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Cholinergic Mechanisms Regulating Cognitive Function and RNA Metabolism

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A thesis submitted in partial fulfillment of the requirements for the Doctor of Philosophy degree in Neuroscience

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Abstract

Acetylcholine (ACh) is one of the main neuromodulators in the mammalian central nervous system (CNS). This chemical messenger has been implicated in the underlying physiology of many distinct cognitive functions. However, the exact role that ACh plays in regulating information processing in the brain is still not fully understood. The vesicular acetylcholine transporter (VACHT) is required for the storage of ACh into synaptic vesicles, and therefore it presents a means to modulate release. Diminished VACHT levels cause a decrease in cholinergic tone, whereas increased VACHT expression has been shown to augment ACh release. Previously published data have shown that elimination of VACHT in the basal forebrain in genetically-modified mice impairs learning and memory.

For our studies we have used different mouse lines in which the expression of the VACHT gene is changed, both increased and decreased. We are therefore able to study the consequences of altered cholinergic tone *in vivo*. Our hypothesis is that changes in cholinergic tone produce specific molecular signatures in target brain areas that underlie alterations in cognitive function. Our studies aimed to elucidate the behavioural and molecular consequences of cholinergic dysfunction. Behavioral testing included classical learning and memory tests as well as sophisticated tasks using novel touch screens chambers to measure attention, learning and memory as well as cognitive flexibility. At the molecular level, the goal was to examine how long-term changes in cholinergic tone impact mechanisms regulating synaptic plasticity and neuronal health. Finally, by aging mouse models of cholinergic dysfunction we were able to elucidate the role that cholinergic tone plays in the classical pathological hallmarks of neurodegenerative disorders.

Ultimately, by establishing the molecular signature of increased and decreased cholinergic tone in targeted brain regions (cortex and hippocampus) it may become possible to find novel targets for therapeutic interventions to improve cognitive deficits due to altered cholinergic tone.

Keywords

Acetylcholine

Cholinergic signaling

Vesicular acetylcholine transporter

Cognition

Alzheimer's Disease

RNA Metabolism

Co-Authorship Statement

Data presented in Chapter 2 of this thesis was previously published in The Journal of Neuroscience on June 19th, 2013 under 33(25)10427-10438. This peer reviewed article is titled “ChAT–ChR2–EYFP mice have enhanced motor endurance but show deficits in attention and several additional cognitive domains”. All of the experiments in Chapter 2, except Figure 2.1A-E, were performed by Benjamin Kolisnyk under the supervision of Dr. Vania F. Prado and Marco A. M. Prado. The confocal microscopy experiments were performed by Dr. Ana Magalhães. The PCR experiments were performed by Jue Fan, and the western blot experiments were performed by Sanda Raulic (University of Western Ontario, London, Canada).

Chapter 3 of this thesis was previously published in The Journal of Neuroscience on September 11th, 2013 under 33(37)14908-14920. This peer reviewed article is titled “Forebrain deletion of the vesicular acetylcholine transporter results in deficits in executive function, metabolic, and RNA splicing abnormalities in the prefrontal cortex”. All of the experiments in Chapter 3, except Figure 3.9, were performed by Benjamin Kolisnyk under the supervision of Dr. Vania F. Prado and Marco A. M. Prado. In vivo magnetic resonance spectroscopy of neuronal metabolites were performed by Dr. Simona Nikolova (University of Western Ontario, London, Canada).

Chapter 4 of this thesis was previously published in the British Journal of Pharmacology on October 1st, 2015 under 170(20)4919-4931. This peer reviewed article is titled “ $\alpha 7$ nicotinic ACh receptor-deficient mice exhibit sustained attention impairments that are reversed by $\beta 2$ nicotinic ACh receptor activation”. All of the experiments in Chapter 4 were performed by Benjamin Kolisnyk with the assistance of Mohamed A. Al-Onaizi under the supervision of Dr. Vania F. Prado and Marco A. M. Prado.

All of the experiments presented in Chapter 5, except for figure 5.1.1B-C, 5.1.3 5.2.1I, 5.3A-B, 5.4.1A-F, H, I, 5.4.2, 5.5.1F, 5.6A were performed by Benjamin Kolisnyk under the supervision of Dr. Vania F. Prado and Marco A. M. Prado. RNA-Seq heat map generation and post-hoc analysis of alternative splicing was performed by Dr. Lilach

Soreq (University College London, United Kingdom). Confocal microscopy, silver staining experiments and Morris Water Maze tests and analysis were carried out by Mohamed A. Al-Onaizi under the supervision of Dr. Vania F. Prado and Marco A. M. Prado (University of Western Ontario, London, Canada). The cumulative distribution function analysis of cholinergic gene expression in the AD brain, as well as the mircoRNA sequencing was performed by Shahar Barbash and Uryia Beckenstein under the supervision of Dr. Hemrona Soreq (Hebrew University of Jerusalem, Israel).

All of the experiments presented in Chapter 6, except for figure 6.2A-E, 6.5A were performed by Benjamin Kolisnyk under the supervision of Dr. Vania F. Prado and Marco A. M. Prado. Confocal microscopy was performed by Mohamed A. Al-Onaizi under the supervision of Dr. Vania F. Prado and Marco A. M. Prado (University of Western Ontario, London, Canada).

All other experiments presented in this thesis were performed by Benjamin Kolisnyk under the supervision of Dr. Vania F. Prado and Dr. Marco A. M. Prado at the University of Western Ontario in the Graduate Program in Neuroscience.

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List of Abbreviations

ACh	Acetylcholine
AChE	Acetylcholinesterase
AD	Alzheimer's Disease
APP	Amyloid Precursor Protein
ChAT	Choline Acetyltransferase
CHT-1	High affinity choline transporter 1
CNS	Central Nervous System
CTL1	<i>Torpedo</i> -like choline transporter
GSK-3	Glycogen-synthase kinase-3
hnRNP	Heterogeneous nuclear ribonucleoproteins
LTD	Long term depression
LTP	Long term potentiation
mAChR	Muscarinic acetylcholine receptors
MS	Medial Septum
MSNs	Medium Spiny Neurons
nAChR	Nicotinic acetylcholine receptors
nBm	Nucleus Basalis Magnocellularis
NFT	Neurofibrillary tangles
OCT2	Organic Cation Transporter 2
PFC	Prefrontal Cortex

PNS	Peripheral Nervous System
PPT	Pedunculo pontine Tegmentum
RNA-Seq	RNA Sequencing
SR	Serine/Arginine-Rich Protein
STP	Short term potentiation
VACHT	Vesicular Acetylcholine Transporter
VGLUT-3	Vesicular glutamate transporter-3
VP	Ventral Pallidum

Chapter 1

1 Introduction

1.1 Central Cholinergic Tone

Acetylcholine (ACh) was the first neurotransmitter to be identified (Loewi 1921). Cells which secrete, and thus signal via ACh, are deemed cholinergic cells. Cholinergic cells are found throughout the mammalian body and they are both neuronal and non-neuronal cell types. Neuronal ACh acts both in the peripheral nervous system (PNS) and in the central nervous system (CNS). In the PNS ACh is the neurotransmitter which activates skeletal muscles, in the neuromuscular junction. Furthermore, ACh in the PNS is the neurotransmitter of the autonomic nervous system which regulates a host of involuntary and unconscious bodily functions. CNS ACh is a neuromodulator affecting synaptic plasticity and regulating many behaviours including learning and memory, attention, and reward (Hasselmo 1999, Picciotto, Higley et al. 2012).

1.1.1 Regulation of ACh Release

Synthesis of ACh relies on the uptake of choline into the presynaptic cholinergic nerve terminal. This process is mediated by the activity of the high affinity choline transporter 1 (CHT-1) (Yamamura and Snyder 1972) Kuhar and Murrin 1978). Choline in the presynaptic cell is then combined with Acetyl-CoA and synthesized into ACh by the choline acetyltransferase enzyme (ChAT) (Hersh 1982, Rylett and Schmidt 1993). Newly synthesized molecules of ACh are then packaged into synaptic vesicles by the vesicular acetylcholine transporter (VACHT) (Prado, Reis et al. 2002, Prado, Roy et al. 2013). VACHT represents the rate limiting step in the release of ACh. Genetic elimination of VACHT has demonstrated that VACHT is required for the storage and release of ACh (Prado, Martins-Silva et al. 2006, de Castro, De Jaeger et al. 2009). Unlike monoamine which have multiple and redundant transporters (Liu, Peter et al. 1992), VACHT is the sole transporter for ACh. Following stimulation of the presynaptic cell, ACh containing

synaptic vesicles fuse with the presynaptic membrane and ACh is released into the synapse (Katz and Miledi 1965, Varoqui and Erickson 1996). In the synapse, ACh can bind and act upon pre and post synaptic ACh receptors. These receptors fall into two main classes, ionotropic nicotinic receptors, and metabotropic muscarinic receptors. Upon dissociation from the receptors, synaptic ACh is broken down into its constituents by the activity of the acetylcholinesterase enzyme (AChE) (Marnay and Nachmansohn 1937, Soreq and Seidman 2001). Schematic of ACh release is depicted in Figure 1.1.

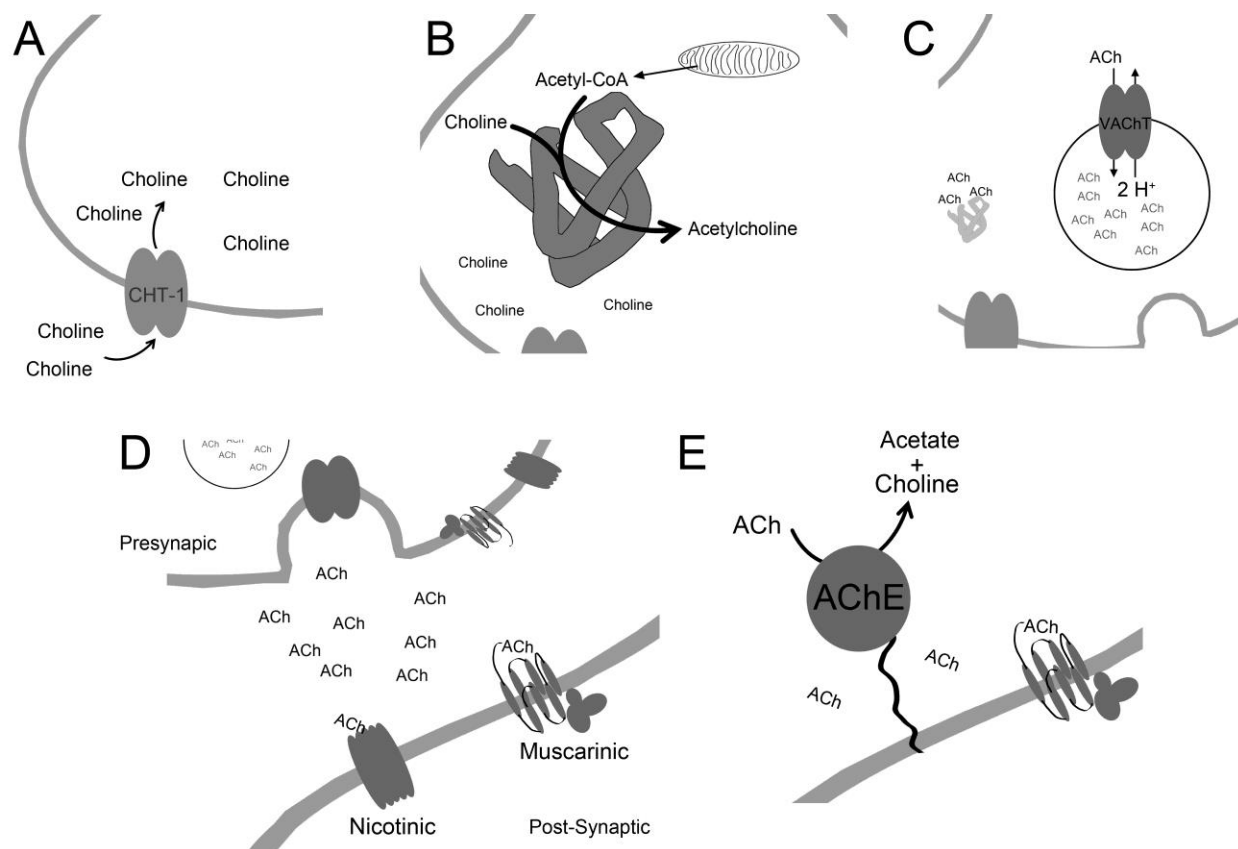


Figure 1.1 The Cholinergic Synapse. (A) Choline is taken up into the pre-synaptic cholinergic neuron by the activity of the high affinity choline transporter, CHT-1. (B) Choline and acetyl-CoA are combined to form acetylcholine by the choline acetyltransferase enzyme. (C) The Vesicular Acetylcholine Transporter packages acetylcholine into synaptic vesicles, exchanging one cytoplasmic molecule of acetylcholine for two vesicular H⁺ ions. (D) Following excitation of the pre-synaptic cholinergic neurons, acetylcholine containing synaptic vesicle fuses with the plasma membrane and acetylcholine is released into the synapse. Acetylcholine can then bind to either ionotropic nicotinic receptors or metabotropic muscarinic receptors. These receptors can be expressed both pre- and post-synaptically. (E) Following dissociation of acetylcholine from its receptors, the molecule is broken down by the acetylcholinesterase enzyme into acetate and choline.

1.1.2 The Vesicular Acetylcholine Transporter

To speed up synaptic transmission, neurotransmitters are packaged into synaptic vesicles, and released as a quantum (Katz and Thesleff 1957, Stevens 1993). This quantal release mechanism allows for the local concentration of neurotransmitters released into the synapse to be orders of magnitude larger than if neurotransmitters were simply released uniformly across the nerve terminal. Release events of ACh from neurons into the synapse have been well characterized as quantal events (Katz and Thesleff 1957, Van der Kloot and Molgo 1994). It has been estimated that roughly 10,000 molecules of ACh are packaged into each vesicle (Linder, Pennefather et al. 1984). As ACh is a cation, it will not simply diffuse passively through membranes. A transport mechanism is required for the packaging of ACh into vesicles for synaptic release. VACHT is the protein responsible for the packaging of ACh into synaptic vesicles (Alfonso, Grundahl et al. 1993). Evidence of how VACHT carries out this transport has been elucidated from models of the proteins structure.

Although the structure of the protein has not been resolved by crystallography or other methods, models of the protein structure have been proposed to explain the biochemical activity of the transporter. It has been suggested, based on the knowledge of other transporters in the same protein family, that VACHT would assume a 12 transmembrane domain structure (Vardy, Arkin et al. 2004). Following the proposed model, the protein would be separated into two distinct large structural halves, allowing for a central transport path to be formed between them (Khare, Ojeda et al. 2010). VACHT is able to pump ACh into synaptic vesicles, by exchanging two intra-vesicular protons, for one cytoplasmic molecule of ACh (Nguyen, Cox et al. 1998). Experimental evidence suggests that this exchange occurs within the described central transport path of the protein (Ojeda, Kolmakova et al. 2004).

In vitro studies have indicated that the activity of VACHT is highly regulated. VACHT will concentrate ACh into vesicles at a rate 30 folds lower than predicted, based on the free energy formed by the exchange of two protons (Parsons 2000). The pharmacological agent vesamicol is a selective non-competitive VACHT inhibitor. Studies using

vesamicol have shown that the compound is able to block ACh storage in vesicles, and also block release of ACh into the synapse (Anderson, King et al. 1983, Collier, Welner et al. 1986, Whitton, Marshall et al. 1986, Prado, Gomez et al. 1992, Van der Kloot 2003). Therefore, synaptic release of ACh is dependent on VACHT packaging the neurotransmitter into vesicles. These findings have been confirmed *in vivo*, where mice with targeted deletions of VACHT no longer release ACh upon KCl stimulation (Prado, Martins-Silva et al. 2006, de Castro, De Jaeger et al. 2009, Lima Rde, Prado et al. 2010, Guzman, De Jaeger et al. 2011). Taken together, these results place VACHT as the rate limiting step in the release of ACh into the synapse.

The majority of total VACHT protein is found within the synaptic vesicles of cholinergic neurons. The VACHT protein however is not locally translated at the synapse (Park, Gondre-Lewis et al. 2011). The intracellular trafficking of VACHT is therefore a key cellular process within cholinergic neurons (Prado and Prado 2002). VACHT trafficking to synaptic vesicles has been shown to be a clathrin-mediated process (Santos, Barbosa et al. 2001, Barbosa, Ferreira et al. 2002, Ferreira, Santos et al. 2005). Experiments using a yeast two hybrid system to investigate protein-protein interaction, have shown that the C-terminal domain of VACHT interacts with the AP-2 adaptor complex (Barbosa, Ferreira et al. 2002). AP-2 is a multimeric protein that is a master regulator of clathrin-mediated endocytosis (Pearse, Smith et al. 2000). A di-leucine motif has been characterized within the C-terminus of the VACHT protein, and plays a critical role in the clathrin-mediated endocytosis of the transporter (Tan, Waites et al. 1998). Mutations in this di-leucine motif abolish the interaction between VACHT and the AP-2 complex (Barbosa, Ferreira et al. 2002). Likewise, the C-terminal segment of vesicular monoamine transporters (VMATs) regulates their trafficking (Tan, Waites et al. 1998). This is not surprising as there is a large degree of homology between VACHT and VMATs (Liu and Edwards 1997). Interestingly, the intracellular trafficking of these proteins is vastly different. In the brain, VMATs are trafficked to many different types of secretory vesicles (Nirenberg, Liu et al. 1995, Nirenberg, Chan et al. 1996). Conversely, VACHT is localized almost exclusively to synaptic vesicles (Gilmor, Nash et al. 1996, Weihe, Tao-Cheng et al. 1996). It appears that the phosphorylation of this C-terminus is important to the subcellular specificity of VACHT trafficking (Krantz, Waites et al. 2000,

Ferreira, Santos et al. 2005). The kinase PKC has been shown to both modulate VACHT phosphorylation as well as ACh release from hippocampal synaptosomes (Tanaka, Fujiwara et al. 1986, Allgaier, Daschmann et al. 1988, Barbosa, Clarizia et al. 1997). VACHT phosphorylation can therefore be highly relevant to cholinergic signalling in the brain (Van der Kloot and Molgo 1994).

1.1.3 Choline Acetyltransferase

Synthesis of ACh within neurons occurs within the cytoplasm of cholinergic nerve terminals. ChAT is the enzyme responsible for the production of ACh within cells. As its name suggests, choline acetyltransferase transfers an acetyl group from an acetyl-CoA to a choline molecule to produce the neurotransmitter ACh (Nachmansohn and Berman 1946). Expression of the ChAT enzyme is extremely sparse, estimated to comprise less than a ten thousandth of a percent of total brain proteins (Eckenstein and Thoenen 1982, Bruce, Wainer et al. 1985). Despite this low abundance, ChAT protein is found within every cholinergic cell in the brain (Docherty, Bradford et al. 1985), its expression pattern therefore follows the anatomical distribution of cholinergic neurons in the brain.

Interestingly, the genes for ChAT and VACHT are present in the same gene locus, termed the cholinergic gene locus (Eiden 1998, Mallet, Houhou et al. 1998). Cloning of the ChAT gene revealed a rather unique structure for the gene (Berrard, Brice et al. 1987, Strauss, Kemper et al. 1991). Upstream of the coding region for ChAT, within the intron between the first and second exons, the VACHT 1590bp open reading frame was discovered (Bejanin, Cervini et al. 1994, Erickson, Varoqui et al. 1994, Roghani, Feldman et al. 1994). The VACHT gene is found in the same transcriptional orientation as ChAT (Berrard, Varoqui et al. 1995). This unique gene organization is evolutionarily conserved and can be found in *C. elegans* (Alfonso, Grundahl et al. 1994, Roghani, Feldman et al. 1994), *drosophila* (Kitamoto, Wang et al. 1998), mice (Misawa, Ishii et al. 1992, Barbosa, Massensini et al. 1999), rats (Bejanin, Habert et al. 1992) and men (Berrard, Brice et al. 1987). Although arising from the same gene locus, VACHT and

ChAT are transcribed as separate transcripts (Alfonso, Grundahl et al. 1994, Erickson, Varoqui et al. 1994).

ChAT is localized predominantly in the cytoplasm (Bruce, Wainer et al. 1985). However, membrane-bound forms of the protein have been reported (Bruce and Hersh 1987). In addition, a variant of the human form of the enzyme can localize to the nucleus, wherein it plays a role in the regulation of gene expression and chromatin modeling (Gill, Bhattacharya et al. 2003, Matsuo, Bellier et al. 2011). The ChAT enzyme is organized as a globular, single strand, protein (Govindasamy, Pedersen et al. 2004). Site-directed mutagenesis studies have shown that a number of critical amino acid residues regulate the catalytic function of the protein (Carbini and Hersh 1993, Dobransky, Davis et al. 2000). This work showed that a histidine residue is the acid/base catalytic residue of the enzyme, while a nearby arginine residue interacts with, and binds the CoA molecule. Further structural biology experiments have confirmed these findings (Kim, Rylett et al. 2006).

Interestingly, there appears to be no correlation between the mRNA level of ChAT within a cellular population, and the enzymatic activity of the cells (Berrard, Brice et al. 1987). This finding suggests that regulation of ChAT protein levels and activity occur at the post-transcriptional level. Translation of the ChAT protein occurs within the soma of neurons (Berrard, Brice et al. 1987) and the enzyme is then transported by an undetermined mechanism to the synapse. The transport of the enzyme represents a means by which cells can regulate their production of ACh. A critical post-translational modification to the ChAT enzyme is its phosphorylation (Bruce and Hersh 1989, Dobransky and Rylett 2003). A number of phosphorylation sites have been demonstrated on the enzyme and it appears that these modifications play a role in regulating the catalytic activity of the enzyme (Dobransky and Rylett 2003). A key phosphatase involved in the regulation of ChAT enzymatic activity is PKC (Dobransky, Doherty-Kirby et al. 2004). Importantly ChAT phosphorylation in synaptosomes is sensitive to Ca^{2+} levels (Dobransky and Rylett 2005). The enzymatic activity of ChAT, and consequently ACh synthesis, can therefore be regulated in response to neuronal depolarization. Deletion of the chat gene from the mouse genome is post-embryonically

lethal (Misgeld, Burgess et al. 2002). Studies of the embryos from these animals have shown in the absence of ChAT there is dramatic restructuring of the PNS in these animals (Brandon, Lin et al. 2003), indicating that ChAT, and therefore ACh, is essential for proper developments of the nervous system.

1.1.4 The High Affinity Choline Transporter

Synthesis of ACh is dependent on the intracellular concentrations of choline. Neurons are unable to synthesise enough of their own choline for cholinergic neurotransmission (Yamamura and Snyder 1972, Collier and Katz 1974). Therefore, ACh releasing neurons are dependent on the activity of a transporter to obtain their choline (Birks, Macintosh et al. 1956, Birks and Macintosh 1957). The transporter responsible for the uptake of choline into neurons is the CHT1 transporter. This transporter regulates choline levels within a cell, by transporting choline into the cell in a Na⁺ dependant manner (Simon and Kuhar 1975, Birks, Worsley et al. 1985). This protein is encoded by the SLC5A7 gene, which was first identified in *C. elegans*, and subsequently identified in the rat, mouse and human (Apparsundaram, Ferguson et al. 2000, Okuda, Haga et al. 2000). There is a very high degree of homology between the rat and human gene (Okuda and Haga 2000) as well as between the rat and mouse gene (Apparsundaram, Ferguson et al. 2001). Importantly, CHT1 is preferentially expressed in cholinergic neurons, and can therefore be used as a specific marker for these cells (Misawa, Nakata et al. 2001).

CHT1 is not the sole choline transporter expressed in the mammalian brain. The *Torpedo*-like choline transporter, CTL1 is highly expressed in oligodendrocytes, where it provides choline for the synthesis of phospholipids (Traiffort, Ruat et al. 2005). CTL1 also differs from CHT1 in that its function is dependent on K⁺ ions rather than Na⁺ ions (Fujita, Shimada et al. 2006). The other choline transporter expressed in the mammalian brain is the organic cation transporter 2 (OCT2). Unlike CTL1, OCT2 is also expressed in cholinergic neurons, being found on synaptic vesicles within these neurons (Nakanishi, Haruta et al. 2011, Nakata, Matsui et al. 2013). OCT2 however is not selective for choline, but rather can transport all organic cations. Given that OCT2 and CHT1 share similar localization in cholinergic neurons, it has been hypothesized

that these two transporters may collaborate to transport choline into cholinergic neurons (Nakata, Matsui et al. 2013).

The CHT1 protein is 580 amino acids long and organized on plasma membranes in a 13 transmembrane domain structure (Apparsundaram, Ferguson et al. 2000, Okuda, Haga et al. 2000, Torres, Gainetdinov et al. 2003). CHT1 has been shown to have consensus PKA and PKC phosphorylation motifs, implicating these signalling pathways in the regulation of this protein (Gates, Ferguson et al. 2004, Brock, Nickel et al. 2007). Experimental inhibition of these signalling pathways has led to decreases in cell surface levels of the transporter (Gates, Ferguson et al. 2004). Although CHT1 carries out its physiological function at the plasma membrane, the vast majority of the protein is found within intracellular vesicles, with only a small portion of the total protein pool found on the plasma membrane (Ferguson, Savchenko et al. 2003, Ribeiro, Alves-Silva et al. 2003, Ribeiro, Black et al. 2005). Inclusion of CHT1 in the plasma membrane of synapses is dependent on the activity of the neuron. Depolarization by action potential of the neuron increases the levels of CHT1 at the plasma membrane in a calcium dependant manner (Collier and Katz 1974, Simon and Kuhar 1975). The trafficking of CHT1 to the plasma membrane is mediated by the clathrin endocytic pathway (Ribeiro, Alves-Silva et al. 2003). Plasma membrane CHT1 then can be internalized in a clathrin dependant manner to either be tagged for proteasome degradation, or to be trafficked back to the plasma membrane (Ribeiro, Black et al. 2005).

Genetic elimination of CHT1 from the mouse genome results in post-natal lethality, within an hour of birth, due to an inability of the animals to breathe (Ferguson, Bazalakova et al. 2004). Mice with a heterozygous null mutation are however viable and are able to maintain the same level of choline uptake as wild-type control animals through posttranslational compensation of CHT1 function, by increased inclusion at the plasma membrane (Ferguson, Bazalakova et al. 2004). Furthermore, in mice with a heterozygous null deletion of the ChAT gene (and therefore a reduced capacity to synthesize ACh), levels of the CHT1 protein were increased in compensation (Brandon, Mellott et al. 2004). Analysis of the prefrontal cortex of rats performing attention based cognitive tasks showed both an increase in choline uptake and in CHT1 protein levels

(Apparsundaram, Martinez et al. 2005). These findings demonstrate that the trafficking of CHT1 to the plasma membrane is a highly dynamic process which plays a role in normal physiological functioning. Importantly polymorphisms in the CHT-1 gene have been identified in patients with Attention Deficit Disorders, related to cholinergic deficits in these patients (English, Hahn et al. 2009). The trafficking of CHT1 to the plasma membrane is thus a critical determinant to the levels of choline within cholinergic cells and a critical process for cognitive functioning.

1.1.5 Nicotinic Receptors

Nicotinic acetylcholine receptors (nAChRs) are ionotropic receptors which are selective for ACh. nAChRs are expressed in both the peripheral and in the CNS. This class of receptors are involved in neuronal excitability and regulation of neurotransmitter release. There are nine different nicotinic receptor subunits that are expressed in the CNS, they are either α subunits ($\alpha 2, 3, 4, 5, 6, 7$) or β subunits ($\beta 2, 3, 4$) all encoded by distinct genes (Le Novere and Changeux 1995, Dani and Bertrand 2007). These subunits combine as either homomeric or heteromeric pentameric receptors. The most prominent homomeric nicotinic receptor in the mammalian CNS is the $\alpha 7$ nicotinic receptor ($\alpha 7$ nAChR). However the most prominently expressed nicotinic receptor in the brain is the $\alpha 4\beta 2$ nAChR (Wada, Wada et al. 1989).

Regardless of their make-up, nicotinic receptors share the same general structure. They are organised as a transmembrane receptor with a central ion channel, an extracellular ligand binding domain with a ligand binding pocket (Karlin and Akabas 1995). Although they share similar structures, $\alpha 7$ nAChRs and $\alpha 4\beta 2$ nAChRs have drastically different functional properties (Giniatullin, Nistri et al. 2005). $\alpha 7$ nAChRs are quick to be activated by ACh and are quickly desensitized (Pidoplichko, DeBiasi et al. 1997). These receptors are permeable to Na^+ , and K^+ , but are highly permeable to Ca^{2+} (Seguela, Wadiche et al. 1993). $\alpha 4\beta 2$ nAChRs on the other hand are slow to be activated by ACh and are also slow to desensitize (Alkondon and Albuquerque 2005). These receptors are only permeable to Na^+ and K^+ ions.

In situ hybridization studies have demonstrated that the $\alpha 4$ and $\beta 2$ nAChR subunits are expressed ubiquitously across the mammalian brain (Wevers, Jeske et al. 1994). Expression of these receptors is highest in the thalamus and cortex and relatively low in the hippocampus (Alkondon, Reinhardt et al. 1994). $\beta 2$ nAChRs is essential for nicotine evoked release of GABA and dopamine from synaptosomes collected from a number of brain regions (Turner 2004, McClure-Begley, King et al. 2009). Furthermore nicotine evoked striatal release of dopamine is abolished in mice lacking the $\beta 2$ subunit (King, Caldarone et al. 2004). This regulation of dopamine release by $\beta 2$ nAChRs is functionally relevant as mice lacking this receptor do not display place preference conditioning to cocaine (Zachariou, Caldarone et al. 2001). Young mice lacking the $\beta 2$ nAChR subunit do not display memory impairments, however as these mice age they display cortical atrophy and cell loss in the hippocampus (Zoli, Picciotto et al. 1999). The age dependant neurodegeneration in these animals is associated with learning and memory impairments.

The $\alpha 7$ nAChR like the $\alpha 4$ and $\beta 2$ is expressed throughout the brain. However the distribution pattern of the $\alpha 7$ nAChR is antithetical to the pattern of the $\alpha 4$ and $\beta 2$ subunits. $\alpha 7$ nAChRs are most expressed in the hippocampus and cortex, but are almost absent in the thalamus (Seguela, Wadiche et al. 1993). Although $\alpha 7$ nAChRs are highly involved in synaptic plasticity in the hippocampus, $\alpha 7$ -subunit knockout mice did not differ from wild-type controls in a host of memory assays including contextual and cued fear-conditioning and on the Morris water maze (Paylor, Nguyen et al. 1998, Fernandes, Hoyle et al. 2006). $\alpha 7$ nAChRs are also expressed on non-neuronal cells in both the brain and in the periphery, including astrocytes and microglia. $\alpha 7$ nAChRs on these non-neuronal cells play a critical role in inflammation (de Jonge and Ulloa 2007) and in neuroprotection (Ren, Puig et al. 2005). On immune cells activation of $\alpha 7$ receptors regulates the production of inflammatory cytokines (Wang, Yu et al. 2003).

1.1.6 Muscarinic Acetylcholine Receptors

ACh can act upon a class of metabotropic receptors, the muscarinic acetylcholine receptors (mAChRs). There have been 5 subtypes of mAChRs that have been

identified, the M1, M2, M3, M4 and M5 receptors. All of these receptors function as classical G-protein coupled receptors (Wess 1996). mAChRs can be subdivided into two categories, the Gq coupled receptors which includes the M1, M3 and M5 receptors (Berstein, Blank et al. 1992, Offermanns, Wieland et al. 1994, Qin, Dong et al. 2011), and the Gi/o coupled M2 and M4 receptors (Winitz, Russell et al. 1993, Migeon and Nathanson 1994). The Gq coupled receptors activate phospholipase C and increase intracellular Ca^{2+} levels; these receptors are therefore deemed excitatory. The Gi/o coupled receptors on the other hand act by decreasing cyclic nucleotide levels, decreasing intracellular Ca^{2+} levels and promoting K^{+} efflux, thus inhibiting the neuron. G proteins can also directly regulate K^{+} channels, which is a common mechanism for M2 muscarinic receptors (Kunkel and Peralta 1995).

All five of the mAChR are expressed in the mammalian nervous system. These receptors are found to be expressed on both neuronal and glial cell types in the nervous system. The expression of the M1, M4 and M5 subtypes is enriched in the CNS, whereas the M2 and M3 receptors are equally found in both the CNS and the PNS (Levey 1993). mAChRs in the brain have been shown to play regulatory roles in many cognitive processes. Each of the five muscarinic receptors are encoded by a unique gene. This has allowed for the genetic manipulation of the individual receptor types and from this their distinct physiological roles in the central nervous system have been elucidated (Wess 2004).

M1 mAChRs are expressed throughout the mammalian forebrain, including cerebral cortex, hippocampus, and in the striatum (Wolfe and Yasuda 1995). It is by its broad level of expression that the receptor is thought to play a role in many cognitive processes. Mice lacking the M1 mAChR have been shown to be hyperactive (Gerber, Sotnikova et al. 2001) and have impaired working memory (Anagnostaras, Murphy et al. 2003) and consolidation (Gould, Dencker et al. 2015). These animals also present a number of biochemical (Berkeley, Gomez et al. 2001) and electrophysiological (Anagnostaras, Murphy et al. 2003) abnormalities that underlie their impaired behaviour.

M3 mAChRs are expressed throughout the brain but are most prominently expressed in the hypothalamus (Wall, Yasuda et al. 1991). Hypothalamic M3 mAChRs regulate food intake and appetite. These receptors are found on melanin-concentrating hormone producing neurons of the hypothalamus, and their activations stimulates production of the appetite regulating hormones (Yamada, Miyakawa et al. 2001). Mice lacking this receptor are lean and have a pronounced reduction in bodyweight and food intake compared to control animals (Yamada, Miyakawa et al. 2001). In the periphery these receptors have been shown to regulate smooth muscle function (Matsui, Motomura et al. 2002) and the salivary response (Bacman, Sterin-Borda et al. 1996).

M5 mAChRs have low levels of expression throughout the brain and are enriched in limited cellular populations (Wei, Walton et al. 1994). M5 mAChRs are expressed on the midbrain dopaminergic neurons, originating from the substantia nigra (Vilario, Palacios et al. 1990), and are therefore highly critical to the regulation of dopamine release in the striatum. M5 mAChRs have been shown to directly regulate striatal dopamine release, although other muscarinic subtypes can also modulate striatal dopamine by indirect mechanisms (Zhang, Yamada et al. 2002). The ventral tegmental area of mice deficient in the M5 mAChR do not respond to cholinergic stimulation demonstrating that these receptors also regulate ventral tegmental area dopamine release (Yeomans, Forster et al. 2001, Forster, Yeomans et al. 2002). Given the role of these receptors in regulating dopamine signalling, mice lacking M5 mAChRs have altered responses to opioids and cocaine (Basile, Fedorova et al. 2002, Thomsen, Woldbye et al. 2005).

The inhibitory M2 and M4 mAChRs function mainly as auto-receptors for ACh in the brain (Starke, Gothert et al. 1989). These receptors are also both present on the GABAergic medium spiny neurons in the striatum (Yan, Flores-Hernandez et al. 2001). For the most part, these receptors are responsible for inhibiting release of ACh (Zhou, Meyer et al. 2002). They are therefore predominantly presynaptic receptors found on

cholinergic neurons (Levey, Edmunds et al. 1995). These receptors therefore play a critical role in the regulation of the timing and release of ACh, processes which are highly relevant to cognitive function (Sarter, Parikh et al. 2009). Mice lacking the M2 receptor show a broad range of hippocampal behavioural and electrophysiological impairments (Seeger, Fedorova et al. 2004). Mice lacking the M4 receptor also present with learning impairments and hyperactivity (Koshimizu, Leiter et al. 2012). Given that these receptors regulate release of ACh; it is difficult to differentiate the specific roles of these receptors to cognition, from general roles of cholinergic tone in the brain.

1.1.7 Basal Forebrain Cholinergic System

The basal forebrain is a collection of nuclei including the medial septum (MS), the ventral pallidum (VP), the diagonal band nuclei, magnocellular preoptic nucleus, and the nucleus basalis magnocellularis (nBm) (Zaborszky, Pang et al. 1999). The neurons found within this brain region have been implicated in many cognitive functions including learning and memory and executive function (Miyamoto, Shintani et al. 1985). The basal forebrain is composed of a highly variable population of neurons. ACh releasing neurons represent roughly 20% of the neurons in the basal forebrain (Semba 2004). Other neurons in the basal forebrain release glutamate, GABA and neuropeptides (Henny and Jones 2008).

The output of basal forebrain cholinergic neurons is dependent on the nuclei from which these neurons are found (Figure 1.2A). Neurons originating in the MS and the diagonal band nuclei provide the major cholinergic innervation to the hippocampus (Mesulam, Mufson et al. 1983). Cholinergic neurons from the diagonal band and from the magnocellular preoptic nucleus project to the olfactory bulb and to the entorhinal cortex (Gaykema, Luiten et al. 1990), while the nBm cholinergic neurons project to both the basolateral amygdala and the entire cortex (Boegman, Cockhill et al. 1992, Power, Thal et al. 2002). Just as the basal forebrain is not a homogenous cell population, the described projections are not purely cholinergic with both GABAergic and glutamatergic projection neurons sharing the same projection tracks as the cholinergic cells (Huh, Goutagny et al. 2010).

Basal forebrain cholinergic neurons receive afferent input from midbrain and brainstem as well as from the hypothalamus. Unlike the non-cholinergic neurons in the basal forebrain, the cholinergic neurons in the basal forebrain do not appear to receive top down input from the cortex (Zaborszky 1989, Zaborszky and Duque 2000).

Hypocretin/orexin positive neurons from the hypothalamus have been identified as the main source of innervation to the basal forebrain (Henny and Jones 2006). These neurons have been shown to synapse onto both cholinergic and non-cholinergic neurons in the basal forebrain. These neurons are histaminergic and are important regulators of arousal. Midbrain afferent connections to the basal forebrain originate from the dopaminergic cells of the substantia nigra and from the ventral tegmental area (Fallon and Moore 1978, Zahm and Trimble 2008). Brainstem structures which project to the basal forebrain cholinergic cells are adrenergic in nature from the medulla and the locus coeruleus and cholinergic from the pedunculopontine nucleus.

Basal forebrain cholinergic neurons role in regulating executive function and memory has largely been investigated by immunotoxin lesioning of these cells (Baxter, Bucci et al. 2013). The 192 IgG-saporin is a specific neurotoxin which, when delivered to the basal forebrain, will selectively kill cholinergic neurons and spare the other cell types in the region (Book, Wiley et al. 1992). An important caveat to the attribution of these behaviours to cholinergic signalling is that these neurons may not be simply cholinergic. In culture, these cholinergic neurons from the basal forebrain have been shown to be able to release glutamate (Allen, Abogadie et al. 2006). Recent optogenetic experiments have demonstrated that basal forebrain cholinergic which project to the cortex co-release GABA from distinct pools of vesicles (Saunders, Granger et al. 2015). The behavioural consequences of this co-transmission have yet to be investigated, but suggest that GABA and/or glutamate co-released with ACh may influence behaviours thought to be regulated by ACh signalling alone (Granger, Mulder et al. 2016).

1.1.8 Striatal Cholinergic System

Contrary to projection cholinergic neurons found in the basal forebrain and the pedunculopontine tegmental nucleus, the cholinergic neurons in the striatum are local

interneurons (Figure 1.2B). As such, they are characterized by shorter axons and form circuits with nearby neuron within the same brain region (Zhou, Wilson et al. 2002). The cholinergic interneurons of the striatum are the primary source of ACh in the striatum, but only comprise less than 1% percent of all cells in the striatum (Bolam, Wainer et al. 1984). Cholinergic neurons in the striatum, relative to other cholinergic neurons, have higher levels of the key cholinergic markers choline acetyltransferase (Hebb and Silver 1961) and acetylcholinesterase (Woolf and Butcher 1981). This enrichment in cholinergic markers demonstrates the importance that these cells play in regulating striatal function. 33 1.2 B.

A key role of the cholinergic interneurons in the striatum is to integrate information from afferent inputs to the striatum. This is achieved by assimilating inputs of a large number of neurons which release various different neurotransmitters, by expressing a large number of different receptor classes for these neurotransmitters. These neurotransmitters can either act in an excitatory manner, such as glutamate (Calabresi, Centonze et al. 1998), serotonin (Bonsi, Cuomo et al. 2007), histamine (Bell, Richardson et al. 2000) and substance P (Aosaki and Kawaguchi 1996). Neurotransmitters can also inhibit cholinergic interneurons, such as GABA (DeBoer and Westerink 1994), adenosine (Brown, James et al. 1990), and endogenous opioids (Rada, Mark et al. 1991). Other neurotransmitters can be both excitatory and inhibitory, depending on which class of receptors they activate such as with dopamine, excitatory D1-like signalling (Aosaki, Kiuchi et al. 1998) and inhibitory D2-like (Chuhma, Mingote et al. 2014). It is therefore the role of these cholinergic interneurons to integrate all of these various signals.

Despite their relatively small cell number, striatal interneurons project throughout the striatum and can therefore have broad physiological effects. GABA-ergic medium spiny neurons (MSNs) are the primary output of the striatum (Chuhma, Tanaka et al. 2011). These neurons are not thought to express nicotinic acetylcholine receptors (Luo, Janssen et al. 2013), though nicotine can indirectly modulate their activity (Liu, Otsu et al. 2007). Cholinergic signalling therefore directly modulates the activity of MSNs by

activation of muscarinic receptors. Activation of M1 muscarinic receptors on these cells is thought to reduce KCNQ potassium inhibition (Shen, Hamilton et al. 2005) and Ca^{2+} entry (Perez-Garci, Bargas et al. 2003), increasing the excitation of MSNs. Nicotinic receptors in the striatum are highly concentrated on both glutamatergic and dopaminergic nerve terminals. Glutamatergic nerve terminals in the striatum are enriched in $\alpha 7$ nicotinic receptors, and activation of these receptors leads to release of glutamate (Campos, Alfonso et al. 2010). Release of dopamine in the striatum is also highly dependent on cholinergic signalling. Unlike glutamate, the release of dopamine in the striatum has been shown to be dependent on the synchrony of cholinergic interneuron firing, and the activation of $\beta 2$ nicotinic receptors on dopaminergic terminals (Cachope, Mateo et al. 2012).

An important caveat for many of the studies of striatal cholinergic neurons, is that these cells co-transmit glutamate. This co-transmission is achieved through synergism between VACHT and the vesicular glutamate transporter-3 (VGLUT-3) (El Mestikawy, Wallen-Mackenzie et al. 2011). VACHT and VGLUT-3 are found on the same vesicles in these neurons and it has been shown that VGLUT-3 enables these vesicles to package additional ACh (Gras, Amilhon et al. 2008). Studies using genetically modified mice have shown that the glutamate and the ACh released from these neurons can have separate and potentially opposite physiological roles in regulating striatal function and behaviour (El Mestikawy, Wallen-Mackenzie et al. 2011, Guzman, De Jaeger et al. 2011, Sakae, Marti et al. 2015). Behavioural studies of mice with lesioned striatal cholinergic interneurons were found to be hyperactive, have a heightened response to cocaine and do not show haloperidol induced catalepsy (Hikida, Kaneko et al. 2001, Kitabatake, Hikida et al. 2003). These behaviours were initially attributed to the cholinergic properties of these cells. However mice lacking release of ACh from the striatum were not hyperactive and did not display heightened responses to cocaine (Guzman, De Jaeger et al. 2011). In fact, it was mice lacking the VGLUT-3 transporter which recapitulated the phenotype of the lesioned animals (Gras, Amilhon et al. 2008). The ACh released from these cells seems to be playing a critical role in regulating release of dopamine. The animals lacking release of ACh from the striatum showed a

functional increase in dopamine receptor expression and activity, assessed by pharmacological MRI (Guzman, De Jaeger et al. 2011). VGLUT-3 and VACht have opposing roles in the regulation of dopamine release. Elimination of VACht from striatal interneurons decreases KCl stimulated dopamine release, whereas elimination of VGLUT-3 from these neurons potentiates the dopamine response (Sakae, Marti et al. 2015). These results suggest that other physiological properties of striatal ACh may potentially be attributable to the glutamate released from these cholinergic interneurons or may be dependent on the combined action of both neurotransmitters.

1.1.9 The Pedunculo pontine Tegmentum Cholinergic System

The pedunculo pontine tegmentum (PPT) is a collection of nuclei found within the brainstem behind the substantia nigra. The nuclei found within the PPT are a heterogeneous population of neurons that differ by the neurotransmitters they release. The three major neurons within the PPT are cholinergic, GABAergic and glutamatergic (Martinez-Gonzalez, Wang et al. 2012). These three types of neurons are largely segregated into separate regions of the PPT. The majority of cholinergic neurons within the PPT are located in the PPT pars compacta (Pahapill and Lozano 2000).

Much of the work to characterize the projection of the cholinergic neurons from the PPT has been done in non-human primates. These experiments have shown that these cholinergic neurons project predominantly to structures within the basal ganglia (Figure 1.2 C). Both the substantia nigra (Futami, Takakusaki et al. 1995) and the ventral tegmental area receive significant input from the cholinergic neurons of the PPT (Charara, Smith et al. 1996). This anatomical data place these cholinergic cells as key regulators of dopamine signalling in the brain. The primary output of the cholinergic neurons from the PPT is the thalamus (Parent, Pare et al. 1988). Additionally the striatum also receives direct input from the cholinergic neurons of the PPT (Dautan, Huerta-Ocampo et al. 2014). The PPT is therefore an alternate source of cholinergic tone in the striatum, besides the cholinergic interneurons. Finally an important target of the cholinergic neurons in the PPT is the contralateral PPT (Benarroch 2013).

Given the anatomical connectivity data, the cholinergic output from the PPT is placed to be a key regulator of dopamine signalling in the brain. Experimental evidence for this was first shown by studying the addictive properties of nicotine; by increasing dopamine release acting specifically through $\beta 2$ nicotinic acetylcholine receptors in the VTA (Picciotto, Zoli et al. 1998). Further work has also demonstrated that M5-type muscarinic receptors can also stimulate dopamine release from the VTA (Corrigall, Coen et al. 2002). Since the cholinergic output from the PPT can robustly modulate dopamine signaling, these neurons are important intermediaries of addiction and reward. Not only do these neurons release more ACh into the VTA during cocaine administration and cocaine seeking behaviours (You, Wang et al. 2008), but these cholinergic neurons will also increase their firing rate in response to environmental cues associated with reward (Goldberg and Reynolds 2011). Given these findings, cholinergic PPT neurons have been proposed to be master regulators of dopamine signalling in the brain (Maskos 2008).

The PPT cholinergic neurons also play a key role in regulating sleep and arousal. PPT cholinergic neurons are completely inhibited during seizures, this inhibition is accompanied by changes in EEG recordings (Motelow, Li et al. 2015). In line with these findings, PPT cholinergic neurons play a critical role in increasing arousal states during sleep. Recent optogenetic studies have found that activation of cholinergic neurons in the PPT is an important modulator of REM sleep and plays a critical role in the initiation of REM sleep (Van Dort, Zachs et al. 2015).

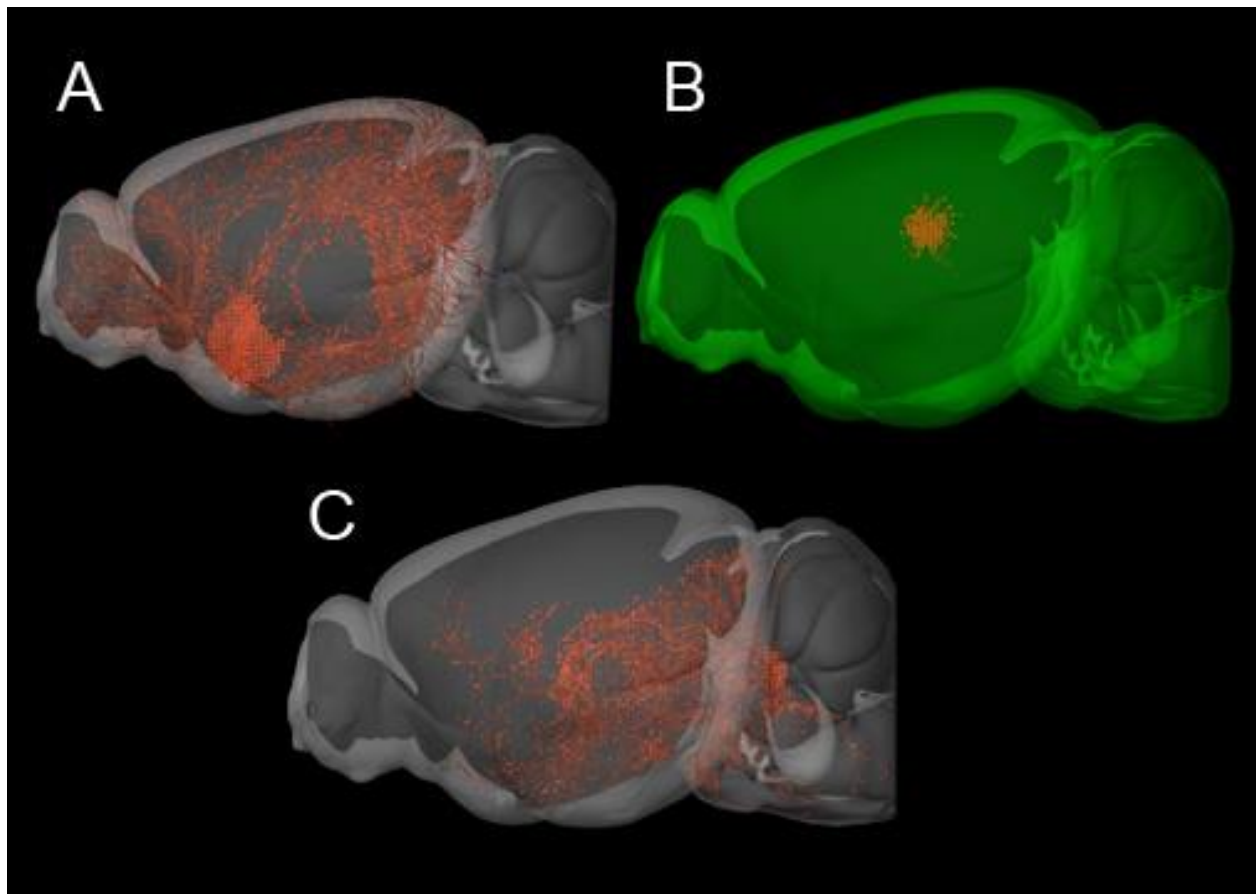


Figure 1.2 The Central Cholinergic System in the Murine Brain. Sagittal 3D reconstructions of the mouse brain. Image data detailing axonal projections labeled by rAAV tracers injections into ChAT-IRES-Cre mice, and visualized using serial two-photon tomography. (A) Cholinergic projections from the basal forebrain. (B) Cholinergic interneurons in the striatum (C) Cholinergic projections from the pedunculopontine tegmental nucleus. Images generated from the Allen Brain Institute Mouse Connectivity Atlas. © 2016 Allen Institute for Brain Science. Allen Mouse Brain Connectivity Atlas [Internet]. Available from: <http://connectivity.brain-map.org>. Oh, S.W. et al. (2014) A mesoscale connectome of the mouse brain, *Nature* 508: 207-214. doi:10.1038/nature13186

1.2 Cholinergic Regulation of Brain Functions

1.2.1 Cholinergic Regulation of Hippocampal Function

The hippocampus has been extensively studied for its role in regulating learning and memory (Squire 1992). This brain region plays an important role in the formation and maintenance of new memories. In Alzheimer's disease (AD) the hippocampus is one of the first brain regions to be affected by pathology (De Leon, George et al. 1997, Padurariu, Ciobica et al. 2012). Hippocampal degeneration mediates some of the learning and memory deficits in AD patients (Graham and Hodges 1997).

The finding in humans that drugs which block cholinergic receptors in brain impair performance on task of learning and memory (Ghoneim and Mewaldt 1975, Atri, Sherman et al. 2004), have placed this neurotransmitter as a central regulator of memory. Functional MRI studies have shown that cholinergic modulation of the hippocampus occurs during learning and memory tasks (Goekoop, Scheltens et al. 2006, Wink, Bernard et al. 2006). Much of the work delineating the mechanism of cholinergic control of hippocampal function has been performed in rodents. In both rodents and man, the cholinergic innervation to the hippocampus arises from the medial septum nucleus within the basal forebrain cholinergic system (Lewis and Shute 1967).

The involvement of the basal forebrain cholinergic system in memory is supported by several works employing various methods ranging from unspecific and specific lesion methods (Wrenn, Lappi et al. 1999, Chudasama, Dalley et al. 2004), pharmacological manipulations (Granon, Poucet et al. 1995) and more recently the use of genetic manipulations (Fernandes, Hoyle et al. 2006, Martyn, De Jaeger et al. 2012, Al-Onaizi, Parfitt et al. 2016). The observation of a transient increase of cholinergic activity during and after a memory tasks can be observed in hippocampus (Durkin and Toumane 1992, Durkin 1994). It is suggested that this increase in neurotransmitter release may support synaptic plasticity in the hippocampus, a mechanism which is essential for learning and

memory (Fadda, Melis et al. 1996, Hironaka, Tanaka et al. 2001).

Synaptic plasticity is a process whereby the nervous system changes the weight of functional connectivity; it can help form, eliminate, potentiate and weaken connections of neuronal circuits (Abbott and Nelson 2000). The mechanism of cholinergic regulation of hippocampal plasticity has been well studied (Hasselmo and Bower 1993, McEwen 1999, Yakel and Shao 2004, Hasselmo 2006, Drever, Riedel et al. 2011, Yakel 2012). The addition of low concentrations of carbachol, a cholinergic mimetic, onto cultured slices induces LTP, an effect dependent of muscarinic receptors (Auerbach and Segal 1996). *In vivo* experiments have consistently demonstrated the role of cholinergic tone in the modulation of LTP. Free walking mice showed reduced LTP in the hippocampus, after cholinergic denervation in the medial septum or following administration of muscarinic receptors antagonists (Leung, Shen et al. 2003, Doralp and Leung 2008). Furthermore, deletion of VACHT from basal forebrain neurons also disrupts hippocampal LTP *ex vivo* (Martyn, De Jaeger et al. 2012) and *in vivo* (Al-Onaizi, Parfitt et al. 2016).

The mechanisms by which cholinergic neurons regulate synaptic plasticity are complex and are likely to involve short-term changes in membrane conductance and also on second messengers. Carbachol can induce another type of synaptic plasticity in the hippocampus and the cortex, long-term depression (LTD), once again requiring muscarinic activation (Jo, Son et al. 2010, Caruana, Warburton et al. 2011). LTD is correlated with learning and information storage, furthermore, it has been related to processes which require cognitive flexibility such as extinction and behavior flexibility (Collingridge, Peineau et al. 2010).

Reports have proposed the notion that cholinergic modulation of synaptic plasticity is highly dependent on time, and that nicotinic receptors serve as a switch between LTP and LTD. Ge and Dani (2005), using a protocol to induce a short-term, transient, potentiation (STP) observed that the STP became an LTP response when ACh was administered multiple seconds prior to the stimulation, however when ACh was

delivered less than a second prior the stimulation then the STD turned into a LTD response. Similarly, cholinergic stimulation 120 ms prior to stimulation lead to an $\alpha 7$ nAChR dependent LTP. When the same cholinergic stimulation was administered 10 ms after electrical stimulation, a muscarinic dependant LTP was observed (Gu and Yakel 2011). Thus depending on the timing of the activation, either induction of LTP or LTD can occur and will depend on the activation of nicotinic or muscarinic receptors.

Cholinergic activity seems necessary to regulate neuronal synchrony (Metherate, Cox et al. 1992). Neuronal synchrony is the simultaneous change in membrane potential across multiple neurons. This process, in the hippocampus, is thought to underlie many different types of cognitive processing, such as learning and memory (Benchenane, Tiesinga et al. 2011). Furthermore, it has been suggested that disruption of neuronal synchrony may underlie cognitive deficits in diseases such as Alzheimer's and Parkinson's (Uhlhaas and Singer 2006).

1.2.2 Cholinergic Regulation of Attention

Release of ACh from the basal forebrain into the prefrontal cortex (PFC) is essential for attentive processing. ACh signalling in the PFC is an important mechanism for neuromodulation of cortical synaptic activity. The efflux of ACh into the PFC, occurs in rapid transients that act on the millisecond time scale and tonically release ACh (Celesia and Jasper 1966). These cholinergic transients are correlated with both cue detection and attentional performance in rodents.

Both selective cholinergic lesions and non-selective lesions of the basal forebrain produce robust deficits in attentional performance in rodents (Robbins, Everitt et al. 1989, Muir, Dunnett et al. 1992, Turchi and Sarter 1997, McGaughy and Sarter 1998). Importantly, the attentional deficits produced by lesions to the basal forebrain cholinergic system are permanent (McGaughy, Kaiser et al. 1996). In addition, these deficits do not alter response times in lesioned animals. On a task where rodents are rewarded for both detecting the presence of salient stimuli and their absence, cholinergic lesions produced drastic deficits in detection of the salient cues, but the rodents had no deficits on trials where they were required to detect the absence of the

stimulus (McGaughy, Kaiser et al. 1996, McGaughy and Sarter 1998). These results implicate basal forebrain cholinergic tone in mediating cue detection. The attention deficits in basal forebrain cholinergic lesioned animals were insensitive to pharmacological administration of nicotinic agonists, suggesting that specifically the release of ACh is critical for cue detection in tasks of attention (McGaughy, Decker et al. 1999).

Microdialysis studies have shown that release of ACh into the PFC is increased when rodents are performing attentional tasks (Passetti, Dalley et al. 2000). Efflux of ACh into the PFC appears to vary based on the difficulty of the attentive task, where the harder the task, the more ACh is released (Dalley, McGaughy et al. 2001). Experiments recording cholinergic signalling in the PFC using enzyme coated microelectrodes demonstrated that attentionally relevant cues correlated with rapid transient increases in ACh levels in the PFC (Parikh, Kozak et al. 2007). These cholinergic transients correlated with attentive behaviour in the animals and were absent when the cues were missed by the animals. Optogenetic stimulation of basal forebrain cholinergic afferents, to simulate cholinergic transients, during tasks of attention produced “false alarms” where rodents behaved as if they had seen a rewarding cue, when no cue had been presented (Gritton, Howe et al. 2016).

Evidence for nicotinic regulation of attention comes from a number of studies which demonstrated the pro-attentive effects of nicotine (Wesnes and Warburton 1984, Rusted and Warburton 1992). The two most prevalent nicotinic receptors in the PFC are the $\alpha 4\beta 2$ nAChRs and the $\alpha 7$ nAChRs. Evidences from animal models suggest that the effects of nicotine on attention are mediated by $\alpha 4\beta 2$ nAChRs (Potter, Corwin et al. 1999, Howe, Ji et al. 2010). Administration of a $\alpha 4\beta 2$ nAChRs agonist had a greater effect on attentive behaviour than nicotine (Howe, Ji et al. 2010). Mice lacking the $\beta 2$ nAChR subunit had impairments in attention as assessed by the 5-choice serial reaction time task. These deficits were reversed by viral mediated expression of the $\beta 2$ subunit specifically in the PFC, demonstrating the necessity and sufficiency of the $\beta 2$ nAChR subunit (Guillem, Bloem et al. 2011). The mechanism of $\alpha 4\beta 2$ nAChRs signalling in attention has been thoroughly studied. Stimulation of $\alpha 4\beta 2$ nAChRs evoked

release of glutamate into the PFC, lesions of the mediodorsal thalamic nucleus eliminated the glutamate release (Parikh, Man et al. 2008). $\alpha 4\beta 2$ nAChRs thus recruit thalamic glutamatergic inputs to regulate cue detection (Howe, Ji et al. 2010). Histological studies have shown that the thalamic glutamatergic nerve terminals in the PFC do indeed express $\alpha 4\beta 2$ nAChRs (Lambe, Picciotto et al. 2003).

The evidence for the involvement of $\alpha 7$ nAChRs in attention is more contentious. Initial studies suggest that mice null for the $\alpha 7$ nAChR have deficits in sustained attention (Hoyle, Genn et al. 2006, Young, Crawford et al. 2007). Others have however reported no deficits in these same mice on the same tasks (Guillem, Bloem et al. 2011). It should be noted that in the latter study the task was substantially easier. The attentional deficits in mice null for the $\alpha 7$ nAChR may therefore be dependent on the difficulty of the task assessing attention. Pharmacological manipulations of $\alpha 7$ nAChRs have also had mixed results, with some showing improvements in attention and others showing no behavioural effects (Grottick and Higgins 2000, Pichat, Bergis et al. 2007, Rezvani, Kholdebarin et al. 2009, Wallace, Callahan et al. 2011).

The role of muscarinic receptors in attention has been investigated in human studies using the muscarinic inhibitor scopolamine. Administration of scopolamine induces cognitive impairments in healthy human subjects (Dunne and Hartley 1986). The effects of muscarinic blockade on attention appear to involve the visual cortex along with the PFC (Davidson and Marrocco 2000). mAChR blockade in the visual cortex prevents V1 neuronal adaptation to attentional stimuli. Stimulation of mAChRs in the PFC potentiates release of ACh from basal forebrain cholinergic neurons. This top down modulation of attention circuitry by mAChRs plays a role in ignoring distracting stimuli (Sarter, Gehring et al. 2006, Broussard, Karelina et al. 2009). The predominant hypothesis is that attentional performance is the result of synergy between nAChRs and mAChRs. Nicotinic receptors would mediate cue detection and the saliency of the attentionally relevant stimuli, and the muscarinic receptors regulate the top-down processes and recruit the relevant circuitry for sustained attention (Greenwood, Lin et al. 2009).

1.2.3 Cholinergic Regulation of Executive function

Executive function is the umbrella term for the collection of cognitive processes that includes attention, working memory, cognitive flexibility and planning. These cognitive processes allow an organism to monitor their own behaviour and allow for the organism to achieve goal directed behaviour. Impairments in executive function are associated with a number of neurological and neuropsychiatric disorders (Tekin and Cummings 2002).

It is by modulating the activity of various cortical networks, that ACh is believed to regulate executive functioning (Hasselmo and Sarter 2011). Of particular interest, ACh in the PFC is thought to function in a signal-to-noise manner to mediate salient cue detection in the environment (Sarter, Hasselmo et al. 2005). Cortical cholinergic tone has been shown to modulate gamma oscillations (Buhl, Tamas et al. 1998); this effect seems to be dependent of muscarinic activation, mainly by M1 muscarinic receptors (Fisahn, Pike et al. 1998, Fisahn, Yamada et al. 2002). Activation of nicotinic receptors in the PFC has been shown to increase post-synaptic activity (Couey, Meredith et al. 2007). Recently, two-photon imaging has been used to explore the role of nicotinic receptors in the regulation of these effects. Poorthuis and colleagues (2013) have demonstrated that cortical pyramidal neurons can be differentially modulated by $\alpha 7$ and $\beta 2$ nAChRs depending on the layer of the cortex.

Of importance for executive function and attention, ACh in the PFC appears to regulate both LTP and LTD (Bueno-Junior, Lopes-Aguiar et al. 2012). However, the effects of cholinergic projections arising from the basal forebrain are highly important in synaptic plasticity all throughout the cortex. It regulates both the function and the development of the visual cortex (Hohmann and Berger-Sweeney 1998, Morishita, Miwa et al. 2010). Finally, cortical cholinergic tone is thought to play a role in synchronizing activity in the motor cortex and regulate responses to attentionally relevant stimuli (Conner, Culbertson et al. 2003). The mechanisms underlying the role of cortical cholinergic tone to regulate synaptic plasticity seem to be divergent from those in the hippocampus. For example, in the hippocampus carbachol induction of LTD does not require PLC or PKC activity,

whereas, in the mPFC carbachol-induced LTD requires the participation of PLC and PKC signaling (Huang and Hsu 2010, Caruana, Warburton et al. 2011). Furthermore, cortical cholinergic tone appears to function synergistically with noradrenaline to modulate cortical plasticity (Bear and Singer 1986, Kirkwood, Rozas et al. 1999).

1.2.3.1 Cholinergic Regulation of Cognitive Flexibility

Cognitive flexibility is defined as the ability of higher organisms to adapt under varying environmental conditions, which is essential for survival. In order to test cognitive flexibility in rodents, tasks such as the pairwise visual discrimination are used (Clark, Cools et al. 2004). All tasks which assess cognitive flexibility require the animal to learn a given “rule”, usually a pairing of a stimulus with a reward, then to abandon this rule in favour of a new one. Performance on such behavioural tasks are highly dependent on the PFC. Specifically, the prelimbic subregion of the PFC, has been shown to be important in regulating anxiety-related behaviours, and reversal learning in a visual discrimination task (Heidbreder, Thompson et al. 1996). Direct lesions or temporary inactivation of the prelimbic regions of the prefrontal cortex has no effect on the acquisition of different stimuli, that is to say the initial “rule” but has a robust consequence when a shift in using another strategy is needed in order to adapt and learn a new “rule” (de Bruin, Sanchez-Santed et al. 1994, Ragozzino, Detrick et al. 1999, Birrell and Brown 2000, Delatour and Gisquet-Verrier 2000, Dias and Aggleton 2000, Ragozzino, Kim et al. 2003). Previous studies have also shown that the striatum, which receives input from the prelimbic region, plays an important role in cognitive flexibility (Dunnett and Iversen 1981, Packard, Hirsh et al. 1989, Knowlton, Mangels et al. 1996, Packard and Teather 1997).

Cholinergic tone in the striatum has been thought to play an important role in mediating cognitive flexibility. Striatal ACh was demonstrated to be critical for regulating synaptic plasticity that underlies forms of learning and memory (Calabresi, Centonze et al. 1998). In addition to the role of ACh in memory functions, Aosaki et al (Aosaki, Tsubokawa et al. 1994) reported that the activity of striatal tonic active neurons was correlated with the presentation of rewards, providing insight on the role of striatal ACh in goal-oriented

behaviors. However, the exact role of striatal ACh in cognitive flexibility is still under investigation. Mice with striatal interneurons deficient for VACHT showed no deficits in a water maze based reversal learning paradigm (Guzman, De Jaeger et al. 2011), a form of cognitive flexibility.

Results from mice lacking forebrain VACHT indicate that cholinergic tone is not required for the initial spatial learning phase in a Morris Water Maze task. However, when the contingencies are changed, and the platform is moved to a different quadrant of the pool, these mutant mice are completely unable to adapt and learn the new “rule”, suggesting that forebrain cholinergic tone is required for such behaviour (Martyn et al., 2012). Although there is a clear role of ACh in cognitive flexibility little is known of the mechanisms by which ACh exerts its effect.

Administration of the M1 muscarinic antagonist scopolamine is one of the most robust means by which impairments in behavioural flexibility can be induced (Ragozzino, Jih et al. 2002, Klinkenberg and Blokland 2010). Furthermore administration of agonists and positive allosteric modulators of M1 improve performance on measures of cognitive flexibility (McCool, Patel et al. 2008, Shirey, Brady et al. 2009). Interestingly, visual discrimination and reversal learning tested in mice deficient for the M1 muscarinic receptor showed no significant differences from control mice on acquisition or reversal (Bartko, Romberg et al. 2011), in contrast to the pharmacological data. Aging induced impairments in cognitive flexibility has been correlated with decreased expression of the M2 muscarinic receptor. Seeger *et al* (2004), investigated the role of M2 receptors, using M2 knockout mice in behavioural tasks assessing working memory and behavioural flexibility. They reported that M2 null mice had deficit in the acquisition phase of the Barnes Maze by their inability to switch from a random strategy to a more efficient strategy. Thereby, concluding that cognitive flexibility could be mediated through M2 receptors.

The role of nicotinic receptors in cognitive flexibility has not been greatly explored. Nicotinic ACh receptors, specifically the $\alpha 7$ nAChR, have been shown to alter both release of glutamate in the PFC (Marchi, Risso et al. 2002, Gomez-Varela and Berg 2013) and trafficking of glutamate receptors (Yang, Paspalas et al. 2013). As Glutamate

signalling (Karlsson, Tanaka et al. 2009) and glutamate receptor trafficking (Brigman, Feyder et al. 2008, Brigman, Daut et al. 2013) play important roles in cognitive flexibility, it is possible that cholinergic modulation of glutamate signalling, via nicotinic receptor activation, may contribute to one's ability to reverse contingency rules and demonstrate cognitive flexibility.

1.3 Alzheimer's Disease

AD is a chronic neurodegenerative disease which is characterized by loss of neurons and synapses in cortical and subcortical brain regions. This cell loss results in atrophy of the effected brain regions. This neuropathology manifests itself symptomatically early on as memory loss, but as the disease progresses the symptoms expand to include long term memory loss, impairments in executive functioning and mood disorders. The pathological hallmarks of the disease are extracellular amyloid plaques, and intracellular neurofibrillary tangles. This pathology has been hypothesised to play a critical role in disease development, however the etiology of the disease remains poorly understood.

1.3.1 Amyloid Pathology in AD

A pathological hallmark of AD, is the appearance of extracellular amyloid plaques. The presence of these plaques are a required diagnostic criteria for AD and plaque burden within the brain is used to determine the Braak staging of AD (Braak, Braak et al. 1986). These amyloid plaques are composed of aggregated fragments of the amyloid precursor protein (APP) (Weidemann, Konig et al. 1989).

APP is an integral membrane protein and within the brain its expression is highest at synapses (Muller and Zheng 2012, Puig and Combs 2013). Mice deficient in the APP gene present subtle cognitive deficits and electrophysiological changes but do not recapitulate an "Alzheimer's-like" phenotype (Zheng, Jiang et al. 1996, Mileusnic, Lancashire et al. 2000, Wang, Yang et al. 2005). It is therefore understood that the amyloid toxicity in the AD brain arises from a gain of function of the protein rather than a loss of the protein normal functions. The normal cellular function of the amyloid precursor protein remains unclear. The protein has been linked to many key neuronal

functions including synaptic formation (Priller, Bauer et al. 2006), neuronal transport (Torroja, Chu et al. 1999), iron export (Rogers, Bush et al. 2008) and hormonal signalling (Bandyopadhyay, Goldstein et al. 2007).

APP under normal conditions undergoes a series of post-translational modifications, most notably proteolytic cleavage of the protein. APP can undergo either an amyloidogenic or a non-amyloidogenic proteolytic cleavage, these cleavage pathways are mediated by distinct proteolytic enzymes. The non-amyloidogenic pathway begins with APP cleavage by α -secretase into a soluble APP α fragment and a C83 fragment (Esch, Keim et al. 1990, Sisodia, Koo et al. 1990). The C83 fragment is subsequently cleaved by the γ -secretase enzyme to form the non-toxic P3 (Haass, Hung et al. 1993) and the APP protein's intracellular domain or AICD C-terminus fragments (Gu, Misonou et al. 2001).

Amyloidogenic proteolytic cleavage of APP is initiated by the β -secretase (BACE1) enzyme (Cai, Wang et al. 2001). Given its role in initiation of toxic APP processing, BACE1 is the rate limiting step in A β production (Stockley and O'Neill 2007). BACE1 will cleave APP into soluble APP β fragments and C99 fragments (Luo, Bolon et al. 2001). It is these C99 fragments which can be cleaved at a number of sites by the γ -secretase enzymatic complex to produce A β species and AICD fragments (Citron, Westaway et al. 1997, Dovey, John et al. 2001). The cleavage pathway by which APP is catabolised is determined by the relative abundance of the α - and β -secretases. However mutations in both the APP gene (De Jonghe, Esselens et al. 2001) and in the secretase enzymes can favour production of A β (Yan, Bienkowski et al. 1999, Jankowsky, Fadale et al. 2004). Changes in the catabolism of APP to produce A β -proteins is thought to trigger the amyloid cascade in the AD brain and is the basis of the amyloid hypothesis of AD (Hardy and Higgins 1992). There are three predominant forms of A β peptides: A β 38, A β 40 and A β 42 (Portelius, Tran et al. 2007). Additionally, an A β 43 peptide has been described in presenilin-1 mutation knockin mice (Xia, Kelleher et al. 2016). There is evidence that the more hydrophobic forms of these peptides, in particular the A β 42, are

more related to severity of AD (Chui, Tanahashi et al. 1999). Specifically, the ratio of A β 42 to A β 40 is most related to disease severity (Jarrett, Berger et al. 1993).

A key component therefore in A β production is the γ -secretase enzymatic complex. This enzymatic complex is composed of four essential core proteins (Edbauer, Winkler et al. 2003): presenilin-1 (Haass and Steiner 2002), nicastrin (Yu, Nishimura et al. 2000), APH-1 (Goutte, Tsunozaki et al. 2002) and presenilin enhancer-2 (Francis, McGrath et al. 2002). Mutations in these core proteins enhance production of A β 42 peptides (Citron, Westaway et al. 1997, Yu, Nishimura et al. 2000). Inhibition of γ -secretase on the other hand reduces beta-amyloid production in the brain (Dovey, John et al. 2001). The individual core proteins have also been shown to play regulatory roles in APP processing beyond their enzymatic activity. Presenilin-1 for example can modulate APP processing by regulating the intracellular trafficking of the protein (Leem, Saura et al. 2002, Cai, Leem et al. 2003). Depictions of the amyloidogenic and non-amyloidogenic APP cleavage pathways are shown in Figure 1.3.

Given the highly neurotoxic nature of A β -oligomers and potentially of A β plaques, many therapeutic approaches have been developed to target the production of A β , by inhibiting BACE1 (Vassar 2001) or the γ -secretase complex (Dovey, John et al. 2001). Although targeting these enzymatic pathways may be promising therapeutic avenues, concerns have been raised that interfering with these enzymes may be detrimental to neuronal health (Hu, Hicks et al. 2006, Haapasalo and Kovacs 2011). The γ -secretase enzymatic complex for instance, plays many other critical roles in the cell including Notch processing (De Strooper, Annaert et al. 1999). Therefore, the general inhibition of this complex has been shown not to be a good approach for therapeutic interventions for AD (Haass and Selkoe 2007). Targeting the amyloidogenic activity of the complex while leaving the Notch signalling unaffected can be achieved by modulating proteins which activate the complex (Netzer, Dou et al. 2003, He, Luo et al. 2010).

Total A β levels, particularly the A β 42 molecule, in the brain can either be elevated by increase in production of the toxic species or by a reduction in their clearance (Selkoe 1993, De Felice and Ferreira 2002). This increase in A β -proteins leads to the

propensity to form A β -oligomers in the brain (Lambert, Barlow et al. 1998, Walsh, Klyubin et al. 2002, Gong, Chang et al. 2003). The oligomers disrupt synaptic function (Wang, Pasternak et al. 2002, Lacor, Buniel et al. 2004, Lacor, Buniel et al. 2007). Eventually the accumulation of these oligomers triggers amyloid plaque formation (Ahmed, Davis et al. 2010) and elicits an inflammatory response (White, Manelli et al. 2005, Sondag, Dhawan et al. 2009). This accumulation of A β -oligomers therefore leads to progressive neuronal injury (Zhang, McLaughlin et al. 2002). A β -oligomers have also been shown to trigger tau hyperphosphorylation (Ma, Yang et al. 2009). These events together have been suggested to underlie neuronal dysfunction and cognitive decline in the AD brain (Cleary, Walsh et al. 2005, Tomic, Pensalfini et al. 2009).

A β -oligomers can produce cytotoxicity by a number of mechanisms. A number of transmembrane receptors have been identified that A β -oligomers can bind to, including the NMDA receptor (Texido, Martin-Satue et al. 2011), α 7nAChR (Wang, Lee et al. 2000, Lilja, Porras et al. 2011), insulin (Zhao, De Felice et al. 2008) and the PrP^c (Lauren, Gimbel et al. 2009, Chen, Yadav et al. 2010). Binding to these membrane proteins can trigger a number of cytotoxic signalling pathways, ultimately leading to cell death (Haass and Selkoe 2007). A β -oligomers have also been proposed to increase membrane permeability and by doing so, disrupt the cationic homeostasis of the affected cells (Lin, Bhatia et al. 2001, Demuro, Mina et al. 2005). A β -oligomers can also trigger cytotoxic cellular signalling when it accumulates within neurons. These intracellular aggregates of A β have been shown to impair proteasome function (Tseng, Green et al. 2008), disrupt mitochondria (Manczak, Anekonda et al. 2006) and increase production of toxic reactive oxygen species (Cenini, Cecchi et al. 2010).

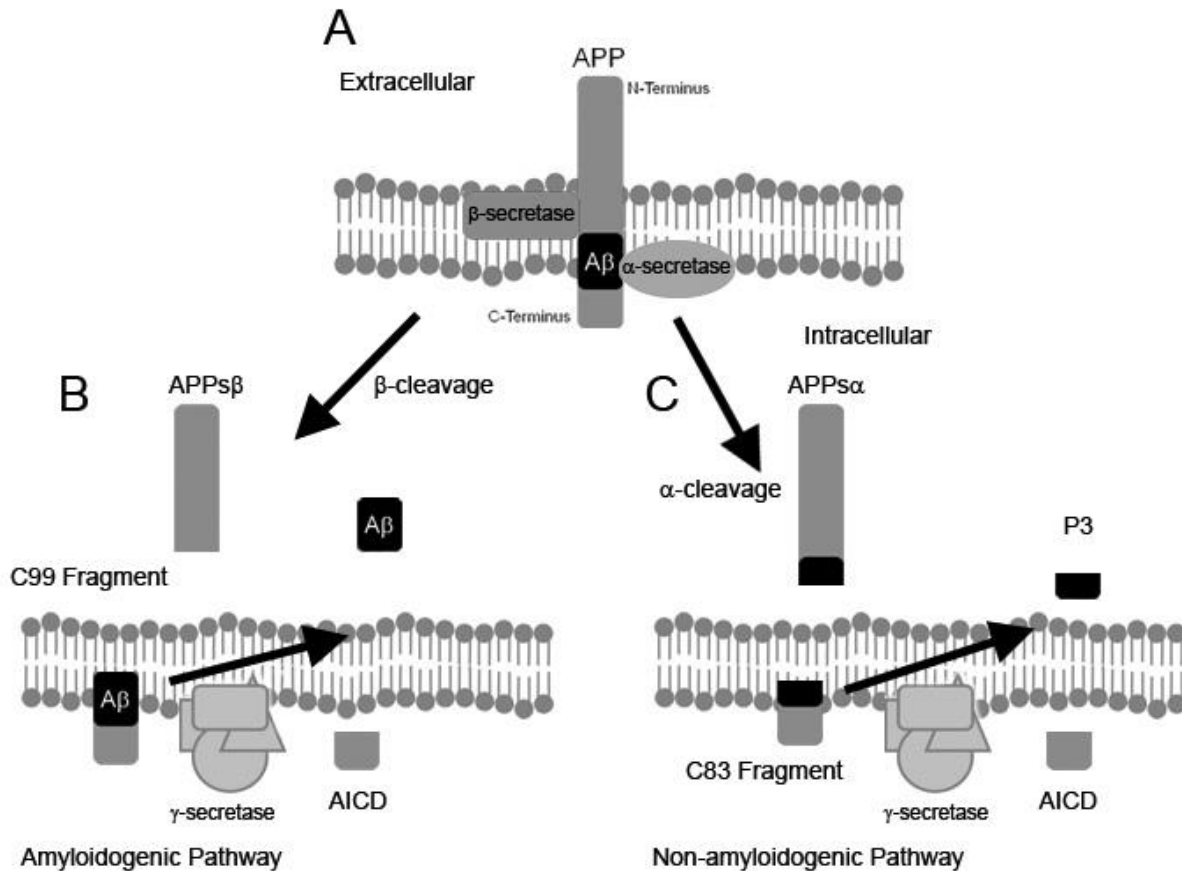


Figure 1.3 Processing of the Amyloid Precursor Protein. (A) Transmembrane APP protein can be cleaved by either the α -secretase or the β -secretase enzymes. Cleavage by the β -secretase enzyme leads to the amyloidogenic processing of the protein, while cleavage by the α -secretase leads to the non-amyloidogenic processing of the protein. (B) The amyloidogenic processing of APP. Following cleavage by the β -secretase enzyme a β soluble APP fragment and a C99 fragment of the protein are formed. The C99 fragment undergoes subsequent cleavage to form toxic A β fragments and AICD fragments. This cleavage is mediated by the γ -secretase complex. (C) The non-amyloidogenic processing of APP. Following cleavage by the α -secretase enzyme an α soluble APP fragment and a C83 fragment of the protein are formed. The C83 fragment undergoes subsequent cleavage to form inert P3 fragments and the AICD fragment. This cleavage is mediated by the γ -secretase complex.

1.3.2 Tau Pathology in Alzheimer's Disease

Another key pathological hallmark of AD, is the appearance of intracellular neurofibrillary tangles (NFTs). Inclusion of NFTs, along with amyloid plaques, are a diagnostic criteria for AD and the severity of the NFT pathology are also important for the Braak staging of AD (Braak, Braak et al. 1986). NFTs are composed of aberrantly phosphorylated microtubule associated protein tau (Goedert, Wischik et al. 1988). The exact relationship between tau pathology and neurodegeneration remains unclear. Specifically, it is not fully understood if tau pathology arises from the loss of the protein normal function, or if tau hyperphosphorylation leads to a toxic gain of function of the protein.

The full length tau protein is 441 amino acid residues long and presents two characteristic domains. Near the C-terminus of the protein, there are a number of tubulin binding domains, and near the N-terminus there are two acidic domains. The predominant function of the tau protein is to stabilize microtubules (Lee, Cowan et al. 1988). This function is mediated by the two characteristic structural domains of the protein, with the tubulin binding domain binding β -tubulin (Maccioni, Rivas et al. 1988), and the acidic domains binding to the negatively charged regions of microtubules (Ennulat, Liem et al. 1989). This interaction between tau and microtubules can be regulated by phosphorylation of the tau protein. Phosphorylation of tau negatively regulates its interaction with microtubules (Steiner, Mandelkow et al. 1990). Aberrant phosphorylation of the tau protein can thus lead to microtubule instability, a potential mechanism of tau neurotoxicity.

The effects of tau phosphorylation are dependent on which amino acid residues on the protein are phosphorylated. Different phosphorylation sites can have different physiological or pathological outcomes. Tau phosphorylation plays an important role in regulating microtubule dynamics in neurons, however when deregulated this process can become neurotoxic. The key inhibitory phosphorylation sites on tau are Ser262, Thr231, and Ser235; tau phosphorylated at any of these amino acids will have inhibited

microtubule binding capacities (Sengupta, Kabat et al. 1998). Furthermore, phosphorylation at Ser199/Ser202/Thr205, Thr212, Thr231/Ser235, Ser262/Ser356, and Ser422, will not only inhibit the function of the protein, but will cause tau to sequester normal tau proteins away from microtubules and inhibit their function as well (Alonso Adel, Mederlyova et al. 2004). Finally phosphorylation at Thr231, Ser396, and Ser422 have also been shown to promote self-aggregation of the tau in vitro (Abraha, Ghoshal et al. 2000).

Phosphorylation of tau is a dynamic process with a number of kinases and phosphatases interacting with the protein. The kinases which have been identified to phosphorylate tau are glycogen-synthase kinase-3 β (GSK-3 β) (Takashima, Noguchi et al. 1993), cyclin-dependent protein kinase 5 (Baumann, Mandelkow et al. 1993), cAMP-dependent protein kinase (Jicha, Weaver et al. 1999), and stress-activated protein kinases (Ferrer, Gomez-Isla et al. 2005). These kinases preferentially phosphorylate tau at different amino acid residues. GSK-3 β in particular has been identified as promoting toxic phosphorylation of tau. This kinase will preferentially phosphorylate at Ser202/Thr205, Ser214/Thr212, Thr231 and Ser396 residues (Song and Yang 1995). PP2A has been identified as the major phosphatase of tau (Goedert, Jakes et al. 1995). Importantly, activity and expression of this phosphatase has been shown to be decreased in the AD brain (Liu, Grundke-Iqbal et al. 2005).

Tau neurotoxicity is likely the result of both the gain and loss of functions resulting from hyperphosphorylated tau. As described above, when tau is hyperphosphorylated it no longer stabilizes microtubules. Hyperphosphorylation of the protein can therefore destabilize microtubules and compromise axonal transport (Zhang, Maiti et al. 2005). Furthermore, tau hyperphosphorylation causes the protein to bind to its un-phosphorylated form and inhibits its own function. This again leads to microtubule instability and compromised axonal transport (Zhang, Maiti et al. 2005). Microtubule instability is highly toxic to neurons (Gornstein and Schwarz 2014), drugs that inhibit microtubule stability are toxic to cultured neurons within hours and can cause neurological impairments within a week *in vivo* (Pisano, Pratesi et al. 2003).

1.3.3 Cholinergic Vulnerability in Alzheimer's Disease

A central hypothesis in AD, is that the cognitive symptoms of the disease arise as a result of the loss of basal forebrain cholinergic signalling. It was first reported in the 1970's that anticholinergic drugs could impair cognitive function in humans (Deutsch 1971). Given these findings, it was hypothesized that this neurotransmitter system may be dysfunctional in dementia. Post mortem analysis of AD brains has revealed significant reductions in levels of the ChAT enzyme in the cortex (Bowen, Smith et al. 1976, Perry, Gibson et al. 1977). Furthermore, it has been shown that in the AD brain there is a reduction in choline uptake (Rylett, Ball et al. 1983), ACh release (Nilsson, Nordberg et al. 1986), VACHT (Efange, Garland et al. 1997, Chen, Reese et al. 2011, Parent, Bedard et al. 2013) and an overall reduction in the number of cholinergic neurons in the basal forebrain region (Davies and Maloney 1976, Whitehouse, Price et al. 1982). This body of evidence lead to the cholinergic hypothesis of AD (Bartus, Dean et al. 1982). This hypothesis is the basis for the use of cholinesterase inhibitors as standard therapy for AD. These drugs have been shown to be effective in improving behavioural symptoms of the disease and delaying the placement of the patients in nursing homes (Cummings 2003).

One of the hypothesis of AD is that the neuronal dysfunction that occurs in the disease precede the cognitive decline (Nestor, Scheltens et al. 2004). That is, the pathological changes observed in the brain cause neuronal dysfunction and cell loss, leading to cognitive decline. It is therefore important to detect AD prior to the clinical manifestation of the disease. It was reported that there was no change in ChAT or AChE levels in the cortex of individuals with mild-AD (Davis, Mohs et al. 1999). Furthermore, the activity of the enzyme was reported as unaltered in the mild-AD brain and activity was increased in the brain of patients with mild cognitive impairment (DeKosky, Ikonomic et al. 2002). These findings led to criticisms of the validity of the cholinergic hypothesis of AD (Morris 2002). A strong counterargument to these criticism, however is that neither total levels nor activity of the ChAT or AChE enzymes represent accurate measures of ACh release. Therefore the levels of these enzymes in the AD brain are not necessarily

indicative of changes in cholinergic signalling (Terry and Buccafusco 2003). Further evidence of cholinergic dysfunction (either for or against), in particular assessment of ACh release, in early AD is therefore still needed.

The main risk factor for AD is aging (Lindsay, Laurin et al. 2002). Therefore, numerous studies have examined the effect of aging on the cholinergic system. It was shown that in mice, ACh synthesis is reduced by 75% when comparing young (3 months old) to aged (30 months old) animals (Gibson, Peterson et al. 1981). Furthermore, as mice age, their cholinergic neurons no longer release as much ACh as their younger counterparts (Gibson and Peterson 1981). These findings were confirmed in rats as well (Wu, Bertorelli et al. 1988). Numerous studies in animals have suggested that cholinergic neurons function “normally” and that the aging process stresses these neurons and decreases their function (Meyer, Crews et al. 1986, Gilad, Rabey et al. 1987, Moore, Stuckman et al. 1996). Accelerating the aging-induced deficits in cholinergic signalling has been shown to have functional consequences in rat model of sustained attention (Burk, Herzog et al. 2002).

Recent evidence has added a new dimension to the cholinergic hypothesis of AD. Clinical findings report that there is an increased incidence of dementia in patients following the cumulative use of anticholinergic drugs (Gray, Anderson et al. 2015, Risacher, McDonald et al. 2016). It is well understood that the use of these compounds can impair cognition while the patient is taking them. However, there is a growing body of clinical evidence suggesting that anticholinergic medications can produce cognitive impairments long after consumption of the medications has been ceased (Carriere, Fourrier-Reglat et al. 2009, Jessen, Kaduszkiewicz et al. 2010). Furthermore, it has been reported that prolonged use of these drugs, specifically anti-muscarinic agents, increases Alzheimer’s pathology in the brains of these patients (Perry, Kilford et al. 2003). *In vitro* models, have confirmed that anti-muscarinic agents have the most potent effect on neuronal and astrocytic cells (Woehrling, Parri et al. 2015). Mechanistic insight, however, into how anticholinergic medications can increase risk of dementia are still largely unknown.

Cholinergic neurons also appear to be highly vulnerable to AD pathology. Post-mortem analysis of AD brains has shown that basal forebrain cholinergic neurons present with both amyloid (Baker-Nigh, Vahedi et al. 2015) and tau pathology (Vana, Kanaan et al. 2011, Ahmadian, Rezvanian et al. 2015). These cholinergic basal forebrain neurons have been shown to be vulnerable to both of these AD related pathologies. This selective vulnerability is mediated by the dependence of these basal forebrain cholinergic neurons on trophic factors. A β species impair trophic signalling in these neurons, resulting in impairment in their function and toxicity to the cells (Cuello and Bruno 2007). Targeting these neurotrophic pathways in mouse models of AD can improve cognitive outcomes in these mice, and at the same time reduce tau and A β related pathology (Nguyen, Shen et al. 2014). Furthermore, it has been shown that A β species promote tau hyperphosphorylation in basal forebrain cholinergic neurons (Zheng, Bastianetto et al. 2002). Cholinergic neurons are therefore highly vulnerable to AD pathology and this is thought to play a role in mediating cognitive dysfunction in the disease. Also, the magnitude of the loss of these neurons correlates to cognitive deficits in patients (Mufson, Ma et al. 2002). It should be noted that other factors have been shown to correlate to cognitive dysfunction including A β oligomers (Cleary, Walsh et al. 2005, Tomic, Pensalfini et al. 2009) and general synaptic dysfunction in the AD brain (DeKosky and Scheff 1990, Selkoe 2002).

Aberrant cholinergic signalling can also impact the signalling pathways related to both tau and amyloid pathology. Immunolesions of basal forebrain cholinergic neurons in the 3xTG mouse model of AD (which has both amyloid and tau pathology), significantly enhanced pathology in these mice (Hartig, Saul et al. 2014). Furthermore administration of an M1 muscarinic agonist to 3xTG mice significantly decreased the pathology and hippocampal specific memory impairments in the animals (Caccamo, Oddo et al. 2006). These effects were purported to be mediated by regulating GSK3 activity and BACE1 expression. Crossing Alzheimer's model mice with mice lacking the M1 muscarinic receptor significantly increased amyloidogenic processing of APP and accumulation of toxic A β species (Davis, Fritz et al. 2010). Further work in mice has shown that

impairing cholinergic signalling accelerates tau hyperphosphorylation (Zhang, Chen et al. 2014). These studies speak to the complexity of AD pathology and provide evidence that cholinergic signalling, along with being highly vulnerable to AD pathology, may also be important in regulating AD pathology.

1.3.4 RNA Metabolism Dysfunction in Alzheimer's Disease

RNA metabolism refers to any events in the life cycle of an RNA molecule, including its synthesis, modification, processing, translation and ultimately its degradation (Stamm, Ben-Ari et al. 2005). Alternative splicing is the process by which the mRNA of a given gene can be edited to form differential transcripts. This process involves the inclusion or the exclusion of particular exons or introns in a transcript (Zahler, Neugebauer et al. 1993). Alternative splicing is a central aspect of neural physiology and is carried by RNA binding proteins. The function of a number of RNA binding proteins is therefore essential for both the development and function of neurons (Jensen, Dredge et al. 2000).

Alternative splicing of mRNAs prior to their translation is an essential regulatory process in eukaryotic cells. It is by alternative splicing that a single gene composed of multiple exons can be translated into proteins which have different structures and functions (Padgett, Grabowski et al. 1986, Breitbart, Andreadis et al. 1987). Furthermore, the alternative splicing of an mRNA plays a critical role in the final cellular localization of the gene product. For example, if a nuclear localization signal of a given protein is added by alternative splicing that protein will now translocate to the nucleus, as is the case with CaM-Kinase (Srinivasan, Edman et al. 1994). Alternative splicing plays a critical role in both the development and in the normal function of the mammalian nervous system (Li, Lee et al. 2007, Raj and Blencowe 2015).

There are multiple patterns of alternative splicing that have been identified in eukaryotic cells (Sammeth, Foissac et al. 2008). Schematic depictions of the different forms of alternative splicing can be found in Figure 1.4. The most common alternative splicing event is the cassette-exon event (Sammeth, Foissac et al. 2008); this is the inclusion or exclusion of a single exonic sequence from the final mRNA transcript (Van der Ploeg,

Liu et al. 1982). A mutually exclusive exon splicing event is when the inclusion of a given exon in a transcript results in the exclusion of another (usually a proximal exon) (Smith and Nadal-Ginard 1989). Alternative splicing can also occur within an exon. Splicing of a sequence which changes the length of the exon at the 5'-end is an alternative 5' splicing event, and an event that does the same at the 3' end of an exon is a 3' alternative splicing event (Fu, Mayeda et al. 1992). Intronic sequences are usually spliced out of a final transcript, however alternative splicing of an mRNA can result in the retention of intronic sequences (Galante, Sakabe et al. 2004). Alternative splicing can also occur within the promoter region of a given transcript, when this event occurs it results in a different first exon for the final transcript (Cramer, Caceres et al. 1999). Alternative splicing also plays a significant role in the regulation of the 3' UTR of a transcript, as it can result in a completely different 3'-UTR (Grimm, Holinski-Feder et al. 1998). The length of the 3'UTR is also prone to alternative splicing, these events are termed alternative polyadenylation events (Proudfoot, Furger et al. 2002). Alternative polyadenylation of a transcript is an important determinant of which microRNA end up binding to the transcript and therefore can effect translation and degradation of the transcript (Sandberg, Neilson et al. 2008).

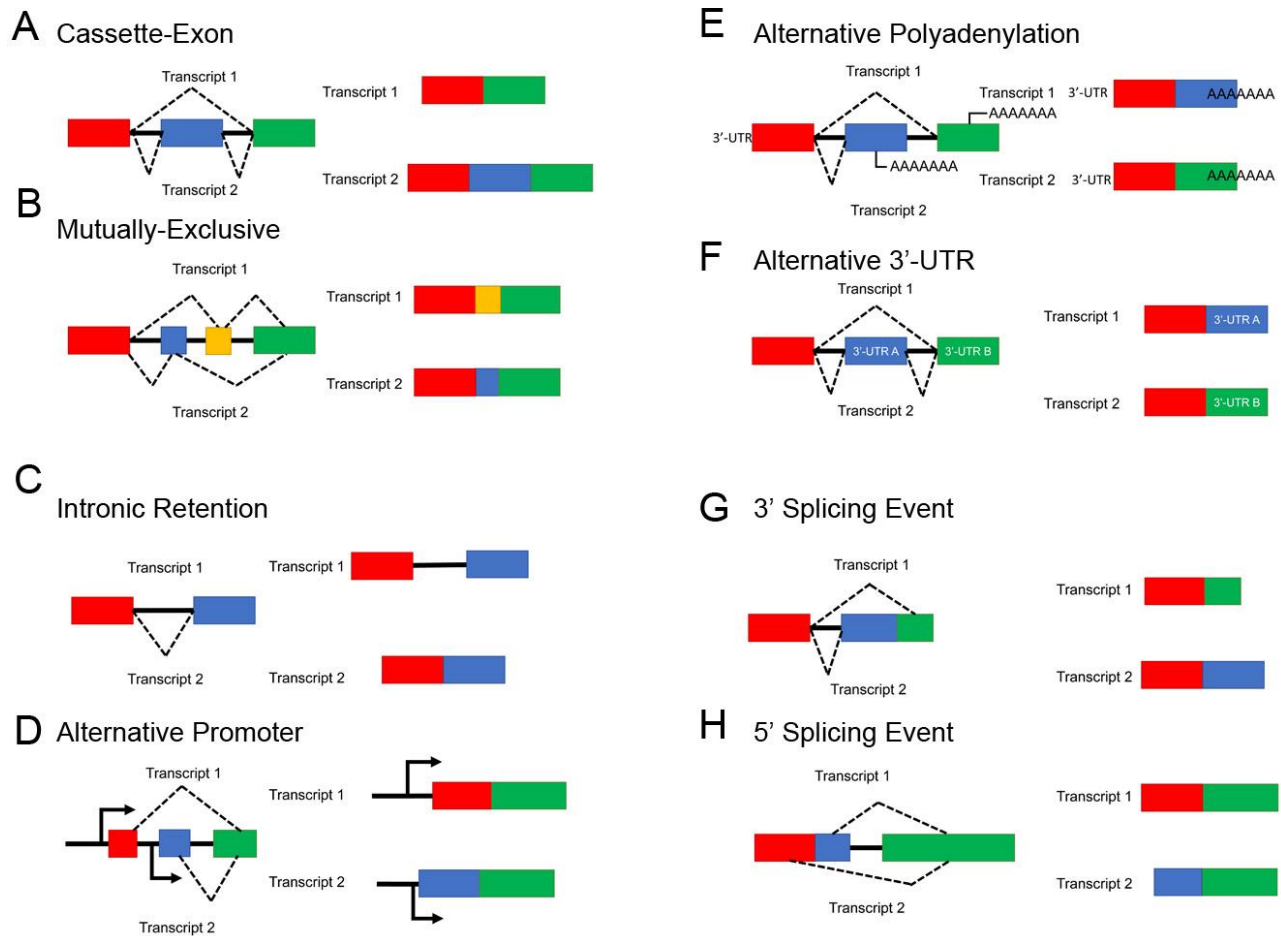


Figure 1.4. Patterns of alternative splicing in eukaryotic cells. (A) Cassette-exon splicing events are the inclusion or exclusion of a single exonic sequence from the final mRNA transcript. (B) Mutually-exclusive splicing events occur when the inclusion of a given exon in a transcript results in the exclusion of another. (C) Intronic retention, when an intronic sequence is retained in the final mRNA transcript. (D) Alternative promoter events are when alternative splicing changes the first exon of a given transcript. (E) Alternative polyadenylation events occur when the length of the 3'-UTR of a transcript is altered. (F) Alternative 3'-UTRs occur when the 3'UTR of a transcript is completely alerted by alternative splicing. (G) 3'-Splicing event. When alternative splicing occurs within the 3' region of an exon. (H) 5'-Splicing event. When an alternative splicing event occurs within the 5' region of an exon.

All of these different patterns of alternative splicing occur concurrently on transcripts within eukaryotic cells. These splicing events are regulated by hosts of RNA-binding

proteins (RBPs) (Mount, Pettersson et al. 1983, Mayeda and Krainer 1992, Wu and Maniatis 1993, Izaurralde, Lewis et al. 1994). RBPs all bind to RNA and either enhance or repel spliceosome formation and ultimately the alternative splicing of specific sequences (Blencowe 2000). Any given RBP can have different effects on a single transcript based on where the RBP binds to the mRNA, post-translational modification to the RBP and interactions with other RBPs (Tacke, Chen et al. 1997, Xiao and Manley 1997, Black 2003). In the mammalian nervous system, there is a significant amount of overlap between the functions of the various RBPs. This creates a complex and finely tuned regulatory network regulating RNA metabolism within each neuron in the brain (Vuong, Black et al. 2016). The interactions between these RNA binding proteins in neurons is complex and plays a vital role in neuronal function (McGlinchey and Smith 2008) and are dysfunctional in AD (Bai, Hales et al. 2013).

Many familial mutations have been identified in key AD related genes that cause alternative splicing of these transcripts. This includes the genes for the amyloid precursor protein (Golde, Estus et al. 1990) and tau (Niblock and Gallo 2012). Furthermore mutations in genes involved in RNA metabolism are central to many familial forms of neurodegeneration, including AD (Lemmens, Moore et al. 2010). In particular, dysfunction of RNA metabolism is an important factor in the etiology of Amyotrophic Lateral Sclerosis (ALS). Many of the key processes in RNA metabolism have been shown to be disrupted in ALS (Strong 2010). Microarray analysis has shown that a large number of key transcripts are both up and down regulated in ALS, suggesting impaired regulation of transcription in the disease (Ferraiuolo, Heath et al. 2007). Furthermore, there is evidence of altered alternative splicing (Rabin, Kim et al. 2010), mRNA transport deficits (Millecamps and Julien 2013) and impairment in RNA translation in ALS (Ling, Polymenidou et al. 2013). Mutations in hnRNPA2/B1 and hnRNPA1 (see below) have been associated with familial forms of ALS. Importantly, these mutations result in the proteins aggregating in stress granules and forming cytoplasmic inclusions (Kim, Kim et al. 2013).

The role of alternative splicing in sporadic AD however is not well defined. The hippocampus was identified as a region vulnerable to changes in RNA metabolism in

the sporadic AD brain. Importantly, these observed changes in RNA metabolism, were uncorrelated to pathological hallmarks of AD (Doebler, Markesbery et al. 1987). Many studies have demonstrated that transcriptome level changes in genes related to neuronal function are a hallmark of AD (Miller, Oldham et al. 2008). Microarray studies of the AD brain temporal lobe found that there was significant amounts of alternative splicing, and that this was reflected by changes in RNA binding protein levels (Tollervey, Wang et al. 2011). Further microarray analysis of post-mortem entorhinal cortices from AD and non-demented control brains, found global changes in alternative splicing in the sporadic AD brain (Berson, Barbash et al. 2012). Importantly, these changes in alternative splicing were linked to hnRNPA/B proteins.

1.3.4.1 hnRNPA/B Proteins

Heterogeneous nuclear ribonucleoproteins (hnRNP) are a large family of protein which associate with and bind pre-mRNA into hnRNP particles. hnRNP particles are complexes of mRNA and protein. A mRNA being in an hnRNP particle indicates to the cell that the mRNA is not mature, and is not ready for translation (Konig, Zarnack et al. 2010). It is within this hnRNP particle that splicing of the mRNA occurs. A subfamily of the hnRNP proteins is the A/B family. The hnRNPA/B family is comprised primarily of the hnRNPA1 hnRNPA2/B1 proteins (Minoo, Martin et al. 1991), although hnRNPA0 (Myer and Steitz 1995) and hnRNPA3 (Matsui, Motomura et al. 2002) are also members of the family. All hnRNPA/B proteins have two RNA-recognition motifs within a glycine rich domain (Dreyfuss, Matunis et al. 1993). All proteins within the family have a relatively high level of homology between these RNA-recognition motifs (Burd, Swanson et al. 1989). hnRNPA/B proteins are the most abundant hnRNP proteins within cells. hnRNPA2/B1 and A1 comprise roughly 60% of all hnRNP proteins within cells (Beyer, Christensen et al. 1977). hnRNPA/B proteins are most abundant within the nucleus of cells (Pinol-Roma, Swanson et al. 1989), however the shuttling of these proteins between the nucleus and the cytoplasm is critical for many of their functions.

The key function of hnRNPA/B proteins is their involvement in RNA-editing. hnRNPA/B proteins are essential components of the spliceosome and are involved in alternative and constitutive splicing events (Jurica, Licklider et al. 2002). hnRNPA/B proteins do not directly splice mRNA, rather, they regulate alternative splicing by attracting or repulsing serine/arginine-rich (SR) proteins (Martinez-Contreras, Cloutier et al. 2007). Therefore, hnRNPA/B proteins can act as either splicing enhancers or repressors, depending on their RNA-recognition motif and the element they bind on a given mRNA, and their effect on SR proteins.

hnRNPA/B proteins can also play important roles in other aspects of RNA metabolism. These proteins can play a role in gene transcription, by binding to promoter regions of genomic DNA (Takimoto, Tomonaga et al. 1993, Campillos, Lamas et al. 2003). The binding of these hnRNPA/B proteins can either promote or inhibit transcription of genes. hnRNPA/B proteins also play a role in shuttling mRNA out of the nucleus. hnRNPA/Bs interact with transportin 1 and 2 proteins (Rebane, Aab et al. 2004) and is then exported from the nucleus by nucleoporins (Bonifaci, Moroianu et al. 1997). hnRNPA/Bs then shuttle mRNAs to polysomes for translation (Visa, Alzhanova-Ericsson et al. 1996). In neurons this can involve transporting key transcripts, in an activity dependant manner, from the nucleus to the synapse, such as *BDNF* mRNA (Leal, Afonso et al. 2014). hnRNPA2/B1 is also found to bind to, and interact with miRNAs. hnRNPA2/B1 will specifically bind miRNAs which have a recognition element for hnRNPA2/B1, the protein controls the loading of miRNAs into exosomes (Villarroya-Beltri, Gutierrez-Vazquez et al. 2013).

1.3.4.2 hnRNPA/B Proteins in AD

The selective loss of hnRNPA/B proteins in the AD brain was an important breakthrough in understanding the mechanism which regulate alternative splicing (Berson, Barbash et al. 2012). In mice, viral mediated knockdown of hnRNPA/B proteins recapitulated many of the alternative splicing events observed in the AD brain (Berson, Barbash et al. 2012). Furthermore knocking down hnRNPA/B proteins produced memory and electrophysiological impairments in the mice (Berson, Barbash et al. 2012). Taken together, these results implicate broad changes in alternative splicing as a causal factor

to cognitive impairments in AD. Importantly, this change in hnRNPA/B protein levels was independent of A β and Tau toxicity in mouse models of AD. Rather, it was shown that cholinergic signalling mediated hnRNPA/B protein levels (Berson, Barbash et al. 2012), and that manipulating cholinergic tone in mice could impair RNA metabolism.

An unbiased analysis of the human brain-insoluble proteome identified a number of protein components of the U1-snRNP, both the U1-70K and the U1A proteins, as being aggregated in the AD brain (Bai, Hales et al. 2013). This complex is a primary component of the spliceosome and mediates spliceosome binding to RNA and the initiation of splicing (Hodnett and Busch 1968, Seraphin and Rosbash 1989). In line with the observation of aggregation of splicing factors in the AD brain, a number of genes were shown to be alternatively spliced in the AD brain, including the BACE1 gene (Bai, Hales et al. 2013). In vitro manipulations of U1-70K expression altered APP processing in cultured neurons and induced production of A β species (Bai, Hales et al. 2013). Experimental evidence has shown that the aberrant aggregation of the U1-70K splicing factor in the AD brain is the result of abnormal truncation of the protein in the AD brain (Bai, Chen et al. 2014).

Taken together, these findings demonstrate multiple neurodegeneration-related alterations in RNA processing which may play a role in AD pathogenesis and disease progression. The mechanisms regulating these disease related changes in RNA-metabolism remain poorly understood, however cholinergic signalling has been demonstrated as an important mediator of this process. Insight into the cellular mechanisms regulating this interaction could provide crucial insight into the pathogenesis of AD.

1.3.4.3 RNA Sequencing as a Tool to study RNA Metabolism

The study of entire transcriptome at once (the sum of all transcripts within a cell, or group of cells) has proven to be an invaluable tool in neuroscience from basic science (Okaty, Sugino et al. 2011), up to clinical research (Gould and Manji 2004). A number of techniques have been developed in order to study the transcriptome. Sequencing based

approaches is one of the powerful tools used to study of RNA metabolism. The depiction of the typical workflow of an RNA-Seq experiment can be found in Figure 1.5.

RNA-Seq can provide an in depth qualitative and quantitative analysis of the transcriptome. The first step in RNA-Seq is the isolation of total RNA from the cell population/tissue of interest. This total RNA is then converted into a library of cDNA and fragmented. Adapter sequences are added to each fragment of cDNA. The adapter sequences provide necessary elements for sequencing and also contain DNA barcodes which allows for the determination of the 5'-3' orientation of the sequence fragment. The cDNA fragments are then sequenced in a high throughput manner, producing "reads" of the fragments. After being sequenced, the resulting "reads" are then aligned using assembly algorithms either with or without a reference genome (Mortazavi, Williams et al. 2008). This mapping process provides the qualitative analysis of the transcriptome, while the quantitative aspect of RNA-Seq comes from the count of the reads from same transcript (Kanitz, Gypas et al. 2015, Conesa, Madrigal et al. 2016). This "reads count" can be used to compare the level of transcripts across experimental conditions.

Given that RNA-Seq can provide quantitative and qualitative analysis of transcripts at an extremely high level of resolution, the technique is an invaluable tool to the study of alternative splicing and RNA processing. The resulting data from RNA-Seq experiments can be analyzed in a number of ways to quantify alternative splicing. The most conservative approach to this kind of analysis is to quantify the number of reads which map to particular transcript isoform which have unique sequences, be they exons, intron or splice junctions (Filichkin, Priest et al. 2010). The normalized count of these reads provides an absolute quantification of the abundance of these transcript variants. This approach however is limited to transcripts which have these unique sequences, or which only have very minor (a couple of base pairs) differences between transcript variants. An alternative approach is to quantify all the reads which map onto a specific gene of interest, and normalizing the reads to the average for that gene. This approach will thus provide the relative abundance of transcript variants, and has led to the discovery of many novel alternative splicing events and splice junctions (Trapnell, Pachter et al. 2009).

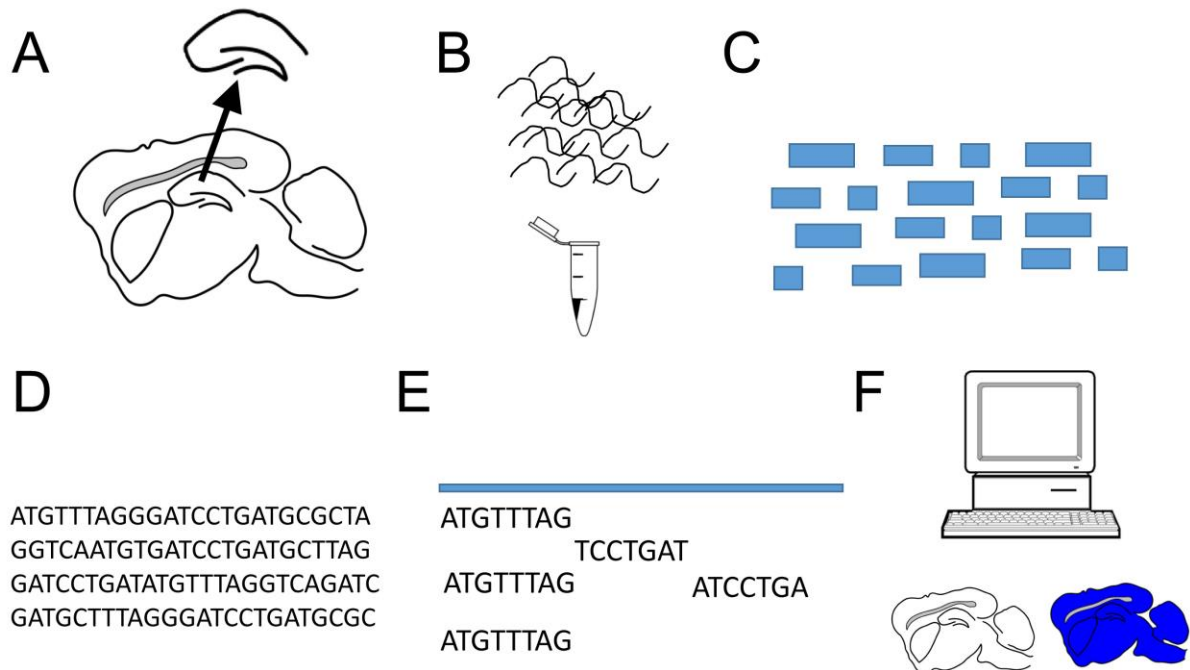


Figure 1.5 Workflow of an RNA-Seq Experiment. (A) A tissue sample of interest is isolated. (B) mRNA is isolated from the tissue sample. (C) The mRNA is converted into cDNA and fragmented into short segments (reads). (D) The reads are sequenced. (E) Sequenced reads are aligned to a reference genome. (F) Aligned sequences are then counted (read counts) to allow for comparisons between samples.

1.4 Rationale and Hypothesis

AD is a progressive neurodegenerative disease and is characterized by a number of key pathological and molecular changes in the brain. These molecular and pathological changes converge to perturb neuronal function, leading to cognitive decline, and ultimately lead to loss of neurons in the brain. A key aspect of AD is the loss of basal forebrain cholinergic neurons. ACh has been implicated in the underlying physiology of many distinct cognitive functions; however the exact role that ACh plays in regulating information processing in the brain is still not fully understood.

Therefore, the overall objective of thesis is to first characterize how altered cholinergic signalling in mice can lead to cognitive dysfunction. Additional objectives include to evaluate the molecular changes that follow long-term cholinergic dysfunction and how they may be related to AD pathology. VACHT is required for the storage of ACh into synaptic vesicles, and therefore it presents a means to modulate release. We can leverage this knowledge to generate mice with brain region specific changes in transporter level. Specifically, the aims of this thesis are:

1. To investigate the consequences of cholinergic dysfunction on distinct cognitive domains in mice and attempt to dissect underlying receptor signalling pathways.
2. Determine the genome-wide transcriptome level changes in mice with long-term cholinergic dysfunction and to determine the molecular mechanisms underpinning these changes.
3. Examine the molecular alterations that contribute to molecular pathology in a mouse model with deficient cholinergic signaling in the forebrain.

Several lines of research suggest that long-term cholinergic dysfunction may lead to cognition dysfunction, suggesting a role for decreased ACh signaling on the broad molecular and pathological changes in the demented brain. *The hypothesis we tested is that changes in cholinergic tone produce specific molecular signatures in target brain areas that underlie alterations in cognitive function.* We combined behavioural and molecular techniques and unique mouse models to test this hypothesis and to define

basic aspects of regulation of behaviour by cholinergic activity. Dysfunction of the cholinergic system has been shown to play a role in a host of neurological and neuropsychiatric disorders beyond just AD. Thus, understanding the basic physiological aspects of this system may lead to the development of novel treatments for neurological and psychiatric disorders.

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Chapter 2

ChAT–ChR2–EYFP mice have enhanced motor endurance but show deficits in attention and several additional cognitive domains

2.1 Chapter Summary

Acetylcholine (ACh) is an important neuromodulator in the nervous system implicated in many forms of cognitive and motor processing. Recent studies have used bacterial artificial chromosome (BAC) transgenic mice expressing channelrhodopsin-2 (ChR2) protein under the control of the choline acetyltransferase (ChAT) promoter (ChAT–ChR2–EYFP) to dissect cholinergic circuit connectivity and function using optogenetic approaches. We report that a mouse line used for this purpose also carries several copies of the vesicular acetylcholine transporter gene (VACHT), which leads to overexpression of functional VACHT and consequently increased cholinergic tone. We demonstrate that these mice have marked improvement in motor endurance. However, they also present severe cognitive deficits, including attention deficits and dysfunction in working memory and spatial memory. These results suggest that increased VACHT expression may disrupt critical steps in information processing. Our studies demonstrate that ChAT–ChR2–EYFP mice show altered cholinergic tone that fundamentally differentiates them from wild-type mice.

2.2 Introduction

Acetylcholine (ACh) has multiple functions in the CNS, including modulation of attention and memory encoding, consolidation, and retrieval (Prado et al., 2013). Understanding the precise roles of ACh in distinct brain regions has remained a challenge because of the myriad of cholinergic receptors that can modulate postsynaptic and presynaptic cholinergic activities (Hasselmo and Sarter, 2011). Genetic approaches have been used to determine the specific roles of ACh in different brain regions (Guzman et al., 2011; Martyn et al., 2012; Patel et al., 2012), as well as to pinpoint precise functions of ACh receptors (for review, see Wess et al., 2007; Changeux, 2010). More recently, optogenetics has also been used to further dissect and understand cholinergic signaling in the CNS (Witten et al., 2010; Nagode et al., 2011; Ren et al., 2011; Zhao et al., 2011; Gu et al., 2012). One of the approaches to specifically activate cholinergic neurons using optogenetics is in vivo injection of Cre-inducible viral vectors carrying the channelrhodopsin-2 (ChR2) gene. Cholinergic specificity is ensured by using bacterial artificial chromosome (BAC) transgenic mice expressing Cre recombinase under the control of the choline acetyltransferase (ChAT) promoter (Gradinaru et al., 2007). Alternatively, BAC transgenic mice expressing ChR2 protein under the control of the ChAT promoter (ChAT–ChR2–EYFP) have also been used, for example, to examine ACh/glutamate cotransmission in neurons thought to be strictly cholinergic (Ren et al., 2011; Zhao et al., 2011). However, a unique characteristic of the ChAT locus, also called cholinergic gene locus (Eiden, 1998), is that the entire open reading frame for the vesicular acetylcholine transporter (VACHT) lies within the intron between the first and second exons of the ChAT gene (Bejanin et al., 1994; Erickson et al., 1994; Roghani et al., 1994; Cervini et al., 1995; Naciff et al., 1997). Thus, the BAC containing the ChAT gene used to generate these mouse lines carries also the VACHT gene.

Importantly, increased expression of VACHT can alter ACh release. For example, in vitro overexpression of the VACHT in *Xenopus* neurons results in increased amplitude of miniature currents and in more synaptic vesicles containing ACh (Song et al., 1997). Moreover, a recent report indicates that a mouse line containing four copies of the ChAT–BAC driving the expression of GFP presents increased ACh release (Nagy and

Aubert, 2012). However, the consequences of VACHT overexpression for cognitive functions are not yet understood. Because ChAT–ChR2–EYFP mice have the potential to become widely used by the neuroscience community as a tool to determine the consequences of cholinergic activation for behavior manifestations, we determined the extent by which VACHT is overexpressed in this mouse line and whether overexpression of VACHT affects mouse behavior.

We report that ChAT–ChR2–EYFP mice have several extra copies of the VACHT gene and express increased VACHT mRNA and protein levels. ACh release is increased threefold in these mice. Importantly, we find that ChAT–ChR2–EYFP have increased physical endurance, consistent with increased cholinergic tone. In contrast with the improved motor function, cognitive tests demonstrated that increased expression of VACHT interferes with multiple domains of cognitive function.

2.3 Material and Methods

2.3.1 Animals

All experiments were performed in compliance with the Canadian Council of Animal Care guidelines for the care and use of animals. The protocol was approved by the University of Western Ontario Institutional Animal Care and Use Committee (2008-127). All efforts were made to minimize the suffering of animals. ChAT–ChR2–EYFP mice [B6.Cg-Tg(Chat-COP4*H134R/EYFP)6Gfng/J; The Jackson Laboratory] and VGAT–ChR2–EYFP mice [B6.Cg-Tg(Slc32a1-COP4*H134R/EYFP)8Gfng/J; The Jackson Laboratory] were described previously (Zhao et al., 2011) and were maintained as hemizygous. Control mice consisted of ChAT–ChR2–EYFP or VGAT–ChR2–EYFP negative littermates. Only male mice were used in these studies. Animals were housed in groups of two to four per cage in a temperature-controlled room with a 14/10 light/dark cycle. Food and water were provided ad libitum. Behavioral assessment started with less demanding (locomotor activity) to more demanding (depression and anxiety-like behavior, spatial memory in the Barnes maze, water maze, and then attention) tasks. Treadmill experiments were done after the water maze and before

attention measurements. There was an interval of 3–5 d between distinct behavioral tasks. The experimenter was blind to the genotypes, and, in most behavioral tasks, software-based analysis was used to score mouse performance. All behavioral experiments were performed from 9:00 A.M. to 4:00 P.M. in the light cycle, except for the light/dark transition (always performed after 7:00 P.M.) and locomotor activity tests (performed from 5:00 P.M. to 9:00 P.M.; lights off at 7:00 P.M.).

2.3.2 Immunofluorescence microscopy

Mice were anesthetized using a ketamine (100 mg/kg)-xylene (20 mg/kg) solution and then killed by transcardial perfusion with 4% paraformaldehyde (v/v) in 1× PBS. Brains were harvested and placed in 4% paraformaldehyde in 1× PBS at 4°C for 4 h, and they were kept at 4°C until being sliced using a vibratome. Brain sections (40 µm) were prepared, and free-floating sections in 1× PBS (one per well in a 24-well plate) were permeabilized with 0.4% Triton X-100 in 1× PBS for 1 h. Nonspecific epitopes were blocked using a solution of 1× PBS/0.4% Triton X-100 containing 0.1% glycine (w/v), 0.1% lysine (w/v), 1% BSA (w/v), and 1% normal donkey serum (w/v). Primary antibody (an FITC-conjugated goat polyclonal anti-GFP; catalog #ab6662; Abcam) was incubated in blocking buffer overnight at 4°C. Sections were then washed five times in 1× PBS/0.4% Triton X-100 (10 min each). Sections were mounted on slides and visualized using an Olympus IX81 laser-scanning microscope (FluoView) using an argon laser with parameters set for GFP. Images were taken using a 10× objective (numerical aperture 0.40) with the tile feature. Acquired images were then used to reconstruct the entire brain using the Olympus software.

2.3.3 qPCR and Western blotting

To genotype mice and to measure gene copies of VACHT, genomic DNA was extracted from tail-snip samples, and qPCR was used with the following primer pair: forward, 5'-GAGAGTACTTTGCCTGGGAGGA-3'; and reverse, 5'-GGCCACAGTAAGACCTCCCTTG-3'. The results were normalized to *Sti1p1* using the following primer pair: forward, 5'-ATGTATCTGAGCATGCCTCTG-3'; and reverse, 5'-

ATTGCCCTTCTCCTTTAGCTC-3'. To measure VACHT mRNA expression, total RNA was extracted using the Aurum Total RNA for fatty and fibrous tissue kit (Bio-Rad) according to the kit manual. cDNA synthesis and qPCR analysis were performed as described previously (Guzman et al., 2011). Immunoblotting was performed as described previously (Martins-Silva et al., 2011). The antibodies used were anti-VACHT (catalog #139103; Synaptic Systems), anti-ChAT (catalog #A144p; Millipore), anti-Synaptophysin (catalog #S5768; Sigma-Aldrich), and anti-Actin (catalog #ab49900; Abcam).

2.3.4 Acetylcholine Release

ACh release from hippocampal brain slices was done as described previously (Guzman et al., 2011), by labeling slices with [3H] methyl-choline, before using KCl to stimulate release of labeled ACh.

2.3.5 Metabolic assessments

Oxygen consumption, carbon dioxide production, respiratory exchange ratio (RER), food and water intake, and physical activity were simultaneously measured for young and adult mice by using the Comprehensive Lab Animal Monitoring System interfaced with Oxymax software (Columbus Instruments) essentially as described previously (Guzman et al., 2013). Mice were individually housed in the metabolic chambers maintained at $24 \pm 1^\circ\text{C}$ and given ad libitum access to powdered standard rodent chow and water. All the measurements were taken every 10 min for 24 h (12 h light/12 h dark) after a 16 h habituation period in the individual metabolic chambers. Total activity, ambulatory activity, and sleep (periods of inactivity) were obtained using the Opto-M3 Activity Monitor and Oxymax software algorithms (Columbus Instruments) as described previously (Guzman et al., 2013).

2.3.6 Glucose tolerance test

Animals were fasted for 5 h and then received an intraperitoneal injection of 2 g/kg glucose. Blood glucose levels were measured at 0 (baseline), 30, 60, 90, 120, and 150

min after glucose injection. Glucose levels were determined in blood samples obtained from a tail snip using ACCU-CHEK Advantage (Roche Diagnostics).

2.3.7 Grip force

Forelimb and hindlimb grip strength were assessed using a previously described protocol (Prado et al., 2006).

2.3.8 Treadmill

To test motor endurance, a rodent treadmill (IITC Life Sciences), with a grid behind the track that delivered a mild electric shock (15–20 V) when the mouse fell off, was used. Before testing, mice were trained for 4 d (3 min/day). On the first day, inclination was set to 5°. The inclination was increased by 5° on each subsequent training day. The initial training speed was 8 m/min, and the treadmill was accelerated by 1 m/min, up to 9 m/min. In the second training session, the initial speed was 10 m/min and was increased to 11 m/min, whereas on the third day and fourth days, the speed was maintained at 12 m/min. On the test day, the initial speed was set to 12 m/min, and the ramp angle was set to 20°. Speed was increased to 20 m/min over the course of the first 15 min of testing, after which it remained constant, until the test was complete. The test ended when 60 min had elapsed or the mouse had reached exhaustion (Lund et al., 2010).

2.3.9 Elevated plus maze, forced swimming test, and tail suspension test

Anxiety-like behavior was assessed using the elevated plus maze test, performed as described previously (Martins-Silva et al., 2011). Sessions were recorded and the video was analyzed using the ANY-Maze Software (Stoelting) to determine total time spent in the open and closed arms. Depressive-like behavior was assessed using the forced swim and tail suspension tests (Martyn et al., 2012). For the forced swim test, mice were placed in a 2 L beaker containing 1.8 L of 25–27°C water, for 6 min. For the tail suspension test, mice were suspended from their tails for 5 min, held in place by a strip

of masking tape placed ~1.5 inches from the base of the tail. Sessions were recorded for both tests, and immobility time and episodes were assessed using the ANY-Maze Software. For the forced swim test, only data obtained after the initial 2 min of the test were used for the analysis.

2.3.10 Rotarod

The rotarod task was conducted as described previously to assess motor learning and acrobatic motor skill (Prado et al., 2006; de Castro et al., 2009a).

2.3.11 Locomotor activity

Spontaneous locomotor activity in a new environment to determine exploratory behavior was recorded using automated locomotor boxes essentially as described previously (Guzman et al., 2013).

2.3.12 Spontaneous alternations Y-maze

The spontaneous alternations Y-maze task to investigate working memory was performed using a symmetrical, three-armed Y-maze as described previously (de Castro et al., 2009a). All sessions were recorded. Both the order and the number of arm entries were recorded. A spontaneous alternation was counted when the mouse visited all three arms in a row without revisiting a previous arm.

2.3.13 Barnes maze

Barnes maze testing to determine spatial memory was performed as described previously (Patil et al., 2009; Martyn et al., 2012) using a white circular platform (92 cm in diameter) with 20 equally spaced holes (5 cm in diameter; 7.5 cm between holes), elevated 105 cm above the floor (San Diego Instruments), and spatial cues (posters, streamers, and plastic props) were placed around the maze. Briefly, animals were given four training trials a day for 4 d, with a 15 min intertrial interval (ITI). On the fifth day, memory was assessed via a probe trial. The probe trial consisted of barring access to

the target hole and assessing nose pokes to the holes within the target quadrant. Sessions were recorded and analyzed using the ANY-Maze Software.

2.3.14 Morris water maze

The spatial version of the Morris water maze (MWM) was conducted as described previously to investigate spatial memory (Vorhees and Williams, 2006; Martyn et al., 2012). Briefly, animals were given four training trials a day (90 s each) for 4 d, with a 15 min ITI. If the mice did not find the platform after 90 s during the learning phase, they were gently directed to the platform. On the fifth day, memory was assessed via a probe trial (60 s), during which the platform is removed and time spent in the target quadrant is measured. The task was performed in a 1.5-m-diameter pool with 25°C water. The platform was submerged 1 cm below the surface of the water, and spatial cues (posters, streamers, and plastic props) were distributed around the pool. Sessions were recorded and analyzed using the ANY-Maze Software.

Both the two-trial and cued variations of the MWM were performed as described previously (Vorhees and Williams, 2006). Briefly, for the two-trial variation, used to assess working or trial-dependent learning and memory, mice were tested over the course of 8 d. The mouse was first given a 90 s trial, and then after a 15 s ITI, the mouse was given a second trial with identical platform location and starting point. This was repeated with four unique starting location/platform location combinations a day. As for the cued variation, used to assess goal-directed behavior, mice were tested for 2 d using novel platform and starting location combinations. For this variation, the platform was at water level and a cue was placed on it (a plastic block). Sessions were recorded for both tests and were analyzed using the ANY-Maze Software.

2.3.15 Five-choice serial reaction time task

The five-choice serial reaction time (5-CSRT) task is used to determine attention in mice (Robbins, 2002; Romberg et al., 2011). Mice were trained in the 5-CSRT in automated Bussey-Saksida Mouse Touch Screen Systems model 81426 (Campden Instruments Limited). Schedules were designed and data were collected using the ABET II Touch

software v.2.15 (Lafayette Instruments). Before being trained on the 5-CSRT task, mice were first put through a pretraining program. This consisted of first habituating the mouse to the testing chamber with the lights off for 15 min. The next day, the mouse was left in the chamber with the lights off for 20 min. At this time, the reward tray was primed with strawberry milkshake (Saputo Dairy Products), and a tone was played when the mouse entered the reward tray. Whenever the mouse returned to the reward tray, it received a reward paired with the tone. This was repeated the next 2 d for 40 min sessions (phase 1).

The next training phase (phase 2) involved pairing the reward with presentation of the stimulus (flash of light in one of the five windows) on the touchscreen. The stimulus appeared randomly, and, after 30 s, it was removed and a reward was given paired with a tone. If the mouse touched the screen while stimulus was displayed, it immediately received a reward. Once the mouse collected the reward, a new trial was initiated. This phase was repeated until the mouse completed 30 trials within 60 min (phase 2).

To further shape behavior, phase 3 involved displaying the stimulus randomly in one of the windows. The mouse had to touch the stimulus on the screen to receive a reward paired with a tone. There was no response to the mouse touching anything but the stimulus. Once again, this was repeated until the mouse completed 30 trials within 60 min. The next phase (phase 4) was identical to phase 3 except that the mouse had to initiate each trial by nose poking the reward tray. Criterion was 30 correct trials within 60 min.

Finally, in the last pre-training phase (phase 5), the previous procedure was repeated, but if the mouse touched an incorrect screen, it received a 5 s timeout, during which the chamber light was turned on. The final phase had a stricter criterion, requiring the mice to perform 30 trials in 60 min with 23 correct responses in 2 consecutive days.

For the 5-CSRT training phase, mice were trained to respond to brief flashes of light pseudo randomly displayed in one of the five spatial locations on the touchscreen. Each trial was initiated after the mouse poked the magazine. In this phase, the stimulus was delivered after a variable 5–10 s delay (delay period), during which the animal was required to attend to the screen. In case the mouse prematurely touched the screen

during this delay, the response was recorded as premature and the mouse was punished with a 10 s timeout. The stimulus duration was initially set to 4 s, followed by a limited holding period of 5 s, during which the stimulus was absent but the mouse could still respond to the location (holding period). Each session lasted 50 trials or 1 h. Responses to the stimulus window during stimulus presence or the holding period were recorded as correct, whereas responses to any other window were recorded as incorrect. A correct choice was rewarded with a tone and food delivery. An incorrect response was punished with a 10 s timeout. A failure to respond to any window either during stimulus display or the holding period was recorded as an omission, and the mouse was punished with a 10 s timeout. Perseverative responses to the screen after premature, correct, and incorrect choices were also recorded. Our initial goal was to have the performance of a mouse reaching criterion at 4 s stimulus duration (80% accuracy, 20% omissions for 3 consecutive days) and reduce the stimulus duration to 2 s. However, ChAT–ChR2–EYFP BAC mice were not able to reach criterion at 4 s stimulus duration. Therefore, we used another training procedure, that is, the same cohort of mice was trained in a 16 s stimulus duration, and when they reached criterion, the stimulus duration was reduced to 8 s. After reaching criterion with the 8 s stimulus, the mice were tested 2 more days, and the mean measures of those additional 2 d were used to assess baseline performance.

After finishing training at 8 s stimulus duration, mice were probed for attentional deficits in the following probe trial schedule: each mouse was tested over two sessions at a given stimulus duration (4 and 2 s). Between each different stimulus duration, the mouse was returned to an 8 s stimulus duration for two baseline sessions. The order of the probe trial sessions was semi randomized using a Latin square method.

On all 5-CSRT task sessions, accuracy was defined as the total number of correct responses divided by the number of correct and incorrect responses (touches to a wrong window while the correct stimulus was still displayed). Rate of omissions were the proportion of omitted responses to total trials. Response latency was the time for the mouse to touch the correct stimulus from its onset. Reward collection latency was the time for the mouse to return to the reward tray once it had touched the correct stimulus.

A premature response was counted when the mouse touched one of the windows before stimulus onset. Finally, a perseverative response was any identical response that occurred after a correct, incorrect, or premature response.

2.3.16 Statistical analyses

Data are expressed as mean $\pm$ SEM. SigmaStat 3.5 software was used for statistical analysis. Comparison between two experimental groups was done by Student's t test or Mann–Whitney rank-sum test when the data did not follow a normal distribution. When several experimental groups or treatments were analyzed, two-way ANOVA or two-way repeated-measures (RM) ANOVA were used as required. When appropriate, a Tukey's HSD post hoc comparison test was used.

2.4 Results

2.4.1 Increased levels of VACHT in the ChAT–ChR2–EYFP BAC mice

Immunofluorescence analysis confirmed previous findings that ChR2–EYFP is highly expressed in different areas of the brain (Zhao et al., 2011), including the striatum and basal forebrain (Fig. 2.1A), as well as interpeduncular nucleus and brainstem motor nuclei (data not shown). qPCR assays showed that ChAT–ChR2–EYFP mice contain ~56 copies of the VACHT gene and 54 copies of the YFP gene (Fig. 2.1B), suggesting that close to 50 copies of the ChAT–BAC were inserted in the mouse genome. RT-qPCR data indicate that these additional copies of the VACHT gene are functional because VACHT mRNA was increased almost 20-fold in the striatum of ChAT–ChR2–EYFP mice when compared with controls; importantly, expression of ChAT, as expected, was not changed (Fig. 2.1C). This increased VACHT mRNA level is consistent with the elevated copy number of ChAT–ChR2–EYFP BAC. Expression of the VACHT protein is also increased (Fig. 2.1D) in this mouse line. In the hippocampus, there is a 550% increase in VACHT protein levels, whereas in the brainstem, VACHT levels are augmented by 350% when compared with control littermates (Fig. 2.1D). Expression of the ChAT protein was unaltered in both brain regions (Fig. 2.1E).

Importantly, increased expression of VACHT protein had functional consequences, because ChAT–Chr2–EYFP BAC mice presented threefold to fourfold increase in the release of newly synthesized [3H]ACh from hippocampal slices (Fig. 2.1F). Moreover, BAC transgenic expression of VACHT was able to rescue postnatal lethality attributable to VACHT elimination. We crossed ChAT–Chr2–EYFP with VACHTdel/wt [heterozygous VACHT knock-out (de Castro et al., 2009b)] mice and then intercrossed heterozygous littermates to obtain ChAT–Chr2–EYFP VACHTdel/del. Screening of the offspring was done by qPCR of the VACHT del allele (de Castro et al., 2009b). Our data show that ChAT–Chr2–EYFP VACHTdel/del mice are viable and survive to adulthood (Table 1).

Figure 2.1- Overexpression of VACHT in ChAT–ChR2–EYFP mice. A, YFP expression in the CNS of ChAT–ChR2–EYFP mice (n = 3). B, VACHT and YFP gene copy numbers determined by genomic qPCR (n = 5). C, VACHT and ChAT mRNA expression in the striatum of wild-type and transgenic mice (n = 6 for both genotypes). D, VACHT protein expression in the hippocampus and brainstem with representative immunoblots (n = 3 for both genotypes). E, ChAT protein expression in the hippocampus and brainstem with representative immunoblots (n = 3 for both genotypes). F, Release of newly synthesized ACh in hippocampal slices (n = 4 for both genotypes). *p < 0.05, **p < 0.01, ***p < 0.001.

Figure 2.1- Overexpression of VACht in ChAT-ChR2-EYFP mice.

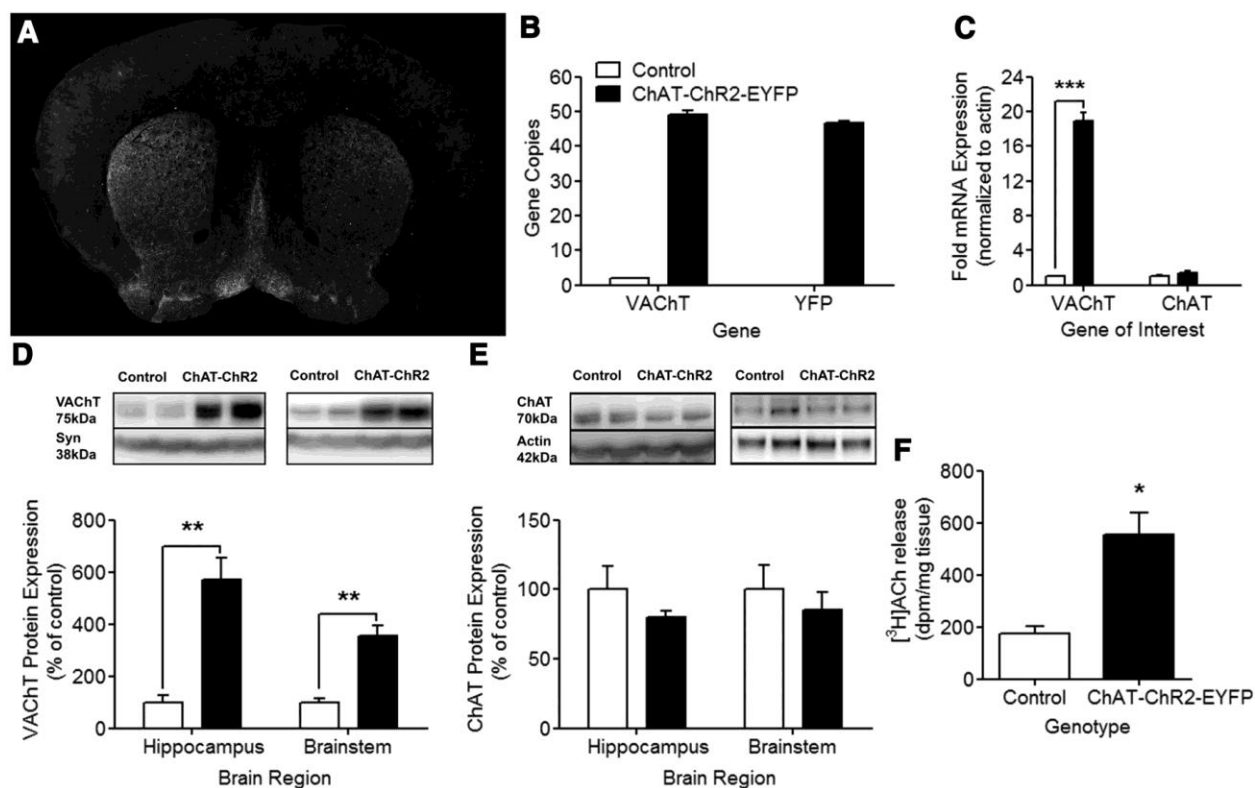


Table 2.1. Rescue of lethality in VACHTdel/del mice. ChAT–ChR2–EYFP mice were crossed to VACHTdel/wt mice and offspring were then intercrossed. Genomic qPCR using primers that amplify the VACHTdel allele was used to identify live VACHTdel/del mice containing the ChaT BAC.

Table 2.1. Rescue of lethality in VACHTdel/del mice.

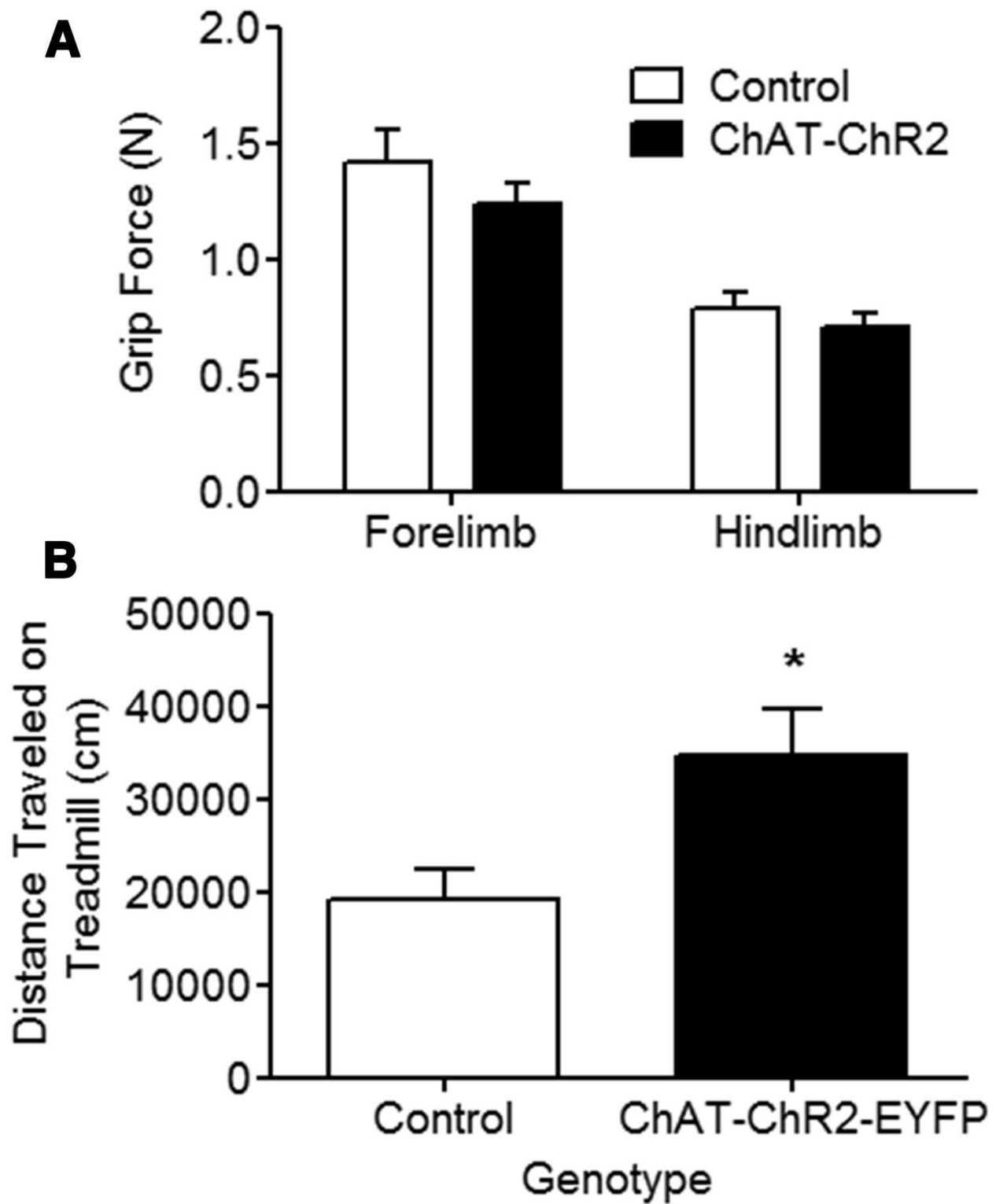
Genotype	Number of mice born
<i>VACHT^{wt/wt}</i>	2
<i>VACHT^{wt/del}</i>	7
<i>ChAT-ChR2-EYFP VACHT^{wt/del}</i>	10
<i>ChAT-ChR2-EYFP VACHT^{del/del}</i>	4
<i>ChAT-ChR2-EYFP VACHT^{wt/wt}</i>	6
Total	29

2.4.2 ChAT–ChR2–EYFP mice have improved motor endurance

To assess neuromuscular function in ChAT–ChR2–EYFP mice, both forelimb and hindlimb grip strength were measured, but there was no statistical difference between ChAT–ChR2–EYFP mice and control littermates (Fig. 2.2A). In contrast, ChAT–ChR2–EYFP mice performed much better than wild-type controls in the treadmill. By using a protocol designed to determine physical fitness, we observed that ChAT–ChR2–EYFP mice were able to run almost twice as much compared with control mice ($t(14) = 2.497$, $p = 0.0256$; Fig. 2.2B).

Figure 2.2 ChAT–ChR2–EYFP mice have increased physical endurance. A, Grip force in wild-type and transgenic mice. B, Treadmill analysis of physical endurance in wild-type and transgenic mice (* $p < 0.05$, $n = 8$ for both genotypes).

Figure 2.2 ChAT-ChR2-EYFP mice have increased physical endurance.

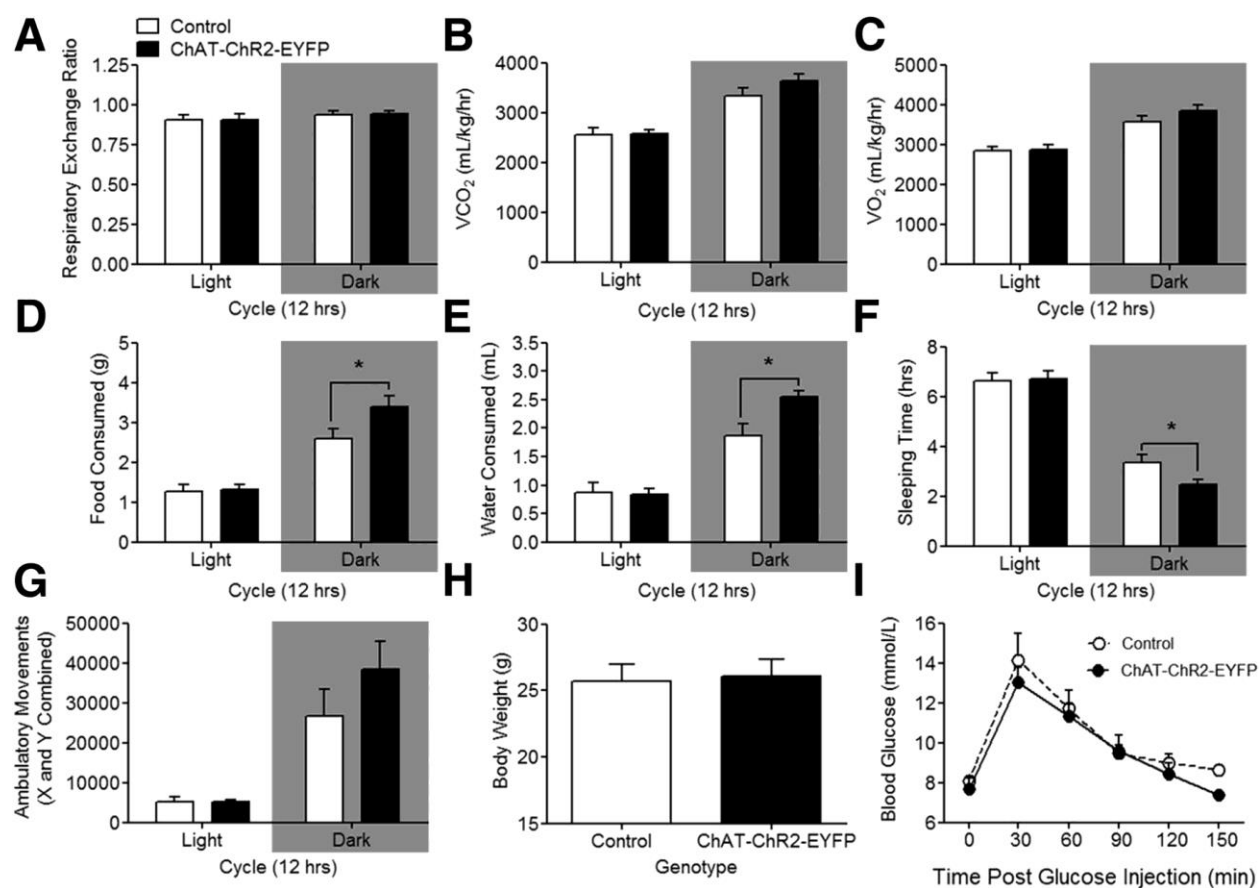


2.4.3 ChAT–ChR2–EYFP mice do not present gross alterations in metabolism

To investigate whether increased copy numbers of VACHT affects homeostasis, transgenic ChAT–ChR2–EYFP mice were assessed in metabolic cages. Transgenic mice had body weight statistically similar to controls ($t(14) = 0.6920$, $p = 0.500$; Fig. 2.3). These mice presented similar metabolic profiles as controls, with no statistical differences in RER, in the light ($t(14) = 0.9898$, $p = 0.831$) or the dark ($t(14) = 0.5414$, $p = 0.702$) cycles (Fig. 2.3A). They did not consume more O₂ during the light cycle ($t(14) = 0.1897$, $p = 0.8523$) or dark cycle ($t(14) = 1.402$, $p = 0.1828$; Fig. 2.3B). Similar results were obtained for CO₂ release during the light ($t(14) = 0.09952$, $p = 0.9221$) or dark ($t(14) = 1.462$, $p = 0.1658$) cycle (Fig. 2.3C). Likewise, locomotor activity, sleep time, or blood glucose levels were not significantly altered in this transgenic mouse line (Fig. 2.3). Interestingly, ChAT–ChR2–EYFP mice consumed both more food and water during the dark cycle than control mice (food consumption, $t(14) = 2.212$, $p = 0.0441$; water consumption, $t(14) = 2.878$, $p = 0.0122$; Fig. 2.3D,E).

Figure 2.3. Metabolic analysis in ChAT–ChR2–EYFP mice. A, Respiratory exchange rate analysis. B, VCO₂ consumption. C, VO₂. D, Food consumption. E, Water consumption. F, Sleep time. G, Home cage activity. H, Body weight at time of analysis. I, Glucose tolerance test. * $p < 0.05$, $n = 8$ for both genotypes.

Figure 2.3. Metabolic analysis in ChAT-ChR2-EYFP mice.

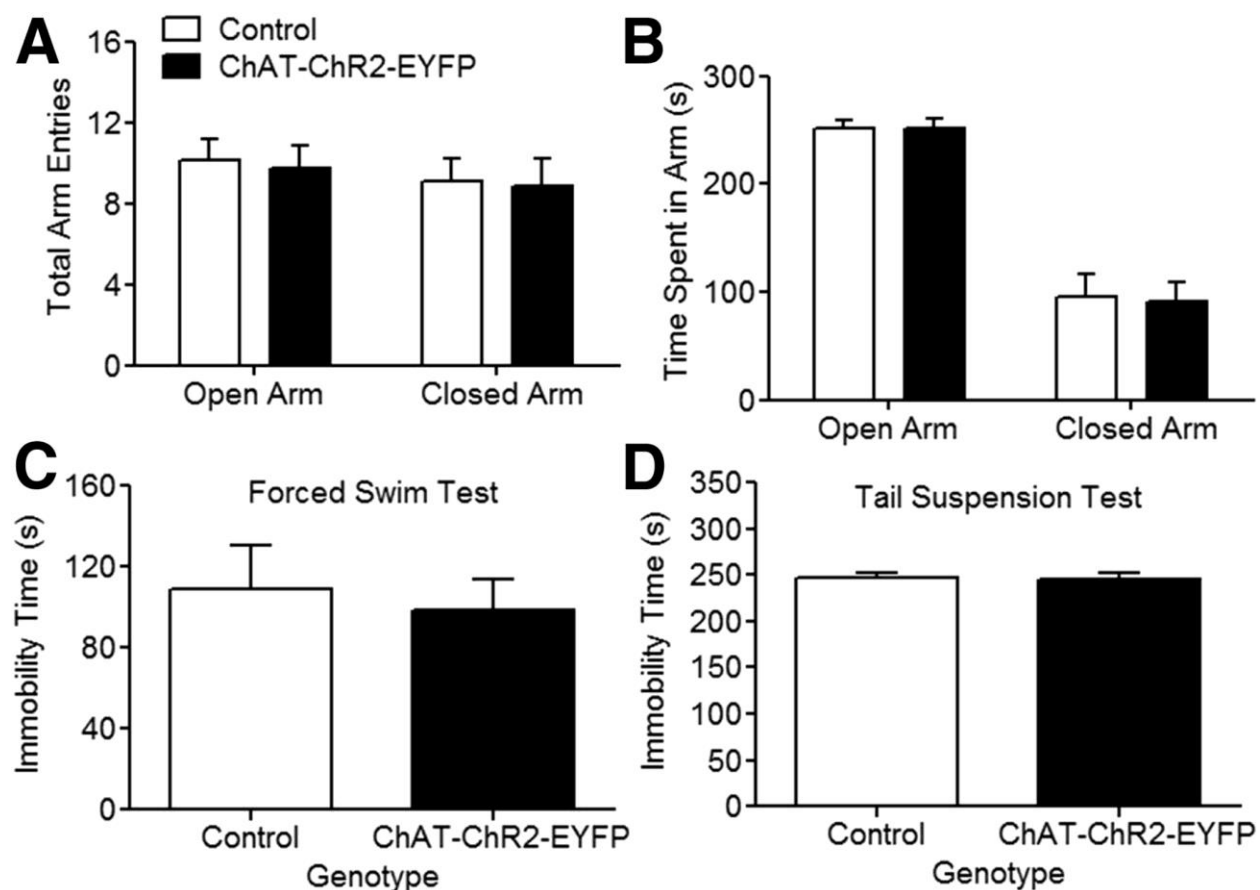


2.4.4 ChAT–ChR2–EYFP mice do not present anxiety or depression-like behavior

We tested ChAT–ChR2–EYFP mice for anxiety using the elevated plus maze paradigm. These mice visited the open ($t(14) = 0.2304$, $p = 0.8211$) or closed ($t(14) = 0.1365$, $p = 0.8934$) arms at rates statistically comparable with those observed in controls (Fig. 2.4A). In addition, they did not spend more time than controls in the open ($t(14) = 0.2304$, $p = 0.8211$) or closed ($t(14) = 0.1314$, $p = 0.8973$) arms (Fig. 2.4B). ChAT–ChR2–EYFP mice were also tested for depressive-like behavior using both the tail suspension and forced swim tests and presented no statistical difference from wild-type controls (swim test, $t(14) = 0.4016$, $p = 0.6941$; tail suspension, $t(14) = 0.04468$, $p = 0.9650$; Fig. 2.3C,D, respectively).

Figure 2.4. Assessment of anxiety and depressive-like behavior in ChAT–ChR2–EYFP mice. A, Number of arm entries in the elevated plus maze. B, Time spent in the open and closed arms. C, Immobility time in the forced swimming test. D, Immobility time in the tail suspension test (n = 8 for both genotypes).

Figure 2.4. Assessment of anxiety and depressive-like behavior in ChAT-ChR2-EYFP mice.



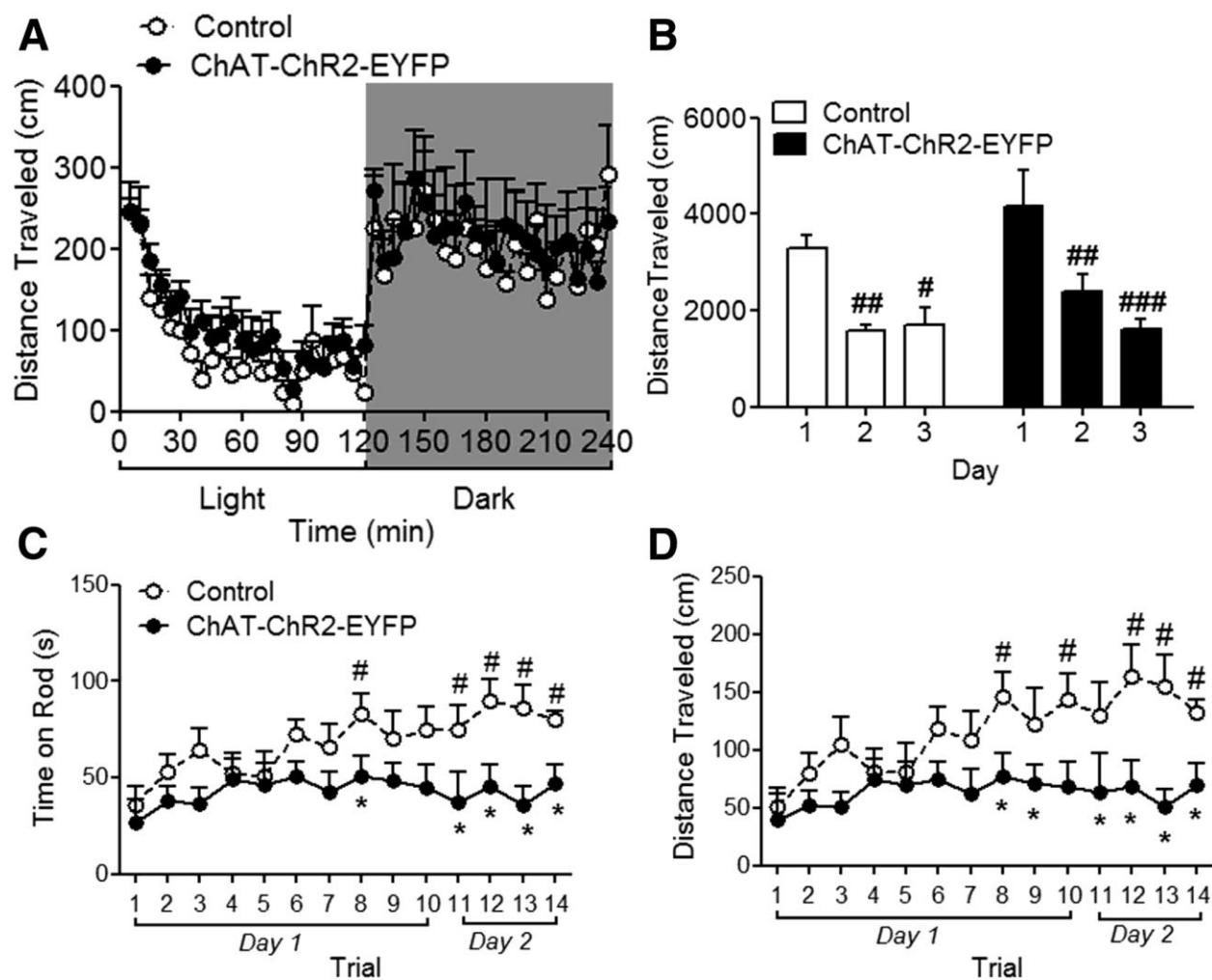
2.4.5 ChAT–ChR2–EYFP mice show normal locomotion but have impaired motor learning

We assessed locomotor activity in ChAT–ChR2–EYFP mice using an automated novel open-field environment for 4 h: 2 h in the light and 2 h in the dark. No statistical differences in locomotor activity were observed between genotypes ($F(1,658) = 0.2468$, $p = 0.6271$; Fig. 2.5A). There was no interaction between time $\times$ genotype ($F(47,658) = 0.4313$, $p = 0.9997$), with both genotypes significantly reducing their locomotor activity during the course of the test in the light phase ($F(47,658) = 9.725$, $p < 0.0001$). Moreover, habituation in the open field was not affected in ChAT–ChR2–EYFP mice [Fig. 2.5B; two-way RM-ANOVA shows a significant effect of day ($F(2,42) = 15.07$, $p < 0.0001$), no effect of genotype ($F(1,42) = 2.653$, $p = 0.1108$), and no interaction ($F(2,42) = 0.880$, $p = 0.4225$)].

Knowing that transgenic mice have increased endurance and no overt deficits in locomotor behavior, the accelerating rotarod task was used to assess motor learning. Surprisingly, the ChAT–ChR2–EYFP mice failed to improve their performance in the rotarod, whereas wild-type control mice improved the time spent on the rotarod as well as distance traveled [Fig. 2.5C,D; two-way RM-ANOVA revealed main effect of genotype ($F(1,182) = 6.015$, $p = 0.0279$) and trial ($F(13,182) = 2.796$, $p = 0.0012$)]. Post hoc analysis confirmed that the ChAT–ChR2–EYFP mice did not significantly improve their performance from their first trial.

Figure 2.5. ChAT–ChR2–EYFP mice have normal locomotor activity but impaired motor learning. A, Locomotor activity of wild-type or ChAT–ChR2–EYFP mice during the light (2 h) and dark (2 h) activity periods in an open arm. The test was done from 5:00 P.M. to 9:00 P.M. B, Habituation in the open field. C, Acrobatic motor performance and motor learning in the rotarod. Time spent on the rod. D, Distance traveled in the rotarod (* $p < 0.05$, significant difference between genotypes; # $p < 0.05$, ## $p < 0.01$, ### $p < 0.001$, significant difference within genotype; $n = 8$ for both genotypes).

Figure 2.5. ChAT-ChR2-EYFP mice have normal locomotor activity but impaired motor learning.



2.4.6 ChAT–ChR2–EYFP mice have impaired spatial memory

To assess other forms of learning, we tested spatial learning and memory in the ChAT–ChR2–EYFP mice using the Barnes maze and MWM. During the acquisition phase of the Barnes maze, there were no statistical differences for the performance between the two genotypes. The two groups made a similar number of errors before reaching the target hole ($F(1,42) = 0.2685$, $p = 0.6124$; Fig. 2.6A). In contrast, during the probe trial, on day 5, ChAT–ChR2–EYFP mice visited the target hole location significantly less than controls ($t(14) = 3.360$, $p = 0.0047$; Fig. 2.6B) and showed a significantly decreased preference for the target hole, as defined by the target hole preference index [target hole visits/mean visits per hole (Holmes et al., 2002), $t(14) = 2.712$, $p = 0.0168$; Fig. 2.6C]. Although both genotypes showed a significant effect of the hole location during the probe trial ($F(1,154) = 26.66$, $p = 0.001$), there was a significant effect of genotype ($F(1,154) = 11.29$, $p = 0.047$) and a significant genotype $\times$ hole location effect ($F(1,154) = 2.819$, $p = 0.022$). Post hoc analysis revealed that wild-type mice preferred the target hole, whereas ChAT–ChR2–EYFP mice did not (Fig. 2.6D,E). Representative traces of two controls (Fig. 2.6F) and two ChAT–ChR2–EYFP mice (Fig. 2.6G) show the performance of the two genotypes in this task.

To further determine the mechanisms involved with potential spatial memory deficits, the MWM was used. Once again during the course of acquisition, the performance of ChAT–ChR2–EYFP mice was indistinguishable from that of controls in terms of latency to find the target ($F(1,42) = 0.8933$, $p = 0.3606$) and the distance traveled to the target ($F(1,42) = 2.783$, $p = 0.1175$; Fig. 2.7A–C). Mutants learned the location of the platform similar to control mice, confirming the observations using the Barnes maze. These results indicate that the ChAT–ChR2–EYFP mice do not have any gross sensorimotor deficits and were able to use the cues to learn the task. However, on the probe trial day, ChAT–ChR2–EYFP mice showed no preference for the target quadrant of the pool (Fig. 2.7D). The occupancy plots in the MWM on the probe trial show that the controls clearly remembered where the platform should be (Fig. 2.7E). In contrast, ChAT–ChR2–EYFP mice did not seem to retrieve this information during the probe trial (Fig. 2.7F).

Figure 2.6. ChAT–Chr2–EYFP mice have spatial memory deficits in the Barnes

maze. Mice were subject to the Barnes maze paradigm, and the average values of four 3-min trials per day are plotted. A, Number of errors before finding the target hole. B, Visits to the target hole during the day 5, 90 s probe trial. C, Preference for the target hole over other holes during the probe trial (target hole visits/average nontarget visits). D, Nose pokes per hole were measured on day 5 in a 90 s probe trial for control mice. T, Target hole. Numbers refer to the location of holes adjacent to the target hole. Op, Opposite hole. E, ChAT–Chr2–EYFP mice. F, Representative path tracings for two control mice during the probe trial (target quadrant highlighted; T). G, Same as in F but for ChAT–Chr2–EYFP mice. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, $n = 8$ for both genotypes.

Figure 2.6. ChAT-ChR2-EYFP mice have spatial memory deficits in the Barnes maze.

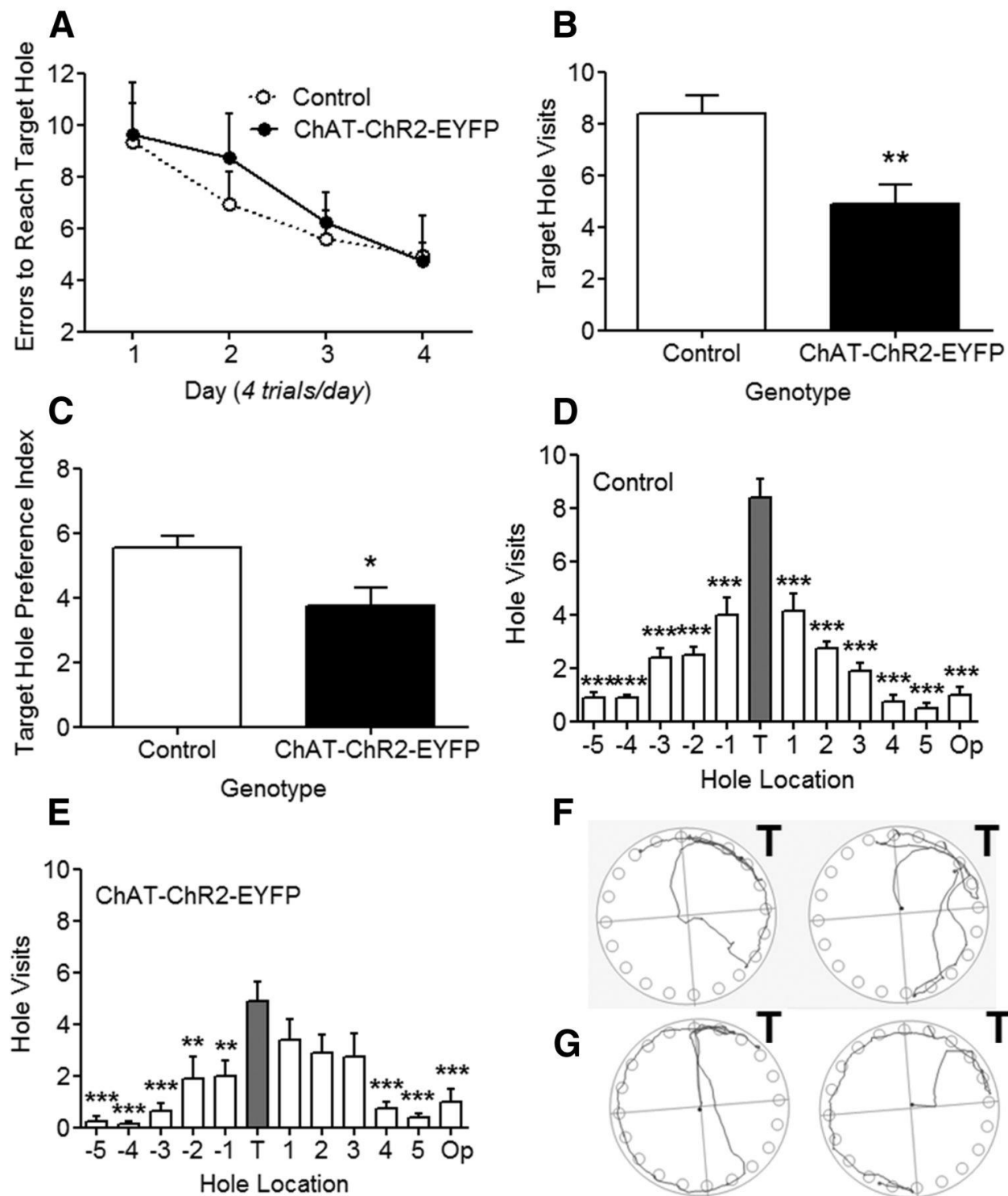
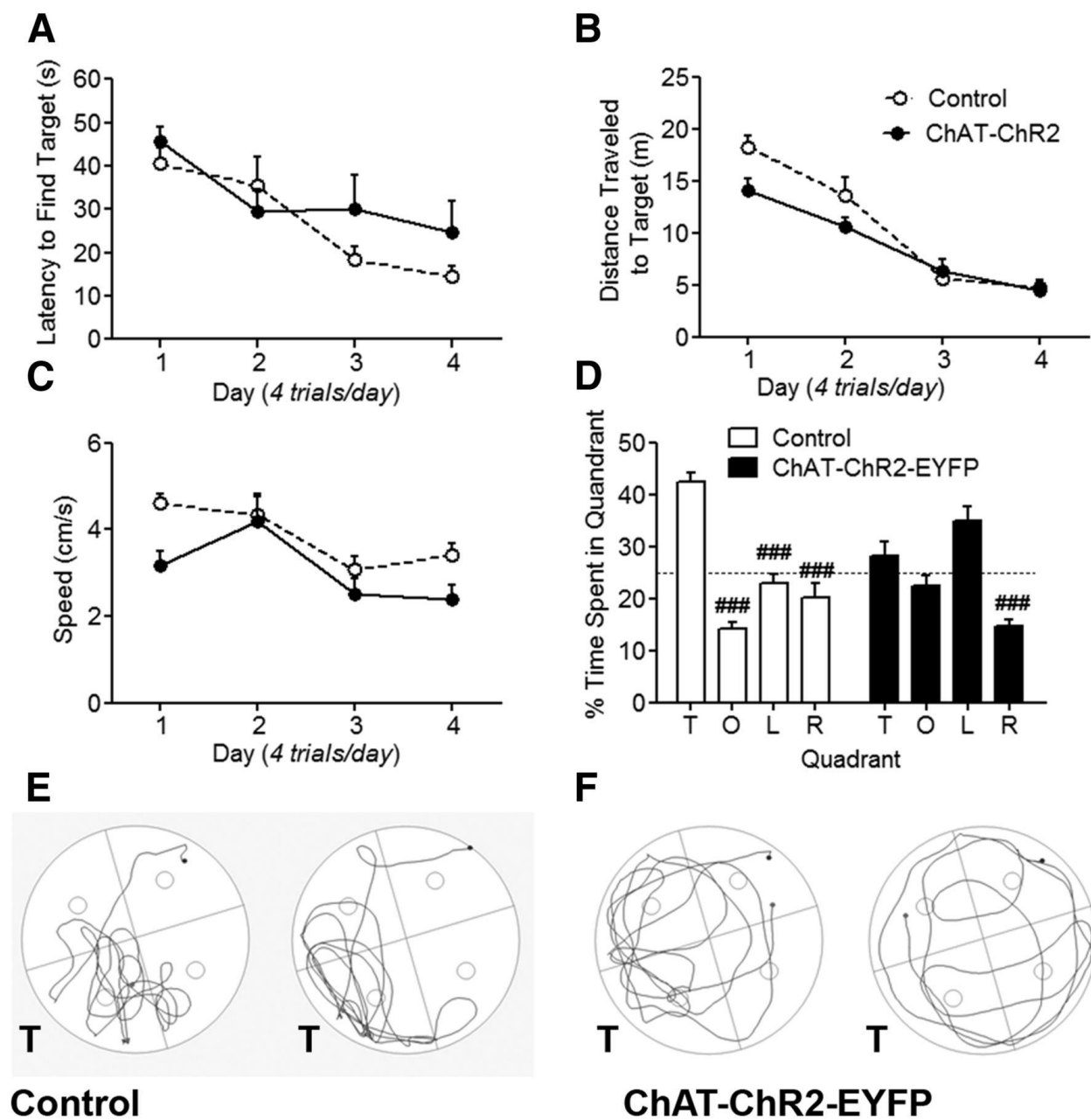


Figure 2.7. ChAT–ChR2–EYFP mice have spatial memory deficits in the MWM.

Mice were subject to the MWM paradigm, and the average values of four 90-s trials per day are plotted. A, Latency to find the platform. B, Distance traveled to the platform. C, Mouse speed. D, Percentage time spent per quadrant was measured on day 5 in a 60 s probe trial with the platform removed. E, Representative occupancy plots for two control mice. F, Representative occupancy plots for two ChAT–ChR2–EYFP mice during the probe trial (T indicates the location of the target quadrant). #### $p < 0.001$, significant difference within genotype, $n = 8$ for both genotypes. L, Left; O, opposite; R, right; T, target.

Figure 2.7. ChAT-ChR2-EYFP mice have spatial memory deficits in the MWM.

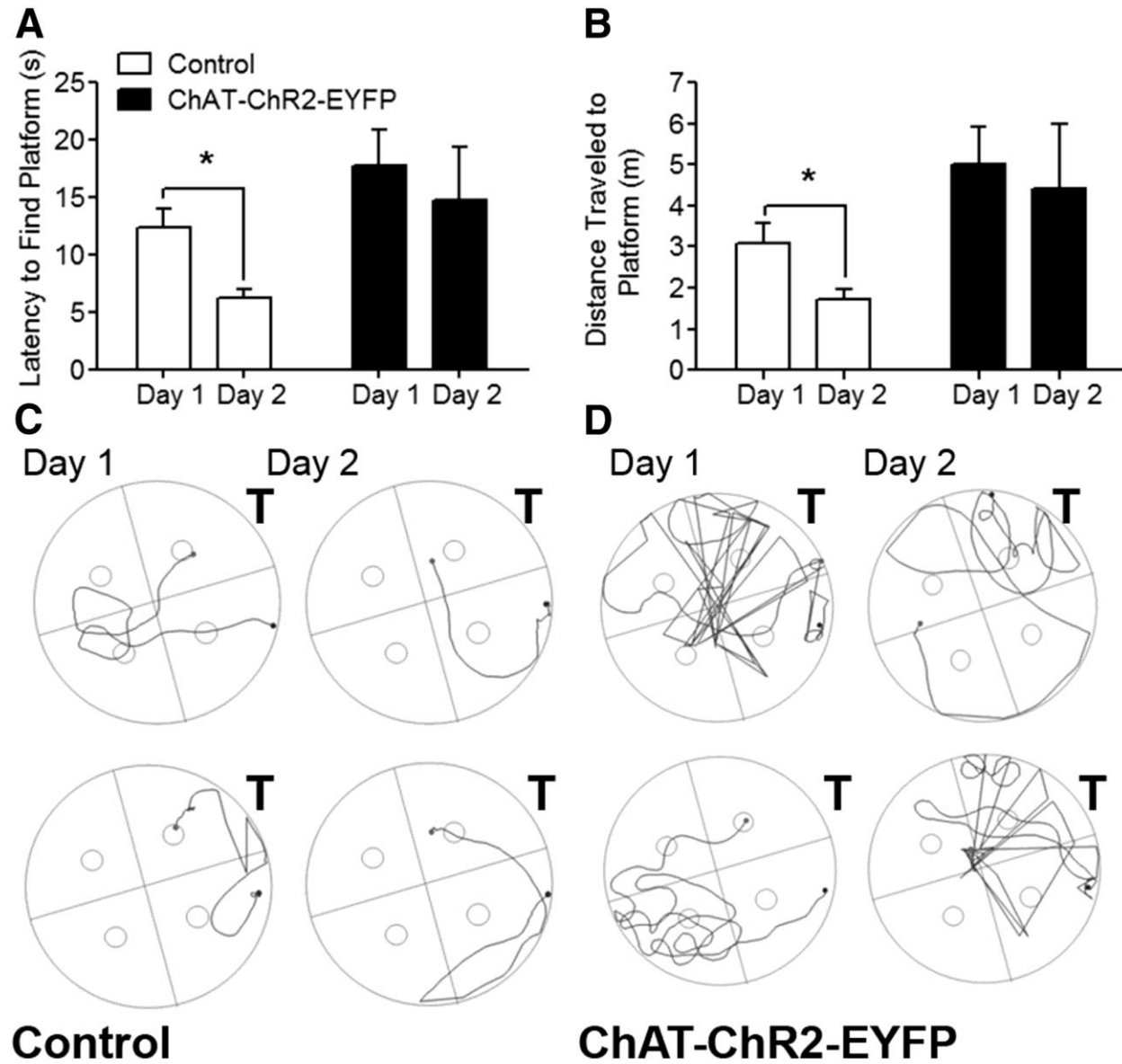


2.4.7 ChAT–ChR2–EYFP mice have deficiencies in cue-directed memory

To assess cue-driven learning in these mice, the cued version of the MWM was used (Vorhees and Williams, 2006). There was a significant difference between genotypes ($F(1,14) = 5.262$, $p = 0.0378$) and a significant effect of day ($F(1,14) = 7.834$, $p = 0.0142$) in terms of latency to find the target (Fig. 2.8A). Post hoc analysis confirmed that control mice improved their performance from day 1 to day 2, whereas ChAT–ChR2–EYFP mice did not (Fig. 2.8A). There was a trend for ChAT–ChR2–EYFP mice to swim a greater distance to the target (Fig. 2.8B), but this failed to reach significance ($F(1,14) = 7.834$, $p = 0.0861$). A closer examination of the path traces revealed that ChAT–ChR2–EYFP mice do not seem to use the cue to find the target on the second day (Fig. 2.8C,D).

Figure 2.8. ChAT–ChR2–EYFP mice have deficits in cue memory. Mice were subject to the cued version of the MWM in which they had to associate the platform with a cue. A, Primary latency to find the platform. B, Distance traveled to the platform. C, Representative path tracings to the target of two control mice. D, Representative path tracings to the target of two ChAT–ChR2–EYFP mice. Traces are from the second trial on the first and second days of the experiment, with T indicating the location of the platform. The average of four 90-s trials per day is plotted. * $p < 0.05$, $n = 8$ for both genotypes.

Figure 2.8. ChAT-ChR2-EYFP mice have deficits in cue memory.



2.4.8 ChAT–Chr2–EYFP have impaired working memory

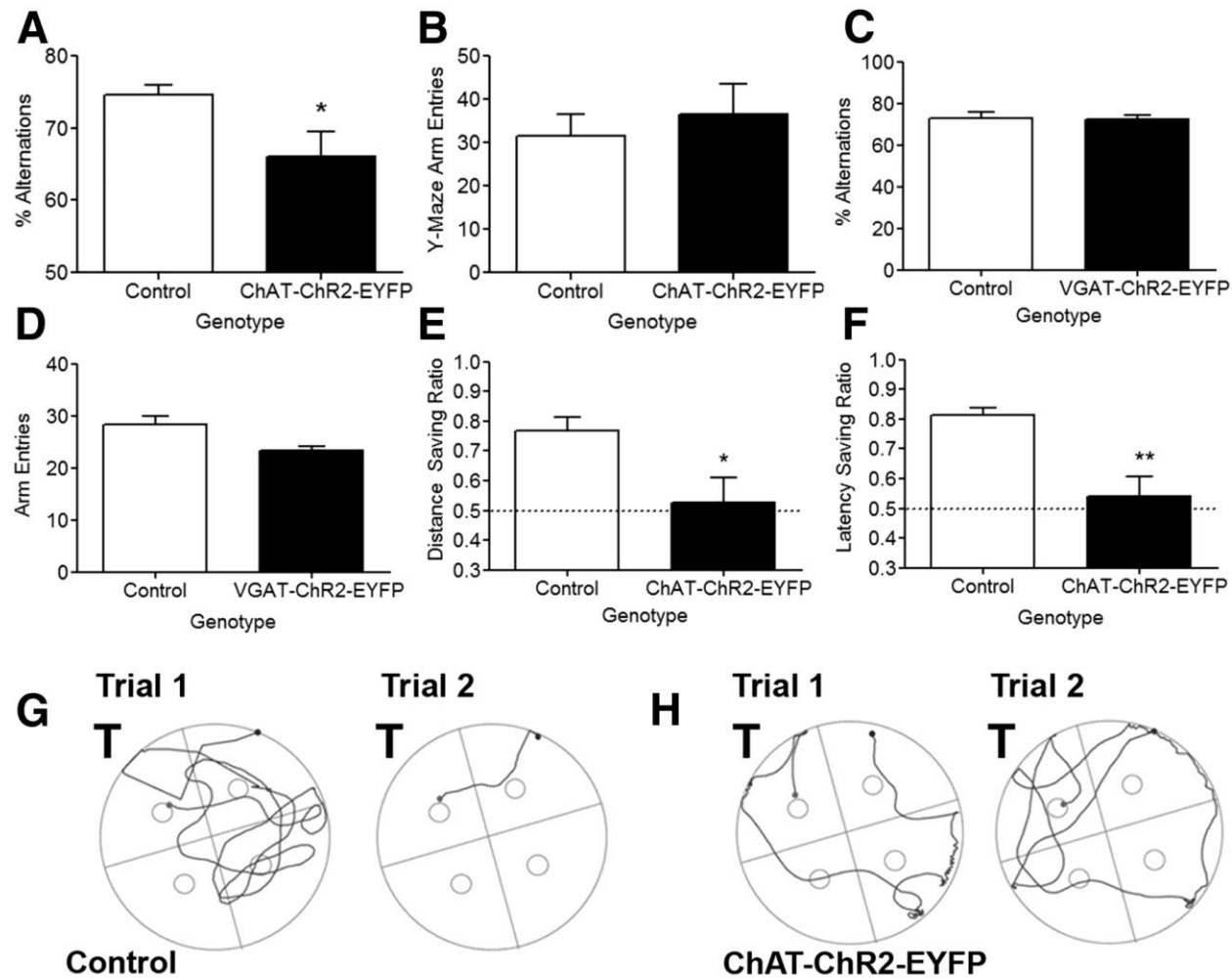
The above experiments suggest that ChAT–Chr2–EYFP mice can learn the spatial version of the MWM, but they have difficulty retrieving that memory trace. Moreover, these transgenic mice show impaired motor learning and cued-driven learning. These results suggest the possibility that chronically increased cholinergic tone disturbs distinct forms of information processing. To evaluate working memory, we first used spontaneous alternations in the Y-maze (de Castro et al., 2009a). In contrast to results obtained with littermate control mice, ChAT–Chr2–EYFP mice revisited the arms of the Y-maze more often, showing significantly less spontaneous alternations ($t(14) = 2.448$, $p = 0.0293$; Fig. 2.9A). The number of arm entries was not affected ($t(14) = 0.6031$, $p = 0.5568$; Fig. 2.9B), nor was distance traveled ($t(14) = 0.5620$, $p = 0.5837$; data not shown). However, performance of ChAT–Chr2–EYFP mice was above chance (>50%) regarding alternations, suggesting that these mice had a partial dysfunction on their working memory. To exclude the possibility that the cognitive deficits observed could be related to the introduction of Chr2 or EYFP, we also tested VGAT–Chr2–EYFP and their littermate controls in the Y-maze alternation. qPCR analysis showed that these mice had ~20 copies of EYFP and therefore 20 copies of the Chr2 gene. Distinct from ChAT–Chr2–EYFP mice, VGAT–Chr2–EYFP mice did not differ statistically from their littermate controls in terms of either spontaneous alternations ($t(10) = 0.1914$, $p = 0.8520$; Fig. 2.9C) or number of arm entries ($t(10) = 1.562$, $p = 0.1494$; Fig. 2.9D).

To further probe working memory in ChAT–Chr2–EYFP mice, the two-trial variation of the MWM was used (Vorhees and Williams, 2006). In this variation of the task, mice must first find a novel platform location by chance and then, after a 10 s ITI, find it again. To analyze mouse performance on this task, we used the latency and distance savings ratio to standardize data (Varvel and Lichtman, 2002). These ratios were calculated by dividing the distance traveled, or latency on the first trial by that on the sum of the first and second trials. Values >0.5 indicate improvement from the first to the second trial. ChAT–Chr2–EYFP mice had significantly lower distance savings ratio ($t(14) = 2.501$, $p = 0.0254$) and latency savings ratio ($t(14) = 3.684$, $p = 0.0025$; Fig.

2.9E–H) than control mice. Together, these results indicate that ChAT–ChR2–EYFP mice have impaired working memory.

Figure 2.9. ChAT–ChR2–EYFP mice have deficits in working memory. A, Spontaneous alternations in the Y-maze were used to assess working memory for ChAT–ChR2–EYFP mice. B, Number of arms visited for ChAT–ChR2–EYFP mice ($n = 8$ for both genotypes). C, Spontaneous alternations in the Y-maze for VGAT–ChR2–EYFP mice. D, Number of arms visited for VGAT–ChR2–EYFP mice. $n = 6$ for both genotypes. E, ChAT–ChR2–EYFP mice were subject to the two-trial MWM paradigm to further assess working memory. Savings ratios were calculated from the average of the first and second 90 s trials across all 4 d of the experiment. The graph shows the mean distance savings ratios. F, Latency saving ratio. G, Representative path tracings to the target for two control mice. H, Representative path tracings to the target for two ChAT–ChR2–EYFP mice. Traces are from the first and second trials during the third day of the experiment. T indicates the location of the platform. $*p < 0.05$, $**p < 0.01$, $n = 8$ for both genotypes.

Figure 2.9. ChAT-ChR2-EYFP mice have deficits in working memory.



2.4.9 ChAT–ChR2–EYFP mice have impaired attentional processing

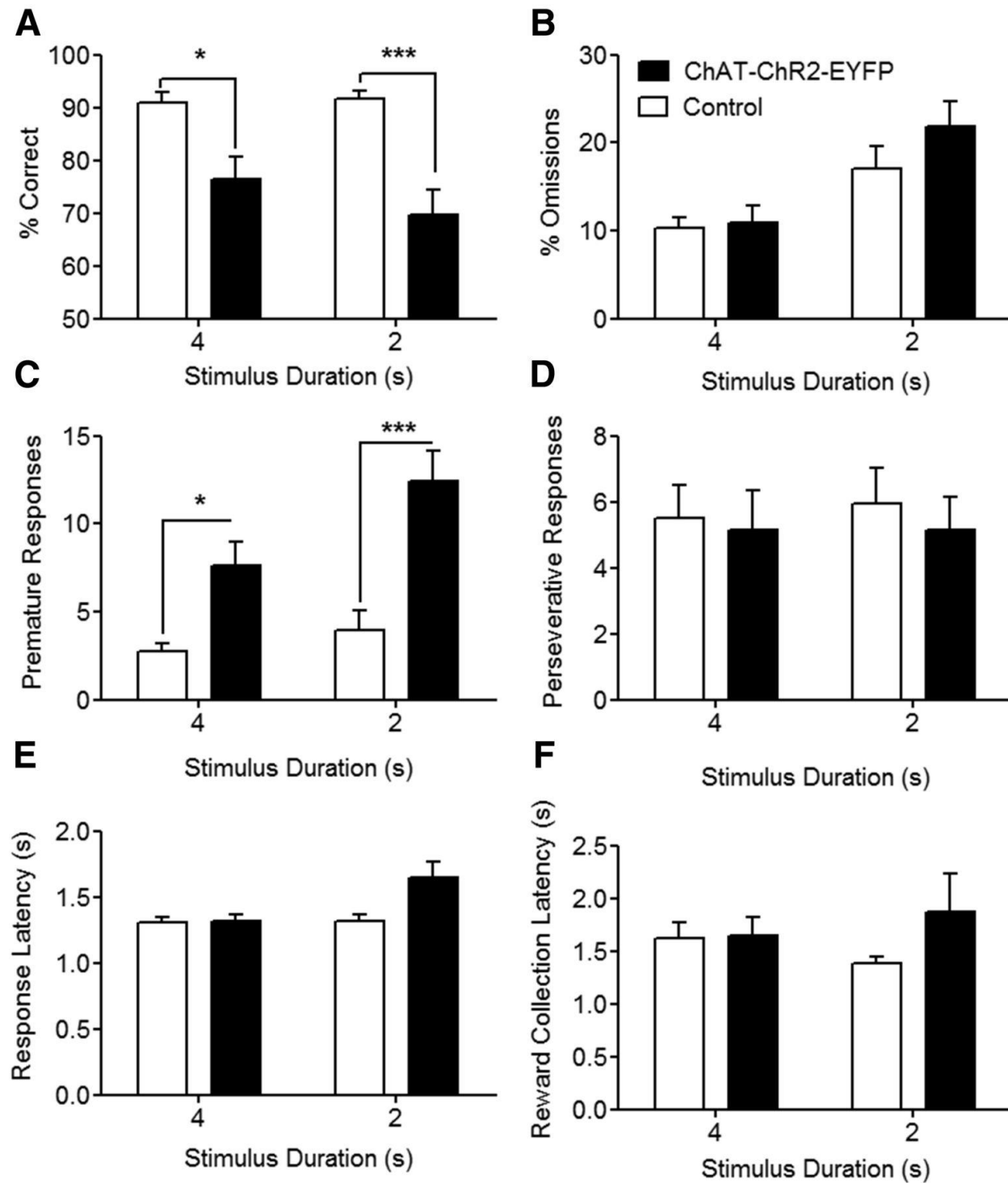
To determine whether ChAT–ChR2–EYFP mice may be affected in other cognitive domains that are sensitive to cholinergic tone and could contribute to the deficits we observed, we used the 5-CSRT task. During pretraining, transgenic mice did not differ from controls in terms of trials needed to achieve criterion [two-way RM-ANOVA; no effect of genotype ($F(1,48) = 0.6766$, $p = 0.4268$) and no effect of training phase ($F(4,48) = 2.306$, $p = 0.0717$)]. It should be noted that one mouse of each genotype never completed the pretraining and were not subjected to training in the 5-CSRT task. Our initial goal was to train mice first using a 4 s stimulus duration and then proceed to 2 s as described previously (Romberg et al., 2011). However, after 12 training sessions at 4 s stimulus duration, whereas all control mice reached criterion with an average of 10.28 ± 1.23 trials, all ChAT–ChR2–EYFP mice failed to acquire the task. Therefore, we increased the stimulus duration time (decreased the attentional demand) to 16 s and then 8 s to do the training. Probe trials were then performed with 4 and 2 s stimulus durations.

Under less demanding attentional conditions, ChAT–ChR2–EYFP mice were able to acquire the task, reaching criteria at both stimulus durations (16 and 8 s) in the same number of sessions as controls [two-way RM-ANOVA; no effect of genotype ($F(1,12) = 1.122$, $p = 0.3103$) and no effect of stimulus duration ($F(1,12) = 2.492$, $p = 0.1404$)]. However, during probe trials, ChAT–ChR2–EYFP mice showed significant impairments in choice accuracy [two-way RM-ANOVA; main effect of genotype ($F(1,12) = 29.86$, $p = 0.0001$) and no effect of stimulus duration ($F(1,12) = 0.6894$, $p = 0.4226$); Fig. 2.10A], with post hoc analysis showing that the ChAT–ChR2–EYFP mice had impaired accuracy at both stimulus durations. The rate of omissions for ChAT–ChR2–EYFP mice was unaffected [two-way RM-ANOVA; no effect of genotype ($F(1,12) = 1.928$, $p = 0.1902$) and main effect of stimulus duration ($F(1,12) = 13.79$, $p = 0.0030$); Fig. 2.10B]. Additionally, ChAT–ChR2–EYFP mice showed a significant increase in premature

responses [two-way RM-ANOVA; main effect of genotype ($F(1,12) = 21.74$, $p = 0.0005$) and main effect of stimulus duration ($F(1,12) = 7.657$, $p = 0.0171$); Fig. 2.10C]. Post hoc analysis revealed that the ChAT–ChR2–EYFP mice had more premature responses at each stimulus duration. No change in perseverative responses was observed in ChAT–ChR2–EYFP mice [two-way RM-ANOVA; no effect of genotype ($F(1,12) = 0.05002$, $p = 0.8268$) and no effect of stimulus duration ($F(1,12) = 0.6894$, $p = 0.4226$); Fig. 2.10D]. Importantly, there were no differences between genotypes in terms of response latency [two-way RM-ANOVA; no effect of genotype ($F(1,12) = 1.570$, $p = 0.2341$) and no effect of stimulus duration ($F(1,12) = 2.112$, $p = 0.1718$)] or reward collection latency [two-way RM-ANOVA; no effect of genotype ($F(1,12) = 1.082$, $p = 0.3189$) and no effect of stimulus duration ($F(1,12) = 0.001394$, $p = 0.9708$); Fig. 2.10E,F].

Figure 2.10. ChAT–ChR2–EYFP mice have deficits in attention. The 5-CSRT task was used to measure attention in the ChAT–ChR2–EYFP mice. A, Mean response accuracy during probe trial sessions. B, Rate of omissions. To assess response patterns, both premature (C) and perseverative (D) responses were monitored during probe trials. E, Mean response latency. F, Mean reward collection latency. * $p < 0.05$, *** $p < 0.001$, $n = 7$ for both genotypes.

Figure 10. ChAT-ChR2-EYFP mice have deficits in attention



2.5 Discussion

Here we report an extensive characterization of the BAC transgenic ChAT–ChR2–EYFP mouse line and reveal two major findings. First, there are several extra copies of the VACHT gene in this mouse line, which led to increased levels of functional transporter, increased release of ACh, and improvement of physical endurance. Second, it seems that this chronic increase in cholinergic tone is deleterious in the CNS, disrupting several distinct cognitive domains. Interestingly, increase in VACHT mRNA expression was approximately fourfold higher than increase in protein expression. This result suggests the existence of translational or posttranslational mechanisms limiting the availability of the VACHT protein in cholinergic neurons.

Vesicular storage of ACh is a required step for ACh release (de Castro et al., 2009b), and decreased VACHT expression leads to motor and cognitive dysfunctions (Prado et al., 2006; Martyn et al., 2012). Specifically, reduction of VACHT levels affects grip strength and fatigue; VACHT knockdown homozygous mice, with 70% reduction in VACHT levels, are unable to run in a treadmill test (Prado et al., 2006). In agreement with these early results, overexpression of the high-affinity choline transporter in motoneurons improves the performance of transgenic mice in the treadmill (Lund et al., 2010). The present results with ChAT–ChR2–EYFP mice further support the notion that physical fitness is related to changes in cholinergic synaptic activity. Increased VACHT levels allowed transgenic mice to run farther than control nontransgenic littermates on the treadmill. However, it is unknown whether the increase in motor endurance results only from increased VACHT levels in motoneurons because, in this mouse line, VACHT is likely to be overexpressed in all cholinergic nerve endings. Decreased VACHT expression in the periphery has been shown to affect cardiac activity by distinct mechanisms (Lara et al., 2010; Rocha-Resende et al., 2012; Roy et al., 2012; Prado et al., 2013). Thus, ChAT–ChR2–EYFP mice will be essential to determine whether increased VACHT expression can improve cardiovascular function.

Although a number of studies indicate that ACh is involved in the regulation of metabolic homeostasis (for review, see Picciotto et al., 2012), no significant difference between

ChAT–ChR2–EYFP and wild-type littermates was observed when an extensive list of metabolic parameters was analyzed, including RER, the volume of oxygen produced (VO₂), the volume of carbon dioxide produced (VCO₂), body weight, sleeping time, ambulatory movement, and serum glucose. However, our data show that ChAT–ChR2–EYFP mice consume significantly more food and water during the dark period. It is possible that the small increase in food and water intake observed in these transgenic mice reflects the fact that, in the home-cage-like environment, they have a small tendency to be more active than controls. Surprisingly, ChAT–ChR2–EYFP mice did not show changes in locomotor activity in a novel environment, anxiety-like behavior, or depression-like behavior. To note, increased cholinergic transmission has been suggested to be pro-depressive (Janowsky et al., 1972; Overstreet et al., 1986; Overstreet, 1993; Fagergren et al., 2005). Moreover, antagonists of nicotinic and muscarinic receptors have antidepressant activity (Rabenstein et al., 2006; Andreasen and Redrobe, 2009). Because chronic increase in cholinergic tone may affect the expression of distinct receptors in specific brain regions, it is unlikely that all phenotypes described previously attributable to cholinesterase inhibition or dysfunction may be affected in ChAT–ChR2–EYFP mice.

Despite their increased motor endurance, ChAT–ChR2–EYFP mice were unable to improve their performance in the rotarod, suggesting that increased cholinergic tone in the CNS is deleterious for learning an acrobatic skill. Previous experiments with mice presenting reduced levels of VACht (40% VACht knockdown heterozygous mice) had indicated that motor learning depends on cholinergic tone (Prado et al., 2006; de Castro et al., 2009b). Together, these results suggest that either too much or too little ACh in the brain is detrimental for motor learning.

We have also detected diminished performance of ChAT–ChR2–EYFP mice in two distinct tasks designed to measure spatial memory. In both the Barnes maze and MWM, ChAT–ChR2–EYFP mice present a specific deficit in the retrieval of information. In both tests, ChAT–ChR2–EYFP mice were able to learn the task (location of the platform or the exit hole), as evidenced by their improved performance over the 4 d of training. However, in probe trials, ChAT–ChR2–EYFP mice performed poorly compared with

their littermate controls in both tests. This phenotype may not be related only to spatial memory deficits, because these mice also presented impairments in the cued version of the MWM. Because ChAT–ChR2–EYFP mice can improve their performance during the 4 d of training in the Barnes maze and MWM, it is unlikely that they present any gross sensory motor deficits that would preclude visualization of cues. Conversely, deficits in the cued version of the MWM suggest that increased cholinergic tone might interfere with the mouse's ability to recognize that the platform is the goal (cue detection). It has been reported that detection of signals depends on cholinergic neurotransmission (Sarter et al., 2005; Parikh et al., 2007). Therefore, the chronic excess of cholinergic tone may disrupt the transmission of salient information related to a cue, preventing these animals from using such information to guide them to their goal.

Working memory is a prefrontal cortical process that is modulated by cholinergic signaling (Croxson et al., 2011). There is strong evidence implicating cholinergic activity in enhancing discrimination of signal-to-noise in the prefrontal cortex (for review, see Hasselmo and Sarter, 2011), a role that is critical in regulating attention (Sarter et al., 2006; Parikh et al., 2007; Hasselmo and Sarter, 2011). However, the focus in the literature has been on hypocholinergic function (McGaughy et al., 2002; Dalley et al., 2004; Harati et al., 2008; Parikh et al., 2013), and to date, there has not been an evaluation of chronic cholinergic deregulation on attentive processing. Additionally, ACh has been shown to be important for feature binding, the process by which the brain processes specific features of an object and compile a unified picture of it (Botly and De Rosa, 2009). Interestingly ChAT–ChR2–EYFP mice showed inattentive behavior related to cholinergic dysregulation; however, they also showed increased premature responses in the 5-CSRT task, a behavior that has been shown to be regulated by serotonergic signaling (Fletcher et al., 2013; Humpston et al., 2013). ACh has been proposed to help filter sensory information by increasing persistent spiking in cortical neurons, compatible with its proposed role in facilitating cue detection (Hasselmo and Stern, 2006). Such a mechanism depends on background tonic level of ACh but also on the transient increase in cholinergic activity (Parikh et al., 2007). Whether tonic cholinergic activity in the ChAT–ChR2–EYFP mice is so high that it precludes additional transient increases in cholinergic tone remains to be determined. However, the

observation that ChAT–ChR2–EYFP mice have working memory and attention deficits suggests the possibility that multiple forms of information encoding are affected in these mice. Therefore, these experiments emphasize the importance of regulated ACh release in cognitive function.

The precise mechanism by which excessive release of ACh in ChAT–ChR2–EYFP mice affects memory is not yet clear. It is likely that cellular regulation of neuronal spiking (Hasselmo and Sarter, 2011) may be affected by chronically increased levels of extracellular ACh. Moreover, increased and sustained cholinergic tone may affect forebrain circuitries by changing the expression of receptors and the regulation of other neurochemical systems, leading to abnormal processing, encoding, or retrieval of information. The overall memory deficits observed in ChAT–ChR2–EYFP mice suggest the need for specific temporal and spatial control of synaptic ACh levels for optimal cognitive performance.

In contrast with the worse performance of ChAT–ChR2–EYFP mice in cognitive tasks, augmented cholinergic tone seems to improve physical fitness, suggesting that increasing cholinergic tone may be beneficial in the periphery. Whether increased cholinergic function will be beneficial in other parameters regulated by the autonomic nervous system, as well as for improving the activity of the cholinergic anti-inflammatory pathway, remains to be determined.

Given that we detect improvement physical endurance and decreased performance in a series of behavioral tasks that have been previously related to cholinergic functions, we have interpreted our results as a potential consequence of increased cholinergic tone. It should be noted that we cannot eliminate the possibility that the large number of copies of the BAC inserted in the mouse genome disrupted a specific gene locus that could both improve physical endurance and disrupt cognition, although this seems unlikely. Also, we cannot discard the possibility that the high copy number of ChR2 or YFP may have unexpected consequences. We attempted to test this possibility by using another mouse line with high copy number of ChR2 and YFP. The VGAT–ChR2–EYFP mice, which have 20 copies of these genes, did not present impairments in working memory. These results support the argument that the effects observed in ChAT–ChR2–EYFP

mice are related to cholinergic hyperfunction. Importantly, these altered phenotypes fundamentally differentiate ChAT–ChR2–EYFP from control mice.

In short, our experiments indicate that ChAT–ChR2–EYFP mice overexpress VACht and show important functional consequences, including unforeseen effects in cognitive processing. Because most studies using optogenetic control of cholinergic neurons have used mice expressing Cre or ChR2 that was inserted in the ChAT–BAC (Witten et al., 2010; Bell et al., 2011; Gu and Yakel, 2011; Nagode et al., 2011; Cachope et al., 2012; Kalmbach et al., 2012), it is important to be aware that VACht overexpression may contribute to behavioral or cellular outputs. Therefore, novel approaches to control cholinergic neurons using optogenetics may be necessary. Inactivation of the VACht gene in the ChAT–BAC is a possible alternative. However, ChAT–ChR2–EYFP mice will be valuable to test current theories of cholinergic function and the consequences of overactive cholinergic signaling for information processing.

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Chapter 3

Forebrain deletion of the vesicular acetylcholine transporter results in deficits in executive function, metabolic, and RNA splicing abnormalities in the prefrontal cortex

3.1 Chapter Summary

One of the key brain regions in cognitive processing and executive function is the prefrontal cortex (PFC), which receives cholinergic input from basal forebrain cholinergic neurons. We evaluated the contribution of synaptically released acetylcholine (ACh) to executive function by genetically targeting the vesicular acetylcholine transporter (VACHT) in the mouse forebrain. Executive function was assessed using a pairwise visual discrimination paradigm and the 5-choice serial reaction time task (5-CSRT). In the pairwise test, VACHT-deficient mice were able to learn, but were impaired in reversal learning, suggesting that these mice present cognitive inflexibility. Interestingly, VACHT-targeted mice took longer to reach criteria in the 5-CSRT. Although their performance was indistinguishable from that of control mice during low attentional demand, increased attentional demand revealed striking deficits in VACHT-deleted mice. Galantamine, a cholinesterase inhibitor used in Alzheimer's disease, significantly improved the performance of control mice, but not of VACHT-deficient mice on the 5-CSRT. *In vivo* magnetic resonance spectroscopy showed altered levels of two neurochemical markers of neuronal function, taurine and lactate, suggesting altered PFC metabolism in VACHT-deficient mice. The PFC of these mice displayed a drastic reduction in the splicing factor heterogeneous nuclear ribonucleoprotein A2/B1 (hnRNPA2/B1), whose cholinergic-mediated reduction was previously demonstrated in Alzheimer's disease. Consequently, several key hnRNPA2/B1 target transcripts involved in neuronal function present changes in alternative splicing in VACHT-deficient mice, including pyruvate kinase M, a key enzyme involved in lactate metabolism. We propose that VACHT-targeted mice can be used to model and to dissect the neurochemical basis of executive abnormalities.

3.2 Introduction

The prefrontal cortex (PFC) is essential for the modulation of executive function, which is loosely defined as a set of cognitive tools that allows hierarchical and timely control of actions leading to specific behaviors (Alvarez and Emory, 2006; Robbins and Roberts, 2007; Chudasama, 2011). Disruption in executive function is a key symptom in neurological and neuropsychiatric disorders, including Alzheimer's disease (AD; Perry and Hodges, 1999; Traykov et al., 2007; McGuinness et al., 2010), schizophrenia (Morice, 1990), autism (Hill, 2004; Sala et al., 2011), and drug addiction (Stalnaker et al., 2009). The basic neurochemical underpinnings of executive function are, however, still poorly understood.

Cholinergic deficits are a hallmark of AD (Perry et al., 1977; Whitehouse et al., 1981, 1982). Moreover, amyloid β ($A\beta$) oligomers, potential toxins in AD, disrupt cholinergic synaptic transmission in the PFC (Chen et al., 2013). Cholinergic deficiency in AD can have widespread effects, including global changes in alternative splicing of genes involved in synaptic plasticity (Berson et al., 2012).

Acetylcholine (ACh) in the PFC has been implicated in controlling attention (Elliott, 2003; Jurado and Rosselli, 2007), one of the components of executive function. Cue detection and top-down modulation of attentive behavior have both been shown to activate PFC cholinergic activity and to be modulated by cholinergic signaling (Sarter et al., 2001; Parikh et al., 2007). Cholinergic transients in the PFC have been linked to cue detection, and both tonic and phasic PFC ACh release seem to regulate attentional demand (Parikh et al., 2007; for review, see Hasselmo and Sarter, 2011), which may depend mainly on nicotinic receptor signaling (McGaughy et al., 1999; Grottick and Higgins, 2000; Parikh et al., 2010; Guillem et al., 2011).

Cognitive flexibility, the ability to alter strategy according to changing environmental cues, is another key component of executive function (Elliott, 2003; Jurado and Rosselli, 2007). The neurochemical basis of cognitive flexibility is not fully understood, but serotonin is thought to play critical roles (Schmitt et al., 2006; Evers et al., 2007; Brigman et al., 2010).

Release of ACh is a tightly regulated process, with the vesicular acetylcholine transporter (VACHT) controlling a limiting key step (de Castro et al., 2009a; Kolisnyk et al., 2013; for review, see Prado et al., 2013). Genetic elimination of VACHT from the forebrain causes deficits in reversal learning assessed using the Morris Water Maze (MWM) (Martyn et al., 2012). Deficits in reversal learning may be related to hippocampal dysfunction, but could also reflect alterations in behavioral flexibility. To examine if decreased levels of VACHT, a change observed in AD (Efange et al., 1997; Chen et al., 2011), affects executive function we have used touchscreen tasks. We report that elimination of forebrain VACHT caused severe deficits in cognitive flexibility and in sustained attention. In addition, we found that these mutant mice have profound changes in RNA processing in the PFC, which correlate with behavioral and metabolic deficits. Our results suggest that elimination of forebrain cholinergic activity in mice provides a model for understanding the neurochemical basis of executive function.

3.3 Material and Methods

3.3.1 Animals

Generation of VACHTSix3-Cre-flox/flox mice was previously described (Martyn et al., 2012). In short, VACHTSix3-Cre-flox/flox mice were generated by crossing VACHTflox/flox (mixed C57BL/6J × 129/SvEv background, backcrossed to C57BL/6J for five generations) with the Six3-Cre mouse line (NMRI background, backcrossed to C57BL/6J for five generations). We then intercrossed VACHTSix3-Cre-flox/wt mice to obtain VACHTSix3-Cre-flox/flox. For the galantamine experiments, the mice used were wild-type C57BL/6J. Mice were housed in groups of three or four per cage without environmental enrichment in a temperature-controlled room with 14/10 h light/dark cycle, and water was provided ad libitum. Only male mice were used in these studies. Mice were restricted to 85% of their free-feed weight and maintained on 85% of their weight for the duration of the study. All procedures were conducted in accordance with guidelines from the Canadian Council of Animal Care at the University of Western Ontario with an approved institutional animal protocol (2008–127).

3.3.2 Western Blotting

Mouse PFC was collected, protein was isolated, and immunoblotting was performed as previously described (Martins-Silva et al., 2011). The antibodies used were anti-VACHT (catalog #139103; Synaptic Systems) at a 1:3000 dilution, anti-Synaptophysin (catalog #S5768; Sigma-Aldrich) at a 1:500 dilution, anti-hnRNP A2/B1 (catalog #sc-10035; Santa Cruz Biotechnology) at a 1:500 dilution, and anti- β -Actin (catalog #ab49900; Abcam), at a 1:15000 dilution. Band intensity was quantified using FluoroChemQ software (Thermo Fisher Scientific).

3.3.3 Acetylcholine Release

ACh release from prefrontal cortical brain slices was quantified by labeling slices with [3H] methyl-choline before using KCl to stimulate release of labeled ACh as previously described (Guzman et al., 2011).

3.3.4 qPCR

To measure mRNA expression, total RNA was extracted from freshly dissected PFC tissue, using the Aurum Total RNA for fatty and fibrous tissue kit (Bio-Rad) according to the manufacturer's instructions. cDNA synthesis and qPCR analysis were performed as previously described (Guzman et al., 2011). Primer sequences used to determine alternative spliced transcripts are found in Table 3.1. β -Actin was used as a reference transcript for all reactions. For alternative splicing experiments, the alternative exon levels were normalized to a constitutively expressed exon from the same gene.

Table 3.1. Primers for alternative splicing assay

Target	Forward primer(5' → 3')	Reverse primer (5' → 3')
<i>CD55</i> exon 8	CCCAGCATGTACCTGTTACC	TCACATGCAAAACCTGTCAAGG
<i>CD55</i> exon 1	TGTCTCTGTTGCTGCTGTCC	TGCTCAGCAAACCTTGAGGTG
<i>DRAM2</i> exon 2	TGATTCAAGGTTACACTCACA	AAAACCTGAGGCCTTGCTGAA
<i>DRAM2</i> exon 4	TTCAGCAAGGCCTCAGTTTT	TCAGGAGGTATTGTCCCTGTG
<i>SIPA1L1</i> intron 5	TCAGGCATGCAGTTCTTTTG	GAAAGCAGGCAGTACCTTCG
<i>SIPA1L1</i> exon 4	TAGTGTGGACGCTGCTGTCT	GGCTCTGTGGTCACCAGAAT
<i>DYSTONIN</i> exon 41	ATGGCATTTCCTCCATTAG	GGAGGTTGGTTTTGCTTCAA
<i>DYSTONIN</i> exon 7	GAGCGGGACAAAGTTCAAAA	CCCGTCCCTCAGATCCTC
<i>REELIN</i> exon 3	ATCATGTCCGACCACCAGTT	ATCATGTCCGACCACCAGTT
<i>REELIN</i> exon 18	GCAGTGCCAGACTTTCCTCT	GCCTCCCATCTTTGTTGAAA
<i>REELIN</i> exon 1	GGCAACCCACCTACTACG	GACTGGATGCTTGTGCGAGGT
<i>mENAH</i>	CGGCAGTAAGTCACCTGTCA	C TTCAGCTTTGCCAGCTCTT
<i>mENAH invasive</i>	GATTCAAGACCATCAGGTTGTG	CAATGTTGGCCCTAAATAGAA
<i>PKM1</i>	CATGCAGCACCTGATAGCTC	TTATAAGAGGCCTCCACGCTG
<i>PKM2</i>	GCAGTGGGGCCATTATCGT	GGGATTTGAGTCACGGCAA

3.3.5 Magnetic resonance imaging

Magnetic resonance spectroscopy of the prefrontal region was performed in four VACHTSix3-Cre-flox/flox mice and four littermates (VACHTflox/flox). Spectroscopic localization of a 24 μ l voxel was achieved by adiabatic selective refocusing (DelaBarre and Garwood, 1998) on a 9.4 tesla horizontal bore small animal Agilent magnetic resonance imaging (MRI) scanner. Water-suppressed full spectra (TR/TE = 3250/20 ms, 128 acquisitions), water-suppressed macromolecule spectra (TR/TE = 5000/20 ms, inversion time TI = 873 ms, 128 acquisitions), and water-unsuppressed spectra (TR/TE = 3250/20 ms, 8 acquisitions) were acquired. All animals were anesthetized with 2% isoflurane during the procedure and were maintained at 37° by blowing warm air into the bore of the magnet using a Model 1025 Small Animal Monitoring and Gating System (SA Instruments).

3.3.6 Metabolite analysis

Magnetic resonance spectra were analyzed using purpose-built software (fitMAN; Bartha et al., 1999) to determine the contribution of each metabolite relative to total creatine as previously described (Bartha, 2007, 2008). Briefly, spectra were lineshape corrected (Bartha et al., 2000b) and the macromolecule and residual water contribution was removed (Kassem and Bartha, 2003). Then, the spectrum was fitted in the time domain to a basis set of 19 metabolite lineshapes (Pfeuffer et al., 1999; Bartha et al., 2000a). Five metabolites (measured relative to creatine) were reliably measured and included in group comparisons: N-acetylaspartate (NAA), myo-inositol (Myo), choline (Cho), taurine (Tau), and lactate (Lac).

3.3.7 Touchscreen behavioral assessment

3.3.7.1 Apparatus and task

Mice were trained in the 5-choice serial reaction time task (5-CSRT) and in the pairwise visual discrimination in automated Bussey–Saksida Mouse Touchscreen Systems

model 81426 (Campden Instruments). Schedules were designed and data were collected using the ABET II Touch software v.2.15 (Lafayette Instruments).

3.3.7.2 Pretraining

Before being trained on the pairwise visual discrimination or the 5-CSRT task, mice were first put through a pretraining program. This consisted of first habituating the mice to the testing chamber with the lights off for 15 min. The next day, mice were left in the chamber with the lights off for 20 min, this time with the reward tray primed with a 150 μ l reward (strawberry milkshake; Saputo Dairy Products), and a tone was played whenever the mouse entered the reward tray. Whenever the mouse returned to the reward tray, it received a reward (7 μ l) paired with the tone. This training was repeated the next 2 d for 40 min sessions (phase 1).

The next training phase (phase 2) involved pairing the reward with the presentation of the stimulus on the touchscreen. The stimulus appeared randomly in one of the windows and after 30 s, it was removed and a reward (7 μ l) was given paired with a tone. If the mouse touched the screen while the image was displayed, it immediately received a reward (7 μ l). Once the mouse collected the reward a new trial was initiated. This phase was repeated until the mouse completed 30 trials within 60 min (phase 2).

Phase 3 was used to further shape behavior. It involved displaying the stimulus randomly in one of the windows. The mouse was required to touch the stimulus on the screen to receive a reward (7 μ l) paired with a tone. There was no response to the mouse touching anything but the stimulus. Once again, this was repeated until the mouse completed 30 trials within 60 min. Phase 4 was identical to phase 3 except that the mouse was required to initiate each trial by nose poking the reward tray. Criterion was 30 correct trials within 60 min.

Finally, in the last pretraining phase (phase 5), the previous procedure was repeated but if the mouse touched an incorrect screen, it received a 5 s time-out, during which the light was turned on. The final phase had a stricter criterion, requiring the mouse to perform 30 trials in 60 min with at least 23 correct responses in 2 consecutive days.

3.3.7.3 Pairwise visual discrimination and reversal

Pairwise visual discrimination and reversal task were performed as previously described (Romberg et al., 2013). Mice used in this experiment were 6–8 months old. At the beginning of each session, the reward tray was primed with 7 μ l of milkshake. Briefly, the mice were first trained to discriminate between two visual stimuli, which were presented simultaneously, with their spatial location randomized over a 30 trial session. If mouse nose poked the correct stimulus (S+), a tone was played and mouse received a reward (7 μ l), whereas if the incorrect stimulus (S–) was nose poked, light in the chamber was turned on for 5 s (time-out) followed by a correction trial. During the correction trial, the trial was repeated until the mouse poked the correct stimulus. Criterion was reached when the mouse selected the correct image (S+) on 80% of the trials, excluding correction trials, for 2 consecutive days. Once mice reached criteria, they were given two sessions to assess baseline performance on the task. For reversal learning the rule associated to each stimulus was switched, that is, the rewarded image (S+) during acquisition became the (S–) image in reversal and was punished, while the (S–) image from acquisition became the correct stimulus and was rewarded. Reversal learning was assessed over the course of 10 sessions.

3.3.7.4 Training in 5-CSRT

The 5-CSRT task was performed as previously described (Romberg et al., 2011). A distinct cohort of mice (8–10 months old) was trained in the 5-CSRT task. At the beginning of each session, the reward tray was primed with 7 μ l of milkshake. Each trial was initiated after the mouse nose poked the magazine. In this phase, the stimulus was delivered after a variable 5–10 s delay (delay period), during which the animal was required to attend to the screen. In case the mouse prematurely touched the screen during this delay, the response was recorded as premature and the mouse was punished with a 10 s time-out. The stimulus duration was initially set to 4 s, followed by a limited holding period of 5 s, during which the stimulus was absent, but the mouse could still respond to the location (holding period). Responses to the stimulus window during stimulus presence or the holding period were recorded as correct and a 7 μ l

reward was administered, while responses to any other window were recorded as incorrect. A correct choice was rewarded with a tone and food delivery. An incorrect response was punished with a 10 s time-out. A failure to respond to any window both during stimulus display, or during the holding period, was recorded as an omission and punished with a 10 s time-out. Perseverative responses to the screen after premature, correct, and incorrect choices were also recorded. Once the performance of a mouse reached criterion at 4 s stimulus duration (80% accuracy, 20% omissions for 3 consecutive days), the stimulus duration was reduced to 2 s. After reaching criterion with the 2 s stimulus, mice were tested for two more days. The mean measurement of those 2 d was used to assess baseline performance. If the mouse completed <30 trials, it was considered not to have reached criteria, even if it met accuracy and omissions thresholds.

3.3.7.5 Probe trial

To probe attention in mice we used a previously described probe trial schedule with reduced stimulus durations (Romberg et al., 2011). Briefly, each mouse was tested for 2 consecutive days at a given stimulus duration (1.5, 1, 0.8, and 0.6 s). After each test, the animal was retested onto the 2 s stimulus duration for 2 d or until criteria were reached (80% accuracy, 20% omission), to assess baseline performance. The order of the probe trial sessions were semi-randomized using a Latin square method.

3.3.7.6 Distraction task

To further test attentional demand, and assess susceptibility to distraction, we developed a distraction version of the 5-CSRT task. During this task, a 1000 ms distractor tone, different from the reward tone, was played semi-randomly at five different time points during the delay period: 0 (corresponding to when the mouse initiates the task), 0.5, 2.5, 4.5, and 5 s (corresponding to when the stimulus is displayed on the touchscreens). Stimulus duration was set to 2 s. For each distractor tone time point mice were tested for five sessions. At the end of the five sessions one baseline task (50 trial, 2 s stimulus duration, no distractor sounds) was performed before moving to the next distractor time point.

3.3.7.7 5-CSRT task measures

On all 5-CSRT task sessions, accuracy was defined as the total number of correct responses, divided by the number of correct and incorrect (touches to a wrong window while the correct stimulus was still displayed) responses. The rate of omissions was the proportion of omitted responses to total trials. Response latency was the time for the mouse to touch the correct stimulus after its onset. Reward collection latency was the time for the mouse to return to the reward tray once it had touched the correct stimulus. A premature response was counted when the mouse touched one of the windows before stimulus onset. Finally, a perseverative response was any identical response that occurred following a correct, incorrect, or premature response.

3.3.7.8 Drug treatments

Galantamine hydrobromide, a cholinesterase inhibitor, (Sigma-Aldrich) was dissolved in physiological saline (0.9% NaCl) before administration. Sixty minutes before being tested on the 5-CSRT mice received an intraperitoneal injection of drug (100 μ l, 1 mg/kg) or saline. The dose for galantamine was selected based on previous studies (Prado et al., 2006; de Castro et al., 2009b; De Jaeger et al., 2013). Previously, we have tested 3 mg/kg galantamine in other tasks, but this dose was no more effective than 1 mg/kg and it produced hypersalivation in mice (de Castro et al., 2009b). Moreover, at 1 mg/kg wild-type mice were able to increase their performance in the 5-CSRT (see below). Mice were tested at the 0.6 s stimulus duration, which represents a high attention demanding task (Romberg et al., 2011). The order of the injections was counterbalanced. Between injections mice had three washout days wherein their performance on the 5CSRT was re-baselined at the 2 s stimulus duration.

3.3.8 Statistical analysis

For the pairwise visual discrimination task response accuracy was calculated as the number of correct trials divided by the total number of trials, excluding correction trials. Data are expressed as mean $\pm$ SEM. SigmaStat 3.5 software was used for statistical analysis. Comparison between two experimental groups was made by Student's t test or

Mann–Whitney rank sum test, when the data did not follow a normal distribution. When several experimental groups or treatments were analyzed, two-way ANOVA or two-way ANOVA with repeated measures was used as required. When appropriate, a Tukey's HSD post hoc comparison test was used. In all comparisons, $p < 0.05$ was considered statistically significant.

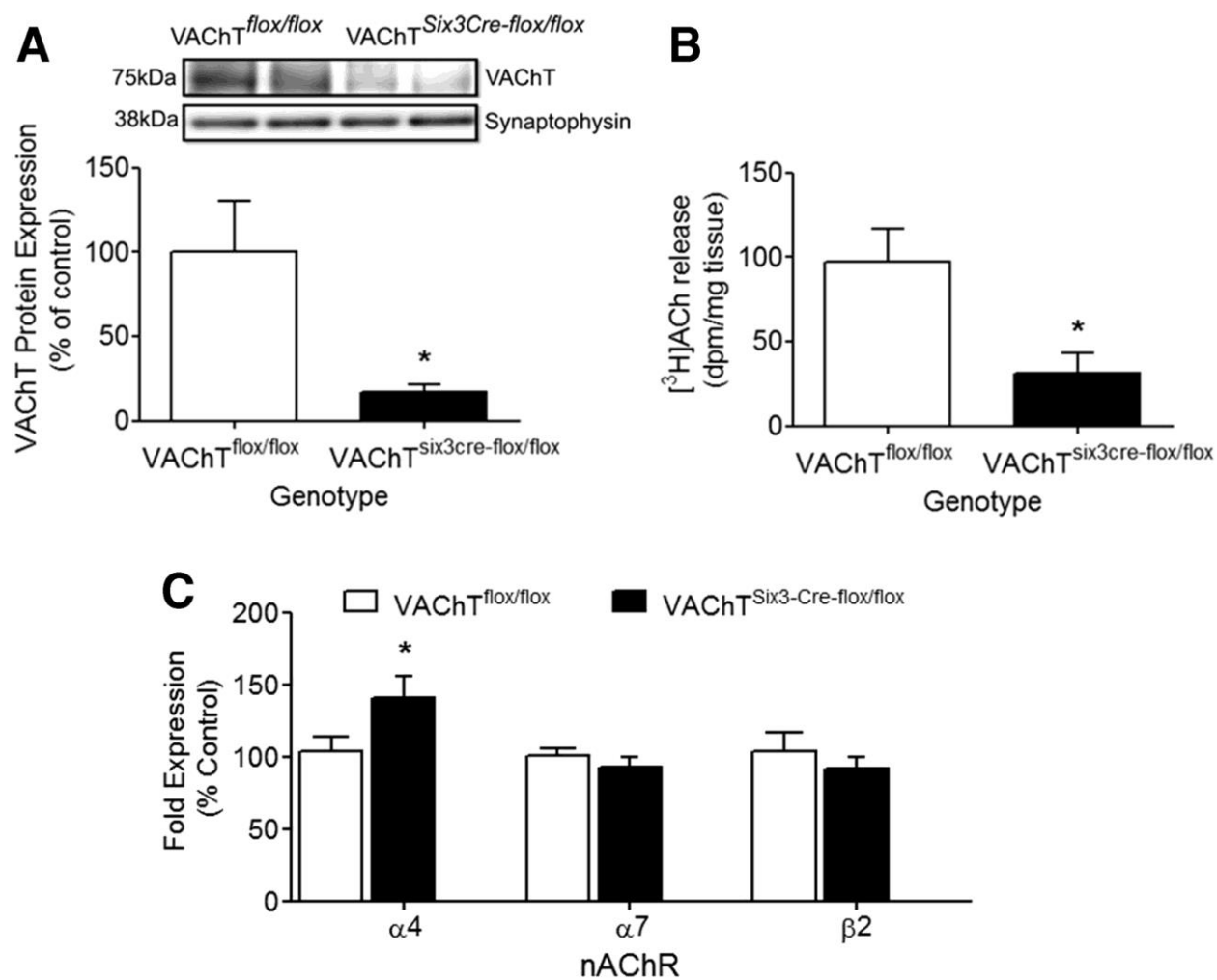
3.4 Results

3.4.1 VACHTSix3-Cre-flox/flox mice have reduced VACHT and ACh release in the PFC

We have previously reported that VACHTSix3-Cre-flox/flox mice have the VACHT gene deleted from >90% of their basal forebrain cholinergic neurons (Martyn et al., 2012). To confirm that this deletion affected prefrontal cortical cholinergic signaling, we performed Western blot analysis to assess VACHT expression. VACHTSix3-Cre-flox/flox mice have a significant reduction in PFC VACHT protein expression ($t(6) = 2.706$, $p = 0.0353$; Fig. 5.1A). Moreover, this reduction in VACHT protein levels results in a significant decrease in newly synthesized [3H] ACh release in slices of PFC from VACHTSix3-Cre-flox/flox mice when compared with control mice ($t(4) = 2.899$, $p = 0.0442$; Fig. 5.1B). We used qPCR to assess the expression of nicotinic receptors (nAChRs), which have been shown previously to be critical for attentional performance. The PFC of VACHTSix3-Cre-flox/flox mice shows no significant change in the expression of $\alpha 7$ nAChR mRNA ($t(10) = 0.9300$, $p = 0.3743$) nor $\beta 2$ nAChR mRNA ($t(10) = 0.8359$, $p = 0.4227$). Interestingly, $\alpha 4$ nAChR mRNA is slightly upregulated ($t(10) = 2.550$, $p = 0.0289$; Fig. 5.1 C).

Figure 3.1 Expression of VACHT in the PFC of VACHT^{Six3-Cre-flox/flox} mice. **A**, VACHT protein expression in the PFC with representative immunoblots inset ($n = 4$). **B**, Release of newly synthesized [^3H]ACh in PFC slices ($n = 3$). **C**, qPCR analysis of nAChR expression ($n = 6$, data are mean $\pm$ SEM, $*p < 0.05$).

Figure 3.1 Expression of VACHT in the PFC of VACHT^{Six3-Cre-flox/flox} mice.



3.4.2 Decreased forebrain cholinergic tone specifically disturbs reversal learning in the pairwise visual discrimination task

We have previously demonstrated that VACHTSix3-Cre-flox/flox mice have impairments in reversal learning in the MWM (Martyn et al., 2012), suggesting the possibility that these mice have behavior flexibility deficits. To determine whether VACHTSix3-Cre-flox/flox mice present alterations in cognitive flexibility we used a “nonhippocampal” pairwise visual discrimination task (Romberg et al., 2013). This task has been previously shown to depend on the PFC and also on striatal-cortical loops (Graybeal et al., 2011). The performance of VACHTSix3-Cre-flox/flox mice did not differ from that of controls (VACHTflox/flox) when they were trained to operate the touchscreen (pretraining phase). The number of sessions the mice took to acquire each training phase did not differ from control (RM-ANOVA, no effect of genotype $F(1,54) = 0.3950$, $p = 0.5398$; main effect of training phase $F(4,54) = 5.227$, $p = 0.0012$; and no interaction effect $F(4,54) = 1.389$, $p = 0.2495$; Figure 3.2A). Acquisition of the pairwise visual discrimination task (Fig. 5.2B; for stimuli used) did not differ between genotypes, in terms of sessions to criteria (Fig. 5.2C; $t(14) = 0.2446$, $p = 0.8117$), correction errors made (Fig. 5.2D; $t(14) = 0.2942$, $p = 0.7746$), response latency (Fig. 5.2E; $t(14) = 1.019$, $p = 0.3256$), or reward collection latency (Fig. 5.2F; $t(14) = 0.2606$, $p = 0.7988$). We have previously reported that these mice are hyperactive in novel environments, but they are able to habituate to the environment (Martyn et al., 2012). Hence, due to the extensive training for the performance in the touchscreen tasks the lack of differences in response and reward collection latencies is not surprising. However, VACHTSix3-Cre-flox/flox mice showed severe reversal learning impairment (Fig. 5.3A; for the stimuli used), measured by the percentage of correct responses (Fig. 5.3B; RM-ANOVA, main effect of genotype $F(1,132) = 19.78$, $p = 0.0008$; main effect of session $F(11,132) = 23.28$, $p = 0.0001$; and significant interaction effect $F(1,12) = 5.035$, $p = 0.0001$) and by its increased correction errors (Fig. 5.3C; RM-ANOVA, main effect of genotype $F(1,132) = 14.72$, $p = 0.0024$; main effect of session $F(11,132) = 14.37$, $p = 0.0001$; and significant interaction effect $F(1,12) = 2.817$, $p = 0.0025$). Post hoc analysis showed that VACHTSix3-Cre-flox/flox mice never improved significantly from the first reversal

session and in 10 sessions they performed only at chance level. Importantly, during the reversal trials, the VAC^hTSix3-Cre-flox/flox mice did not differ from controls in terms of response latency (Fig. 5.3D; RM-ANOVA, no effect of genotype $F(1,154) = 0.4233$, $p = 0.5258$; main effect of session $F(11,154) = 4.705$, $p = 0.0001$; and no interaction effect $F(11,154) = 0.9997$, $p = 0.4493$) or reward collection latency (Fig. 5.3E; RM-ANOVA, no effect of genotype $F(1,154) = 1.107$, $p = 0.3105$; main effect of session $F(11,132) = 3.965$, $p = 0.0001$; and no interaction effect $F(11,154) = 1.141$, $p = 0.3333$). These results suggest that forebrain cholinergic tone is important for cognitive flexibility.

Figure 3.2. VACHT^{Six3-Cre-flox/flox} mice show normal visual discrimination

learning. **A**, Mean number of trials required to reach criteria during the operant conditioning, pretraining phases. **B**, Image of a mouse performing the task, with the fan shown as the S+ and the marbles as the S-. **C**, Number of sessions to criteria in the pairwise visual discrimination learning task. **D**, Correction errors made to achieve discrimination criteria. **E**, Mean response latency. **F**, Mean reward collection latency. $n = 8$, data are mean $\pm$ SEM.

Figure 3.2. VACHT^{Six3-Cre-flox/flox} mice show normal visual discrimination learning.

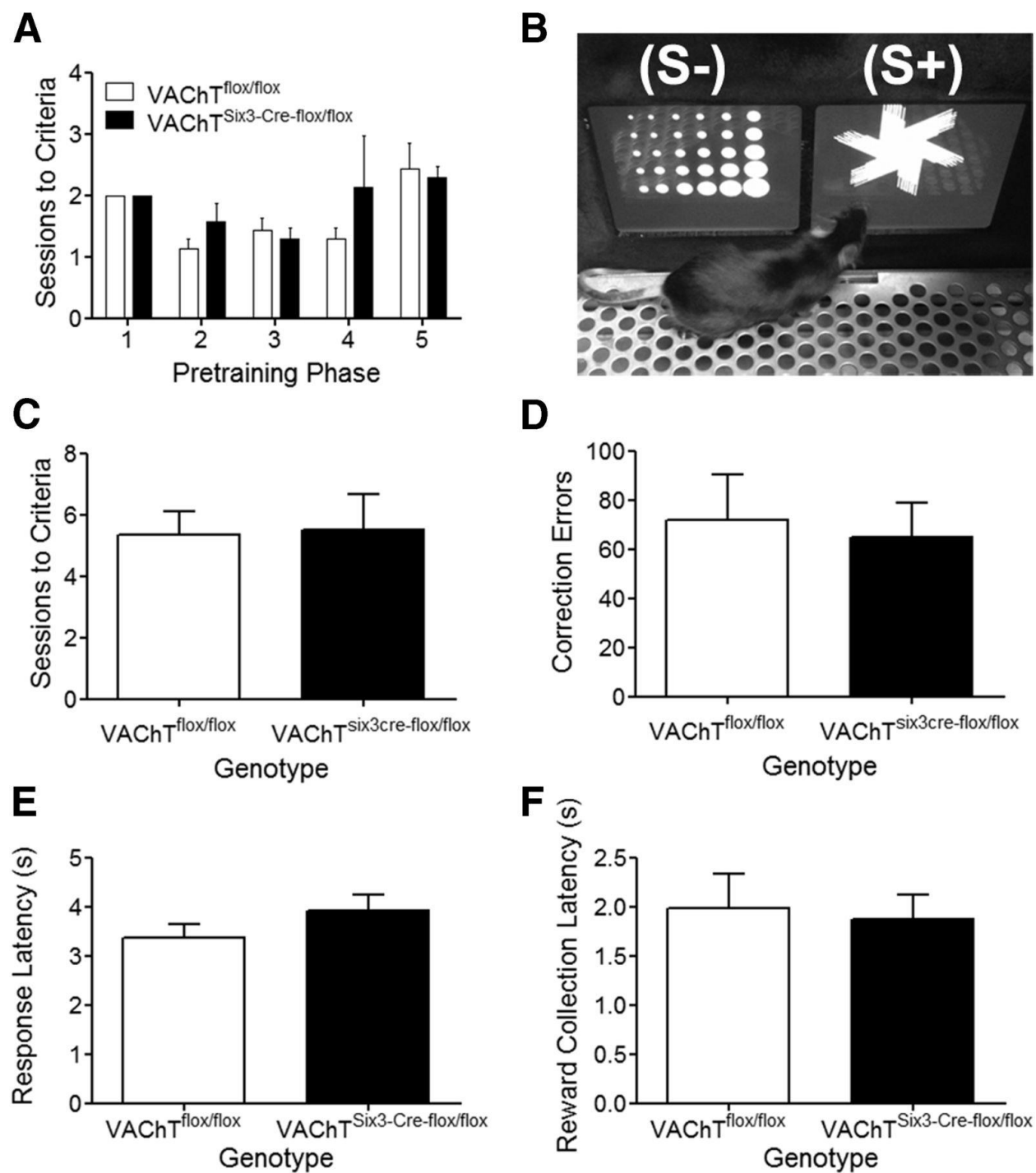
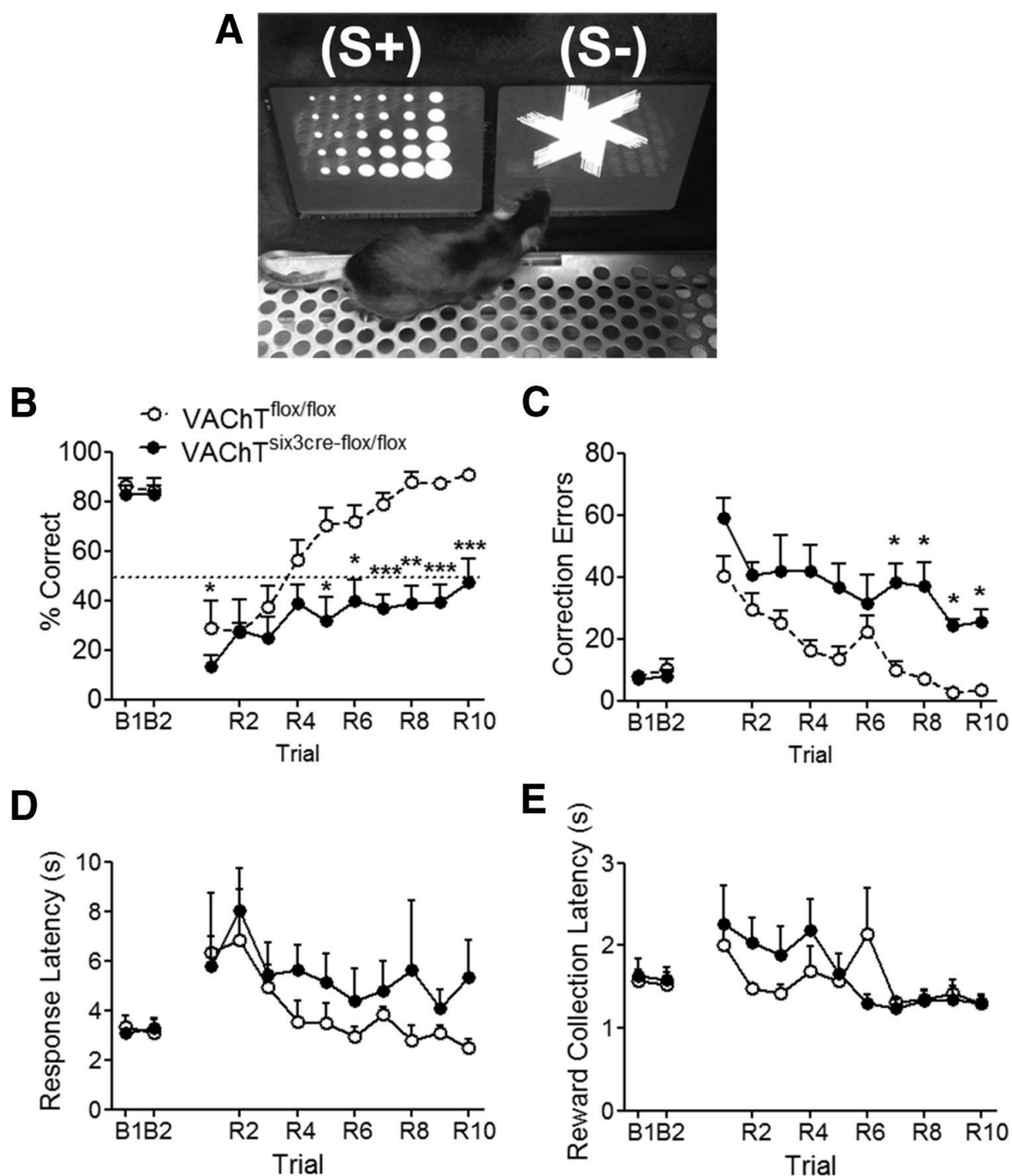


Figure 3.3. VACHT^{Six3-Cre-flox/flox} mice have impaired reversal learning. **A**, Image of a mouse performing the task, this time with the fan shown as the S- and the marbles as the S+. **B**, Choice accuracy before (B1 and B2) and during reversal trials (R2–R10), dashed line denotes chance (50%). **C**, Number of correction errors made across reversal trials. **D**, Response latency across reversal trials. **E**, Reward collection latency across reversal trials ($n = 8$, data are mean $\pm$ SEM, $*p < 0.05$, $**p < 0.01$, and $***p < 0.001$).

Figure 3.3. VACHT^{Six3-Cre-flox/flox} mice have impaired reversal learning.

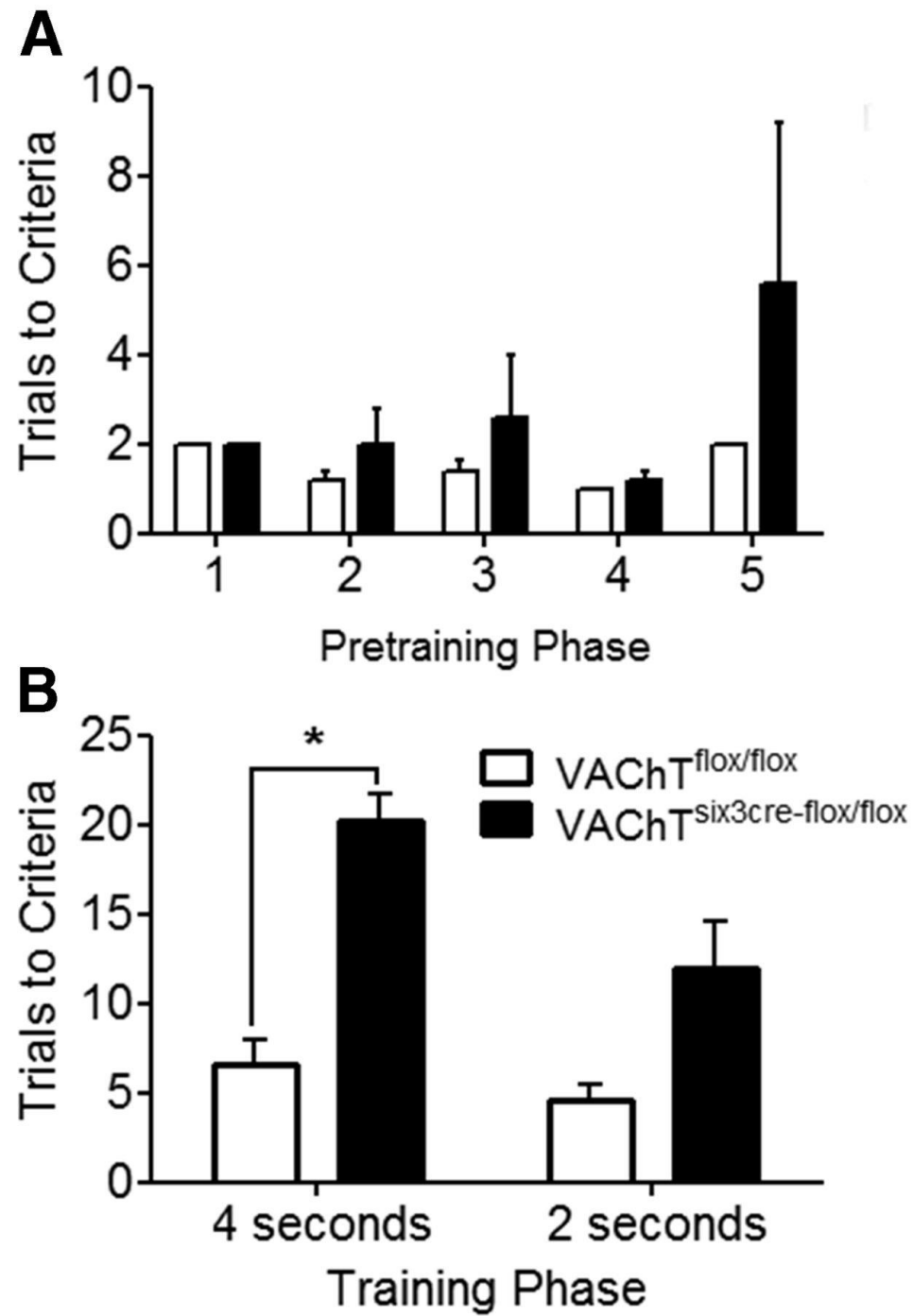


3.4.3 VACHTSix3-Cre-flox/flox mice have impaired acquisition of the 5-CSRT task

Similar to the results for visual discrimination experiments, the performance of the second cohort of VACHTSix3-Cre-flox/flox mice did not differ from that of control mice for touchscreen operation training (pretraining phase). The number of sessions necessary to reach criteria across all pretraining phases did not differ between genotypes (RM-ANOVA, no effect of genotype $F(1,32) = 1.528$, $p = 0.2515$; no effect of training phase $F(4,32) = 1.492$, $p = 0.2280$; Figure 3.4A). However, when mice were trained to respond to flashes of light displayed in one of the five spatial locations on the touchscreen (training phase), VACHTSix3-Cre-flox/flox showed a significantly worse performance, needing more sessions to reach criteria (RM-ANOVA, main effect of genotype, $F(1,8) = 10.06$, $p = 0.0132$; main effect of stimulus duration, $F(1,8) = 5.731$, $p = 0.0436$, no interaction effect, $F(1,8) = 4.252$, $p = 0.0731$; Fig. 5.4B).

Figure 3.4. Training in the 5-CSRT task. **A**, Mean number of trials required to reach criteria during the operant conditioning, pretraining phases. **B**, Mean number of trials required to reach criteria at 4 and 2 s stimulus duration ($n = 6$, data are mean $\pm$ SEM, $*p < 0.05$).

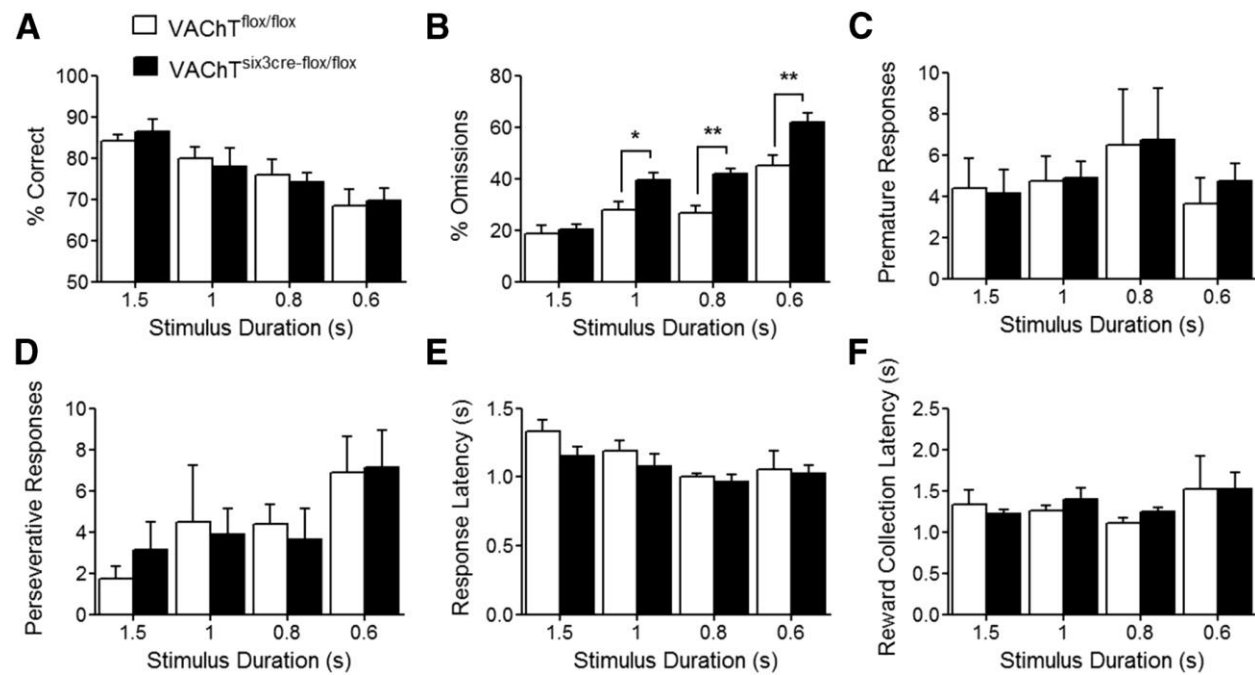
Figure 3.4. Training in the 5-CSRT task



3.4.4 Deletion of forebrain VACHT results in inattentive but not impulsive or compulsive behavior

Once mice reached criteria they were tested for attentional performance by decreasing stimulus duration to 1.5, 1, 0.8, and 0.6 s as previously described (Romberg et al., 2011). At 1.5 s, VACHTSix3-Cre-flox/flox mice were able to perform identically to control mice in both accuracy and omissions (Fig. 5.5A,B). In contrast, increasing attentional demand by diminishing the stimuli period revealed an attentional deficit in VACHTSix3-Cre-flox/flox mice. Response accuracy did not differ between genotypes (RM-ANOVA, no effect of genotype $F(1,24) = 0.0007548$, $p = 0.9788$; main effect of stimulus duration $F(3,24) = 10.28$, $p < 0.001$; Figure 3.5A). However, VACHTSix3-Cre-flox/flox mice presented an increased rate of omission (RM-ANOVA, main effect of genotype $F(1,24) = 57.99$, $p < 0.0001$; main effect of stimulus duration $F(3,24) = 36.44$, $p < 0.0001$; no interaction effect $F(3,24) = 2.176$, $p = 0.1171$; Figure 3.5B). Post hoc analysis revealed that VACHTSix3-Cre-flox/flox mice omitted more at 0.6–1 s stimulus durations. Interestingly, VACHT-deficient mice had no alterations in premature responses (RM-ANOVA, no effect of genotype $F(1,24) = 0.07440$, $p = 0.7874$; no effect of stimulus duration $F(3,24) = 0.9891$, $p = 0.4146$; Figure 3.5C) or perseverative responses (RM-ANOVA, no effect of genotype $F(1,24) = 0.04610$, $p = 0.9695$; no effect of stimulus duration $F(3,24) = 1.244$, $p = 0.3232$; Figure 3.5D). Additionally, mutant mice did not differ from littermate controls in response latency (RM-ANOVA, no effect of genotype $F(1,24) = 2.279$, $p = 0.1818$; no effect of stimulus duration $F(3,24) = 0.09686$, $p = 0.7662$; Figure 3.5E) and reward collection latency (RM-ANOVA, no effect of genotype $F(1,24) = 2.279$, $p = 0.1818$; no effect of stimulus duration $F(3,24) = 1.189$, $p = 0.3420$; Figure 3.5F).

Figure 3.5. VACHT^{Six3-Cre-flox/flox} mice have attentional deficits. Performance and response measures during 5-CSRT task probe trials. Mice were subjected to a series of probe trials and the average values of 50 trial sessions are plotted. **A**, Mean accuracy. **B**, Mean rate of omissions. **C**, Mean premature responses. **D**, Mean perseverative responses. **E**, Mean response latency. **F**, Mean reward collection latency ($n = 6$, data are mean $\pm$ SEM, $*p < 0.05$ and $**p < 0.01$).

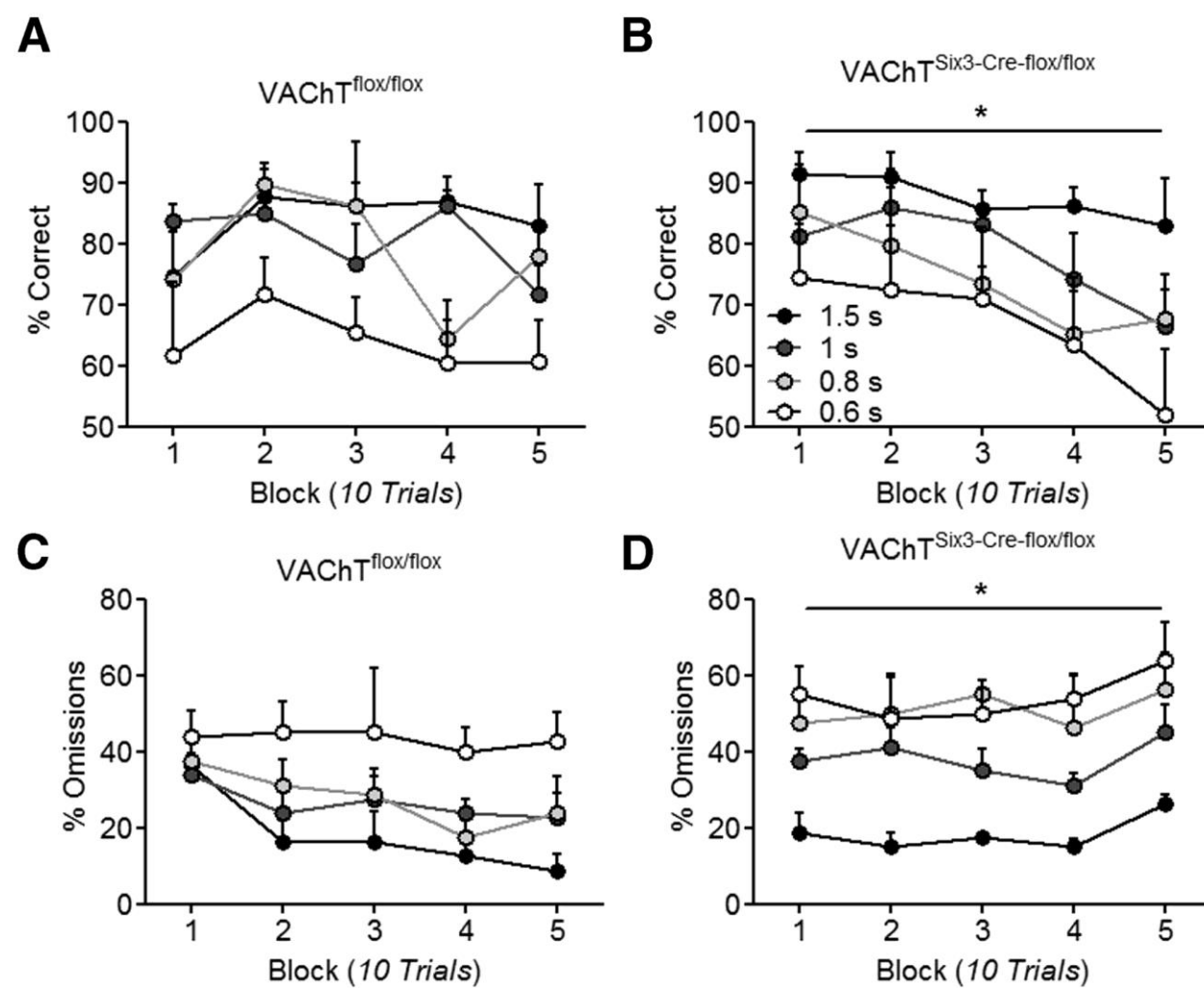
Figure 3.5. VACHT^{Six3-Cre-flox/flox} mice have attentional deficits

3.4.5 Deletion of forebrain VAcHT impairs sustained attention

To assess sustained attention (vigilance), we analyzed both response accuracy and rate of omissions over blocks of 10 trials (Romberg et al., 2011). Response accuracy of control mice did not significantly vary across blocks, but did reduce significantly with decreases in stimuli duration (RM-ANOVA, main effect of stimulus duration $F(3,48) = 5.893$, $p = 0.0104$; no effect of block $F(4,48) = 1.214$, $p = 0.317$; Figure 3.6A). In contrast, response accuracy of VAcHTSix3-Cre-flox/flox mice reduced significantly across blocks and stimuli duration (RM-ANOVA, main effect of stimulus duration $F(3,48) = 4.257$, $p = 0.0077$; main effect of block $F(4,48) = 3.933$, $p = 0.0289$; Figure 3.6B). As with response accuracy, rate of omissions of control mice did not vary across blocks, only with stimuli duration (RM-ANOVA, main effect of stimulus duration $F(3,48) = 5.803$, $p = 0.0228$; no effect of block $F(4,48) = 0.5352$, $p = 0.7105$; Figure 3.6C), whereas rate of omissions of VAcHTSix3-Cre-flox/flox mice increased significantly across stimuli duration and blocks (RM-ANOVA, main effect of stimulus duration $F(3,48) = 9.387$, $p = 0.0018$; main effect of block $F(4,48) = 2.803$, $p = 0.0360$; Figure 3.6D). Together the data suggest that VAcHTSix3-Cre-flox/flox mice have impaired ability to sustain attention.

Figure 3.6. VACHT^{Six3-Cre-flox/flox} mice have impaired sustained attention. Mean response accuracy for blocks of 10 trials for (A) VACHT^{flox/flox} and (B) VACHT^{Six3-Cre-flox/flox} mice. Mean rate of omission for blocks of 10 trials for (C) VACHT^{flox/flox} and (D) VACHT^{Six3-Cre-flox/flox} mice ($n = 6$, data are mean $\pm$ SEM, $*p < 0.05$).

Figure 3.6. VACHT^{Six3-Cre-flox/flox} mice have impaired sustained attention.

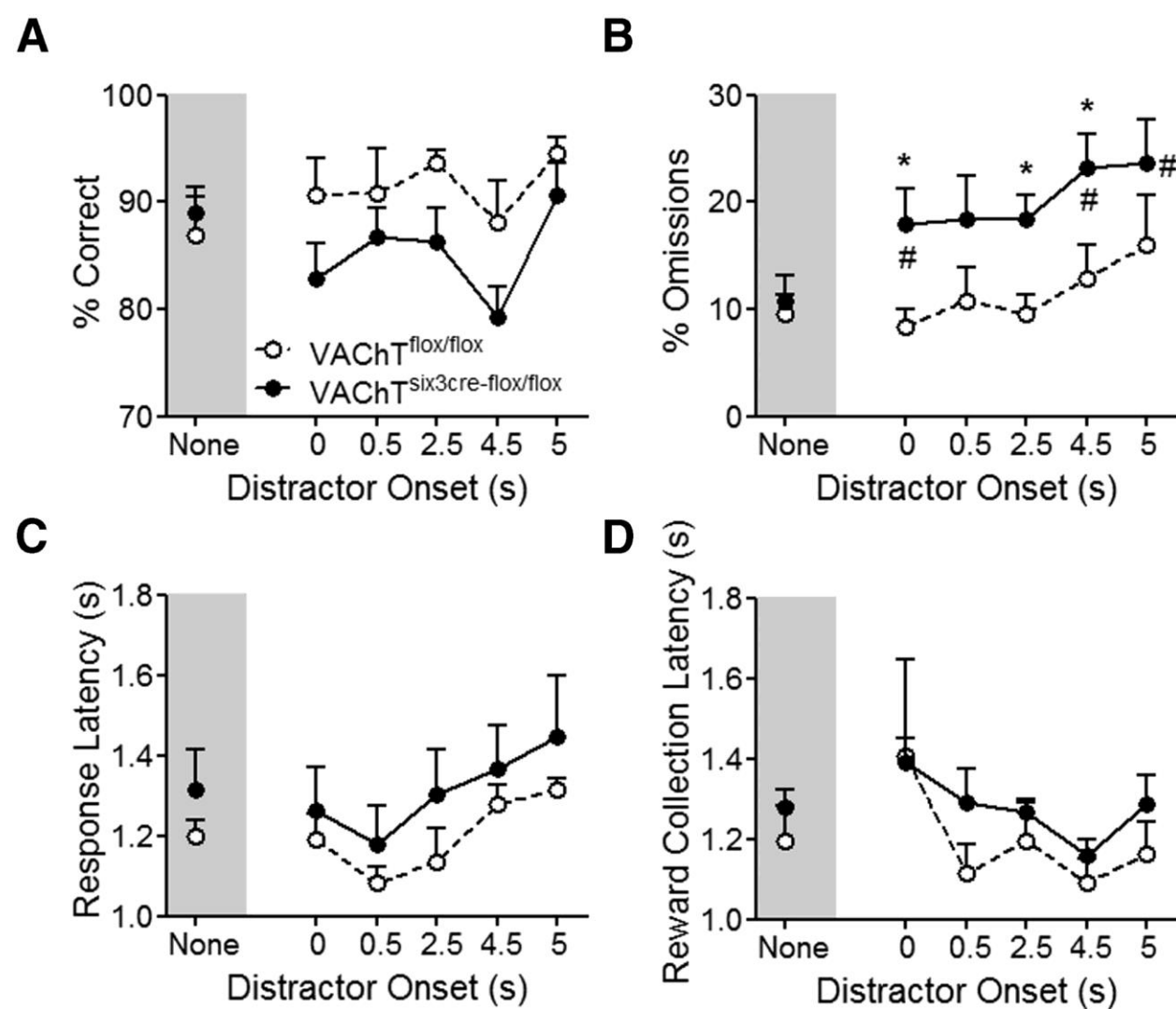


3.4.6 Deletion of forebrain VAcHT increases susceptibility to distractions

To assess distractibility of VAcHTSix3-Cre-flox/flox mice, we increased attentional demand by testing them on a distraction variation of the 5-CSRT. Stimulus duration was set to 2 s, where performance of both genotypes was identical, and distractor sounds were played at set time points during trials. Response accuracy of VAcHTSix3-Cre-flox/flox mice tended to be reduced by distractions compared with controls (RM-ANOVA, near significant effect of genotype $F(1,32) = 4.825$, $p = 0.0589$; main effect of distractor onset $F(4,32) = 3.583$, $p = 0.0159$; Figure 3.7A). Rate of omission was significantly higher in VAcHTSix3-Cre-flox/flox mice than controls (RM-ANOVA, significant effect of genotype $F(1,32) = 6.809$, $p = 0.0312$; no effect of distractor onset $F(4,32) = 2.564$, $p = 0.0572$; Figure 3.7B). Importantly, neither response latency (RM-ANOVA, no effect of genotype $F(1,32) = 1.045$, $p = 0.3367$; main effect of distractor onset $F(4,32) = 7.069$, $p = 0.0003$; Figure 3.7C) nor reward collection latency varied between genotypes (RM-ANOVA, no effect of genotype $F(1,32) = 0.7467$, $p = 0.4127$; main effect of distractor onset $F(4,32) = 3.226$, $p = 0.0248$; Figure 3.7D).

Figure 3.7 VACHT^{Six3-Cre-flox/flox} mice are more susceptible to distraction. Mice were subjected to a series of distraction trials and the average values of 50 trial sessions per distractor onset are plotted. **A**, Mean response accuracy. **B**, Mean rate of omission. **C**, Mean response latency. **D**, Mean reward collection latency ($n = 6$, data are mean $\pm$ SEM, * represents significant differences between genotypes, # represents significant differences within genotypes; $*p < 0.05$).

Figure 3.7 VACHT^{Six3-Cre-flox/flox} mice are more susceptible to distraction.



3.4.7 Galantamine improves attention in wild-type mice on a demanding task

Detection of pro-attentive effects of pharmacological manipulations on the 5-CSRT is hampered by possible ceiling effects (Robbins, 2002). To detect differences in mice it is important to test the drug on challenging conditions, which can be achieved by shortening the duration of the stimulus presentation (Romberg et al., 2011). To find a suitably challenging task in which we could observe increased attention, we trained a group ($n = 8$) of wild-type mice on the 5-CSRT, and ran them through the probe trial series, serially reducing stimulus duration (1.5, 1, 0.8, and 0.6 s). Choice accuracy ($F(4,31) = 13.77$, $p < 0.0001$; Fig. 3.8A) and rate of omissions ($F(4,31) = 6.716$, $p = 0.0024$; Fig. 3.8B) were significantly affected by reducing stimulus duration. Post hoc analysis revealed that at 0.6 s stimulus duration the rate of accuracy was significantly reduced, and omissions significantly increased from the 1.5 s stimulus duration. We therefore chose both, 0.8 s stimulus duration and the more challenging 0.6 s stimulus duration, for pharmacological testing. Administration of galantamine (1 mg/kg, i.p.) 1 h before 5-CSRT testing at 0.8 s did not improve accuracy (paired t test, $t(7) = 1.287$, $p = 0.2544$; Fig. 3.8C) or omissions (paired t test, $t(7) = 0.4581$, $p = 0.6661$; Fig. 3.8D). However, when administered before a 0.6 s stimulus duration session, galantamine (1 mg/kg) significantly improved accuracy compared with saline (paired t test, $t(7) = 2.405$, $p = 0.0471$; Fig. 3.8E) and significantly reduced the rate of omission (paired t test, $t(7) = 2.379$, $p = 0.0489$; Fig. 3.8F). Response latency (paired t test, $t(7) = 1.296$, $p = 0.2360$), and reward collection latency (paired t test, $t(7) = 0.390$, $p = 0.7080$) were not changed by galantamine injections (data not shown). These results suggest that increased cholinergic tone can increase attentional performance when the probe trial is sufficiently demanding to avoid a potential ceiling effect.

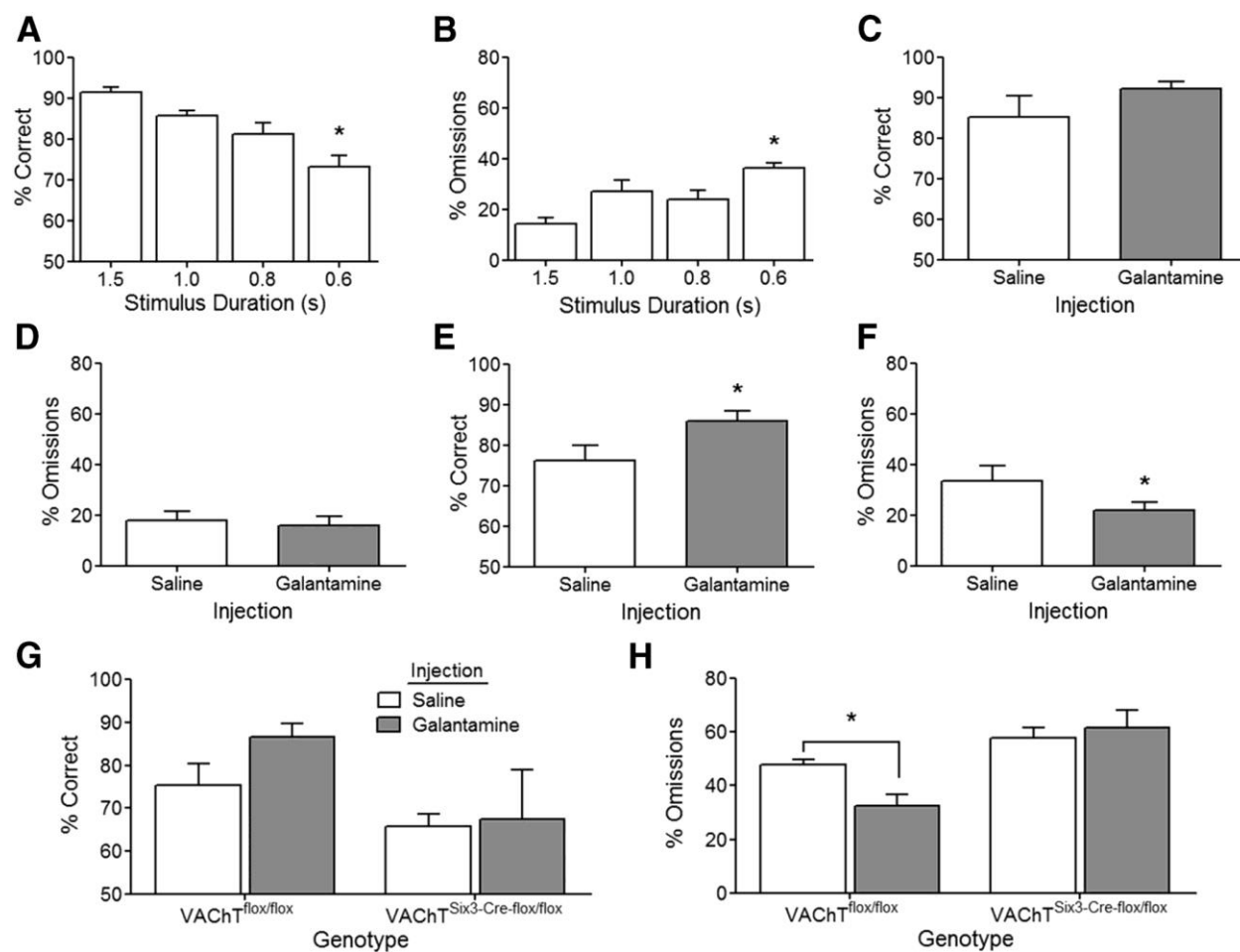
3.4.8 Galantamine does not improve attention deficits in VACHTSix3-Cre-flox/flox mice

To investigate if the deficits observed in VACHTSix3-Cre-flox/flox are exclusively related to decreased levels of synaptic ACh, we injected mice with galantamine (1 mg/Kg IP), a

dose that effectively improved performance of wild-type mice (Fig. 3.8), and tested both VACHTSix3-Cre-flox/flox and VACHTflox/flox mice at 0.6 s (50 trials). Galantamine tended to improve choice accuracy, albeit this effect did not reach statistical significance (paired t test, $t(5) = 1.954$, $p = 0.1224$; Fig. 3.8G). However, the drug was able to significantly reduce rate of omissions (paired t test, $t(5) = 3.383$, $p = 0.0277$; Fig. 3.8H) in VACHTflox/flox mice. Interestingly, galantamine had no effect on the performance of VACHTSix3-Cre-flox/flox mice, neither improving accuracy (paired t test, $t(5) = 0.162$, $p = 0.880$; Fig. 8G) nor rate of omission (paired t test, $t(5) = 0.868$, $p = 0.434$; Fig. 3.8H).

Figure 3.8 Galantamine improves attention in wild-type, but not in VACHT^{Six3-Cre-flox/flox} mice. Wild-type mice ($n = 8$) were subjected to a series of probe trials and the average values of 50 trial sessions are plotted. **A**, Mean accuracy. **B**, Mean rate of omissions. Effect of galantamine (1 mg/kg i.p.) on **(C)** response accuracy and **(D)** rate of omission in wild-type mice at a 0.8 s stimulus duration ($n = 8$). Effect of galantamine on **(E)** response accuracy and **(F)** rate of omission in wild-type mice at a 0.6 s stimulus duration ($n = 8$). Effect of galantamine (1 mg/Kg I.P.) on **(G)** choice accuracy and **(H)** rate of omission in VACHT^{flox/flox} and VACHT^{Six3-Cre-flox/flox} mice ($n = 6$, data are mean $\pm$ SEM, $*p < 0.05$).

Figure 3.8 Galantamine improves attention in wild-type, but not in VACHT^{Six3-Cre-flox/flox} mice.

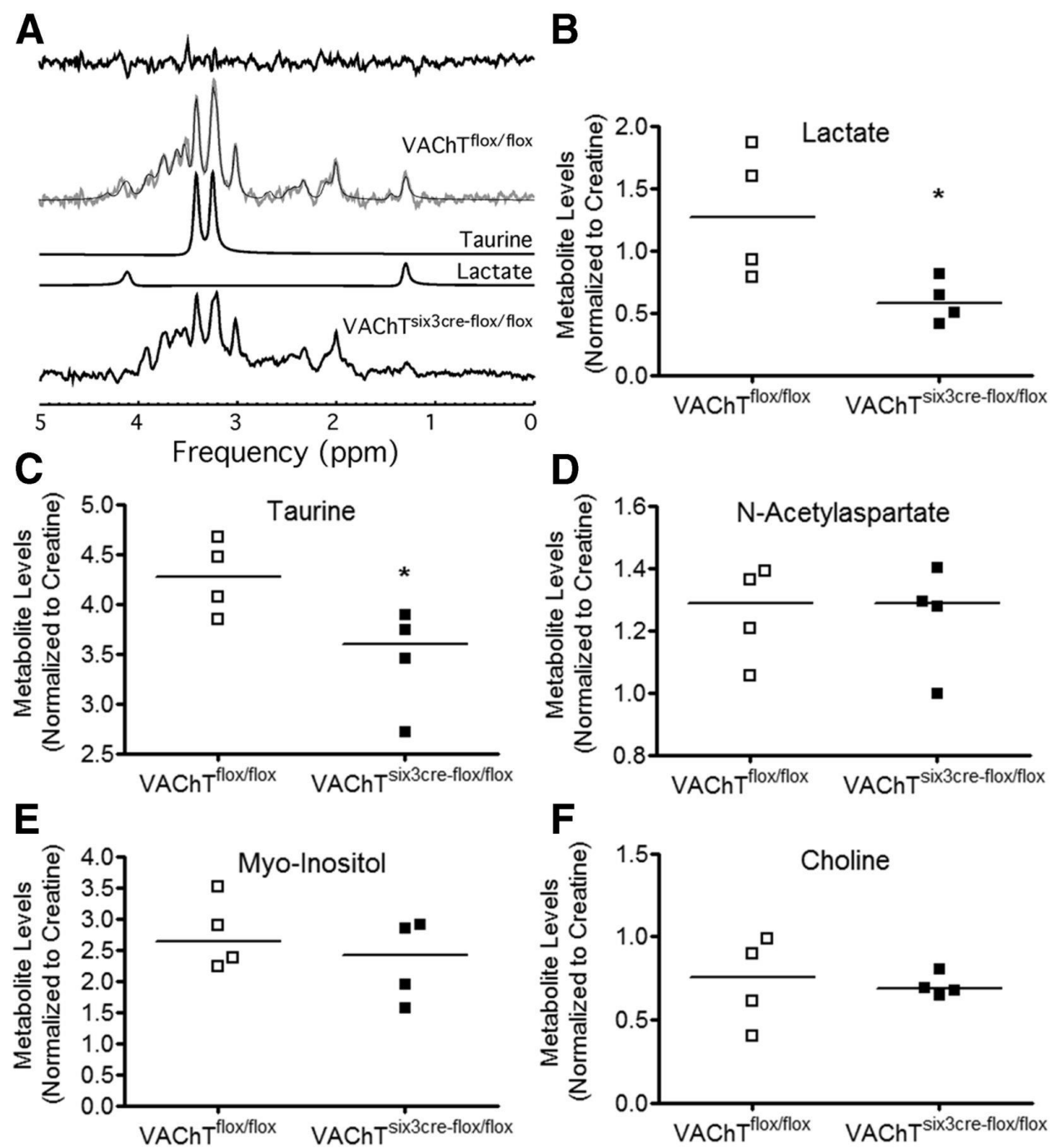


3.4.9 Deletion of forebrain VACHT results in metabolic abnormalities in the PFC

The lack of effect of galantamine in VACHTSix3-Cre-flox/flox suggests that diminished ACh release in mutant mice may not be sufficiently increased by galantamine to reverse the attentional deficits in these mice. In addition to that, a chronic decrease in cholinergic tone may cause circuitry or metabolic changes that could affect how neuronal circuitries are recruited for specific cognitive tasks. We used in vivo magnetic resonance spectroscopy to assess if metabolic parameters were affected in the prefrontal region of VACHT-deficient mice (Fig. 3.9A; representative spectra). This analysis revealed that VACHTSix3-Cre-flox/flox mice had significantly less Lac ($t(6) = 2.600$, $p = 0.0428$; Fig. 3.9B) and Tau ($t(6) = 2.522$, $p = 0.0452$; Fig. 3.9C) than controls. Levels of NAA ($t(6) = 0.0907$, $p = 0.9307$; Fig. 3.9D), Myo ($t(6) = 0.9598$, $p = 0.3742$; Fig. 3.9E), and Cho ($t(6) = 0.1461$, $p = 0.8886$; Fig. 3.9F) remained unchanged.

Figure 3.9. VACHT^{Six3-Cre-flox/flox} mice have metabolic abnormalities in the PFC. *In vivo* magnetic resonance spectroscopy of neuronal metabolites. **A, 9.4 tesla ¹H magnetic resonance spectroscopy data from VACHT^{flox/flox} (top) and VACHT^{Six3cre-flox/flox} (bottom) mice. The VACHT^{flox/flox} data are shown in gray with fit superimposed (black line) and residual shown above. Individual component spectra for Tau and Lac are also provided. **B**, Levels of Lac. **C**, Levels of Tau. **D**, Levels of NAA. **E**, Levels of Myo. **F**, Levels of Cho ($n = 4$, data shown are the median and individual values per mouse, $*p < 0.05$).**

Figure 3.9. VACHT^{Six3-Cre-flox/flox} mice have metabolic abnormalities in the PFC.



3.4.10 Deletion of forebrain VACHT results in altered RNA metabolism in the PFC

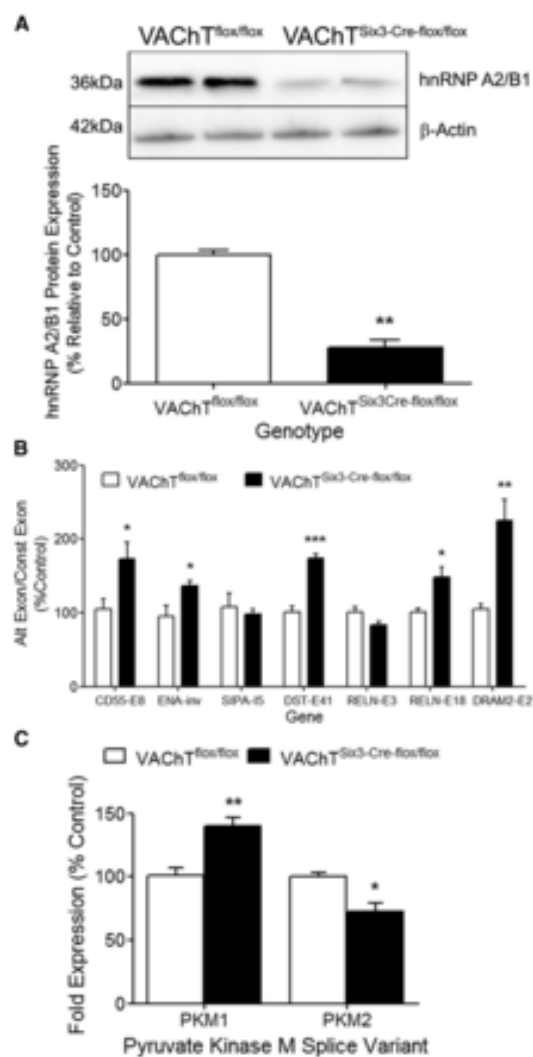
Cholinergic deficits in AD have been proposed to cause major transcriptome changes via aberrant hnRNPA2/B1 expression (Berson et al., 2012). hnRNPA2/B1 refers to a family of proteins that functions as splicing factors and mRNA chaperones (Hoek et al., 1998; Kamma et al., 1999). This gene family is critical for regulating alternative splicing in numerous genes involved with synaptic plasticity and cognition (Berson et al., 2012). Its expression is severely reduced in Alzheimer brain and appears enhanced in primary mouse neurons under carbachol induction (Berson et al., 2012), suggesting cholinergic regulation of hnRNPA2/B1 proteins. To determine whether the PFC of VACHTSix3-Cre-flox/flox shows parallel suppression of the hnRNPA2/B1 proteins, their levels were assessed. Compared with controls, the PFC of VACHTSix3-Cre-flox/flox mice showed a significant reduction in hnRNPA2/B1 expression (75% decrease, $t(6) = 4.941$, $p = 0.0026$; Fig. 3.10A). We then used qPCR to assess whether the decrease in hnRNPA2/B1 could have a functional impact on RNA processing in the PFC. We evaluated the alternative splicing of the key genes, SIPA1L1(SIPA), REELIN(RELN), DRAM2, CD55, DYSTONIN (DST), and ENAH, as manifested by increased exon inclusion tested both in Alzheimer's brain and in mouse brain depleted of its cholinergic neurons by saporin-mediated treatment (Berson et al., 2012). This analysis revealed that VACHTSix3-Cre-flox/flox mice had significant changes in the splicing of these genes in the PFC, with significantly increased inclusion of exon 8 of CD55 ($t(10) = 2.550$, $p = 0.0289$), exon 41 of DST ($t(10) = 7.436$, $p = 0.0001$), exon 18 of RELN ($t(10) = 3.230$, $p = 0.0090$), and exon 2 of DRAM2 ($t(10) = 3.990$, $p = 0.0260$). In addition the inv isoform of the ENAH gene was also significantly increased ($t(10) = 2.522$, $p = 0.0303$). In contrast, intron 5 of SIPA ($t(10) = 0.5449$, $p = 0.5978$) and exon 3 of RELN ($t(10) = 2.215$, $p = 0.0511$), which have also been shown to be affected in AD, were unchanged, although we detected a trend for the latter (Fig. 3.10B).

hnRNPA2/B1 has been shown to regulate the splicing of pyruvate kinase M (PKM) enzyme, which in turn dictates lactate metabolism (David et al., 2010). Knockdown of hnRNPA2/B1 expression in vitro favors the PKM1 isoform, which leads to reduced

levels of Lac, whereas upregulation hnRNPA2/B1 favors the PKM2 isoform and increased Lac levels (Clower et al., 2010; for review, see Chen et al., 2010). To test whether alternative splicing of PKM occurs in VACHTSix3-Cre-flox/flox mice, we performed qPCR to determine the expression of the PKM1 and PKM2 splice variants. Interestingly the VACHTSix3-Cre-flox/flox mice showed a significant upregulation of the PKM1 variant ($t(10) = 4.277$, $p = 0.0016$), and a significant reduction in the PKM2 variant ($t(10) = 3.073$, $p = 0.0110$; Fig. 3.10C), effectively changing the ratio between these two enzymes.

Figure 3.10. VACHTSix3-Cre-flox/flox mice have abnormal RNA processing in the PFC. A, hnRNPA2/B1 protein expression in the PFC with representative immunoblots (inset, n = 4). B, qPCR analysis of alternative splicing events for CD55, ENAH, SIPA, Dystonin (DST), Reelin (RELN), and DRAM2. C, Expression of the PKM1 and PKM2 isoforms. Alternative exon levels are normalized to a constitutive exon from the same gene (n = 6, data are mean $\pm$ SEM, *p < 0.05, **p < 0.01, and ***p < 0.001).

Figure 3.10. VACHT^{Six3-Cre-flox/flox} mice have abnormal RNA processing in the PFC.



3.5 Discussion

In this report we show that forebrain VAcHT knock-out mice present deficits in two domains of executive function, cognitive flexibility and attention. Additionally, VAcHT-deficient mice exhibit metabolic deficits in the PFC suggestive of changes in PFC circuitry. Furthermore, these mice have reduced expression of a key splicing factor, hnRNPA2/B1, which has been previously implicated in synaptic plasticity deficits in AD (Berson et al., 2012) and in mutations that were recently discovered in rare proteinopathies (Kim et al., 2013). These changes have a functional impact on RNA metabolism in the PFC of VAcHT-deficient mice. These results suggest that VAcHTSix3-Cre-flox/flox mice may represent a powerful tool to dissect the molecular and neurochemical basis of executive dysfunction.

3.5.1 Cognitive flexibility in VAcHTSix3-Cre-flox/flox mice

VAcHTSix3-Cre-flox/flox mice were able to associate an image with a reward, and another with a punishment, in the pairwise visual discrimination task. Acquisition of this task has been shown to be dependent on glutamatergic signaling, with mice lacking the GLAST glutamate transporter being unable to acquire the task (Karlsson et al., 2009). Evidence suggests that the NMDA receptor is an important molecular switch for the acquisition of the task (Brigman et al., 2008; Barkus et al., 2012). Our results indicate that cholinergic signaling is not required for such learning. In contrast, when contingencies of the pairwise task were reversed, forebrain VAcHT knock-out mice were unable to adapt and learn the new rule. Reversal learning in a visual discrimination task has been proposed to serve as a measure of cognitive flexibility in rodents (Izquierdo et al., 2006; Brigman et al., 2008). Neurochemical modulation of reversal learning is complex, as it can be enhanced by targeting multiple neurotransmitter signaling systems including serotonergic (Brigman et al., 2010), dopaminergic (Izquierdo et al., 2006), and glutamatergic (Balschun et al., 2010). The role of cholinergic signaling has been focused predominantly on muscarinic receptors (Ridley et al., 1984, 1985). Determining the exact mechanism has been difficult, as M1 receptor agonists facilitate cognitive flexibility (McCool et al., 2008; Shirey et al., 2009), but no

effects on cognitive flexibility were observed in M1-null mice (Bartko et al., 2011). There is evidence suggesting that M2 and M4 receptors may be involved in cognitive flexibility (Nieves-Martinez et al., 2012). Our results indicate that cholinergic signaling is essential for modulation of cognitive flexibility.

3.5.2 Attention deficits in VACHT-deficient mice

To further understand the role of forebrain ACh in executive function we evaluated attention on forebrain VACHT knock-out mice using the 5-CSRT task, a test suggested to be dependent on PFC cholinergic signaling (Guillem et al., 2011; for review, see Robbins, 2000; Dalley et al., 2004a). In line with our previous finding with the VACHTSix3-Cre-flox/flox mouse line having learning and memory deficits (Martyn et al., 2012), these mice showed impairments in acquisition of the 5-CSRT, taking nearly twice as long as controls to reach criteria at the 4 and 2 s phase of the training process. Interestingly, they were not impaired during the pretraining phase, wherein mice are taught to respond to the touchscreen. These results suggest that simple operant conditioning is not dependent on forebrain cholinergic signaling, but rather that forebrain ACh is responsible for the use of such information to perform higher order cognitive tasks. Attentional demand deficits were probed by reducing stimulus duration. Choice accuracy, perseverative, and premature responses of VACHTSix3-Cre-flox/flox mice were unaffected. However, the rate of omission for VACHTSix3-Cre-flox/flox was significantly increased. Additionally, in the presence of a noise distractor VACHTSix3-Cre-flox/flox mice were significantly less attentive than controls, showing a much higher rate of omissions. This test was performed under a condition in which the performance of VACHT-deficient mice was on par with controls without the auditory distraction. The auditory distraction task gives a clear indication that the attention deficits observed in VACHTSix3-Cre-flox/flox mice were not due to visual abnormalities. These findings are aligned with previous work, given that cue detection has been shown to involve transient rises in ACh release (Himmelheber et al., 2000; Parikh et al., 2007). Our experiments agree with previous work indicating a key role for cholinergic activity in improving response to distractors in attentional tasks (Gill et al., 2000; Terry et al., 2002;

Newman and McGaughy, 2008; Broussard et al., 2009; Howe et al., 2010; St Peters et al., 2011).

Regulation of attentional performance by endogenous ACh has been investigated in rats using immunolesion with IgG-192 saporin (Walsh et al., 1996; Risbrough et al., 2002; Lehmann et al., 2003; Chudasama et al., 2004; Dalley et al., 2004b). Specifically, deficits in choice accuracy and increases in perseverative responses were observed in rats following 192 IgG-saporin-induced lesions (McGaughy et al., 2002; Dalley et al., 2004b). In these studies no effects were observed on rates of omissions. Our experiments show a somewhat distinct feature, demonstrating increased rates of omission, without changes in perseverative response. Interestingly, selective elimination of the $\beta 2$ nAChR in mice also revealed an increase in rate of omissions (Guillem et al., 2011). The differences between genetically modified and lesioned animals could therefore be species related. Alternatively, this difference may reflect the capacity of cholinergic neurons to secrete more than one neurotransmitter (El Mestikawy et al., 2011; Prado et al., 2013). Basal forebrain cholinergic neurons can release glutamate in vitro (Allen et al., 2006). There is also evidence that these neurons possess the machinery to release GABA (Henny and Jones, 2008). Recent experiments targeting striatum cholinergic neurons revealed striking behavioral differences between mice that had cholinergic elimination, using immunolesion, or mice that were genetically targeted to eliminate striatal ACh release (Kitabatake et al., 2003; Guzman et al., 2011; for review, see Prado et al., 2013). Immunolesion of cholinergic neurons can therefore have effects beyond impairing ACh release and could affect cotransmission. Whether cotransmission has a role in the small phenotypic differences between our experiments and previous work using rats injected with IgG-192-saporin remains to be determined.

Galantamine was unable to rescue the attention deficits in VAcHTSix3-Cre-flox/flox mice. We have previously shown, using a mouse line with decreased VAcHT expression, that galantamine could reverse social memory deficits (Prado et al., 2006) and object recognition memory deficits (de Castro et al., 2009b; De Jaeger et al., 2013). Hence, the fact that galantamine can improve performance of control mice, but not of VAcHTSix3-Cre-flox/flox mice, suggests that the latter may not release sufficient

synaptic ACh to be enhanced by galantamine. Alternatively, these sophisticated tasks may be more affected by changes in neuronal circuitry. The *in vivo* ¹H spectroscopy data suggest that critical metabolic changes occur in VACHT-deficient mice; namely, reduced levels of both Tau and Lac in the prefrontal region. Lac has been proposed as the preferred metabolic substrate for neurons (for review, see Pellerin et al., 2007), suggesting that decreased cholinergic tone may lead to a general decrease in neuronal activity.

3.5.3 Alterations in PFC function in VACHT-deficient mice

The reduction in PFC hnRNPA2/B1 observed in VACHTSix3-Cre-flox/flox mice is in line with previous work indicating cholinergic-mediated regulation of its expression in AD (Berson et al., 2012). Furthermore, we found that alternative splicing alteration pattern in the PFC of these mice is similar to the pattern found in both AD patient samples and hypocholinergic animal models (Berson et al., 2012). Overall, these changes suggest alterations in the PFC circuitry. Furthermore, the splicing change found in the PKM gene indicates a potential mechanism for cholinergic regulation of Lac metabolism. Of note, nearly significant differential expression of the PKM variants was observed in exon array datasets from the entorhinal cortices of three AD patients and three matched controls studied previously, despite the small number of samples (Berson et al., 2012; $p < 0.051$; raw data deposited in the GenBank).

Decreased Lac levels have been observed in mouse models of AD (Du Yan et al., 2000; Marjanska et al., 2005). Moreover, in the CRND8 transgenic mouse model of AD, lower levels of Tau were observed *in vivo* by H1-NMR (Salek et al., 2010). Interestingly, high levels of Lac in cultured neurons decrease susceptibility to A β -derived peptides and oxidative stress *in vitro* (Newington et al., 2012). Together, these data suggest that VACHTSix3-Cre-flox/flox mice may be useful for understanding metabolic abnormalities that occur in dementia.

3.6 Conclusion

In summary, by eliminating VACHT from the forebrain we determined that cholinergic signaling regulates executive function, affects metabolism, and also RNA processing in the PFC. The PFC has been shown to mediate salient cue detection (Himmelheber et al., 2000; Parikh et al., 2007), and it serves as a hub that regulates numerous neurotransmitter interactions (Dalley et al., 2004a; Carr et al., 2007; Tait and Brown, 2008). Our work helps to define the specific role played by ACh in behaviors related to cortical functioning, and its potential underlying mechanisms. Decreased levels of VACHT in the brain have been reported in AD (Efange et al., 1997; Chen et al., 2011), therefore the executive dysfunction and mRNA processing abnormalities we observed in VACHT-deficient mice may be of relevance to model this specific deficiency in humans. Therefore, this work provides novel insights into the basic neurochemical contributors governing executive function.

3.7 Acknowledgements

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Chapter 4

$\alpha 7$ nicotinic ACh receptor-deficient mice exhibit sustained attention impairments that are reversed by $\beta 2$ nicotinic ACh receptor activation

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4.2 Chapter Summary

Disruptions of executive function, including attentional deficits, are a hallmark of a number of diseases. ACh in the prefrontal cortex regulates attentive behaviour; however, the role of $\alpha 7$ nicotinic ACh receptor ($\alpha 7$ nAChR) in attention is contentious. In order to probe attention, we trained both wild-type and $\alpha 7$ nAChR knockout mice on a touch screen-based five-choice serial reaction time task (5-CSRT). Following training procedures, we then tested sustained attention using a probe trial experiment. To further differentiate the role of specific nicotinic receptors in attention, we then tested the effects of both $\alpha 7$ nAChR and $\beta 2$ nAChR agonists on the performance of both wild-type and knockout mice on the 5-CSRT task. At low doses, $\alpha 7$ nAChR agonists improved attentional performance of wild-type mice, while high doses had deleterious effects on attention. $\alpha 7$ nAChR knockout mice displayed deficits in sustained attention that were not ameliorated by $\alpha 7$ nAChR agonists. However, these deficits were completely reversed by the administration of a $\beta 2$ nAChR agonist. Furthermore, administration of a $\beta 2$ nAChR agonist in $\alpha 7$ nAChR knockout mice elicited similar biochemical response in the prefrontal cortex as the administration of $\alpha 7$ nAChR agonists in wild-type mice. Our experiments reveal an intricate relationship between distinct nicotinic receptors to regulate attentional performance and provide the basis for targeting $\beta 2$ nAChRs pharmacologically to decrease attentional deficits due to a dysfunction in $\alpha 7$ nAChRs.

4.3 Introduction

Attentional performance can be severely compromised in different neuropsychiatric and neurodegenerative diseases, including schizophrenia and Alzheimer's disease (Mega and Cummings, 1994; Buckner, 2004). ACh release in the prefrontal cortex (PFC), a brain area known to play a central role in attention (Kastner and Ungerleider, 2000; Corbetta and Shulman, 2002; Buschman and Miller, 2007), is important for the regulation of attentive behaviour (Elliott, 2003). Schizophrenic patients present severe physiological and molecular dysfunctions in the PFC (Weinberger et al., 1986; Mirnics et al., 2000; Guillozet-Bongaarts et al., 2014). One of the more profound molecular changes is the loss of the $\alpha 7$ nicotinic ACh receptor ($\alpha 7$ nAChR), encoded by the

CHRNA7 gene. Although the genetic linkage between the CHRNA7 gene and schizophrenia is complex, with studies pointing towards and against CHRNA7 as a risk gene for the disease (Xu et al., 2001; Zammit et al., 2007), robust decreases in protein and mRNA expression of the $\alpha 7$ nAChR have been shown in the PFC of patients with schizophrenia (Guan et al., 1999; Guillozet-Bongaarts et al., 2014). Moreover, in Alzheimer's disease, A β peptides can bind to $\alpha 7$ nAChRs (Wang et al., 2000) and disrupt their function (Chen et al., 2006).

There is accumulating evidence demonstrating that cue detection during attentional efforts is mediated by nicotinic receptor signalling (McGaughy et al., 1999a; Grottick and Higgins, 2000; Parikh et al., 2007, 2010). $\beta 2$ nAChRs are both necessary and sufficient to regulate attention in mice using a non-demanding five-choice serial reaction time task (5-CSRT) paradigm (Guillem et al., 2011). On the other hand, the role of $\alpha 7$ nAChRs in attention is still not completely understood. Initial studies suggest that CHRNA7 $^{-/-}$ mice present deficits in sustained attention (Hoyle et al., 2006; Young et al., 2007). However, it has been reported that for less demanding tasks no deficits were observed in $\alpha 7$ nAChR-null mice (Guillem et al., 2011). Taken together, these results suggest that attentional deficits in CHRNA7 $^{-/-}$ mice may depend on the attentional load.

Pharmacological manipulations of $\alpha 7$ nAChRs have also produced conflicting results, most likely because of the poor selectivity of the drugs used (Grottick and Higgins, 2000; Pichat et al., 2007; Rezvani et al., 2009; Wallace et al., 2011a). Interestingly, studies in humans have shown that agonists for the $\alpha 7$ nAChR can improve the performance of patients suffering from schizophrenia on neurocognitive tests (Olincy et al., 2006; Olincy and Stevens, 2007).

Here, we report that $\alpha 7$ nAChR-null mice present deficits in their ability to sustain attention in a demanding paradigm. Moreover, we found that activation of $\alpha 7$ nAChRs increased biochemical signalling and attention in wild-type (WT) mice, but not in CHRNA7 $^{-/-}$ mice. Interestingly, activation of $\beta 2$ nAChRs triggered similar biochemical pathways as $\alpha 7$ nAChR agonists and reversed attentional deficits in $\alpha 7$ nAChR-null mice. These results suggest that $\alpha 7$ nAChRs may contribute to attention performance, but activation of $\beta 2$ nAChRs can bypass the deficits triggered by deficient $\alpha 7$ nAChR

signalling. Our results suggest that the $\alpha 7$ nAChR plays a role in sustained attention during demanding tasks and that $\beta 2$ nAChR drugs may be of potential use for correcting cognitive and molecular signalling deficits seen in psychiatric or neurological disorders in which $\alpha 7$ nAChRs are affected.

4.4 Material and Methods

4.4.1 Animals

CHRNA7^{-/-} mice (B6.129S7 nAChR Chrna7^{tm1Bay/J}) were purchased from Jackson Laboratories (Bar Harbor, ME, USA). Mice were housed in groups of three or four per cage in a temperature-controlled room with 12/12 h light/dark cycle (07:00–19:00 h), and water was provided ad libitum. Only male mice were used in these studies. For the 5-CSRT studies, mice were housed in pairs and restricted to 85% of their free-feed weight and maintained on 85% of their weight for the duration of the studies as described (Kolisnyk et al., 2013a,b). All behavioural experiments were conducted between 12:00 and 17:00 h. We followed the ARRIVE guidelines (Kilkenny et al., 2010); hence, mice were randomized for behavioural tests, and the experimenter was blind to the genotype. All procedures were conducted in accordance with guidelines from the Canadian Council of Animal Care at the University of Western Ontario with an approved institutional animal protocol (2008-127).

4.4.2 Five-choice serial reaction time task training

A cohort of WT and CHRNA7^{-/-} mice ($n = 7$ per genotype, 5–6 months old) was trained in the 5-CSRT task using the automated Bussey–Saksida Mouse Touch Screen System model 81426 (Campden Instruments, Lafayette, IN, USA). Schedules were designed, and data were collected using the abet ii touch software v.2.15 (Lafayette Instruments, Lafayette, IN, USA). Mice were trained to respond to the touch screen chambers using a previously described operant training procedure (Kolisnyk et al., 2013a, 2013b).

Training on the 5-CSRT task was performed as previously described (Romberg et al., 2011). Once the performance of a mouse reached criterion (80% accuracy, 20%

omissions for three consecutive days) at 4 s stimulus duration, stimulus duration was reduced to 2 s. After reaching criterion at a 2 s stimulus duration, the mouse was tested on probe trials.

4.4.3 Probe trial

To probe attention in mice, we used a previously described probe trial schedule with reduced stimulus durations (Romberg et al., 2011; Kolisnyk et al., 2013a). Mice were tested for 2 days at a given stimulus duration (1.5, 1, 0.8 or 0.6 s). Each day, sessions lasted 50 trials or 1 h. After each test, the animal was retested at the 2 s stimulus duration for 2 days, until the mice had been tested at all stimulus durations. The order of the probe trial sessions was semi-randomized using a Latin square method. Behavioural data were averaged over the 2 days of each stimulus duration.

4.4.4 Drug injections

For all drug experiments, mice were tested at the 0.6 s stimulus duration. The same mice used for the initial 5-CSRT experiments were used for the drug studies. Animals were injected 30 min before testing for the PHA-543,613 (Sigma-Aldrich, St Louis, MO, USA) and PNU-228,927 (Tocris Bioscience, Bristol, UK) experiments and 15 min before testing for the ABT-418 (Sigma-Aldrich) experiment (McGaughy et al., 1999b). Doses of PHA-543,613 [0.33, 1 and 3 mg·kg⁻¹, i.p. (Acker et al., 2008)], PNU-282,927 [1, 3 and 5 mg·kg⁻¹, i.p. (Hajos et al., 2005; Vicens et al., 2013)] and ABT-418 [0.04, 0.13 and 0.39 mg·kg⁻¹, i.p. (McGaughy et al., 1999a)] were chosen based on previous studies. In control experiments, vehicle (saline) was injected. The order of drug injections was semi-randomized using a Latin square method. Between different doses in the drug injection experiments, mice were given two washout days during which they were baselined with a 2 s stimulus duration.

4.4.5 Analysis of 5-CSRT task

On all 5-CSRT task sessions, accuracy was calculated as the number of correct responses divided by the number of correct and incorrect responses (touches to a

wrong window while the correct stimulus was still displayed). Omissions were calculated as the total number of omitted trials divided by the number of total trials. Response latency was the time the mouse took to touch the correct stimulus after the onset of its display. Reward collection latency was defined as the time it took the mouse to enter the reward magazine following a correct response. A premature response was counted when the mouse touched one of the windows prior to the stimulus being displayed. Finally, a perseverative response was any identical response that occurred following a correct, incorrect or premature response.

4.4.6 Food intake in food-deprived mice

Feeding behaviour was analysed as previously described (Semenova and Markou, 2007). Naive groups of WT and *CHRNA7*^{-/-} mice (n = 8 per genotype) were housed individually and were deprived of food overnight before the test. During the test, mice were placed in a clean cage and given 20 g of standard chow. Food intake was measured 20, 40, 60 and 80 min after the start of the test. Food intake was normalized to the body weight of the animals.

4.4.7 qPCR

Total RNA was extracted from freshly dissected PFC tissue, using the Aurum Total RNA for fatty and fibrous tissue kit (Bio-Rad Laboratories, Hercules, CA, USA); cDNA synthesis and quantitative PCR (qPCR) analysis of nicotinic receptor expression were performed as previously described (Guzman et al., 2011; Kolisnyk et al., 2013a).

4.4.8 Western Blotting

Western blotting was performed as previously described (Martins-Silva et al., 2011). For analysis of phospho-proteins in the PFC, mice were given i.p. drug injections and were killed 30 min later. Tissue was then homogenized in lysis buffer supplemented with protease and phosphatase inhibitor cocktails (Thermo Fisher Scientific, Waltham, MA, USA). The antibodies used were anti-vesicular ACh transporter (VAChT) (catalogue #139103; Synaptic Systems, Göttingen, Germany), anti-ChAT (catalogue #1DB-001-

0000849693; Millipore, Billerica, MA, USA), anti-synaptophysin (catalogue #S5768; Sigma-Aldrich), anti-ERK1/2 (catalogue #4695; Cell Signaling Technology, Danvers, MA, USA), anti-phospho-ERK1/2 (catalogue #4372; Cell Signaling Technology), anti-cFos (catalogue #4384; Cell Signaling Technology) and anti- β -actin (catalogue #ab49900; Abcam, Cambridge, UK). Band intensity was quantified using fluorochemq software (Thermo Fisher Scientific).

4.4.9 Statistical analyses

All data are expressed as mean $\pm$ SEM. sigmastat 3.5 (Systat Software, San Jose, CA, USA) was used for all statistical analysis. Comparisons between two experimental groups were made by Student's t-test. When several experimental groups or treatments were analysed, one-way ANOVA or two-way ANOVA with repeated-measures tests were used as required. Statistically significant effects were further analysed using Tukey's honestly significant difference post hoc tests. In all analyses, $P < 0.05$ was considered statistically significant.

4.5 Results

4.5.1 $\alpha 7$ nAChR-null mice present normal acquisition on the 5-CSRT task

No difference between CHRNA7 $^{-/-}$ mice and WT controls was observed in the number of sessions required to reach criterion at any of the pre-training phases for the 5-CSRT task [Fig. 4.1.1; RM-ANOVA: no effect of genotype, $F(1,14) = 2.814$, $P = 0.1156$; main effect of training phase, $F(4,14) = 104.3$, $P < 0.0001$; no interaction effect, $F(4,14) = 1.126$, $P = 0.3535$]. During training on the 5-CSRT task as well, CHRNA7 $^{-/-}$ mice took as many sessions as WT controls to achieve criterion at both the 4 and 2 s stimulus durations [RM-ANOVA: no effect of genotype, $F(1,14) = 2.552$, $P = 0.1325$; main effect of stimulus duration, $F(1,14) = 57.78$, $P < 0.0001$; no interaction, $F(1,14) = 4.472$, $P = 0.0529$; Fig. 4.1.1B]. It should be noted that there was a strong tendency for the CHRNA7 $^{-/-}$ mice to take longer to learn the task at the 4 s stimulus

duration, which may reflect previously documented impairments in procedural learning in these mice (Young et al., 2011).

4.5.2 $\alpha 7$ nAChR-null mice have impaired sustained attention

Once mice reached criterion at 2 s stimulus duration, we assessed attention performance by using a probe trial, with reduced stimulus durations (1.5, 1, 0.8 and 0.6 s stimulus durations) as previously described (Romberg et al., 2011). Across all four stimulus durations, $CHRNA7^{-/-}$ mice performed similarly to controls in both total measures of omissions [RM-ANOVA: no effect of genotype, $F(1,36) = 3.235$, $P = 0.0972$; main effect of stimulus duration, $F(3,36) = 14.50$, $P < 0.001$; no interaction, $F(3,36) = 0.5136$, $P = 0.6755$; Figure 4.1.2A] and accuracy [RM-ANOVA: no effect of genotype, $F(1,36) = 0.06134$, $P = 0.8086$; main effect of stimulus duration, $F(3,36) = 9.208$, $P < 0.001$; no interaction, $F(3,36) = 0.6347$, $P = 0.5975$; Figure 4.1.2B]. To assess sustained attention, we analysed rate of omissions and response accuracy over blocks of 25 trials across the various stimulus durations of the probe trial experiment. As each probe trial session ends after 50 trials or 1 h, analysing blocks of 25 trials divided the performance between two halves: block A and block B. This procedure allowed us to determine if mice can sustain attention during the full period of the probe trial and maintain performance between the first and second periods of testing. Performance of control WT mice did not differ across the probe trial in terms of omissions [RM-ANOVA: no difference between blocks A and B, $F(1,6) = 1.904$, $P = 0.2168$; main effect of stimulus duration, $F(3,18) = 8.661$, $P < 0.001$; and no interaction, $F(3,18) = 0.4736$, $P = 0.7045$; Figure 4.1.2C] or accuracy [RM-ANOVA: no effect of blocks, $F(1,6) = 4.319$, $P = 0.0829$; main effect of stimulus duration, $F(3,18) = 4.897$, $P = 0.0166$; and no interaction, $F(3,18) = 0.4947$, $P = 0.6905$; Figure 4.1.2D]. In contrast, $CHRNA7^{-/-}$ mice displayed increased omission errors in the second half of the probe trial experiment compared with the first half [RM-ANOVA: main effect of block, $F(1,6) = 20.59$, $P < 0.001$; main effect of stimulus duration, $F(3,18) = 9.471$, $P < 0.001$; and main interaction effect, $F(3,18) = 12.13$, $P < 0.001$; Figure 4.1.2E]. Post hoc analysis confirmed that $CHRNA7^{-/-}$ mice had significantly more omission errors during the second half of the task at both the 0.8 and 0.6 s

stimulus durations, suggesting that these mice display impaired ability to sustain attention. Interestingly, *CHRNA7*^{-/-} mice did not present accuracy impairments across the two blocks [RM-ANOVA: no effect of block, $F(1,6) = 1.348$, $P = 0.2897$; main effect of stimulus duration, $F(3,18) = 5.877$, $P = 0.0056$; and no interaction effect, $F(3,18) = 0.6404$, $P = 0.5989$; Figure 4.1.2F].

Increases in omission on the 5-CSRT task have been proposed to be due to lack of attention, lack of motivation or motor impairments (Robbins, 2002). Given that *CHRNA7*^{-/-} mice were no different from controls in terms of latency to respond to stimulus or latency to collect the reward, it is unlikely that motivation or motor impairments are causing the deficits in sustained attention (Robbins, 2002; Spinelli et al., 2004). To address this, we measured several other parameters to test for motivational or aberrant behaviour in *CHRNA7*^{-/-} mice. $\alpha 7$ nAChR-null mice showed no difference in latency to respond to the stimulus [RM-ANOVA: no effect of genotype, $F(1,36) = 0.01533$, $P = 0.9035$; no effect of stimulus duration, $F(3,36) = 2.003$, $P = 0.1310$; no interaction, $F(3,36) = 1.223$, $P = 0.3154$; Figure 4.1.3A]. We then assessed response latency across blocks of trials to determine if the sustained attention deficits in *CHRNA7*^{-/-} mice may be due to delayed responsiveness. Response latency did not differ across blocks for either the WT [RM-ANOVA: no effect of block, $F(1,6) = 0.07218$, $P = 0.7972$; no effect of stimulus duration, $F(3,18) = 2.749$, $P = 0.0792$; and no interaction effect, $F(3,18) = 0.7886$, $P = 0.5159$; Figure 4.1.3B] or *CHRNA7*^{-/-} mice [RM-ANOVA: no effect of block, $F(1,6) = 0.2481$, $P = 0.6362$; no effect of stimulus duration, $F(3,18) = 2.2557$, $P = 0.1166$; and no interaction effect, $F(3,18) = 1.490$, $P = 0.2501$; Figure 4.1.3C]. We also assessed the time to retrieve their reward following a correct response [RM-ANOVA, no effect of genotype, $F(1,36) = 0.2025$, $P = 0.6607$; no effect of stimulus duration, $F(3,36) = 1.153$, $P = 0.3410$; no interaction, $F(3,36) = 0.2954$, $P = 0.8284$; Figure 4.1.3D] when compared with WT controls. Furthermore, we assessed reward latency across blocks of trials, and neither the WT [RM-ANOVA: no effect of block, $F(1,6) = 2.345$, $P = 0.1766$; no effect of stimulus duration, $F(3,18) = 2.176$, $P = 0.1262$; and no interaction effect, $F(3,18) = 0.5404$, $P = 0.6677$; Figure 4.1.3E) nor *CHRNA7*^{-/-} mice [RM-ANOVA, no effect of block, $F(1,6) = 0.02162$, $P = 0.8879$; no effect of stimulus duration, $F(3,18) = 0.6190$, $P = 0.6617$; and no

interaction effect, $F(3,18) = 0.3581$, $P = 0.7839$; Figure 4.1.3F) showed alteration in reward collection latency. To test whether $CHRNA7^{-/-}$ mice differ from WT controls in satiety, we measured food intake following food restriction in a group of naive mice. Compared with controls, $CHRNA7^{-/-}$ mice did not differ in food consumption over the course of the test [RM-ANOVA: no effect of genotype, $F(1,48) = 1.280$, $P = 0.2800$; main effect of time, $F(4,48) = 73.88$, $P < 0.001$; and no interaction effect, $F(4,48) = 1.296$, $P = 0.2849$; Figure 4.1.3G]. This is in line with previous work showing that these mice have normal motivation (Hoyle et al., 2011) and suggests that $CHRNA7^{-/-}$ mice have specific deficits in sustained attention.

Impulsivity and compulsivity were also assessed in $CHRNA7^{-/-}$ mice during the probe trial experiment. Compared with controls, $CHRNA7^{-/-}$ mice were no different in terms of premature responses, a measure of impulsivity [RM-ANOVA: no effect of genotype, $F(1,36) = 0.9222$, $P = 0.3575$; no effect of stimulus duration, $F(3,36) = 0.4541$, $P = 0.7161$; no interaction effect, $F(3,36) = 0.09521$, $P = 0.9621$; Fig. 4.1.4A, B], or perseverative responses, a measure of compulsive behaviour [RM-ANOVA: no effect of genotype, $F(1,36) = 0.04477$, $P = 0.8363$, main effect of stimulus duration, $F(3,36) = 4.105$, $P = 0.0140$; no interaction effect, $F(3,36) = 0.8660$, $P = 0.4685$, Fig. 4.1.4C, D].

The ability to release normal levels of ACh is critical to attention (Kolisnyk et al., 2013a,b); therefore, we investigated expression levels of the cholinergic machinery in the PFC of $CHRNA7^{-/-}$ mice. Compared with WT controls, $CHRNA7^{-/-}$ mice showed no significant change in expression of the VACHT [$t(4) = 0.375$, $P = 0.7291$] or ChAT. The sustained attention deficits in $CHRNA7^{-/-}$ mice are therefore not a result of an inherent dysfunction in the machinery required for ACh release (Figure 4.1.5A).

$\alpha 7$ nicotinic ACh receptor deletion has been suggested to cause compensatory changes in other nicotinic receptors during development (Yu et al., 2007). To determine if the PFC of adult $CHRNA7^{-/-}$ mice displayed altered expression of nicotinic receptors, we examined their expression by qPCR analysis. The PFC of $CHRNA7^{-/-}$ mice showed no significant change in the expression of $CHRNA4$ [$t(8) = 1.104$, $P = 0.3016$] or of $CHRNA2$ expression [$t(8) = 0.4893$, $P = 0.6378$]. In addition, we evaluated the

expression of the enzyme AChE and observed no significant difference between genotypes [$t(8) = 0.0409$, $P = 0.9684$]. As expected, we did not detect CHRNA7 expression in CHRNA7^{-/-} animals (Figure 4.1.5B).

To evaluate the biochemical correlates of neuronal activity in the PFC of CHRNA7^{-/-} mice, we determined protein levels of the immediate-early gene cFos, a known marker of activated neurons. Compared with the WT control, CHRNA7^{-/-} mice showed no significant change in cFos protein levels [$t(4) = 0.779$, $P = 0.4792$, Figure 4.1.5C]. Moreover, to test if the CHRNA7^{-/-} had impaired activation of relevant second messenger signalling cascades involved with nicotinic response in attention (Wallace and Porter, 2011b), we evaluated the phosphorylation status of ERK1/2 and observed no significant difference between genotypes [$t(4) = 0.331$, $P = 0.7575$, Figure 4.1.5D].

Figure 4.1.1. Pre-training on the 5-CSRT task. (a) Sessions to criteria during pretraining for the 5-CSRT task. Numbers designate phases of the pre-training (1 – ‘habituation’, 2 – ‘initial touch’, 3 – ‘must touch’, 4 – ‘must initiate’, 5 – ‘punish incorrect’). (b) Sessions to criteria during training on the 5-CSRT task. (Data are presented as mean $\pm$ SEM.).

Figure 4.1.1. Pre-training on the 5-CSRT task.

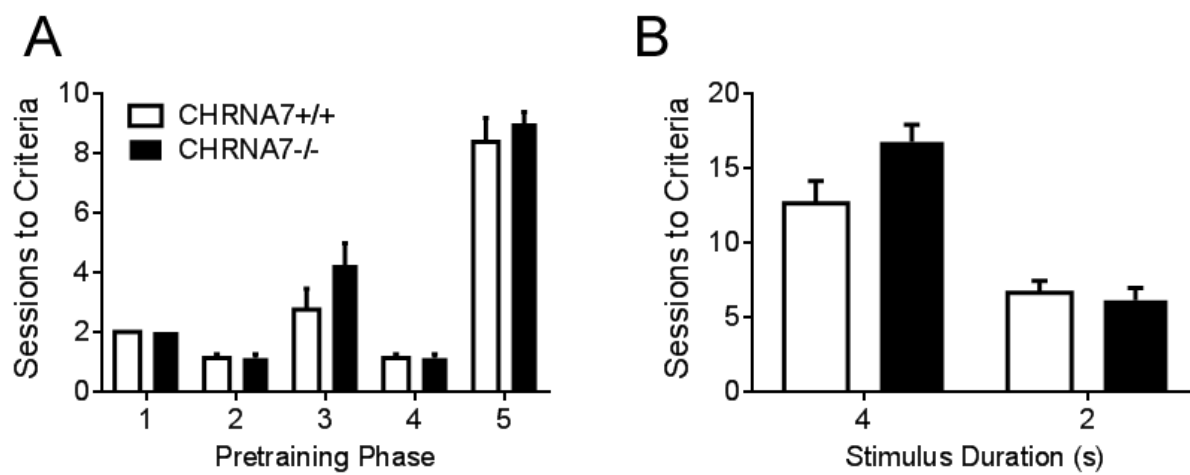


Figure 4.1.2. CHRNA7^{-/-} mice have impaired sustained attention. Comparison between genotypes of (A) omissions and (B) accuracy during the probe trial experiment using the 5-CSRT task. (C) Omissions and (D) accuracy across bins of 25 trials in WT mice. (E) Omissions and (F) accuracy across bins of 25 trials in CHRNA7^{-/-} mice (data are presented as mean $\pm$ SEM; *P < 0.05, **P < 0.01, ***P < 0.001).

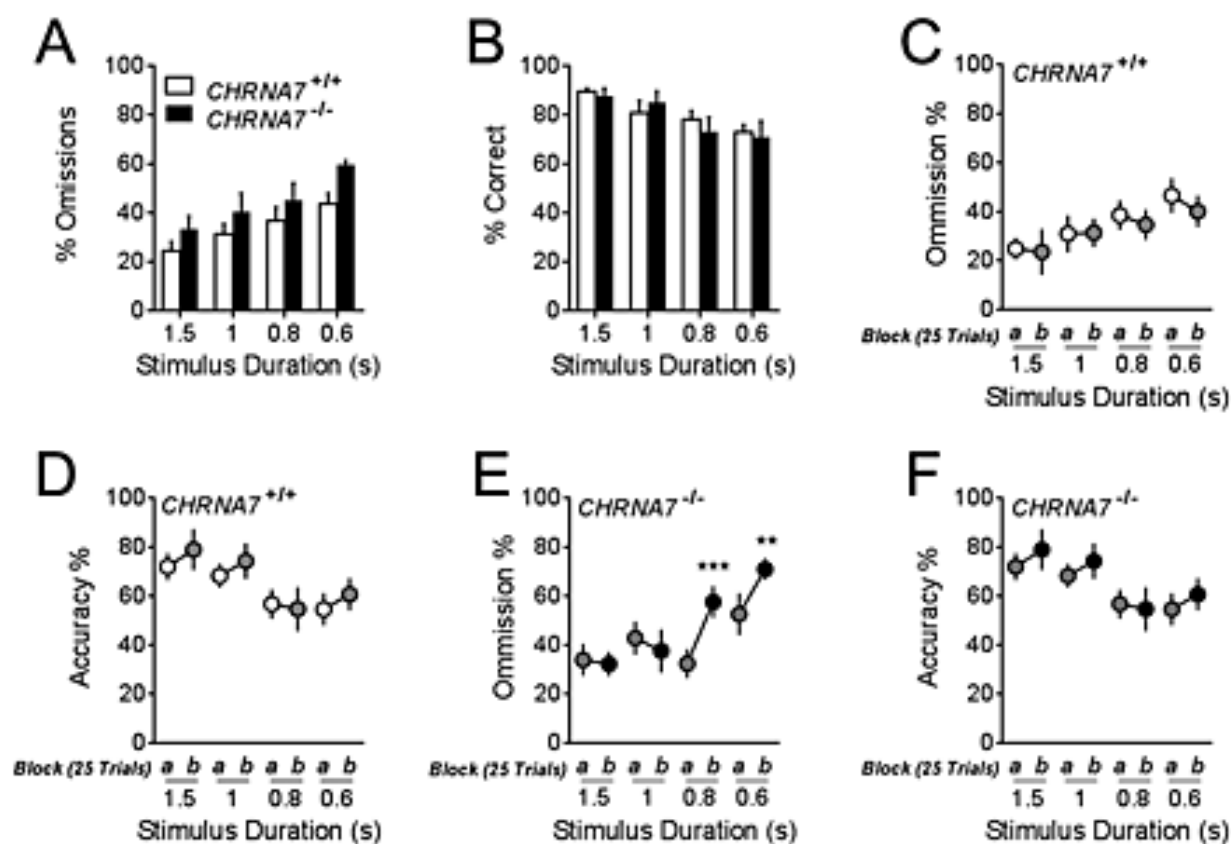
Figure 4.1.2. *CHRNA7*^{-/-} mice have impaired sustained attention.

Figure 4.1.3. CHRNA7^{-/-} mice have normal motivation and motor function during the 5-CSRT task. Comparison between genotypes of response latencies (A). Response latencies across bins of 25 trials in wild-type (B) and CHRNA7^{-/-} mice (C). Comparison between genotypes of reward collection latencies (D). Reward collection latencies across bins of 25 trials in wild-type (E) and CHRNA7^{-/-} mice (F). (G) Food consumption following food deprivation as a measure of motivation (data are presented as mean $\pm$ SEM).

Figure 4.1.3. *CHRNA7*^{-/-} mice have normal motivation and motor function during the 5-CSRT task.

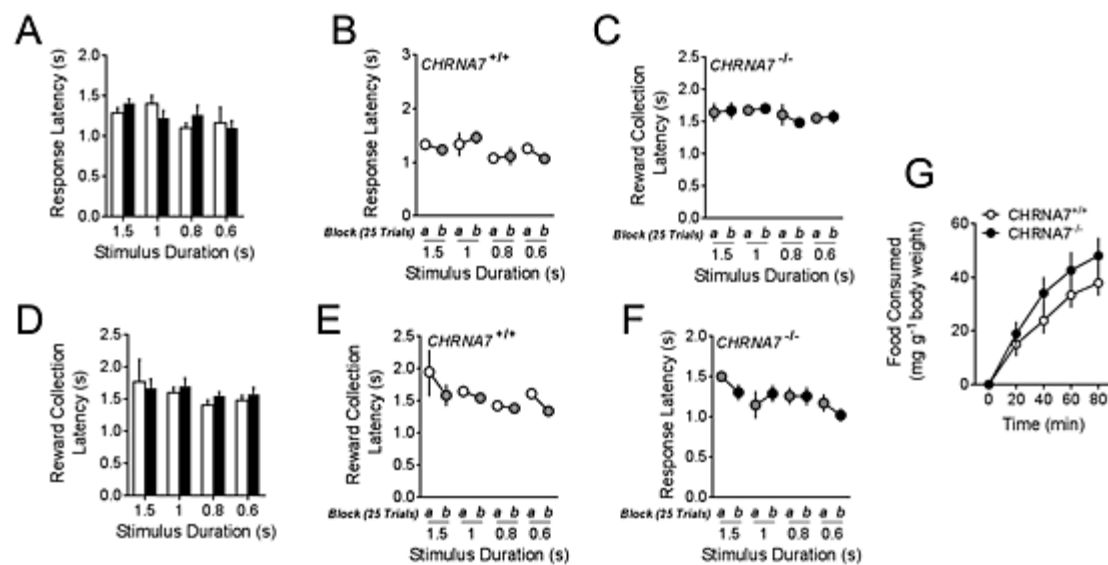


Figure 4.1.4. Response patterns did not differ in $\alpha 7$ nAChR null mice on the 5-CSRT task probe trial. Premature (a) and perseverative (b) responses between WT (clear bars) and CHRNA7^{-/-} mice (dark bars). (Data are presented as mean $\pm$ SEM.)

Figure 4.1.4. Response patterns did not differ in $\alpha 7$ nAChR null mice on the 5-CSRT task probe trial.

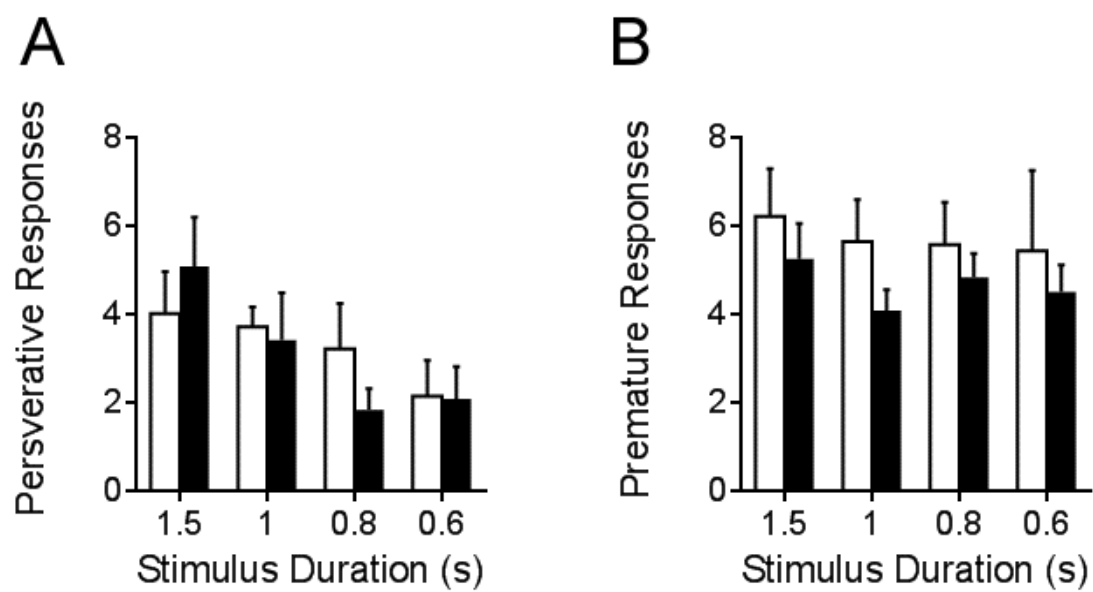
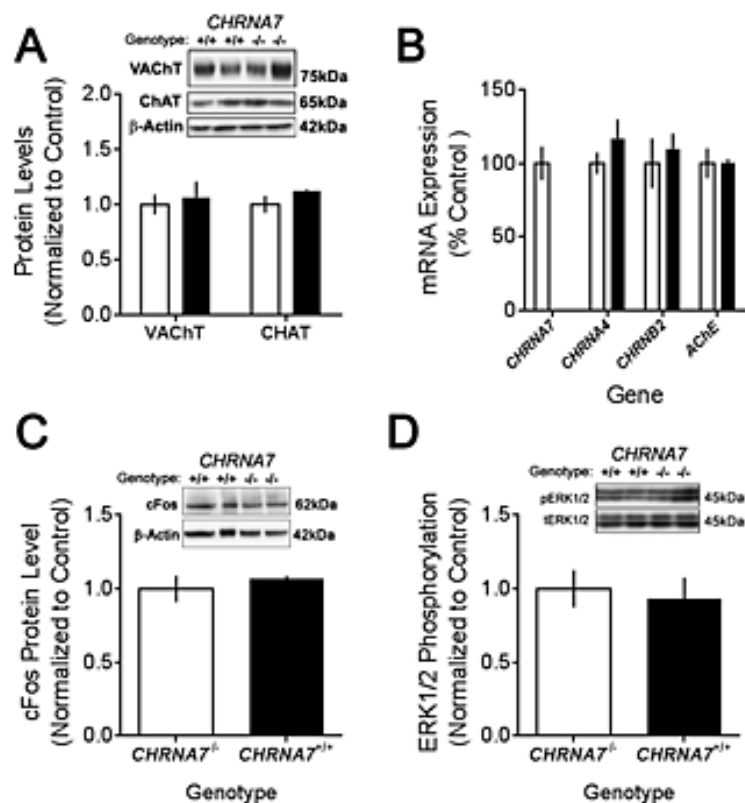


Figure 4.1.5. Evaluation of the expression of cholinergic markers and relevant signalling pathways in the PFC of *CHRNA7*^{-/-} mice. (A) Immunoblot of VACht and ChAT expression in the PFC. (B) qPCR expression of nicotinic receptors and AChE in the PFC. (C) cFos protein levels and (D) ERK1/2 phosphorylation in the PFC (data are presented as mean $\pm$ SEM).

Figure 4.1.5. Evaluation of the expression of cholinergic markers and relevant signalling pathways in the PFC of *CHRNA7*^{-/-} mice.



4.5.3 Effect of $\alpha 7$ nAChR agonists on attention

To evaluate acute roles of $\alpha 7$ nAChR in regulating sustained attention behaviour, we investigated two selective $\alpha 7$ nAChR agonists, PHA-543,613 (Acker et al., 2008) and PNU-282,987 (Hajos et al., 2005), in WT mice using the 5-CSRT task. Mice were tested at a 0.6 s stimulus duration, which represents a cognitively demanding version of the task (Romberg et al., 2011; Kolisnyk et al., 2013a). PHA-543,613 significantly improved rate of omissions [RM-ANOVA: main effect of dose, $F(3,18) = 12.52$, $P < 0.001$; Figure 4.2.1A], with post hoc analysis confirming that the $1 \text{ mg}\cdot\text{kg}^{-1}$ dose significantly improved performance over saline. Conversely, PHA-543,613 significantly altered response accuracy in higher doses [RM-ANOVA: main effect of dose, $F(3,18) = 12.55$, $P < 0.001$; Figure 4.2.1B]. Post hoc analysis revealed that at the highest dose tested ($3 \text{ mg}\cdot\text{kg}^{-1}$), PHA-543,613-injected mice performed significantly worse than mice injected with saline. PHA-543,613 did not significantly alter response latency [RM-ANOVA: no effect of dose, $F(3,18) = 1.568$, $P = 0.2318$, Fig. 4.2.2A] or reward collection latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.7517$, $P = 0.5382$; Fig. 4.2.2B]. In addition, PHA-543,613 did not alter premature [RM-ANOVA: no effect of dose, $F(3,18) = 0.7599$, $P = 0.4930$] nor perseverative responses [RM-ANOVA: no effect of dose, $F(3,18) = 0.1404$, $P = 0.8821$, Fig. 4.2.2C, D]. To address the effects of PHA-543,613 on sustained attention, we analysed performance of mice over blocks of 25 trials and observed that PHA-543,613 did not significantly alter sustained omissions between the two blocks of testing [RM-ANOVA: main effect of dose, $F(3,36) = 13.20$, $P < 0.0001$; no effect of block, $F(1,12) = 0.7069$, $P = 0.4327$; and no interaction, $F(3,36) = 1.288$, $P = 0.3088$; Figure 4.2.1C], nor did it alter accuracy in WT mice [RM-ANOVA: main effect of dose, $F(3,36) = 14.63$, $P < 0.0001$; no effect of block, $F(1,12) = 1.729$, $P = 0.101$; and no interaction effect, $F(3,18) = 0.0713$, $P = 0.9749$; Figure 4.2.1D]. At $1 \text{ mg}\cdot\text{kg}^{-1}$, the percentage of omissions seemed to be slightly reduced in the second block, suggesting modest improvement in the performance.

The second $\alpha 7$ nAChR agonist tested, PNU-282,987, also significantly improved rate of omissions [RM-ANOVA: main effect of dose, $F(3,18) = 2.767$, $P = 0.0437$, Figure 4.2.1E], with post hoc analysis confirming that both the 1 and $3 \text{ mg}\cdot\text{kg}^{-1}$ doses

significantly improved performance over saline. Conversely, PNU-282,978 significantly altered response accuracy [RM-ANOVA: main effect of dose, $F(3,18) = 5.637$, $P = 0.0066$; Figure 4.2.1F]. Post hoc analysis revealed that at the highest dose tested ($5 \text{ mg} \cdot \text{kg}^{-1}$) mice injected with PNU-282,978 performed significantly worse than mice injected with saline. PNU-282,978 did not significantly alter response latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.9985$, $P = 0.4018$; Fig. 4.2.2E] nor reward collection latency [RM-ANOVA: no effect of dose, $F(3,18) = 1.131$, $P = 0.3375$; Figure 4.3.2.2.1F]. PNU-282,978 did not alter the number of premature [RM-ANOVA: no effect of dose, $F(3,18) = 3.015$, $P = 0.1157$] or perseverative responses [RM-ANOVA: no effect of dose, $F(3,18) = 0.4522$, $P = 0.6707$, Fig. 4.2.2G, H]. In terms of the effects of PNU-282,978 on sustained attention, analysis of injected mice over two blocks of 25 trials showed that PNU-282,978 did alter the rate of omissions, with $3 \text{ mg} \cdot \text{kg}^{-1}$ improving omission rates over the two blocks [RM-ANOVA: main effect of dose, $F(3,36) = 6.095$, $P = 0.0031$; no effect of block, $F(1,12) = 0.5240$, $P = 0.4761$; and main interaction effect, $F(3,36) = 3.218$, $P = 0.0407$; Figure 4.2.1G], but did not alter sustained accuracy [RM-ANOVA: main effect of dose, $F(3,36) = 6.044$, $P = 0.0019$; no effect of block, $F(1,12) = 0.222$, $P = 0.6458$; and no interaction effect, $F(3,18) = 0.0701$, $P = 0.9755$; Figure 4.2.1H].

To evaluate the biochemical correlates of acute $\alpha 7 \text{nAChR}$ agonist activation in the PFC, we injected PHA-543,613 on WT mice and determined protein levels of cFos and the phosphorylation status of ERK1/2. These experiments used a separate cohort of mice, which were injected with drug or saline and then killed 30 min later and had their PFC dissected to obtain protein extracts. Compared with saline, PHA-543,613 injected in mice led to a significant increase in the levels of cFos protein in their PFC [one-way ANOVA: main effect of dose, $F(2,6) = 7.404$, $P = 0.0240$; Figure 4.2.1I], with post hoc analysis showing that cFos levels were increased at both doses of PHA-543,613. Similarly, injections of PHA-543,613 significantly increased ERK1/2 phosphorylation levels in a dose-dependent way [one-way ANOVA: main effect of dose, $F(2,6) = 28.80$, $P < 0.001$; Figure 4.2.1J].

Figure 4.2.1 $\alpha 7$ nAChR agonists improve attention in wild-type mice. (A) Omission and (B) accuracy following injections of PHA-543,613 in WT mice. (C) Omissions and (D) accuracy over bins of 25 trials following administration of PHA-543,613. (E) Omission and (F) accuracy following injections of PNU-282,987 in WT mice. (G) Omissions and (H) accuracy over bins of 25 trials following administration of PNU-282,987. (I) cFos protein levels and (J) ERK1/2 phosphorylation following injection of PHA-543,613 (data are presented as mean $\pm$ SEM; *P < 0.05, **P < 0.01, *P < 0.001).**

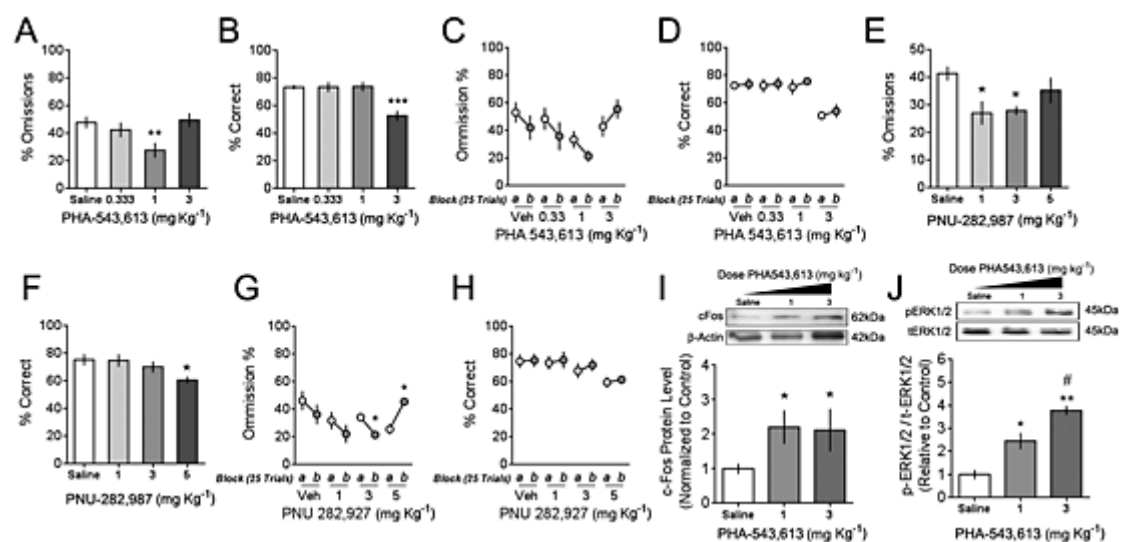
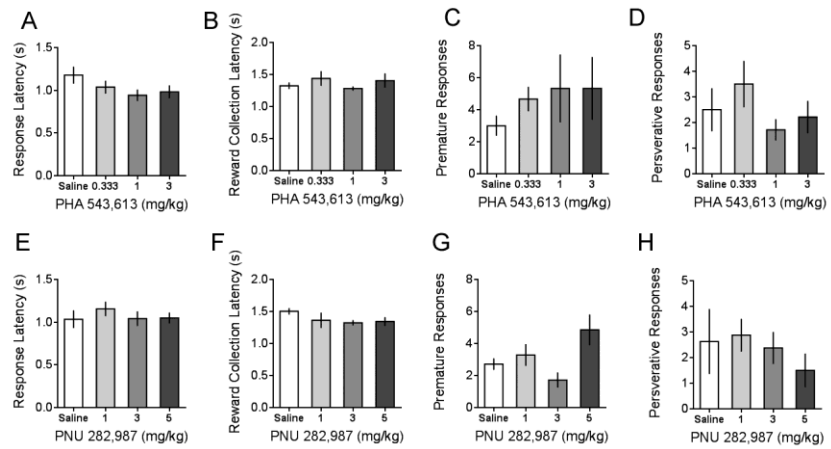
Figure 4.2.1 $\alpha 7$ nAChR agonists improve attention in wild-type mice.

Figure 4.2.2 $\alpha 7$ nAChR agonists did not alter response patterns in wild-type mice.

Premature responses (a), perseverative responses (b), response (c) and reward collection (d) latencies following PHA-543,613 injections in WT mice. Premature responses (e), perseverative responses (f), response (g) and reward collection (h) latencies following PNU-282,927 injections in WT mice. (Data are presented as mean $\pm$ SEM.)

Figure 4.2.2 $\alpha 7$ nAChR agonists did not alter response patterns in wild-type mice.



4.5.4 Positive and negative effects of $\alpha 7$ nAChR agonists are abolished in CHRNA7 $^{-/-}$ mice

To confirm the specificity of both PHA-543,613 and PNU-282,987 for $\alpha 7$ nAChRs, we administered both compounds to CHRNA7 $^{-/-}$ mice prior to testing them on the 5-CSRT task with a 0.6 s stimulus duration. Compared with saline, PHA-543,613 had no effect on the performance of the mice at any dose tested. PHA-543,613 did not alter rate of omissions [RM-ANOVA: no effect of dose, $F(3,18) = 1.528$, $P = 0.2515$; Figure 4.3.1A] or response accuracy [RM-ANOVA: no effect of dose, $F(3,18) = 0.1121$, $P = 0.8733$; Figure 4.3.1B], response latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.2490$, $P = 0.7348$; Figure 4.3.2A] or reward collection latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.3018$, $P = 0.6621$; Figure 4.3.2B]. PHA-543,613 did not alter the number of premature [RM-ANOVA: no effect of dose, $F(3,18) = 1.104$, $P = 0.3579$] or perseverative responses [RM-ANOVA: no effect of dose, $F(3,18) = 2.101$, $P = 0.1738$, Figure 4.3.2C, D]. Furthermore, when we analysed performance over blocks of 25 trials, we observed that PHA-543,613 did not alter impaired omission deficit of CHRNA7 $^{-/-}$ mice at 0.6 s, which remained significantly higher in block B across all doses [RM-ANOVA: no effect of dose, $F(3,36) = 1.528$, $P = 0.2414$; main effect of block, $F(1,12) = 14.89$, $P = 0.0084$; and no interaction $F(3,12) = 0.2209$, $P = 0.8806$; Figure 4.3.1C]. PHA-543,613 did not alter sustained accuracy in CHRNA7 $^{-/-}$ mice either [RM-ANOVA: no effect of dose, $F(3,36) = 0.2017$, $P = 0.8945$; no effect of block, $F(1,12) = 0.00701$, $P = 0.9343$; and no interaction, $F(3,36) = 0.02177$, $P = 0.9956$; Figure 4.3.1D].

As with the PHA-543,613, PNU-282,987 had no effect on the performance of CHRNA7 $^{-/-}$ mice at any of the tested doses. The drug did not alter rate of omissions [RM-ANOVA: no effect of dose, $F(3,18) = 0.1515$, $P = 0.9277$; Figure 4.3.1E], response accuracy [RM-ANOVA: no effect of dose, $F(3,18) = 0.1458$, $P = 0.9310$; Figure 4.3.1F], response latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.0586$, $P = 2.808$, Figure 4.3.2E] or reward collection latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.8089$, $P = 0.4603$, Figure 4.3.2F]. PNU-282,987 did not alter the number of premature [RM-ANOVA: no effect of dose, $F(3,18) = 0.2767$, $P = 0.8316$] or perseverative responses [RM-ANOVA: no effect of dose, $F(3,18) = 0.2218$, $P = 0.8036$, Figure 4.3.2G, H]. Also,

analysis of performance of injected mice over blocks of 25 trials showed that the $\alpha 7$ nAChR agonist had no effect on the impaired omission deficit that we consistently observed on CHRNA7 $^{-/-}$ mice [RM-ANOVA: main effect of block, $F(1,6) = 9.112$, $P = 0.0234$; no effect of dose, $F(3,18) = 0.2542$, $P = 0.8573$; and no interaction, $F(3,18) = 0.2546$, $P = 0.8570$; Figure 4.3.1G] nor on sustained accuracy [RM-ANOVA: no effect of blocks, $F(1,6) = 0.0258$, $P = 0.9945$; no effect of dose, $F(3,18) = 1.123$, $P = 0.3729$; and no interaction, $F(3,18) = 0.2665$, $P = 0.8491$; Figure 4.3.1H]. Taken together, these results demonstrate that modulation of attention performance on the 5-CSRT task by both PHA-543,613 and PNU-282,987 depends on their activity on $\alpha 7$ nAChR.

Additionally, to confirm the selectivity of the molecular changes observed following PHA-543,613 administration in WT mice, we injected CHRNA7 $^{-/-}$ mice with the highest dose of the drug ($3 \text{ mg} \cdot \text{kg}^{-1}$) and then, 30 min later, measured the effects on cFos protein levels and ERK1/2 phosphorylation in the PFC. Unlike PHA-543,613-injected WT mice, CHRNA7 $^{-/-}$ mice exhibited no change in cFos levels [$t(4) = 0.387$, $P = 0.7186$; Figure 4.3.1I] or ERK1/2 phosphorylation [$t(4) = 0.1029$, $P = 0.9230$; Figure 4.3.1J], suggesting that both the behaviour and molecular effects of the drug are specific to activation of $\alpha 7$ nAChR.

Figure 4.3.1. $\alpha 7$ nAChR agonists do not alter attention in mice lacking $\alpha 7$ nAChR.

(A) Omission and (B) accuracy following injections of PHA-543,613 in CHRNA7^{-/-} mice. (C) Omissions and (D) accuracy over bins of 25 trials following administration of PHA-543,613 in CHRNA7^{-/-} mice. (E) Omission and (F) accuracy following injections of PNU-282,987 in CHRNA7^{-/-} mice. (G) Omissions and (H) accuracy over bins of 25 trials following administration of PNU-282,987. (I) cFos protein levels and (J) ERK1/2 phosphorylation following injection of PHA-543,613 (data are presented as mean $\pm$ SEM; *P < 0.05, **P < 0.01, ***P < 0.001).

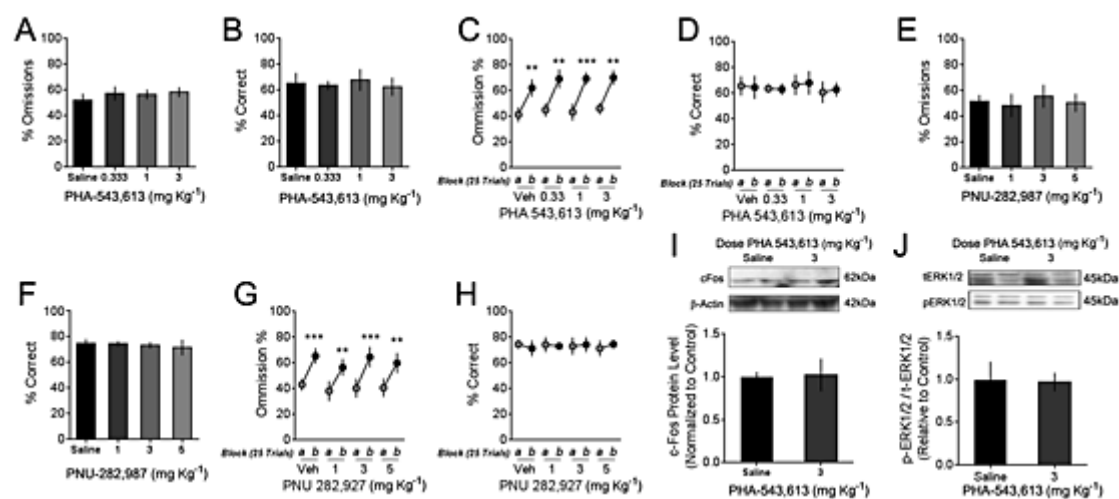
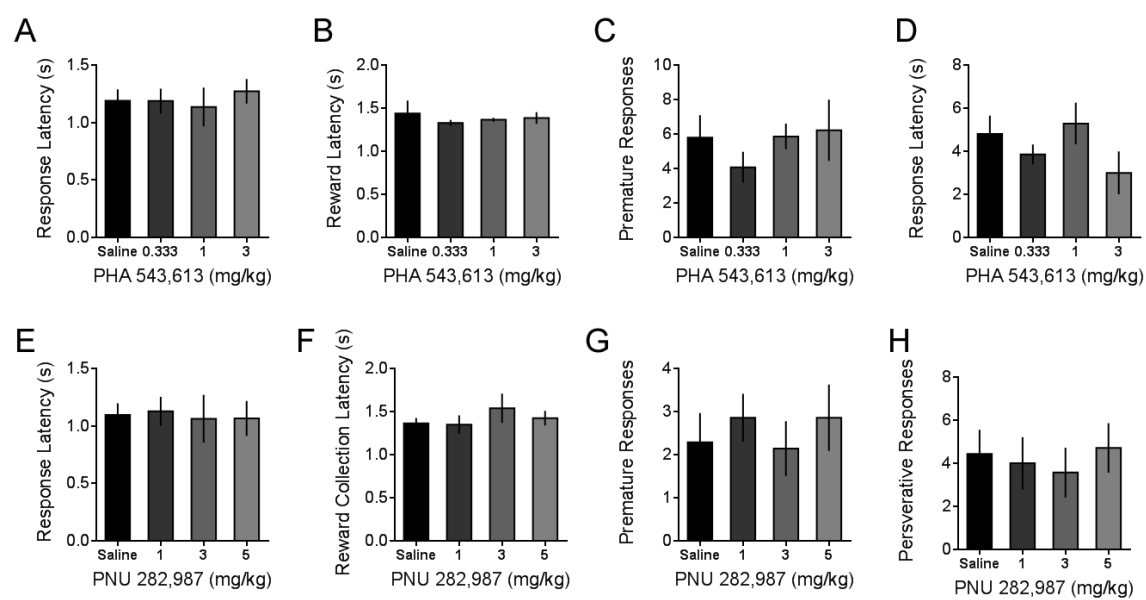
Figure 4.3.1. $\alpha 7$ nAChR agonists do not alter attention in mice lacking $\alpha 7$ nAChR.

Figure 4.3.2. $\alpha 7$ nAChR agonists did not alter response patterns in CHRNA7-null mice. Premature responses (a), perseverative responses (b), response (c) and reward collection (d) latencies following PHA-543,613 injections in CHRNA7^{-/-} mice. Premature responses (e), perseverative responses (f), response (g) and reward collection (h) latencies following PNU-282,927 injections in CHRNA7^{-/-} mice. (Data are presented as mean $\pm$ SEM.).

Figure 4.3.2. $\alpha 7$ nAChR agonists did not alter response patterns in CHRNA7-null mice.



4.5.5 The $\beta 2nAChR$ agonist ABT-418 improves attention

In order to explore the relationship between distinct types of nicotinic receptors on attentional performance, we used ABT-418, a $\beta 2nAChR$ agonist, and treated WT mice that were tested with the 0.6 s stimulus duration paradigm. Injections of ABT-418 were able to significantly improve both rate of omissions [RM-ANOVA: main effect of dose, $F(3,18) = 4.544$, $P = 0.0132$; Figure 4.4.1A] and response accuracy [RM-ANOVA: main effect of dose, $F(3,18) = 6.950$, $P = 0.0020$; Figure 4.4.1B] without altering response latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.06377$, $P = 0.9014$; Figure 4.4.2A] or reward collection latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.2936$, $P = 0.8797$; Figure 4.4.2B]. ABT-418 did not alter the number of premature [RM-ANOVA: no effect of dose, $F(3,18) = 1.228$, $P = 0.3103$] or perseverative responses [RM-ANOVA: no effect of dose, $F(3,18) = 0.3062$, $P = 0.6764$, Figure 4.4.2C, D]. To evaluate the effects of ABT-418 on sustained attention, we analysed accuracy and omissions across blocks of 25 trials. ABT-418 did not significantly alter sustained omissions across blocks for WT mice [RM-ANOVA: no effect of block, $F(1,6) = 0.6582$, $P = 0.6013$; main effect of dose, $F(3,18) = 0.2542$, $P = 0.8573$; and no interaction, $F(3,18) = 0.6582$, $P = 0.5847$; Figure 4.4.1C]. ABT-418 had no effect on sustained accuracy in WT mice, with the improvements brought on by the drug spanning across both blocks of trials [RM-ANOVA: no effect of block, $F(1,6) = 0.7267$, $P = 0.4083$; main effect of dose, $F(3,18) = 7.744$, $P = 0.0003$; and no interaction $F(3,18) = 1.084$, $P = 0.3662$; Figure 4.4.1D).

Given that nicotinic receptors may be expressed in similar populations of neurons and could crosstalk (Azam et al., 2003), we evaluated whether $\beta 2nAChR$ receptor activation could impact attention in mice lacking $\alpha 7nAChR$. As with the WT mice, ABT-418 was able to significantly improve both omissions [RM-ANOVA: main effect of dose, $F(3,18) = 5.466$, $P = 0.0066$; Figure 4.4.3A] and accuracy [RM-ANOVA: main effect of dose, $F(3,18) = 3.383$, $P = 0.0373$; Figure 4.4.3B] in $CHRNA7^{-/-}$ mice, without altering response latency [RM-ANOVA: no effect of dose, $F(3,18) = 1.622$, $P = 0.2495$; Figure 4.4.4A] or reward collection latency [RM-ANOVA: no effect of dose, $F(3,18) = 0.8793$, $P = 0.4359$; Figure 4.4.4B]. ABT-418 did not alter the number of premature [RM-

ANOVA: no effect of dose, $F(3,18) = 0.1450$, $P = 0.81133$] or perseverative responses [RM-ANOVA: no effect of dose, $F(3,18) = 0.1254$, $P = 0.8336$; Figure 4.4.4C, D].

Importantly, ABT-418 was able to reverse the sustained attention deficits observed in *CHRNA7*^{-/-} mice (Figure 4.4.3C) and improved the sustained omission deficits in these mice [RM-ANOVA: main effect of block, $F(1,6) = 11.82$, $P = 0.0138$; main effect of dose, $F(3,18) = 7.640$, $P = 0.0017$; and no interaction effect, $F(3,18) = 1.707$, $P = 0.2013$; Figure 4.4.3C]. Post hoc analysis revealed that this occurred even at the lowest dose administered. Sustained accuracy was not altered [RM-ANOVA: no effect of block, $F(1,6) = 0.1284$, $P = 0.7324$; main effect of dose, $F(3,18) = 5.017$, $P = 0.0106$; and no interaction, $F(3,18) = 1.054$, $P = 0.3929$; Figure 4.4.3D].

To determine the biochemical correlates of treatment with ABT-418 on *CHRNA7*^{-/-} mice, we injected a new cohort of *CHRNA7*^{-/-} mice with $0.39 \text{ mg} \cdot \text{kg}^{-1}$ of ABT-418 and 30 min later evaluated cFos and ERK1/2 phosphorylation levels in the PFC of the mice. Compared with saline-injected mice, *CHRNA7*^{-/-} mice injected with ABT-418 showed a significant increase in cFos protein levels 30 min after injection [$t(4) = 5.610$, $P = 0.0050$; Figure 4.4.3E]. ABT-418 was also able to significantly increase ERK1/2 phosphorylation levels in the PFC of mice lacking $\alpha 7\text{nAChR}$ [$t(4) = 5.300$, $P = 0.0061$; Figure 4.4.3F].

Importantly, given that the mice had been exposed to the task numerous times, we evaluated the performance of the mice over the course of the various injections in order to ensure that the improvements brought on by the ABT-418 were not due to the mice becoming better at the task. We compared the performance (both rates of omission and accuracy) of the mice from the vehicle injections of each drug experiment with their naive performance (the performance at a 0.6 s stimulus duration during the probe trial experiments). Both the WT {omission [one-way ANOVA: no effect of treatment, $F(6,18) = 0.7467$, $P = 0.4692$; Figure 4.4.57A] and accuracy [one-way ANOVA: no effect of treatment, $F(6,18) = 0.6749$, $P = 0.6716$; Figure 4.4.57B]} and *CHRNA7*^{-/-} mice {omission [one-way ANOVA: no effect of treatment, $F(6,18) = 2.565$, $P = 0.1154$; Figure 4.4.57C] and accuracy [one-way ANOVA: no effect of treatment, $F(6,18) = 1.005$, $P = 0.3876$; Figure 4.4.57D]} demonstrated no significant change in performance in both omissions and accuracy from their naive performance across all injections.

Figure 4.4.1. β 2nAChR agonists improve attention in wild-type mice. (A) Omission and (B) accuracy following injections of ABT-418 in WT mice. (C) Omissions and (D) accuracy over bins of 25 trials following administration of ABT-418 in WT mice (data are presented as mean $\pm$ SEM; *P < 0.05, **P < 0.01).

Figure 4.4.1. β_2 nAChR agonists improve attention in wild-type mice.

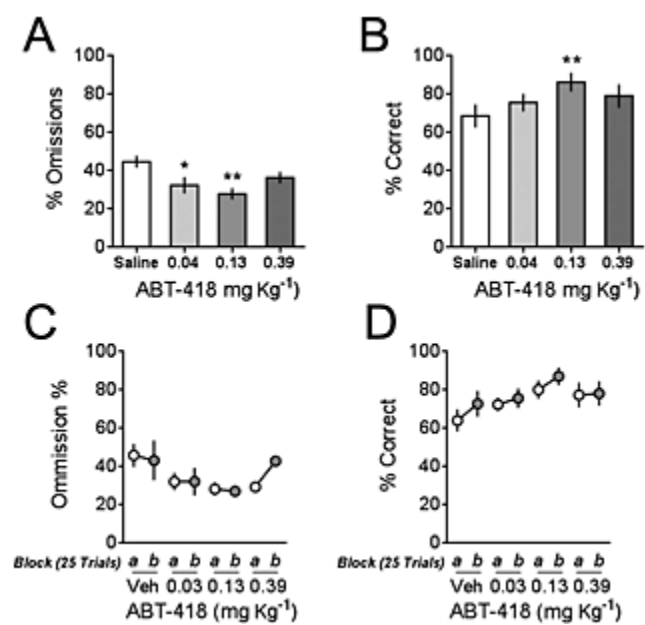


Figure 4.4.2. ABT-418 did not alter response patterns in wild-type mice. Premature responses (a), perseverative responses (b), response (c) and reward collection (d) latencies following ABT-418 injections in WT mice. (Data are presented as mean $\pm$ SEM.).

Figure 4.4.2. ABT-418 did not alter response patterns in wild-type mice.

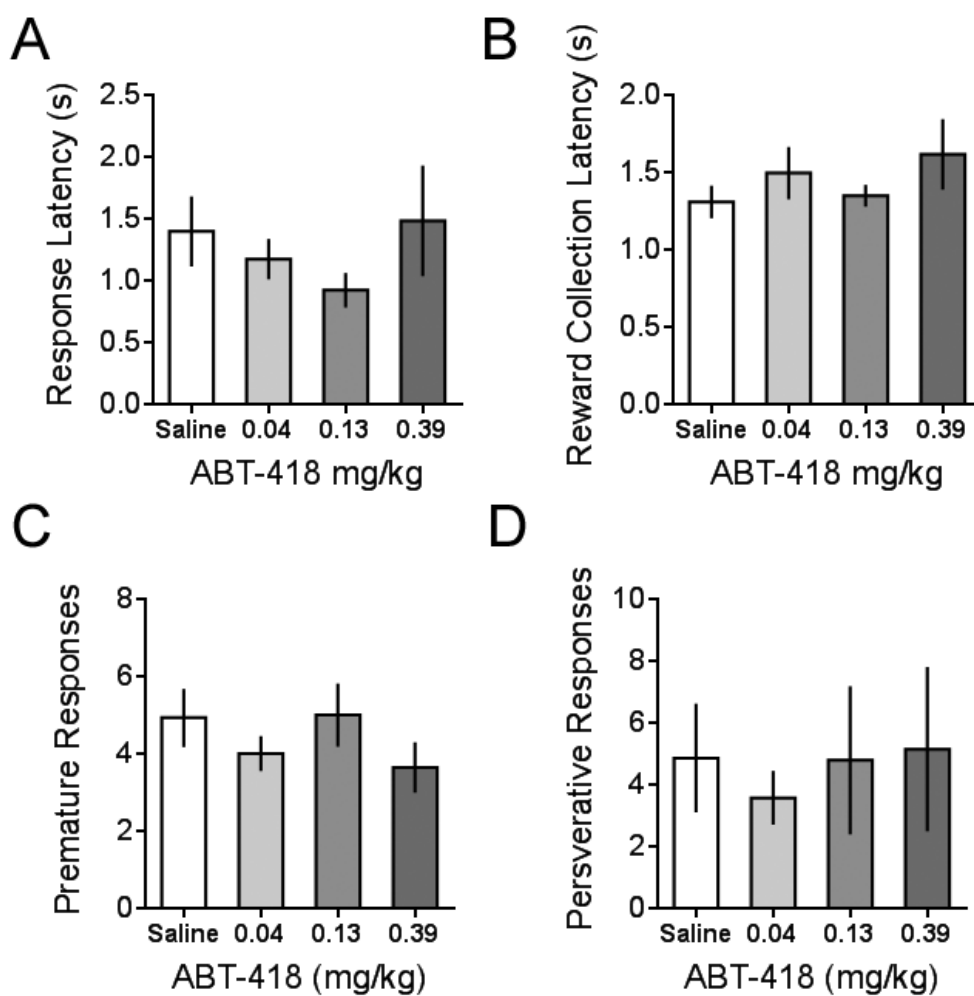


Figure 4.4.3. Sustained attention deficits of CHRNA7 null mice are reversed by $\beta 2nAChR$ agonists. (A) Omission and (B) accuracy following injections of ABT-418 in CHRNA7^{-/-} mice. (C) Omissions and (D) accuracy over bins of 25 trials following administration of ABT-418. (E) cFos protein levels and (F) ERK1/2 phosphorylation following injection of ABT-418 (data are presented as mean $\pm$ SEM; * P < 0.05, ** P < 0.01).

Figure 4.4.3. Sustained attention deficits of CHRNA7 null mice are reversed by β 2nAChR agonists.

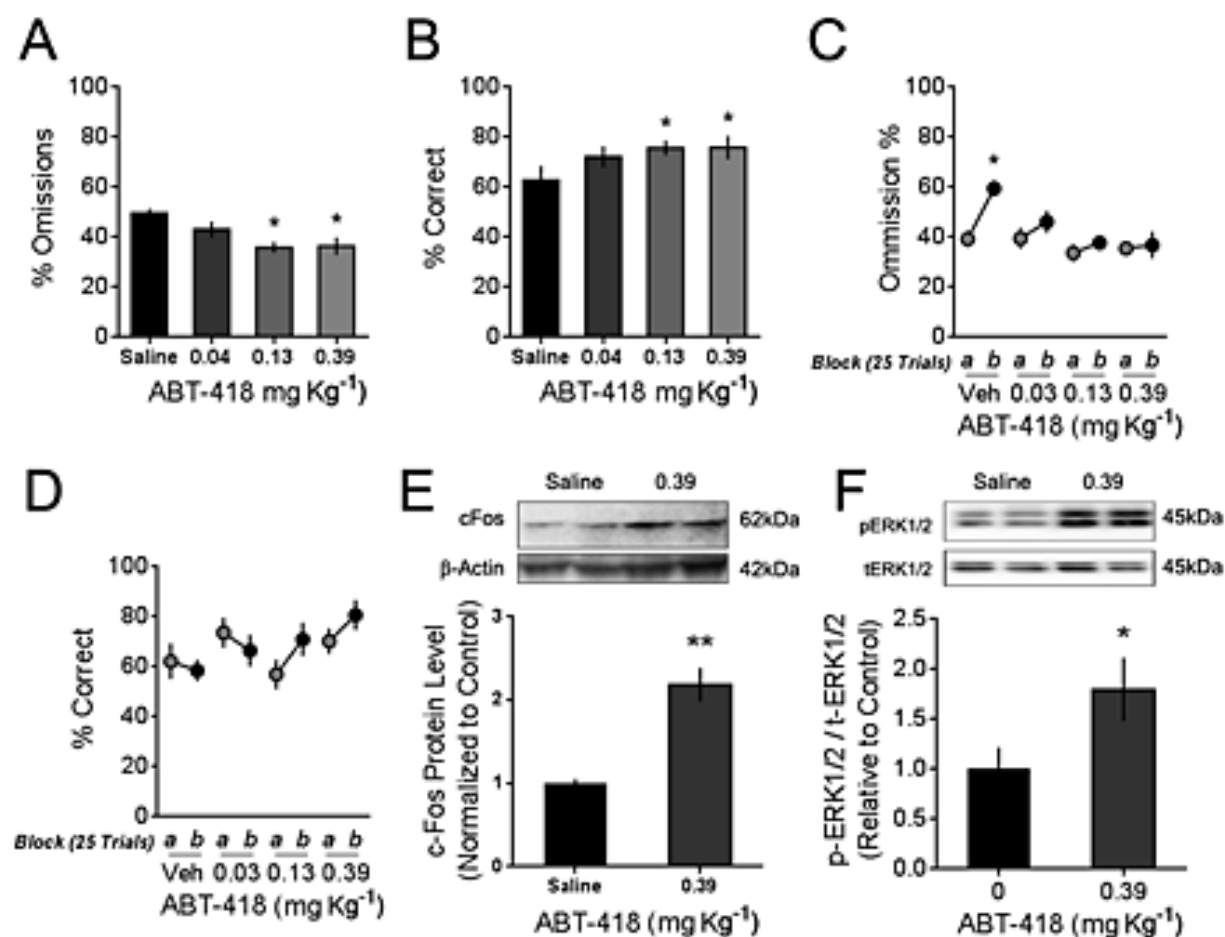


Figure 4.4.4. ABT-418 did not alter response patterns in CHRNA7 null mice.

Premature responses (a), perseverative responses (b), response (c) and reward collection (d) latencies following ABT-418 injections in CHRNA7^{-/-} mice. (Data are presented as mean $\pm$ SEM.).

Figure 4.4.4. ABT-418 did not alter response patterns in CHRNA7 null mice.

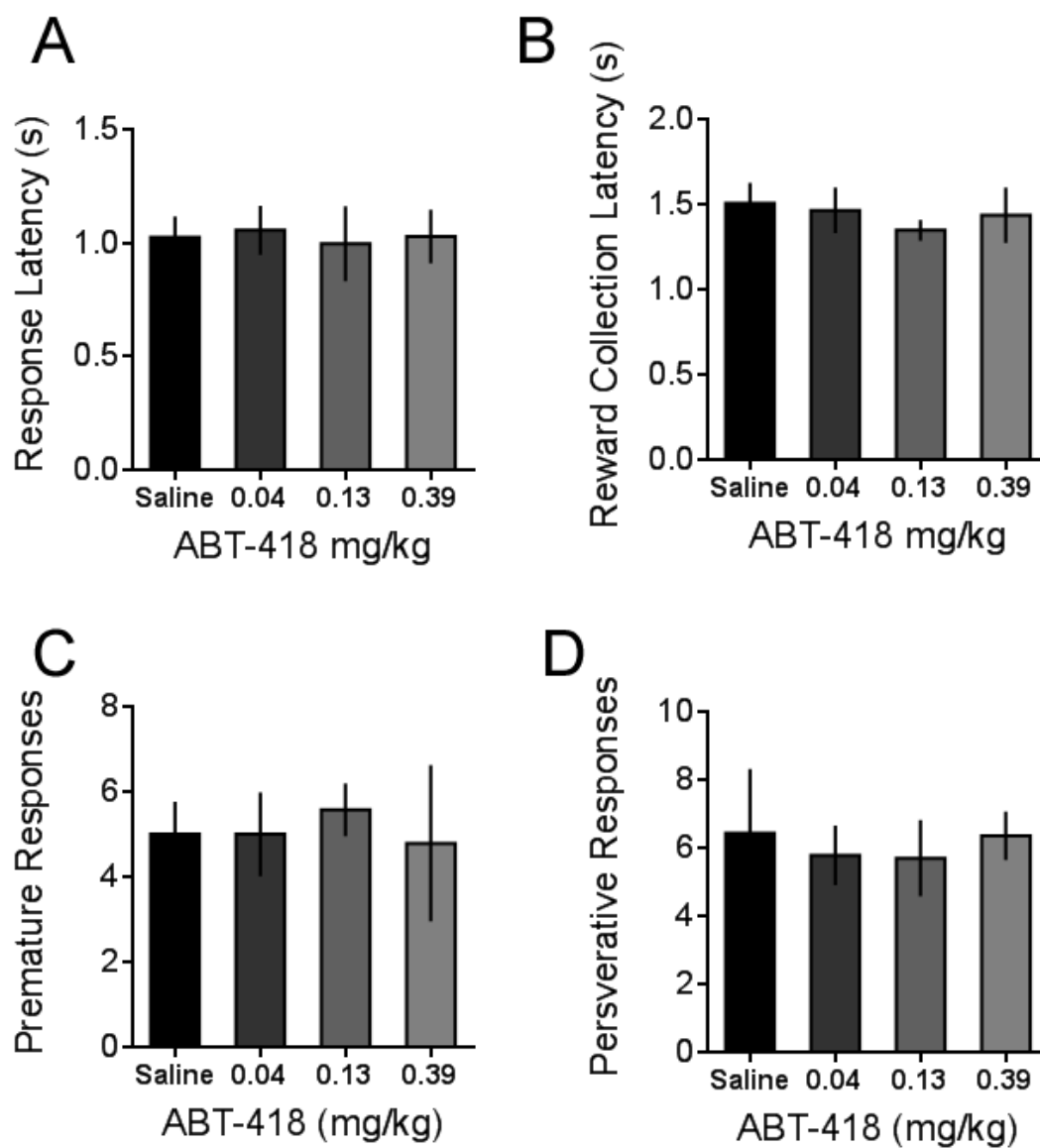
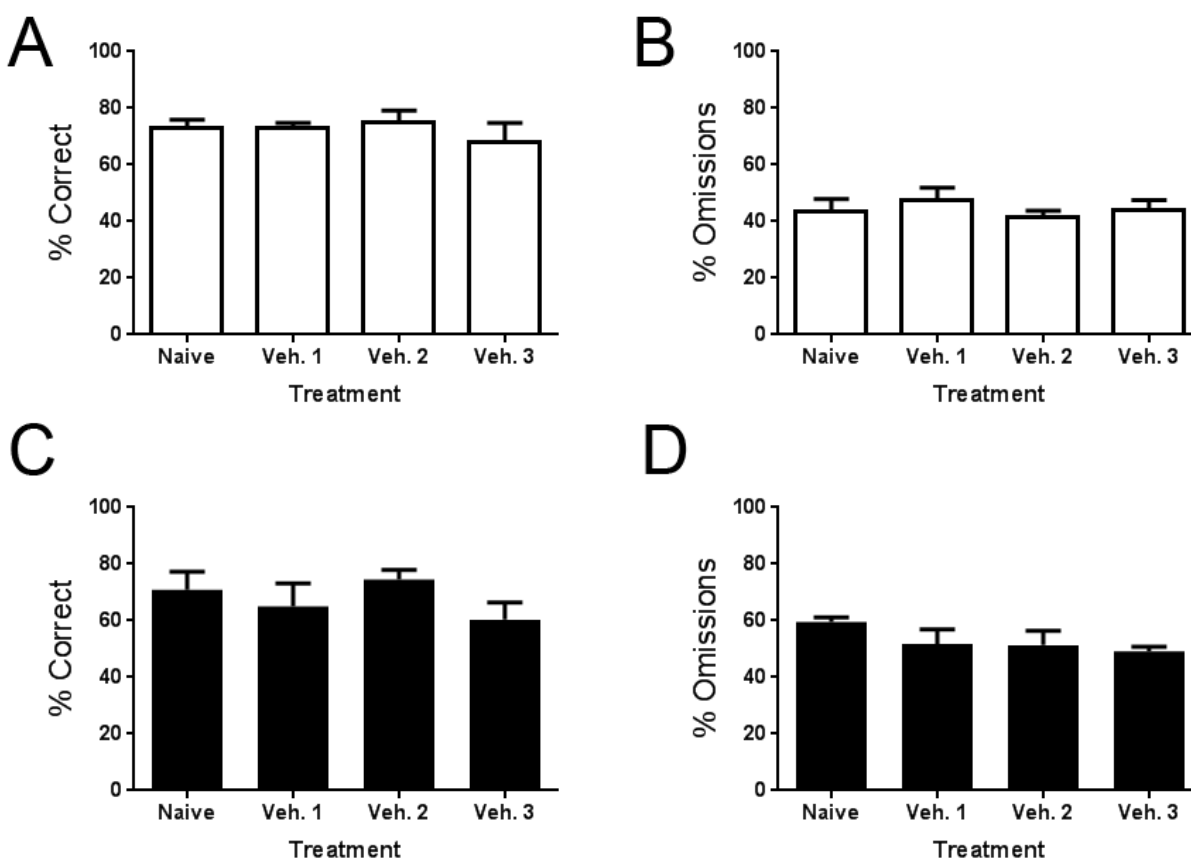


Figure 4.4.5. Performance of mice did not differ across all drug treatments.

Evaluation of accuracy (a) and omissions (b) from vehicle treatments from all drug trials in wild-type mice. Evaluation of accuracy (c) and omissions (d) from vehicle treatments from all drug trials in wild-type mice *CHRNA7*^{-/-} mice. (Data are presented as mean $\pm$ SEM.).

Figure 4.4.5. Performance of mice did not differ across all drug treatments.



4.6 Discussion

In this study, we demonstrated that the genetic elimination of the *CHRNA7* gene disturbs sustained attentional performance, as measured by the 5-CSRT task, and that this deficit is reversed by administration of ABT-418, a β 2nAChR agonist. *CHRNA7*^{-/-} mice exhibited impaired performance (increased omission errors) during the second half of testing sessions of the 5-CSRT, suggestive of deficits in sustained attention, or vigilance. Increases in omission errors on the 5-CSRT task may reflect either decreased attentional processing or a lack of motivation (Robbins, 2002; Spinelli et al., 2004).

However, given the normal performance of *CHRNA7*^{-/-} mice on the food intake test, this phenotype is unlikely to represent a motivational issue, suggesting that the lack of α 7nAChRs impairs the ability to maintain performance levels during the task.

Pharmacological activation of α 7nAChRs in WT mice by two distinct α 7nAChR agonists, PHA-543,613 and PNU-282,987, in lower doses improved attentional performance but did not change sustained attention. These effects were specific to their actions on α 7nAChRs, as these compounds were ineffective on *CHRNA7*^{-/-} mice.

Pharmacological activation of the β 2nAChR by ABT-418 was able to reverse the sustained attention deficit in *CHRNA7*^{-/-} mice, suggesting that the deficits observed in these mice can be rescued by β 2nAChR signalling.

Post-mortem analysis of human patient samples has shown that ERK1/2 MAP kinase signalling is reduced in brains of schizophrenic patients (Yuan et al., 2010). Moreover, an inability to induce phosphorylation of ERK1/2 MAP kinases in the PFC is thought to underlie certain cognitive deficits in animal models of schizophrenia (Kamei et al., 2006). α 7nAChR activation has been shown to induce phosphorylation of ERK1/2 MAP kinases both in vitro and in vivo (Bitner et al., 2007). Similar effects have been observed in second-generation antipsychotics (Lu et al., 2004). We showed that pharmacological activation of the α 7nAChR by PHA-543,613 induced a dose response increase in both ERK1/2 phosphorylation levels and cFos in WT mice. These effects were not detected in *CHRNA7*^{-/-} mice. Whether this biochemical correlation of α 7nAChR activation relates to the biochemical and attentional deficits observed in schizophrenia is unknown. Interestingly, when *CHRNA7*^{-/-} mice were treated with the β 2nAChR agonist

ABT-418, both ERK1/2 phosphorylation and cFos protein levels were increased and were correlated with the reversal of the sustained attention deficits. Although it is currently unclear if the neurons that respond to ABT-418 and the $\alpha 7$ nAChR drugs PHA-543,613 and PNU-282,987 are the same, one potential important implication of the behavioural data is that ABT-418 can reverse the sustained attention deficits due to abnormal CHRNA7 expression.

Interestingly, in WT mice, all $\alpha 7$ nAChR targeting drugs used presented an inverted 'U'-shaped behavioural response. This is not uncommon with nicotinic signalling with similar responses observed across cognitive domains and even species (Picciotto, 2003; Olincy et al., 2006; Wallace et al., 2011a; Braida et al., 2013). Desensitization of the receptor is often suggested as a potential mechanism underlying this U-shaped behavioural response. Our data suggest that this may not be the case for $\alpha 7$ nAChR activation, given that we see increases in the levels of phospho-ERK1/2 following administration of a high dose of $\alpha 7$ nAChR agonist in WT mice, which results in poor performance on the 5-CSRT task. Interestingly, it has been proposed that overactivity of this second messenger signalling pathway can actually impair executive function and lead to distractibility (Birnbaum et al., 2004). We have also recently shown that increased cholinergic tone by overexpression of VACHT and increased cholinergic signalling in BAC ChAT-Chr2-EYFP mice disturbs attentional processing (Kolisnyk et al., 2013b).

The ability of nicotine to improve attention has been well documented in rodents (Young et al., 2004), non-human primates (Prendergast et al., 1998) and humans (Lawrence et al., 2002). A common technique to evaluate the role of $\alpha 7$ nAChR signalling in attention has been to co-treat rodents with both nicotine and the $\alpha 7$ nAChR antagonist MLA. These studies have, however, provided mixed results. Some investigators obtained evidence for $\alpha 7$ nAChR signalling in the pro-attentive effects of nicotine (Hahn et al., 2011), and others failed to implicate $\alpha 7$ nAChR signalling in nicotine-induced improvements in attention (Grottick and Higgins, 2000). Studies using AR-R17779, a full agonist of the $\alpha 7$ nAChR, have failed to demonstrate pro-attentive effects of $\alpha 7$ nAChR stimulation (Grottick and Higgins, 2000; Grottick et al., 2003; Hahn et al., 2003). This

compound, however, has also been shown to poorly penetrate the blood brain barrier (Mullen et al., 2000). On the other hand, R3487/MEM 3454, an $\alpha 7$ nAChR agonist and 5-HT₃ receptor antagonist, has been shown to improve measures of sustained attention in both rats (Rezvani et al., 2009) and macaque monkeys (Wallace et al., 2009). Our experiments utilized both PHA-543,613 and PNU-282,987, $\alpha 7$ nAChR agonists, which have been previously reported to easily cross the blood brain barrier (Acker et al., 2008). Indeed, the biochemical activation reflected by increased cFos levels or phospho-ERK supports the contention that these drugs were able to activate the PFC in mice. Importantly, our data further support results from previous studies, suggesting that $\alpha 7$ nAChR signalling has a role in sustained attention (Young et al., 2007), specifically characterized by increased omission errors on the 5-CSRT task in $\alpha 7$ nAChR-null mice (Young et al., 2004).

Cholinergic transients in the PFC have been shown to be important for cue detection and attentional processing (Parikh et al., 2007). $\alpha 7$ nAChR activation increases the duration of these transients 10–15-fold, and interestingly, this effect is lost when dopaminergic afferents to the PFC are eliminated, suggesting a complex interplay between neurotransmitter systems (Parikh et al., 2010).

An important role of nicotinic receptors in the CNS is to influence the release of other neurotransmitters. Nicotinic receptors have been shown to influence the release of glutamate (Gioanni et al., 1999), dopamine (Zhou et al., 2001), GABA (Alkondon et al., 1999), noradrenaline (Fu et al., 1998), 5-HT (Kenny et al., 2000) and ACh itself (Rowell and Winkler, 1984). Efflux of all of these neurotransmitters in PFC has been associated with performance on the 5-CSRT task (reviewed in Robbins, 2002). Electron microscopy studies point to ACh release potentially being auto-regulated by presynaptic $\alpha 7$ nAChRs in the PFC (Duffy et al., 2009). On the other hand, post-synaptic $\beta 2$ nAChRs have been shown to be necessary and sufficient to regulate performance on the 5-CSRT task (Guillem et al., 2011; Poorthuis and Mansvelder, 2013). In addition to the possibility that $\alpha 7$ and $\beta 2$ receptors can form functional heteromeric receptors (Liu et al., 2009; Moretti et al., 2014), our data reveal a complex interplay between these two receptors in regulating sustained attention. Given that our results suggest that activation

of $\beta 2nAChRs$ can bypass $\alpha 7nAChRs$, it is possible that activation of $\alpha 7nAChRs$ could induce ACh release in the PFC, which would then activate post-synaptic $\beta 2nAChRs$ to regulate sustained attention. If this model is correct, it may explain the inconsistency amongst studies using non-selective nicotinic agonists and antagonists. Co-treatment with nicotine and methyllycaconitine, a $\alpha 7nAChR$ antagonist, would still activate $\beta 2nAChRs$ and thus improve attentive processing. Therefore, these previous experiments would not exclude a role of $\alpha 7nAChRs$ in attentional performance.

In conclusion, our data support a role for $\alpha 7nAChRs$ in sustained attention and reveal an intricate relationship between distinct nicotinic receptors to regulate attentional performance. Our results indicate that activation of $\beta 2nAChRs$ can bypass attentional deficits due to $\alpha 7nAChR$ deficiency, suggesting that $\beta 2nAChRs$ may be an important pharmacological target in cognitive dysfunctions in which impaired $\alpha 7nAChRs$ have been implicated, such as schizophrenia and Alzheimer's disease (Parri et al., 2011).

4.7 Acknowledgements

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4.8 References

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Chapter 5

Cholinergic surveillance over hippocampal RNA metabolism and Alzheimer's-like pathology

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5.1 Chapter Summary

The relationship between long-term cholinergic dysfunction and risk of developing dementia is poorly understood. Here we used mice with deletion of the vesicular acetylcholine transporter (VACHT) in the forebrain to model cholinergic abnormalities observed in dementia. Whole genome RNA-sequencing of hippocampal samples revealed that cholinergic failure causes changes in RNA metabolism. Remarkably, key transcripts related to Alzheimer's disease are affected. *BACE1* for instance, shows abnormal splicing caused by decreased expression of the splicing regulator hnRNPA2/B1. Resulting BACE1 overexpression leads to increased APP processing and accumulation of soluble A β ₁₋₄₂. This is accompanied by age-related increases in GSK3 activation, tau hyper-phosphorylation, caspase-3 activation, decreased synaptic markers, increased neuronal death and deteriorating cognition. Pharmacological inhibition of GSK3 hyperactivation reversed deficits in synaptic markers and tau hyperphosphorylation induced by cholinergic dysfunction, indicating a key role for GSK3 in some of these pathological changes. Interestingly, in human brains there was a high correlation between decreased levels of VACHT and hnRNPA2/B1 levels with increased tau hyperphosphorylation. These results suggest that changes in RNA processing caused by cholinergic loss can facilitate Alzheimer's-like pathology in mice, providing a mechanism by which decreased cholinergic tone may increase risk of dementia.

5.2 Introduction

Alzheimer's disease (AD), the predominant form of dementia, is pathologically characterized by accumulation of amyloid plaques and neurofibrillary tangles that ultimately lead to neuronal death. One of the early alterations identified in AD-affected individuals with cognitive decline is a profound decrease in basal forebrain cholinergic neurons (Whitehouse et al., 1982), which gave rise to the cholinergic hypothesis of AD (Bartus et al., 1982). Accordingly, Alzheimer's Disease Neuroimaging Initiative data reveal atrophy of the basal forebrain in individuals with mild cognitive impairment (Grothe et al., 2014), and increased forebrain cholinergic atrophy in Alzheimer's-affected individuals (Grothe et al., 2013). Cholinergic dysfunction correlates with decreased hippocampal volume and pathology (Teipel et al., 2014). Furthermore, recent epidemiological data suggest that long-term use of drugs with anti-cholinergic activity by elderly individuals increases the future risk of dementia (Gray et al., 2015). These observations reveal an intimate, but poorly understood relationship, between cholinergic dysfunction and the pathological and cognitive deficits in AD. However, whether cholinergic malfunction has a causal role in increasing the risk of dementia or regulating pathology is unknown. Moreover, the causal and temporal relationships between cholinergic malfunctioning and long-term changes in hippocampal neurons in AD are still unclear.

To test the capacity of cholinergic tone to regulate long-term functions in target cells we examined the hippocampal transcriptome in genetically-modified mice with compromised hippocampal cholinergic tone. Using forebrain-specific deletion of the vesicular acetylcholine transporter (VACHT), a protein required for acetylcholine (ACh) release (de Castro et al., 2009; Prado et al., 2013), we unveil that long-term cholinergic deficiency causes global changes in gene expression and alternative splicing in the hippocampus. This leads to abnormal alternative splicing of BACE1 with consequent age-dependent changes in amyloid precursor protein (APP) processing, tau hyperphosphorylation, hippocampal neuronal loss and cognitive decline. Comparative analyses in the AD brain enabled us to identify links between cholinergic deficiency and AD pathology, together supporting the notion that early cholinergic dysfunction may be

a pivotal step in AD pathology initiation and progression. Our data provide potential mechanisms to explain how cholinergic deficiency may facilitate pathology in AD.

5.3 Materials and Methods

5.3.1 Mouse lines

Generation of VAcHTflox/flox mice was previously described (de Castro et al., 2009). VAcHTNkx2.1-Cre-flox/flox mice were generated by crossing VAcHTflox/flox (crossed for 5 generations with C57BL/6J) with the Nkx2.1-Cre mouse line (C57BL/6J-Tg(Nkx2-1-cre)2Sand/J), purchased from The Jackson Laboratory (JAX stock no. 008661). Unless otherwise stated, all control mice used were VAcHTflox/flox littermates. All procedures were conducted in accordance with guidelines of the Canadian Council of Animal Care (CCAC) and in accordance with ARRIVE guidelines, at the University of Western Ontario with an approved institutional animal protocol (2008-127). Only male mice were used for all experiments.

5.3.2 RNA Sequencing

Mouse hippocampal tissue was rapidly dissected and total RNA was extracted from individual samples using the PureLink RNA Mini Kit (Ambion). 2 µg of total RNA were then sent to the Centre for Applied Genomics, The Hospital for Sick Children, where the cDNA library was prepared using the TruSeq Stranded Total Sample Preparation kit (Illumina) and run in a HiSeq 2500 platform with coverage of 200-250 million pair reads per lane. 5 animals were run per lane to obtain enough coverage for alternative splicing analysis (50 million pair reads per sample). The sequenced reads were aligned to the mouse genome using the TopHat program against the mouse genome in Ensembl (version EnsMart72) to enable quantification of splice junctions in addition to gene level measurements. Differential gene expression analysis was conducted using the Bioconductor DESeq package which accounts for the counts binomial distribution

(Anders and Huber, 2010). Datasets are available on ArrayExpress (<http://www.ebi.ac.uk/arrayexpress/>) under accession number E-MTAB-3897.

For human brains, we used the SQUARE™ RNA library construction approach which utilizes different sets of 5'- and 3'-site specific primers to segregate all full-length transcripts into sub-pools defined by the selective nucleotides in the respective primers. Unlike traditional sequencing, which is based on the use of universal primers that produce a pool of fragmented RNA products for a given gene, we used 12 different sets of 3'-primers that complement all distinct di-nucleotides at transcript 3'-polyadenylation sites and enable separate sequencing of the corresponding intact RNA molecules for each of the primer sets through barcoding. This unprecedented depth of segregated brain RNA-Seq data was made publicly accessible by establishing a user-friendly website where the sequenced variants for any given brain-expressed transcript can be found (<http://apainad.weebly.com/>). Sequencing files were processed and analyzed for differential expression and functional enrichment.

RNA sequencing libraries made from the temporal gyrus samples yielded an average of 6.0×10^6 (STD= 2.0×10^6) uniquely aligned 75 base pair (bp) single end reads, or approximately 7.0×10^7 (STD= 1.8×10^7) total read counts when combining all 12 SQUARE fields for each sample. These reads were mapped against the GRCh37/hg19 version of the Homo sapiens genome (<http://genome.ucsc.edu/>). Transcripts with more than 1 read per kilobase per million (RPKM) per SQUARE field were defined as being detected (Hebenstreit and Teichmann, 2011). An average of 6610 ± 1367 genes per field were detected across the 12 fields (details in Supplementary Table 5.6.2). Expression criteria were set to RPKM>1 in at least one of the SQUARE fields, in at least 80% of the tested donor cohorts.

5.3.3 Immunofluorescence

Immunofluorescence experiments were performed as previously described (de Castro et al. 2009). Primary antibodies used were anti-Choline Transporter (CHT1; 1:200), which was kindly donated by Dr. R. Jane Rylett, University of Western Ontario, London, Ontario, anti-hnRNPA2/B1 (1:200 Santa Cruz Biotechnology Catalog no. sc-10035),

anti-Cleaved caspase-3 (1:500 Thermo Fisher Scientific, Catalog no. PA5-16335), anti-AT180 (1:1000 Thermo Fisher Scientific, Catalog no. EN-MN1040), anti-NeuN (1:200 PhosphoSolutions, Catalog no. 583-FOX3), anti-GFAP, anti-PSD95. Sections were visualized by Zeiss LSM 510 Meta (Carl Zeiss, Oberkochen, Germany) confocal system (40x, 63x objectives, with an N.A. of 1.3 and 1.4, respectively) and by Leica TCS SP8 (Leica Microsystems Inc, Ontario, Canada) confocal system (63x objective, with an N.A. of 1.4), a 488-nm Ar laser and 633-nm HeNe laser were used for excitation of fluorophores.

5.3.4 Western Blotting

Mouse hippocampi were collected, protein was isolated, and immunoblotting was performed as previously described using RIPA lysis buffer supplemented with protease and phosphatase inhibitors (Guzman et al., 2011). Band intensities were quantified using FluoroChemQ software (Thermo Fisher Scientific).

5.3.5 Gene Ontology Analysis

Gene ontology functional analysis was performed using the GOrilla software through the web application. Using the two-un-ranked lists method as described (Eden et al., 2009). KEGG pathway analysis was performed using the ClueGO plug-in of Cytoscape (Bindea et al., 2009).

5.3.6 RNA Binding Protein Analysis

To predict potential RNA-binding proteins that may be implicated in the observed changes in alternative splicing, alternatively spliced sequences were run through the RBPmap software (Paz et al., 2014) to detect potentially altered RNA binding proteins. The list of RNA binding proteins that were suggested by the software were then run through the Allen Brain Atlas (<http://mouse.brain-map.org/>) in order to ensure that they were expressed in the murine hippocampus. All RNA binding proteins not expressed in the hippocampus were excluded.

5.3.7 qPCR

To measure mRNA expression, total RNA was extracted from freshly dissected hippocampal tissue, using the Aurum Total RNA for fatty and fibrous tissue kit (Bio-Rad) according to the manufacturer's instructions. cDNA synthesis and qPCR analysis were performed as previously described (Guzman et al., 2011). For alternative splicing experiments, the alternative exon levels were normalized to a constitutively expressed exon from the same gene.

5.3.8 Primary Neuronal Cultures

Primary mouse hippocampal neurons were produced from E16 embryos as previously described (Ostapchenko et al., 2013). Neurons were cultured for 15 days. Knockdown of hnRNPA2/B1 from the cultured neurons was achieved by treatment with a shRNA, as previously described (Berson et al., 2012). A separate set of cultured neurons was treated with 10 μ M of carbachol, 10 μ M of carbachol and 100 μ M Atropine, or 100 μ M Atropine alone for 48 hours.

5.3.9 APP Processing

Biochemical analysis of the processing of APP was performed as previously described (Dewachter et al., 2002). Forebrains from VACHT deficient and control mice were homogenized in 50mM Tris-HCl (pH 8.5), samples were then ultracentrifuge at 135,000g for 1 hour at 4°C, and the supernatant was collected and analyzed by Western blotting and ELISA. The pellet was re-suspended and ultracentrifuged again and diluted in 8M guanidine HCl to obtain the insoluble fraction for ELISA analysis.

5.3.10 ELISA

Murine β -amyloid was measured from the hippocampal homogenate using the Wako Human/Rat (Mouse) β -Amyloid (42) ELISA High-Sensitive Kit (Catalog Number: 292-64501). The ELISA assay was performed according to the manufacturer's protocol.

5.3.11 Congo Red Staining

Congo red staining was performed as previously described (Thompson and Walker, 2015), using a Congo-Red solution (Sigma C-6277) in 100% ethanol.

5.3.12 Silver staining

Assessment of argyrophilic cells in the hippocampus was done by using NeuroSilverTM staining kit II (FD NeuroTechnologies, Inc., Baltimore, MD), which provides detection of degenerating neurons, including neuronal somata, axons, and terminals.

5.3.13 Estimation of Hippocampal Volume

NeuN immunohistochemistry was performed in order to estimate the volume of and number of neurons of hippocampal regions CA1, CA3, and the dentate gyrus (DG) as described (Beauquis et al., 2014). Briefly, tissue sections were stained with mouse monoclonal anti-NeuN (1:500 PhosphoSolutions, Catalog no. 583-FOX3), using the ABC kit (Vector Laboratories) and developed with 2 mM diaminobenzidine (Sigma, USA) and 0.5 mM H₂O₂ in 0.1 M Tris buffer. The total number of NeuN (T) cells in the various hippocampal regions was estimated using the following formula: $T=(N*V)/t$, where N is the cell density, V is the volume of the structure, and t is the thickness of the section.

5.3.14 GSK3 Inhibition

To inhibit GSK3 in VAcHTNkx2.1-Cre-flox/flox mice, a cohort of aged animals (12 months old, n=5 AR-A014418 treated, n=4 saline treated) were implanted with Alzet micro-osmotic pumps (Model 1004; DURECT Corp, Cupertino, Calif). The pumps were implanted subcutaneously in the intra-scapular region of each mouse. The reservoir of each pump was preloaded with 96 μ L of either sterile saline solution or the GSK3 inhibitor AR-A014418. The pumps administered 5 mg/kg/d of AR-A014418, a dose shown to produce a significant inhibition of GSK3 in vivo (Ly et al., 2013). During the

implantation procedure, mice were anesthetized with ketamine (100 mg/kg) and xylazine (15 mg/kg). Drug treatment lasted for 28 days.

5.3.15 Morris Water Maze

The spatial version of the Morris water maze (MWM) was conducted as described previously to investigate spatial memory (Kolisnyk et al., 2013b; Martyn et al., 2012; Vorhees and Williams, 2006). Briefly, animals were given four training trials a day (90 s each) for 4 d, with a 15 minute inter-trial interval. If the mice did not find the platform after 90 s during the learning phase, they were gently directed to the platform. On the fifth day, memory was assessed via a probe trial (60 s), during which the platform is removed and time spent in the target quadrant is measured. The task was performed in a 1.5-m-diameter pool with 25°C water. The platform was submerged 1 cm below the surface of the water, and spatial cues (posters, streamers, and plastic props) were distributed around the pool. Sessions were recorded and analyzed using the ANY-Maze Software.

The classification of search strategies mice employed during training was defined as previously described (Garthe et al., 2009). An experimenter blind to genotypes scored search strategies as follows: (1) thigmotaxis, characterized by maintaining close proximity to the wall (>70% trial within 10-cm of wall); (2) random search, illustrated by global swimming with no classified strategy; (3) scanning, characterized by a preference for the central pool area (>50% trial within 35-cm of pool center); (4) chaining, characterized by searching near the correct radial distance of the platform to the wall (>75% trial 20–50-cm from the pool center, <15% within 10-cm of wall, and <10% within 20-cm of pool center); (5) directed search, characterized by a preference for a passageway toward the platform or platform quadrant (>80% trial within a 50-cm-wide region from the start point to the platform); (6) focal search, characterized by a highly localized search near the platform ($\geq$ 50% trial in a circular target zone with a 15-cm radius); (7) direct swim, characterized by a maintained heading toward the platform (Little to no deviation in path to reach platform from start point). Total block lengths were the sum of all blocks for one strategy and one mouse.

5.3.16 Protein Isolation from Human post-mortem brain tissue

Samples from parietal cortical tissues from age/ sex-matched controls (n = 6, 3 females and 3 males) and AD-affected individuals (n = 6, 3 females and 3 males) and information related to age and demographics have been previously published (Ostapchenko et al., 2013). The samples were homogenized in RIPA buffer supplemented with protease inhibitor cocktail (Calbiochem), and Western blotting was performed as described above.

5.3.17 Statistical analysis

Sigmastat 3.5 software was used for statistical analysis. Student's t-test was used for comparison between two experimental groups. Two-way ANOVA or two-way ANOVA with repeated measures (RM) were used when more than two groups were compared.

5.4 Results

5.4.1 Forebrain Cholinergic dysfunction modifies expression levels of hippocampal transcripts and alternative splicing

To determine the contribution of cholinergic tone to the regulation of hippocampal transcript levels, we used VACHTNKx2.1-Cre-flox/flox mice, a mouse line with selective deletion of the VACHT gene from forebrain regions, including the medial septum, which contains cholinergic neurons that project to the hippocampus. VACHT has been shown to be essential for ACh packaging and release (de Castro et al., 2009; Lima Rde et al., 2010; Prado et al., 2006). Non-biased whole genome transcriptome RNA-sequencing of hippocampal samples from three VACHT-deficient and four control mice yielded a total of 14,200 expressed genes. Comparative analysis revealed that 1,098 genes were differentially expressed in VACHTNKx2.1-Cre-flox/flox hippocampi compared to control mice (Figure 5.1.1A-B, FDR corrected $p < 0.05$). Of those, 763 genes were upregulated and 362 down-regulated in the transgenic mice. In addition, a linear regression analysis

on reciprocal junction pairs detected roughly 4% of hippocampal transcripts in VACHTNKx2.1-Cre-flox/flox mice as alternatively spliced in high confidence as compared with control mice. Equal proportion of exon inclusion and exclusion events was observed; mainly events of cassette exons were detected (Figure 5.1.1C), suggesting widespread changes in several splicing regulation related pathways and/or cellular mechanisms (Soreq et al., 2014).

We interrogated these differentially expressed/spliced genes for involvement in neuronal function and AD-like pathology. A number of genes involved in critical pathways including PI3K-Akt signalling pathway [a regulator of neuronal vulnerability (Endo et al., 2006; Gary and Mattson, 2001)], spliceosome regulation and regulation of microtubule-based processes were identified using Gene Ontology (GO) KEGG pathway analysis (Figure 5.1.1D, Table 5.1). qPCR validation and correlation between changes observed in RNA-Seq and in an independent mouse cohort are shown in Fig. 5.1.2 for the different gene pathways and alternative splicing events. These results suggest that abnormal cholinergic signalling can effectively modulate several major gene pathways with potential to influence the function of target cells in the hippocampus.

We also performed small molecule RNA-Seq and additional miRNA microarray hybridization experiments, and observed limited changes in miRNA expression in the hippocampus of VACHT-deficient mice (Fig. 5.1.3). VACHTNKx2.1-Cre-flox/flox hippocampus showed a mature miRNA expression profile with only marginal differences from controls. Only 7 of 700 detectable miRNAs were differentially expressed, and of the 20 miRNAs most highly expressed in the hippocampus, comprising 82% of total counts, none were differentially expressed (Fig. 5.1.3). These findings point to alternative splicing and transcription, or changes in mRNA turnover, rather than miRNA, as potential main contributors to phenotypes in VACHT-deficient mice.

Figure 5.1.1. Forebrain deletion of VACHT induces alterations in hippocampal transcriptome. (A) Principal component analysis of transcripts from the hippocampi of control (VACHT^{flox/flox}; gray circles) and VACHT^{NKx2.1-Cre-flox/flox} (red circles) mice. (B) Cluster analysis of differentially regulated transcripts in the hippocampus of VACHT^{NKx2.1-Cre-flox/flox} (n=3) mice compared to controls (n=4). (C) Number of genes at indicated significance cut-off that were found to have an exon inclusion or exclusion event and summary of alternative splicing events. (D) List of genes from the PI3K-AKT pathway (grey shading), Spliceosome pathway (blue shading), Microtubule polymerization pathway (green shading) and other AD genes of interest (yellow shading), identified from KEGG pathway analysis of altered transcripts in VACHT^{NKx2.1-Cre-flox/flox} mice. For each gene corresponding fold change, corrected statistical significance levels, and RNA expression change is also shown. Altered mRNA expression of these genes has been confirmed by qPCR (see Fig. 5.1.2).

Figure 5.1.1. Forebrain deletion of VACHT induces alterations in hippocampal transcriptome.

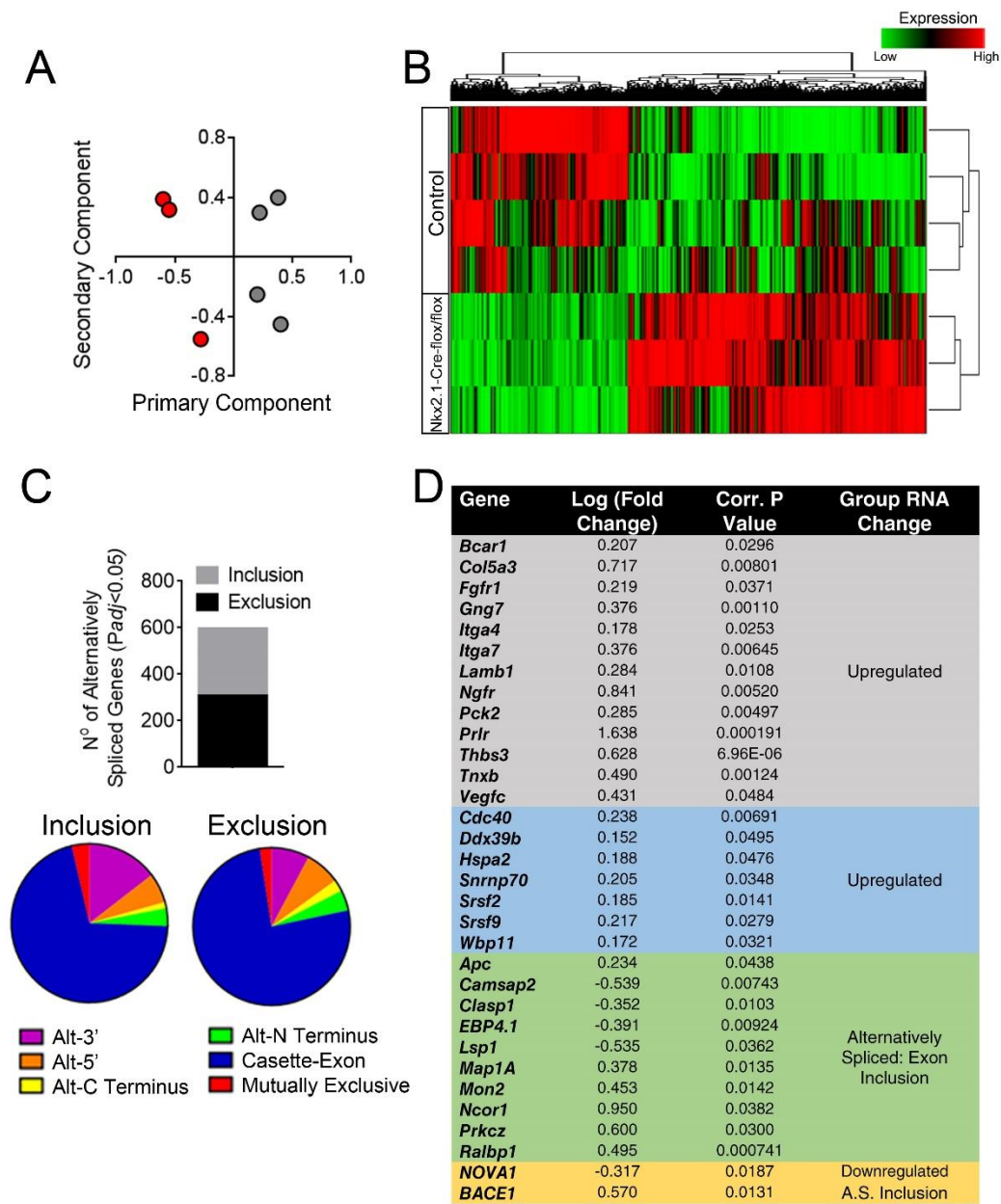


Figure 5.1.2. qPCR validation of RNA-Seq data. (A) qPCR validation and Pearson's correlation analysis on transcripts annotated to the spliceosome KEGG pathway quantified by RNA-Seq data from the hippocampus of VACHT^{NKx2.1-Cre-flox/flox} mice and controls [(r=0.8528, p=0.001), n=6 data are mean $\pm$ SEM.]. (B) qPCR validation and Pearson's correlation analysis with RNA-Seq data of transcripts annotated to the PI3k-AKT KEGG pathway [(r=0.8528, p=0.001)]. (C) qPCR validation and Pearson's correlation analysis of transcripts annotated to the microtubule polymerization pathway [(r=0.8528, p=0.001)].

Figure 5.1.2. qPCR validation of RNA-Seq data.

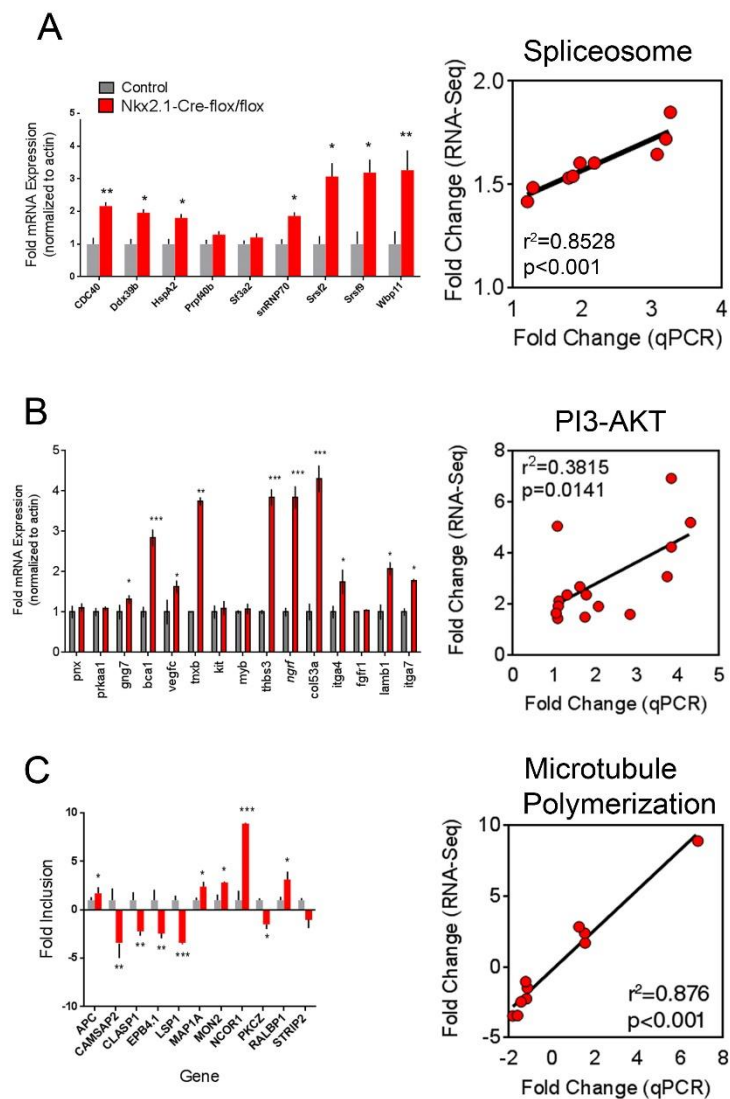


Figure 5.1.3. Global hippocampal expression of miRNA is not altered in VACHT

deficient mice. (A) Small RNA sequencing from six VACHT^{Nkx2.1-Cre-flox/flox} mice and five controls demonstrated miR-592-5p, miR-219-2-3 and 148a-3p as differentially expressed (DE) after FDR correction ($P < 0.05$). (B) Principal Component Analysis (PCA) showed marginal separation of the two groups, suggesting that VACHT transcript removal does not induce a global change in small RNA expression. (C) Extent of absolute change was limited, as none of the top 20 miRNAs expressed in the hippocampus were modified, leaving 82% of hippocampal miRNAs unchanged. (D) Similar fractions of small RNA reads mapped to parts of the pre-miRNA molecules other than the mature-miRNA in VACHT^{Nkx2.1-Cre-flox/flox} mice and controls (E) Processing rate and/or efficacy might be affected, as a set of 7 seemingly unmodified miRNAs presented drastically reduced pre-miRNA levels when quantified by long RNA sequencing in VACHT^{Nkx2.1-Cre-flox/flox} mice.

Figure 5.1.3. Global hippocampal expression of miRNA is not altered in VACHT deficient mice.

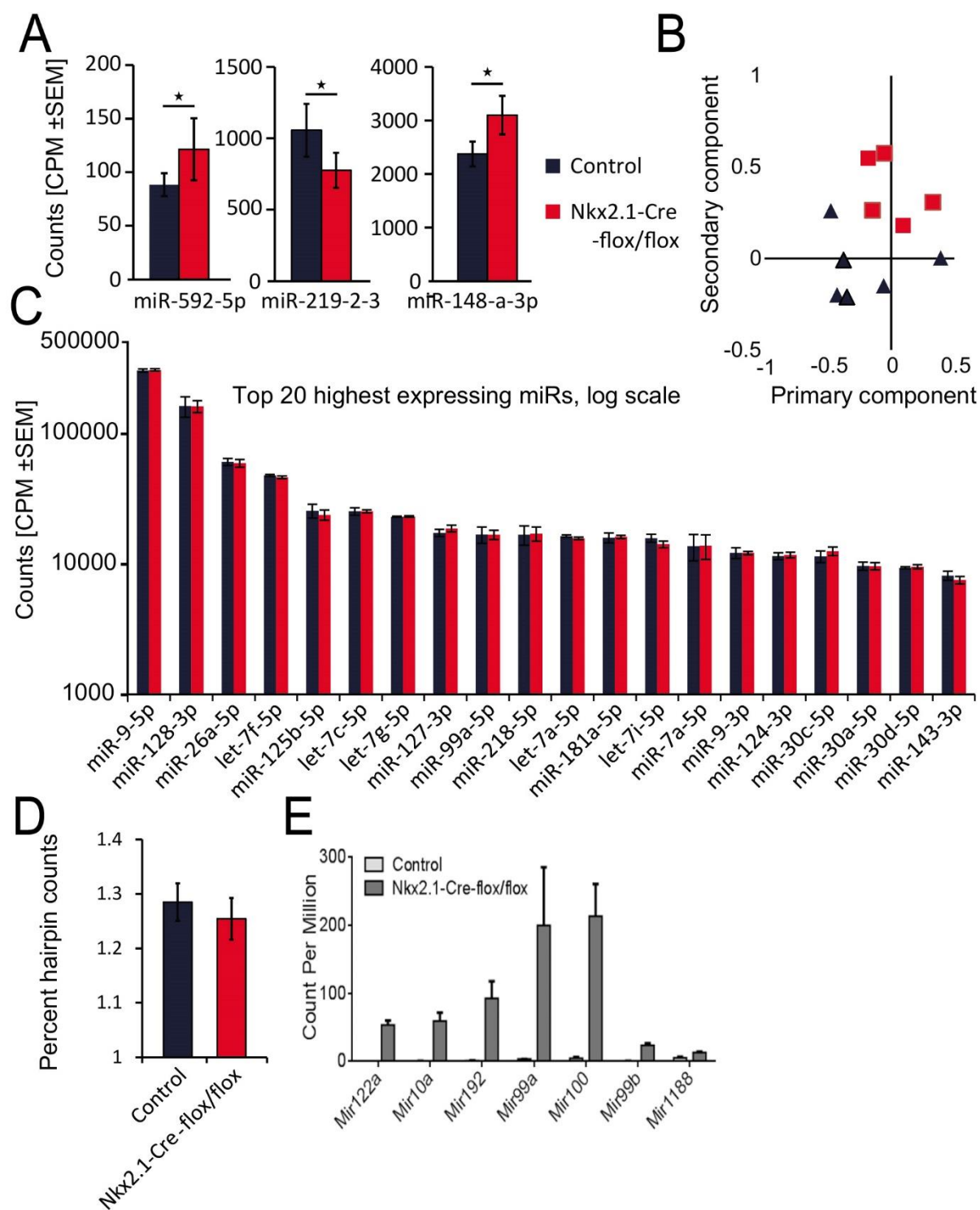


Table 5.1 AD Related Genes Identified in RNA-Seq Data. Genes in either the AKT pathway (grey shading), Spliceosome pathway (blue shading), or Regulation of Microtubule Polymerization (green shading) and role(s) in AD-like pathology.

Table 5.1 AD Related Genes Identified in RNA-Seq Data.

Gene	Link to AD
<i>Bcar1</i>	Linked to APP transcription (Seenundun and Robaire, 2007).
<i>Col5a3</i>	SNP linked to AD (Silver et al., 2012).
<i>Fgfr1</i>	Altered expression in aging (Walker et al., 1998).
<i>Gng7</i>	Associated with depression in the elderly (Schol-Gelok et al., 2010). Protein alterations in animal model of neurodegeneration (Karlsson et al., 2012).
<i>Itga4</i>	Upregulated in astrocytes in AD brain (Orre et al., 2014). Potential to bind Ab (Sabo et al., 1995).
<i>Itga7</i>	Potential to bind Ab (Sabo et al., 1995).
<i>Kit</i>	Mediates cell survival and apoptosis via AKT (Blume-Jensen et al., 1998)
<i>Lamb1</i>	SNP linked to AD (Taguchi et al., 2005)
<i>Myb</i>	Regulates neuronal apoptosis (Liu et al., 2004)
<i>Ngfr</i>	Up-regulated in AD brain (Scott et al., 1995) SNP linked to AD (Cozza et al., 2008)
<i>Pck2</i>	SNP linked to AD (Taguchi et al., 2005) Altered transcription in AD brain (Brooks et al., 2007)
<i>Prkaa1</i>	SNP linked to AD (Clarimon et al., 2009)
<i>Prlr</i>	Up-regulated in rat model of AD (Bakalash et al., 2011)
<i>Pxn</i>	Up-regulated in AD brain (Liang et al., 2012)
<i>Thbs3</i>	Altered transcription in AD brain (Kalback et al., 2004)
<i>Tnxb</i>	SNP linked to AD (Meda et al., 2012; Sherva et al., 2011)
<i>Vegfc</i>	Increased levels in CSF of AD patients (Tarkowski et al., 2002)
<i>Cdc40</i>	Linked to alternative splicing in neurodegeneration (Tollervey et al., 2011)
<i>Ddx39b</i>	SNP linked to Late-Onset-AD (Mohsen et al., 2015)
<i>Hspa2</i>	SNP linked to Late-Onset-AD (Broer et al., 2011; Clarimon et al., 2003)
<i>Prpf40b</i>	Implicated in human neurodegeneration (Passani et al., 2000)
<i>Sf3a2</i>	Altered in aging mouse brain (Meshorer and Soreq, 2002)
<i>Snrnp70</i>	Up-regulated and aggregated in AD brain (Bai et al., 2013)
<i>Srsf2</i>	Regulates splicing events in AD (Raj et al., 2014)

<i>Srsf9</i>	Regulates splicing events in AD (Qian and Liu, 2014)
<i>Wbp11</i>	Upregulated in accelerated aging murine model (Carter et al., 2005)
<i>APC</i>	Increased expression in AD brain (Leroy et al., 2001)
<i>CAMSAP2</i>	Altered protein levels in animal model of neurodegeneration (McGorum et al., 2015)
<i>CLASP1</i>	No known link to AD
<i>EBP4.1</i>	Interacts with APP protein in vivo (Bai et al., 2008)
<i>LSP1</i>	Epigenetic modifications in AD mouse model (Cong et al., 2014)
<i>MAP1A</i>	Upregulated in tau deficient mice (Ma et al., 2014) Binds soluble A β <i>in vitro</i> (Clemmensen et al., 2012)
<i>MON2</i>	No known link to AD
<i>NCOR1</i>	Protein expression altered by A β and tau (Hoerndli et al., 2007)
<i>PKCZ</i>	Altered activity in AD brain (Moore et al., 1998)
<i>RALBP1</i>	Transcription altered in AD brain (Zhang et al., 2015)
<i>STRIP2</i>	Decreased expression in neurodegeneration (Desplats et al., 2006)

5.4.2 Cholinergic deficit triggers abnormal BACE1 alternative splicing and APP Processing

One of the detected abnormally alternatively spliced genes in our database was the protease BACE1 (Figure 5.2.1D), which is responsible for the cleavage of APP (Luo et al., 2001). The predicted alternative splicing event in VACHT-deficient mice is expected to increase expression of BACE1-501, the active protein isoform (Mowrer and Wolfe, 2008). qPCR analysis validated the predicted splicing event and demonstrated increased exon 3/4 inclusion for BACE1 (Figure 5.2.1A).

Bioinformatics analysis using the RBP-Map tool revealed an enrichment of binding sites for hnRNPA2/B1 in BACE1 mRNA. hnRNPA2/B1 is part of a family of RNA binding proteins that regulate pre-mRNA splicing, trafficking and maturation (Bekenstein and Soreq, 2013). Notably, AD-associated impairments in cholinergic signalling are accompanied by decreased expression of hnRNPA2/B1 protein in the AD cerebral cortex and in cholinergic impaired mice (Berson et al., 2012; Kolisnyk et al., 2013a). Correspondingly, the hippocampus of VACHT^{tnx2.1-Cre-flox/flox} mice showed reduced hnRNPA2/B1 protein levels (Figure 5.2.1 B). We then investigated whether hnRNPA2/B1 regulates BACE1 splicing by exposing primary hippocampal cultured neurons to lentivirus carrying shRNA against hnRNPA2/B1. Our results showed changes in BACE1 splicing similar to cholinergic deficiency (Figure 5.2.1C), directly implicating hnRNPA2/B1 in the regulation of BACE1 splicing. To test for the role of cholinergic signalling and the different cholinergic receptors in mediating this splicing event, we treated cultured hippocampal neurons with the cholinergic mimetic carbachol. This treatment was able to decrease the proportion of BACE1-501. This decrease was blocked by co-treatment with the muscarinic antagonist atropine (Figure 5.2.1D). These data implicate muscarinic receptors in the regulation of BACE1 splicing. This splicing event in BACE1 predicts an increase in the levels of the mature BACE1 protein and indeed, immunoblot analysis revealed a 2-fold increase of BACE1 levels in the hippocampus of VACHT-deficient mice (Figure 5.2.1E).

In late onset AD BACE1 expression is upregulated (Hebert et al., 2008) and it is thought to contribute to age-dependent progression in AD pathology (Ly et al., 2013). We therefore tested for changes in APP processing in VACHTNkx2.1-Cre-flox/flox mice. Aged VACHT-deficient mice (11-14 month old) displayed a modified pattern of Tris-soluble APP fragments (Figure 5.2.1 F), similar to that of mouse models with APP/PS1 mutations (Jankowsky et al., 2004; Oddo et al., 2003). In contrast, membrane-bound C-terminal fragments of APP (α and β CTFs), alterations of which can suggest impaired proteolytic processing of the protein [Reviewed in (Selkoe, 2000)], were similar in VACHT-deficient mice and controls (Figure 5.2.1 G). APP processing was not modified in aged Nkx2.1-Cre mice (Figure 5.2.2 A), suggesting that this effect is due to cholinergic dysfunction rather than to Cre expression.

We then assessed the levels of mouse amyloid peptides using an ELISA kit validated for both mouse and human A β peptides (Teich et al., 2013). The hippocampus of aged VACHTNkx2.1-Cre-flox/flox mice showed increased levels of soluble mouse A β peptide compared to controls (Figure 5.2.1 H), reaching about one third of the levels of those found in aged 5XFAD mouse model of AD, which is one of the most aggressive models of AD amyloidosis. In comparison, insoluble amyloid peptide was undetectable in the brains of VACHT-deficient mice, whereas it was highly abundant in the 5XFAD mice (Figure 5.2.1 H). In addition, neither control nor VACHT-deficient mice displayed positive Congo red staining, unlike brain sections from 5XFAD mice, which exhibited numerous Congo red plaques (Figure 5.2.1 I). These data indicate that although VACHT-deficient mice show increased levels of soluble A β peptides, they do not seem to accumulate in extracellular amyloid plaques. Indeed, the murine amyloid peptide is much less prone to aggregation than human A β due to two amino acid changes (Jankowsky et al., 2007).

Figure 5.2.1 Disrupted APP processing and alternative splicing of BACE1 in cholinergic deficient mice. (A) qPCR analysis of alternative splicing events for BACE1 in the hippocampus of controls and (VACHT^{flox/flox}; gray bars) and VACHT^{NKx2.1-Cre-flox/flox} (red bars). Alternative exon levels are normalized to a constitutive exon from the same gene (n=6, data are mean $\pm$ SEM. **P<0.01). (B) Representative Western blot and quantification of hnRNPA2/B1 protein expression in the hippocampus of controls (VACHT^{flox/flox}; gray bars) and VACHT^{NKx2.1-Cre-flox/flox} (red bars) mice. hnRNPA2/B1 expression was normalized to actin (n=4, data are mean $\pm$ SEM. **P<0.01). (C) Quantification of the BACE1 alternative splicing in primary neuron cultures treated with hnRNPA2B1-shRNA (*P<0.05). (D) Quantification of the BACE1 alternative splicing in primary neuron cultures treated with 10mM Carbachol and Atropine (n=4, data are mean $\pm$ SEM. **P<0.05). (E) Representative Western blot and quantification of BACE1 protein levels in the hippocampus of controls (VACHT^{flox/flox}; gray bars) and VACHT^{NKx2.1-Cre-flox/flox} (red bars) mice. BACE1 expression was normalized to actin (n=3, data are mean $\pm$ SEM. *P<0.05). (F) Biochemical analysis and quantification of murine APP fragments in brain homogenates of aged expressed as a % [(Signal intensity of the fragment/signal intensity of full-length protein) x100]. 11-14 month old controls (VACHT^{flox/flox}; gray bars), VACHT^{NKx2.1-Cre-flox/flox} (red bars) and APP^{swe}/PS1dE9 (green bars) hippocampal tissue extracts were resolved by Western blotting (data are mean $\pm$ SEM n=3). (G) Analysis of membrane-bound APP fragments in aged controls (VACHT^{flox/flox}; gray bars) and VACHT^{NKx2.1-Cre-flox/flox} (red bars) and APP^{swe}/PS1dE9 (green bars) (data are mean $\pm$ SEM n=3). (H) Murine soluble and insoluble levels of A β 42 in aged (11-14 months old) controls (VACHT^{flox/flox}; gray bars), VACHT^{NKx2.1-Cre-flox/flox} (red bars) and 5xFAD (black bars) measured by ELISA (n=4) (I) Congo red staining in the CA1 region of the hippocampus in aged (11-14 months old) controls, VACHT^{NKx2.1-Cre-flox/flox}, and 5xFAD mice. Arrowheads indicate positive-Congo red staining suggestive of amyloid plaques. (n=3, Scale bar, 100 μ m).

Figure 5.2.1 Disrupted APP processing and alternative splicing of BACE1 in cholinergic deficient mice.

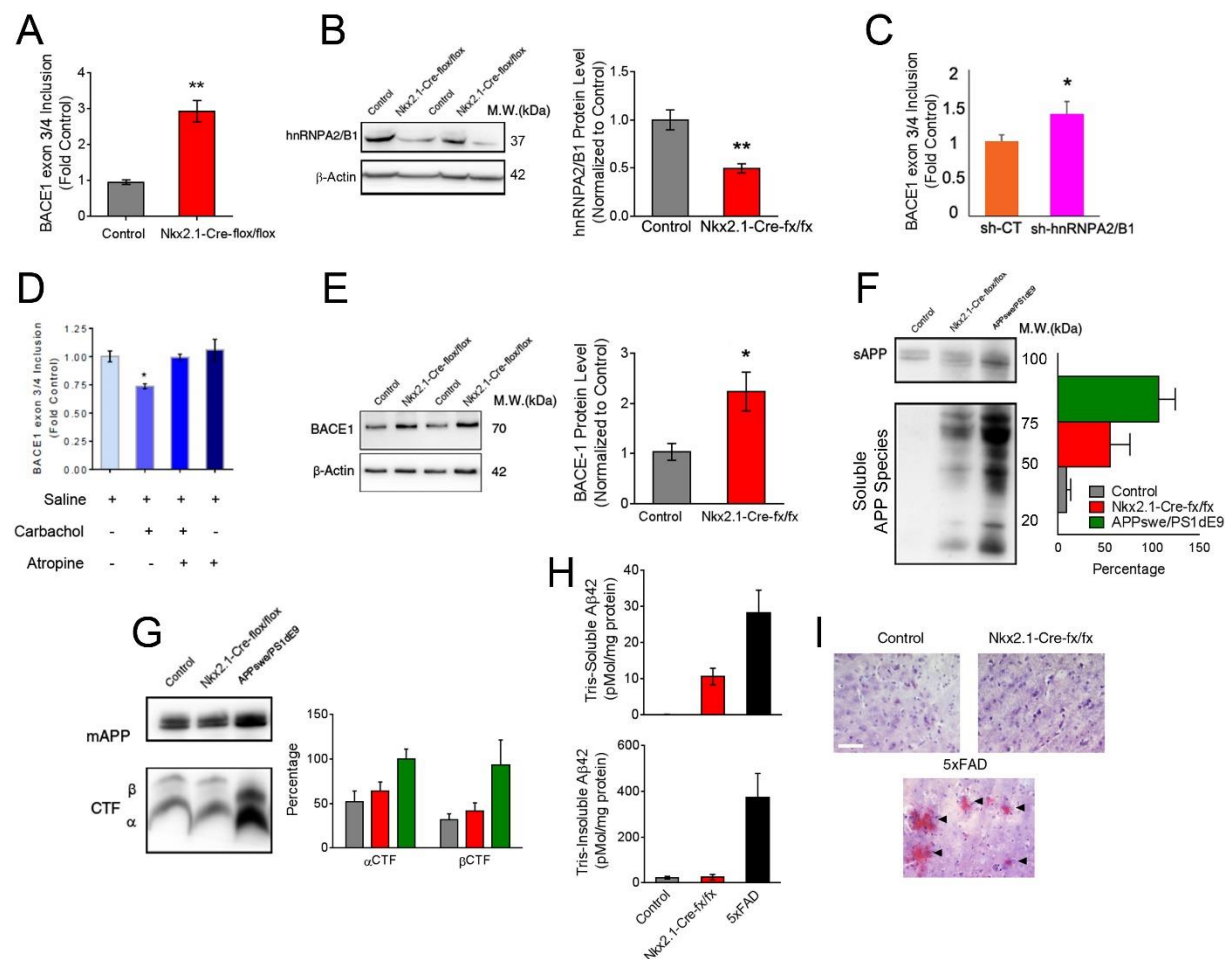
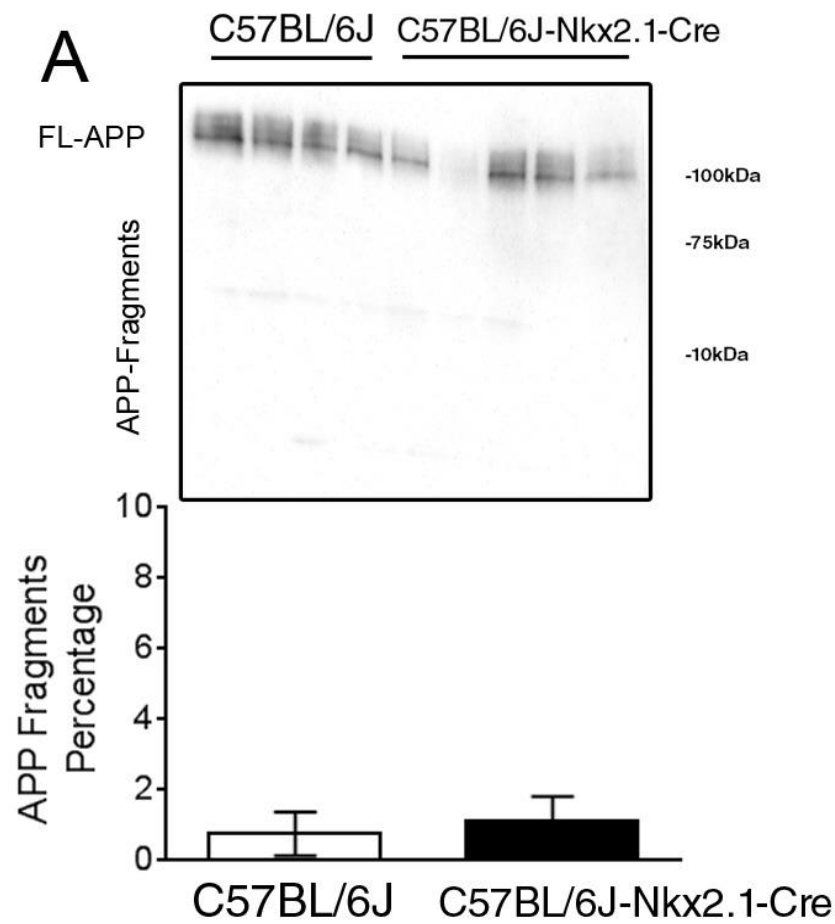


Figure 5.2.2 Absence of altered APP processing in aged (11-14 month old) C57/BJ6-Nkx2.1-Cre mice. (A) Western blot of APP processing from Tris-soluble fraction and quantification of APP fragments detected in aged C57BL/6J-Nkx2.1-Cre mice (11-14 month old) showing no significant differences compared to controls (n=4). (Data are mean $\pm$ S.E.M.).

Figure 5.2.2 Absence of altered APP processing in aged (11-14 month old) C57/BJ6-Nkx2.1-Cre mice.



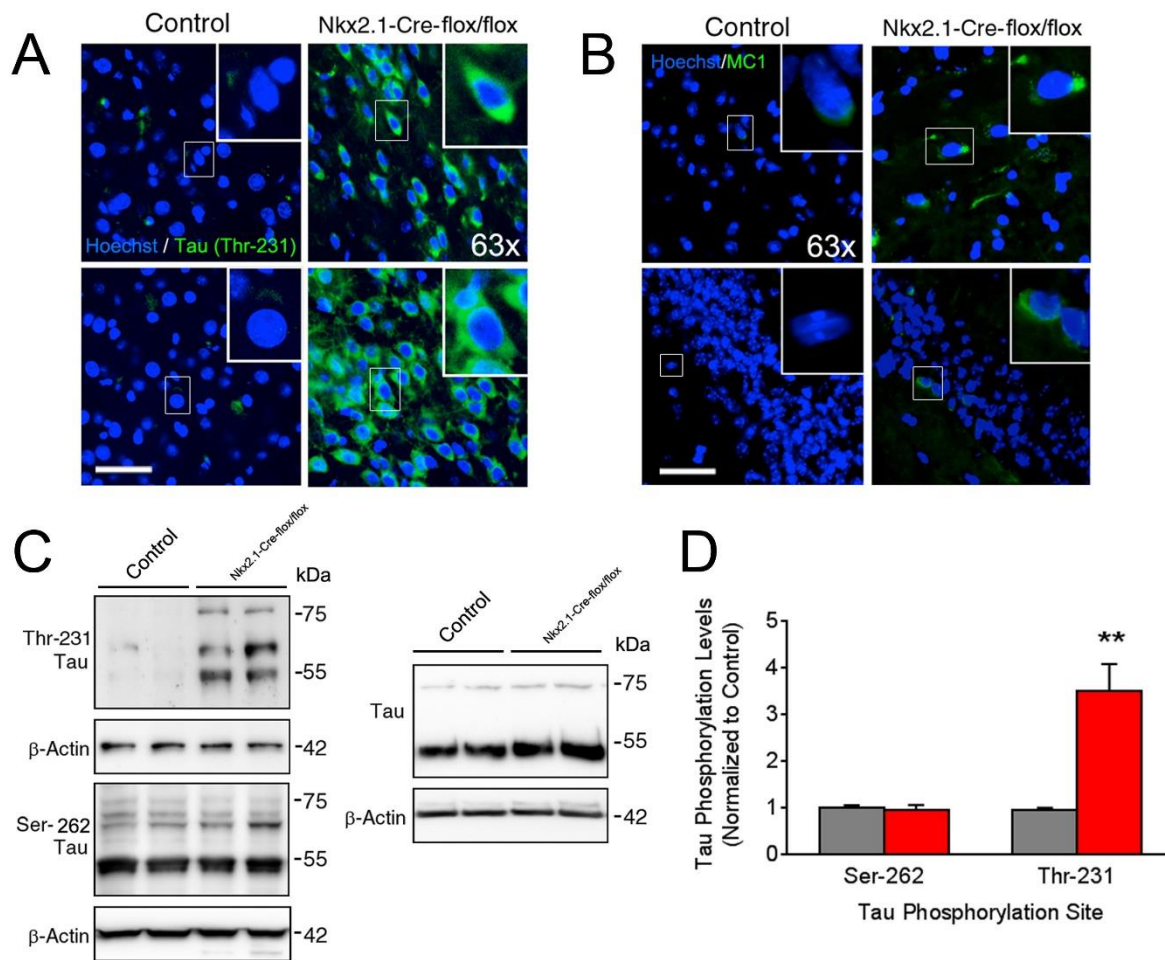
5.4.3 Cholinergic deficit leads to age-dependent hippocampal tauopathy

In AD, increased levels of soluble A β peptides are thought to precede abnormal phosphorylation of the microtubule associated protein tau (Iqbal et al., 2010). Previous reports suggested that cholinergic activity and tau phosphorylation might be inter-related (Hellstrom-Lindahl, 2000). Therefore, we used immunofluorescence to assess levels of the AT180 tau epitope (T231/S235) in the hippocampus of VAcHT-deficient mice. This phosphorylation-dependent antibody specific to pT231 has been shown to label approximately 70% of paired helical filaments (PHF) in AD brains (Goedert et al., 1994). Phosphorylation at this epitope reduces the binding of tau to microtubules potentially increasing its toxicity (Lim et al., 2008). Immunofluorescence imaging revealed a robust increase of AT180 immunoreactivity in the hippocampus of VAcHTNkx2.1-Cre-flox/flox mice compared to aged-matched controls (Figure 5.3A- 11-14 month-old mice). To test if the positive immunoreactivity of pTau in VAcHT-deficient mice is associated with an induction of pathological tau, immunofluorescence with MC1 antibody was performed. Positive reactivity of conformation-dependent MC1 antibody depends on the proximity of N terminal (a.a. 7-9) and C-terminal (313-333) amino acid sequences of tau, which is one of the earliest alterations of tau in AD (Weaver et al., 2000; Wolozin et al., 1986). Immunostaining with MC1 revealed positive immunoreactivity in the hippocampus of aged cholinergic-deficient mice, but not in age-matched controls (Figure 5.3B).

In agreement with the immunofluorescence data, hippocampal extracts of VAcHTNkx2.1-Cre-flox/flox mice showed approximately four-fold increases in pTau immunoreactive bands, including higher order oligomers detected with AT180, when compared to controls (Figure 5.3C and D). On the other hand, total tau and pTauS262 levels were unmodified in VAcHT-deficient mice (Figure 5.3C and D). Taken together, our data indicate that deletion of hippocampal VAcHT induces hyper-phosphorylation of tau and leads to tau pathological conformation as detected by MC1, both of which are consistently observed in AD. These data suggest the potential for neuronal toxicity due to cholinergic dysfunction.

Figure 5.3. Hippocampal cholinergic failure triggers tauopathy in an age-dependent manner. (A) Phosphorylated Tau levels monitored by immunolabeling with phosphorylation-dependent antibodies specific to pT231. Representative images of pT231 and Hoeschst labeling in the hippocampus of aged (11-14 month old) controls (left) and VACHT^{NKx2.1-Cre-flox/flox} (right) mice. (n=3, Scale bar, 100μm). (B) Representative images of MC1 and Hoeschst labeling in the CA1 region of the hippocampus of controls (left) and VACHT^{NKx2.1-Cre-flox/flox} (right) mice. (n=3, Scale bar, 100μm). (C) Western blot analysis of controls (VACHT^{flox/flox}) and VACHT^{NKx2.1-Cre-flox/flox} aged (11-14 month old) hippocampal samples for tau using phosphorylation-dependent anti-tau antibodies pT231, Ser 262 and for total Tau protein expression. (D) Quantification of Western blots. pT231, Ser 262, and total tau expression were normalized to actin (n= 4, data are mean ± SEM. **P<0.01).

Figure 5.3. Hippocampal cholinergic failure triggers tauopathy in an age-dependent manner.



5.4.4 Cholinergic deficiency exacerbates age-dependent neuronal vulnerability and impaired learning

Synaptic health is compromised in mouse models of AD and synaptic loss is a consistent finding in AD-affected individuals (Klein, 2006). To examine synaptic integrity we stained hippocampal sections with the synaptic marker PSD95. Aged VACHTNKx2.1-Cre-flox/flox mice displayed hippocampal decreases in PSD95-immunoreactivity, increased microglial activation and up-regulation of inflammatory markers, in comparison to age-matched controls, suggesting large-scale synaptic dysfunction in these mutants (Figure 5.4.1A-C). These observations predict neuronal vulnerability; therefore, we stained brain sections with silver, which accumulates in neurons that are more vulnerable to neurodegeneration (DeOlmos and Ingram, 1971). Aged VACHT-deficient mice presented intensified silver staining compared to controls; this increased silver staining was not observed in young VACHT-deficient mice (Figure 5.4.1D-E), suggesting that long-lasting decrease in cholinergic signalling may increase the vulnerability of hippocampal neurons. Parallel staining of hippocampal sections from aged 5XFAD mice compared to control mice performed as a positive control revealed similar increases in silver staining as that for VACHT-deficient mice (Figure 5.4.2).

Activated caspase-3, a marker of apoptosis, was augmented in young VACHTNKx2.1-Cre-flox/flox mice compared to controls (Figure 5.4.1F). However, aging significantly increased the number of activated caspase-positive cells in VACHT-deficient mice when compared to controls (Figure 5.4.1F). Also, young VACHT-deficient mice showed no alteration in the number of NeuN positive cells across all regions of the hippocampus (Figure 5.4.1G, Figure 5.4.2); while NeuN positive cells in CA1 and CA3 region, but not dentate gyrus were decreased in aged VACHT-deficient mice (Figure 5.4.1G, Figure 5.4.2), predicting functional implications for this aging-related hippocampal neuronal vulnerability. Thus, impaired cholinergic signalling induces global changes in transcript levels, followed by age-related exacerbation of synaptic and neuronal vulnerability.

To test whether long-lasting cholinergic failure may have age-dependent consequences in cognitive function, we subjected aged (11-14 months old) VACHT-deficient mice to

the MWM task. Young VAcHT-deficient mice (3-6 months old) show little difference from controls in acquisition performance on the Morris Water Maze (MWM) task (Al-Onaizi et al., 2016). In contrast, aged VAcHT-deficient mice took significantly longer and swam a greater distance than age-matched controls to find the platform across the four days of acquisition (Figure 5.4.1E-F). Furthermore, aged VAcHT-deficient mice used distinct strategy preferences to find the platform, indicating that their deteriorated performance was due to modified learning capacities. Briefly, the analysis of search strategies used by each animal was based on a fixed set of criteria (Figure 5.4.1H). At a young age, both controls and VAcHTNkx2.1-Cre-flox/flox mice predominantly used a more direct strategy to reach the platform (strategies 5/6/7, Figure 5.4.1I). In contrast, aged VAcHT-deficient mice used random swimming predominantly as their strategy to acquire the task (strategy 2, Figure 5.4.1I), while aged control mice maintained the use of more direct strategies. Aged VAcHT-deficient mice also exhibited deficits in the probe trial (Figure 5.4.1G). Taken together, these results suggest that long-term cholinergic deficiency in VAcHTNkx2.1-Cre-flox/flox mice led to progressive loss of neurons in the hippocampus that worsened spatial information acquisition and cognitive functioning.

Figure 5.4.1. Hippocampal cholinergic failure leads to increased neuronal vulnerability and worsens cognitive functioning.

(A) Immunofluorescence imaging showing PSD-95 protein levels in the hippocampus of aged controls or VACHT^{NKx2.1-Cre-flox/flox} mice and corresponding (B) Western blot analysis for PSD-95 protein levels in the hippocampus of VACHT^{NKx2.1-Cre-flox/flox} mice compared to controls ($t_{(6)}=4.286$, $p=0.0052$, $n=4$). (C) Immunofluorescence imaging and quantification showing CD-68 immunoreactivity in the hippocampus of aged VACHT^{NKx2.1-Cre-flox/flox} mice as well as levels of IL-1 transcripts as measured by qRT-PCR ($t_{(10)}=2.312$, $p=0.0434$, $n=6$) and IL-6 transcripts as measured by qRT-PCR ($t_{(10)}=2.882$, $p=0.0204$) (Data are mean $\pm$ S.E.M., * $P<0.05$, $n=6$). (D) Representative images of silver staining in the CA1 region of young (3-6 months) and aged (11-14 months) mice. Scale bar, 100 μ m. (E) Quantification of silver stain-positive cells between young and aged hippocampi of controls (VACHT^{flox/flox}; gray bars) and VACHT^{NKx2.1-Cre-flox/flox} (red bars). ($n=5$, data are mean $\pm$ SEM. ** $P<0.01$). (F) Representative immunofluorescence images for activated-caspase 3 labelling in the hippocampi of young (Top) and aged (Bottom) mice. Quantification of activated caspase-3 immunolabelling in young and aged hippocampi of controls (VACHT^{flox/flox}; gray bars) and VACHT^{NKx2.1-Cre-flox/flox} (red bars). ($n=3$, data are mean $\pm$ SEM. * $P<0.05$, ** $P<0.01$, Scale bar, 100 μ m). (G) Distribution of neuron-specific nuclear antigen (NeuN)-positive neurons in the CA1 region of the hippocampus in young (top) and aged (bottom) mice (Scale bar, 100 μ m). Quantitative comparison of the number of neurons labelled by NeuN in the CA1 region of the hippocampus in young (top) and aged (bottom) mice ($n=6$, data are mean $\pm$ SEM. * $P<0.05$). (H) Representative examples of the 7 classified criteria to score the strategies mice used to perform in the MWM. Strategies are color coded. (I) Strategy plot reflecting the mean strategy-recruitment values for the first and fourth trials of each day for young (left) and aged (right) mice. Quantification comparison of total block length values of individual mice and their employed strategies over the course of 4-day training period. Grey bars represent control mice and red bars represent VACHT-deficient mice. ($n=8$, data are mean $\pm$ SEM. * $P<0.05$ ** $P<0.01$).

Figure 5.4.1. Hippocampal cholinergic failure leads to increased neuronal vulnerability and worsens cognitive functioning.

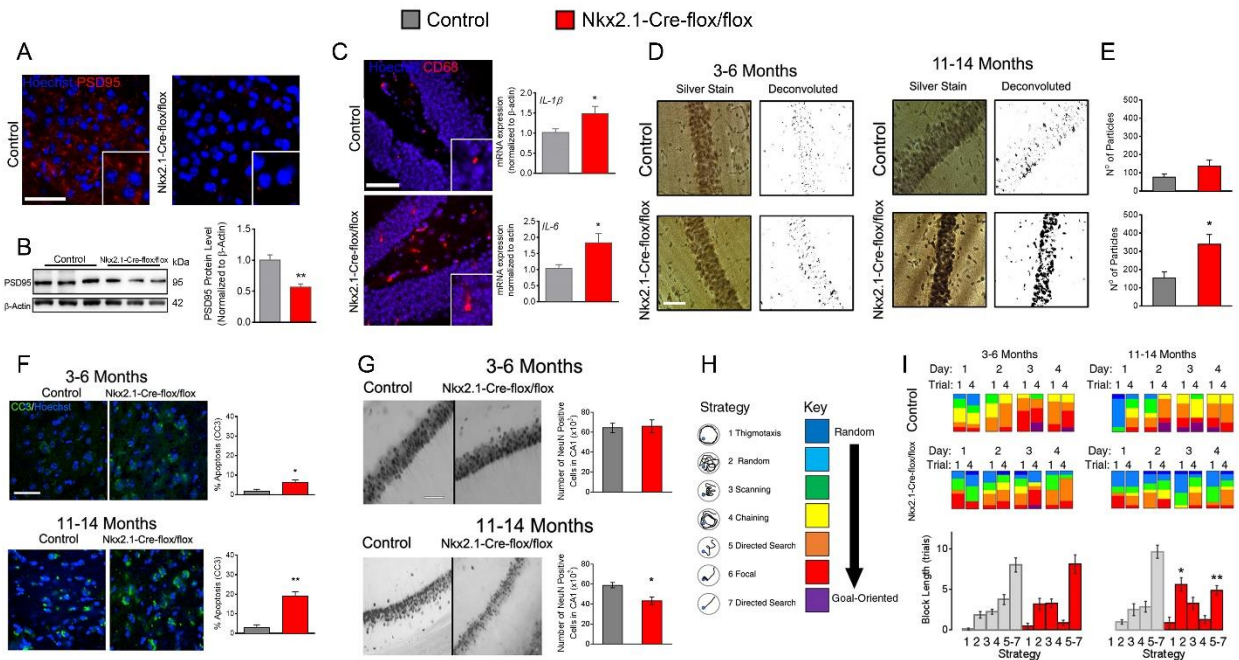
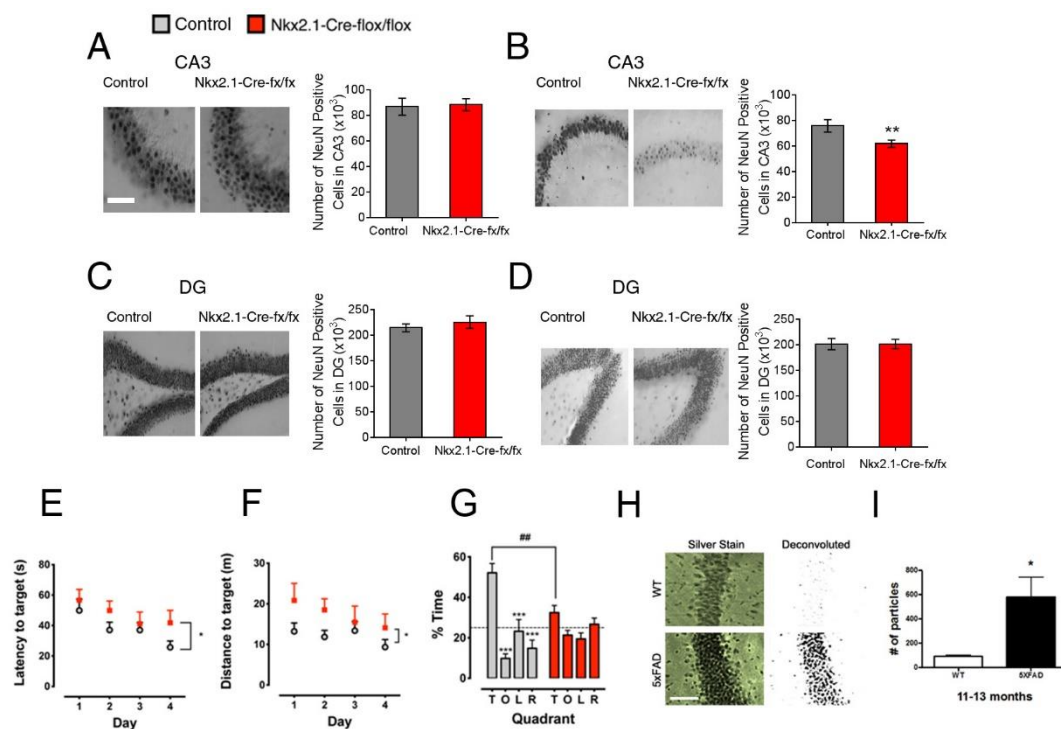


Figure 5.4.2 Estimation of neuronal volume in the CA3 and DG region of the hippocampus of young (3-6) and aged (11-14) month old cholinergic deficient mice as well as cognitive deficits in aged cholinergic deficient mice. (A) Young VACHT^{Nkx2.1-Cre-flox/flox} mice show no change in number of NeuN positive cells in the CA3 ($t_{(18)}=0.1894$, $p=0.8519$), However in (B) there is a significant reduction in number of NeuN positive cells in the CA3 of aged VACHT^{Nkx2.1-Cre-flox/flox} mice ($t_{(18)}=2.454$, $p=0.0246$). No change in the number of NeuN positive cells in the DG region was observed in either young (C) ($t_{(18)}=0.7814$, $p=0.4447$) or old (D) ($t_{(18)}=0.01758$, $p=0.9862$) VACHT^{Nkx2.1-Cre-flox/flox} mice (Data are mean $\pm$ S.E.M., $**p<0.01$, $n=9$). Significantly impaired latency (E) (RM-ANOVA, main effect of genotype $F_{(1,7)}=6.359$, $p=0.0397$), and distance to reach the platform (F) (RM-ANOVA, main effect of genotype $F_{(1,7)}=7.845$, $p=0.0265$) in aged (11-14 month old) VACHT^{Nkx2.1-Cre-flox/flox} mice. (G) Aged (11-14 month old) VACHT^{Nkx2.1-Cre-flox/flox} mice do not show a preference for the target platform during the probe trial portion of the MWM task (RM-ANOVA, main effect of interaction $F_{(3,21)}=6.068$, $p<0.0038$). (Data are mean $\pm$ S.E.M., $*p<0.05$, $**p<0.01$, $***p<0.001$, $n=8$). (H) Representative images of silver staining procedure from 11-14 month old wild-type and 5xFAD mice. (I) Quantification of percent silver stain area from 11-14 month old wild-type and 5xFAD mice (Data are mean $\pm$ S.E.M., $***p<0.001$, $n=3$). Scale bar 100 μm .

Figure 5.4.2 Estimation of neuronal volume in the CA3 and DG region of the hippocampus of young (3-6) and aged (11-14) month old cholinergic deficient mice as well as cognitive deficits in aged cholinergic deficient mice.



5.4.5 Cholinergic mediated age dependent pathology is partially mediated by GSK3 activation

In addition to APP processing and tau hyperphosphorylation, we observed other critical biochemical pathways altered in response to cholinergic deficiency, including aberrant GSK3 signalling, which has also been shown to play multiple roles in AD (Endo et al., 2006; Gary and Mattson, 2001). As several genes that regulate the PI3-AKT pathway were upregulated in VAcHT-deficient mice (Fig. 5.1.1D, 5.1.2), we tested for dysregulation of PI3-AKT signalling pathway in these mice by evaluating the phosphorylation status of the AKT protein and its downstream target GSK3. AKT presented decreased phosphorylation at residue Ser473, with unmodified Thr308 phosphorylation, in VAcHTNKx2.1-Cre-flox/flox hippocampus compared to controls (Figure 5.5.1A). Additionally, GSK3 α/β tyrosine phosphorylation, which reflects activation of GSK3, was increased in these mutants (Figure 5.5.1B). Hence in addition to increased levels of proteins involved in AD pathology, these results suggest potential contributions of GSK3 activation in cholinergic-induced deficits.

To test the role of GSK3 in the abnormal hippocampal changes in cholinergic-deficient mice, we chronically treated a cohort of aged (11 months old) VAcHTNKx2.1-Cre-flox/flox mice with the GSK3 inhibitor AR-A014418 (Figure 5.5.1C). After 28 days of treatment, we found that VAcHT-deficient mice treated with AR-A014418 showed a significant decrease in GSK3 α and β tyrosine phosphorylation when compared to VAcHTNKx2.1-Cre-flox/flox mice treated with saline (Figure 5.5.1D). Increased phosphorylation at Tyr residues 216 or 279 augments GSK3 activity (Hur and Zhou, 2010) and examining GSK3 phosphorylation at these residues has been used to determine the effectiveness of AR-A014418 (Carter et al., 2014; Yadav et al., 2014). We then assessed some of the key alterations detected in the hippocampus of aged VAcHTNKx2.1-Cre-flox/flox mice. AR-A014418 treatment was able to significantly decrease tau T231 hyperphosphorylation and MC1-immunopositive tau in Western blots (Chai et al., 2011; Petry et al., 2014), by approximately 50% in VAcHTNKx2.1-Cre-flox/flox mice when compared to saline VAcHTNKx2.1-Cre-flox/flox mice. Total levels of tau were unchanged (Figure 5.5.1E). Immunofluorescence staining (Figure 5.5.1F)

also demonstrated reduced levels of T231 hyperphosphorylated tau in AR-A014418 treated mice. Compared to saline treated animals, AR-A014418 treatment was able to significantly increase levels of PSD-95 protein (Figure 5.5.1G).

Interestingly, we observed no changes in protein levels of BACE1 following AR-A014418 treatment in aged VChTNKx2.1-Cre-flox/flox mice (Fig. 5.5.2A). Furthermore AR-A014418 treatment did not alter the alternative splicing event in the BACE1 gene (Figure 5.5.2A). Together, these data suggest that the hnRNPA2/B1-mediated alternative splicing and subsequent increase in BACE1 protein level are not mediated by GSK3 activation. Surprisingly, despite reduced levels of hyperphosphorylated tau, 1-month AR-A014418 treatment was unable to decrease the elevated levels of activated caspase-3, (Figure 5.5.2B).

Figure 5.5.1 Cholinergic mediated tau hyperphosphorylation is regulated by GSK3 activation. (A) Representative Western-blot and quantification analysis of pAKT(S473) and pAKT(Thr308) levels in the hippocampus of VACHT^{NKx2.1-Cre-flox/flox} mice. (n=4, data are mean $\pm$ SEM. *P<0.05 (B) Representative Western blot and quantification analysis of phospho-GSK3 α and β in the hippocampus of aged (11-14 month old) controls (left) and VACHT^{NKx2.1-Cre-flox/flox} (right) mice. Levels of pGSK3 α and β to the respective GSK3 (n= 5 and 3, data are mean $\pm$ SEM. **P<0.01, ***P<0.001). (C) Implantation of osmotic pumps and delivery of AR-A014418 to aged VACHT^{NKx2.1-Cre-flox/flox} mice. (D) Representative Western blot and quantification analysis of phospho-GSK3 α and β in the hippocampus of aged VACHT^{NKx2.1-Cre-flox/flox} mice treated with AR-A014418 or saline. (E) Western blot analysis aged VACHT^{NKx2.1-Cre-flox/flox} treated with AR-A014418 or saline for Tau hyper-phosphorylation at T231, MCI immunopositive tau and total Tau protein expression. (F) Representative immunolabelling of reduced T231 Tau in the hippocampus of aged VACHT^{NKx2.1-Cre-flox/flox} mice (Scale bar, 100 μ m). (G) Western blot analysis for PSD-95 protein levels in the hippocampus of VACHT^{NKx2.1-Cre-flox/flox} mice treated with AR-A014418 or saline. (n= 4 saline treated, n=5 AR-A014418 treated, data are mean $\pm$ SEM. *P<0.05 ***P<0.001).

Figure 5.5.1 Cholinergic mediated tau hyperphosphorylation is regulated by GSK3 activation.

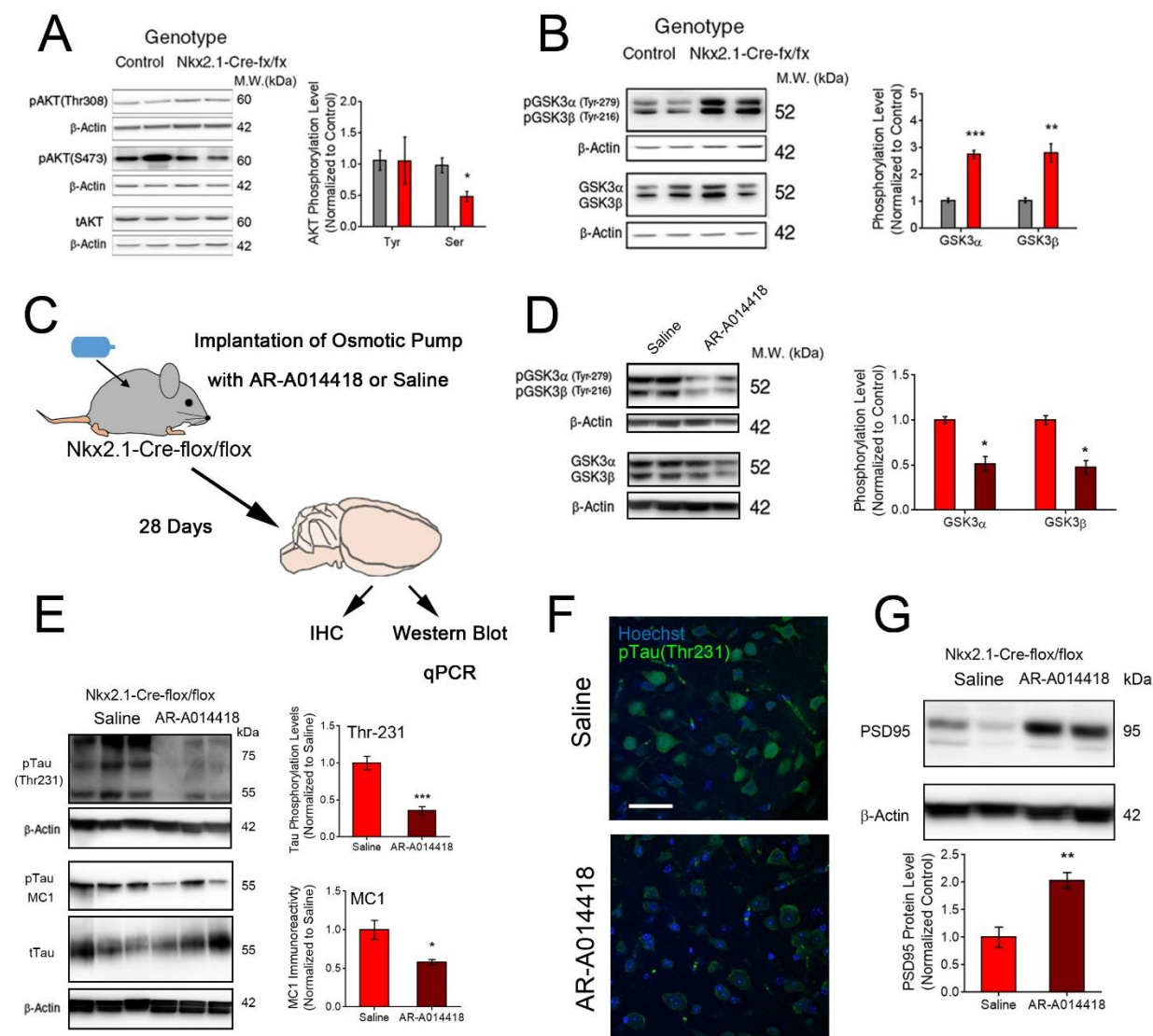
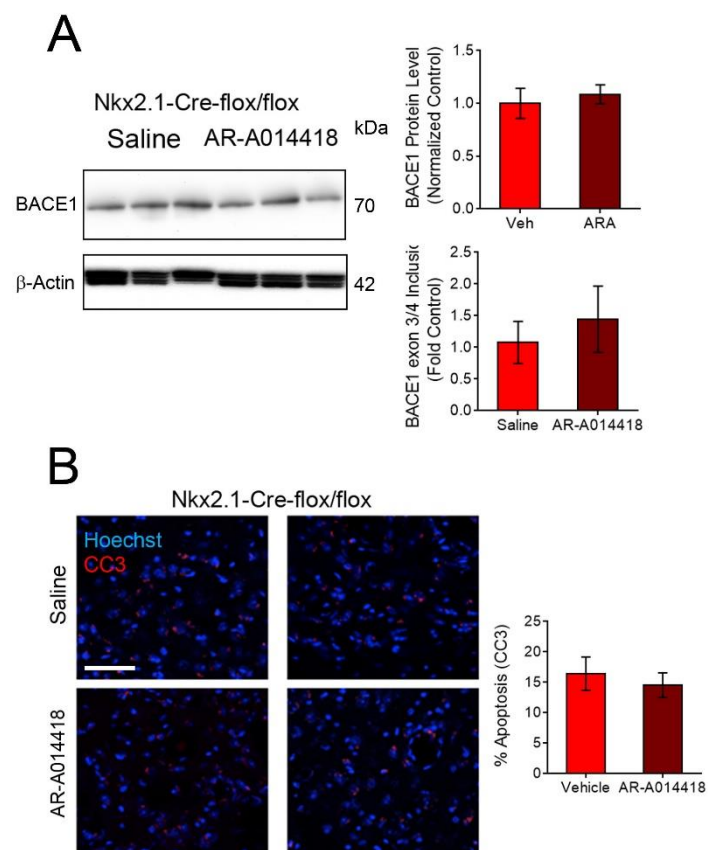


Figure 5.5.2 Cholinergic mediated age dependent pathology is partially mediated by GSK3 hyper-phosphorylation. (A) Representative Western blot and quantification analysis of BACE1 protein levels, along with qPCR analysis of alternative splicing of exon 3/4 of the BACE1 gene in hippocampus of VACHT^{NKx2.1-Cre-flox/flox} treated with AR-A014418 or saline. (B) Quantification of activated caspase-3 immunolabelling in the hippocampus of VACHT^{NKx2.1-Cre-flox/flox} mice treated with AR-A014418 or saline (Scale bar, 100µm) (n= 4 saline treated, n=5 AR-A014418 treated, data are mean ± SEM. *P<0.05 **P<0.01).

Figure 5.5.2 Cholinergic mediated age dependent pathology is partially mediated by GSK3 hyper-phosphorylation.



5.4.6 Cholinergic dysfunction in human AD brains

Whether cholinergic genes are expressed in lower levels in human AD brain compared to cognitively alert controls and may contribute to phenotypes detected herein is not fully understood. To examine that, we extracted total RNA from a cohort of 24 adult human temporal gyrus samples collected at the Netherland Brain Bank (sample information in Table 5.61), including 8 sporadic AD patients and 16 from age-matched controls. We then profiled AD-related transcript differences by adopting the particularly deep SQUARETM RNA library construction approach (Hebenstreit and Teichmann, 2011). Of those, 10,885 genes that were expressed showed a significant change. Next, we quantified the levels of those transcripts composing the expanded family of cholinergic regulator genes (Soreq, 2015). Detected cholinergic transcripts showed significantly lower expression levels than other protein-coding genes in the temporal gyrus of AD patients compared to aged-matched controls (Figure 5.6A).

Brain samples from a distinct cohort of AD patients (Ostapchenko et al., 2013) supported the RNA-Seq analysis results by showing a significant VACHT loss in AD brains compared to age and sex-matched controls (Figure 5.6B), in agreement with previous observations (Chen et al., 2011; Efanget al., 1997). Furthermore, the cohort of AD brains exhibited 50% decrease in hnRNPA2/B1 protein levels compared to age/gender-matched controls (Figure 5.6C), confirming previous results obtained with a distinct AD cohort (Berson et al., 2012). Additionally, we found a significant positive correlation between VACHT and hnRNPA2/B1 protein levels (Figure 5.6D). AD brain samples also showed drastic increases in tau-Thr231 phosphorylation (Figure 5.6E), which was inversely proportional to the levels of VACHT (Figure 5.6F). Our findings using cholinergic-deficient mice support an intricate timeline whereby cholinergic dysfunction per se precedes and may have strong influence in pathological changes observed in AD.

Figure 5.6 Cholinergic Failure in the human AD Brain associates with loss of hnRNPA2/B1 and hyperphosphorylation of tau. (A) Cholinergic Genes are down-regulated in the AD temporal gyrus. Shown are cumulative distribution functions (CDFs) for the global change in the expanded family of cholinergic genes (as listed in Soreq, 2015) compared to global expression patterns between AD and control brain tissues (n= 8, Kolmogorov Smirnov $p=0.03$, red and blue lines, correspondingly). (B) Western blot analysis of VACHT protein levels in AD brains. (C) Western blot analysis of hnRNPA2/B1 protein levels in AD brains. (D) Correlation between hnRNPA2/B1 protein levels and VACHT protein levels in AD brains. (E) Western blot analysis of Tau-Thr231 phosphorylation levels and (F) correlation between VACHT protein levels and Tau Thr-231 phosphorylation levels. (n= 6, data are mean $\pm$ SEM. * $P<0.05$ ** $P<0.01$).

Figure 5.6 Cholinergic Failure in the human AD Brain associates with loss of hnRNPA2/B1 and hyperphosphorylation of tau.

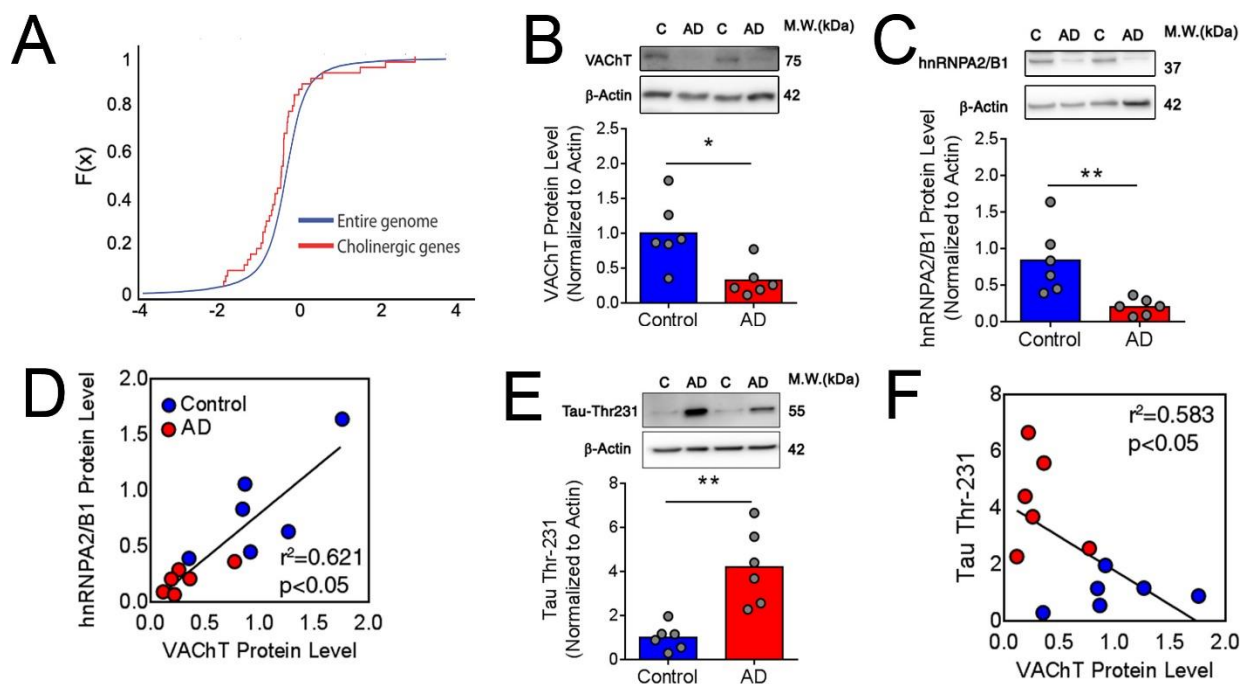


Table 5.6.1 Data for cohort of human brain samples. Samples collected from the Netherland Brain Bank, from which total RNA was extracted and sequenced, n=24.

Table 5.6.1 Data for cohort of human brain samples.

NBB id	sex	age	Post mortem delay	ph	weight	region
2008-047	M	77	06:35	6.10	1250	superior temporalis gyrus
2000-066	M	80	04:20	7.08	1160	inferior temporalis gyrus
2007-025	M	82	05:15	6.34	1182	superior temporalis gyrus
2007-052	M	82	04:15	6.41	1205	medial temporalis gyrus
2009-040	M	83	06:10	5.91	1102	superior temporalis gyrus
2008-029	M	84	08:05	5.95	1195	superior temporalis gyrus
2001-044	M	85	04:25	6.20	1383	superior temporalis gyrus
2001-063	M	85	04:45	6.38	1215	superior temporalis gyrus
2010-016	M	86	06:15	?	1211	superior temporalis gyrus
2009-107	M	88	04:40	6.22	1054	superior temporalis gyrus
2005-010	M	93	04:30	6.46	1040	superior temporalis gyrus
2002-087	M	71	07:40	6.20	1150	superior temporalis gyrus
2001-016	M	77	08:25	7.19	1118	superior temporalis gyrus
2000-015	M	78	05:35	6.63	1417	inferior temporalis gyrus
2005-044	M	80	07:15	5.80	1331	superior temporalis gyrus
2001-021	M	82	07:40	6.07	1318	inferior temporalis gyrus
2009-005	M	82	05:10	6.75	1087	superior temporalis gyrus
2001-086	M	88	07:00	6.84	1368	superior temporalis gyrus
2003-035	M	96	06:30	6.65	1300	superior temporalis gyrus
2005-019	M	74	05:00	6.70	1115	superior temporalis gyrus
2003-084	M	82	10:00	6.53	1488	superior temporalis gyrus
2009-039	M	82	12:55	6.21	1406	superior temporalis gyrus
2005-073	M	87	06:05	6.96	1468	superior temporalis gyrus
2009-075	M	88	07:00	6.76	1230	superior temporalis gyrus

Table 5.6.2 Number of detected genes per patient. Number of detected genes (RPKM>1) per patient, per SQUARE field. Rows are patients and columns are SQUARE fields.

Table 5.6.2 Number of detected genes per patient.

		1	2	3	4	5	6	7	8	9	10	11	12
AD	1	6152	6729	6154	7224	9942	6284	4273	5176	6504	7879	5815	7500
	2	6961	6995	6251	7516	9611	6478	4549	5294	6698	7778	6204	7747
	3	6945	7107	6627	7388	9746	6221	4529	5037	6789	7983	6145	6059
	4	6811	6704	6530	7555	9664	6193	2877	4868	6250	7976	6246	8079
	5	6123	6417	5848	7628	9529	5953	4637	4639	6140	7481	5814	7654
	6	6956	7093	6308	7469	9927	6730	4542	4951	6091	7465	5699	6550
	7	6310	6217	5749	7176	9410	5910	4393	4695	6247	7203	5531	7122
	8	6770	6999	6436	7352	9675	6730	4451	5233	6761	7500	6114	7589
Con	9	6374	6456	5957	6785	9250	6039	3889	4726	6506	7182	5307	6633
	10	6820	6919	6083	6883	9270	5950	4367	4861	6763	7729	5266	6545
	11	5771	6029	5191	6705	9445	5654	4197	4565	6188	6804	5649	6986
	12	5660	7181	6486	7208	10160	7867	5148	5422	6939	8082	6243	6555
	13	6332	6962	6220	6468	9430	6576	3876	5126	6959	7805	5361	6657
	14	6103	6486	5507	7139	9583	5781	4467	4604	6150	7328	5632	7412
	15	6380	6414	5592	6486	9377	5557	3940	4277	6225	7869	5571	7090
	16	6511	6673	6217	7495	9710	6147	4238	4947	6788	8011	5732	7296
	17	6265	6450	5903	7247	9142	5907	4403	4718	6022	7212	5424	7478
	18	7153	7552	6945	7596	9822	6549	4382	5424	7282	8388	5926	7285
	19	6294	5943	5668	7300	9259	5648	4255	4416	6108	7468	5690	7321
	20	6268	6583	5753	7391	9732	6125	4635	4815	5896	7847	5733	7395
	21	7674	7822	6969	8201	10588	7826	5027	5787	7348	8095	6059	7434
	22	7274	7185	6793	7824	9945	6982	4755	5377	7258	8310	6185	7737
	23	7149	7073	6654	7206	9895	6774	4890	5274	6915	8485	5796	8190
	24	5676	6113	5303	6938	9863	6393	4630	4835	6651	7721	5964	6474

5.5 Discussion

We employed transcriptome and biochemical assays on cholinergic-deficient mouse brain samples to explore the impact of long-lasting forebrain cholinergic dysfunction. Whole-genome RNA sequencing demonstrated that cholinergic deficiency modifies expression levels and isoform abundance of several key transcripts related to Alzheimer's disease in the hippocampus of VACHT-deficient mice. Cholinergic-mediated abnormal BACE1 mRNA splicing in VACHT-mutant mice increased BACE1 protein levels and APP processing. Accordingly, cholinergic deficiency caused a 10-fold increase in soluble mouse A β peptides, age-dependent hippocampal tauopathy, synaptic abnormalities, neuronal inflammation, neuronal vulnerability and cognitive decline. We also showed that GSK3 activation is critical for cholinergic modulation of tau hyperphosphorylation and synaptic vulnerability. Furthermore, we confirmed that human AD brains present cholinergic dysfunction and showed that it correlates to changes in the levels of hnRNP A2/B1 and hyperphosphorylated tau. Our findings indicate that cholinergic impairments confer widespread hippocampal damage and malfunction. Furthermore, our data support a causal role for cholinergic signalling as a surveillance mechanism controlling hippocampal transcript levels, maintenance of cognitive function and neuronal viability in mice.

Our RNA sequencing analysis revealed a group of differentially expressed transcripts related to spliceosome regulation in the hippocampus of VACHTNkx2.1-Cre-flox/flox mice, suggesting that the splicing machinery in these mutants could be altered. In fact, a significant number of alternative splicing event abnormalities were observed in the hippocampus of VACHT-deficient mice. These results are consistent with previously reported global changes of alternative splicing in the AD brain (Bai et al., 2013; Berson et al., 2012; Tollervey et al., 2011). Importantly, spliceosome signalling pathway changes can have broad implications for gene regulation [reviewed in (Shin and Manley, 2004)].

Alternative splicing in the nervous system is particularly widespread and is essential for multiple aspects of neuronal function (Raj and Blencowe, 2015). However, the signal-

transduction pathways that regulate splicing are not well known (Shin and Manley, 2004). Our study adds a role for cholinergic signalling in the maintenance of balanced alternative splicing. At least part of the cholinergic-control of alternative splicing seems to involve hnRNPA2/B1. We have shown that cholinergic deficiency in the cortex (Berson et al., 2012; Kolisnyk et al., 2013a) and hippocampus (Figure 2B) leads to decreased expression of the hnRNPA2/B1 protein. Related work demonstrated that hnRNPA2/B1 is a cholinergic regulated splicing factor (Kolisnyk et al submitted). Importantly, knockdown of hnRNPA2/B1 in cultured hippocampal neurons shifted splicing of BACE1 mRNA towards increased expression of mRNA species coding for the BACE1-501 protein isoform as observed in the hippocampus of VACHT-deficient mice. This splicing change led to increased expression of the BACE1 protein that was accompanied by a pattern of APP processing similar to that observed in commonly used mouse models of AD. The alternative splicing event in BACE1 observed in VACHT-mutant mice is regulated by M1 muscarinic receptors (Kolisnyk et al., submitted).

Cholinergic tone has been thought to regulate APP processing through muscarinic receptors (Davis et al., 2010; Nitsch et al., 1992). Specifically, M1 signalling has been shown to regulate the stability of the BACE1 protein (Davis et al., 2010). BACE1-501 is a more stable and active form of the protein (Mowrer and Wolfe, 2008). Remarkably, BACE1 expression is increased in late-onset AD (Hebert et al., 2008). Our data suggest potential mechanisms by which cholinergic regulation can affect BACE1 expression and AD pathology. Interestingly, our data suggest changes in alternative splicing occurs post-transcriptionally and independent of GSK3 signalling. Thus, cholinergic deficiency may affect BACE1 expression differently than previously described in AD, in which GSK3 can regulate BACE1 transcription by increasing promoter activity (Ly et al., 2013). Our findings promote upstream cholinergic mechanisms as a target for diminishing aberrant APP processing in AD.

In addition to increased levels of soluble A β , VACHTNkx2.1-Cre-flox/flox mice also show tau hyper-phosphorylation, which destabilizes microtubules and significantly disrupts axonal transport. Tau hyper-phosphorylation may also contribute to increased vulnerability leading to neuronal death (Billingsley and Kincaid, 1997). In fact, VACHT-

deficient mice show age-dependent increases in hippocampal argyrophilic staining and neuronal death.

Oligomeric protein aggregation has been linked to toxicity and to neurodegenerative disorders, including AD (Maeda et al., 2006). The formation of NFTs alone is insufficient for neurodegeneration, yet oligomeric tau may contribute to neurodegeneration and synaptic loss in AD (Berger et al., 2007; de Calignon et al., 2012). These observed changes in tau in VACHT-deficient mice (i.e. increased oligomer formation), the associated age-dependent increase in immunoreactivity of activated caspase-3, and ultimately neuronal loss all support a relationship between cholinergic failure and AD-like pathology in mice.

Tau hyper-phosphorylation can occur due to the increased activity of GSK3, which subsequently leads to an array of impairments, including disruption of LTP (Hooper et al., 2007) and cell death in vitro (Zheng et al., 2002). GSK3 over-activation is an important hallmark in AD (Hooper et al., 2008). Thus, the GSK3 overactivation observed in VACHT-mutant mice represents a potential mechanism by which reduced cholinergic activity may have multiple influences in AD pathology in target cells. We tested this hypothesis by pharmacological inhibition of GSK3 in aged VACHT-deficient mice. GSK3 inhibition was able to decrease tau hyperphosphorylation. Also, GSK3 inhibition partially restored PSD95 protein levels, but did not decrease caspase-3 activation. These findings demonstrate that cholinergic-induced changes in tau and in amyloid processing are potentially independent of each other and suggest that cholinergic dysfunction is contributing to the pathological outcomes in these animals by altering multiple pathways. The pharmacological inhibition of GSK3 was tested in mice in which certain pathology was already present (11-12 month-old mice). Hence, further experiments should test longer treatments with the compound or genetic ablation of GSK3 genes in VACHT-deficient mice to comprehensively dissect the contribution of overactive GSK3 in other phenotypes.

Aged VACHT-deficient mice showed a decrease in the number of hippocampal neurons, a deficiency that was not observed in young mutants, suggesting that cholinergic tone may play a role in guarding hippocampal neuronal health. Additionally, aged VACHT-

deficient mice showed increased neuroinflammation and reduced number of synapses; which are pathologies observed in AD brains (DeKosky and Scheff, 1990; Rogers and Shen, 2000; Smale et al., 1995). Mice with excess acetylcholinesterase, which present decreased cholinergic function, also show neuroinflammation (Shaked et al., 2009). Furthermore, similar to our observation, mice lacking the $\beta 2$ nicotinic receptor subunit show age-dependent loss of hippocampal neurons (Zoli et al., 1999). Of note, hippocampal neuronal loss is a critical feature in AD, which is not observed in mouse models overexpressing APP and or presenilin 1 with human AD mutations (Stein and Johnson, 2002). Hence, long-term cholinergic deficiency may model this aspect of AD in a better way. Potential mechanisms involved in cholinergic dysfunction induced pathology are shown on Figure 5.7.

In line with an age-dependent loss of hippocampal neurons, we found that aged VACHT-deficient mice showed significant impairments in their learning strategy in the MWM task. Poor performance and acquisition on the MWM task has been associated with loss of neurons in the hippocampus (Olsen et al., 1994). This suggests that neuronal loss in the hippocampus has functional consequences in mice as well.

In AD brains, we found evidence of cholinergic decline and showed a striking relationship between VACHT levels and tau hyper-phosphorylation. Together with the mouse data, these observations support the notion that deficient cholinergic signalling in AD may correlate to key pathological events, including Tau hyper-phosphorylation.

Our data reveal that cholinergic deficiency can affect a number of transcriptional processes, disturb splicing of key genes and interfere with protein networks that normally protect neurons. Interestingly, recent work revealed that basal forebrain cholinergic neurons present intraneuronal A β accumulation even in young adults, which may contribute to their selective vulnerability in AD (Baker-Nigh et al., 2015).

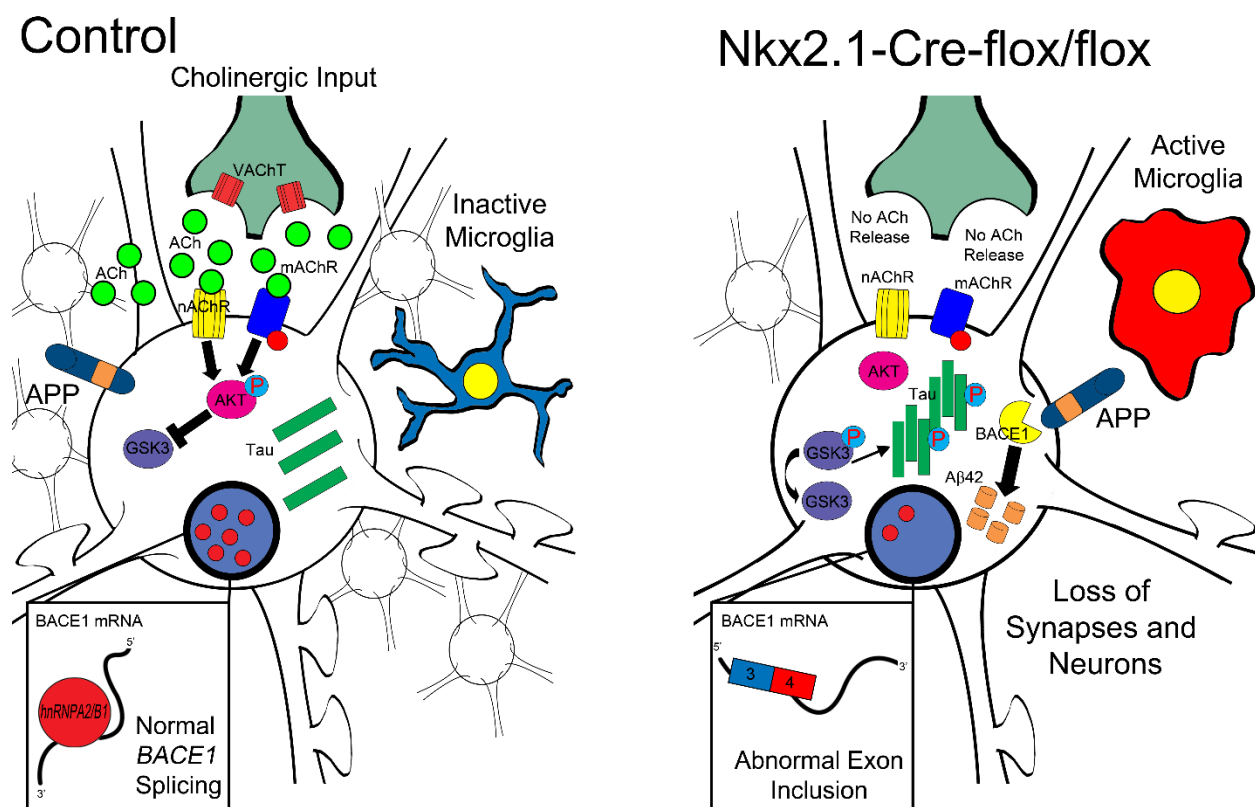
Cholinergic neurons are thought to be highly dependent on the presence of trophic factors for their optimal function and survival (Boskovic et al., 2014; Naumann et al., 2002), which may also contribute to their demise. Regardless of the mechanisms for increased cholinergic vulnerability in AD, it seems that cholinergic dysfunction persisting

for a long period is highly related to hippocampal pathology and amyloid accumulation (Teipel et al., 2014).

In short, our results suggest that long-term cholinergic failure per se, which we model by disrupting synaptic cholinergic function, can trigger AD-like pathology in mice. More importantly, we find that long-term cholinergic deficiency leads to age-dependent cognitive decline that is related to neuronal death, a key feature of late-onset AD that is not modeled in mice overexpressing human genes with AD-related mutations. Our experiments provide a mechanism to explain how decreased cholinergic tone, for example due to long-term use of anti-cholinergic drugs, could lead to increased risk of dementia (Gray et al., 2015), which may depend on global changes of RNA metabolism, including alternative splicing and gene expression. It remains to be determined if rescuing cholinergic function prior to development of AD could have an impact in the risk of dementia or AD-related pathology. However, it is noteworthy that recent observations in potential prodromal AD-affected individuals indicate that cholinesterase inhibition decreases the rate of hippocampal atrophy by 45% during one-year treatment (Dubois et al., 2015). Our data points towards cholinergic signalling being a global mediator of several distinct processes that when dysfunctional lead to pathology. Developing effective strategies to reverse the cholinergic deficits in the AD brain may therefore prove to be more fruitful than specific therapies based on reversing the individual processes it regulates.

Figure 5.7. Summary of findings. (A) In control animals, cholinergic input from the medial septum regulates target neurons in the hippocampus, through nicotinic and muscarinic acetylcholine receptors. Long-term cholinergic signaling maintains transcriptome integrity likely by a combination of muscarinic and nicotinic activation. These maintain balance of signaling pathways that regulate AD-like pathology. (B) Conversely, in cholinergic deficient mice, which models long-term cholinergic dysfunction, lack of signaling by muscarinic and nicotinic receptors affects differential expression of spliceosome-related genes and reductions in hnRNPA2/B1. BACE1 mRNA is abnormally spliced leading to an increase of BACE1 expression. As a consequence, APP processing is altered, yielding accumulation of soluble A β peptides. Furthermore, abnormal gene expression influences AKT-GSK3 modulatory genes with consequences for AKT and GSK3 phosphorylation. These changes contribute to increases in pathological tau phosphorylation and misfolding, neuroinflammation, synaptic loss, hippocampal neuronal death and ultimately leading to cognitive decline in these animals.

Figure 5.7. Summary of findings.



5.6 Acknowledgements

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Chapter 6

Cholinergic Regulation of hnRNPA2/B1 Translation by M1 Muscarinic Receptors

6.1 Chapter Summary

Cholinergic vulnerability, characterized by loss of acetylcholine (ACh), is one of the hallmarks of Alzheimer's disease (AD). Recent work has suggested that decreased ACh activity in AD may contribute to pathological changes through global alterations in alternative splicing. This occurs, at least partially, via the regulation of the expression of a critical protein family in RNA processing, hnRNP A/B proteins. These proteins regulate several steps of RNA metabolism, including alternative splicing, RNA trafficking, miRNA export and gene expression, providing multilevel surveillance in RNA functions. To investigate the mechanism by which cholinergic tone regulates hnRNPA2/B1 expression, we employed a combination of genetic mouse models and *in vivo* and *in vitro* techniques. Decreasing cholinergic tone reduced levels of hnRNPA2/B1, while increasing cholinergic signalling *in vivo* increased expression of hnRNPA2/B1. This effect is not due to decreased hnRNPA2/B1 mRNA expression, increased aggregation or degradation of the protein, but rather to decreased mRNA translation by nonsense mediated decay regulation of translation. Cell culture and knockout mice experiments demonstrated that M1 muscarinic signalling is critical for cholinergic control of hnRNPA2/B1 protein levels. Our experiments suggest an intricate regulation of hnRNPA2/B1 levels by cholinergic activity that interferes with alternative splicing in targeted neurons mimicking deficits found in AD.

6.2 Introduction

Dementia affects roughly 44 million individuals worldwide and represents a large economic burden (Wimo et al., 2013). Individuals affected with Alzheimer's disease (AD) present a profound decrease in basal forebrain cholinergic neurons (Whitehouse et al., 1982). These findings led to the cholinergic hypothesis of AD and the use of cholinesterase inhibitors to mitigate cholinergic failure (Bartus et al., 1982). Recent work suggests that the use of cholinesterase inhibitors for one year in possible prodromal AD-affected individuals halved rates of hippocampal atrophy, suggesting an intricate relationship between cholinergic tone and neurodegeneration (Dubois et al., 2015).

Cholinergic tone can modulate signal processing by changing electrical properties of cells and by modulating intracellular signalling (Dajas-Bailador and Wonnacott, 2004; Soreq, 2015). In addition, it has become clear that cholinergic signalling can also regulate long-term gene expression, miRNAs (Shaked et al., 2009; Soreq, 2015) and alternative splicing (Berson et al., 2012; Kolisnyk et al., 2013a), all of which can modulate functional properties of cells (Blencowe, 2006; Novarino et al., 2014). A key protein that regulates splicing events in AD is the heterogeneous nuclear ribonucleoprotein (hnRNP) A2/B1, which is reduced in brains of AD patients due to cholinergic deficiency (Berson et al., 2012) and is reduced in mice with a conditional deletion of the Vesicular Acetylcholine Transporter in the forebrain (VACHT) (Kolisnyk et al., 2013a).

hnRNPs are a large family of proteins which package pre-mRNA into larger hnRNP particles (Dreyfuss et al., 1993). Each of the hnRNPs contain distinct RNA binding motifs, which allows them to exert their roles in pre-mRNA processing (Black, 2003; Weighardt et al., 1996). hnRNPA2/B1 is one of the major hnRNP isoforms in the brain regulating alternative splicing and the transport of mRNA to distal cellular processes (Han et al., 2010). Importantly, knockdown of hnRNPA2/B1 in vivo caused impairments in learning and memory (Berson et al., 2012). Taken together, these findings suggest a critical role for this RNA binding protein in neuronal function and cognition.

Previous work suggests that cholinergic tone can regulate levels of hnRNPA2/B1, however the mechanisms involved are unclear. Here we show that hnRNPA2/B1 is a cholinergic controlled splicing factor. M1 muscarinic receptor activity is critical for cholinergic regulation of hnRNPA2B1 translation. This work provides a new mechanism by which acetylcholine (ACh) can influence targeted neurons, leading to potential widespread changes in neuronal function.

6.3 Materials and Methods

6.3.1 Mouse lines

All animals with targeted elimination of VACHT were generated using the VACHTflox/flox mouse described in (Martins-Silva et al., 2011). To eliminate VACHT from the forebrain, VACHTflox/flox mice were crossed with C57BL/6J-Tg(Nkx2-1-cre)2Sand/J mice (Xu et al., 2008) to generate VACHTNkx2.1-Cre-flox/flox (Al-Onaizi et al., 2016). To eliminate VACHT from the striatum the VACHTflox/flox mice were crossed with D2-Cre mice (Drd2, Line ER44) to generate VACHTD2-Cre-flox/flox (Guzman et al., 2011). VACHT overexpressing, ChAT-ChR2-EYFP mice were from the Jackson Laboratory, B6.Cg-Tg(Chat-Cop4*H134R/EYFP)6Gfng/J (Zhao et al., 2011). Generation of TgR (Shaked et al., 2009), M1-KO (Hamilton et al., 1997) and M4-KO mice (Gomez et al., 1999) were previously described. All procedures were conducted in accordance with guidelines of the Canadian Council of Animal Care (CCAC) at the University of Western Ontario with an approved institutional animal protocol (2008-127). Only male mice were used for all experiments.

6.3.2 Immunofluorescence

Immunofluorescence experiments were performed as previously described (Guzman et al., 2011). Primary antibodies used were anti-hnRNPA2/B1 (1:200 Santa Cruz Biotechnology Catalog no. sc-10035), anti-NeuN (1:200 PhosphoSolutions, Catalog no.

583-FOX3), and anti-GFAP (1:500 AbCam, Catalogue no. ab7260). Sections were visualized by Zeiss LSM 510 Meta (Carl Zeiss, Oberkochen, Germany) confocal system (10x, 40x, 63x objectives), a 488-nm Ar laser and 633-nm HeNe laser were used for excitation of fluorophores.

6.3.3 Western Blotting

Mouse hippocampi were collected, proteins were isolated, and immunoblotting was performed as previously described using RIPA lysis buffer supplemented with protease and phosphatase inhibitors (Guzman et al., 2011). Band intensities were quantified using FluoroChemQ software (Thermo Fisher Scientific).

6.3.4 Subcellular Fractionation

To isolate nuclear and cytoplasmic proteins from hippocampal tissue, the NE-PER Nuclear Protein Extraction Kit (Thermo Scientific, USA) was used following the manufacturer's instructions.

6.3.5 Sarkosyl Insolubility

Isolation of Sarkosyl insoluble protein was performed as described (Bai et al., 2013). Hippocampal tissue was homogenized in a low salt buffer (10 mM Tris, pH 7.5, 5 mM EDTA, 1 mM DTT, 10% (wt/vol) sucrose, Sigma protease inhibitor cocktail, ~10 ml buffer per gram tissue) to detect total protein, a detergent buffer (the low salt buffer with the addition of 1% (wt/vol) sarkosyl, N-Lauroylsarcosine) for the sarkosyl soluble fraction, and finally 8 M urea with 2% (wt/vol) SDS for the sarkosyl insoluble fraction.

6.3.6 Ubiquitination Assay

The ubiquitination status of the hnRNPA2/B1 protein was determined using previously described protocols (Choo and Zhang, 2009). Briefly, the hnRNPA2/B1 protein was immunoprecipitated using the Santa Cruz sc-10035 antibody and run on an SDS-Page gel. The gel was then blotted with an anti-ubiquitin antibody (Abcam ab7780).

6.3.7 Stereotaxic injections of adeno-associated virus

Injection of AAV virus has been described (Al-Onaizi et al., 2016). Briefly, mice were anesthetized with ketamine (100 mg/kg) and xylazine (25 mg/kg, and 1 μ l (titer of ~10¹³ GC/ml) of AAV8-GFP-Cre-GFP or control virus (AAV8-GFP, Vector BioLabs, Eagleville, PA, USA) was injected into the medial septum (0.98 AP, 0.1 LL and 4.1 DV) of VAcHtflox/flox mice. A recovery period of 4 weeks was given to allow transgene expression, prior to subsequent analyses.

6.3.8 RNA Sequencing

Total RNA was extracted from hippocampal tissues. cDNA library was prepared using TruSeq Stranded Total Sample Preparation kit (Illumina) and ran in a HiSeq 2500 platform. Datasets are available on ArrayExpress (<http://www.ebi.ac.uk/arrayexpress/>) under accession number E-MTAB-3897. Full description and analysis of the results of the RNA-Sequencing dataset are found in chapter 5.

6.3.9 qPCR and RT-PCR

To measure mRNA expression, total RNA was extracted from freshly dissected hippocampal tissue, using the Aurum Total RNA for fatty and fibrous tissue kit (Bio-Rad) according to the manufacturer's instructions. cDNA synthesis and qPCR analysis were performed as previously described (Guzman et al., 2011). For alternative splicing experiments, the alternative exon levels were normalized to a constitutively expressed exon from the same gene. RT-PCR was performed as previously described (Ribeiro et al., 2007).

6.3.10 Isolation of Polysomal RNA

Isolation of polysomal RNA was performed as described (Wagnon et al., 2012). Samples were homogenized in 1.5 ml of ice-cold lysis buffer (20 mM Tris-HCl, pH 7.4, 3 mM MgCl₂, 10 mM NaCl, 2% sucrose, 0.3% Triton X-100, 2 mM vanadyl ribonucleoside complexes [VRC] supplemented with protease inhibitors (complete mini, EDTA-free,

Roche, Indianapolis, IN). The homogenate was then centrifuged at 10,000 g for 10 minutes at 4°C, and the supernatant was transferred to a fresh tube. The lysate was treated with either 30 mM EDTA or 0.1 mg/ml RNase A for 30 minutes on ice or if they were to be treated with EDTA, VRC was not included in the lysis buffer. Lysates were then carefully layered onto 15–55% of sucrose in 25 mM Tris-HCl, pH 7.4, 25 mM NaCl, 5 mM MgCl₂ (and 30 mM EDTA for the EDTA Samples). Gradients were ultracentrifuged in a Beckman Instruments SW40Ti rotor at 150,000g for 2 hours and 25 minutes at 4°C.

To isolate RNA from the fractions, RNA was collected into 1.5 ml of 7.7 M guanidine-HCl, 2 ml of 100% ethanol was added, and samples were stored at –20°C. Samples were then centrifuged at 4000 for 50 minutes at 4°C. The supernatant was removed and 200 µL DEPC-treated H₂O was added to the pellet. To precipitate the RNA, 500 µL of 100% ethanol, 20 µL of 3 M sodium acetate, pH 5.2, and 10 µg glycogen were added, and the samples were stored overnight at –20°C. The samples were then centrifuged at 14,000g for 30 minutes at 4°C. Pellets were washed with ice-cold 75% ethanol and air dried for 15 minutes at room temperature. RNA was re-suspended in 30 µL DEPC-treated H₂O and quantified by nanodrop, before being converted into cDNA using the Applied biosystems cDNA conversion kit. RT-PCR was then performed using primers designed to amplify hnRNPA2/B1 or β-Actin.

6.3.11 Primary Neuronal Cultures

Primary cultures of hippocampal neurons from E17 mouse embryos were obtained as described previously (Beraldo et al., 2013). Cultures were maintained in Neurobasal medium with 2% B-27 supplement (Invitrogen). On day 4, cytosine arabinoside (2 µM; Sigma) was added to prevent astrocyte growth. Half of the culture medium was changed every 2–3 days. Neurons were cultured for 15 days

6.3.12 Pharmacological manipulations in Primary Neuronal Cultures

On the 15th day of culture, the neurons were treated with different doses of carbachol (0, 5, 10, or 50 μ M) dissolved in saline and, 48 hours later, total protein was isolated and levels of hnRNPA2/B1 were determined by Western blotting and immunofluorescence. To evaluate the contribution of nicotinic and muscarinic receptors in regulating hnRNPA2/B1 protein levels, neurons were pre-treated with either mecamylamine (100 μ M), atropine (100 μ M), or both. Then, 1 hour later, neurons were treated with carbachol (10 μ M). Finally, to assess the effect of M1 muscarinic activation, neurons were treated with different doses of AF102B (0, 10, 100, 500 μ M) dissolved in saline.

6.3.13 Statistical Analysis

Data are presented as mean $\pm$ SEM, unless otherwise stated. GraphPad Prism 6 software was used for statistical analysis. Comparison between two experimental groups was done by Student's t test. When several experimental groups or treatments were analyzed, one-way ANOVA and, when appropriate, a Tukey's HSD post hoc comparison test was used.

6.4 Results

6.4.1 Cholinergic Modulation of hnRNPA2/B1 Protein Levels

Previous experiments indicated that hnRNPA2/B1 is decreased in the AD brains, but this is not modeled in genetic mouse models of AD (Berson et al., 2012). In contrast, either genetic or immunotoxin disruption of cholinergic tone led to decreased expression of hnRNP A2/B1 (Berson et al., 2012; Kolisnyk et al., 2013a). As expected VACHTNx2.1-Cre-flox/flox animals presented a robust decrease in hnRNPA2/B1 levels in the hippocampus (Fig. 6.1 A).

The Nk2.1 promoter turns on Cre expression early during development (Xu et al., 2008) and therefore the resulting decrease in hnRNPA2/B1 levels could potentially be a result of developmental suppression of cholinergic tone, rather than being cholinergic regulated in adult mice. To test this possibility, we deleted the VACHT gene specifically in medial septum neurons and parts of the diagonal band (Al-Onaizi et al., 2016), which provides most of the hippocampal cholinergic innervation, of adult VACHT^{flox/flox} mice using AAV8-Cre virus. AAV8-Cre-injected mice showed inter-related decline of both VACHT and hnRNPA2/B1 proteins, whereas AAV8-GFP-injected mice did not (Fig. 6.1B). There was a significant relationship between VACHT and hnRNP A2/B1 levels ($r^2=0.755$, $p<0.001$) (Fig. 6.1B). In addition, we tested whether, in the striatum, elimination of cholinergic tone would affect hnRNPA2/B1 expression by using VACHTD2-Cre-flox/flox mice, with selective striatal VACHT deficiency (Guzman et al., 2011). These mice showed no changes in hnRNPA2/B1 in their striatum (Fig. 6.1C), indicating hippocampal specificity of these effects.

If expression of hnRNPA2/B1 is a cholinergic-regulated process, one would expect that increased cholinergic tone should have opposite effects than those observed by decreased VACHT expression. ChAT-ChR2-EGFP mice overexpress VACHT in the hippocampus and consequently present increased cholinergic tone and ACh release (Kolisnyk et al., 2013b). These mice present increased hnRNPA2/B1 protein levels (Fig. 6.1D), suggesting that VACHT levels critically regulate hnRNPA2/B1 expression.

Decline of hnRNPA2/B1 could be solely related to VACHT depletion, or alternatively, it could reflect the functional loss of ACh signalling in the CNS. To distinguish between these possibilities, we tested the hippocampus of TgR mice over-expressing soluble AChE (Shaked et al., 2009), which causes cholinergic insufficiency. TgR mice showed decrease in hnRNPA2/B1 levels similar to mice with decreased VACHT (Fig. 6.1E), suggesting that ACh synaptic levels are causally involved in the regulation of hnRNPA2/B1 expression. Cre expression by itself had no effect on hnRNPA2/B1 levels as can be seen when we compared expression of hnRNPA2/B1 in the hippocampus of Nkx2.1-Cre and WT mice (Fig. 6.1F). Taken together these data give strong support for the hypothesis that hnRNPA2/B1 is a cholinergic regulated splicing factor.

RNA binding proteins such as hnRNPA2/B1 are predominantly expressed in the nucleus, but they can accumulate in the cytoplasm and cause neuronal toxicity (Kim et al., 2013; Wolozin, 2012). We therefore determined by immunofluorescence staining if the localization of hnRNP A2/B1 is changed in response to decreased cholinergic tone. Compared to controls VChTNKx2.1-Cre-flox/flox had a decrease in hnRNPA2/B1 immunostaining in the CA1, CA3, and Dentate Gyrus regions of the hippocampus (Fig 6.2A-D). hnRNPA2/B1 was present mainly in the nucleus of both neurons (labeled by NeuN, Fig. 2-A-D) as well as in astrocytes (Fig. 6.2E) in control mice. We did not observe any shift in the localization of hnRNPA2/B1 in VChT-deficient mice, only an overall decrease in the levels of staining. To confirm these observations we used subcellular fractionation to assess if VChTNKx2.1-Cre-flox/flox mice show changes in hnRNPA2/B1 distribution between the nuclear and cytoplasmic fractions (Fig. 6.2F). In both control and VChT-deficient mice, hnRNPA2/B1 was predominantly nuclear, following the distribution of the nuclear enzyme PIAS1 (Soares et al., 2013). However, VChTNKx2.1-Cre-flox/flox mice showed consistently reduced nuclear hnRNPA2/B1 levels (Fig. 6.2F).

Figure 6.1. Analysis of hnRNPA2/B1 protein levels in genetically modified mice with differential expression of VACHT. (A) Representative Western blot and quantification of hnRNPA2/B1 protein expression in the hippocampus of VACHT^{flox/flox} and VACHT^{NKx2.1-Cre-flox/flox} mice. hnRNPA2/B1 expression was normalized to actin (n=6). (B) hnRNPA2/B1 protein levels positively correlate with AAV induced reduction of VACHT. The graph shows values for each individual mice injected either with GFP or CRE. The image is from the medial septum of a virus-injected mice (C) Striatal elimination of VACHT does not alter hnRNPA2/B1 protein levels in the striatum of VACHT^{D2-Cre-flox/flox} mice (n=4). (D) Transgenic mice over-expressing VACHT have increased hnRNPA2/B1 protein levels compared to controls (n=4). (E) hnRNPA2/B1 protein levels from the hippocampus of TgR transgenic mice (n=3). (F) No change in hnRNPA2/B1 protein levels compared to controls in the hippocampus of c567BL/6J-Nkx2.1-Cre mice (n=3) (Data are mean +/- S.E.M., *p<0.05, **p<0.01).

Figure 6.1. Analysis of hnRNPA2/B1 protein levels in genetically modified mice with differential expression of VACHT.

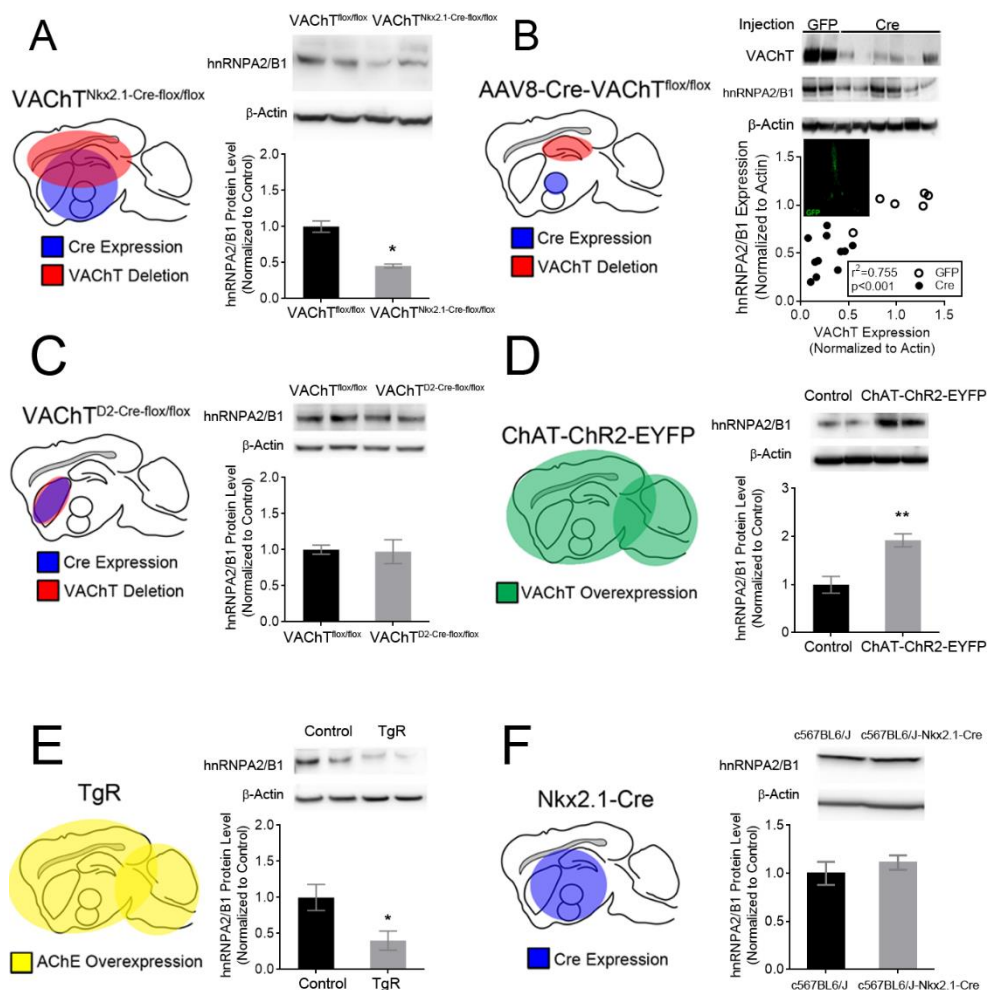
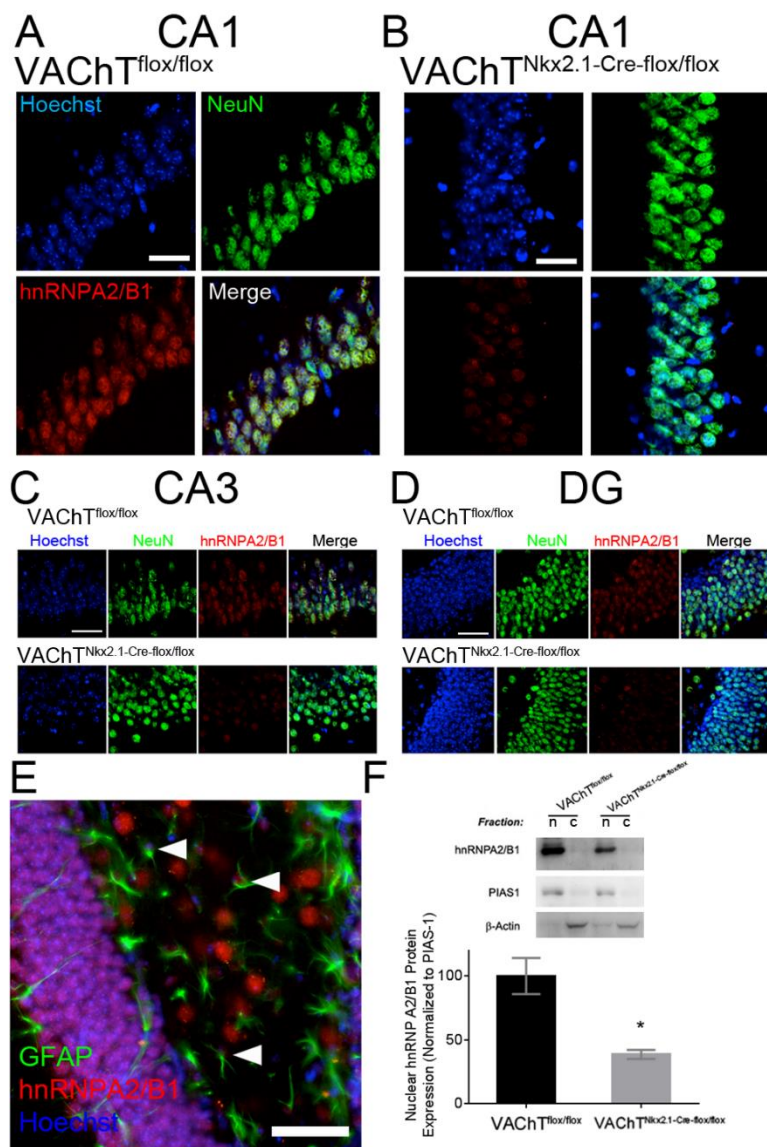


Figure 6.2. Characterization of decreased hnRNPA2/B1 protein levels in the hippocampus of VACHT-deficient mice. (A) Representative images of staining for NeuN, hnRNPA2/B1 and Hoeschst in the CA1 region of the hippocampus in controls (A) and VACHT^{NKx2.1-Cre-flox/flox} mice (B) (Scale bar, 50 μ m). Expression of hnRNPA2/B1 in the CA3 (C) and dentate gyrus (D) by immunofluorescence reveals general decrease of the protein and nuclear localization in VACHT-deficient mice. (E) Localization of hnRNPA2/B1 with GFAP glial marker in the hippocampus of VACHT^{NKx2.1-Cre-flox/flox} mice. (F) Subcellular fractionation assay of hnRNPA2/B1 protein shows hnRNPA2/B1 expression is mainly nuclear (data are mean $\pm$ SEM, * P <0.05).

Figure 6.2. Characterization of decreased hnRNPA2/B1 protein levels in the hippocampus of VACHT-deficient mice.



6.4.2 Mechanisms of cholinergic modulation of hnRNPA2/B1

To investigate mechanisms by which cholinergic tone may regulate the levels of hnRNPA2/B1 protein, we evaluated ubiquitination, a modification that can facilitate protein degradation by the proteasome (Hochstrasser, 1996). Immunoprecipitated hnRNPA2/B1 from the hippocampus of controls and VACHTNKx2.1-Cre-flox/flox mice was resolved by SDS-PAGE and probed with ubiquitin antibodies. VACHT-deficient mice showed no change in ubiquitination status of hnRNPA2/B1 protein, when normalized to total hnRNPA2/B1 protein levels (Fig. 6.3A).

We also examined whether cholinergic tone affects aggregation of hnRNPA2/B1. Notably, hnRNPA2/B1 has a prion-like domain that favours increased aggregation when mutated (Kim et al., 2013). Protein aggregation was investigated by fractionating hippocampal extracts into sarkosyl soluble and insoluble fractions (Fig. 6.3B). In both controls and VACHT-deficient mice, hnRNPA2/B1 was mainly present in soluble fractions, unlike the U1-70k snRNP which has been shown to be present in insoluble fractions (Bai et al., 2013) (Fig. 6.3B). This result excluded the option that cholinergic tone increases aggregation of hnRNPA2/B1. Interestingly, despite different levels of hnRNPA2/B1 protein expression, both control and VACHT-deficient mice exhibited similar hnRNPA2/B1 mRNA levels as determined by RNA-Sequencing (Fig. 6.3C), as observed in AD brains (Berson et al., 2012).

It has been previously reported that protein levels of hnRNPA2/B1 are directly proportional to changes in the RNA editing of the 3' UTR of its mRNA, with a shift away from a nonsense mediated decay (NMD) sensitive transcript increasing protein levels (Bonomi et al., 2013) (Fig. 6.3D). We evaluated by qPCR the ratio of NMD sensitive to NMD insensitive versions of the hnRNPA2/B1 transcript in the hippocampus of VACHTNKx2.1-Cre-flox/flox mice. Compared to controls, we observed a significant shift towards the NMD+ product in VACHT-deficient mice (Fig. 6.3E).

We then tested whether cholinergic tone modulation of NMD+ transcript could regulate hnRNPA2/B1 protein expression levels by limiting protein translation. For this, we studied the recruitment of hnRNPA2/B1 mRNA to ribosomes. Ribonucleotide-protein

complexes (RNPs) were isolated from hippocampal lysates, and sucrose density gradient fractionation was used to separate polyribosomes from large neuronal RNA granules (Fig. 6.4A) (Wagnon et al., 2012). Distribution of hnRNPA2/B1 transcripts in individual fractions was determined by RT-PCR in three individual mice of each genotype (Fig. 6.4B-C). In control mice, hnRNPA2/B1 mRNAs associated with polysomes and RNA granules, and treatment with EDTA, which dissociates mRNA from polysomes, equally distributed hnRNPA2/B1 mRNAs across fractions (Fig. 6.4D-E). However, in VACHTNkx2.1-Cre-flox/flox mice, distribution of hnRNPA2/B1 mRNAs was widespread throughout the fractions, resembling the distribution observed after EDTA treatment (Fig. 6.4D-E). The abundant β -actin mRNA remained unaltered between genotypes, demonstrating specificity towards hnRNPA2/B1 (Fig. 6.3F-G). These results indicate that decreased cholinergic tone leads to diminished translational capacity of hnRNPA2/B1 mRNA transcripts to modulate the efficiency of hnRNPA2/B1 protein translation.

Figure 6.3. Mechanisms of cholinergic regulation of hnRNPA2/B1 protein levels.

(A) No change in ubiquitination status of hnRNPA2/B1 was observed when hnRNPA2/B1 from the hippocampus of VACHT deficient mice ($p=0.3067$, $n=7$ Control and $n=6$ VACHT^{Nkx2.1-Cre-flox/flox} mice) was immunoprecipitated using anti-hnRNPA2/B1 antibody and probed with anti-ubiquitin antibody. (B) Sarkosyl insolubility assay shows no aggregation of hnRNPA2/B1 in VACHT^{Nkx2.1-Cre-flox/flox} mice ($n=4$). (C) Transcript level of hnRNPA2/B1 in the RNA-Seq dataset ($p=0.9124$, $FDR=1$). (D) Cartoon of the alternative splicing in the 3'UTR of hnRNPA2/B1 transcripts (Figure adapted from (Bonomi et al., 2013), the FL transcript is predicted to be stable and undergo translation whereas the NMD sensitive transcript is not; primers used to assay this event are shown in the schematic. (E) Increased in the proportion of NMD+ hnRNPA2/B1 transcripts in the hippocampus of VACHT^{Nkx2.1-Cre-flox/flox} mice ($n=4$, $p<0.01$).

Figure 6.3. Mechanisms of cholinergic regulation of hnRNPA2/B1 protein levels.

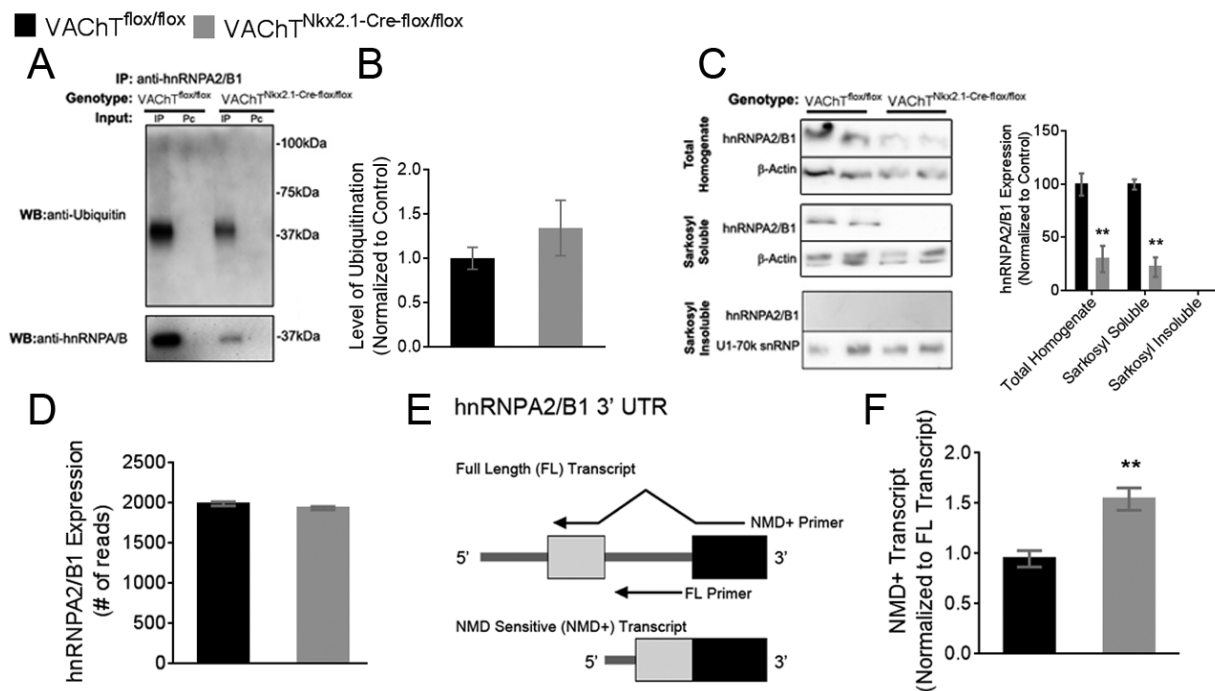
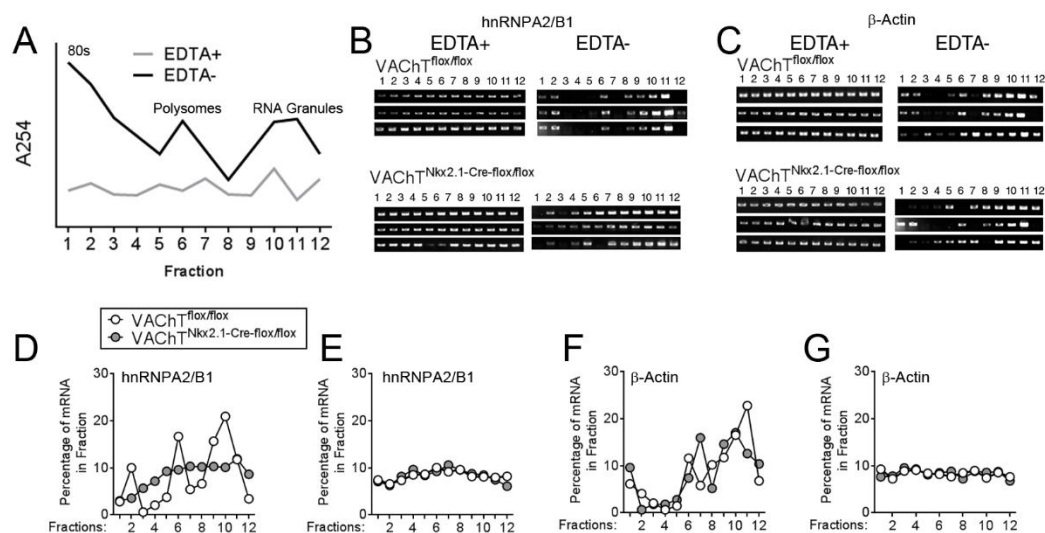


Figure 6.4. Forebrain cholinergic tone regulates translation of hnRNPA2/B1 in the hippocampus. (A) Hippocampal brain tissue was fractionated on a linear sucrose gradient. Fractions were collected and analyzed by spectrophotometry to determine position of monosome (80s), polysomes and RNA granules. (B) RT-PCR of hnRNPA2/B1 transcripts in VACHT^{flox/flox} and VACHT^{Nkx2.1-Cre-flox/flox} mice in the absence or presence of EDTA. (C) RT-PCR of β -Actin transcripts in VACHT^{flox/flox} and VACHT^{Nkx2.1-Cre-flox/flox} mice in the absence or presence of EDTA. (D-E) show quantification of data for the hnRNPA2/B1 transcripts from the three different VACHT-deficient and three control mice in the absence or presence of EDTA. (F-G) show quantification results for β -Actin transcripts from the three different VACHT-deficient and three control mice in the absence or presence of EDTA. 1-12 are the fraction numbers. The values plotted are averaged from gels in (C) (Data are mean).

Figure 6.4. Forebrain cholinergic tone regulates translation of hNRNPA2/B1 in the hippocampus.



6.4.3 Muscarinic Signalling Regulates hnRNPA2/B1 Translation by an NMD Mechanism

To further understand how cholinergic signalling regulates hnRNPA2/B1 levels, we treated neuronal hippocampal cultures from wild-type mice with the cholinergic mimetic carbachol (10 μ M) (Fig 6.5 A-B). This treatment effectively increased hnRNPA2/B1 protein levels in immunofluorescence and immunoblot experiments, and this effect could be blocked by muscarinic, but not by nicotinic antagonist treatment (Fig. 6.5C).

To study the contribution of muscarinic receptor subtypes, we evaluated hnRNPA2/B1 levels in the hippocampus of muscarinic receptor knockout mice. Compared to wild-type mice, M1, but not M4 receptor knockout mice, showed a decrease in hnRNPA2/B1 protein levels, resembling VACHTNkx2.1-Cre-flox/flox mice (Fig. 6.5D). Taken together, these experiments suggest that decreased cholinergic tone, likely due to insufficient M1 receptor activation, changes hnRNPA2/B1 protein levels by regulating mRNA translation.

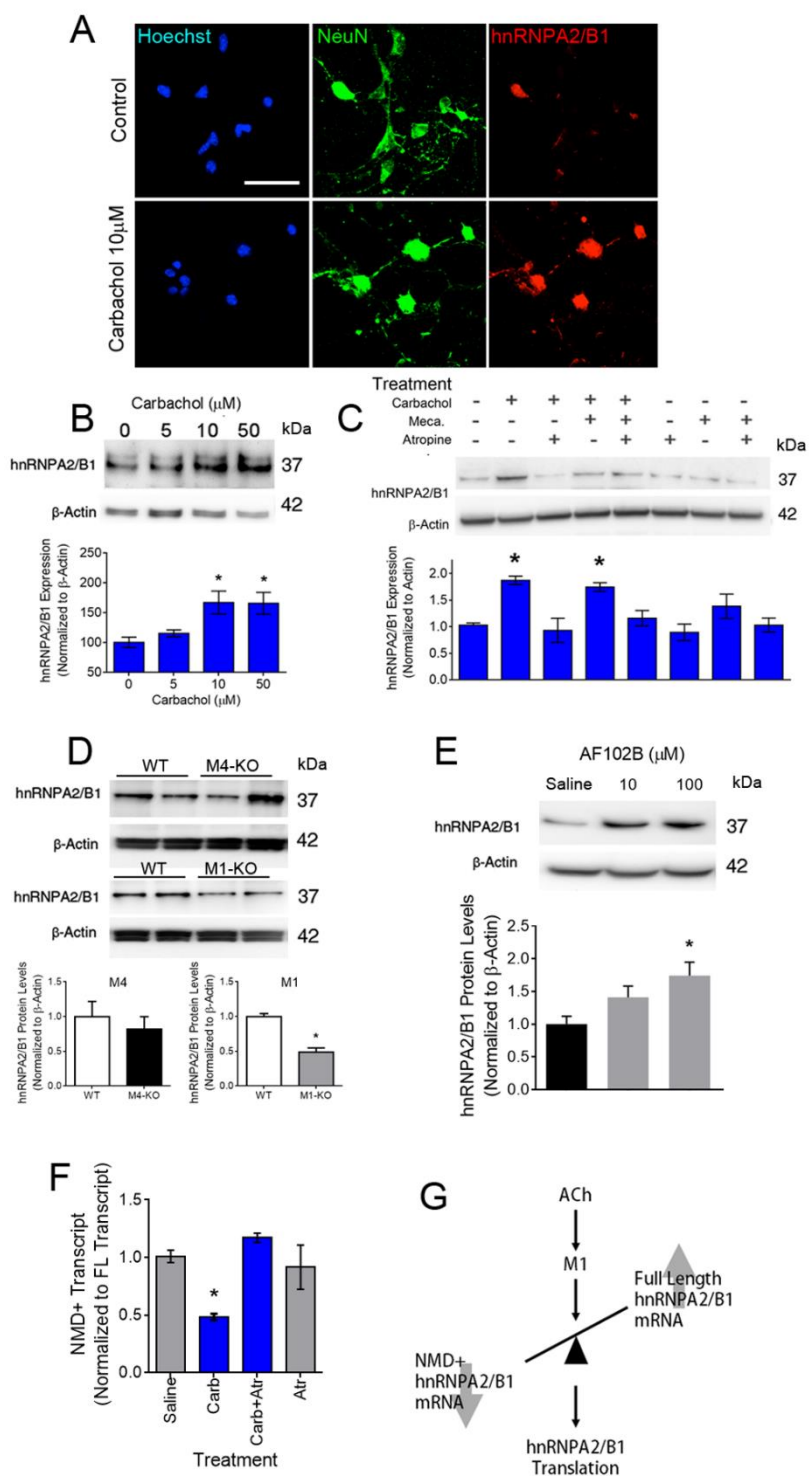
To further investigate the importance of M1 muscarinic receptors in the regulation of hnRNPA2/B1 protein levels in hippocampal neurons we treated neuronal hippocampal cultures from wild-type mice with the M1 muscarinic agonist AF102B (Fisher et al., 1989). Compared to saline treated neurons, those treated with 100 μ M of AF102B showed a significant increase in protein levels of hnRNPA2/B1 (Fig. 6.5E). Interestingly, neurons treated with 500 μ M of the compound did not show this effect, suggesting a “U-shaped” dose-effect function for this effect, a reported effect for M1 muscarinic receptors (Thomsen et al., 2012).

We then evaluated whether in vitro cholinergic regulation also changes the NMD+ product. Compared to saline treatment, carbachol shifted the expression of hnRNPA2/B1 RNA towards the NMD insensitive full-length mRNA product (Fig 6.5F). Furthermore co-treatment with atropine blocked this effect and returned the ratio to control levels, similar to what we observed for hnRNPA2/B1 protein levels (Fig. 6.5C). These data suggest that the ratio of NMD+ hnRNPA2/B1 gene products predict change

in protein levels, and that the regulation of NMD sensitivity is dependent on muscarinic signalling.

Figure 6.5. Muscarinic Regulation of hnRNPA2/B1 Translation. (A) Representative immunofluorescence images and (B) Western blots with quantification of hnRNPA2/B1 protein levels in primary hippocampal neurons after treatment with carbachol for 48 hours. hnRNPA2/B1 expression was normalized to actin (n=3, Data are mean $\pm$ SEM. *p<0.05). (C) Representative Western blot and quantification of hnRNPA2/B1 expression in primary hippocampal neurons after treatment with carbachol, mecamylamine, and atropine. hnRNPA2/B1 expression was normalized to actin (n=4, *p<0.05). The values plotted are averaged from the gels of each individual experiment. (D) Representative Western blot and quantification of hnRNPA2/B1 expression in hippocampal tissue of M4 muscarinic knockout mice (n=7), and M1 receptor knockout mice (n=7 Control and n= 8 M1 KO mice *p<0.05). (E) M1 muscarinic receptor agonist AF102B significantly increased hnRNPA2/B1 protein levels in primary hippocampal cultures (n=5 *p<0.05). (F) Increased expression of the full-length hnRNPA2/B1 transcripts of cells treated with carbachol is blocked by the administration of atropine (n=5, *p<0.05). (G) Proposed model wherein muscarinic M1 receptors signaling would shift the ratio of hnRNPA2/B transcripts, favouring the full length transcripts, and therefore increase translation of the protein.

Figure 6.5. Muscarinic Regulation of hnRNP2/B1 Translation.



6.5 Discussion

In this study we combined a variety of *in vivo* and *in vitro* techniques to evaluate the contribution of cholinergic signalling to expression levels of hippocampal hnRNPA2/B1 protein. Using a number of mouse lines, we demonstrated that hnRNPA2/B1 protein levels in the hippocampus are exquisitely sensitive to changes in cholinergic tone.

Interestingly, we observed no change in hnRNPA2/B1 protein levels in striatum- specific VACHT mutants, whereas there is a body of evidence that cholinergic signalling can affect the levels of this protein in both cortical and hippocampal regions *in vivo* (Berson et al., 2012; Kolisnyk et al., 2013a). Given these findings it is likely that it is an intrinsic property of the target cells themselves that dictate their change in hnRNPA2/B1 translation in response to cholinergic activity. Our results highlight the critical role of the Gq coupled M1 muscarinic receptor in governing hnRNPA2/B1 protein levels.

Unlike the rare hnRNPA2/B1 mutation that increases aggregation and nuclear exclusion (Kim et al., 2013), we did not find aggregation of hnRNPA2/B1 in mice with forebrain cholinergic deficiency, suggesting that in these mice, and likely in AD brains, hnRNPA2/B1 dysfunction occurs by a separate and distinct mechanism. Furthermore, we did not see an increase in ubiquitination, suggesting that changes in hnRNPA2/B1 protein levels do not occur at the post-translational level. In line with this, we found that it may in fact be abnormal translation that drives regulation of hnRNPA2/B1.

A common mechanism for the regulation of the translation of RNA binding proteins is regulation by unproductive splicing and translation (RUST), where the alternative splicing of a transcript affects its translation efficiency (Lareau et al., 2007; McGlincy and Smith, 2008). This may serve as a potential mechanism for cholinergic control of the translation of this RBP. Accordingly, we found that the levels of hnRNPA2/B1 transcripts were maintained in cholinergic-deficient mice or AD brains (Berson et al., 2012), but hnRNPA2/B1 translation was selectively decreased. Notably, hnRNPA2/B1 has been shown to be auto-regulated by a RUST mechanism involving alternative splicing in its 3'-untranslated region that leads to NMD driven by mTOR1C (Dempsey, 2012; McGlincy et al., 2010), which is a key effector of muscarinic receptor signalling (Slack

and Blusztajn, 2008). Correspondingly, we found that cholinergic control of hnRNPA2/B1 translation is mediated by M1 muscarinic receptors (Figure 6.5G).

Targeting the interactions between RBPs and RNA may serve as a new potential therapeutic avenue to restore the RNA-editing deficits observed in neurodegenerative diseases (Bai et al., 2013; Berson et al., 2012; Qian and Liu, 2014; Tollervey et al., 2011). A number of substances, including regularly prescribed antibiotics, have been shown to non-selectively alter alternative splicing in the brain (Graveley, 2005; Kole et al., 2012; Tollervey et al., 2011), however this approach lacks the ability to specifically target “impaired” RBP-RNA interactions.

Cholinergic failure is one of the hallmarks of AD, with the basal forebrain cholinergic system being heavily affected by the disease (Whitehouse et al., 1982). Data from the ADNI (Alzheimer’s Disease Neuroimaging Initiative) consortium, has linked cholinergic failure in AD to both pathological outcomes (Teipel et al., 2014) as well as cognitive impairments in AD (Grothe et al., 2014). Further evidence for the importance of cholinergic signalling to the etiology of AD comes from clinical evidence that the long-term use of anticholinergic medication, specifically anti-muscarinic drugs, significantly increases the risk of developing dementia (Gray et al., 2015). Interestingly, administration of anti-muscarinic agents to AD patients exacerbates their symptoms (Lim et al., 2015). Together these results suggest a crucial role for cholinergic tone in AD, with specific importance of muscarinic signalling.

The main pathological hallmarks of AD are the accumulation of A β plaques and of hyperphosphorylated tau (Huang and Jiang, 2009). M1 muscarinic signalling has been linked to both of these processes. Activation of the receptor has been shown to alter tau phosphorylation both in vitro (Sadot et al., 1996) and in vivo (Genis et al., 1999).

Moreover, deletion of M1 muscarinic receptors increases A β related pathology in a transgenic mouse model overexpressing mutated APP (Davis et al., 2010).

Furthermore, M1 agonists have been shown to reverse A β related pathology in mouse models of AD (Caccamo et al., 2006). These findings suggest that M1 receptors are key mediators of AD pathology. How hnRNPA2/B1 protein expression may contribute to pathology remains to be determined.

Cholinergic failure also plays an important role in one of the most important and apparent cognitive deficits of AD, memory loss (Bartus et al., 1982). There is a strong correlation between loss of basal forebrain cholinergic neurons and cognitive functioning in AD patients. Furthermore, mice with a forebrain specific deletion of VACHT have severe deficits in performance on the Paired-associates learning (PAL) touchscreen task (Al-Onaizi et al., 2016), a rodent version of the Cambridge Neuropsychological Test Automated Battery (CANTAB) tests used in humans, which has been shown to be selective for the memory impairments in AD patients (Egerhazi et al., 2007). Importantly, lentiviral mediated knockdown of hnRNPA2/B1 also produced cognition impairments in mice (Berson et al., 2012).

Taken together, our findings indicate an intricate relationship between M1 muscarinic signalling and hnRNPA2/B1 translation. These findings lay the ground work for new therapeutic avenues for the treatment of AD. Specifically, it points to the potential of M1 muscarinic positive allosteric modulators to improve long-term changes in RNA metabolism and cognitive deficits due to cholinergic malfunction in AD. Noteworthy M1 muscarinic positive allosteric modulators have shown promising results to improve cognition in non-human primates (Lange et al., 2015). Our results show novel mechanisms by which long-term cholinergic dysfunction can regulate target cells.

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7 Chapter 7

Summary and Conclusion

7.1 Summary of Major Findings

Cholinergic dysfunction is a hallmark of Alzheimer's disease. This dysfunction is hypothesized to underlie cognitive symptoms of the disease. However, the exact contribution of cholinergic dysfunction to the etiology of the disease is unclear. In this thesis, we sought out to determine whether alterations in cholinergic signalling in the brain (either increased or decreased) leads to changes in cognitive functioning. Furthermore our goal was to determine the molecular mechanisms of cholinergic dysfunction, and how changes in these mechanisms can contribute to the pathological outcomes in Alzheimer's disease.

In chapter 2 of this thesis, we characterized a mouse line which carries several copies of the vesicular acetylcholine transporter (*VACht*) gene. We showed that increase in *VACht* gene copy number leads to overexpression of functional *VACht* with consequent increase in cholinergic tone. We then carried out a series of behavioural assays to determine the implications on cognition of increased cholinergic tone. We demonstrated that these mice have marked improvement in motor endurance. However, they also have severe cognitive deficits, including attention deficits and dysfunction in working memory and spatial memory. These data, taken together, showed that increased *VACht* expression increases acetylcholine release in the brain and that this is severely detrimental to the cognitive processing of the animals. Although cholinergic tone is reduced in the Alzheimer's brain, the data presented highlight the importance of striking a balance in cholinergic signalling in the brain.

In chapter 3, we endeavoured to evaluate the effect of long-term cholinergic dysfunction in the forebrain. We evaluated the involvement of acetylcholine to forebrain function by genetically eliminating *VACht* from this population of neurons. Included in the

acetylcholine innervated forebrain regions is the PFC, a key brain region in the regulation of executive functioning. We therefore tested mice on measures of executive function. This was assessed using both a pairwise visual discrimination test and a 5-choice serial reaction time task (5-CSRT). Results of the pairwise test showed that VACHT-mutant mice were able to learn the initial stimulus pairing, however when the stimulus pairings were switched the mice failed to learn the new stimulus-reward rule. Similarly, on the 5-CSRT the VACHT mutant animals were able to learn the task, but once the stimulus presentation length was reduced (increasing attentional demand), the mice showed prominent impairments on the task compared to controls.

Given the impaired cognition of the animals, we performed *in vivo* magnetic resonance spectroscopy, to assess potential changes in PFC circuitry and neuronal function. This analysis showed changed levels of the metabolites taurine and lactate. The results suggested changes in neuronal metabolism in the PFC of the VACHT-deficient mice. The PFC of the mice showed a severe decrease in the protein levels of the RNA binding protein heterogeneous nuclear ribonucleoprotein A2/B1 (hnRNPA2/B1). Accordingly, a number of genes in the PFC of VACHT-deficient mice were found to be alternatively spliced. Amongst these genes was pyruvate kinase M, a key enzyme involved in lactate metabolism. In chapter 3, we were able to determine the impact of cholinergic dysfunction in the forebrain and furthermore were able to determine some of the molecular mechanisms that result from cholinergic dysfunction. We therefore sought to expand upon these two key findings in the following chapters.

Chapter 4 was specifically designed to dissect the mechanism underlying cholinergic control of attention, based on our findings in chapter 3 that mice lacking release of acetylcholine into the PFC were impaired on a task of attention. Chapter 4 was dedicated to determining the roles of nicotinic cholinergic receptors in this task. Significant literature exists examining the role of $\beta 2$ nicotinic receptors ($\beta 2$ nAChR) on the 5-CSRT, however, the role of the $\alpha 7$ nicotinic ACh receptor ($\alpha 7$ nAChR) in attention is ambiguous. To clarify the role of the receptor on the task, we trained $\alpha 7$ nAChR knockout mice on the 5-CSRT task. $\alpha 7$ nAChR knockout mice showed impairments in

measures of sustained attention. This was assessed by comparing the performance on the first half of the task to the second half. We were able to completely reverse these impairments by treating mutant mice with an agonist of the $\beta 2nAChR$. In addition, treating $\alpha 7nAChR$ knockout mice with $\beta 2nAChR$ agonist activated the same biochemical response in the PFC as did the administration of a $\alpha 7nAChR$ agonists in control, non-transgenic mice. The work presented in chapter 4 of this thesis details a complex interplay between the $\alpha 7nAChR$ and $\beta 2nAChR$ receptors. This complex relationship regulates attentional performance on the 5CSRT task in mice. These data provide detailed mechanistic insight into cholinergic regulation of attention.

In chapter 5, we pursued the specific molecular mechanisms that underlie long-term cholinergic dysfunction in the brain. To achieve this, we used mice with a deletion of VACHT in the forebrain in order to model cholinergic aberrations. We then employed RNA-sequencing of hippocampal samples from these mice to study genome-wide transcriptome changes. Using this approach we were able to show that cholinergic dysfunction produces alterations in RNA metabolism. We then determined the impact of these changes in RNA metabolism by focusing our studies on changes in key transcripts. We showed that VACHT-mutant mice had abnormal splicing of the *BACE1* gene, and that this was regulated by hnRNPA2/B1. This change in *BACE1* splicing lead to an overall increase in protein levels of *BACE1*, altered APP processing and accumulation of soluble $A\beta_{1-42}$ in the brain of these animals. These pathological changes also involved age-related increased tau hyper-phosphorylation, and other neuronal abnormalities, ultimately leading to neuronal death in the hippocampus. These results indicate that alterations in RNA metabolism are a key mechanism by which cholinergic signalling in the brain can trigger Alzheimer's-like pathology in mice.

In chapter 6, we identified specific cellular mechanisms underpinning cholinergic regulation of hnRNPA2/B1. In both chapters 3 and 5 we provided evidence of the importance of this relationship to neuronal function. To study this relationship, we employed a series of genetically modified mouse models, pharmacology, and a

combination of *in vivo* and *in vitro* techniques. In VACHT^{Nkx2.1-Cre-flox/flox} transgenic mice, we showed that reducing cholinergic signalling decreased protein levels of hnRNPA2/B1. Genetic manipulations that increased cholinergic signalling, by increasing gene copy number of VACHT, had the opposite effect, increasing hnRNPA2/B1 protein levels. We then provided biochemical evidence that regulation of hnRNPA2/B1 protein levels is not mediated by transcription, protein aggregation, or protein degradation. We found however that cholinergic signalling regulates the translation of hnRNPA2/B1. Furthermore, by combining *in vitro* and *in vivo* experiments, we demonstrated that M1 muscarinic receptors control hnRNPA2/B1 protein levels. In this chapter we outlined a sophisticated regulatory mechanism of hnRNPA2/B1 by cholinergic activity, complimenting findings of previous chapters.

7.2 Limitations and Future Studies.

The mouse line used for studies presented in Chapter 2, the ChAT-ChR2-EYFP mice were originally designed for optogenetic experiments. In these mice, the BAC construct was engineered to express an excitatory rhodopsin specifically in cholinergic neurons. However given the unique organization of the cholinergic gene locus (See Chapter 1.2.1), the VACHT gene is present in the BAC. Given our findings that these mice present several additional functional gene copies of VACHT, the utility of these mice for optogenetic experiments is questionable. Therefore future endeavours should focus on this question. A second mouse line was also generated using this same approach (Zhao et al., 2011), the B6.Cg-Tg(Chat-COP4*H134R/EYFP,Slc18a3)5Gfng/J mouse line. Evaluating whether or not this second mouse line also has additional copy numbers of VACHT would be critical. If these mice do not have a functional increase in VACHT it would be of importance to compare findings from optogenetic stimulation in the ChAT-ChR2-EYFP mice to evaluate the contribution of VACHT overexpression to these studies.

In chapter 3 of this thesis we used a genetic method to target the elimination of VACHT from the basal forebrain. This method is not without limitations and differential approaches should be used to confirm our findings. We have validated the use of stereotaxic injection of Cre viruses into specific populations of neurons to delete VACHT (Al-Onaizi et al., 2016). Delivering a Cre virus to the nucleus basalis magnocellularis (NBM) would provide a means to evaluate the specific contribution of cholinergic tone in the PFC, without manipulating acetylcholine release in other brain regions. Viral mediated elimination of VACHT to the NBM would also rule out potential developmental changes contributing to the phenotype of forebrain VACHT-deficient mice.

The major phenotype we identified for $\alpha 7$ nAChR knockout mice in chapter 4 was impaired sustained attention. We were able to reverse this phenotype by activating $\beta 2$ nAChRs. A critical step would be to provide electrophysiological evidence that the drug effects occur in the PFC, as we only provided correlative evidence that the interaction between these receptors occurs in the PFC. One possibility is that the interplay between these receptors occurs at the same synapses in the PFC.

Conversely, it is possible that the $\alpha 7$ nAChR signalling and the $\beta 2$ nAChR signalling are separate and distinct. In agreement with the former possibility, $\alpha 7$ nAChR (Duffy et al., 2009) and $\beta 2$ nAChR (Poorthuis et al., 2013) are found both pre and post-synaptically in the PFC. Genetically eliminating these receptors from specific synaptic locations would provide valuable insight into the exact interaction between these receptors and their relative contributions to attention.

In Chapter 5 of the thesis we used an *in silico* analysis of the data from our RNA-Sequencing experiment, to identify hnRNPA2/B1 as one of the RNA binding protein which mediates the alternative splicing in the hippocampus of forebrain VACHT-mutant mice. However hnRNPA2/B1 was not the sole RNA-binding protein identified by this analysis. Other candidates for potential splicing factors, identified in chapter 5 are RNA binding proteins that have also been implicated in neurodegenerative disorders such as CLEF4 (Gallo and Spickett, 2010), SRSF2 (Raj et al., 2014) and SART3 (Stamper et al., 2008). Similar *in vivo* and *in vitro* approaches used to study hnRNPA2/B1 in

chapters 5 and 6 could elucidate how cholinergic tone could regulate these proteins. Furthermore, the RNA binding protein analysis was limited to exon inclusion events, leaving an entire half of the data (the exon exclusion events) to be subjected to the same analysis. Analysing the exon exclusion event data will allow us to expand upon our findings and determine novel mechanisms by which cholinergic signalling can regulate RNA-metabolism.

The basis of the argument in chapter 5 is that VACHT deficiency leads to increased BACE1 activity, by mediating hnRNPA2/B1 protein levels. We proposed that this increase in BACE1 alters APP processing and increases soluble A β . It will therefore be critical to evaluate this hypothesis *in vivo*. To determine a causal role for BACE1 in the observed altered APP processing in the forebrain VACHT mutant mice, it would be important to inhibit BACE1 *in vivo*. This could be done either genetically or pharmacologically, and APP processing and soluble A β levels should then be assessed.

In chapter 6 we provided evidence that M1 muscarinic receptors regulate the translation of hnRNPA2/B1 in hippocampal neurons. The M1 muscarinic receptor is a G_q coupled receptor and can signal through G _{α q} and G _{α s} (Thomas et al., 2008). This receptor can signal through various second messenger pathways including PKC signalling, PIP2 and modulation of intracellular calcium levels (Delmas and Brown, 2005). Given the potential signalling diversity of this receptor, determining the specificity of how M1 muscarinic receptors increases translation of hnRNPA2/B1 is critical to target this interaction for potential therapeutic benefits.

It would also be an important line of study to determine the time course of cholinergic regulation of hnRNPA2/B1. All *in vitro* studies presented in chapter 6 involved treating cultured neurons for 48 hours. Determining the shortest amount of time needed to change hnRNPA2/B1 protein levels would be critical for understanding the mechanism of regulation. These findings could then be validated *in vivo*. This could be achieved by pharmacological or chemogenetic based approaches, to stimulate M1 muscarinic pathway in mice.

7.3 Significance of Research and Conclusion.

Although the specific mechanisms by which cholinergic signalling in the brain can regulate cognition and neuronal function remain elusive, the data put forward in this thesis demonstrate the importance of cholinergic tone to both cognition and AD molecular pathology. A long line of literature has examined the role of cholinergic signalling in cognitive functioning. The data presented in this thesis advance this body of knowledge and expands upon how the different receptors for acetylcholine regulate different cognitive functions. In addition, we categorized for the first time the molecular hallmarks of long-term cholinergic dysfunction, using a wide range of approaches. In this thesis, I demonstrated a clear link between cholinergic dysfunction and the development of age-dependant molecular pathology in mice. Notably, I showed that some of these molecular changes brought on by long term cholinergic dysfunction are mediated by M1 muscarinic receptors. The data provided evidence that targeting this receptor may be beneficial to correct molecular alteration in patients with neurodegenerative disorders.

The current primary treatment for Alzheimer's disease in the clinic are acetylcholinesterase inhibitors. This line of treatment has shown improvements in cognition have been observed in patients, and are viewed as being moderately beneficial for patients (Courtney et al., 2004; Dubois et al., 2015; Kaduszkiewicz et al., 2005; Raina et al., 2008; Winblad et al., 2006). The data put forward in the thesis highlights key mechanisms by which cholinergic signalling in the brain can regulate cognition and molecular pathology. These mechanisms may serve as novel targets for the development of novel therapeutic interventions in humans affected by dementia. The discovery and development of positive allosteric modulators of cholinergic receptors (especially M1 muscarinic receptors) present an exciting new approach to the development of therapeutics for dementia, which could serve to target many of the mechanisms studied in this thesis.

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Appendix A

Regulation of cholinergic activity by the vesicular acetylcholine transporter

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REVIEW ARTICLE

Regulation of cholinergic activity by the vesicular acetylcholine transporter

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Acetylcholine, the first chemical to be identified as a neurotransmitter, is packed in synaptic vesicles by the activity of VACHT (vesicular acetylcholine transporter). A decrease in VACHT expression has been reported in a number of diseases, and this has consequences for the amount of acetylcholine loaded in synaptic vesicles as well as for neurotransmitter release. Several genetically modified mice targeting the VACHT gene have been generated, providing novel models to understand how changes in VACHT affect transmitter release. A surprising finding is that most cholinergic neurons in the brain also can express a second type of vesicular neurotransmitter transporter that allows these neurons to secrete two distinct neurotransmitters. Thus a given neuron

can use two neurotransmitters to regulate different physiological functions. In addition, recent data indicate that non-neuronal cells can also express the machinery used to synthesize and release acetylcholine. Some of these cells rely on VACHT to secrete acetylcholine with potential physiological consequences in the periphery. Hence novel functions for the oldest neurotransmitter known are emerging with the potential to provide new targets for the treatment of several pathological conditions.

Key words: Alzheimer's disease, heart failure, Parkinson's disease, sepsis, synaptic vesicle, vascular dementia.

INTRODUCTION

Cholinergic neurons in the CNS (central nervous system) and in the periphery secrete the neurotransmitter ACh (acetylcholine) to regulate a plethora of physiological functions. In addition to ACh, many cholinergic neurons in the brain can also secrete the neurotransmitter glutamate [1], whereas cholinergic neurons in the periphery can also secrete a number of peptides and ATP, suggesting the potential for sophisticated modulation of physiological functions by these neurons. Moreover, ACh is also present in a number of non-neuronal cells, where it may have paracrine or autocrine functions [2,3]. Given its cationic nature, ACh does not diffuse effectively through membranes; therefore, a transport mechanism is required for this neurotransmitter to be secreted. Although certain organic cation transporters can carry ACh [2], both in neurons, as well as certain non-neuronal tissues, this chemical messenger is first stored in vesicles prior to being released by exocytosis [4–6].

ACh synthesis (Figure 1) depends on the uptake of the ACh precursor choline by CHT1 [high-affinity choline transporter/SLC5A7 (solute carrier family 5 member 7)] that is mainly expressed in cholinergic neurons [7], although it can also be found in certain non-neuronal cells [2,5]. In the cytoplasm of nerve endings, ACh is synthesized by the enzyme ChAT (choline acetyltransferase) (EC 2.3.1.6) and is then loaded into synaptic vesicles by VACHT [vesicular ACh transporter/SLC18A3 (solute carrier family 18 member 3)] [4,8]. VACHT is a 12 transmembrane domain protein that is part of a Major Facilitator Superfamily of transporters [9]. This superfamily also includes the neurotransmitter transporters VMAT (vesicular monoamine transporter) 1 and VMAT2, which share a high degree of

homology with VACHT in their transmembrane segments. These transporters use the electrochemical gradient generated by a V-type proton ATPase to transport and accumulate neurotransmitters in vesicles [8].

Synaptic vesicles accumulate thousands of ACh molecules to form a quantum. Interestingly, *in vitro* analysis suggests that VACHT is a very slow transporter [10], thus serving as a limiting factor in the recycling of functional cholinergic synaptic vesicles (loaded with ACh) to maintain neurotransmitter release. Indeed, recent experiments in neurons using glutamate uncaging indicate that the VGLUT (vesicular glutamate transporter) is also a very slow transporter [11]. Therefore expression of vesicular transporters and their activity may have major influences on the release of ACh. In the present review we will evaluate novel genetic insights regarding the role of VACHT for transmitter release in neuronal and non-neuronal cells as well as the functional consequences of alterations in VACHT expression. Excellent reviews on the use of genetically modified mice to probe for the specific roles of subtypes of muscarinic and nicotinic receptors have been published previously [12–18], so we will not discuss these results.

VACHT BIOCHEMISTRY AND CELL BIOLOGY

The structure of VACHT has not been resolved experimentally, but a three-dimensional model for this transporter has been proposed based on structural information from two members of the Major Facilitator Superfamily (lactose permease and glycerol 3-phosphate) [9]. The 12 transmembrane domains of VACHT are proposed to fold into two main bundles comprising

Abbreviations used: ACh, acetylcholine; ChAT, choline acetyltransferase; CHT1, high-affinity choline transporter 1; CNS, central nervous system; DA, dopamine; GABA, γ -aminobutyric acid; GI, gastrointestinal; hnRNP, heterogeneous nuclear ribonucleoprotein; IL, interleukin; KD, knockdown; KD^{HET}, heterozygous KD; KD^{HOM}, homozygous KD; KO, knockout; LDCV, large-dense core vesicle; LTP, long-term potentiation; MEPP, miniature-endplate potential; MSN, medium spiny neuron; MWM, Morris water maze; NMJ, neuromuscular junction; OCT, organic cation transporter; PKC, protein kinase C; VACHT, vesicular ACh transporter; VGLUT, vesicular glutamate transporter; VMAT, vesicular monoamine transporter.

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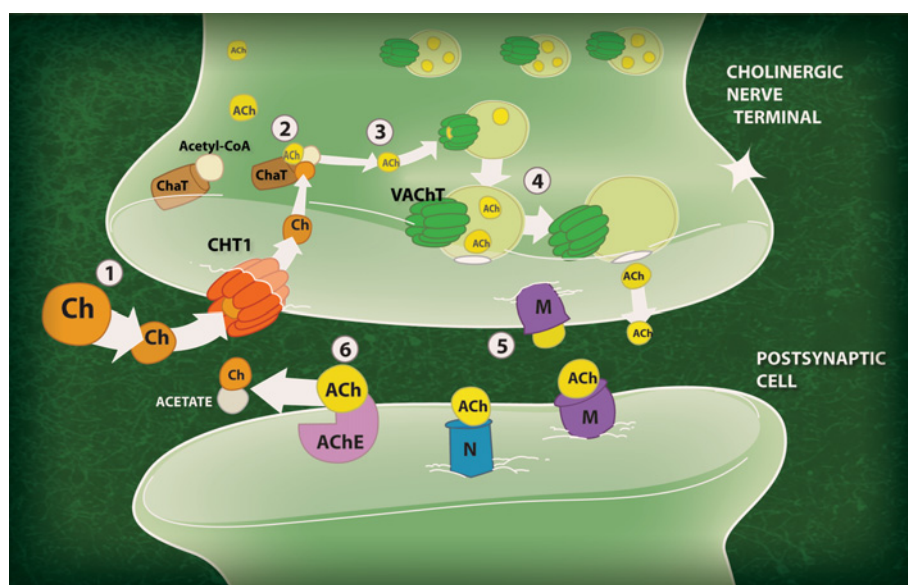


Figure 1 Schematic drawing of ACh storage and release

(1) Uptake of the ACh precursor choline by CHT1 that is mainly expressed in cholinergic neurons. (2) In the cytoplasm of nerve endings, ACh is synthesized by the enzyme ChAT, and then it is loaded into synaptic vesicles (3) by VACHT. (4) Upon arrival of the nerve impulse, vesicles fuse to the plasma membrane and release the neurotransmitter that can then signal through nicotinic (N) and muscarinic (M) receptors (5). ACh is rapidly degraded into acetate and choline (6) by the enzyme AChE (acetylcholinesterase). The number of transmembrane domains for CHT1 is 13 [160] and for VACHT is 12. These are not shown faithfully in the Figure due to space limitations. Ch, choline.

transmembrane helices I–VI and VII–XII respectively [19], with N- and C-terminal regions directed to the cytoplasm. According to this model, a central transport path is formed by these two bundles and a rocker motion of the bundles allows for exposure of the substrate-binding site to the cytoplasm or to the interior of the synaptic vesicle. VACHT exchanges two luminal protons for each cytoplasmic ACh molecule [20]. Site-directed mutagenesis studies suggest that the ACh-binding site is located close to Trp³³¹ at the beginning of transmembrane helix VIII, in the luminal part of the transport channel [21]. Asp³⁹⁸ is suggested to be involved in translocation of one of the protons [22,23].

Studies in PC12 cells overexpressing human VACHT [10] indicate that transport of [³H]ACh by VACHT is saturable, with an apparent K_m value of 1 mM and a V_{max} value of 580 pmol/min/mg. *In vivo*, VACHT concentrates ACh inside synaptic vesicles by 100-fold. This gradient is around 30-fold smaller than that predicted from the available free energy from the exchange of two protons [8], suggesting that ACh storage is regulated [4,24]. Although the mechanisms for regulation are unknown, it has been demonstrated that the amount of ACh stored per vesicle depends on the amount of VACHT that is expressed [25–27]. Thus VACHT is likely to be rate limiting for ACh release. Indeed, early pharmacological experiments using the drug vesamicol [(–)-*trans*-2-(4-phenylpiperidino) cyclohexanol], the prototype VACHT inhibitor, provided evidence that ACh storage in synaptic vesicles is critical for release; although considerations of pharmacological specificity *in vivo* need to be considered (for a review see [24]). For example, early work used high concentrations of vesamicol and binding to other unrelated targets was observed in the peripheral nervous system [28]. Also, interaction with sigma receptors in the brain has been described. However, novel vesamicol analogues have been produced showing higher specificity for VACHT [29,30].

In the striatum, cholinergic neurons were shown to express VGLUT3, and this transporter activity influences ACh loading in

synaptic vesicles by a process named vesicular synergy [31]. The exact mechanism is not yet clear, but it is likely that negatively charged glutamate may affect the ΔpH value to increase transport activity [1,32]. Hence, in addition to accumulating glutamate inside cholinergic vesicles, VGLUT3 may also influence ACh storage. Dopaminergic neurons, on the other hand, express VGLUT2, and DA (dopamine)/glutamate co-transmission has been suggested to play important roles during development and to regulate DA-dependent functions [33,34]. Interestingly, recent experiments suggest that the closely related transporter, VMAT2, mediates release of GABA (γ -aminobutyric acid) in the striatum [35]. This adds to the remarkable lack of specificity for these transporters. Indeed, choline can also be taken up by VACHT, although the affinity for ACh is 7-fold higher than that of choline [36,37].

Vesamicol, a tertiary amine that spontaneously passes through membranes, binds to VACHT and inhibits the transport of ACh [8,22,23,38]. Vesamicol is a non-competitive inhibitor of ACh transport, exhibiting a dissociation constant of 20 nM. Phosphorylation of VACHT at a PKC (protein kinase C) site in the C-terminal domain of VACHT blocks inhibition of transport by vesamicol and a high-affinity analogue of vesamicol [39–41]. However, it has not been determined whether VACHT phosphorylation is important for the modulation of ACh storage *in vivo*. Vesamicol and related compounds bind to VACHT with high affinity and readily cross the blood–brain barrier, therefore intensive efforts have been dedicated to develop analogues of vesamicol that emit either a positron or a gamma photon, suitable for imaging by PET (positron emission tomography) or SPECT (single-photon emission computed tomography) respectively [29,30,42–44]. These compounds have potential applications in the diagnosis of a number of diseases characterized by cholinergic dysfunction including Alzheimer's disease, Down's syndrome, Parkinson's disease, autonomic dysfunction in cardiovascular diseases and schizophrenia.

VACHT LOCALIZATION AND TRAFFICKING

The molecular basis for localization of vesicular transporters in synaptic vesicles has been reviewed elsewhere [45,46]. VACHT is found predominantly in synaptic vesicles in nerve terminals [47]. Early work on the trafficking of VMATs and VACHT indicated that, in cultured cells, these transporters differ in their localization; VACHT was predominantly present in synaptic vesicles, whereas VMATs were found mostly in LDCVs (large-dense core vesicles) [48–50]. Synaptic vesicles and LDCVs are present in most neurons and may regulate the secretion of classical neurotransmitters and peptides or other neuromodulators respectively. Additional studies demonstrated that the C-terminal region of VACHT contains a di-leucine motif required for clathrin-mediated endocytosis [51–54]. Interestingly, this di-leucine motif is regulated by a phosphorylation site that can alter the proportion of VACHT present in small synaptic vesicles or LDCVs [49], suggesting that ACh storage in distinct types of vesicles might occur and be subject to regulation. The C-terminal region of VACHT is also important for its localization in small synaptic vesicles [50,53,55]. Extensive mutational analysis failed to uncover other motifs in the C-terminal tail, other than the di-leucine motif, that can influence VACHT trafficking [53,55]. Interestingly, endocytosis of CHT1, which is also located in synaptic vesicles, is dependent on clathrin and on a di-leucine-like motif present in its C-terminal tail [7,56–58].

A small number of proteins have been described to interact with VACHT. Notably, clathrin adaptor proteins interact with the C-terminal tail of VACHT [52]. In addition, a functional interaction between VACHT and synaptobrevin has also been described in *Caenorhabditis elegans* [59]. These interactions are believed to participate in VACHT trafficking. SEC14, a phosphatidylinositol transfer protein, has also been shown to interact with VACHT [60]; however, the functional consequences of this interaction are unknown.

VACHT expression levels have been shown to change in response to drug treatments [61], as well as in diseases including Alzheimer's disease [62,63], sepsis [64], hypertension [65] and Huntington's disease [66]. Small changes in the expression of VACHT in vesicles may have the potential to change synaptic transmission, as the amount of transmitter released by a single vesicle does not seem to be enough to saturate post-synaptic receptors [67]. This appears to be the case at the neuromuscular junction, as suggested by the extensive variability of quantum size [24]. In central cholinergic terminals, especially where cholinergic terminals do not have opposed post-synaptic cells forming classical synapses, volume transmission may not be enough to saturate ACh receptors [68]. However, classical forms of neurotransmission may also be relevant for ACh in the brain. For example, VACHT-expressing terminals are found close to $\alpha 7$ nicotinic ACh receptors thus suggesting that classical synapses are involved in fast transmission of information by ACh in the brain, in addition to volume transmission [69].

REGULATION OF ACh RELEASE BY VACHT

The relationship between ACh storage and release is complex [24]. Experiments using vesamicol and vesamicol analogues have demonstrated that inhibition of ACh transport into synaptic vesicles decreases ACh release from nerve terminals [8,24]. Overexpression of VACHT in immature neurons [25] has also been used to investigate the *in vitro* relationship between ACh storage and release. These elegant experiments demonstrated that increased VACHT expression augmented the amplitude (quantal size) and frequency of miniature excitatory currents, presumably

by increasing the number of vesicles capable of storing ACh [25]. In addition, mice with increased VACHT expression show increased ACh release [70]. Other experiments demonstrated that VACHT activity is required for physiological storage of ACh, as VACHT-KO (knockout) mice do not survive following birth owing to compromised respiratory activity [71]. Decreased levels of VACHT affect both the peripheral nervous system and the CNS [26,27,71–76], suggesting that, in contrast with the VMAT family which has two members [77], VACHT is the unique transporter for ACh. Neuromuscular phenotypes in VACHT-KO mice were similar, if not identical, to phenotypes described for ChAT-KO mice [78,79]. The normal apoptotic process that prunes the number of motoneurons during development is compromised by lack of VACHT and motoneuron numbers are increased. At the NMJ (neuromuscular junction), nerve endings show increased size and number. Moreover, skeletal muscle presents degeneration and atrophy indicating that, during development, secretion of ACh required for neuromuscular development depends mainly on VACHT activity. Remarkably, the levels of ACh in terminals lacking VACHT were increased, suggesting that feedback inhibition of ACh synthesis is not operational in cholinergic nerve terminals [71].

Surprisingly, electrophysiological analysis of VACHT-KO mice detected small-amplitude MEPPs (miniature-endplate potentials) of very low frequency in the NMJ preparations of null embryos, suggesting that some diffusion and accumulation of ACh in synaptic vesicles occurs in the absence of VACHT. However, this process is insufficient to sustain minimal levels of ACh release at the NMJ. In agreement with these data, release of newly synthesized ACh from brain synaptosomes is completely abolished in VACHT-KO mice [71].

Interestingly, a 50 % decrease in VACHT expression in heterozygous VACHT-KO mice did not affect muscular function [72]. Conversely, these mutant mice present behavioural deficits in object recognition memory [72,80]. These results suggest that central cholinergic synapses are much more dependent on VACHT than NMJ terminals to sustain neurotransmitter release. This is probably because of reduced numbers of synaptic vesicles, or their frequent reuse, in central nerve terminals compared with the NMJ. Further insight into the mechanisms through which altered VACHT expression regulates ACh release came from studies using VACHT-KD (knockdown) mice [26,27]. VACHT-KD^{HET} (heterozygous KD) mice show a 40 % decrease in VACHT expression. Similar to heterozygous VACHT-KO mice, VACHT-KD^{HET} mice do not present muscular dysfunction. Microdialysis analysis in freely moving mice showed that VACHT-KD^{HET} mice have decreased levels of ACh release in the brain. These mutants show deficits in object recognition memory and social recognition memory [26]. These results suggest that the NMJ has a much higher safety factor than central synapses to maintain ACh release. VACHT-KD^{HOM} (homozygous KD) mice have a 70 % decrease in VACHT expression and provide a model for understanding the consequences of profound decrease in VACHT expression for ACh release. Quantal analysis demonstrated that VACHT-KD^{HET} mice have normal MEPP frequency and slightly reduced MEPP amplitude, indicative of the amount of ACh within vesicles. In contrast, VACHT-KD^{HOM} mice show reduced amplitude of MEPPs, consistent with decreased ACh storage, but also a 50 % decrease in the frequency of MEPPs [26,27]. As a consequence of these molecular changes, VACHT-KD^{HOM} mice are myasthenic. Moreover, endplate potentials were also reduced in these mutants [27]. Independent analysis of exocytosis and endocytosis using the fluorescent dye FM1-43 indicated that synaptic vesicle fusion and recycling were not affected in these mutant mice. Furthermore, post-tetanic potentiation is compromised in the NMJ of these

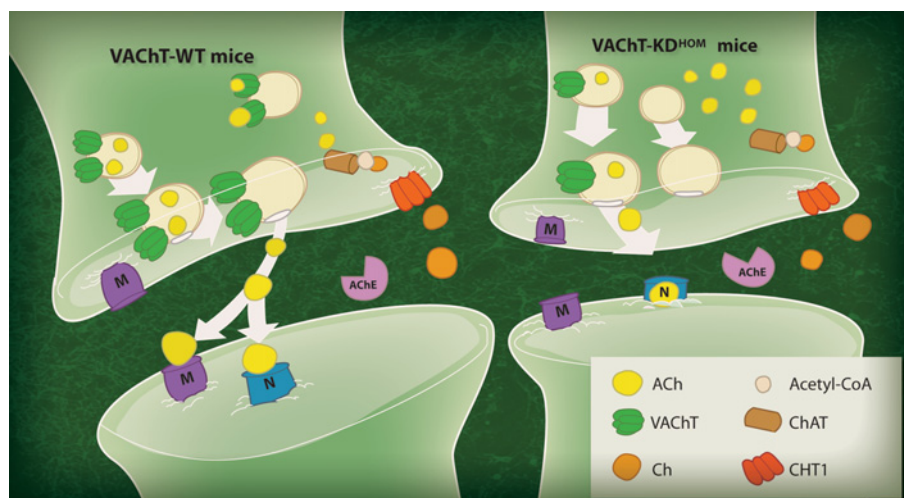


Figure 2 Cholinergic nerve terminal in mice with decreased VACHT expression

The left-hand side shows a nerve terminal in wild-type (WT) mice. The right-hand side shows a nerve terminal in VACHT-KD^{HOM} mice. Some synaptic vesicles will have no transporter and will be unable to store significant levels of ACh. These vesicles will compete for release sites and decrease fusion of vesicles fully loaded with ACh. An animated version of this Figure can be found at <http://www.biochemj.org/bj/450/0265/bj4500265add.htm>. Ch, choline; M, muscarinic receptor; N, nicotinic receptor.

VACHT mutant mice, suggesting that ACh storage can regulate synaptic plasticity [27]. Together, these experiments suggest that reduced levels of VACHT affect ACh storage in synaptic vesicles (Figure 2).

The number of copies of VACHT in a synaptic vesicle is unknown. Studies considering other vesicular transporters estimated that one to three transporters are present in one synaptic vesicle [24]. However, central synapses may contain up to ten copies of neurotransmitter transporters [81]. It is tempting to hypothesize that, in conditions of reduced VACHT expression, some synaptic vesicles will have no transporter and will be unable to store significant levels of ACh (Figure 2). These vesicles would not be able to sustain ACh release; however, because exocytosis and endocytosis in these ACh-empty vesicles is normal, they would compete for releasing sites at the NMJ. The net effect would be a reduction in the frequency of fusion of vesicles containing ACh, which can be detected using electrophysiology (MEPP frequency). These results suggest that even small changes in the levels of VACHT found in Alzheimer's disease and other pathological conditions would have drastic effects on ACh release in the brain, with a reduction in the amount of transmitter released by vesicles, but also a decrease in the number of synaptic vesicles capable of sustaining ACh release.

VACHT AND CHOLINERGIC TONE IN THE CNS

Cholinergic tone has been proposed to modulate a number of brain functions including learning, memory, attention, arousal, sleep, food intake and drug abuse [82–88]. Owing to space limitations we will not discuss these effects in the present review; rather, we will focus on novel aspects of cholinergic neurotransmission uncovered in recent years.

It has been shown that a large number of cholinergic neurons in the CNS co-express a member of the vesicular glutamate-transport protein family and therefore have the potential to co-release glutamate. To note, cholinergic neurons in the habenula co-express VGLUT1 [89], whereas basal forebrain cholinergic neurons projecting to the amygdala [90] as well as tonically active

cholinergic interneurons in the striatum co-express VGLUT3 [91]. In the retina, GABA has been shown to be co-released with ACh [92]. In cultured cholinergic neurons from the basal forebrain, glutamate release has been shown to occur [90]. More recently, evidence from optogenetic studies indicates that cholinergic neurons can co-release glutamate in brain slices [89,93]. Brief photostimulation of cholinergic axonal terminals was shown to induce fast excitatory post-synaptic currents mediated by glutamate receptors [89,93], whereas tetanic photostimulation generated slow post-synaptic currents mediated by nicotinic receptors in the habenula [89].

Genetic approaches have been used to investigate the physiological significance of ACh/glutamate co-transmission in the striatum (Figure 3). Studies using mice with null expression of VGLUT3 (VGLUT3-KO) show evidence that VGLUT3 is co-expressed with VACHT in synaptic vesicles and facilitates ACh filling of these vesicles [31]. VGLUT3-KO mice are hyperactive, more responsive to cocaine and less prone to haloperidol-induced catalepsy than their wild-type littermates [31]. Given that mice with ablated cholinergic neurons in the striatum show a similar phenotype [94,95], it was initially suggested that these behavioural changes resulted from the decreased striatal ACh release observed in VGLUT3-KO mice [31]. Recently it was demonstrated that mice with selective elimination of VACHT from striatal cholinergic interneurons (VACHT^{D2-Cre} flox/flox mice) are not hyperactive and show minimal alteration in behavioural responses to cocaine. These results strongly suggest that glutamate released from cholinergic neurons, rather than ACh, is critical for cocaine-induced behavioural manifestations [76]. Conversely, it was shown that elimination of striatal ACh release affects DA metabolism. It also appeared to affect the response of MSNs (medium spiny neurons) to DA where up-regulation of DA receptors and a change in behavioural responses to dopaminergic agonists was observed [76]. These data indicate that cholinergic interneurons use two distinct neurotransmitters to differentially regulate behaviour. Moreover, synchronized activity of cholinergic interneurons was shown to depolarize DA nerve terminals directly and evoke DA release, independently of the action potentials in DA soma [96,97], indicating that the

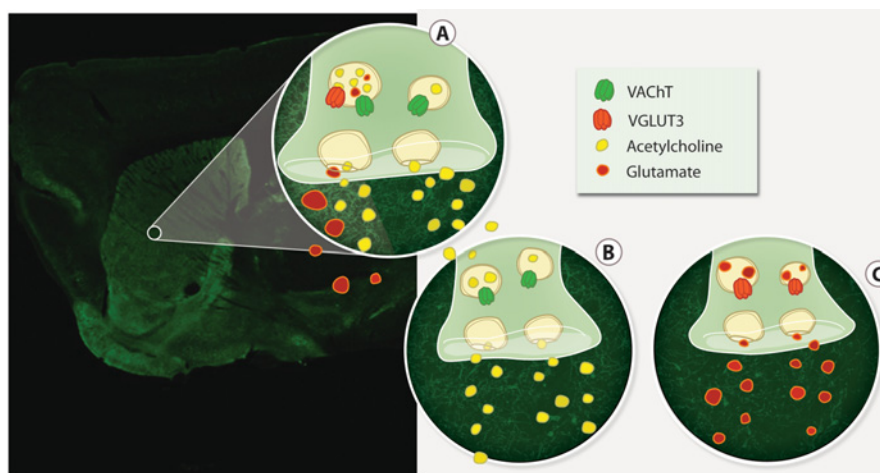


Figure 3 ACh/glutamate co-transmission in the mammalian striatum, and the effects of molecular manipulations

(A) Schematic representation of the normal ACh/glutamate co-transmission and vesicular synergy in the striatum. (B) Loss of VGLUT3 results in elimination of glutamate release. (C) Targeted KO of VACHT in the striatum results in loss of ACh release.

ACh-driven DA signal has crucial outcomes for DA nerve function. Striatal cholinergic neurons can also regulate MSNs by activating GABA release from interneurons and silencing MSNs [98]. Importantly, these findings demonstrate that co-transmission has the potential to significantly affect the functioning of striatal neurons and hence of basal ganglia. Additionally, these results suggest that other roles previously attributed to ACh in striatal function might either result from glutamate released from cholinergic interneurons or depend on the combined action of both transmitters.

Basal forebrain cholinergic neurons, which provide the major input to the cortex and hippocampus, undergo moderate degenerative changes during normal aging, and the resulting cholinergic hypofunction has been associated with age-related memory deficits [99]. A more profound alteration in basal forebrain cholinergic cells is thought to underlie some of the cognitive and behavioural symptoms observed in both Alzheimer's disease and vascular dementia as well as in Parkinson's disease [100–102]. Importantly, VACHT levels are decreased in the brains of Alzheimer's disease patients [62,63].

Studies using animal models of cholinergic dysfunction generated by ablation of basal forebrain cholinergic neurons using electrolytic or excitotoxic methods, as well by the more selective strategy of cholinergic immunolesion, have given inconsistent results concerning the cognitive and behavioural processes that are affected by altering cholinergic transmission [103]. These studies have been hampered by the fact that both non-cholinergic and cholinergic projection neurons are destroyed in many cases, or that the lesions produced do not fully deplete cholinergic neurons. Moreover, these studies cannot separate potential roles of ACh and glutamate that have the potential to be secreted together by these neurons. Genetically modified mice with selective elimination of VACHT expression in forebrain cholinergic neurons provide a model to isolate the consequences of cholinergic deficiency in dementia [75]. Behavioural analysis of mice with selective forebrain VACHT deficiency (VACHT^{Six3-Cre-flox/flox} mice) indicates that these mice are hyperactive [75]. Other mouse lines with decreased cholinergic tone also show augmented locomotion [74]. Hyperactivity in mice is related to a number of possible psychiatric-like behaviours, including a potential increase in anxiety-like behaviour, but this is not the case in these mutant mice. Importantly, the hyperactivity observed

in VACHT^{Six3-Cre-flox/flox} mice is not due to elimination of VACHT in the striatum [76]. Thus these data highlight the importance of basal forebrain cholinergic neurotransmission for the modulation of locomotor activity. Additionally, forebrain VACHT deficiency compromised the ability of mice to use spatial cues to find the platform in the MWM (Morris water maze) [75]. Although these mice show deficits on MWM acquisition, they develop alternative strategies to recall the correct location of the platform in probe trials. Interestingly, forebrain VACHT deficiency impaired the capacity of mice to extinguish a previous location and learn a new platform location, suggesting that ACh is important for behavioural flexibility. Accompanying this spatial memory impairment, we found an impairment in LTP (long-term potentiation) in VACHT^{Six3-Cre-flox/flox} mice. This effect on LTP did not involve changes in glutamatergic synaptic transmission, as input/output relationship and paired-pulse facilitation were not affected [75]. Together, these results suggest that VACHT^{Six3-Cre-flox/flox} mice have cellular and behavioural deficits that prevent proper encoding of spatial memory information, which is one of the first behavioural deficits observed in Alzheimer's disease patients. Hence, these mice may provide a more reliable model of neurochemical changes in Alzheimer's disease and other types of dementia. Potential long-term functions affected by cholinergic deficiency are still largely unknown. Exciting new data suggest that loss of the nuclear ribonucleoproteins hnRNP (heterogeneous nuclear ribonucleoprotein) A/B family, which is observed in the entorhinal cortex of Alzheimer's disease patients, is induced by cholinergic deficiency [104]. Furthermore, loss of the hnRNP splicing factors was shown to cause alternative splicing impairments, dendrite loss in primary neurons and cognitive impairments [104].

REGULATION OF CHOLINERGIC TONE IN THE AUTONOMIC NERVOUS SYSTEM BY VACHT

ACh is the primary chemical neurotransmitter at parasympathetic nerve endings and modulates the function of many peripheral organs in the body. VACHT-positive neurons have been identified in several different organs including the retina, GI (gastrointestinal) tract and respiratory tract, as well as the heart [105].

In the heart, co-ordinated interplay between the two branches of the ANS (autonomic nervous system) is important in maintaining proper function. Activation of the sympathetic branch increases heart rate and contractile force, whereas activation of the parasympathetic branch reduces heart rate by altering the conduction velocity of both the sinoatrial and atrioventricular nodes [106]. It has long been recognized that overactivation of the sympathetic tone contributes to cardiac dysfunction [107–109]; in contrast, much less is known about the role of failing cholinergic neurotransmission in cardiac disease. Vagal stimulation has been shown to improve the outcomes in experimental heart failure [110–118] and it is an approach currently being explored to ameliorate a number of diseases in humans. Recent studies using VACHT-KD^{hOM} mice, which show a systemic reduction in VACHT, provided direct evidence that decreased cholinergic neurotransmission also causes plastic alterations that contribute to heart dysfunction [73,119]. The hearts of VACHT-KD^{hOM} mice have altered calcium handling, show changes in myocyte contractility and express several markers of cardiac stress, which are activated during cardiac remodelling and heart failure [73]. Importantly, all of these changes can be reversed through treatment with pyridostigmine, a peripheral cholinesterase inhibitor, suggesting that cardiac dysfunction in these mice results from a deficiency in cholinergic tone [73]. Mice lacking M₂ muscarinic receptors show increased cardiac stress [120], and experiments using mice lacking one of the high-affinity choline transporter alleles confirmed that decreased cholinergic tone affects heart function [121].

The cholinergic system is important in regulating the innate immune response. In fact, several studies have provided novel insight into the specific mechanisms through which neuronal ACh can act peripherally to control the immune response. This inflammatory reflex, termed the cholinergic anti-inflammatory pathway, is dependent on the peripheral actions of ACh released from the vagus nerve [110,122,123]. ACh binds to $\alpha 7$ nAChRs (nicotinic acetylcholine receptors) on macrophages and thereby inhibits the release of pro-inflammatory cytokines including TNF α (tumour necrosis factor α), IL (interleukin)-1 β and IL-6 [122,123]. Inhibition of cytokine release has been shown to be beneficial in several disease states, including endotoxaemia, sepsis and heart failure [124–127]. Consistent with these results, VACHT-KD^{hOM} mice have been shown to develop an increased inflammatory immune response when infected with parasites [128], indicating disturbance of the cholinergic anti-inflammatory reflex in this mutant.

In the retina, ACh is released in response to light stimulation and leads to direct and rapid excitation of the retinal ganglion cells [129]. Release of ACh in the enteric nervous system induces smooth muscle contractions in the GI tract [130,131]. Cholinergic signalling also leads to smooth muscle contraction in the respiratory tract [132]. Whether decreased cholinergic tone has pathological implications related to eye function, the enteric system or the respiratory tract has not yet been systematically investigated.

NON-NEURONAL CHOLINERGIC MACHINERY

ACh is also produced in many different cell types, leading to the idea that a non-neuronal cholinergic system plays a significant role in regulating various physiological functions [133]. Indeed, the machinery necessary to produce ACh as well as the neurotransmitter itself has been identified in a range of cells including lymphocytes [134,135], epithelial cells [136–138], vascular endothelial cells [139] and the α -cells of the

pancreas [6]. Furthermore, this machinery has been identified in cardiomyocytes [5,140,141].

Immune cells, including lymphocytes, possess the machinery necessary to synthesize ACh [134,135,142,143]. It has been recently demonstrated that a small population of T-lymphocytes can synthesize and release ACh in response to autonomic nervous system activity in the spleen as part of the cholinergic anti-inflammatory pathway [144]. It is important to note that T-cells as well as macrophages express both muscarinic and nicotinic ACh receptors and are also able to produce ACh [145]. The exact mechanism by which ACh is released from these cells to regulate the immune system has not yet been uncovered.

The ability of epithelial cells to synthesize ACh is well characterized; in fact, it has previously been reported that this molecule can be secreted from cultured bronchial epithelial cells [137]. However, ACh release from epithelial cells does not appear to be dependent on VACHT, but rather on the organic cation transporters OCT (organic cation transporter) 1 and OCT2 [146,147]. ACh released by epithelial cells acts through both nicotinic as well as M₁ muscarinic receptors and increases their proliferation rate [148]. Moreover, in a number of cancer cells, particularly in lung cancer, ACh has been shown to play an autocrine role [149–151].

ACh is important in regulating insulin release from β -cells of the pancreas. It has long been suggested that the source of this ACh is the parasympathetic nerve endings in the endocrine pancreas, which can trigger insulin release following binding to the M₃ muscarinic receptor [152,153]. Interestingly, recent work has revealed that, although insulin secretion from β -cells is regulated by neuronal parasympathetic signalling in mice, humans possess the machinery to synthesize and release ACh from α -cells. VACHT plays an important role in the release of ACh from α -cells as positive immunostaining was observed for the transporter in these cells and pharmacological manipulation blocked ACh release. This suggests that ACh is maintained in exocytotic vesicles within α -cells and is released quantally in a manner similar to that observed in neurons [6]. Owing to the fact that β -cells are mostly localized close to α -cells in the pancreatic islets, the non-neuronal ACh released by α -cells can act as a paracrine molecule on neighbouring β -cells and initiate the insulin secretion cascade [6].

Vascular endothelial cells play a critical role in the regulation of blood pressure by inducing the relaxation of vascular smooth muscle cells. This pathway is well characterized and ACh is known to mediate vasodilation through binding to muscarinic ACh receptors on endothelial cells. This interaction leads to the production of the EDRF (endothelium-derived relaxing factor), now known to be nitric oxide, which leads to vasodilation [154]. Although ACh appears to have a profound effect on vascular function, it is important to note that parasympathetic innervation of endothelial cells is virtually non-existent and there are high levels of acetylcholinesterases in circulation. It is now evident that endothelial cells have the ability to synthesize and secrete ACh via a PKC-independent mechanism [139,155]. Importantly, previous work has confirmed the presence of VACHT in two different endothelial cell culture models, suggesting that ACh may be released from these cells via a VACHT-dependent mechanism [156,157].

It has previously been proposed that cardiomyocytes are able to synthesize and release ACh at the cellular level as they possess the machinery for production of ACh [140,141]. Owing to limited innervation of ventricular cardiomyocytes by parasympathetic neurons [158,159], it has been suggested that ventricular cardiomyocytes may synthesize ACh. VACHT was shown to be present in vesicles in cardiomyocytes [141]

suggesting a quantal release of ACh from these cells [5]. In cell culture models, isoproterenol and other adrenergic activators can induce cellular hypertrophy and remodelling. ACh released by cardiomyocytes plays an important role in protecting these cells against isoproterenol-induced cardiomyocyte remodelling [5]. Furthermore, expression of both VACHT and ChAT was increased in cultured cardiomyocytes treated with adrenergic drugs [5], suggesting a potential mechanism for regulation of this machinery. This non-neuronal ACh may then act in an autocrine/paracrine fashion to enhance neuronal cholinergic signalling. Although demonstrated only *in vitro*, these results suggest a novel mechanism to protect the heart under stressful conditions. These data provide for an unanticipated mechanism by which non-neuronal ACh, secreted from VACHT-positive vesicles, may play an important role in cardiac function.

CONCLUSION

The potential to uncover novel physiological functions of ACh using genetically modified mice, in which the cholinergic machinery can be spatially and temporally targeted, has already changed our understanding of functions by this neurotransmitter. Otto Loewi's [161] findings of ACh as a neurotransmitter can now be expanded to a role in paracrine/autocrine communication in a number of non-neuronal cells. By using the *Cre/lox* system, BAC (bacterial artificial chromosomes) transgenic mice and optogenetics, we now have the ability to activate or inactivate the cholinergic machinery or cholinergic neurons at will. These novel approaches will lead to increased knowledge of how ACh contributes to different bodily functions. Additionally, these approaches will be fundamental to unravelling how different populations of cholinergic neurons in the brain can regulate distinct biochemical and physiological processes. It is tempting to speculate that optogenetics, used to activate or inactivate cholinergic neurons in the peripheral nervous system, may be effectively used in the future as treatment for a number of pathologies involving dysregulated sympathetic or parasympathetic activity. Finally, inactivation of cholinergic machinery in non-neuronal tissues using genetically modified mice will provide the ultimate proof for the physiological significance of non-neuronal release of ACh.

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Appendix B

Hyperactivity and attention deficits in mice with decreased levels of stress inducible phosphoprotein 1 (STIP1)

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Contributions to publication: BK performed self-grooming behaviour analyses.

RESEARCH ARTICLE

Hyperactivity and attention deficits in mice with decreased levels of stress-inducible phosphoprotein 1 (STIP1)

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ABSTRACT

Stress-inducible phosphoprotein 1 (STIP1, STI1 or HOP) is a co-chaperone intermediating Hsp70/Hsp90 exchange of client proteins, but it can also be secreted to trigger prion protein-mediated neuronal signaling. Some mothers of children with autism spectrum disorders (ASD) present antibodies against certain brain proteins, including antibodies against STIP1. Maternal antibodies can cross the fetus blood-brain barrier during pregnancy, suggesting the possibility that they can interfere with STIP1 levels and, presumably, functions. However, it is currently unknown whether abnormal levels of STIP1 have any impact in ASD-related behavior. Here, we used mice with reduced (50%) or increased STIP1 levels (fivefold) to test for potential ASD-like phenotypes. We found that increased STIP1 regulates the abundance of Hsp70 and Hsp90, whereas reduced STIP1 does not affect Hsp70, Hsp90 or the prion protein. Interestingly, BAC transgenic mice presenting fivefold more STIP1 show no major phenotype when examined in a series of behavioral tasks, including locomotor activity, elevated plus maze, Morris water maze and five-choice serial reaction time task (5-CSRTT). In contrast, mice with reduced STIP1 levels are hyperactive and have attentional deficits on the 5-CSRTT, but exhibit normal performance for the other tasks. We conclude that reduced STIP1 levels can contribute to phenotypes related to ASD. However, future experiments are needed to define whether it is decreased chaperone capacity or impaired prion protein signaling that contributes to these phenotypes.

KEY WORDS: Touchscreen, Autism, ASD, Stress-inducible phosphoprotein 1, Attention deficits, Mouse model, BAC

INTRODUCTION

In autism spectrum disorders (ASD), alterations in genetic variance and neurodevelopmental are both thought to contribute to phenotype heterogeneity. Womb environment and autoimmune responses have been proposed to contribute to the complex

behavioral alterations observed in ASD, which include, but are not limited to, abnormal socialization and communication and stereotyped behavior (Brimberg et al., 2013; Goldani et al., 2014). Several distinct groups have investigated the existence of antibodies against fetal brain tissue in mothers of ASD children (Bauman et al., 2013; Braunschweig et al., 2012b, 2013; Dalton et al., 2003; Nordahl et al., 2013). Passive transfer of maternal anti-brain antibodies to pregnant experimental animal models (including mice, rats and non-human primates) has shown that their offspring develop a number of endophenotypes that resemble phenotypes in ASD (Bauman et al., 2013; Braunschweig et al., 2012b; Dalton et al., 2003). Indeed, a recent study indicated that the prevalence of antibodies against fetal brain proteins is increased fourfold in mothers of an ASD child compared with control groups (Brimberg et al., 2013). Proteomics analysis has identified six brain proteins as targets for ASD antibodies, including lactate dehydrogenase A and B (LDH), cypin, stress-inducible phosphoprotein 1 (STIP1), collapsin response mediator proteins 1 and 2 (CRMP1, CRMP2) and Y-box-binding protein (YBX1) (Braunschweig et al., 2013). Interestingly, injection of maternal antibodies that recognize LDH, STIP1 and CRMP1 in developing mouse embryos causes an increase in cortical neural precursor proliferation and cortical neuron volume, with consequent increase in brain size and weight (Martinez-Cerdeno et al., 2014). These phenotypes are consistent with the notion that the presence of maternal autoantibodies can affect neuronal development.

STIP1, also known as heat-shock organizing protein (Hop) or STI1, is a co-chaperone that interacts concomitantly with heat-shock proteins 70 and 90 (Hsp70 and Hsp90) (Abbas-Terki et al., 2002; Chen et al., 1996; Nicolet and Craig, 1989; Picard, 2002; Smith et al., 1993). The chaperone machinery is thought to provide a buffer for cells to respond to environmental challenges; disturbance of Hsp70/90 chaperone activity decreases cellular resilience to stress (Chen et al., 2015; Hashimoto-Torii et al., 2014; Taipale et al., 2010, 2014). The absence of STIP1 in mice has important consequences for development, including increased apoptosis, DNA damage and death (Beraldo et al., 2013). These phenotypes are rescued by transgenic BAC expression of STIP1 (Beraldo et al., 2013).

In addition to its intracellular role as a co-chaperone, STIP1 is also secreted by a variety of cells (Erlich et al., 2007; Eustace and Jay, 2004; Hajj et al., 2013; Lima et al., 2007; Wang et al., 2010) via extracellular vesicles (Hajj et al., 2013). Extracellular STIP1 can signal via the prion protein (PrP^C) to produce a myriad of effects related to brain development (Beraldo et al., 2010, 2013; Caetano et al., 2008; Lopes et al., 2005; Soares et al., 2013). Here, we used *Stip1* heterozygous mice (*STI1*^{-/+} mice), as well as mice overexpressing four- to fivefold more STIP1 (*STI1*^{TGA} mice), to investigate the consequences of alteration of STIP1 levels *in vivo*.

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TRANSLATIONAL IMPACT

Clinical issue

Autism spectrum disorders (ASD) represent a range of neurodevelopmental disorders with no cure. ASD is characterized by difficulties in communication and socialization, repetitive movements, hyperactivity, impulsivity, and an impaired ability to concentrate and attend to simple tasks. Genetic variance and neurodevelopmental alterations are both thought to contribute to the heterogeneity of the ASD phenotype. Recent studies have demonstrated that some mothers of children with ASD produce antibodies against six specific proteins present in the fetal brain; presumably, these antibodies can interfere with protein function in the developing brain. One of these antibodies targets a protein known as stress inducible phosphoprotein 1 (STIP1). Moreover, a polymorphism for STIP1 was recently identified as a potential risk factor in attention deficit hyperactivity disorder, which shares some phenotypes with ASD. STIP1 is a co-chaperone that mediates the Hsp70/Hsp90 exchange of client proteins. It also triggers prion protein-mediated neuronal signaling.

Results

Here, to investigate the potential involvement of STIP1 in ASD, the authors examine mice that express reduced (50%) or increased (fivefold) levels of STIP1. They show that increased STIP1 levels regulate the abundance of Hsp70 and Hsp90. By contrast, reduced STIP1 levels have no effect on Hsp70, Hsp90 or prion protein levels. Notably, however, mice expressing increased levels of STIP1 show no major phenotype when examined using a range of behavioral tasks, whereas mice expressing reduced levels of STIP1 exhibit attention deficits and are hyperactive.

Implications and future directions

Because attention deficits and hyperactivity are present in ASD, these findings suggest that interference with STIP1 functions (but not increased STIP1 levels) can contribute to ASD-like phenotypes. Changes in STIP1 levels, possibly triggered by the presence of maternal anti-STIP1 antibodies during brain development, might interfere with the development of brain circuits that affect ASD-like behavior. Additional experiments are required to determine whether decreased STIP1 contributes to ASD-like phenotypes by decreasing chaperone capacity in the developing brain, by impairing prion protein signaling, or through some other mechanism, and to define fully the consequences of disturbed STIP1 activity in ASD.

We report that decreased, but not increased, STIP1 levels affect attention and cause hyperactivity in mice, two phenotypes that are related to ASD-like phenotypes. Our results suggest that interference with STIP1 functions, which presumably occur in the presence of STIP1 antibodies, has the potential to contribute to ASD-like phenotypes.

RESULTS

We initially confirmed previous data to show that *STII*^{-/-} mice present 50% of *STIP1* mRNA levels in their brain, whereas *STII*^{TGA} mice express almost sixfold more mRNA (Fig. 1A; one-way ANOVA; revealed main effect of genotype $F_{(2,15)}=8.521$, $P<0.0001$). In contrast, mRNA levels of known STIP1 interaction partners PrP^C (Fig. 1B; one-way ANOVA $F_{(2,16)}=1.475$, $P=0.2580$), Hsp70 (Fig. 1C; one-way ANOVA $F_{(2,16)}=0.301$, $P=0.744$) and Hsp90 (Fig. 1D; one-way ANOVA $F_{(2,8)}=1.249$, $P=0.337$) were not altered in the brain of the two lines, compared with control mice.

Protein levels for STIP1 followed mRNA levels for both *STII*^{TGA} (Fig. 2A; $t_{(15)}=4.721$, $P=0.003$) and *STII*^{-/-} (Fig. 2B; $t_{(14)}=6.433$,

$P<0.0001$). PrP^C protein levels were not different from controls in both lines (Fig. 2C,D; $t_{(10)}=1.049$, $P=0.391$ and $t_{(13)}=1.128$, $P=0.279$, respectively). Interestingly, levels of Hsp70 were decreased by 50% in *STII*^{TGA} brains (Fig. 2E; $t_{(7)}=5.846$, $P=0.0006$), whereas no change in Hsp70 levels was detected in *STII*^{-/-} mice (Fig. 2F; $t_{(7)}=0.123$, $P=0.9051$), compared with controls. Additionally, Hsp90 levels detected with a pan Hsp90 antibody were doubled in *STII*^{TGA} brains (Fig. 2G; $t_{(22)}=4.618$, $P=0.0001$) but not changed in *STII*^{-/-} brains (Fig. 2H; $t_{(10)}=0.308$, $P=0.7639$), compared with controls. We then evaluated expression levels of Hsp90 α (inducible form) and Hsp90 β (constitutive form) in the brains of *STII*^{TGA} mice and observed that both forms were significantly increased (Fig. 2I,J; $t_{(22)}=4.618$, $P=0.0016$ and $t_{(16)}=5.954$, $P<0.0001$, respectively).

Spontaneous locomotor activity in a new environment can provide information on neuropsychiatric phenotypes in mice associated with genetic mutations. The increased number of *Stip1* copies, with concomitant overexpression of Hsp90 and decreased expression of Hsp70 in *STII*^{TGA} mice did not seem to have any major impact on spontaneous locomotion (Fig. 3A,B; $t_{(29)}=1.140$, $P=0.942$) or time spent in the center of the box, which provides insight on anxiety-like behavior (Fig. 3C; $t_{(29)}=1.236$, $P=0.8669$). In contrast, locomotor activity and total locomotion in a new environment were increased in *STII*^{-/-} mice (Fig. 3D,E; $t_{(44)}=1.879$, $P=0.0078$). However, *STII*^{-/-} mice did not show increased anxiety-like behavior, as determined by the time spent in the center of the box (Fig. 3F; $t_{(40)}=1.221$, $P=0.341$). We also examined another cohort of *STII*^{-/-} mice using automated metabolic cages. In this experiment, which mimics the home cage environment, *STII*^{-/-} mice again showed hyperactivity during the day and night periods, considering both total activity (Fig. 3G; $t_{(14)}=2.558$, $P=0.0228$ and $t_{(14)}=2.230$, $P=0.0426$) and ambulatory activity (Fig. 3H; $t_{(14)}=2.420$, $P=0.00297$ and $t_{(14)}=2.230$, $P=0.0426$). Given this increased motor activity, *STII*^{-/-} mice also demonstrated less sleep time (periods of inactivity) (Fig. 3I; $t_{(14)}=3.949$, $P=0.0015$ and $t_{(14)}=2.724$, $P=0.0165$). Also, *STII*^{-/-} mice showed increased consumption of O₂ during the light and dark cycle (Fig. 3J; $t_{(14)}=2.464$, $P=0.027$ and $t_{(14)}=2.169$, $P=0.047$) and CO₂ production during the dark cycle, but not in the light cycle (Fig. 3K; $t_{(14)}=2.307$, $P=0.036$ and $t_{(14)}=1.360$, $P=0.195$). No differences were observed in other parameters such as respiratory ratio (Fig. 3L; $t_{(14)}=0.4455$, $P=0.6627$ and $t_{(14)}=0.459$, $P=0.653$), food consumption (Fig. 3M; $t_{(14)}=0.5216$, $P=0.6101$ and $t_{(14)}=0.6134$, $P=0.5494$), water consumption (Fig. 3N; $t_{(14)}=1.801$, $P=0.0933$ and $t_{(14)}=0.2752$, $P=0.7872$), and heat production (Fig. 3O; $t_{(14)}=1.014$, $P=0.3276$ and $t_{(14)}=0.1935$, $P=0.8494$) comparing *STII*^{-/-} to *STII*^{+/+} mice for both cycles (light and dark).

In order to test for other neuropsychiatric-like behaviors as a result of altered STIP1 levels we tested both *STII*^{TGA} and *STII*^{-/-} mice for anxiety-like behavior (Fig. 4A-D) and depression-like behavior (Fig. 4E,F). Given the hyperactivity of *STII*^{-/-} mice, we also decided to investigate whether they had alterations in compulsive-like behavior, assessed by measurement of self-grooming and marble burying (Fig. 4G-I). There was no difference in the behavior of either *STII*^{TGA} (Fig. 4A,B,E) or *STII*^{-/-} (Fig. 4C,D,F-I) mice compared with control mice in all these behavioral tasks: time spent in the open arm (Fig. 4C; $t_{(9)}=0.310$, $P=0.7590$), time spent in the closed arm (Fig. 4D; $t_{(19)}=0.3730$, $P=0.7133$), forced swim test (Fig. 4F; $t_{(12)}=1.184$, $P=0.2594$), grooming bouts (Fig. 4H; $t_{(20)}=0.7848$, $P=0.4418$), time grooming (Fig. 4G; $t_{(20)}=0.6072$, $P=0.5505$) and marble burying (Fig. 4I; $t_{(21)}=0.4956$, $P=0.6253$).

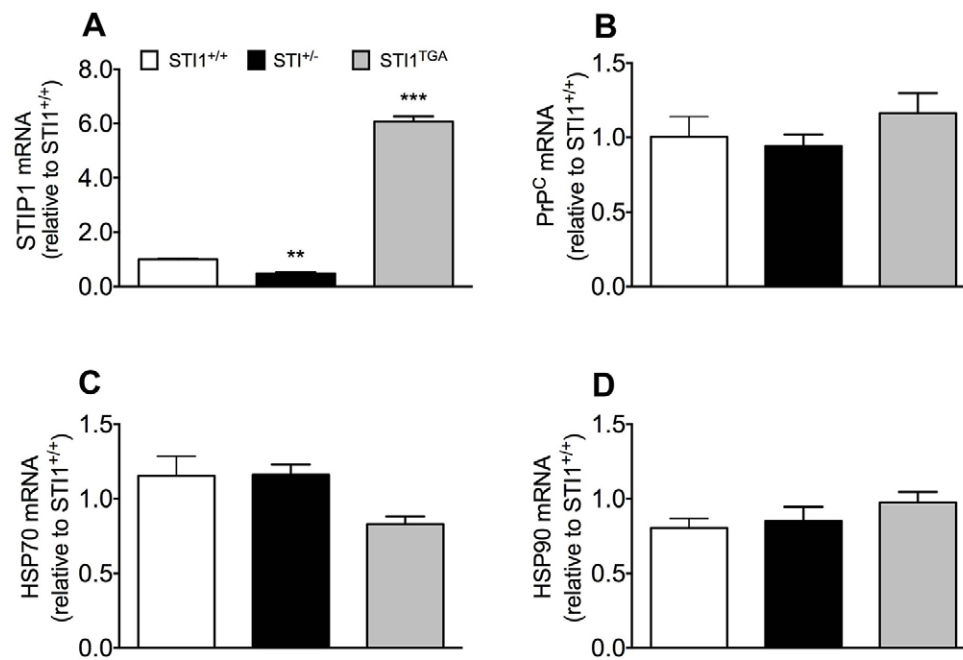


Fig. 1. Analyses of mRNA for STIP1 partners in *STII*^{+/+}, *STII*^{-/-} and *STII*^{TGA} mouse brains. (A) *STIP1* mRNA expression ($n=9$ *STII*^{+/+}, $n=5$ *STII*^{TGA} and $n=4$ *STII*^{-/-}). (B) *PrPC* mRNA expression ($n=8$ *STII*^{+/+}, $n=4$ *STII*^{TGA} and $n=7$ *STII*^{-/-}). (C) *Hsp70* mRNA expression ($n=8$ *STII*^{+/+}, $n=4$ *STII*^{TGA} and $n=7$ *STII*^{-/-}). (D) *Hsp90* mRNA expression ($n=3$ *STII*^{+/+}, $n=4$ *STII*^{TGA} and $n=4$ *STII*^{-/-}). Results are presented as means $\pm$ s.e.m.; data were analyzed and compared by one-way ANOVA and Bonferroni multiple comparisons post-hoc test; ** $P<0.001$ and *** $P<0.0001$ compared with control.

Next, we investigated spatial navigation memory in both *Stip1* mutant mice using the Morris water maze (MWM). Neither *STII*^{TGA} nor *STII*^{-/-} mice presented deficits in acquisition or retrieval of spatial memory in the MWM. For both *STII*^{TGA} and *STII*^{-/-}, performance during the 4-day acquisition phase was indistinguishable from their wild-type controls in terms of latency to find the target (Fig. 5A; RM-ANOVA $F_{(1,13)}=0.062$, $P=0.806$) or speed (Fig. 5C; $F_{(1,10)}=0.215$, $P=0.652$). When spatial memory retrieval was performed on the day-5 probe trial, again no differences were observed between *STII*^{TGA} and *STII*^{-/-} mice, compared with their wild-type controls, for time spent investigating the target quadrant (Fig. 5D; $F_{(1,13)}=1.046$, $P=0.3251$) or latency (Fig. 5E; $F_{(1,10)}=0.215$, $P=0.294$).

Given the hyperactivity phenotype and genetic data suggesting the potential of STIP1 to be linked to ADHD (Mick et al., 2011), a trait commonly found in ASD (Gadow et al., 2006; Goldstein and Schwabach, 2004; Lee and Ousley, 2006; Mulligan et al., 2009), we also determined whether changes in STIP1 levels affected attentional processing. For this, we used the 5-CSRTT. After mice were trained to perform to a criterion (>80% accuracy, <20% omissions) at a 2 s stimulus duration, we assessed attentional performance by using reduced stimulus durations in probe trials (1.5, 1, 0.8 and 0.6 s stimulus durations) as previously described (Romberg et al., 2011). We observed no differences in attentional performance in *STII*^{TGA} mice compared with their littermate controls. There was no difference in accuracy (Fig. 6A; RM-ANOVA showed no effect of genotype $F_{(1,20)}=0.0057$, $P=0.9403$, main effect of stimulus duration $F_{(3,60)}=12.14$, $P<0.0001$ and no significant interaction $F_{(3,60)}=0.1328$, $P=0.9402$) or omission rates (Fig. 6B; RM-ANOVA showed no effect of genotype $F_{(1,18)}=0.2429$, $P=0.6281$, main effect of stimulus duration $F_{(3,54)}=17.62$, $P<0.0001$ and significant interaction $F_{(3,54)}=3.854$, $P=0.0143$). Post-hoc analysis showed that there was no significant difference between *STII*^{TGA} mice and controls. There was also no difference in premature responses, a measure of impulsivity (Fig. 6C; RM-ANOVA showed no effect of genotype $F_{(1,9)}=0.00056$, $P=0.9419$, no effect of stimulus duration $F_{(3,27)}=0.8254$, $P=0.4914$ and no significant interaction

$F_{(3,27)}=1.109$, $P=0.3625$). Moreover, we did not find any difference in motivation, measured as latency to touch the screen (Fig. 6D; RM-ANOVA showed no effect of genotype $F_{(1,9)}=3.399$, $P=0.0983$, main effect of stimulus duration $F_{(3,30)}=4.281$, $P=0.0125$ and no significant interaction $F_{(3,30)}=2.332$, $P=0.0941$). Compulsivity and motivation were not altered either, as assessed by perseverative responses (Fig. 6F; RM-ANOVA, showed no effect of genotype $F_{(1,9)}=3.974$, $P=0.0774$, main effect of stimulus duration $F_{(3,27)}=4.808$, $P=0.0083$ and no significant interaction $F_{(3,27)}=0.1773$, $P=0.9108$) and reward collection latency (Fig. 6E; RM-ANOVA showed no effect of genotype $F_{(1,10)}=1.291$, $P=0.2824$, no effect of stimulus duration $F_{(3,30)}=2.162$, $P=0.1132$ and no significant interaction $F_{(3,30)}=0.7372$, $P=0.5381$).

In contrast, when attentional demand was increased, *STII*^{-/-} mice presented decreased accuracy (Fig. 6G; RM-ANOVA, main effect of genotype $F_{(1,25)}=6.872$, $P=0.0147$, main effect of stimulus duration $F_{(3,75)}=41.95$, $P<0.0001$, significant interaction effect $F_{(3,75)}=4.170$, $P=0.0087$) and increased omission rates (Fig. 6H; RM-ANOVA, main effect of genotype $F_{(1,25)}=6.584$, $P=0.0167$, main effect of stimulus duration $F_{(3,75)}=24.62$, $P<0.0001$, significant interaction effect $F_{(3,75)}=3.401$, $P=0.0220$). Post-hoc analysis revealed that the *STII*^{-/-} mice were significantly impaired in both accuracy and omissions at the 0.6 s stimulus duration. The worse performance of *STII*^{-/-} mice was not related to changes in motivation (latency to respond to the stimulus, RM-ANOVA, no effect of genotype $F_{(1,25)}=0.01856$, $P=0.8925$, no effect of stimulus duration $F_{(3,75)}=1.720$, $P=0.1702$, no interaction $F_{(3,75)}=1.070$, $P=0.3669$). There was also no difference in latency to retrieve the reward following a correct response (RM-ANOVA, no effect of genotype $F_{(1,25)}=0.03176$, $P=0.8600$, no effect of stimulus duration $F_{(3,75)}=0.3997$, $P=0.7536$, no interaction $F_{(3,75)}=1.785$, $P=0.8284$). Moreover, we detected no increase in premature responses (RM-ANOVA, no effect of genotype $F_{(1,25)}=0.0958$, $P=0.7595$, main effect of stimulus duration $F_{(3,75)}=2.907$, $P=0.0401$, no interaction effect $F_{(3,75)}=2.017$, $P=0.1187$) or perseverative responses (RM-ANOVA, no effect of genotype $F_{(1,25)}=0.04188$, $P=0.8395$, main effect of stimulus duration $F_{(3,75)}=6.975$, $P=0.0003$, no interaction effect $F_{(3,75)}=1.139$, $P=0.3389$).

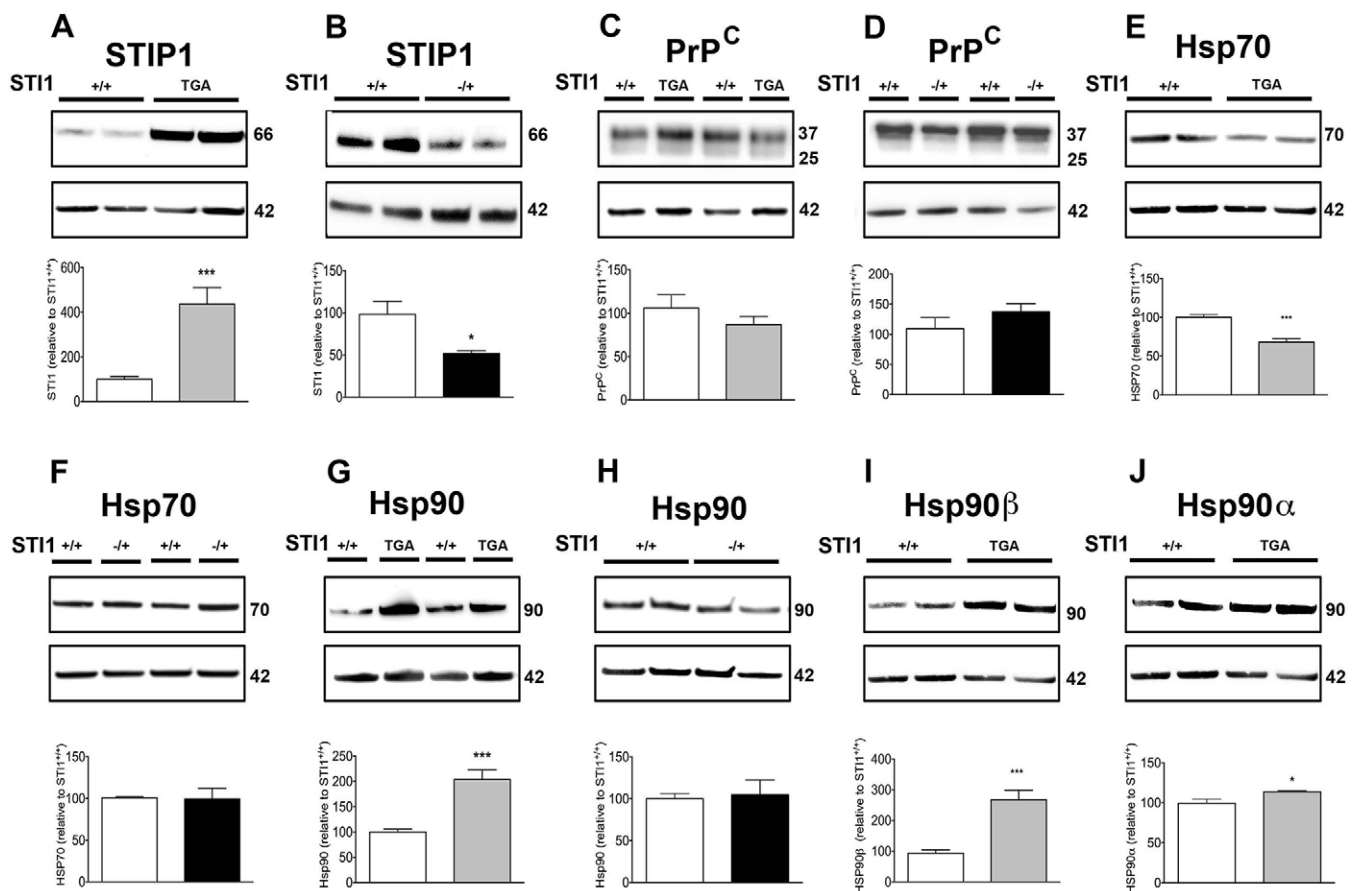


Fig. 2. Analyses of protein levels for STIP1 partners in *STII*^{+/+}, *STII*^{-/-} and *STII*^{TGA} mouse brains. (A,B) STIP1 expression in *STII*^{TGA} ($n=9$ *STII*^{+/+} and $n=8$ *STII*^{TGA}) and *STII*^{-/-} mice ($n=8$ *STII*^{+/+} and $n=8$ *STII*^{-/-}). (C,D) PrP^C expression in *STII*^{TGA} ($n=6$ *STII*^{+/+} and $n=6$ *STII*^{TGA}) and *STII*^{-/-} mice ($n=6$ *STII*^{+/+} and $n=9$ *STII*^{-/-}). (E,F) Hsp70 expression in *STII*^{TGA} ($n=5$ *STII*^{+/+} and $n=4$ *STII*^{TGA}) and *STII*^{-/-} mice ($n=5$ *STII*^{+/+} and $n=4$ *STII*^{-/-}). (G,H) HSP90 expression in *STII*^{TGA} ($n=10$ *STII*^{+/+} and $n=14$ *STII*^{TGA}) and *STII*^{-/-} mice ($n=6$ *STII*^{+/+} and $n=6$ *STII*^{-/-}). (I,J) Hsp90β ($n=10$ *STII*^{+/+} and $n=8$ *STII*^{TGA}) and Hsp90α ($n=5$ *STII*^{+/+} and $n=4$ *STII*^{TGA}) in *STII*^{TGA} mice. Results are presented as means±s.e.m.; data were analyzed and compared by Student's *t*-test; **P*<0.05 and ****P*<0.0001 compared with control.

DISCUSSION

The present experiments tested whether alterations in STIP1 levels have consequences for psychiatric-like behaviors in mice. Our results suggest that decreased, but not increased, STIP1 levels cause significant behavioral alterations in mice. Spatial learning and memory, as well as anxiety and depression-like behavior do not seem to be affected by reduced STIP1 levels. However, mutant mice deficient for STIP1 are hyperactive and present attention deficits.

STIP1 has recently emerged as a protein of potential interest in ASD and endophenotypes related to ASD. Maternal autoantibodies against STIP1 have been identified in mothers of children with ASD (Braunschweig et al., 2013). Moreover, recent global-wide association study (GWAS) analysis identified a polymorphism in *STIP1* (the human gene coding for STIP1/HOP) as a potential risk factor in a population of individuals diagnosed with attention-deficit disorder (Mick et al., 2011), a co-morbidity often associated with ASD (Brimberg et al., 2013; Goldani et al., 2014). The consequences of this polymorphism for STIP1 expression is unknown, but the presence of autoantibodies against STIP1 might affect expression levels of the protein, given that antibodies can penetrate the blood brain barrier of the fetus during pregnancy (Braunschweig et al., 2012a; Diamond et al., 2009; Fox et al., 2012; Zhang et al., 2012). Indeed, maternal antibodies that recognize STIP1 and other targets when injected in pregnant rodents or developing pups can lead to offspring with abnormal neurons and behaviors that relate to ASD

(Braunschweig et al., 2012b; Camacho et al., 2014). To a degree, *STII*^{-/-} mice model this early developmental deficit in STIP1 levels. However, in *STII*^{-/-} mice STIP1 expression is persistently decreased through life, which could also have important consequences for the phenotypes described.

STIP1 is a modular protein containing several tetratricopeptide (TRP) repeat domains and aspartate-proline (DP) reach domains (Taipale et al., 2010). TRP1 and TRP2B can interact with Hsp70 (Flom et al., 2007; Scheufler et al., 2000), whereas TRP2A is required for interaction with Hsp90 (Flom et al., 2007, 2006). Hsp90 activity is regulated by STIP1 and previous work has shown that in mice no other co-chaperone can replace STIP1 (Beraldo et al., 2013). Recent experiments have indicated that the chaperone machinery, activated by the transcription factor heat shock factor 1 (HSF1), is responsible for preventing damaging effects from environmental factors in the developing brain (Hashimoto-Torii et al., 2014). Indeed, the chaperone machinery can buffer many stresses at the cellular level and, therefore, it is not surprising that functional changes in its components have physiological consequences.

In addition to its intracellular chaperone function, STIP1 is also secreted by a myriad of cells, including astrocytes via an extracellular vesicle population, which includes exosomes (Haji et al., 2013). Extracellular STIP1 also mediates important physiological responses in the brain. Acting as a trophic factor to engage PrP^C to signal in neurons, it regulates neurogenesis and

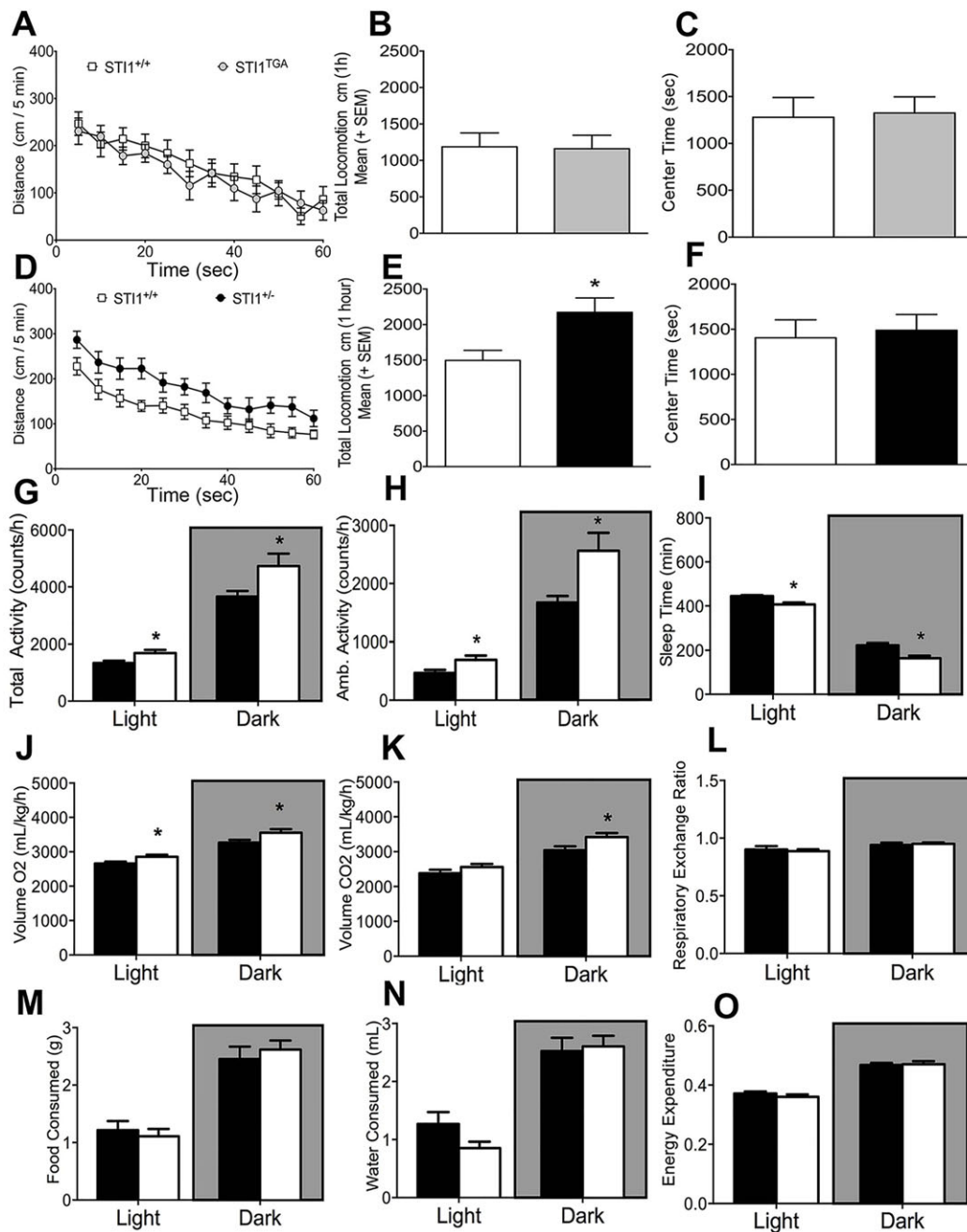


Fig. 3. Locomotor activity in *STI1*^{TGA} and *STI1*^{-/-} mice and metabolic analyses in *STI1*^{-/-} mice. (A) Horizontal locomotor activity in an open-field for *STI1*^{TGA} ($n=14$) and *STI1*^{+/+} control mice ($n=14$). (B) Cumulative 1 h locomotion for *STI1*^{TGA} ($n=14$) and *STI1*^{+/+} control mice ($n=14$). (C) Time spent in the center of the locomotion boxes for *STI1*^{TGA} ($n=14$) and *STI1*^{+/+} control mice ($n=14$). (D) Horizontal locomotor activity in an open-field for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (E) Cumulative 1 h locomotion for *STI1*^{-/-} ($n=22$) and *STI1*^{+/+} control mice ($n=24$). (F) Time spent in the center of the locomotion boxes for *STI1*^{-/-} ($n=22$) and *STI1*^{+/+} control mice ($n=24$). (G) Total activity in metabolic cages for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (H) Ambulatory activity in metabolic cages for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (I) Sleep time for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (J) VO₂ for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (K) VCO₂ for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (L) Respiratory exchange ratio for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (M) Food consumption for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (N) Water consumption for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). (O) Energy expenditure for *STI1*^{-/-} ($n=8$) and *STI1*^{+/+} control mice ($n=8$). Results are presented as means $\pm$ s.e.m.; data were analyzed and compared by Student's *t*-test; * $P < 0.05$ compared with control.

neuronal survival (Beraldo et al., 2010; Lopes et al., 2005; Roffe et al., 2010). STIP1 has a role in functional recovery in stroke (Beraldo et al., 2013; Lee et al., 2013). Moreover, STIP1 also modulates toxicity of A β peptides in models of Alzheimer's disease (Brehme et al., 2014; Ostapchenko et al., 2013).

It is remarkable that mice with increased levels of STIP1 (up to almost fivefold) do not present any major behavioral alteration. In

the extensive evaluation of cognitive phenotypes in this study, which included anxiety and depression-like behaviors, spatial memory and attention, we showed that *STI1*^{TGA} mice perform as well as littermate controls. These results suggest that strategies to increase STIP1 levels should not cause toxicity with consequences for brain functions. This is important, given that increased STIP1 levels might be protective against insults such as stroke-mediated

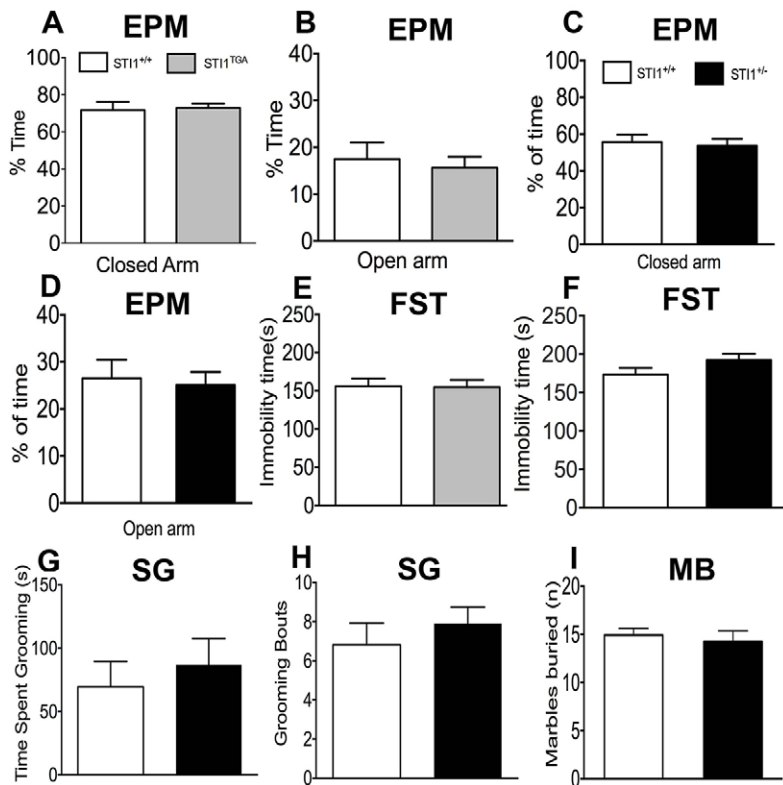


Fig. 4. Anxiety-like behavior, depression-like behavior, social behavior and compulsivity in *STI1*^{TGA} and *STI1*^{-/-} mice.

(A) Percentage of time spent in the closed arm for *STI1*^{TGA} ($n=17$) and control mice ($n=14$). (B) Percentage of time spent in the open arm for *STI1*^{TGA} ($n=17$) and control mice ($n=14$). (C) Percentage of time spent in the closed arm for *STI1*^{-/-} ($n=13$) and control mice ($n=10$). (D) Percentage of time spent in the open arm for *STI1*^{-/-} ($n=13$) and control mice ($n=10$). (E) Immobility time in the forced-swimming test for *STI1*^{TGA} ($n=17$) and control mice ($n=14$). (F) Immobility time in the forced-swimming test for *STI1*^{-/-} ($n=6$) and control mice ($n=8$). (G,H) Time spent grooming and number of grooming bouts for *STI1*^{-/-} ($n=11$) and control mice ($n=11$). (I) Marbles buried by *STI1*^{-/-} ($n=12$) and control mice ($n=12$).

cell death and in Alzheimer's disease (Beraldo et al., 2013; Ostapchenko et al., 2013). Interestingly, whereas increased levels of STIP1 seem to affect the chaperone machinery, prion protein expression is not affected by decreasing the level of Hsp70 and increasing Hsp90. These consequences of increased STIP1 seem to occur at the post-translational level, given that mRNAs for Hsp70 and 90 were not affected. It is unknown at the moment whether increased STIP1 levels stabilize a complex containing Hsp90, preferentially leading to increased turnover of Hsp70.

At present, the exact mechanism by which decreased STIP1 levels affect psychiatric-like behavior is still unknown. Although it is possible that decreased levels of STIP1 during early development have persistent effects in brain circuits, culminating with hyperactivity and attentional deficits, we cannot discard the possibility that STIP1 plays a role in regulating circuitry function in the adult brain. Our experiments at the moment do not discriminate whether the phenotypes observed in mutant mice result from decreased STIP1 co-chaperone function, diminished STIP1 extracellular signaling or both. Our results suggest that reduced levels of STIP1 have important consequences for behavior and seem to affect brain circuits that regulate attention. It is possible that exposure to STIP1 antibodies during pregnancy could reduce STIP1 levels, which, based on the present results, would have important consequences. Future experiments are required to define potential mechanisms as well as the consequences of disturbed STIP1 activity in ASD.

MATERIALS AND METHODS

Animals

STI1^{-/-} and *STI1*^{TGA} mice were generated as described (Beraldo et al., 2013). Both mouse lines were in the C57BL/6J background. All experimental procedures were conducted in compliance with the Canadian Council of Animal Care guidelines for use and care of animals and in accordance with approved animal use protocols at the University of Western Ontario (2008/127). Animals were housed in groups of two or four

per cage. Mice were kept in a temperature-controlled room with a 12/12 light/dark cycle (7 am/7 pm) with food and water provided *ad libitum* unless stated otherwise. For behavioral studies, only male mice were used. Mice were randomized and the experimenter was blind to genotypes. For most of the behavioral tasks, software-based analyses were used to score mice performance with minimum human interference.

qPCR and Western blot

For real-time quantitative PCR (qPCR), brain tissues were homogenized in Trizol and total RNA was extracted using the Aurum Total RNA kit for fatty and fibrous tissue (Bio-Rad, Hercules, CA, USA). qPCR were performed as previously described (Martins-Silva et al., 2011). Primer sequences: STIP1-F, 5'-GCCAAGAAAGGAGACTACCAG-3'; STIP1-R, 5'-TCATAGGTTCTGTTGGCTTCC-3'; Hsp90-F, 5'-CCACCCTGCTCTGTACTACT-3'; Hsp90-R, 5'-CCAGGGCATCTGAAGCATT-3'; Hsp70-R, 5'-ACCTTGACAGTAATCGGTGC-3'; Hsp70-F, 5'-CTCCCGGTGTGGTCTAGAAA-3'; PRP-F, 5'-GAACCATTTCACCGAGCTG-3'; PRP-R, 5'-CATAGTCACAAAGAGGGCCAG-3'; Actin-F, 5'-TGGAATCCTGTGGCATCCATGA-3'; and Actin-R, 5'-AATGCCTGGGTACATGGTGGTA-3'. Immunoblot analysis was carried out as described previously (Beraldo et al., 2013). The antibodies used were anti-STIP1 (1:5000, in-house antibody generated by Bethyl Laboratories Montgomery, USA using recombinant STIP1) (Beraldo et al., 2013), anti-Hsp90 (1:1000), anti-Hsp70 (1:1000), anti-Hsp90 α (1:1000), anti Hsp90 β (1:1000) (Cell Signaling, Danvers, USA) and anti-PrP 8H4 (1:2000) (Abcam, Cambridge, UK).

Locomotor activity

Mice were acclimated to the testing room for 30 min prior to beginning the test; locomotor activity was automatically recorded (Omnitech Electronics Inc., Columbus, USA). Mice were placed in the center of the apparatus and locomotor activity was measured at 5 min intervals for 1 h as described previously (Martyn et al., 2012).

Elevated plus maze

To access anxiety-like behavior, mice were acclimated to the testing room for 30 min prior to beginning the test and then placed in the center of the

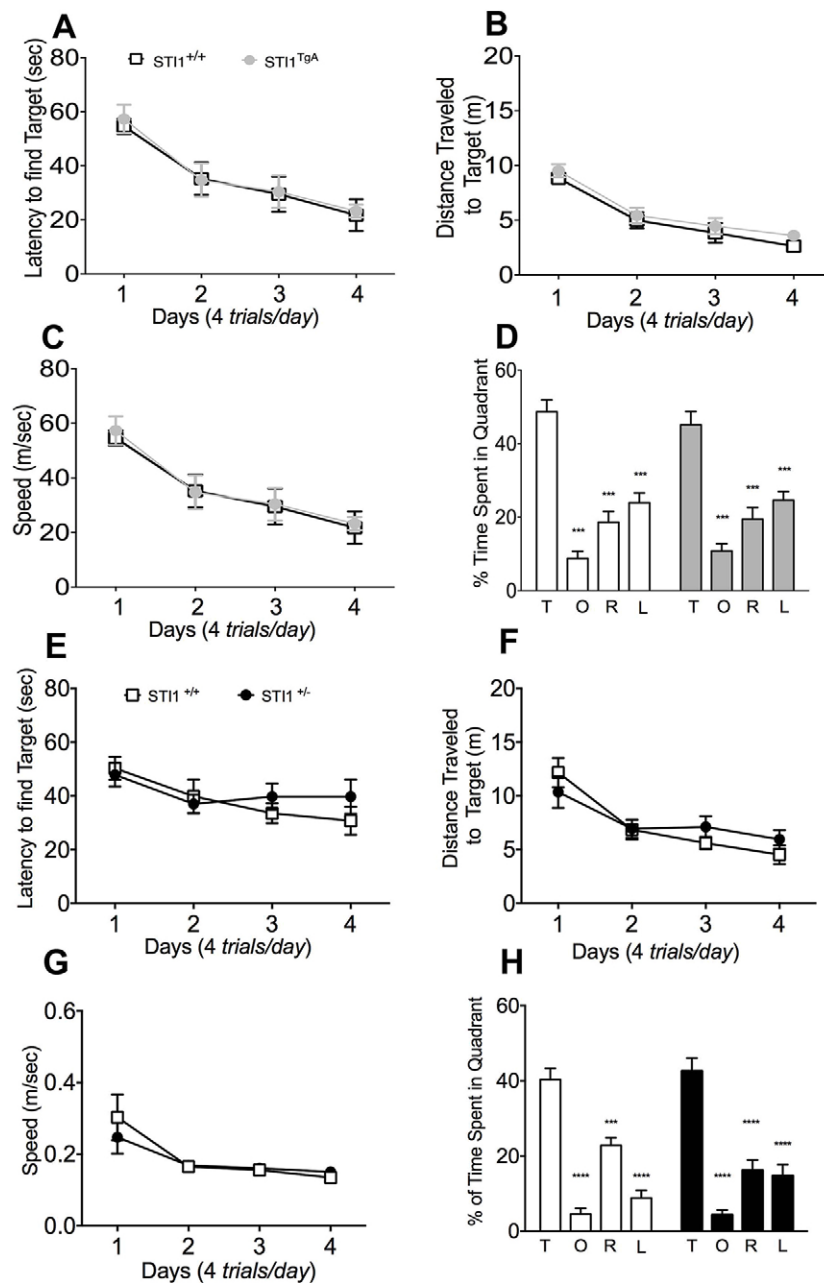


Fig. 5. Spatial memory in $ST11^{TGA}$ and $ST11^{-/-}$ mice. For the tests, $n=14$ $ST11^{+/+}$ and 14 $ST11^{TGA}$ mice were used to test spatial memory in $ST11^{TGA}$ mice and $n=11$ $ST11^{+/+}$ and 11 $ST11^{-/-}$ for $ST11^{-/-}$ mice. (A) Latency to find the platform. (B) Distance traveled. (C) Speed for $ST11^{TGA}$ mice. (D) Percentage time spent by $ST11^{TGA}$ mice and controls in target quadrant (T) and in opposite (O), right (R) and left (L) quadrants was measured on day 5 in a 60 s probe trial with the platform removed. (E) Latency to find the platform. (F) Distance traveled. (G) Speed for $ST11^{-/-}$ mice. (H) Percentage time spent by $ST11^{-/-}$ mice and controls in each quadrant was measured on day 5 in a 60 s probe trial with the platform removed. Results are presented as means $\pm$ s.e.m.; data were analyzed and compared by two-way ANOVA: *** $P<0.001$ and **** $P<0.0001$ compared with time spent in target quadrant.

elevated plus maze (Med Associates Inc., St Albans, USA). The activity was recorded and videos were analyzed using ANY-maze software (Stoelting Co., USA) to determine the amount of time spent in the closed and open sections of the maze.

Forced swimming test

Depressive-like behavior was assessed by a forced swim test (FST) as described previously (Martyn et al., 2012). Briefly, mice were placed in a 2 l beaker containing 1.7 l of water at 25–27°C for 6 min. Experimental sessions were recorded and immobility time was evaluated using ANY-Maze Software (Stoelting Co., USA). Data obtained from the last 4 min of testing were used for the analysis.

Morris water maze

The spatial version of Morris water maze (MWM) was conducted as described previously (Kolitsnyk et al., 2013; Martyn et al., 2012; Vorhees and Williams, 2006). Briefly, the task was performed in a 1.5-m diameter/1-m deep pool filled with water at 25°C. Spatial cues, 40×40 cm boards containing

black symbols (vertical and horizontal stripes, triangles, squares and circles), were placed on the walls distributed around the pool and the platform was submerged 1 cm below the surface of the water. Mice were submitted to four training trials a day (90 s each) for four consecutive days with a 15 min intertrial interval. On day 5, memory was assessed by a single 60 s trial on which the platform was removed and the time spent in the target quadrant was evaluated. All the experimental sessions were recorded and analyzed using the ANY-Maze Software.

Five-choice serial reaction time task

The five-choice serial reaction time task (5-CSRTT) was used to evaluate attention in mice as described previously (Kolitsnyk et al., 2013; Romberg et al., 2011). Mice were trained in the 5-CSRTT in automated Bussey-SaksidaTouch screen systems (Campden Instruments Limited, Loughborough, EN) and the data collected using ABET II Touch software V.2.18 (Lafayette Instruments, Lafayette, USA). Mice were submitted to a pre-training program, which consisted of first habituating the mouse to the testing chamber with the lights off for 10 min. The next day, the mouse was

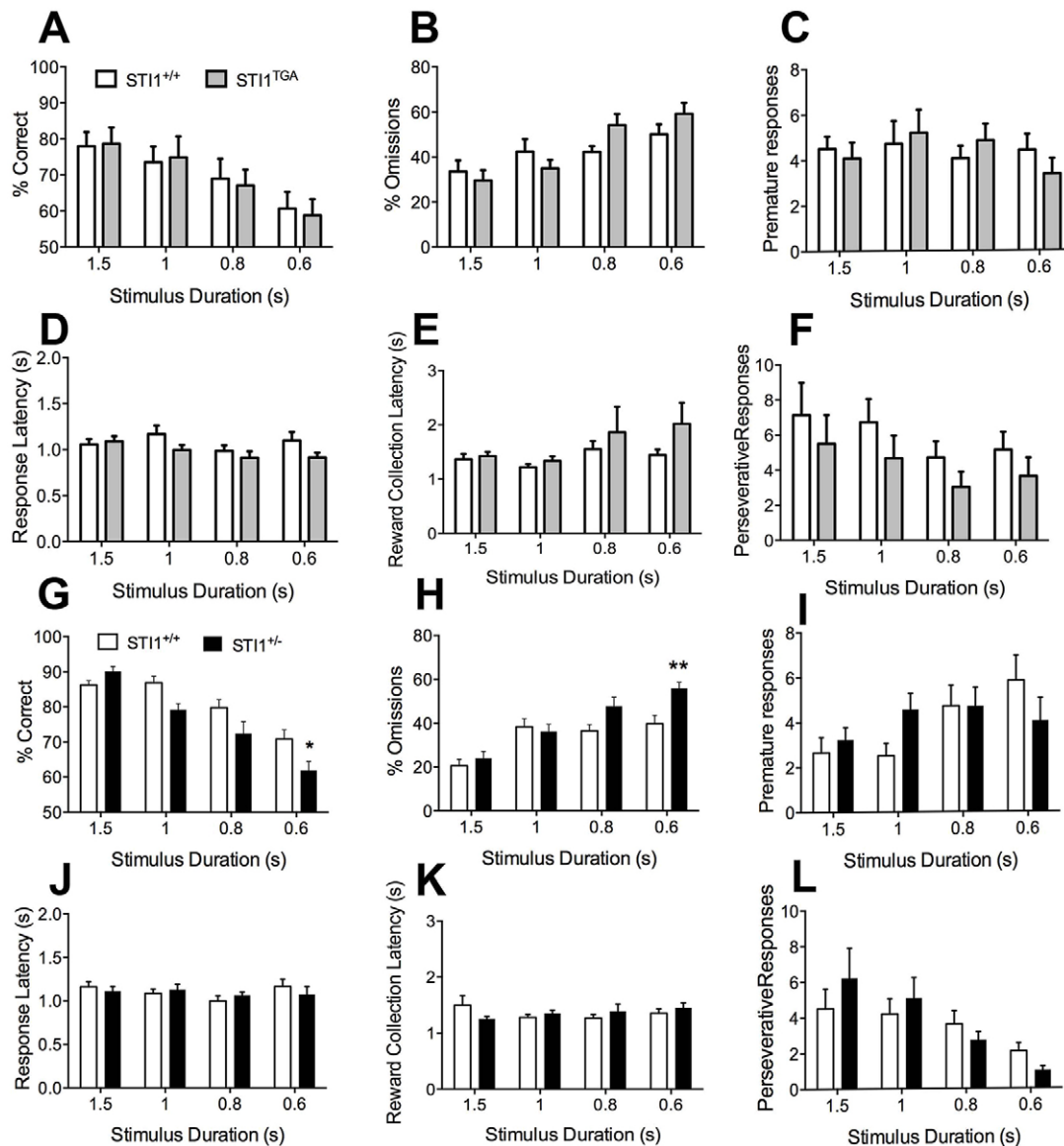


Fig. 6. Five-choice serial reaction time task used to measure attention in *STII*^{TGA} and *STII*^{-/-}. For the tests, $n=10$ *STII*^{+/+} and 10 *STII*^{TGA} mice were used to test attention in *STII*^{TGA} mice and $n=13$ *STII*^{+/+} and 13 *STII*^{-/-} for *STII*^{-/-} mice. (A) Accuracy during probe trial sessions. (B) Rate of omission. (C) Premature responses. (D) Response latency. (E) Reward collection latency. (F) Perseverative responses for *STII*^{TGA} mice. (G) Accuracy during probe trial sessions. (H) Rate of omission. (I) Premature responses. (J) Response latency. (K) Reward collection latency. (L) Perseverative response for *STII*^{-/-} mice. Results are presented as means $\pm$ s.e.m.; data were analyzed and compared by RM-ANOVA; * $P<0.05$, ** $P<0.001$ compared with control.

put in the chamber with the lights off for 20 min. After two days of habituation with no reward been offered, the reward tray was primed with 11% fat strawberry milkshake (Nielson - Saputo Dairy Products) and a tone was played when the mouse entered the reward tray. This was repeated for the next 2 days for 40 min sessions. Whenever the mouse returned to the reward tray, the reward was offered and paired with a tone (phase I). The following training phase consisted in pairing the reward with the presentation of a random stimulus (flash of light in one of the five windows), which is removed after 30 s. At this phase, if the mouse touched the screen when the stimulus was displayed, it received a reward. This cycle was repeated until the mouse completed 30 trials or 60 min timeout (phase II). At phase III of the training, the stimulus was displayed randomly in one of the five windows. The mouse had to touch the window where the stimulus was displayed to receive the reward paired with a tone. Similar to phase II, this cycle was repeated until the mouse completed 30 trials or 60 min timeout. The next step (phase IV) was identical to phase III except by the fact that the mouse had to poke its nose into the reward trail to initiate the task. This process was repeated in the last phase of the pre-training (phase V); however, if the mouse

touched an incorrect screen, it received a 5 s timeout and the light in the chamber was turned on. After the mouse had finished pre-training and reached criterion at 4 s and 2 s stimulus duration (80% accuracy, 20% omission for three consecutive days), mice were probed for attention deficits following probe trial schedules: each mouse was tested over two sessions at 1.5, 1.0, 0.8 and 0.6 s stimulus duration (the order of the probe trial sessions was randomized and the groups counterbalanced). Between each different stimulus duration, each mouse was returned to a 2 s stimulus for two consecutive sessions. Number of trials to criterion, accuracy, omission, reward collection latency and perseverative response were analyzed.

Metabolic assessments

Oxygen consumption, carbon dioxide production, respiratory exchange ratio (RER), carbon dioxide production, water and food intake and physical activity were simultaneously measured for adult *STII*^{+/+} and *STII*^{-/-} mice by using the Comprehensive Lab Animal Monitoring System (CLAMS) interfaced with Oxymax Software (Columbus Instruments, Columbus, OH, USA) as previously described in detail (Guzman et al., 2013; Kolisnyk et al.,

2013). Briefly, mice were individually housed in the metabolic chambers with *ad libitum* access to water and food. Following a 16-h habituation period, all measurements were obtained every 10 min for 24 h (12 h light/12 h dark).

Marble burying task

A marble burying task was used to assess repetitive and anxiety-like behavior as previously described (Deacon, 2006).

Assessment of self-grooming

Self-grooming was assessed to evaluate repetitive behavior, as previously described (McFarlane et al., 2008). Briefly, each mouse was placed individually in a clean, empty, cage and given a 10 min habituation period, after which the mice were filmed for another 10 min. Cumulative time spent grooming and number of grooming bouts were counted by an experimenter blinded to the genotypes of the mice.

Statistical analyses

Data are presented as mean±s.e.m. Statistical analyses were performed using SigmaStat 3.5 software. Student's *t*-test was used to compare two experimental groups and for comparison of several experimental groups, two-way ANOVA or two-way repeated-measures ANOVA were used as required. Tukey's post hoc comparison was used when required.

Competing interests

The authors declare no competing or financial interests.

Author contributions

F.H.B., M.A.M.P., V.F.P., and R.G. conceived and designed experiments. F.H.B., A.T., B.K., P.H.H., R.G., X.D.J., A.C.M., J.F., D.F.G., M.F.C. and T.M. performed the experiments. V.R.M. contributed with specific reagents. F.H.B., A.T., B.K., A.C.M., V.F.P., R.G., V.R.M. and M.A.M.P. analyzed the data. F.H.B., V.F.P. and M.A.M.P. wrote the paper.

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Appendix C

Regulation of cognitive processing by hippocampal cholinergic tone

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Contributions to publication: BK performed working memory experiments with the VACHTNkx2.1-Cre-flox/flox animals as well as the PAL experiments in the AAV8-Cre injected animals.

ORIGINAL ARTICLE

Regulation of Cognitive Processing by Hippocampal Cholinergic Tone

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Abstract

Cholinergic dysfunction has been associated with cognitive abnormalities in a variety of neurodegenerative and neuropsychiatric diseases. Here we tested how information processing is regulated by cholinergic tone in genetically modified mice targeting the vesicular acetylcholine transporter (VACHT), a protein required for acetylcholine release. We measured long-term potentiation of Schaffer collateral-CA1 synapses *in vivo* and assessed information processing by using a mouse touchscreen version of paired associates learning task (PAL). Acquisition of information in the mouse PAL task correlated to levels of hippocampal VACHT, suggesting a critical role for cholinergic tone. Accordingly, synaptic plasticity in the hippocampus *in vivo* was disturbed, but not completely abolished, by decreased hippocampal cholinergic signaling. Disrupted forebrain cholinergic signaling also affected working memory, a result reproduced by selectively decreasing VACHT in the hippocampus. In contrast, spatial memory was relatively preserved, whereas reversal spatial memory was sensitive to decreased hippocampal cholinergic signaling. This work provides a refined roadmap of how synaptically secreted acetylcholine influences distinct behaviors and suggests that distinct forms of cognitive processing may be regulated in different ways by cholinergic activity.

Key words: Alzheimer's disease, long-term potentiation, Morris water maze, paired associates learning, vesicular acetylcholine transporter, working memory

Introduction

Basal forebrain cholinergic neurons provide input to the entire cortex and hippocampus. In particular, the hippocampus receives most of its cholinergic innervation from neurons in the medial septal nucleus (MS) and vertical limb of the diagonal band of Broca (vDB), whereas the cerebral cortex and the amygdala receive cholinergic inputs from neurons located in the nucleus basalis of Meynert (NBM) (Mesulam et al. 1992; Kitt et al. 1994). Abnormalities in forebrain cholinergic nuclei have been implicated in several

cognitive disorders (Bartus 2000; Mesulam 2004), including Alzheimer's disease (AD; Grothe, Schuster, et al. 2014; Teipel et al. 2014). Moreover, cumulative use of drugs with anticholinergic activity is associated with increased risk for dementia and AD (Gray et al. 2015). However, the relationship between cholinergic dysfunction and maintenance of cognitive abilities in these diseases is not fully understood, due to concomitant pathologies that may contribute to cognitive abnormalities (Mesulam 2013).

Cholinergic signaling is involved in the regulation of hippocampal synaptic transmission and plasticity (Ji et al. 2001;

Leung et al. 2003; Seeger et al. 2004; Ge and Dani 2005; Gu and Yakel 2011). Septal cholinergic activation, either by electrical stimulation or by optogenetics, allows the expression of distinct time-dependent forms of hippocampal plasticity (Gu and Yakel 2011). Pharmacological (Decker and Majchrzak 1992; Anagnostaras et al. 1999; Gale et al. 2001; Wallenstein and Vago 2001; Chudasama et al. 2004; Pichat et al. 2007; Timmermann et al. 2007; Ragozzino et al. 2012) and genetic studies (Anagnostaras et al. 2003; Seeger et al. 2004; Poulin et al. 2010) have shown that modulation of cholinergic receptors influence learning and memory processes. Indeed, both nicotinic receptors (nAChRs) and muscarinic receptors (mAChRs) have been linked with various forms of plasticity (Vidal and Changeux 1993; Gray et al. 1996; Ji and Dani 2000; Seeger et al. 2004; Gautam et al. 2006; Giessel and Sabatini 2010; Zheng et al. 2012). For example, M1 knockout mice exhibit selective cognitive impairments in tasks requiring interactions between the hippocampus and cortex (Anagnostaras et al. 2003), while M2 knockout mice display impairments in working memory, cognitive flexibility, and hippocampal plasticity (Seeger et al. 2004). Moreover, recent evidence shows that activation of M1 mAChRs induces long-term potentiation (LTP), suggesting that M1 mAChRs could play a role in regulating hippocampal plasticity (Dennis et al. 2015). Furthermore, the nAChR $\beta 2$ -subunit knockout mice are impaired in learning the MWM, suggesting that the $\beta 2$ -subunit may mediate effects of ACh on learning and memory (Zoli et al. 1999). However, long-term changes in cholinergic activity, as observed in a number of neurodegenerative diseases, are more complex to model using specific receptor knockouts, given the plethora of subtypes of muscarinic and nicotinic receptors.

One widespread alternative to mimic cholinergic dysfunction is the selective elimination of these neurons using toxins in rodents (Baxter and Bucci 2013; Prado et al. 2013). It is somewhat controversial whether selective 192 IgG-saporin lesion of septohippocampal cholinergic neurons can lead to significant impairments in hippocampal-dependent learning and memory tasks in rodents, with some authors finding little effect (Berger-Sweeney et al. 1994; Baxter and Gallagher 1996; Pizzo et al. 2002; Frick et al. 2004; Parent and Baxter 2004), whereas others find a myriad of deficits (Walsh et al. 1996; Janis et al. 1998; Gil-Bea et al. 2011). In addition, cholinergic neurons have been shown to contain more than one class of neurotransmitter transporters and secrete 2 neurotransmitters (Gras et al. 2008; El Mestikawy et al. 2011; Guzman et al. 2011; Prado et al. 2013; Nelson et al. 2014; Saunders et al. 2015). Therefore, it is difficult to interpret results with toxin lesions for specific contributions of neurotransmitters in neurons that release 2 chemical messengers. Indeed, recent work has shown that some basal forebrain cholinergic neurons can also secrete GABA which acts as a neurotransmitter in the cortex (Saunders et al. 2015).

Genetic targeting of either the vesicular acetylcholine transporter (VACHT; Guzman et al. 2011; Martyn et al. 2012) or choline acetyltransferase (ChAT; Patel et al. 2012) using the Cre/lox system has provided a way for investigating specific contributions of ACh when there is co-transmission (Prado et al. 2013). Decreased VACHT levels severely compromise packaging of acetylcholine (ACh) into synaptic vesicles and thus reduce ACh release by nerve terminals (Prado et al. 2006; de Castro, De Jaeger, et al. 2009). Conversely, overexpression of VACHT enhances ACh secretion proportionally (Song et al. 1997; Kolisnyk, Guzman, et al. 2013).

The recent development of automated touchscreen behavioral testing for rodents has greatly improved mouse behavioral assessment. Touchscreen tasks were designed using almost identical paradigms and methodologies used in humans,

facilitating translational studies between species (Morton et al. 2006; Talpos et al. 2009, 2010; Romberg et al. 2011; Mar et al. 2013). The paired associates learning (PAL) test has been shown to efficiently detect cognitive alterations that are consistently observed in AD (Swainson et al. 2001; Blackwell et al. 2004; de Rover et al. 2011) and schizophrenia (Wood et al. 2002; Barnett et al. 2005). In dementia, PAL has been shown to differentiate between mild cognitive impairment and AD (Blackwell et al. 2004). Here we investigated cognitive performance in mice with deletion of VACHT, a protein required for synaptic release of ACh, in either forebrain cholinergic neurons or selectively in septohippocampal cholinergic neurons. Our experiments reveal that dysfunction in hippocampal cholinergic activity influences synaptic plasticity in vivo and disturbs performance in PAL and working memory, whereas spatial navigation seems relatively preserved.

Material and Methods

Animals

Generation of VACHT^{fllox/fllox} mice was previously described (Martins-Silva et al. 2011). VACHT^{fllox/fllox} mice (mixed C57BL/6J $\times$ 129/SvEv background, backcrossed to C57BL/6J for 5 generations) were crossed to VACHT^{Nkx2.1-Cre-fllox/fllox} mice so that offspring from this mating provided control and test littermates. VACHT^{Nkx2.1-Cre-fllox/fllox} mice were generated by crossing VACHT^{fllox/fllox} with the Nkx2.1-Cre mouse line (C57BL/6J-Tg(Nkx2-1-cre)2Sand/J), purchased from The Jackson Laboratory (JAX stock no. 008661). This line has been previously used to eliminate ChAT from forebrain neurons (Patel et al. 2012). Unless otherwise stated, all control mice used for behavioral studies were VACHT^{fllox/fllox} littermates. The reporter mouse line Nkx2.1^(td-Tomato) was generated by crossing B6.Cg-Gt(ROSA)26Sor^{tm9(CAG-tdTomato)Hze/J} mice, purchased from The Jackson Laboratory (JAX stock no. 007909) with the Nkx2.1-Cre mouse line (JAX stock no. 008661).

Animals were housed in groups of 3 per cage without environmental enrichment in a temperature controlled room (12:12 light to dark cycles), and food and water were provided ad libitum for most experiments. Animals that underwent touchscreen testing were housed in pairs; food restricted to no more than 85% of their original weight, and they were maintained at the target weight for the duration of behavioral testing. Male mice 3 months old were used for behavioral studies. We followed the ARRIVE guidelines (Kilkenny et al. 2010); hence, mice were randomized for behavioral tests and the experimenter was blind to the genotype. All procedures were performed in accordance with the Canadian Council of Animal Care guidelines at the University of Western Ontario with an approved animal protocol (2008-127).

Immunofluorescence Microscopy

Mice were anesthetized with ketamine (100 mg/kg) and xylazine (25 mg/kg) in 0.9% sodium chloride, and then sacrificed by transcardial perfusion: phosphate-buffered saline (PBS, pH = 7.4) for 3 min and 4% paraformaldehyde for 5 min. Brains were harvested and placed in 4% paraformaldehyde in 1 $\times$ PBS at 4 $^{\circ}$ C for 4 h; they were kept at 4 $^{\circ}$ C until sliced using a vibratome. Brain sections (40 μ m) were prepared and free-floating sections in 1 $\times$ PBS (1 per well in a 24-well plate) were permeabilized with 0.4% Triton X-100 in 1 $\times$ PBS for 1 h. Non-specific epitopes were blocked using a solution of 1 $\times$ PBS/0.4% Triton X-100 containing 0.1% glycine (wt/vol), 0.1% lysine (wt/vol), 1% BSA (wt/vol), and 1% normal donkey serum (wt/vol). The primary antibodies used were anti-VACHT (catalog no. 139103; Synaptic Systems), anti-ChAT

(1:200) (catalog no. AB144P, Merck Millipore), and anti-Choline Transporter (CHT1; 1:200), which was kindly donated by Dr R. Jane Rylett, University of Western Ontario, London, Ontario. The primary antibody was incubated in blocking buffer overnight at 4 °C. Sections were then washed 5 times in 1× PBS/0.4% Triton X-100 (10 min each). Hoechst 3342 (Life Technologies, Gibco, Carlsbad, CA, USA) (2–5 µg/mL) and secondary antibodies (1:500; anti-488, catalog no. A-11034, ThermoFisher; 1:500 anti-633, catalog no. A-21082, ThermoFisher) were diluted in blocking buffer and slices were incubated for 1 h at RT. Sections were visualized by Zeiss LSM 510Meta (Carl Zeiss, Oberkochen, Germany) confocal system (63× objective, 488-nm Ar laser and 633-nm HeNe laser were used for excitation of fluorophores).

Western Blotting

Immunoblotting was performed as previously described (Martins-Silva et al. 2011; Kolisnyk, Al-Onaizi, et al. 2013; Kolisnyk, Guzman, et al. 2013). Antibodies used were anti-VACHT (catalog no. 139103; Synaptic Systems) and anti-Synaptophysin (catalog no. S5768; Sigma-Aldrich).

Training on the PAL Task

Prior to training, both groups of mice (3 months old) were food restricted until they reached approximately 85% of their original weight. Training of the animals to the PAL task was previously described (Talpos et al. 2009). Briefly, the training phase for the mice in the touchscreen chambers involved a habituation session, where they were placed in the chambers with the lights off for 20 min to habituate to the environment for 2 days. Next, mice were put in the chamber with the same parameters as in the habituation phase, but this time a 150 µL reward (strawberry milkshake; Saputo Dairy Products, Canada) was introduced in the reward receptacle. Every time the mouse attended to the reward in the reward receptacle, a tone was played. This 40 min training session was done for the next 2 days until mice completed 36 trials in 60 min (Habituation; Phase 1).

The mice were then trained to associate the reward with a 30 s presentation of training stimuli, which varied in brightness, shape, and pattern, on one of the 3 screens (Initial touch training; Phase 2). Mice were required to touch any of the screens whenever the stimulus was presented to receive the reward, which was paired with a tone. A new trial was automatically initiated once the mice collected the reward. This was done until the mice completed 36 trials in 60 min for 1 day. Next, mice are required to touch the stimulus that is displayed randomly in one of the 3 windows to receive the reward (must touch stimuli training; Phase 3). Mice are only moved to next training after completing 36 trials in 60 min for 1 day. In the next training phase, food is delivered and tray light is turned on. The mouse must nose poke and exit the reward tray before a stimulus is displayed randomly on the screen (Must initiate; Phase 4). This was done until mice completed 36 trials in 60 min for 1 day. Next, animals go to the last phase of the training program required for the PAL task. This training phase is referred to as “punish incorrect” (Phase 5). This phase is similar to the previous one, but if the mouse touched the incorrect screen, that is, one of the blank screens, it was presented with a 5-s time-out. This time-out was accompanied by the presentation of a bright light in the chamber. Criterion to successfully proceed from this training phase was 23 correct responses out of 30 trials in 60 min for 2 consecutive days. Next, both experimental groups were subjected to acquisition training, where 2 stimuli are displayed at the same

time during a trial. One will be in the correct location (S+) and the other will be in the incorrect location (S–). Mice were required to touch the correct stimulus (S+) presented on one of the 3 screens to complete a trial and receive the reward. In this acquisition phase, mice were on an unpunished version in which touching the S– was ignored. A completion of a trial was only considered when the mouse touches the S+. Criterion for this training phase is completion of 36 trials in 1 session (1 day). All mice from both experimental groups were able to reach criterion in acquisition training.

PAL Task

After successfully completing the training phase, the mice were placed on a PAL task (dPAL), which involves a different stimulus being presented in each trial. A trial starts in dPAL when the mouse initiates it by touching the food receptacle, which triggers the display of both S+ and S– on the screen. S+ refers to when the stimulus is in the correct location, and S– refers to when the stimulus is in the incorrect location. There were 6 possible trial types and 3 different stimuli were presented (flower, plane, and spider). Within trials, an S+ is the flower presented in the left window, the plane in the middle window, or the spider in the right window. Thus, mice are required to learn to associate a stimulus to its correct location. A response by touching the S– resulted in a 10 s time-out and the chamber light was activated for 10 s, acting as an indication for an incorrect response for the mouse. After 10 s, the next initiation by the mouse was considered a correction error trial, where the same S+ and S– were presented as for the unsuccessful previous trial. The number of correction trials was not counted toward the total number of trials performed per session. An S+ response, however, led to a tone, as well as the reward being dispensed in the receptacle.

Electrophysiology

Animals were anesthetized with urethane (1 g/kg i.p.) and placed in a stereotaxic apparatus. Atropine methyl nitrate was administered (5 mg/kg i.p.) to reduce airway secretions during stereotaxic surgery. Animal body temperature was monitored between 36.5 °C and 37 °C using a feedback controlled rectal thermometer and heating pad. Stimulating electrodes were placed into stratum radiatum at P 1.8, L 2.3 or P 2.5, L2.4 (Franklin and Paxinos 2008) to stimulate Schaeffer collaterals projecting from CA3 to CA1 (Hutchison et al. 2009). A silicon probe, with 16 electrodes separated by 50 µm on a vertical shank, was placed in area CA1 at P 2.2, L 1.8. Laminar profiles of the average (4 sweeps) field excitatory postsynaptic potentials evoked by single pulse stimulation of the Schaeffer collaterals at 1.5–2 × threshold stimulus intensity. Current-source density analysis using 100 µm step size was used to determine current sources and sinks. The maximal slope (of 1 ms duration) during the rising phase of the excitatory sink, at its maximum in CA1 stratum radiatum, was used for LTP assessment. After a stable baseline of the excitatory sink slope was established for 30 min (coefficient of variation [SEM/mean] of the sink slopes <0.05), a high-frequency tetanus (100 Hz for 1 s) was delivered at 2–3 times the threshold intensity, and the response was measured for 120 min after the tetanus. For each mouse, the slope of the excitatory sink was normalized by the average value of the baseline, and LTP across mice was averaged and reported as a multiple of the baseline slope.

Rotarod and Neuromuscular Tests

The rotarod task was conducted as previously described (Prado et al. 2006; de Castro, Pereira, et al. 2009). Forelimb and hind

limb grip strength was assessed using a previously described protocol (Prado et al. 2006). The hang-wire experiments were performed as described (Sango et al. 1996).

Morris Water Maze

The spatial version of the MWM was performed as previously described (Vorhees and Williams 2006; Martyn et al. 2012; Kolisnyk, Guzman, et al. 2013). Testing was performed in a 1.5-m diameter pool with 25 °C water. A hidden platform was submerged in a constant location 1 cm below the surface of the water in one of the 4 arbitrarily defined quadrants, and spatial cues were distributed around the pool. Briefly, mice were given four 90-s trials for the duration of 4 days to find the hidden platform, with an ITI of 15 min. The animals were introduced to the pool from different locations within the pool for each trial. Mice that did not find the platform within the 90 s were gently guided to the platform. On the fifth day, spatial memory recall was tested by a 60-s probe trial, where the hidden platform is removed and the amount of time the animal spends in the target quadrant is calculated. To test reversal learning, the hidden platform was relocated to the opposite quadrant, where the animals were given four 90-s trials for 4 days. On the fifth day, the animals were given a 60-s probe trial. Data were analyzed using ANY-Maze video tracking software (Stoelting Co.).

Two-Trial Morris Water Maze

A task used to assess working memory was the 2-trial variation of the MWM. The task was carried out using previously described protocols (Vorhees and Williams 2006; Kolisnyk, Guzman, et al. 2013). The mice were trained on the task over the course of 5 days. During the training period, the mouse was first given a 90-s trial with a 15 s inter-trial interval. Next, the mouse was given a second trial with the same platform location and starting point; this was repeated 3 additional times. After completing the training phase, the mouse was first given a 90 s trial with a 15 s inter-trial interval. The mouse was then given a second trial with identical platform location and starting point. This was repeated with 4 unique starting location/platform location combinations a day. Mean latency and distance savings ratios were then calculated as previously described (Kolisnyk, Guzman, et al. 2013). Sessions were recorded for both tests and were analyzed using the ANY-Maze video tracking software (Stoelting Co.).

Spontaneous Alterations Y-maze

To assess working memory in the mice, we used the spontaneous alternations Y-maze as previously described (Kolisnyk, Guzman, et al. 2013). Briefly, mice were placed in a symmetrical plastic Y-maze apparatus, and both the number and order of arm entries were recorded. A spontaneous alternation was defined as when the mouse visited all 3 of the arms in a row, without having revisited a previous arm of the maze. Sessions were recorded and analyzed using the ANY-Maze Software.

Stereotaxic Injections of Adeno-Associated Virus

To obtain selective deletion of VACHT in the medial septum, mice were anesthetized with ketamine (100 mg/kg) and xylazine (25 mg/kg) in 0.9% sodium chloride, and 1 μ L (titer of $\sim 10^{13}$ GC/mL) of adeno-associated virus (AAV)8-GFP-Cre- or control virus (AAV8-GFP, Vector BioLabs, Eagleville, PA, USA) was injected into the medial septum/vertical limb of the diagonal band (0.98 AP, 0.1 LL and 4.1 DV) of VACHT^{fllox/flox} mice. The injecting

micropipette was inserted and left for 2 min to stabilize. After stabilization, a 0.2 μ L/min infusion was performed using a micro-pump followed by a 30 min rest period to allow local diffusion of the virus and avoid virus efflux. The micropipette was then slowly removed and the scalp sutured. A recovery period of 4 weeks was given before behavioral testing to allow transgene expression.

Statistical Analysis

All data are expressed as mean $\pm$ SEM. Sigstat 3.5 software was used for statistical analysis. Comparison between 2 experimental groups was done with Student's t-test. When several experimental groups or treatments were analyzed, 2-way analysis of variance (ANOVA) or 2-way ANOVA with repeated measures (RM) were used as required. When appropriate, a Bonferroni post hoc analysis test was used.

Results

Deletion of VACHT in Forebrain Projection Neurons

Nkx2.1-driven Cre is expressed in forebrain cholinergic neurons as assessed using a reporter mouse line (see [Supplementary Fig. 1A](#) and [Table 1](#)). Immunoblot analysis shows that VACHT levels in the prefrontal cortex ($t_{(4)} = 6.162$, $P = 0.0035$), hippocampus ($t_{(4)} = 4.461$, $P = 0.0097$), and striatum ($t_{(4)} = 8.625$, $P = 0.0010$) were severely diminished in VACHT^{Nkx2.1-Cre-flox/flox} mice (see [Supplementary Fig. 1B–D](#)). In contrast, VACHT levels remained unchanged in the brainstem of VACHT^{Nkx2.1-Cre-flox/flox} compared with controls ($t_{(4)} = 1.040$, $P = 0.3571$, see [Supplementary Fig. 1E](#)). Moreover, immunofluorescence imaging indicated decreased VACHT immunoreactivity in the hippocampus of VACHT^{Nkx2.1-Cre-flox/flox} mice compared with controls (Fig. 1A,B). Importantly, these mice presented no neuromuscular deficits (see [Supplementary Fig. 2A–C](#)). We have previously shown that reduced VACHT levels proportionally decrease the release of ACh in vivo and in vitro (Prado et al. 2006; Guzman et al. 2011; Kolisnyk, Al-Onaizi, et al. 2013; Kolisnyk, Guzman, et al. 2013).

Forebrain VACHT is Required for Performance in the PAL Task

We tested VACHT^{Nkx2.1-Cre-flox/flox} mice on the PAL task, which requires sophisticated processing of information for proper association of images with specific locations. VACHT^{Nkx2.1-Cre-flox/flox} mice and their matched controls were assessed on the dPAL task using an automated touchscreen system (Fig. 1C and see [Supplementary Videos 3 and 4](#)). Prior to being subjected to the PAL task, both experimental groups are trained on a different training sessions (initial touch, must touch stimuli, must initiate, and punish incorrect) to learn how to operate the touchscreen, which includes learning to touch the screen when a stimulus is presented and initiating the task by inserting the head into the reward chamber. In the “punish incorrect” training, when only one stimulus is presented randomly in one of the 3 screens, mice are taught to touch the screen that shows the stimulus. Mice from both experimental groups were able to reach criterion in this phase of the training and no differences were observed between the 2 genotypes ($t_{(12)} = 0.0749$) (Fig. 1D), indicating that VACHT-deficient mice are able to learn that they need to touch the screen when an image is shown. Additionally it argues that VACHT-deficient mice do not present any major visual impairment. During the course of the 9 weeks that mice were tested on the dPAL task, we observed that control mice significantly improved their accuracy performance, while VACHT deletion

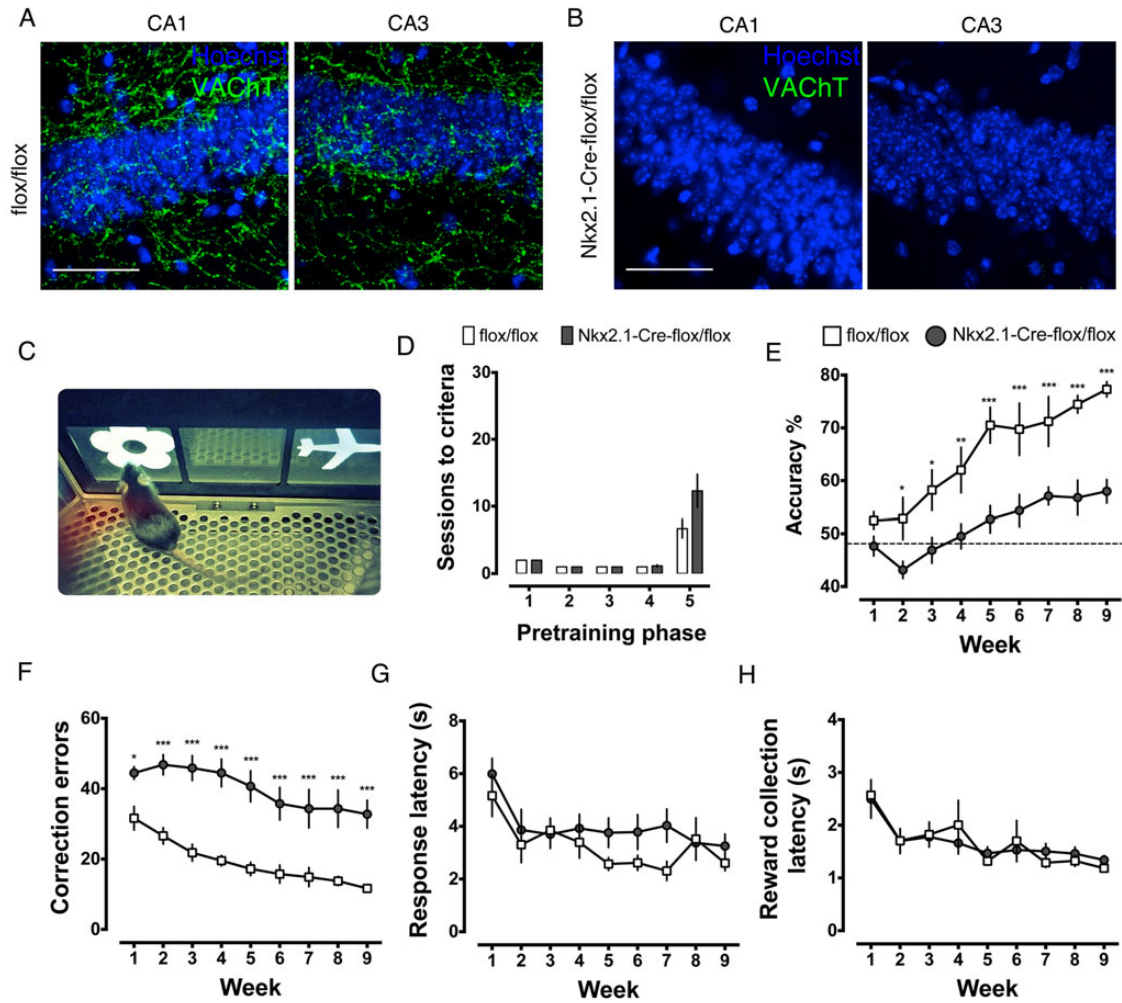


Figure 1. VACHT^{Nkx2.1-Cre-flox/flox} mice display impairments in the acquisition of dPAL. (A) Representative 3-dimensional reconstructed Z stack immunofluorescence images of VACHT (green) and Hoechst (blue) in the CA1 and CA3 regions of the hippocampus in VACHT^{flox/flox} ($n = 3$) and (B) VACHT^{Nkx2.1-Cre-flox/flox} mice ($n = 3$) (Scale bar = 100 μ m). (C) Image depicting a mouse performing the task, where the flower is shown as S+ and the airplane as S-. (D) Number of sessions required by both experimental groups to reach criterion during the operant conditioning, pretraining, and training phases. (E-H) Data for the acquisition of the dPAL task for VACHT^{flox/flox} ($n = 7$ clear squares) and VACHT^{Nkx2.1-Cre-flox/flox} ($n = 7$ dark circles) mice. Each week represents 5 testing sessions of 36 trials. (E) Mean accuracy; (F) Mean correction errors; (G) Response latency; (H) Reward collection latency (Data are mean $\pm$ SEM. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.0001$).

mutants did not (2-way RM ANOVA shows significant effect of weeks $F_{8,48} = 21.11$, $P < 0.0001$, an effect of genotype $F_{1,6} = 56.94$, $P = 0.0003$, and an interaction effect $F_{8,48} = 2.871$, $P = 0.0074$, Fig. 1E). VACHT^{flox/flox} mice (controls) were able to improve performance reaching $77 \pm 1\%$ accuracy by Week 9 (Fig. 1E). In contrast, peak accuracy performance of VACHT^{Nkx2.1-Cre-flox/flox} mice in the dPAL task during the same period was $58 \pm 2\%$ (Fig. 1E). Although VACHT^{Nkx2.1-Cre-flox/flox} mice were able to perform the 36 trials required in each 1-h session, they failed to associate the stimulus to its correct location. Their poorer performance was also reflected in the number of correction errors performed (Fig. 1F). VACHT^{Nkx2.1-Cre-flox/flox} mice failed to decrease the number of correction errors made over the course of 9 weeks, while control mice improved the number of correction errors performed during the course of the study (2-way RM ANOVA shows significant effect of weeks $F_{8,48} = 12.05$, $P < 0.0001$, an effect of genotype $F_{1,6} = 39.41$, $P = 0.0008$, and an interaction effect $F_{8,48} = 1.224$, $P = 0.0306$, Fig. 1F). Correct response latency was not different between the 2 groups over the course of 9 weeks (2-way RM ANOVA shows significant effect of weeks $F_{8,48} = 7.508$, $P < 0.0001$, no effect of genotype $F_{1,6} = 2.437$, $P = 0.1695$, and no interaction $F_{8,48} = 1.195$, $P = 0.3220$, Fig. 1G). Furthermore, VACHT^{Nkx2.1-Cre-flox/flox}

mice were no different from controls when the latency to collect the reward was measured, which indicated that motivation was not a factor in their poorer performance (2-way RM ANOVA shows a significant effect of weeks $F_{8,48} = 7.596$, $P < 0.0001$, no effect of genotype $F_{1,6} = 0.0001380$, $P = 0.7681$, and no interaction $F_{8,48} = 0.6061$, $P = 0.7681$ Fig. 1H). In summary, VACHT^{Nkx2.1-Cre-flox/flox} mice were able to learn that they had to touch the screen when the images were shown; however, they failed in making associations, that is, they were unable to assign each image to a specific position.

Hippocampal LTP is Disrupted in Forebrain-Specific VACHT Knockout Mice In Vivo

Formation of associations might depend on lasting increases in synaptic strength. To determine whether VACHT^{Nkx2.1-Cre-flox/flox} mice have intact synaptic plasticity, we examined LTP of the synapse of the Schaffer collaterals on hippocampal CA1 neurons in anaesthetized mice in vivo. VACHT^{Nkx2.1-Cre-flox/flox} mice showed decreased LTP which lasted about 90 min post-tetanus delivery while LTP in VACHT^{flox/flox} mice was maintained for 120 min (Fig. 2A,B). This indicated that the lack of cholinergic signaling disturbs synaptic plasticity in hippocampal CA1 area in vivo.

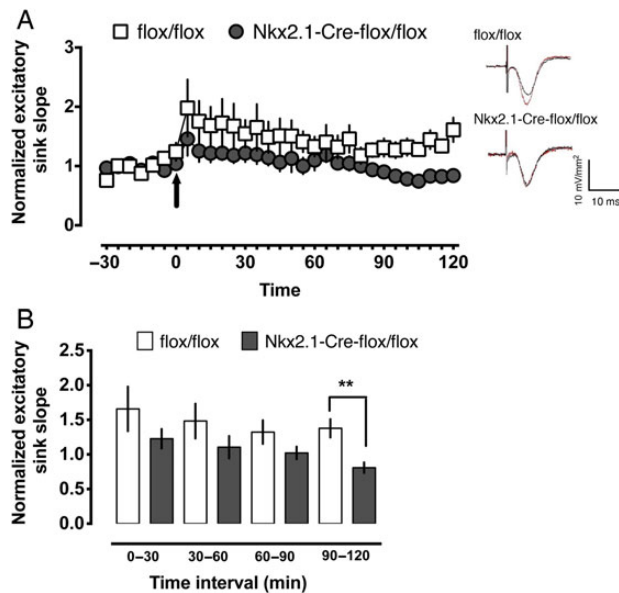


Figure 2. Hippocampal LTP is disrupted in forebrain-specific VACHT knockout mice in vivo. (A) Normalized slopes of the excitatory sink recorded at CA1 stratum radiatum (apical dendrites) of VACHT^{flox/flox} (clear squares, $n = 5$) and VACHT^{Nkx2.1-Cre-flox/flox} (dark circles, $n = 6$) mice. Baseline was monitored for 30 min prior to tetanus delivery ($t = 0$), and posttetanic response was monitored for 120 min. A 1-s 100 Hz train, delivered at 2–3 times the threshold intensity (arrow), induced higher and more prolonged potentiation in VACHT^{Nkx2.1-Cre-flox/flox} mice than VACHT^{flox/flox} controls. Insets show representative current sink time response taken at 80 min (red traces), overlaid on the pretetanus baseline response (black traces), from each genotype. (B) Normalized excitatory sink slope averaged across 30-min time intervals (mean $\pm$ SEM) in VACHT^{flox/flox} and VACHT^{Nkx2.1-Cre-flox/flox} mice, with significant difference between mouse groups at 90–120 min ($t_{(9)} = 3.911$, $P = 0.0036$).

To specifically evaluate the contribution of hippocampal cholinergic tone to PAL performance, we stereotactically injected AAV8-GFP-Cre or AAV8-GFP virus to the medial septum and vertical limb of the diagonal band (MS/VDB) of VACHT^{flox/flox} mice (AAV8-GFP-Cre $n = 13$; AAV8-GFP $n = 7$). Mice were trained on the dPAL task 1 month after viral injection. Following completion of the task, mice were sacrificed to evaluate VACHT protein levels. Given the length of the experiment (≈ 4 months), and the observation that viral injection was only partially effective to reduce hippocampal VACHT levels (see [Supplementary Fig. 6B](#)), we did not exclude any mouse from the analysis, even if viral mediated recombination was not effective to eliminate the transporter. Instead, we correlated VACHT levels in the hippocampus from both AAV8-GFP-Cre and AAV8-GFP to their performance on the PAL task.

Performance on the final week of the experiment was positively correlated to VACHT protein levels in terms of response accuracy (Pearson's $r = 0.5208$, $CI = 0.1015$ – 0.7829 , $P = 0.0186$, [Fig. 3A](#)) and negatively correlated to number of correction errors (Pearson's $r = -0.6518$, $CI = -0.8494$ to -0.2940 , $P = 0.0018$, [Fig. 3B](#)). We also evaluated the relationship between hippocampal VACHT protein levels to learning the PAL task. We calculated the rate of learning as the slope of the learning curve of both response accuracy and correction errors across all the weeks of the task. VACHT protein level was positively correlated to the rate of learning of response accuracy (Pearson's $r = 0.5053$, $CI = 0.08072$ – 0.7747 , $P = 0.0231$, [Fig. 3C](#)) and negatively correlated to the correction error rate of learning (Pearson's $r = -0.1799$, $CI = -0.7982$ to -0.1418 , $P = 0.0120$, [Fig. 3D](#)). Importantly, VACHT protein levels

did not correlate to mean response latency across the task (Pearson's $r = 0.1349$, $CI = -0.3273$ to 0.5450 , $P = 0.5708$, [Fig. 3E](#)) or mean reward collection latency across the task (Pearson's $r = -0.1799$, $CI = -0.5676$ to 0.2731 , $P = 0.4352$, [Fig. 3F](#)), suggesting that response patterns and motivation are unaltered by reduced VACHT levels. Taken together these results show that the less VACHT protein in the hippocampus the worse is the mouse performance in the dPAL task, indicating that dPAL learning is modulated by septohippocampal cholinergic signaling.

VACHT and Spatial Navigation

Given the strong deficit of association of the image with its correct location in the PAL task, it seemed of importance also to evaluate spatial memory in these mice. Spatial memory is widely used to assess information acquisition and storage in the hippocampus, but cholinergic dysfunction has only mild effects in the MWM in mice ([Moreau et al. 2008](#); [Martyn et al. 2012](#)). Our data showed that spatial learning on the MWM was relatively normal in VACHT^{Nkx2.1-Cre-flox/flox} mice compared with controls (see [Supplementary Fig. 5A–C](#)). On the probe trial of the MWM, both groups of mice spent significantly more time in the target quadrant compared with the opposite quadrant (2-way ANOVA shows a significant effect of quadrant, $F_{3,80} = 39.58$, $P < 0.0001$, and an interaction effect $F_{3,80} = 2.914$, $P = 0.0394$, see [Supplementary Fig. 5D](#)), post hoc analysis revealed that both groups spent significantly more time in the target quadrant. However, VACHT^{Nkx2.1-Cre-flox/flox} mice had significantly fewer platform crosses compared with littermate controls ($t_{(20)} = 2.795$, $P = 0.0112$, see [Supplementary Fig. 5E](#)).

To specifically evaluate the contribution of hippocampal cholinergic tone to learning and memory performance in the spatial version of the MWM, we stereotactically injected AAV8-GFP-Cre ($n = 25$) virus to the MS/VDB in another cohort of VACHT^{flox/flox} mice (see [Supplementary Fig. 6A,B](#)). VACHT^{flox/flox} mice injected with AAV8-GFP ($n = 14$) were used as controls. AAV8-GFP-Cre-injected mice that showed more than 50% of hippocampal VACHT protein levels ($n = 11$) compared with controls were excluded from the analysis (see [Supplementary Fig. 6E](#)). In AAV8-GFP-Cre-injected mice with reduced hippocampal VACHT levels, VACHT protein in the prefrontal cortex was not changed (97% of AAV8-GFP VACHT levels, $t_{(4)} = 0.453$, $P = 0.665$, see [Supplementary Figure 6C,D](#)). AAV8-GFP-Cre-mediated deletion of VACHT from the medial septum did not significantly alter acquisition of the spatial version of the MWM (Latency, 2-way RM ANOVA shows an effect of days $F_{3,39} = 22.84$, $P < 0.0001$, no effect of Cre virus injection $F_{1,13} = 0.2228$, $P = 0.6447$, and no interaction, $F_{3,39} = 1.302$, $P = 0.2876$, [Fig. 4A](#)). Similar results were obtained for distance travelled (2-way RM ANOVA shows an effect of days, $F_{3,39} = 23.5$, $P < 0.0001$, no effect of Cre expression $F_{1,13} = 0.3125$, $P = 0.5856$, and no interaction, $F_{3,39} = 1.329$, $P = 0.2787$, [Fig. 4B](#)). In the probe trial, mice injected with the AAV8-GFP-Cre virus did not differ from controls in terms of preference for the target quadrant (2-way ANOVA shows a significant effect of quadrant, $F_{3,104} = 37.81$, $P < 0.0001$, no effect of Cre expression, $F_{1,104} = 0.6452$, $P = 0.4237$, and no interaction $F_{3,104} = 0.3988$, $P = 0.7541$, [Fig. 4D](#)) or platform crosses ($t_{(26)} = 0.9547$, $P = 0.3603$, [Figure 4E](#)). Taken together, these results suggest that decreased levels of hippocampal cholinergic activity do not seem to affect MWM performance.

VACHT^{Nkx2.1-Cre-flox/flox} mice were also tested on the reversal learning protocol of the MWM. During the course of 4 days, control mice significantly improved in their latency to find the hidden platform in contrast to VACHT^{Nkx2.1-Cre-flox/flox} mice (2-way RM ANOVA shows a significant effect of days $F_{3,30} = 8.632$, $P = 0.0003$, main effect of genotype $F_{1,10} = 11.17$, $P = 0.0075$, and

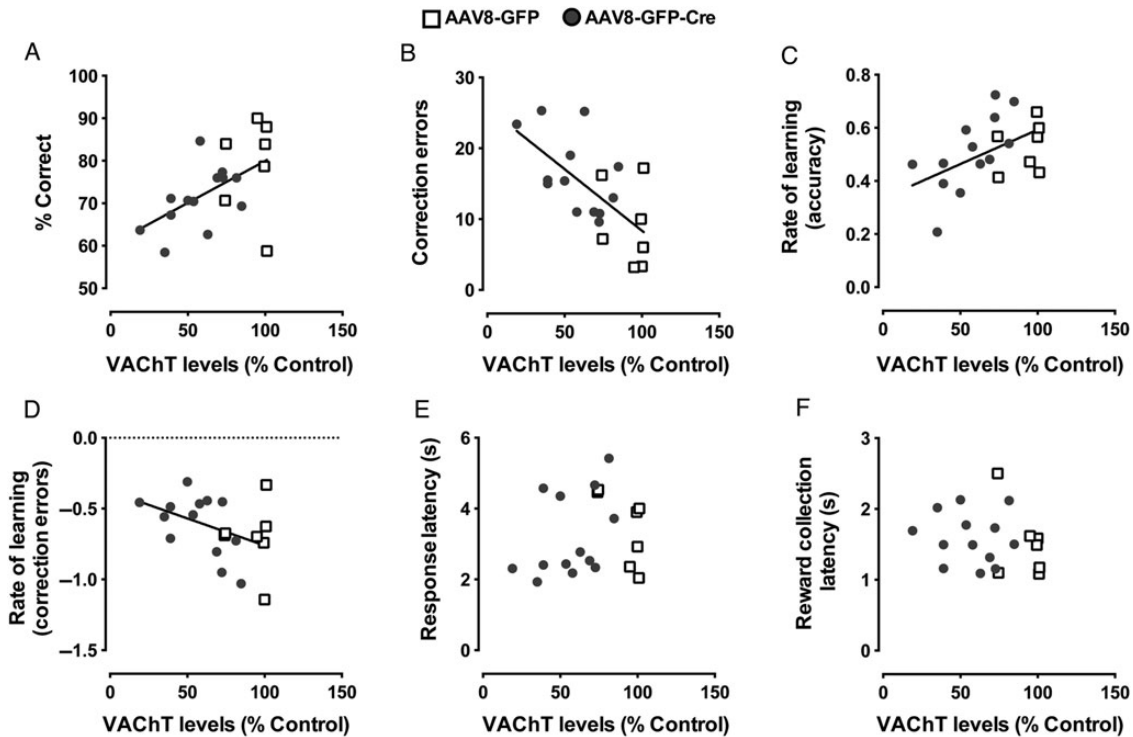


Figure 3. Medial septum AAV8-GFP-Cre-injected mice show deficits in dPAL. (A,B) Linear regression and correlation between response accuracy ($r = 0.5208$, $P = 0.0186$) and correction errors ($r = -0.5154$, $P = 0.0168$) on Week 9 and hippocampal VACHT protein expression levels for AAV8-GFP (clear squares, $n = 7$) and AAV8-GFP-Cre (dark circles, $n = 13$) injected mice. (C,D) Linear regression and correlation between response accuracy ($r = 0.4460$, $P = 0.0487$) and correction errors ($r = -0.1799$, $P = 0.0120$) across all the weeks of the PAL task and hippocampal VACHT protein expression levels. (E,F) The relationship between response latency ($r = 0.1349$, $P = 0.5708$) and reward collection latency ($r = -0.1799$, $P = 0.4352$) across all the weeks of the PAL task and VACHT expression levels.

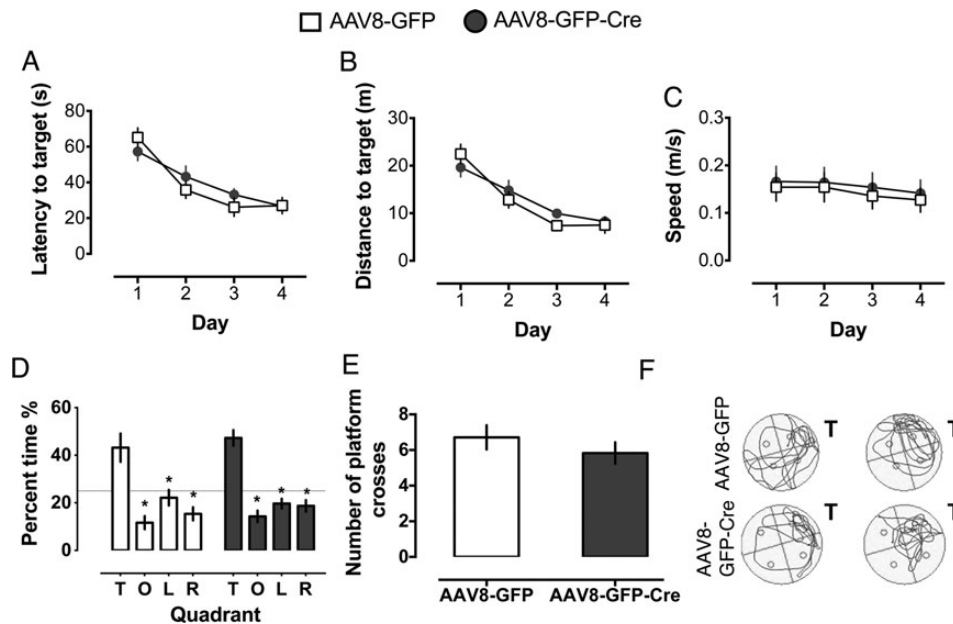


Figure 4. Performance of medial septum AAV8-GFP-Cre-injected mice in the MWM. $VACHT^{fllox/fllox}$ injected with AAV8-GFP virus (clear squares, $n = 14$) or AAV8-GFP-Cre virus (dark circles, $n = 14$) were tested in the spatial paradigm of the MWM. Data average of four 90-s trials per day were plotted. (A) Latency to reach the platform, (B) distance to reach the platform, (C) speed to reach the platform, (D) the percentage of time spent in each quadrant of the pool measured on Day 5 in a 60-s probe trial with the platform removed. (E) Number of platform crosses during the probe trial. (F) Representative path traces of 2 AAV8-GFP and 2 AAV8-GFP-Cre-injected mice in the probe trial. The target quadrant is in the upper right. Data are mean $\pm$ SEM. * $P < 0.05$. T, target; O, opposite; L, left; R, right.

no interaction $F_{3,30} = 1.501$, $P = 0.2342$, Fig. 5A–C). Notably, on the probe trial, control mice spent considerably more time in the target quadrant compared with the other quadrants (2-way ANOVA

shows a significant effect of quadrant, $F_{3,80} = 7.226$, $P = 0.0002$, and an interaction effect $F_{3,80} = 3.133$, $P = 0.0301$, Fig. 5D), while $VACHT^{Nkx2.1-Cre-fllox/fllox}$ mice visited all quadrants almost equally.

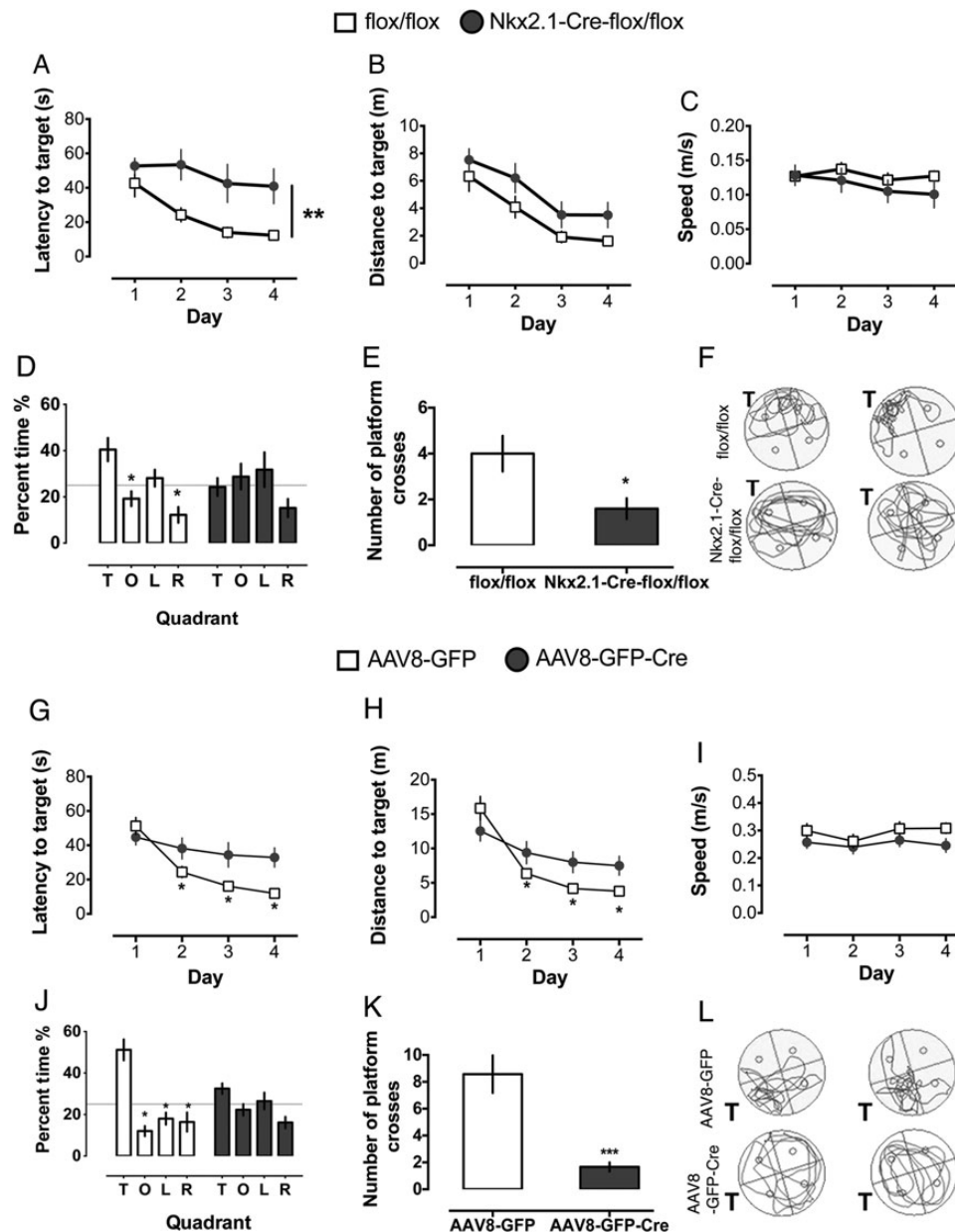


Figure 5. Reversal learning is affected in *VACHT^{Nkx2.1-Cre-flox/flox}* and medial septum AAV8-GFP-Cre-injected mice. *VACHT^{flox/flox}* (clear squares, $n = 11$) and *VACHT^{Nkx2.1-Cre-flox/flox}* (dark circles, $n = 11$) were tested in the reversal paradigm of the MWM. Data average of four 90-s trials per day were plotted. (A) Latency to reach the platform, (B) distance to reach the platform, (C) speed to reach the platform, (D) the percentage of time spent in each quadrant of the pool measured on Day 5 in a 60-s probe trial with the platform removed. (E) Number of platform crosses during the probe trial. (F) Representative path traces for 2 *VACHT^{flox/flox}* and 2 *VACHT^{Nkx2.1-Cre-flox/flox}* in the probe trial. The target quadrant is in the upper left. (G–L) AAV8-GFP (clear squares, $n = 14$) or AAV8-GFP-Cre (dark circles, $n = 14$)-injected mice were tested in the reversal paradigm of the MWM. The data average of four 90-s trials per day were plotted. (G) Latency to find the platform, (H) distance, (I) speed, (J) the percentage of time spent in each quadrant of the pool was measured on Day 5 in a 60-s probe trial with the platform removed. (K) Number of platform crosses during the probe trial. (L) Two AAV8-GFP- and 2 AAV8-GFP-Cre-injected mice in the probe trial. The target quadrant is indicated with a T. Data are mean $\pm$ SEM. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.0001$. T, target; O, opposite; L, left; R, right.

The number of platform crosses was also higher for control mice compared with *VACHT* mutants ($t_{(20)} = 2.797$, $P = 0.0111$, Fig. 5E). These results indicate that, different from control mice, *VACHT^{Nkx2.1-Cre-flox/flox}* mice were unable to extinguish the previously learned position and relearn the new position of the hidden platform.

To account for compromised striatal cholinergic signaling in *VACHT^{Nkx2.1-Cre-flox/flox}* mice for the performance in the MWM (see Supplementary Fig. 1D), we also tested a mouse line with

selective deletion of *VACHT* in striatal neurons (*VACHT^{D2-Cre-flox/flox}*), but spared hippocampal *VACHT* (Guzman et al. 2011; see Supplementary Fig. 7). Interestingly, *VACHT^{D2-Cre-flox/flox}* mice did not differ from controls (*VACHT^{flox/flox}*) in both acquisition and reversal versions on the MWM (see Supplementary Fig. 7D–H). These results suggest that deficits seen in reversal learning in *VACHT^{Nkx2.1-Cre-flox/flox}* mice are not likely due to impaired striatal cholinergic transmission, but rather a result of hippocampal or cortical deficits or combined cortical hippocampal

dysfunction. To discern among these possibilities, we used virus-injected mice.

Selective reduction of hippocampal cholinergic tone in virus-injected mice also increased latency to find the platform in reversal learning (2-way RM ANOVA shows an effect of days, $F_{3,39} = 21.96$, $P < 0.0001$ and a significant interaction effect, $F_{3,39} = 7.507$, $P = 0.0004$), with post hoc analysis revealing that AAV8-GFP-Cre-injected mice performed significantly worse on Day 4 compared with controls (Fig. 5G). During the probe trial, mice injected with AAV8-GFP-Cre virus showed significant impairments, failing to show a preference for the target quadrant (2-way ANOVA shows a significant effect of quadrant, $F_{3,104} = 23.3$, $P < 0.0001$, and an interaction effect, $F_{3,104} = 7.173$, $P = 0.002$, Fig. 5J). Post hoc analysis revealed that the AAV8-GFP-Cre mice did not prefer the target quadrant compared with the other quadrants, while the AAV8-GFP-injected controls had a strong preference for the target quadrant. Furthermore, the AAV8-GFP-Cre-injected mice showed a decrease in the number of platform crosses ($t_{(26)} = 0.9547$, $P = 0.0010$, Fig. 5K). These results reveal that disruption of hippocampal cholinergic tone, but not striatal or cortical cholinergic activity, compromises information processing in the MWM reversal learning.

Regulation of Working Memory by Septohippocampal VACHT

To determine whether other cognitive domains of importance in neuropsychiatric disorders that could contribute to the PAL deficits may also be regulated by synaptically released ACh, we evaluated the performance of the VACHT^{Nkx2.1-Cre-flox/flox} mice on 2 measures of working memory: the working memory version of the MWM and spontaneous alternations in the Y-maze. In the working memory version of the MWM, VACHT^{Nkx2.1-Cre-flox/flox} mice failed to improve their performance from the first to the second trial resulting in significant impairments in measures of latency savings ($t_{(12)} = 3.580$, $P = 0.0030$, Fig. 6A) and distance savings ($t_{(12)} = 2.852$, $P = 0.0127$, Fig. 6B), suggesting that the

VACHT^{Nkx2.1-Cre-flox/flox} mice have impaired working memory. Similarly, VACHT^{Nkx2.1-Cre-flox/flox} mice revisited arms in the maze more often than controls resulting in a significant decrease in spontaneous alternations in the Y-maze ($t_{(12)} = 2.674$, $P = 0.0182$, Fig. 6C), suggesting that forebrain VACHT is required for normal working memory performance.

When tested on the working memory MWM test, mice with selective elimination of septohippocampal VACHT by virus injection (same cohort used in the MWM) also showed impaired latency savings ratio ($t_{(26)} = 2.847$, $P = 0.0111$, Fig. 6D) and distance savings ratio ($t_{(26)} = 2.149$, $P = 0.0473$, Fig. 6E). On the spontaneous alternations Y-maze task, AAV8-GFP-Cre-injected mice showed impairments on working memory, measured as a significant decreased rate of spontaneous alternations ($t_{(26)} = 3.347$, $P = 0.0041$, Fig. 6F). It is interesting to note that working memory deficits observed for AAV8-GFP-Cre-injected mice were similar to deficits observed for VACHT^{Nkx2.1-Cre-flox/flox} mice. Taken together these results indicate that working memory is highly sensitive to hippocampal cholinergic tone.

Discussion

The present work shows that selective inhibition of cholinergic signaling in the hippocampus in mice leads to disruption of synaptic plasticity and specific cognitive impairments. In particular, we show that hippocampal cholinergic signaling is important for the modulation of cognitive tasks shown to be impaired in schizophrenia and dementia, including the PAL task. Interestingly, some hippocampal-dependent tasks appear to be more sensitive to decreased cholinergic signaling than others. Our results provide a comprehensive map of cholinergic-regulated hippocampal cognitive processing that may be useful to understand similar deficits in humans with cholinergic deficiency.

Notably, we report novel data indicating the importance of cholinergic signaling in regulating the PAL task. Clinically, the PAL task has been suggested as a potential cognitive marker of decline in psychosis (Wood et al. 2002). Significant impairments

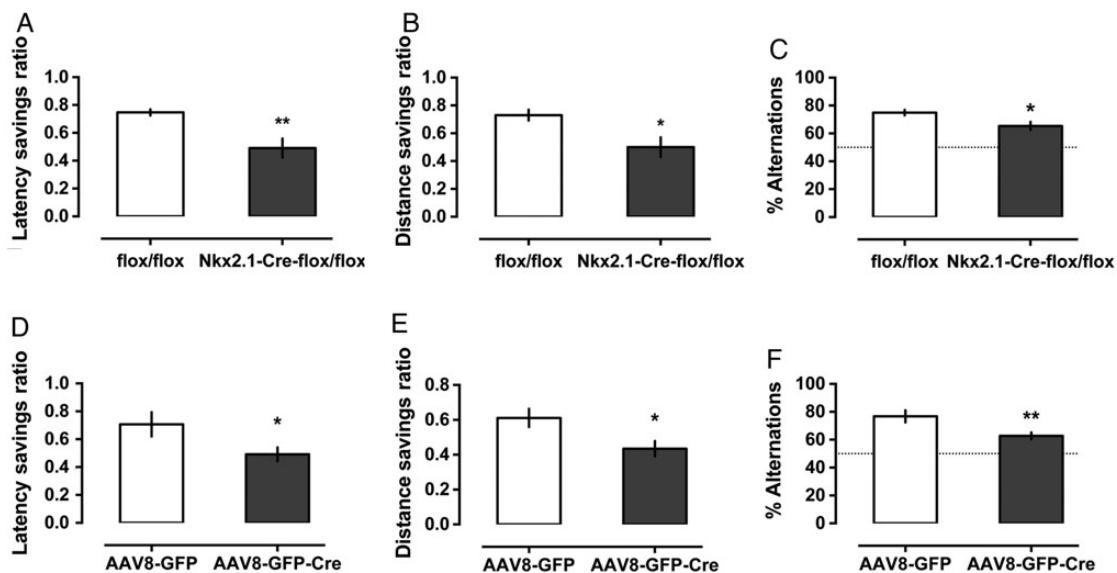


Figure 6. Working memory depends on hippocampal cholinergic tone. (A) Latency savings ratio and (B) distance savings ratio for VACHT^{flox/flox} (clear, $n = 7$) and VACHT^{Nkx2.1-Cre-flox/flox} (dark, $n = 7$) mice in the working memory version of the MWM. (C) Spontaneous alternations in the Y-maze for VACHT^{Nkx2.1-Cre-flox/flox}. (D) Latency savings ratio and (E) distance savings ratio for AAV8-GFP (clear, $n = 14$) and AAV8-GFP-Cre (dark, $n = 14$) mice in the working memory version of the MWM. (F) Spontaneous alternations in the Y-maze for virus-injected mice. Data are mean $\pm$ SEM. * $P < 0.05$, ** $P < 0.01$.

in PAL have been observed in patients with schizophrenia with a positive correlation between failure on the PAL task and negative symptoms (Barnett et al. 2005). Additionally, hippocampal activation during PAL is changed in patients with mild cognitive impairment compared with aged-matched controls (de Rover et al. 2011). Hence, PAL has also been considered a sensitive task for predicting cognitive decline in AD (Swainson et al. 2001; Blackwell et al. 2004).

Nonetheless, whether cholinergic signaling is required for acquisition of the task has not been clearly established. Systemic administration of donepezil, a cholinesterase inhibitor, improved post-acquisition PAL performance in mice, an effect that was attenuated with administration of muscarinic antagonists (Bartko, Vendrell et al. 2011). Similar results have been observed in monkeys where both mecamlamine (nicotinic antagonist) and scopolamine (muscarinic antagonist) induced deficits in PAL performance (Taffe et al. 2002; Katner et al. 2004). These results suggest that cholinergic signaling might be relevant for PAL. Also, rats previously trained in PAL that received injections into the dorsal hippocampus of either scopolamine or mecamlamine and that were re-tested did not show deficits in performance, suggesting that hippocampal cholinergic signaling might not modulate recall in this task (Talpos et al. 2009). Our results indicate that disruption in forebrain cholinergic tone disturbs PAL learning. Additionally, our data suggest that dysfunctional hippocampal cholinergic signaling may decrease PAL performance, as performance of mice in the PAL task correlates with hippocampal VACHT protein levels. Importantly, these deficits occurred in the absence of alterations in latency to touch the screen or to collect the reward, indicating that motivation was not a factor in the poorer performance of mice with lower cholinergic tone. Interestingly, mice deficient for the M1 receptor presented no differences compared with controls in their acquisition of the PAL task (Bartko, Romberg et al. 2011), suggesting that nicotinic and/or other muscarinic receptors might be involved in mediating learning in this hippocampal-dependent task.

Performance in PAL, as well as in other paired-associated tasks, may depend on intact hippocampal function in humans and rats (Talpos et al. 2009; de Rover et al. 2011). For example, short-lasting inactivation of the rat hippocampus using lidocaine (non-selective Na⁺ channel blocker) significantly impairs performance postacquisition of the PAL task, suggesting that the hippocampus is required at least for performance in this task (Talpos et al. 2009). In addition, human fMRI studies have shown bilateral BOLD activation of the hippocampus during the encoding phase of the PAL task (de Rover et al. 2011). Interestingly, subjects with memory deficits showed decreased hippocampal activation with increased memory demand, whereas healthy controls showed the opposite (de Rover et al. 2011). Moreover, PAL performance correlates with hippocampal volume loss in schizophrenia and mild cognitive impairment (MCI) (Keri et al. 2012). Intriguingly, recent reports indicate that mice with hippocampal lesions are still able to acquire the PAL task (Delotterie et al. 2015; Kim et al. 2015). One possible explanation (Kim et al. 2015) regarding these findings is that with a functional hippocampus the task is acquired in a hippocampal-dependent manner, but with a dysfunctional hippocampus, the task can be learnt using an alternative hippocampal-independent strategy. For example, mice with hippocampal lesions could have used the dorsal striatum to acquire the task (Delotterie et al. 2015). Indeed, the development of such behavioral plasticity has been shown in rats with unilateral hippocampal lesions (Zou et al. 1999). Our findings that forebrain VACHT-deficient mice seem unable to acquire the task, whereas decreased VACHT levels in the

hippocampus decrease acquisition performance, suggest that the hippocampal cholinergic tone may facilitate acquisition of the PAL task. However, it is unlikely that only one brain region is involved in such a complex task.

The mechanisms by which ACh tone facilitates PAL performance are not fully understood. It is possible that cholinergic tone is required for specific types of synaptic plasticity. Indeed, hippocampal LTP in vitro is disturbed in a different mouse line lacking forebrain VACHT (Martyn et al. 2012). We corroborated this finding in vivo in VACHT^{Nkx2.1-Cre-flox/flox} mice and demonstrated that in the absence of VACHT expression, hippocampal LTP is compromised, suggesting that disturbances of synaptic plasticity might contribute to the deficit. To note, previous studies have shown that levels of VACHT are correlated to levels of ACh release (Prado et al. 2006; de Castro, Pereira, et al. 2009, reviewed in Prado et al. (2013)); an increase in VACHT levels increases ACh release whereas decreased levels have the opposite effect (Song et al. 1997; Prado et al. 2006; Kolisnyk, Guzman, et al. 2013). VACHT is decreased in AD (Parent et al. 2013). These results suggest that correlating levels of VACHT detected with PET ligands (Efang 2000) to performance in the PAL test (Harel et al. 2013) might provide a potential biomarker of remaining cholinergic function and cognitive reserve.

We showed that acquisition of the spatial version of the MWM and recall of platform location was mildly affected in VACHT^{Nkx2.1-Cre-flox/flox} mice, while AAV8-GFP-Cre-injected mice did not show any deficit in this behavioral task. Similarly, impairments in the spatial version of the MWM have been observed in rats with combined lesions of MS/VDB and nucleus basalis magnocellularis (NBM) cholinergic neurons produced by immunotoxin 192 IgG-saporin (Pizzo et al. 2002), while rats with immunotoxin lesions restricted to MS/VDB did not show any impairment (Berger-Sweeney et al. 1994; Baxter and Gallagher 1996; Pizzo et al. 2002; Frick et al. 2004). Interestingly, rats with 192 IgG-saporin lesions restricted to NBM also did not show behavioral impairments in the MWM (Pizzo et al. 2002). These data suggest that forebrain cholinergic signaling is necessary for reference spatial learning and memory assessed using the MWM; however, it seems that both the cortical and hippocampal cholinergic projections need to be compromised to produce a severe spatial deficit. Thus, providing that cortical cholinergic projections are intact, hippocampal cholinergic activity is not absolutely required for this behavioral task. It remains to be established whether GABA or glutamate, which could potentially be co-released with ACh (Guzman et al. 2011; Saunders et al. 2015) in both the hippocampus and cortex, may contribute to regulation of spatial memory by cholinergic neurons.

In contrast to the reference memory test, both VACHT^{Nkx2.1-Cre-flox/flox} and AAV8-GFP-Cre-GFP-injected mice when tested in the MWM reversal learning task presented extensive deficits, suggesting a prominent role for hippocampal cholinergic signaling in reversal learning. The impairments seen in VACHT-deficient mice in reversal learning could relate to the loss of muscarinic presynaptic inhibition of excitatory feedback within cortical circuits (Hasselmo and McGaughy 2004), which would slow the extinction of a previously learned strategy (Hasselmo et al. 2002; Hasselmo 2006). To note, the findings with VACHT^{Nkx2.1-Cre-flox/flox} mice recapitulated the deficits seen in reversal learning in a different mouse line with deficient forebrain cholinergic tone we generated previously (Martyn et al. 2012; Kolisnyk, Al-Onaizi, et al. 2013). Interestingly, rats with 192 IgG-saporin lesions restricted to NBM also show behavioral flexibility impairments (Cabrera et al. 2006). Taken together, these results suggest that both NBM-cortical and septohippocampal cholinergic

signaling might be critical for the mediation of this form of cognitive flexibility.

The most common form of LTP underlying hippocampal synaptic plasticity in spatial memory depends on the activation of NMDARs (Collingridge et al. 1983; Martin et al. 2000; MacDonald et al. 2006). Intracerebroventricular administration of a NMDAR antagonist (AP5) significantly impaired performance of rats during reversal testing in the MWM (Morris et al. 1990). Moreover, genetically modified mice with deletion of the GluN2B subunit of NMDARs in the CA1 region of the hippocampus exhibited impairments in reversal learning (von Engelhardt et al. 2008). Similarly, mice with corticohippocampal deletion of GluN2B present deficits in hippocampal synaptic plasticity, highlighted by abolished long-term depression (LTD), a partial deficiency of LTP, and memory impairments (Brigman et al. 2010). The impairments observed in VACHT^{Nkx2.1-Cre-flox/flox} mice in LTP and reversal learning suggest that long-term cholinergic signaling may regulate NMDAR-mediated synaptic plasticity required for reversal learning in the MWM.

Both prefrontal cortex and hippocampus have been implicated in working memory (Yoon et al. 2008). A number of studies indicate that cholinergic neurotransmission is crucial for modulation of working memory in various behavioral tasks (Levy et al. 1991; Baxter et al. 1995; Furey et al. 2000; Hironaka et al. 2001). Whether cholinergic modulation of working memory is dependent on ACh acting on prefrontal cortex, hippocampus, or in both structures simultaneously is not known. Our results show that deficits in the working memory version of the MWM task and the Y-maze alternating task are equally severe in both forebrain VACHT mutants (VACHT^{Nkx2.1-Cre-flox/flox} mice) and hippocampus VACHT mutants (AAV8-GFP-Cre-injected mice), suggesting that hippocampal cholinergic tone is vital in regulating information processing in working memory tasks. Taken together, these results suggest that ACh may exert important roles in working memory via modulation of hippocampal function. Whether these working memory deficits somehow contribute to the poor performance in PAL remains to be established.

Imaging studies involving volumetric measurement of basal forebrain cholinergic nuclei in humans reveal a drastic decrease in the volume of basal forebrain neurons in AD and MCI patients, in comparison to healthy elderly controls (Grothe et al. 2010, 2012; Grothe, Ewers, et al. 2014; Teipel et al. 2014). Given that individuals with dementia may present long-term changes in cholinergic tone, our mouse lines and approaches may be directly relevant to understand molecular, cellular, circuitry, and behavioral consequences of cholinergic malfunction. The present work is relevant to understand how drug-induced cholinergic dysfunction or degenerative changes in cholinergic neurons contribute to cognitive alterations in several neuropsychiatric disorders (Severance and Yolken 2008; Scarr et al. 2009). In summary, hippocampal cholinergic activity does not seem to be critical for spatial reference learning and memory, but has fundamental roles on working memory, reversal learning, and paired associates learning. As PAL performance may be dependent on cholinergic integrity, it is tempting to speculate that the PAL task could be used to identify individuals with cognitive dysfunction linked to cholinergic abnormalities.

Supplementary Material

Supplementary material can be found at <http://www.cercor.oxfordjournals.org/> online.

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Notes

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Curriculum Vitae

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Trainee, Robarts Research Institute

Graduate Program in Neuroscience, Schulich School of Medicine & Dentistry

EDUCATION:

UNIVERSITY	DEGREE	DEPARTMENT	YEAR
The University of Ottawa	BSc. Hons	Psychology & Biochemistry	2008-12
The University of Western Ontario	PhD	Neuroscience	2012-Current

Thesis Title: Cholinergic Mechanisms Regulating Cognitive Function and RNA Metabolism

Ph. D. Supervisor: Drs. Marco & Vania Prado

ACADEMIC EMPLOYMENT HISTORY:

TEACHING ASSISTANT

UNIVERSITY	SUPERVISOR	DEPARTMENT	YEAR
The University of Western Ontario	Dr. Michelle Belton	Medical Sciences	2013-Current
	Dr. Rhodri Cusak	Neuroscience	2014

AWARDS AND DISTINCTIONS

2014-2017	The Alzheimer Society Research Program Fellowship The Annie Dakens Research Fund Award
2015	ISN-APSN Travel Award
2012-2014	OGS Graduate Scholarship 2012-2013, 2013-2014
2012	CPA Certificate of Academic Excellence - Prize / Award Canadian Psychological Association for Best Thesis

PRESENTATIONS

Posters Presented

Kolisnyk B, Al-Onaizi MA, Hirata PH, Guzman MS, Nikolova S, Barbash S, Soreq H, Bartha R, Prado MA, Prado VF "Deletion of the vesicular acetylcholine transporter in the murine forebrain results in metabolic abnormalities in the prefrontal cortex and disruption in executive function.", Neuropsychopharmacology Meeting 2013, U.S.A, California, San Diego.

Kolisnyk B, Hirata PH, Prado MA, and Prado VF. "Cholinergic Tone And Attention: A Possible Role Of The $\alpha 7$ Nicotinic Acetylcholine Receptor", Canadian Neuroscience Meeting 2013, Canada, Ontario, Toronto

Kolisnyk, B, Al-Onaizi, M.A, Parfitt, G.M, Kish, M.T, Xu, J, Hanin,G, Soreq, H, Prado MA, and Prado VF "Cholinergic regulation of cognitive function and underlying molecular mechanisms", Canadian Neuroscience Meeting 2014, Canada , Quebec, Montreal **and invited to present at** the Canadian Student Health Research Forum 2014, Canada, Manitoba, Winnipeg.

Kolisnyk, B, Al-Onaizi, M.A, Prado MA, and Prado VF "Elucidating the role of the $\alpha 7$ nicotinic acetylcholine receptor in attention", Neurex Meeting: "Cholinergic Tone: Where from, what for?" 2014, France, Alsace, Strasbourg.

Kolisnyk, B, Al-Onaizi, M.A, Prado MA, and Prado VF " $\alpha 7$ nicotinic acetylcholine receptor-deficient mice exhibit sustained attention impairments that are reversed by ABT-418", ISN 2015 Biennial Meeting of the Society of Neurochemistry , Australia, Queensland, Cairns.

PUBLICATIONS

Journal Articles

Al-Onaizi, MA, Parfitt, GM, **Kolisnyk, B**, Law, CSH, Guzman, MS, Barros, DM, Leung, SL, Prado, MAM, Prado, VF "Regulation of cognitive processing by hippocampal cholinergic tone". *Cerebral Cortex*, pii**bhv349** (2016)

Beraldo FH, Thomas A, **Kolisnyk B**, Hirata PH, De Jaeger X, Martyn AC, Fan J, Goncalves DF, Cowan MF, Masood T, Martins VR, Gros R, Prado VF, Prado MA. [Hyperactivity and attention deficits in mice with decreased levels of stress inducible phosphoprotein 1 \(STIP1\)](#). *Dis Model Mech*. 2015 Sep 17

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Nogueira Kde O, Sartori SS, Araújo VA, Neves CA, **Kolisnyk B**. (2015) [Sperm storage in Hemidactylus mabouia: Morphological and ultrastructural aspects of a reproductive strategy](#). *Anim Reprod Sci*. 2015 Aug;159:212-6.

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Kolisnyk, B., Guzman, M. S., Raulic, S., Fan, J., Magalhães, A. C., Feng, G., ... & Prado, M. A. (2013). [ChAT–ChR2–EYFP Mice Have Enhanced Motor Endurance But Show Deficits in Attention and Several Additional Cognitive Domains](#). *The Journal of Neuroscience*, 33(25), 10427-10438.

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