Molecular identification and characterization of host DEAD-box RNA helicases that are associated with Turnip mosaic virus infection

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Graduate Program in Biology
A thesis submitted in partial fulfillment of the requirements for the degree in Doctor of Philosophy
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MOLECULAR IDENTIFICATION AND CHARACTERIZATION OF
HOST DEAD-BOX RNA HELICASES THAT ARE ASSOCIATED WITH
TURNIP MOSAIC VIRUS INFECTION

(Thesis format: Monograph)

By

Yinzi Li

Graduate Program in Biology

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

The School of Graduate and Postdoctoral Studies
The University of Western Ontario
London, Ontario, Canada

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ABSTRACT

Plant viruses have small and compact genomes whose coding capacity is not sufficient to fulfill the viral life cycle. Thus, they are largely dependent on the host by recruiting many host components such as proteins and membranes. Many efforts have been made towards understanding the role of host factors and recent progress has led to the identification and characterization of a number of important host factors recruited for plant virus replication. DEAD-box RNA helicases (RHs) have been shown to play multiple roles in RNA metabolism, including remodeling RNA structures and promoting RNA-protein association/dissociation. During viral replication, RHs are implicated in several key steps of the infection process, such as viral genome translation, unwinding double-stranded RNA intermediates, and maintaining viral gene integrity by suppression of viral RNA recombination. Here, we used Turnip mosaic virus (TuMV), a member of potyviruses, as a model virus to explore RHs' role in viral infection. Firstly, we screened Arabidopsis T-DNA insertion mutants corresponding to RHs and identified three Arabidopsis DEAD-box RNA helicases (AtRHs) that are associated with TuMV infection. We further characterized an Arabidopsis DEAD-box RNA helicase, PRH75, which is required for TuMV infection as downregulation of PRH75 in Arabidopsis impedes the viral infection. We also found that PRH75 interacts with several viral proteins including TuMV helicase CI, RNA-dependent RNA polymerase (RdRP) NIb and viral genome-linked protein VPg. In TuMV-infected cells, PRH75 colocalizes with the 6K2-induced viral replication complex (VRC) and viral dsRNA. The recruitment of PRH75 to the VRC is possibly through its interactions with viral replicase components CI, NIb and VPg. As an RNA helicase, PRH75 may assist in unwinding viral RNA duplexes during TuMV replication. Moreover, the work here also presents evidence demonstrating that the nuclear transport of TuMV viral proteins is mediated by Arabidopsis importin α. Taken together, these data suggest that PRH75 is an essential host factor required for TuMV infection.

Keywords: plant viruses, potyviruses, Turnip mosaic virus (TuMV), viral replication and translation, viral replication complex (VRC), recessive resistance, host factor(s), Arabidopsis DEAD-box RNA helicase (AtRH), nuclear transport, Arabidopsis importin α.
First, I would like to give my heartfelt gratitude to my supervisor and mentor, Dr. Aiming Wang for his guidance, patience and encouragement. It was an invaluable and deeply rewarding experience to learn from him and work in his team. His supervision and intelligence inspired me to complete my journey of pursuing my Ph.D degree. More than anything, his diligence, generosity and wisdom have been instrumental in my personal growth.

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My earnest thanks go to my group fellows, Dr. Ruyi Xiong, Dr. Changwei Zhang, Dr. Chowda Reddy, Dr. Hui Chen, Dr. Lingrui Zhang, Dr. Xiaofei Cheng and Dr. Hongguang Cui. It was a great pleasure to work with them. Also, I am grateful towards other group members and friends for their companionship and help. I have learned and benefited so much from them.

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I am deeply indebted to my parents and my husband. It was their endless love and sacrifices to enable me to succeed. I am so proud of my baby girl who changed my life and makes it joyful.
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<th>Definition</th>
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</thead>
<tbody>
<tr>
<td>::</td>
<td>fused to (in the context of reporter-gene fusion constructs)</td>
</tr>
<tr>
<td>°C</td>
<td>Degrees Celsius</td>
</tr>
<tr>
<td>35S</td>
<td><em>Cauliflower mosaic virus</em> 35S RNA promoter</td>
</tr>
<tr>
<td>[A]</td>
<td>poly(A) tail</td>
</tr>
<tr>
<td>At</td>
<td><em>Arabidopsis thaliana</em></td>
</tr>
<tr>
<td>aa</td>
<td>amino acids</td>
</tr>
<tr>
<td>AAFC</td>
<td>Agriculture and Agri-Food Canada</td>
</tr>
<tr>
<td>ABRC</td>
<td>Arabidopsis Biological Resource Center</td>
</tr>
<tr>
<td>ACT</td>
<td><em>Arabidopsis</em> Actin2</td>
</tr>
<tr>
<td>AD</td>
<td>activation domain</td>
</tr>
<tr>
<td>Ade</td>
<td>adenine</td>
</tr>
<tr>
<td>AGO</td>
<td>Argonaute protein</td>
</tr>
<tr>
<td>AtRH</td>
<td><em>Arabidopsis</em> DEAD-box RNA helicase</td>
</tr>
<tr>
<td>ATP</td>
<td>adenosine 5'-triphosphate</td>
</tr>
<tr>
<td>AV-3</td>
<td><em>Asparagus virus 3</em></td>
</tr>
<tr>
<td>Avr</td>
<td>avirulence gene</td>
</tr>
<tr>
<td>BiFC</td>
<td>bimolecular fluorescence complementation</td>
</tr>
<tr>
<td>BK</td>
<td>binding domain</td>
</tr>
<tr>
<td>BLAST</td>
<td>basic local alignment search tool</td>
</tr>
<tr>
<td>BMV</td>
<td><em>Brome mosaic virus</em></td>
</tr>
<tr>
<td>bp</td>
<td>base pair</td>
</tr>
<tr>
<td>CaMV</td>
<td><em>Cauliflower mosaic virus</em></td>
</tr>
<tr>
<td>cDNA</td>
<td>complementary DNA</td>
</tr>
<tr>
<td>CFP</td>
<td>cyan fluorescent protein</td>
</tr>
<tr>
<td>Chl</td>
<td>chloroplast autofluorescence</td>
</tr>
<tr>
<td>CI</td>
<td>the cylindrical inclusion protein</td>
</tr>
<tr>
<td>CIYVV</td>
<td><em>Clover yellow vein virus</em></td>
</tr>
<tr>
<td>cm</td>
<td>centimeter (s)</td>
</tr>
<tr>
<td>CMV</td>
<td><em>Cucumber mosaic virus</em></td>
</tr>
<tr>
<td>Col-0</td>
<td>ecotype Columbia</td>
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<tr>
<td>CP</td>
<td>coat protein or viral capsid</td>
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<tr>
<td>CTAB</td>
<td>cetyltrimethyl-ammonium bromide</td>
</tr>
<tr>
<td>C-terminal</td>
<td>carboxyl-terminal</td>
</tr>
<tr>
<td>CVYV</td>
<td><em>Cucumber vein yellowing virus</em></td>
</tr>
<tr>
<td>DBP1</td>
<td>DNA-binding protein phosphatase 1</td>
</tr>
<tr>
<td>Dbp3</td>
<td>DEAD-box protein 3</td>
</tr>
<tr>
<td>Dbp5</td>
<td>DEAD-box protein 5</td>
</tr>
<tr>
<td>Dbp2p</td>
<td>DEAD-box protein 2</td>
</tr>
<tr>
<td>DCL</td>
<td>Dicer-like ribonuclease (s)</td>
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<td>DDX</td>
<td>DEAD-box RNA helicase</td>
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<tr>
<td>DEAD</td>
<td>Asp-Glu-Ala-Asp</td>
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<td>DEAH</td>
<td>Asp-Glu-Ala-His</td>
</tr>
<tr>
<td>DED1</td>
<td>DEAD-box helicase 1</td>
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<tr>
<td>Ded1p</td>
<td><em>DED1</em>-encoded protein</td>
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DENV  Dengue virus
DIC  differential interference contrast
DMSO  dimethyl sulfoxide
DNA  deoxyribonucleic acid
DNase  deoxyribonuclease
DO  dropout
dpi  days post inoculation/infiltration
DRB  dsRNA-binding protein
dRBFC  dsRNA-binding dependent fluorescence complementation
dsRNA  double-stranded RNA
EDTA  ethylenediaminetetraacetic acid
eEF1A  eukaryotic elongation factor 1A
eIF  eukaryotic translation initiation factor(s)
eIF4A  eukaryotic translation initiation factor 4A
eIF4B  eukaryotic translation initiation factor 4B
eIF4E  eukaryotic translation initiation factor 4E
eIF(iso)4E  eukaryotic translation initiation factor isoform 4E
eIF4F  eukaryotic translation initiation factor 4F
eIF4G  eukaryotic translation initiation factor 4G
eIF(iso)4G1  eukaryotic translation initiation factor isoform 4G1
eIF(iso)4G2  eukaryotic translation initiation factor isoform 4G2
eIF4H  eukaryotic translation initiation factor 4H
ELISA  enzyme-linked immunosorbent assay
ER  endoplasmic reticulum
ETI  effector-triggered immunity
ETS  effector-triggered susceptibility
FAL1  Translation initiation factor 4AIII-like protein 1
FHV  Flock house virus
FRET  fluorescence resonance energy transfer
g  gram (s)
GFP  green fluorescent protein
GUS  β-glucuronidase
h  hour (s)
HBV  Hepatitis B virus
HC-Pro  the helper component protease
HCV  Hepatitis C virus
His  histidine
HIV-1  Human immunodeficiency virus type 1
HM  homozygous
HR  hypersensitive response
Hsc70  heat shock cognate 70 kDa protein
IBV  Infectious bronchitis virus
IMPA  importin α
ISE  increased size exclusion limit
iso  isoform
JAX1  jacalin-type lectin required for Potexvirus resistance 1
<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Definition</th>
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<tbody>
<tr>
<td>6K1</td>
<td>the first 6 kDa protein</td>
</tr>
<tr>
<td>6K2</td>
<td>the second 6 kDa protein (also referred to as 6K)</td>
</tr>
<tr>
<td>kb</td>
<td>kilobase (s)</td>
</tr>
<tr>
<td>kDa</td>
<td>kilodalton (s)</td>
</tr>
<tr>
<td>kV</td>
<td>kilovolt (s)</td>
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<tr>
<td>l</td>
<td>litre</td>
</tr>
<tr>
<td>LB</td>
<td>Luria Bertani</td>
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<td>LB T</td>
<td>T-DNA left border</td>
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<td>Leu</td>
<td>leucine</td>
</tr>
<tr>
<td>LiAc</td>
<td>lithium acetate</td>
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<tr>
<td>LMV</td>
<td><em>Lettuce mosaic virus</em></td>
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<tr>
<td>LOS4</td>
<td><em>Arabidopsis</em> osmotically responsive genes 4</td>
</tr>
<tr>
<td>LP</td>
<td>left genomic primer</td>
</tr>
<tr>
<td>LRR</td>
<td>leucine-rich repeat</td>
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<td>μg</td>
<td>microgram</td>
</tr>
<tr>
<td>μl</td>
<td>microlitre</td>
</tr>
<tr>
<td>μM</td>
<td>micromolar</td>
</tr>
<tr>
<td>MAMP</td>
<td>microbe-associated molecular pattern</td>
</tr>
<tr>
<td>MARV</td>
<td><em>Marburg virus</em></td>
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<tr>
<td>MES</td>
<td>2-N-morpholino-ethanesulfonic acid</td>
</tr>
<tr>
<td>mg</td>
<td>milligram</td>
</tr>
<tr>
<td>min</td>
<td>minute</td>
</tr>
<tr>
<td>miRNA</td>
<td>microRNA</td>
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<td>millimolar</td>
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<td>mRNA</td>
<td>messenger RNA</td>
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<tr>
<td>MW</td>
<td>molecular weight</td>
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<tr>
<td>ng</td>
<td>nanogram</td>
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<td>nanometer</td>
</tr>
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<td>nt</td>
<td>nucleotide(s)</td>
</tr>
<tr>
<td>NB</td>
<td>nucleotide binding</td>
</tr>
<tr>
<td>NCBI</td>
<td>National Center for Biotechnology Information</td>
</tr>
<tr>
<td>N1a</td>
<td>the nuclear inclusion a protein</td>
</tr>
<tr>
<td>N1a-Pro</td>
<td>the nuclear inclusion a protease</td>
</tr>
<tr>
<td>N1b</td>
<td>the nuclear inclusion b protein</td>
</tr>
<tr>
<td>NLS</td>
<td>nuclear localization signal</td>
</tr>
<tr>
<td>NLoS</td>
<td>nucleolar localization signal</td>
</tr>
<tr>
<td>NPC</td>
<td>nuclear pore complex</td>
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<tr>
<td>N-P-K</td>
<td>nitrogen (N)-phosphorus (P)-potassium (K)</td>
</tr>
<tr>
<td>N-terminal</td>
<td>amino-terminal</td>
</tr>
<tr>
<td>OD</td>
<td>optical density (absorbance)</td>
</tr>
<tr>
<td>ORF</td>
<td>open reading frame</td>
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<tr>
<td>OsBIRH1</td>
<td><em>Oryza sativa</em> BTH-induced RNA helicase 1</td>
</tr>
<tr>
<td>P1</td>
<td>the first protein</td>
</tr>
<tr>
<td>P1b</td>
<td>the second copy of P1</td>
</tr>
<tr>
<td>P3</td>
<td>the third protein</td>
</tr>
</tbody>
</table>
P3N-PIPO  pipo as a translational fusion with the N-terminus of P3
PABP  poly(A)-binding protein
PAMP  pathogen-associated molecular pattern
PCaP1  plasma membrane associated cation-binding protein 1
PCD  programmed cell death
PCR  polymerase chain reaction
PD  plasmodesmata
PDS  phytoene desaturase
PEG  polyethylene glycol
PIPO  pretty interesting Potyviridae ORF
PIAMV  Plantago asiatica mosaic virus
PLRV  Potato leaf roll virus
PMH1  Putative Mitochondrial RNA Helicase1
Poly(A)  polyadenylate
PpDDXL  Prunus persica DDX-like
PPV  Plum pox virus
PRR  pattern recognition receptor
Pro  protease
PSbMV  Pea seed-borne mosaic virus
PTI  PAMP-triggered immunity
PVA  Potato virus A
PVIP  potyvirus VPg-interacting protein
PVX  Potato virus X
PVY  Potato virus Y
qRT-PCR  real-time quantitative RT-PCR
R gene  resistance gene
RecA  recombinase A
REN  RNA replication enhancer
Rev  HIV-1 regulator of virion expression
RDR  RNA-dependent RNA polymerase (plant)
RdRp  RNA-dependent RNA polymerase (virus)
RH  RNA helicase
RISC  RNA-induced silencing complex
RNA  ribonucleic acid
(+)-RNA  (viral) positive-sense RNA
(-)-RNA  (viral) negative-sense RNA
RNase  ribonuclease
RNP  ribonucleoprotein
RP  right genomic primer
rpm  revolutions per minute
RT-PCR  reverse transcription polymerase chain reaction
RTM  restricted TEV movement
RubisCO  ribulose-1,5-bisphosphate carboxylase/oxygenase
Rx  PVX resistance gene
SA  salicylic acid
SAR  systemic acquired resistance
<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Full Name</th>
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<tbody>
<tr>
<td>SARS</td>
<td>severe acute respiratory syndrome</td>
</tr>
<tr>
<td>SARS-CoV</td>
<td>SARS-associated coronavirus</td>
</tr>
<tr>
<td>SCE1</td>
<td>SUMO conjugation enzyme 1</td>
</tr>
<tr>
<td>SD</td>
<td>synthetic defined</td>
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<tr>
<td>SF</td>
<td>superfamily</td>
</tr>
<tr>
<td>siRNA</td>
<td>small interfering RNA</td>
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<tr>
<td>SMV</td>
<td><em>Soybean mosaic virus</em></td>
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<tr>
<td>sRNA</td>
<td>small RNA</td>
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<tr>
<td>ssRNA</td>
<td>single-stranded RNA</td>
</tr>
<tr>
<td>(+) ssRNA</td>
<td>positive-sense single-stranded RNA</td>
</tr>
<tr>
<td>STRS1</td>
<td>Stress Response Suppressor 1</td>
</tr>
<tr>
<td>STRS2</td>
<td>Stress Response Suppressor 2</td>
</tr>
<tr>
<td>SUMO</td>
<td>small ubiquitin-related modifier</td>
</tr>
<tr>
<td>TAIR</td>
<td>The Arabidopsis Information Resource</td>
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<tr>
<td>TAS-ELISA</td>
<td>triple-antibody sandwich enzyme-linked immunosorbent assay</td>
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<tr>
<td>TBSV</td>
<td><em>Tomato bushy stunt virus</em></td>
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<tr>
<td>TCV</td>
<td><em>Turnip crinkle virus</em></td>
</tr>
<tr>
<td>T-DNA</td>
<td>transfer DNA</td>
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<tr>
<td>TEV</td>
<td><em>Tobacco etch virus</em></td>
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<tr>
<td>TMV</td>
<td><em>Tobacco mosaic virus</em></td>
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<tr>
<td>ToMV</td>
<td><em>Tomato mosaic virus</em></td>
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<tr>
<td>Tris</td>
<td>tris-hydroxymethyl aminomethane</td>
</tr>
<tr>
<td>Trp</td>
<td>tryptophan</td>
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<tr>
<td>TRV</td>
<td><em>Tobacco rattle virus</em></td>
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<td>TuMV</td>
<td><em>Turnip mosaic virus</em></td>
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<tr>
<td>TVMV</td>
<td><em>Tobacco vein mottling virus</em></td>
</tr>
<tr>
<td>UTR</td>
<td>untranslated region</td>
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<tr>
<td>UWO</td>
<td>The University of Western Ontario</td>
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<tr>
<td>VIGS</td>
<td>virus-induced gene silencing</td>
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<tr>
<td>VPg</td>
<td>the viral genome-linked protein</td>
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<tr>
<td>VPg-Pro</td>
<td>VPg fused to a protease domain at the C terminus</td>
</tr>
<tr>
<td>VRC</td>
<td>viral replication complex</td>
</tr>
<tr>
<td>WCIMV</td>
<td><em>White clover mosaic virus</em></td>
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<tr>
<td>WNIV</td>
<td><em>West Nile virus</em></td>
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<tr>
<td>WT</td>
<td>wild-type</td>
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<tr>
<td>Y2H</td>
<td>yeast two-hybrid</td>
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<tr>
<td>YC</td>
<td>C-terminal fragment of the YFP protein</td>
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<td>yellow fluorescent protein</td>
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<tr>
<td>YN</td>
<td>N-terminal fragment of the YFP protein</td>
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<tr>
<td>YPD</td>
<td>yeast extract-peptone-dextrose</td>
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<td>YPDA</td>
<td>YPD medium supplemented with adenine hemisulfate</td>
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Chapter 1: Introduction

1.1 An overview of plant viruses

In the late 19th Century, a tiny infectious agent was found to cause a mosaic disease on tobacco plants, which was proven to be irrelevant to bacteria. Unlike bacteria, the infectious agent was in fact filterable. Subsequently, the term “virus”, the Latin word meaning “slimy liquid” or “poison” was coined to indicate the non-bacterial nature of this plant disease and *Tobacco mosaic virus* (TMV) was shown to be the culprit of the tobacco mosaic disease (Beijerinck, 1898). From then on, the concept of a virus as a distinct infectious entity has been established, and a lot of plant diseases that have caused substantial economic losses in the agriculture community have been found to be associated with viruses. Along with the breakthroughs of new biotechnology, numerous viral pathogens have been identified.

In essence, viruses can be regarded as the ultimate and prototypical paradigm of "selfish genes". Like all cellular life forms, viruses carry genetic information constructed by either deoxyribonucleic acid (DNA) or ribonucleic acid (RNA) in a single-stranded or double-stranded form (Astier *et al.*, 2001). However, the genetic code carried by viruses, which must be decoded by the molecular machinery of the host cell that it infects (Wagner *et al.*, 1999), is directed towards only for virus own replication. Besides the genetic materials, all viruses have coat proteins (CPs) that function as a shell to protect the viral genome from degradation, and some are wrapped by an outer membrane envelop that surrounds them during their time outside a cell. The coordinated interactions between CPs and viral nucleic acid are essential to regulate virion assembly and disassembly (Callaway *et al.*, 2001).

All viruses are obligate parasites since they can be maintained only inside living cells. Most of RNA viruses have a small genome ranging from 4 to 15 kilobases (kb) in length and have a very limited coding capacity, encoding a set of proteins that vary from 3 to 10-15 of the upper limit (Matthews and Hull, 2002). Therefore, viruses have to largely depend upon their hosts to complete almost all major steps of their infection process (Whitham and Wang, 2004).
As for a plant virus, a successful infection begins with the efficient penetration of the viral particle into plant cells such as epidermal or mesophyll cells. Then, the viral particle undergoes disassembly for translation and replication in the initially infected cell. Subsequently, the newly assembled viral particle traffics into the adjacent healthy cells via plasmodesmata (PD). Finally, the virus enters the vascular tissue to reach remote sites, thus infecting the whole plant (Schoelz et al., 2011) (Figure 1).

Viruses replicate, evolve and are adapted to the host cells they infect. Viruses are known to be able to infect all types of living organisms including eukaryotes (vertebrates, invertebrates, plants and fungi) and prokaryotes (bacteria and archaea) (Carter and Saunders, 2007). This could be attributed to the fact that viruses themselves are extremely adaptable, using different replication strategies and are highly mutable to generate genetic variation through mutation and recombination in response to various environmental pressures.

In an infected cell, viruses can cause extensive remodeling of the intracellular environment in favor of the replication process (Laliberté and Sanfaçon, 2010). For instance, some plant viruses induce the proliferation of endoplasmic reticulum (ER) membranes for the formation of membranous vesicles to facilitate the assembly of viral replication complexes (Salonen et al., 2005), whereas others may reshape cellular organelles such as chloroplasts, mitochondria, or peroxisomes (Wei et al., 2010).

Plant pathogenic viruses often rely on insect, nematode and/or fungal vectors to gain entry into host plants, move from plant to plant and move over distant regions (Thresh, 2006). In addition, viruses can also be transmitted by human activities such as propagation of infected vegetative materials, grafting of infected materials, as well as through pollen and seed produced by the infected plants (Andret-Link and Fuchs, 2005).

As one of the main threats to agricultural production, viruses cause many important plant diseases, and are responsible for losses in crop yield and quality all over the world. Therefore, a great deal of effort is needed to develop a better comprehension of plant virology and the interplay between plants and viruses, in order to develop more potent strategies against virus infection.
Figure 1 Schematic depiction of potyvirus infection cycle.

After viral entry into the cell, the virion is disassembled and viral positive-sense RNA (+(+)RNA) is released into the cytoplasm for translation. Newly translated viral proteins such as RNA-dependent RNA polymerase (RdRp) and helicase direct the assembly of viral replication complex (VRC) and recruit the viral RNA to the VRC for replication. Viral negative-sense RNA ((-)RNA) is synthesized and serves as template for amplification of viral (+(+)RNA progeny. The new viral (+(+)RNA is released from the VRC and starts a new cycle of translation and replication or is encapsidated into new progeny virions and transport to the adjacent cells. Modified from (Nagy and Pogany, 2011).
1.1.1 Replication of positive-sense RNA viruses

The majority of known plant viruses have positive-sense RNA genomes and most viral RNA genomes are made of single-stranded RNA (van Regenmortel et al., 2000). Upon entry into the host cell, the viral positive-sense RNA readily serves as a messenger RNA (mRNA) to direct biosynthesis of viral proteins for viral genome replication (Khan and Dijkstra, 2006). This type of viruses includes many important human and animal viruses, such as Hepatitis C virus (HCV), West Nile virus (WNV), Dengue virus (DENV) and severe acute respiratory syndrome coronavirus (SARS CoV) (Nagy and Pogany, 2011). For plant viruses, the vast majority characterized to date are positive-sense RNA viruses as well, and only the viruses classified into the Caulimoviridae, Geminiviridae and Nanoviridae families store their genetic information in DNA genomes (Astier et al., 2001).

Viral genome replication generally refers to the cellular process by which viral genomic nucleic acid is multiplicato. As for a positive-sense RNA virus, the first step of viral genome replication is to synthesize the viral proteins required for viral replication. These viral proteins include viral RdRp, helicase and other essential viral replicase components, and are mainly involved in membrane targeting, template recruitment and amplification as well as RNA capping (Novak and Kirkegaard, 1994; Ivanov and Mäkinen, 2012). However, since viruses do not encode translation factors or ribosomes, they have to hijack the host translational machinery to complete protein synthesis and genome replication (Patarroyo et al., 2012).

Assembly of the viral replication complex (VRC) is a prerequisite for viral genome replication, and provides an environment in which viral RNA can be synthesized and sheltered from the cytoplasmic environment of the cell to avoid antiviral RNA silencing (Laliberté and Sanfaçon, 2010). A growing body of evidence suggests that for all positive-sense RNA viruses, viral genome replication occurs on different types of intracellular membranes (Belov et al., 2007). Hence, VRCs that contain both viral and host components are anchored in a virus-induced membrane compartment. In plants, VRCs have been found to target different subcellular organelles, varying considerably
among viruses, such as the ER, chloroplast, vacuole, peroxisome, Golgi and mitochondria (Salonen et al., 2005). In addition, specific cellular membranes can also be modified by different viruses to facilitate their RNA replication. The requirement for membrane rearrangements and modifications during viral genome replication indicates that the host membranes are essential and functional components of VRCs. Moreover, many viruses encode integral membrane proteins that associate with particular intracellular membranes and act as anchors for the formation of VRCs (Sanfaçon, 2012). In addition, these integral membrane proteins may play a vital role in recruiting other viral proteins and host components into VRCs.

Within VRCs, viral RdRp and helicase are the two most critical components. These two proteins are associated with other viral proteins as well as host cellular factors for viral genome replication. As noted, all the positive-sense RNA viruses encode viral polymerase proteins, which are responsible for catalyzing synthesis of progeny viral RNA genomes from the parental viral RNA genome. A complementary negative-sense RNA is synthesized by the viral RdRp using the positive-sense RNA as a template. As for viral helicase, it functions as a necessary component to help unwind local double-stranded RNA regions during replication. With its assistance, the newly generated negative-sense RNA serves as a template for the synthesis of the progeny positive-sense RNA. It is worth mentioning that not all RNA viruses have a helicase function, as only those with genomes that exceed 6 kb contain genes encoding helicases (Gorbalenya and Koonin, 1993). The progeny positive-sense RNA is synthesized 10 to 100 fold faster than the negative-sense RNA, indicating that viruses have evolved sophisticated mechanisms for temporal and spatial control of RdRp during negative-sense and positive-sense RNA synthesis (Sanfaçon, 2005).

Importantly, the fact that viral genomes of positive-sense RNA viruses serve both as the mRNA for translation and the template for replication raises the possibility that the replication process is tightly coupled to translation. Ribosomes travel from 5' to the 3' end of the viral RNA during protein translation while viral RdRp travels from the 3' to the 5' end of the viral RNA for replication (Ahlquist et al., 2003). As a consequence, successful
viral infection depends on the precise execution of regulatory mechanisms to control the
switch from the translation mode to the replication mode (Sanfaçon, 2005).

1.1.2 Picorna-like plant viruses, *Potyviridae*

Potyviruses represent the largest group of known plant viruses. They are members of the
genus *Potyvirus* in the family *Potyviridae*. The family contains seven additional genera:
*Brambyvirus*, *Bymovirus*, *Ipomovirus*, *Macluravirus*, *Poacevirus*, *Rymovirus*, and
*Tritimovirus*. Among 176 species in the family, 146 species belong to the *Potyvirus*
genus (Fauquet *et al.*, 2005; King *et al.*, 2012). Viruses of the family *Potyviridae* share
similarities in genome organization and replication strategies with members of the family
*Picornaviridae* of human/animal viruses. Therefore, together with plant bipartite como-
and nepoviruses in the sub-family *Comovirinae*, viruses in the family *Potyviridae* and
picornaviruses are classified into the *Picornavirales* (Goldbach, 1987).

Many of potyviruses are economically important pathogens of agricultural crops. They
have a broad geographical distribution and can infect a wide range of hosts including
mono- and dicotyledonous plant species and lead to significant losses in crop yield and
economy worldwide each year. For example, as the most devastating viral pathogen of
stone fruit crops, *Plum pox virus* (PPV) can infect a variety of fruit species including
peaches, apricots, plums, cherries and almonds, leading to a dramatic reduction of fruit
yields (Sochor *et al.*, 2012; García *et al.*, 2014). *Potato virus Y* (PVY), as the type species
of *Potyvirus*, is a destructive virus that can cause significant damage to potato, tobacco
and pepper production. Together with *Potato virus A* (PVA; genus *Potyvirus*) and *Potato
leaf roll virus* (PLRV; genus *Polerovirus*), they are three major plant viruses that can
pose the biggest threat to potato production worldwide. Due to their high biological and
economic importance, PPV and PVY are considered among the top 10 most important
plant viruses (Scholthof *et al.*, 2011).

Most of potyviruses are spread in a non-persistent manner by aphids or via grafting and
wounding during agricultural practices and some are also seed-transmitted. Potyviruses
produce non-enveloped, flexuous filamentous particles, about 680-900 nm in length and
11-13 nm in diameter. Each encapsidated genome contains a positive-sense single-
stranded RNA of approximately 10,000 nucleotides (Gibbs and Ohshima, 2010). Due to their diverse transmission modes and wide host range, it is very difficult to control and prevent potyvirus infection in agriculture (Gibbs et al., 2008).

1.1.3 Genome organization of potyviruses

The potyviral genome is a positive-sense, single-stranded RNA with a virus-encoded protein VPg covalently linked to the 5' end, and a polyadenylated [poly(A)] tail at its 3' end. The viral genome contains a single open reading frame (ORF) that is translated into a long polyprotein of about 350 kDa. This large polyprotein is ultimately cleaved by three different virus-encoded proteases into at least ten multifunctional proteins (from N- to C-terminus): P1, helper component protease (HC-Pro), P3, 6K1, cylindrical inclusion (CI) protein, 6K2, viral genome-linked protein (VPg), nuclear inclusion a (Nia), nuclear inclusion b (Nib), and capsid protein (CP) (Urcuqui-Inchima et al., 2001). In addition to the large polyprotein, there is a small ORF called “pretty interesting Potyviridae ORF” (PIPO) embedded in the P3 cistron (Chung et al., 2008). PIPO results from a ribosomal frameshift during translation and is produced as a translational fusion with the N-terminus of P3 coding region. The resulting fusion protein is about ~25 kDa, termed P3N-PIPO (Wei et al., 2010; Vijayapalani et al., 2012) (Figure 2).

Unlike many other plant viruses, the Potyviridae family do not regulate expression of specific viral genes quantitatively and temporally through synthesis of subgenomic RNAs (Sztuba-Solińska et al., 2011). As the result of translational frameshift at P3, three viral proteins P1, HC-Pro and P3N-PIPO are theoretically produced more than other eight viral proteins, dependent on the frameshift efficiency. However, viral proteins within each of these two groups are translated in an equimolar ratio. It is therefore important for potyviruses to employ different strategies to dynamically regulate viral protein expression during their infection cycle (Ivanov et al., 2014).

1.1.4 Functions of potyviral proteins

P1, which is the first protein that is translated, is the most variable potyviral protein. It is located at the beginning of the viral genome of potyviruses, as a serine protease which is
Figure 2  Potyviral genome organization and polyprotein processing strategy.

(A) Genome organization of the genus *Potyvirus*. The genome of potyvirus is the (+)ssRNA molecule covalently linked to VPg at the 5’ end and poly(A) at the 3’ end. The VPg is shown in cycle. The poly(A) tail is shown in [A]n. The viral open reading frame is depicted as a large box in which individual viral proteins are delineated by vertical lines. 5’ and 3’ untranslated regions are indicated as two short horizontal lines, respectively. Modified from (Ivanov et al., 2014).

(B) Schematic representation of potyviral polyprotein processing strategy. The potyviral genome is translated into a single polyprotein which is then processed by three virus-encoded proteases into individual mature proteins. Proteolytic sites are marked with arrows. P1 protease is responsible for P1/HC-Pro cleavage site. HC-Pro protease is responsible for HC-Pro/P3 cleavage site. NIa-Pro protease is responsible for all other cleavage sites. PIPO derived from a frameshift in the P3 cistron is indicated as a short grey bar. PIPO fused with the N-terminal portion of P3, termed P3N-PIPO is indicated as a red bar. Modified from (Wei et al., 2010).
responsible for cis-cleavage of the polyprotein between P1 and HC-Pro (Rohožková and Navrátil, 2011). Although it has been well known that the cleavage is carried out by a serine protease domain within the C-terminus of P1, no other conserved functional domains in P1 have been discovered so far. This is likely due to the fact that P1 is the most divergent potyviral protein in terms of both length and amino acid sequence (Verchot et al., 1991). Swapping experiments between P1 proteins from PPV and Tobacco vein mottling virus (TVMV) suggest that P1 may play a critical role in host compatibility and pathogenicity (Salvador et al., 2008). Recently, it has been shown that an amino-acid substitution in the P1 cistron could overcome eIF4E-mediated recessive resistance against Clover yellow vein virus (CIYVV) in pea (Nakahara et al., 2010). In addition, although it has long been known that P1 cleavage is required for viral infectivity, the functions of P1 during the virus life cycle remained largely unknown. Over the last decade, accumulated evidence suggests that P1 might be able to play a vital role in effectively counteracting the antiviral defense mediated by RNA silencing. This notion was subsequently strengthened by the findings obtained in Cucumber vein yellowing virus (CVYV), a member of the genus Ipomovirus, the fourth monopartite genus of the Potyviridae family. Unlike the viruses from the genus Potyvirus, CVYV does not contain a sequence coding for HC-Pro in its genome, but has two P1 copies organized in tandem. It was revealed that P1 can enhance the activity of HC-Pro in members of the genus Potyvirus, and, moreover, the second copy (P1b) in CVYV is able to suppress RNA silencing in a manner similar to that of HC-Pro from the genus Potyvirus, suggesting that P1b is replacing HC-Pro in this function (Valli et al., 2006). From an evolitional angle, this finding may suggest that viruses have evolved to counteract RNA silencing by similar mechanisms using very different proteins within the Potyviridae family.

Potyviral HC-Pro is a multifunctional protein that is directly involved in diverse aspects of the potyvirus infection process. It is initially known to act as the helper component for aphid-mediated plant-to-plant transmission (Govier and Kassanis, 1974). In addition, HC-Pro has a cysteine protease activity that autocatalytically cleaves at its own C-terminus, between HC-Pro and P3. Notably, HC-Pro functions as an RNA-silencing suppressor of host antiviral defense mechanism by specifically binding viral 21-nucleotides (nt) small RNAs (Shibolet et al., 2007; Hasiów-Jaroszewska et al., 2014).
P3, the third protein, is similar to the P1 in its variability among different potyviruses. The roles of P3 involved in symptom development and as a pathogenicity determinant are supported by independent studies from several laboratories (Sáenz et al., 2000; Jenner et al., 2003; Suehiro et al., 2004; Chowda-Reddy et al., 2011; Wen et al., 2011). Recently, a yeast two-hybrid (Y2H) study has provided the evidence that potyviral P3 interacts with the subunit of host ribulose-1,5-bisphosphate carboxylase/oxygenase (RubisCO) protein and the interaction may contribute to the potyvirus symptom development (Lin et al., 2011). In addition, subcellular localization studies of Tobacco etch virus (TEV) P3 have revealed that P3 localizes to the ER membrane and forms punctate inclusions associated with the Golgi apparatus. Moreover, the P3 punctate structure could traffic along the actin filaments and colocalize with the replication vesicles, suggesting that the function of P3 may be related to viral replication as well (Cui et al., 2010).

Recent research on P3N-PIPO has indicated that it is essential for potyviral cell-to-cell movement (Wei et al., 2010; Wen and Hajimorad, 2010). This capability was attributed to the role of P3N-PIPO that modulates targeting of CI to form the conical structure at PD. Using a Y2H screen, a host plasma membrane associated cation-binding protein (PCaP1) was found to interact with P3N-PIPO. Knockout of PCaP1 in Arabidopsis could confer enhanced resistance against Turnip mosaic virus (TuMV) (Vijayapalani et al., 2012), suggesting PCaP1 may affect viral intercellular transport through regulation of P3N-PIPO function.

6K1 is a short polypeptide whose function is poorly understood. The analysis of Pea seed-borne mosaic virus (PSbMV) 6K1 has suggested that the P3-6k1 region may function as a host-specific pathogenicity determinant (Johansen et al., 2001). Recent study of one isolate of Soybean mosaic virus (SMV) has provided evidence that 6K1 protein is likely to play a role in the cell-to-cell movement during potyvirus infection (Hong et al., 2007).

CI is a versatile protein that forms pinwheel-shaped cylindrical cytoplasmic inclusions in infected cells. CI processes NTPase and RNA helicase activities, which are involved in unfolding of structured RNA duplexes during viral genome replication. Potyviral CI may
also contribute to symptom determination and elicitation of dominant resistance responses (Zhang et al.; Seo et al., 2009). Additionally, interactions between CI protein and host proteins originating from the ER and chloroplast have been pointed out, suggesting the presence of CI in virus-induced vesicles (Jiménez et al., 2006). The role of CI in potyvirus cell-to-cell movement through PD has been demonstrated by analyzing TEV CI-mutants (Carrington et al., 1998). Intriguingly, CI protein that expressed transiently in TuMV-infected cells is further targeted to PD, accumulating as spike-like structures in proximity to the viral vesicles, in addition to structures penetrating the cell wall (Wei et al., 2010). The targeting of CI to PD is mediated by P3N-PIPO (Wei et al., 2010). Taken together, CI protein acts as an RNA helicase involved in viral genome replication inside viral vesicles, and also exhibits different functions, such as facilitating virus transport to adjacent cells (Sorel et al., 2014).

6K2, the second 6 kDa polypeptide, is a putative membrane-anchor protein that plays a critical role in anchoring the potyviral VRCs to intracellular membrane structures through its highly hydrophobic domain (Restrepo-Hartwig and Carrington, 1992). 6K2 is also responsible for membrane modifications and rearrangements of the early secretory pathway in infected cells. It can induce the formation of viral vesicles from ER membranes in the host cell, leading to the formation of the VRCs that contain all components required for viral genome replication (Schaad et al., 1997). Recently, 6K2 was also found to be involved in intracellular movement of viral vesicles along actin microfilaments (Grangeon et al., 2013). In addition, a variety of intermediate polyprotein precursors containing the domain for the 6K2 protein, including CI-6K2 and 6K2-NIa, have been identified in infected cells through an alternative cleavage of the large viral polyprotein.

Potyviral NIa localizes to the nucleus where nuclear inclusions are induced. NIa is processed to yield two viral proteins, VPg and NIa-Pro by its C-terminal protease domain. NIa has recently been observed to interact with fibrillain in the nucleus and this interaction may play a role in suppression of antiviral gene silencing (Rajamäki and Valkonen, 2009).
VPg is a virus-encoded protein that is covalently linked to the 5' end of viral genome and serves as a protein primer for viral genome replication and a functional equivalent to the eukaryotic mRNA cap structure for protection of the viral RNA genome and translational initiation (Wittmann et al., 1997). Accordingly, VPg is a versatile protein that controls many processes leading to viral proliferation. Various precursor forms of VPg have been detected in infected cells resulting from the cleavage of polyprotein and maturation of viral proteins. For example, VPg-Pro (Nla) is detected in the cytoplasm and nucleus of infected cells (Léonard et al., 2004). 6K2-VPg-Pro is found to be associated with intracellular membranes and within vesicular structures derived from the ER (Jiang and Laliberté, 2011). VPg is suggested to be a hub protein, interacting with host proteins as well as viral proteins during the potyvirus life cycle (Jiang and Laliberté, 2011). VPg can bind eukaryotic translation initiation factor 4E (eIF4E) and its isoform eIF(iso)4E (Wittmann et al., 1997; Leonard et al., 2000). Knockout of eIF(iso)4E can lead to resistance to potyvirus in Arabidopsis (Lellis et al., 2002). Other host factors interacting with VPg include a cysteine-rich protein termed potyvirus VPg-interacting protein (PVIP) (Dunoyer et al., 2004), AtRH8, an Arabidopsis DEAD-box RNA helicase-like protein (Huang et al., 2010), eukaryotic elongation factor eEF1A (Thivierge et al., 2008) and poly(A)-binding proteins (PABP) (Dufresne et al., 2008).

Nla-Pro is located at the C-terminal region of the Nla protein and is responsible for cleavage of at least six cleavage sites in the potyviral polyprotein. As a cysteine protease, Nla-Pro shares structural similarity with cellular serine protease (Adams et al., 2005). The nuclear distribution of Nla-Pro is manifested as a formation of inclusion bodies and observed in the late stage of viral infection (Schaad et al., 1996). Since Nla-Pro has non-substrate-specific DNase activity, it is likely that Nla-Pro may play a role in degradation of the host DNA (Anindya and Savithri, 2004). The ability of interacting with viral RdRp (Nlb) and non-specific binding of RNA suggests that Nla-Pro is involved in the viral genome replication process (Li et al., 1997; Guo et al., 2001). A recent study has shown that overexpression of Nla-Pro can attract aphid vectors and increase their reproduction in order to promote virus transmission (Casteel et al., 2014).
Potyviral NIb acts as a viral RdRp and interacts with VPg and Nla-Pro. During viral infection, NIb functions in combination with other viral and host factors to catalyze synthesis of new viral progeny genomes (Hong and Hunt, 1996). It has been shown that the interaction of NIb with 6K2-VPg-Pro is required for the recruitment of NIb into the virus-induced membrane-bound vesicles that house VRC (Li et al., 1997). Additionally, uridylylation of VPg protein by NIb plays a pivotal role in regulation of viral RNA synthesis (Puustinen and Mäkinen, 2004). More recently, SUMOylation of NIb by Arabidopsis SCE1 has been demonstrated to be essential for viral infection. It has also been proposed that the SUMOylation may directly regulate the function(s) of NIb involved in viral replication. Considering that NIb from not only TuMV but also TEV and SMV can interact with SCE1, the SUMOylation of NIb within the host cell is most likely conserved in the potyvirus replication process (Xiong and Wang, 2013).

Potyviral CP forms the capsid that mainly functions to encapsidate the potyviral RNA. The functions of CP have been related to viral translation, replication and transmission (Dolja et al., 1994). Moreover, accumulating evidence indicates that CP can bind HC-Pro, and the interaction is essential for efficient virus transmission mediated by aphid (Blanc et al., 1997). In addition, based on the similarity of CPs among different potyviruses, the amino acid sequence of CP has been used for determination of relationship within potyviruses. CP has also been suggested to participate in potyvirus intercellular movement, together with HC-Pro, CI and P3N-PIPO (Lucas, 2006; Hofius et al., 2007; Wei et al., 2010).

1.1.5 *Turnip mosaic virus* (TuMV)

TuMV is a member of the genus *Potyvirus*. Historically, TuMV was first reported in the USA on *Brassica rapa* in 1921 (Gardner and Kendrick, 1921), but is now known to occur in many regions of the world including the temperate and tropical climate areas of Africa, Asia, Europe, Oceania and the Americas (Ohshima et al., 2002). As one of the most prevalent viral pathogens, TuMV infects a wide range of plant species, mostly (although not exclusively) in the family *Brassicaceae* (Sánchez et al., 2003). Other non-brassica crops (radish, lettuce, endive, escarole, horseradish, peas, and rhubarb) and ornamentals
were also found to be naturally susceptible to TuMV infection. By 1991, TuMV had been found to infect over 318 species in 156 genera of 43 plant families (Edwardson and Christie, 1991). As it causes significant economic losses in many infected vegetable and horticultural crops, TuMV was ranked second after Cucumber mosaic virus (CMV, genus Cucumovirus) amongst the most damaging plant viruses worldwide (Tomlinson, 1987). Given the fact that TuMV is able to infect the model plants Arabidopsis thaliana (Arabidopsis) and Nicotiana benthamiana (N. benthamiana), it makes TuMV an ideal model to study plant-virus interactions from both plant and virus perspectives (Walsh and Jenner, 2002).

Like other potyviruses, TuMV is transmitted by phloem-feeding insects, such as aphids, in a non-persistent manner (Edwardson and Christie, 1986). It has been reported that at least 89 species of aphids are able to transport TuMV virions to a healthy plant after feeding on the diseased plants (Shukla et al., 1994).

In general, disease symptoms caused by TuMV infection appear on virtually all parts of the infected plants, including leaves, stems, roots, fruits, flowers and seeds. The characteristic symptoms of TuMV infection include mosaic, mottling, chlorotic rings on leaves or color break on flowers, fruits, and stems. In severe cases, infected plants are stunted with leaf distortion and necrosis, fruit and stem malformations, as well as fruit drop (Shukla et al., 1994). Basically, symptoms that develop on plants in response to TuMV infection are usually regarded as harmful effects on the infected plants.

1.2 Host factors required for viral infection

1.2.1 Host factors

Plant viruses have small and compact genomes whose coding capacity is not sufficient to fulfil the viral life cycle. However, as successful pathogens, plant viruses can replicate efficiently within host cells. It is very clear that they have evolved with the ability to hijack host proteins and reprogram host metabolites to support the infection process (Nagy and Pogany, 2011).
Many efforts have been made towards understanding the role of host factors and recent progress has led to the identification and characterization of a number of important host factors recruited for plant virus replication. Different approaches have been employed, such as genome-wide screening and proteome-wide screening (Nagy and Pogany, 2010). In *Saccharomyces cerevisiae* (*S. cerevisiae*), several genome-wide screenings have identified approximately 130 genes that affect *Tomato bushy stunt virus* (TBSV, genus *Tomusvirus*, family *Tomusviridae*) replication (Panavas et al., 2005; Jiang et al., 2006). In the case of *Brome mosaic virus* (BMV, genus *Bromovirus*, family *Bromoviridae*), around 100 yeast genes have also been shown to play a role in viral replication (Kushner et al., 2003; Gancarz et al., 2011).

Diverse approaches have also been used to identify host factors from plants required for viral infections by several plant viruses including potyviruses (Dufresne et al., 2008; Hafrán et al., 2010), *Tomato mosaic virus* (ToMV, genus *Tobamovirus*) (Nishikiori et al., 2006) and TBSV (Serva and Nagy, 2006). An emerging picture from these studies is that host factors play versatile roles during plant RNA virus replication, including: 1) assistance in the proper assembly of VRCs and cellular membrane remodelling; 2) recruitment of viral proteins and template RNA to the VRC; 3) regulation of the switch from viral genome translation to replication; 4) participation in the intracellular transport of viral proteins and viral RNA; and 5) facilitating folding of viral proteins as protein chaperones (Nagy and Pogany, 2011; Hyodo and Okuno, 2014).

For instance, the potyviral replication factory is associated with intracellular membranous structures derived from the ER (Wei et al., 2010) and where a number of host proteins are recruited to form the VRC for viral replication (Wang, 2013). These host factors include eukaryotic translation initiation factors (eIFs) (Wittmann et al., 1997; Schaad et al., 2000), a cysteine-rich protein PVIP (Dunoyer et al., 2004), Heat shock cognate 70-3 (Hsc70-3) (Dufresne et al., 2008), PABP (Dufresne et al., 2008), eEF1A (Thivierge et al., 2008), DEAD-box RNA helicase (Huang et al., 2010) and DNA-binding protein phosphatase 1 (DBP1) (Castelló et al., 2010). Among them, eIFs and DEAD-box RNA helicases are relatively well characterized.
1.2.2 Eukaryotic translation initiation factors (eIFs)

Translation of the viral genome is fully dependent on the host translation machinery. Translation initiation is the highly-regulated and rate-limiting step of protein synthesis (Sonenberg and Hinnebusch, 2009). It is initiated by the recruitment of the eIF4F complex to the viral RNA (Bushell and Sarnow, 2002). The eIF4F complex is composed of factors eIF4E, eIF4G and eIF4A. eIF4E is a cap binding protein that binds to the 5’ cap structure of mRNA or the viral protein linked to the 5' end of the viral genomic RNA. eIF4E is associated with eIF4G, a scaffold protein that interacts with other components of the eIF4F complex (Sonenberg and Hinnebusch, 2009; Jackson et al., 2010). eIF4A is responsible for recruiting ternary 40S ribosomal complexes and unwinding double-stranded RNA structures (Rogers et al., 1999).

Previous studies have shown that potyviruses selectively recruit one of eIF4E and eIF4G or their corresponding isoforms for their infection (Nicaise et al., 2007). The recruitment of these translation initiation factors occurs through their physical interactions with the viral protein VPg or its precursor NIa. Mutations or knockout of eIF4E or eIF4G or their isoforms eIF(iso)4E and eIF(iso)4G1 or eIF(iso)4G2, could confer resistance against certain potyvirus infection without compromising regular plant growth and development (see section 1.4.2) (Gallois et al., 2010).

1.2.3 Eukaryotic translation initiation factor 4A, eIF4A

Among eIFs, eIF4A is the prototype of DEAD-box RNA helicases (Rogers et al., 1999). It was first characterized through its requirement in translation and was further identified as a component of eIF4F complex (Grifo et al., 1982). Together with the central scaffolding protein eIF4G and the cap-binding protein eIF4E, eIF4A forms the eIF4F complex accompanied by accessory proteins eIF4B and eIF4H (Jackson et al., 2010). The eIF4F complex is essential for the translation of most cellular mRNAs and is an important target for regulation (Jackson et al., 2010).

eIF4A possesses both ATP-dependent RNA helicase activity and RNA remodelling activity. It is suggested that eIF4A is responsible for unwinding RNA secondary
structures in the 5' UTR which would inhibit ribosome scanning (Svitkin et al., 2001). eIF4A also facilitates viral translation initiation by exhibiting RNA helicase activities (Robaglia and Caranta, 2006). RNA helicase activities of eIF4A are largely dependent on stimulation from other translation initiation factors. In the eIF4F complex, the helicase activities of eIF4A are increased which suggests that the helicase activity requires the recruitment of eIF4A to a specific mRNA, preventing the unwinding of RNA structures not targeted by the binding partners (Lu et al., 2014). Hence, the research on eIF4A, as one of the first DEAD-box RNA helicases that have been studied extensively, has led to the discovery of the fundamental principles underlying the functions of DEAD-box RNA helicases (Andreou and Klostermeier, 2013).

1.3 DEAD-box RNA helicase

RNA helicases, which function as highly conserved enzymes, can utilize ATP to catalyze the separation of RNA duplexes and the structural rearrangement of RNA and RNA/protein complexes (ribonucleoprotein (RNP) complexes) in all aspects of RNA metabolism, from transcription, mRNA splicing and translation, RNA modification and transport, ribosome biogenesis, RNP complex assembly to mRNA degradation (Cordin et al., 2006; Pyle, 2008). RNA helicases are present in all eukaryotic cells and many bacteria and some viruses also encode one or more helicase proteins (Hilbert et al., 2009).

Based on sequence and structural features, RNA helicases are classified into five main groups, namely superfamily (SF) 1 to SF5 (Gorbalenya and Koonin, 1993). DEAD-box RNA helicases belong to the helicase superfamily 2 (SF2), together with DEAH, DExH and DExD families, which are commonly referred to as the DExD/H helicase family (Fairman-Williams et al., 2010).

1.3.1 Structure and functions

DEAD-box RNA helicases represent a large family of proteins which have been shown to be involved in almost every step of RNA metabolism (Cordin et al., 2006). The name of the family was derived from the highly conserved amino acid sequence D-E-A-D (Asp–Glu–Ala–Asp) of its motif II (Linder and Jankowsky, 2011).
It has been suggested that some DEAD-box RNA helicases may act as RNA chaperones, promoting the formation of optimal RNA structures through local RNA unwinding, or as RNPases by mediating RNA-protein association/dissociation (Fuller-Pace, 2006). DEAD-box RNA helicases play essential roles in regulating cellular RNA metabolism. For example, they function as part of the spliceosome complexes and/or the eukaryotic translation initiation machinery (Rocak and Linder, 2004).

DEAD-box RNA helicases are characterized by a set of conserved motifs, namely Q, I, Ia, Ib, Ic, II, III, IV, IVa, V, Va, and VI, which contribute to ATP binding and hydrolysis, RNA binding and duplex unwinding (Cordin et al., 2006). Motifs Ia, Ib, Ic, IV, IVa and V participate in RNA binding, whereas motifs Q, I, II and VI have been implicated in ATP binding and hydrolysis (Rocak and Linder, 2004). The motifs III and Va are responsible for coupling ATPase and duplex separation (Tanner et al., 2003). These characteristic sequence motifs are located within a conserved spatial arrangement in the helicase core, which is formed by two recombinase A (RecA)-like domains with flexible central regions (Singleton et al., 2007; Linder and Jankowsky, 2011).

Although DEAD-box RNA helicases share the highly conserved structure of the helicase core, they have been associated with a variety of ATP-dependent cellular functions (Rocak and Linder, 2004). RNA unwinding activity is the main function performed by DEAD-box RNA helicases, and involves ATP-dependent binding and RNA or RNP structure remodelling (Pyle, 2008). DEAD-box RNA helicases load directly onto the duplex region and then separate the strands apart in an ATP-dependent manner instead of translocation on the RNA. This evident unwinding style is termed local strand separation (Yang et al., 2007). The highly targeted unwinding process prevents large-scale unravelling of exquisite-assembled RNA or RNP structures. Each RNA unwinding event utilizes one single ATP molecule through ATP binding and hydrolysis (Chen et al., 2008). In addition to ATP-dependent RNA unwinding, DEAD-box RNA helicases may also participate in export of mRNA from the nucleus to the cytoplasm. For example, the DEAD-box protein Dbp5 has been shown to mediate mRNA export to the cytoplasm (Tran et al., 2007).
1.3.2 Association with abiotic stress

Plants are immobile organisms and are subject to a wide range of environmental insults, including biotic and abiotic stresses. Abiotic stresses, such as low temperatures, high salinity and drought, have an adverse influence on the plant growth, development and productivity (Knight and Knight, 2001). Plants respond to abiotic stresses in different ways and have evolved a complex variety of strategies to increase their tolerance to environmental stresses through physical adaptation and molecular and cellular changes (Takken et al., 2006). As part of plant stress responses, plants regulate gene expression in order to activate and integrate various tolerance mechanisms. The targeted genes encode proteins involved in different biological functions, including nucleic acid metabolism (Chinnusamy et al., 2004; Zhu et al., 2007).

Recent studies have revealed that RNA helicases play a critical role in plant stress responses (Owttrim, 2006; Vashisht and Tuteja, 2006). Notably, when exposed to low temperatures, RNA molecules form stable non-functional secondary structures, and hence require RNA chaperones to perform the proper functions (Lorsch, 2002). It is possible that DEAD-box RNA helicases, which can operate as RNA chaperones, are able to unwind misfolded RNA structures using energy derived from ATP hydrolysis, thereby ensuring correct RNA folding (Vashisht and Tuteja, 2006).

An Arabidopsis osmotically responsive gene, LOS4 encoding a DEAD-box RNA helicase (AtRH38), which has been reported to be crucial for expression of cold-responsive genes under conditions of low temperatures. LOS4 functions in cold tolerance through regulating mRNA export from the nucleus to the cytoplasm (Gong et al., 2002; Gong et al., 2005). Moreover, two Arabidopsis DEAD-box RNA helicase genes, Stress Response Suppressor 1 (STRS1) and 2 (STRS2) have been identified to suppress responses to abiotic stresses (Kant et al., 2007). Mutations of either STRS1 or STRS2 in Arabidopsis led to an increased tolerance to salt, osmotic, and heat stresses, and thus both STRS1 and STRS2 appear to play critical roles in response to abiotic stresses by attenuating expression of upstream stress signaling components (Kant et al., 2007). Interestingly, in a similar study to characterize functional roles of DEAD-box RNA helicases in response to
abiotic stresses, AtRH25 (STRS2) was shown to be up-regulated in response to low temperature treatment and contribute to enhanced cold tolerance in *Arabidopsis* by exerting RNA chaperone activity (Kim et al., 2008).

In addition to the functional roles in abiotic stress response, some DEAD-box RNA helicases also participate in modulating defence against biotic stresses. For instance, a rice gene *Oryza sativa* BTH-induced RNA helicase 1 (*OsBIRH1*), encoding a DEAD-box RNA helicase, has been implicated in stress response to oxidative stress. Overexpression of *OsBIRH1* confers enhanced disease resistance against fungal pathogen infection in *Arabidopsis* (Li et al., 2008).

### 1.3.3 Association with viral infection

During the past decade, accumulating evidence suggests that RNA helicases likely play several essential roles during viral infection including (i) facilitating viral genomic RNA translation, (ii) recruiting viral RNA for replication, (iii) coordinating viral RNA template for translation or replication, and (iv) regulating viral RNA stability or degradation (Huang et al., 2010). However, detailed studies towards understanding the functions of RNA helicases in positive-sense RNA virus life cycle are very limited.

In a seminal work, Noueiry and colleagues showed that the yeast gene *DED1*, encoding a DEAD-box RNA helicase is required for the translation of BMV, a bromovirus. A point-mutation in *DED1* inhibits BMV RNA replication via disrupting expression of viral-encoded polymerase protein 2a but not affect yeast growth (Noueiry et al., 2000). Coincidentally, through a genome-wide screening of yeast genes, *DED1* has also been identified as a host gene required for replication of TBSV, a tombusvirus. Down-regulation of *DED1* affects TBSV viral infection by inhibiting the accumulation of virus-encoded replication proteins (Jiang et al., 2006). Recently, it has been shown that *DED1*-encoded protein Ded1p is required for viral replication of TBSV and *Flock house virus* (FHV, genus *Alphanodavirus*) by binding to the negative-sense viral RNA and promoting positive-sense viral RNA synthesis. Ded1p is recruited to TBSV VCR as an important host component, and ATPase-defective Ded1p mutant fails to initiate TBSV replication, suggesting that helicase activity is required for TBSV replication (Kovalev et al., 2012).
Similar to Ded1p, another RNA helicase Dbp2p (the homolog of the human p68 protein) also binds to the 3' end of the viral negative-sense RNA of TBSV and unwinds the local secondary structure to promote positive-sense RNA replication in yeast (Kovalev et al., 2012). AtRH20, an RNA helicase in Arabidopsis sharing high sequence similarity with DED1, can stimulate TBSV positive-sense RNA synthesis, suggesting RNA helicases in plants may assist viral replication in a similar manner (Kovalev et al., 2012). More recently, two additional cellular RNA helicases, e.g., the eIF4AIII-like yeast FAL1 and the DDX5-like Dbp3 and their orthologs in Arabidopsis, AtRH2 and AtRH5, have been shown to be present in the tombusviruses RVCs (Kovalev and Nagy, 2014). They bind to the 5' proximal RIII (-) replication enhancer (REN) element in the TBSV negative-sense RNA and unwind the dsRNA structure within the RIII(-) REN region (Kovalev and Nagy, 2014). Coordinated unwinding of the dsRNA at the 5' region by this group of RNA helicases and the secondary structure at the 3' terminal region by the DED1/AtRH20 would bring the 5' and 3' terminal sequence of the negative-sense RNA in close vicinity via long-range RNA-RNA base pairing and facilitate asymmetrical viral replication by recycling the viral replicase proteins for multiple rounds of positive-sense viral RNA synthesis (Kovalev and Nagy, 2014). It is also worth to note that an Arabidopsis DEAD-box RNA helicase, AtRH8 and a Prunus persica DDX-like protein, PpDDXL, have been identified to interact with potyviral VPg. AtRH8 colocalizes with the viral replication vesicles, indicating that AtRH8 is necessary for potyvirus infection by facilitating viral genome translation and replication (Huang et al., 2010).

Interestingly, several lines of evidence obtained in recent years indicate that DEAD-box RNA helicases play critical roles in human virus replication. It has been demonstrated that DEAD-box RNA helicase 1 (DDX1) functions as a Rev cellular co-factor supporting Human immunodeficiency virus type 1 (HIV-1) replication. HIV-1 Rev protein is responsible for the transport of viral RNA from the nucleus to cytoplasm by remodeling VRC and is required for HIV-1 virion assembly (Fang et al., 2004; Fang et al., 2005). In addition to DDX1, DEAD-box RNA helicase 3 (DDX3) has also been reported to be required for HIV-1 replication. Functioning as a nucleo-cytoplasmic shuttling protein, DDX3 is responsible for restructuring viral RNAs and facilitating the translocation through the nuclear pore complex. Knockdown of DDX3 suppressed the export of HIV-1
viral RNAs from the nucleus (Yedavalli et al., 2004). Intriguingly, HCV also recruits DDX3 for viral RNA replication. DDX3 might be associated with HCV assembly and the lack of DDX3 would cause a significant decrease of HCV viral RNA accumulation by 95% (Ariumi et al., 2007). A very recent study revealed that DDX3 can also interact with the viral polymerase of *Hepatitis B virus* (HBV), a DNA virus whose replication is dependent on reverse transcription of the viral genome. DDX3 restricts HBV genome replication by inhibition of its reverse transcription (Wang et al., 2009). More recently, DEAD-box RNA helicase 56 (DDX56), a nucleolar helicase has been found to interact with WNV capsid protein. This observation suggests that DDX56 is required for assembly of WNV viral particles. Mutations of DEAD motif of DDX56 would impair the function in packaging viral RNA into virions (Xu et al., 2011; Xu and Hobman, 2012).

Taken together, these studies reinforce the idea that DEAD-box RNA helicases play an essential role in viral infection but the functional mechanisms may differ from helicase to helicase and from virus to virus.

### 1.4 Plant defense responses against viral pathogens

#### 1.4.1 Dominant resistance

Plants are constantly exposed to invasion by a multitude of pathogenic microbes, including viruses. Over the course of evolution, there has always been an "arms race" between plants and plant viruses, in which the viruses evolve mechanisms to survive by invading plants to acquire biosynthetic products and energy, while plants evolve ways to prevent the invasion. Since plants lack mobile defender cells and an adaptive immune system like animals, they rely on an elaborate innate immune system to defend themselves against the viral intruders. There are two general types of antiviral strategies that plants employ to combat viral infections. The better-characterized mechanism is the one mediated by resistance (*R*) genes (Mandadi and Scholthof, 2013). The other is an antiviral RNA silencing pathway, which is triggered by double-stranded RNA, leading to the cellular defense against foreign nucleic acids (Soosaar et al., 2005).
R-gene mediated resistance pathways are often associated with the hypersensitive response (HR) which usually induces programmed cell death (PCD) surrounding the infection site. The phenotype of HR is the appearance of necrotic lesions at the site of local infection. The HR functions to limit viral proliferation, thus the virus is constrained to the lesions and unable to spread to adjacent healthy tissues (Ross, 1961; Moffett, 2009). Following HR in the local infection area, R-gene mediated resistance responses could also lead to systemic acquired resistance (SAR) in tissues distant from local infected area and result in an enhanced resistance to later pathogen attack (Ross, 1961). SAR is considered to be a broad-spectrum, long-lasting resistance through the whole plant (Ryals et al., 1996). This response is activated by the induction of expression of a set of pathogenesis-related genes which encode antimicrobial compounds (Durrant and Dong, 2004; Kang et al., 2005) and results in the generation of the immune signal molecule salicylic acid (SA) (Gaffney et al., 1993).

R-gene mediated resistance is known to be triggered when a pathogen-encoded avirulence factor (Avr) is recognized by a dominant R-gene encoded product in the plant (Bent and Mackey, 2007; Moffett, 2009). The classic model of the "gene-for-gene" resistance is that the N gene of tobacco plants could confer resistance to TMV (genus Tobamovirus) and most tobamoviruses (Erickson et al., 1999). It was first reported by F.O. Holmes in 1938 (Holmes, 1938). The N gene product from Nicotiana glutinosa specifically recognizes the helicase domain of the TMV replicase protein and triggers the HR (Abbink et al., 1998).

The pathogen is recognized through its conserved structures or proteins associated with the pathogen by plant pattern recognition receptors (PRRs), termed pathogen associated molecular patterns (PAMPs) or microbe-associated molecular patterns (MAMPs). The induced immunity responses are noted as PAMP-triggered immunity (PTI) response (Boller and Felix, 2009). After successful invasion, pathogens deliver specific effector molecules into the plant cell to enhance pathogen virulence and impair host defense signaling cascade. The effectors employed by the pathogen could interfere with PTI response, leading to effector-triggered susceptibility (ETS) (Bent and Mackey, 2007). To contribute defense against the pathogen effectors, plant R genes encode a class of
nucleotide binding (NB) and leucine rich repeat (LRR) domain (NB-LRR)-containing proteins which can directly or indirectly recognize the specific effectors to induce effector-triggered immunity (ETI) response (Collier and Moffett, 2009). NB-LRR proteins represent the major class of plant R gene products (R proteins) (Moffett, 2009). Compared with PTI response, ETI occurs faster and acts as a stronger response usually associated with HR at the infection site (Jones and Dangl, 2006; Dodds and Rathjen, 2010).

To date, several dominant R genes against plant viruses have been identified. For example, an Arabidopsis jacalin-type lectin, restricted TEV movement (RTM1), has been shown to prevent the systemic spread of several potyviruses (Chisholm et al., 2000). In addition to RTM1, RTM2 and RTM3 physically interact with RTM1 and also contribute to viral resistance responses (Chisholm et al., 2001; Mandadi and Scholthof, 2013). Lately, another jacalin-type lectin, JAX1, was shown to confer broad resistance against multiple potexviruses including Potato virus X (PVX), Plantago asiatica mosaic virus (PlAMV), White clover mosaic virus (WCIMV), and Asparagus virus 3 (AV-3), suggesting lectins play an important role in plant antiviral immunity (Yamaji et al., 2012). JAX1-mediated resistance against PlAMV occurs via inhibition of viral replication whereas RTM1 impedes viral movement by interference with viral movement-associated proteins (Yamaji et al., 2012). Moreover, tomato (S. hirsutum) resistance gene Tm-1-encoded protein can bind to the replication protein of ToMV which confers resistance to ToMV by inhibiting viral RNA replication (Ishibashi et al., 2007). Potato (Solanum tuberosum) resistance genes Rx1 and Rx2 both impart resistance to PVX through recognition and interaction with the PVX CP and are required to block virus replication (Bendahmane et al., 1999; Bendahmane et al., 2000).

1.4.2 Recessive resistance

As discussed above, plant viruses recruit many host factors to complete their life cycle. The inability to recruit an essential host component may result in resistance against viruses, termed recessive resistance. Genes encoding dysfunctional host factors are referred to as recessive resistance genes (Fraser and Van Loon, 1986).
Recessive resistance is prevalently found to confer resistance to potyviruses (Kang et al., 2005). More than half of the recessive resistance genes reported so far are effective against potyviruses (Diaz-Pendon et al., 2004). The recessive genes involved in the potyvirus-related resistance mainly encode eIF4E and eIF4G or their isoforms (Truniger and Aranda, 2009) and are related to the binding capabilities between potyvirus VPg and eIF4E/eIF4G and their isoforms (Wittmann et al., 1997; Leonard et al., 2000; Schaad et al., 2000).

eIF4E is a crucial component of the eukaryotic translation initiation machinery that binds to 5' cap structure of mRNA to initiate mRNA translation (Sonenberg and Hinnebusch, 2009). Potyviruses encode the VPg which is covalently linked to the 5' end of the viral genomic RNA and allows the translation of viral RNA in a cap-independent manner. Potyviral VPg is found to physically associate with eIF4E/eIF4G and their isoforms (Wang and Krishnaswamy, 2012). Disrupting or eliminating the interactions between VPg and eIF4E/eIF4G proves to be sufficient to prevent potyvirus infection in planta (Leonard et al., 2000). In all cases, the resistance phenotypes result from a few amino acid changes in the eIF4E or eIF(iso)4E proteins, which are grouped in two regions of the eIF4E structure located near the cap binding pocket and at the surface of the protein (Robaglia and Caranta, 2006). Different potyviruses may selectively recruit eIF4E or the respective isoforms for their replication. Moreover, the same potyvirus may utilize different eIF4E or its isoforms for successful infection of different host plants. For example, Arabidopsis eif(iso)4e knockout mutants are resistant to TuMV, Lettuce mosaic virus (LMV), TEV and PPV, while Arabidopsis eIF4E is required for successful infection of CIYVV (Duprat et al., 2002; Lellis et al., 2002; Sato et al., 2005; Decroocq et al., 2006). In addition, mutations in eIF4G could impart recessive resistance to CMV (genus Cucumovirus) and Turnip crinkle virus (TCV, genus Carmovirus) in Arabidopsis (Yoshii et al., 2004). Altogether, these data provide the evidence of a conserved relationship between plant RNA viruses and the host translation initiation machinery during viral life cycle.
1.4.3 RNA silencing and its suppression

Upon viral infection, in addition to the aforementioned dominant $R$ gene- or recessive gene-mediated resistance, RNA silencing plays a pivotal role in directing antiviral immunity in plants. RNA silencing machinery is a complicated system that recruits unique genetic components to perform their functions. There are four conserved classes of proteins involved in RNA-based antiviral defense, which include Dicer-like ribonucleases (DCLs), Argonaute proteins (AGO), dsRNA-binding proteins (DRB), and RNA-dependent RNA polymerases (RDR) (Vaucheret, 2006).

The RNA silencing pathway is largely mediated by a variety of small RNAs (sRNAs) (Rana, 2007). sRNAs are 18 to 25-nt- long noncoding RNA molecules that can regulate gene expression either transcriptionally or post-transcriptionally (Ruiz-Ferrer and Voinnet, 2009; Katiyar-Agarwal and Jin, 2010). Pathogen-regulated, host endogenous microRNAs (miRNAs) and small interfering RNAs (siRNAs) are the most important sRNA regulators regarding plant-pathogen interaction (Jin, 2008). RNA silencing is considered to be highly specific since it targets mRNA transcripts based on sequence complementarity between the sRNAs and its target RNA (Baulcombe, 2004).

Antiviral RNA silencing is an innate immune response triggered by viral dsRNA, which is derived from viral replication intermediates or secondary RNA folding structures. Antiviral RNA silencing begins with the activity of DCLs that target viral dsRNA and results in the generation of 21-24-nt viral siRNAs, the central components of the RNA silencing pathway (Ding and Voinnet, 2007). Processed viral siRNA duplexes are unwound and recruited by AGOs, which are the catalytic component of RNA-induced silencing complexes (RISCs). RISCs can bind the viral genome and transcripts, and direct the cleavage of homologous mRNAs to achieve post-transcriptional silencing (Ding, 2010). DRBs have been found to modulate the function of DCLs, while RDRs are encoded by the host plant to produce viral secondary siRNAs or some of the dsRNA precursors that serve as templates for DCLs (Brodersen and Voinnet, 2006).

The viral siRNAs involved in the RNA silencing pathway share similar features with host siRNAs and miRNAs (Sharma et al., 2013). They are classified into two groups. One
group, the primary siRNAs, is processed from DCL-mediated cleavage of the initial invading viral RNA. The other type of siRNAs, the secondary siRNAs, recruits host RDRs for their biogenesis (Ruiz-Ferrer and Voinnet, 2009). The amplification of secondary siRNAs has been linked to the long-distance spread of the RNA silencing signals, which allows viral siRNAs move from cell-to-cell for effective RNA silencing responses to viral infection (Hamilton et al., 2002; Himber et al., 2003).

The RNA silencing pathways in *Arabidopsis* have been well characterized and comprise four DCLs, six RDRs, ten AGOs and six DRBs that participate in at least four different endogenous RNA silencing pathways (Vaucheret, 2006). These components have distinct but partially overlapping functions in different RNA silencing pathways. It has been reported that all four DCLs perform the antiviral defense activity in plants (Blevins et al., 2006). Among them, DCL2 and DCL4 are two primary regulators while DCL3 plays a minor role and DCL1 acts negatively as it down-regulates DCL2 and DCL4 functions (Garcia-Ruiz et al., 2010). *Arabidopsis* RDRs play an essential role in RNA silencing defense by amplifying the majority of viral secondary siRNAs. Disease susceptibility to plant RNA viruses was dramatically enhanced in RDR-defective *Arabidopsis* mutant plants (Qu et al., 2005). Accumulating evidence suggests that AGOs which associate with siRNAs to guide sequence-specific silencing, are regulated by DNA methylation (Mallory and Vaucheret, 2010). AGO1 and AGO2 are the key components of the RNA silencing pathways and are recruited for efficient cleavage of viral RNA and processing viral secondary siRNAs in a cooperative manner (Cao et al., 2014). RDR2 is required for the biogenesis of endogenous 24-nt siRNAs that directs DNA methylation in plants (Xie et al., 2004). Moreover, extensive studies have shown that viral siRNA biogenesis is facilitated by RDR1, RDR2 and RDR6 (Qi et al., 2009). Compared to the rapid R gene-mediated defense responses, which can constrain further virus spread within 3-4 days, antiviral RNA silencing is a relatively slow process and could not lead to complete clearance of viral infection (Ding, 2010).

Plant viruses have evolved a variety of effective counter-defense strategies to overcome the antiviral RNA silencing of the host. One of the best-characterized strategies plant viruses employ is to encode RNA silencing suppressors, which are viral proteins that can
interfere with the components of RNA silencing pathways and inhibit the effectiveness of plant defense (Qu and Morris, 2005). Virus-encoded silencing suppressors from different virus families are diverse in sequences and structures. They are able to target different steps of RNA silencing pathways and utilize various strategies to obstruct host antiviral defense (Burgyán and Havelda, 2011). The functions of silencing suppressors can partially or completely disable the activities of silencing components but the mechanism of the viral suppressors remains to be determined (Levy et al., 2008). There are five possible models to describe how viral suppressors of RNA silencing may work: 1) inhibition of the biogenesis of viral siRNAs; 2) blocking loading of viral siRNAs into the RISC by sequestration of viral siRNAs; 3) manipulation of the formation of components of the RISC; 4) inhibition of the AGO-mediated cleavage of viral RNA; and 5) blocking silencing by interacting with plant components which are required for the antiviral silencing machinery (Katiyar-agarwal and Jin, 2010).

For instance, TBSV encodes the P19 protein, which is recognized as a suppressor of RNA silencing by a variety of different tombusviruses (Qu and Morris, 2002). P19, which targets and directly binds double-stranded siRNAs, preferentially binds 20-22 nt duplexes to prevent them from being incorporated into the RISC (Silhavy et al., 2002). Given the fact that siRNAs is the key indicator of RNA silencing, the affinity of P19 for siRNAs is essential for viral pathogenesis (Hsieh et al., 2009). The protease HC-Pro, encoded by different potyviruses is one of the first viral silencing suppressors to be characterized. The silencing suppressor function of HC-Pro is likely to act by inhibiting the unwinding of siRNA duplexes and RISC assembly (Chapman et al., 2004). As a multifunctional protein, HC-Pro is also involved in aphid transmission, viral polyprotein processing, and long distance movement (Kasschau et al., 1997). Mutations in HC-Pro that abolish its suppressor function could cause the virus to lose the ability to replicate the viral genome and move from cell to cell (Kasschau and Carrington, 2001). The 2b protein of cucumoviruses is another example of well-studied viral silencing suppressor. It has been demonstrated that CMV 2b protein can enhance viral long distance movement and interfere with systemic spread of RNA silencing signals (Guo and Ding, 2002). P25 of PVX, which was previously shown to be required for cell-to-cell movement of PVX, can suppress RNA silencing by blocking the silencing signals from moving systemically
between the cells (Azevedo et al., 2010). TCV encodes the P38 protein, which has been reported to have the silencing-suppressing function. P38 binds dsRNA of variable lengths and competes with DCL4 to prevent from binding viral dsRNA (Deleris et al., 2006). The suppressor activity of P38 is further supported by the observed interaction between P38 and AGO1, which leads to blocking the RNA silencing pathways (Voinnet et al., 2000). Since many viral silencing suppressors can bind short dsRNA, it is suggested that binding viral siRNAs duplexes might represent an effective silencing suppression strategy employed by plant viruses (Mérai et al., 2006).

1.5 Research objectives and goals

It is well known that plant viruses pose a major threat to a broad range of plant species in agriculture. Genetic resistance is the practical approach to the control of viral diseases. Unfortunately, natural genetic resistance is rare. To develop novel genetic resistance, it is essential to better understand the viral infection process. Virus infection in plants is a complicated process that requires specific interactions between viral and host proteins. Due to the complexity of plant genomes and the diversity of plant viruses, identification of the host proteins in these interactions has been limited. Towards the development of novel viral disease resistance in crops, which is the long term goal of this research, my thesis focuses on the molecular isolation of host factors required for viral infection and functional characterization of their working mechanisms in viral infection.

To isolate host factors required for viral infection, I proposed to screen Arabidopsis T-DNA insertion lines using TuMV as a model virus. Since DEAD-box RNA helicases likely play essential and regulatory roles in the viral RNA replication and translation of positive-sense RNA viruses, I further selected Arabidopsis T-DNA insertion mutants corresponding to this gene family for analysis. Thus, the central hypotheses of this research are that (1) Arabidopsis DEAD-box RNA helicases are involved in TuMV infection, and (2) down-regulation or mutation of one of these host factors will lead to recessive resistance against TuMV infection. The specific objectives of this thesis are:

(1) To identify AtRHs essential for TuMV infection through a reverse genomic approach by screening Arabidopsis atrh T-DNA insertion mutant lines;
(2) To functionally characterize the identified candidate AtRHs associated with TuMV infection using the model plants Arabidopsis and N. benthamiana;

(3) To identify TuMV proteins interacting with candidate AtRHs;

(4) To identify plant proteins involved in the interaction between AtRHs and TuMV proteins;

(5) To study the involvement of the identified AtRHs as host factors required for viral replication and/or translation.
Chapter 2: Materials and Methods

2.1 Plant materials and growth conditions

*Arabidopsis* (*Arabidopsis thaliana*) ecotype Col-0 and *Nicotiana benthamiana* (*N. benthamiana*) were used in this study. *Arabidopsis* and wild-type *N. benthamiana* plants were maintained in a growth chamber under constant conditions of 60% relative humidity and a day/night regime of 16 h in the light at 22ºC followed by 8 h at 18ºC in the dark. Plants were watered daily as needed and fertilized (20-8-20 [N-P-K], 0.5g/l) weekly. Seeds for *Arabidopsis* T-DNA insertion mutant lines were obtained from the Arabidopsis Biological Resource Center (ABRC) at Ohio State University, Columbus, Ohio, USA. T-DNA insertion information was obtained from the Salk Institute Genomic Analysis Laboratory website (http://signal.salk.edu/).

2.2 Virus materials

The pCambiaTunos/GFP plasmid (TuMV-GFP) containing the full-length cDNA of the TuMV genome and pCambiaTunos/6KmCherry (TuMV::6K-mCherry) having an additional copy of the 6K2-coding sequence tagged with fluorescent protein mCherry between P1 and HC-Pro were obtained from Dr. Jean-François Laliberté at the Institut Armand-Frappier, Institut National de la Recherche Scientifique, Laval, Québec, Canada (Cotton et al., 2009). The recombinant TuMV infectious clone carrying an additional copy of the 6K2-coding sequence fused to yellow fluorescent protein (YFP) at the junction of P1 and HC-Pro (TuMV::6K-YFP) was described previously (Huang et al., 2010).

2.3 Bacterial strains and growth conditions

*Escherichia coli* (*E. coli*) strain DH10B was used for DNA plasmid propagation and isolation. *E. coli* DH10B was grown in Luria-Bertani (LB) liquid medium (tryptone 1%, yeast extract 0.5%, NaCl 1%) or on LB solid medium supplemented with 1.5% w/v agar at 37ºC. Ampicillin (100 µg/ml) or kanamycin (100 µg/ml) was added to LB liquid and agar medium based on the selectable markers of the plasmids used. *Agrobacterium*
*Agrobacterium tumefaciens* (A. tumefaciens) strain GV3101 was employed for plant transformation. *Agrobacterium* strain GV3101 was grown in LB medium containing 100 μg/ml of kanamycin, 50 μg/ml of rifamycin and 25 μg/ml of gentamicin at 28ºC.

### 2.4 Yeast strains and cell culture

Yeast strain AH109 was used for Y2H assay. Yeast cells were grown at 30ºC in rich YPD medium supplemented with adenine hemisulfate (YPDA) or in minimal synthetic defined (SD) base medium (0.17% yeast nitrogen base without amino acids, 2% glucose) combined with appropriate dropout (DO) supplement. For SD solid medium, minimal SD base medium was supplemented with 1.5% w/v agar. Selective medium for yeast transformants was a combination of minimal SD base with -Ade (Adenine)/-His (Histidine)/-Leu (Leucine)/-Trp (Tryptophan) DO supplement.

### 2.5 Plasmid construction

Gateway technology (Invitrogen, Burlington, Ontario, Canada) was used to generate all the plasmid constructs used in this study except where otherwise stated. Gene sequences were amplified by polymerase chain reaction (PCR) using Phusion® High-Fidelity DNA Polymerase (New England Biolabs, Pickering, Ontario, Canada) for cloning purposes. GoTaq® Flexi DNA Polymerase (Promega, Madison, WI, USA) was employed for genotyping and other analysis.

The full-length P1, HC-Pro, P3, 6K1, CI, 6K2, VPg, NIa-Pro, NIb and CP coding regions of TuMV (GenBank accession NC_002509) were obtained by PCR amplification from the pCambiaTunos/GFP infectious clone (Cotton et al., 2009) using the primer sets indicated (Table 1). *Arabidopsis AtRH9* (AT3G22310), *AtRH26* (AT5G08610), *PRH75* (AT5G62190), *IMPA1* (AT3G06720), *IMPA2* (AT4G16143), *eIF(iso)4E* (AT5G35620), and *fibrillarin* (AT5G52470) coding sequences were generated using the primer pairs listed (Table 2) from cDNA derived from *Arabidopsis* leaves. The resulting DNA fragments were purified and transferred into the entry vector pDONR221 (Invitrogen) by recombination using BP Clonase® (Invitrogen) following the standard conditions and procedures recommended by the supplier (Karimi et al., 2002). Insertions in the resulting
Table 1  Primers used for plasmid construction to express TuMV viral proteins in plants. The *attB* recognition site is underlined.

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Primer sequence (5'-3')</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAT</td>
</tr>
<tr>
<td>P1-Gate-R</td>
<td>GGGGACCACTTTGTACAAAAAACAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>HC-Pro-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>HC-Pro-Gate-R</td>
<td>GGGGACCACTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>P3-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>P3-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>6K1-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>6K1-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>CI-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>CI-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
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<tr>
<td>6K2-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>6K2-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>VPg-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>VPg-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>Nla-Pro-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>Nla-Pro-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>Nlb-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
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<td>Nlb-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>CP-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
<tr>
<td>CP-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTTCATGATGGCAGCAGTTACATTTGCGAC</td>
</tr>
</tbody>
</table>
Table 2  Primers used for construction of plasmids to express *Arabidopsis* proteins.
The *attB* recognition site is underlined.

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Primer sequence (5'-3')</th>
</tr>
</thead>
<tbody>
<tr>
<td>AtRH9-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGATTAGCACAGTACTTCGCGAT</td>
</tr>
<tr>
<td>AtRH9-Gate-R</td>
<td>GGGGACCACCTTTGTACAAGAAAGCTGGTGTAAGATCTTTTACCATCGTTTGAT</td>
</tr>
<tr>
<td>AtRH26-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGTCCTCGAAGTTCCCTCGGT</td>
</tr>
<tr>
<td>AtRH26-Gate-R</td>
<td>GGGGACCACCTTTGTACAAGAAAGCTGGTTGTTCTTAAGACCAGGAACG</td>
</tr>
<tr>
<td>PRH75-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGCTTCCCTAATGTTATCTGA</td>
</tr>
<tr>
<td>PRH75-Gate-R</td>
<td>GGGGACCACCTTTGTACAAGAAAGCTGGGTCAGTATCTTCGCTCTACCACCA</td>
</tr>
<tr>
<td>IMPA1-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGCCTAAGACCAACGCTAAG</td>
</tr>
<tr>
<td>IMPA1-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGCCTAAGACCAACGCTAAG</td>
</tr>
<tr>
<td>IMPA2-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGCTTCCCTAATGTTATCTGA</td>
</tr>
<tr>
<td>IMPA2-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGCTTCCCTAATGTTATCTGA</td>
</tr>
<tr>
<td>eIF(iso)4E-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGCGACCGATGATGTGAAC</td>
</tr>
<tr>
<td>eIF(iso)4E-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGCGACCGATGATGTGAAC</td>
</tr>
<tr>
<td>fibrillarin-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGAGACCCGCTCTCTTC</td>
</tr>
<tr>
<td>fibrillarin-Gate-R</td>
<td>GGGGACAAGTTTGTACAAAAAAAGCAGGCTTCATGAGACCCGCTCTCTTC</td>
</tr>
</tbody>
</table>
pDONR221 clones were verified by DNA sequencing.

Forward primers PRH75-F, PRH75-115F, PRH75-356F and PRH75-451F (Table 3) were designed to amplify regions of *Arabidopsis* PRH75 starting at amino acids 1, 115, 356 and 451, respectively. Reverse primers PRH75-R, PRH75-114R, PRH75-355R and PRH75-450R were designed to amplify regions of PRH75 ending at amino acids 114, 355, 450 and 671, respectively.

To construct vectors for the targeted Y2H assay, inserts of the resulting intermediate pDONR221 clones were further transferred into modified Gateway-compatible vectors pGADT7-DEST (prey) or pGBKT7-DEST (bait) (Lu et al., 2010) by recombination using LR Clonase® (Invitrogen) to yield pGAD-NIb, pGAD-NIa-Pro, pGAD-VPg, pGAD-CI, pGAD-IMPA1, pGAD-IMPA2 and pGBK-eIF(iso)4E, pGBK-PRH75, pGBK-IMPA1, pGBK-IMPA2, respectively.

For bimolecular fluorescence complementation (BiFC) assay, the coding sequences of *TuMV* NIb, VPg, NIa-Pro, CI and 6K2 cistrons and the full-length coding sequences of *Arabidopsis* AtRH9, PRH75, IMPA1 and IMPA2 were introduced into the BiFC vectors pEarleyGate201-YN or pEarleyGate201-YC (Lu et al., 2010) to produce NIb-YN, NIb-YC, VPg-YN, VPg-YC, NIa-Pro-YN, NIa-Pro-YC, CI-YN, CI-YC, 6K2-YN, IMPA1-YN, IMPA1-YP, IMPA2-YN, IMPA2-YP, AtRH9-YN, AtRH9-YC, PRH75-YN and PRH75-YC, respectively.

For transient expression analysis in plant cells, the entire NIb, VPg, NIa-Pro and CI coding regions of *TuMV*, the full-length coding sequences of *Arabidopsis* AtRH9, AtRH26 and PRH75, *Arabidopsis* fibrillarin, IMPA1, IMPA2 and eIF(iso)4E were transferred by recombination into the binary destination vectors pEarleyGate101 or pEarleyGate102 (Earley et al., 2006) to generate plant expression vectors for transient expression of AtRH9-YFP, PRH75-YFP, NIb-YFP, NIa-Pro-YFP, VPg-YFP, CI-YFP, IMPA1-YFP, IMPA2-YFP and eIF(iso)4E-YFP; AtRH26-CFP (cyan fluorescent protein), PRH75-CFP and fibrillarin-CFP, respectively.

For nuclear localization signal (NLS) analysis, PRH75(1-114), PRH75(115-355), PRH75(356-
Table 3  Primers used for construction of plasmids for PRH75 domain analysis. The *attB* recognition site is underlined.

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Primer sequence (5'-3')</th>
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</thead>
<tbody>
<tr>
<td>PRH75-Gate-F</td>
<td>GGGGACAAGTTTGTACAAAAAACAGGCTTCATGCTCCCTAATGTTATCTG</td>
</tr>
<tr>
<td>PRH75-Gate-R</td>
<td>GGGGACCACCTTTGTACAAGAAAGCTGGGTCATATCTCTGGCCTCTACCA</td>
</tr>
<tr>
<td>PRH75-Gate-115F</td>
<td>GGGGACAAGTTTGTACAAAAAACAGGCTTCATGCTCCCTAATGTTATCTG</td>
</tr>
<tr>
<td>PRH75-Gate-114R</td>
<td>GGGGACCACCTTTGTACAAGAAAGCTGGGTCATATCTCTGGCCTCTACCA</td>
</tr>
<tr>
<td>PRH75-Gate-356F</td>
<td>GGGGACAAGTTTGTACAAAAAACAGGCTTCATGCTCCCTAATGTTATCTG</td>
</tr>
<tr>
<td>PRH75-Gate-355R</td>
<td>GGGGACCACCTTTGTACAAGAAAGCTGGGTCATATCTCTGGCCTCTACCA</td>
</tr>
<tr>
<td>PRH75-Gate-451F</td>
<td>GGGGACAAGTTTGTACAAAAAACAGGCTTCATGCTCCCTAATGTTATCTG</td>
</tr>
<tr>
<td>PRH75-Gate-450R</td>
<td>GGGGACCACCTTTGTACAAGAAAGCTGGGTCATGCTCCCTAATGTTATCTG</td>
</tr>
</tbody>
</table>
PRH75(451-671), PRH75(1-355), PRH75(1-450), PRH75(115-450), PRH75(115-671) and PRH75(356-671) were transferred by recombination into the binary destination vectors pEarleyGate101-GUS to generate plant expression vectors for transient expression of PRH75(1-114)-GUS-YFP, PRH75(115-355)-GUS-YFP, PRH75(356-450)-GUS-YFP, PRH75(451-671)-GUS-YFP, PRH75(1-355)-GUS-YFP, PRH75(1-450)-GUS-YFP, PRH75(115-450)-GUS-YFP, PRH75(115-671)-GUS-YFP and PRH75(356-671)-GUS-YFP, respectively. The coding sequence of \( \beta \)-glucuronidase (GUS) was obtained by PCR from plasmid pENTR-GUS (Invitrogen) and ligated into AvrII-restricted pEarleyGate101 to yield GUS-YFP (Xiong and Wang, 2013).

For Tobacco rattle virus (TRV)-based virus induced gene silencing (VIGS), a 110 base-pair (bp) of AtRH9 fragment and a 125 bp of PRH75 fragment were amplified from Arabidopsis cDNA with two pairs of primers that contained an EcoRI and BamHI site specific to the 5’ and 3’ end of the fragments, respectively (AtRH9-EcoRI-F/AtRH9-BamHI-R and PRH75-EcoRI-F/PRH75-BamHI-R) (Table 4). The amplified fragment was digested with EcoRI and BamHI, then ligated into the corresponding sites of EcoRI and BamHI-restricted pTRV2 vector (Burch-Smith et al., 2006) to generate the vectors pTRV2-AtRH9 and pTRV2-PRH75, respectively.

2.6 Bacterial transformations

2.6.1 E. coli transformation

E. coli strain DH10B competent cells were thawed on ice for 10 min prior to mixing with the plasmid DNA. The mixture of competent cells and the recombinant plasmid was incubated on ice for 30 min and followed by a heat shock at 42°C for 90 seconds and then cooled on ice. LB medium was added and the transformed cells were incubated at 37°C for one hour with agitation to allow expression of antibiotic resistance genes. The resulting culture was then spread on LB agar plates containing the appropriate antibiotics to select for the transformed bacteria. The plates were incubated overnight at 37°C and colonies that were able to form in the presence of antibiotics were counted as successful plasmid DNA transformations after 12-16 h. The colonies were checked by colony PCR to confirm the presence of plasmid/gene.
Table 4  Primers used to amplify *AtRH9* and *PRH75* DNA fragments that are inserted into the TRV-based vector. The *EcoRI* and *BamHI* sites are underlined.

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Primer sequence (5'-3')</th>
</tr>
</thead>
<tbody>
<tr>
<td>AtRH9-EcoRI-F</td>
<td>CCGGAATTCTGATGTTGCTGCCGTGGACT</td>
</tr>
<tr>
<td>AtRH9-BamHI-R</td>
<td>CGCGGATCCCACGACCAGTTCGCCCGCTT</td>
</tr>
<tr>
<td>PRH75-EcoRI-F</td>
<td>CGCGAATTCCGCCAACAGGAAGAGCTGGCA</td>
</tr>
<tr>
<td>PRH75-BamHI-R</td>
<td>CGCGGATCCAGGTTGAGGTCAGCAAGGTC</td>
</tr>
</tbody>
</table>
2.6.2 Agrobacterium transformation

Agrobacterium transformation of plasmid DNA was carried out using the electroporation following the Bio-Rad *E. coli* Pulser (Bio-Rad) manual. The plasmid DNA from BP/LR reaction or ligation products were mixed with *Agrobacterium* strain GV3101 competent cells on ice for 10 min. The mixture was transferred to a cold 0.1 cm Gene Pulser® cuvette (Bio-Rad) and kept on ice for 10 min. A single electric pulse of 1.8 kV voltage was applied using a Bio-Rad MicroPulser. Following electroporation, 200 μl of liquid LB medium was immediately added to the mixture and incubated at 28°C with shaking for 2 h. The resulting culture was spread on LB agar plates containing the appropriate antibiotics. The plates were incubated at 28°C for 48 h and colonies were selected for further analysis.

2.7 Plant genomic DNA extraction

*Arabidopsis* leaf tissue (200 mg) was collected and ground in liquid nitrogen. Extraction buffer (500 μl) [10 mM Tris-HCl, 1.4 M NaCl, 20 mM ethylenediaminetetraacetic acid (EDTA), 2% cetyltrimethyl-ammonium bromide (w/v) (CTAB)] (Porebski et al., 1997) was added to each sample, then 500 μl of chloroform:isoamyl alcohol (24:1) was added and mixed well, followed by a centrifugation at 10,000 rpm for 5 min. The upper aqueous phase was transferred to a clean tube and DNA was precipitated by adding 0.7 volume of isopropanol. Samples were incubated at -20°C for 1 h, kept on ice for 10 min and then centrifuged at 10,000 rpm for 20 min to collect the pellets. After two washes with 500 μl 70% ethanol and centrifugation, the pellet was air-dried for 20 min at room temperature and resuspended in 50 μl of milli-Q water.

2.8 RNA isolation

Total RNA was isolated from *Arabidopsis* leaf tissue using the RNeasy Plant Mini Kit (Qiagen) following the manufacturer's instructions. DNase I treatment was performed to remove genomic DNA contamination prior to elution in RNase free water (Invitrogen).

The concentration of total RNA was determined by measuring absorbance at 260 nm/280 nm using a spectrophotometer (Nanodrop1000, ABI). Reverse transcription was
performed by synthesizing first-strand cDNA from 1.5 µg of total RNA (pretreated with DNase I) as the template using Superscript III reverse transcriptase (Invitrogen) and an oligo(dT)$_{12-18}$ primer (Invitrogen) following the manufacturer's protocols.

2.9 Functional analysis of *Arabidopsis* T-DNA insertion lines of *AtRHs*

2.9.1 Selection of *Arabidopsis* T-DNA insertion lines of *AtRHs*

Genebank accession numbers were used to select *Arabidopsis* T-DNA insertion lines of *Arabidopsis* DEAD-box RNA helicases (*AtRHs* or *RHs*). So far, approximately 113 sequences from *Arabidopsis* genome have been annotated in the TAIR unigene set as putative RNA helicase genes (Umate *et al.*, 2010). Based on their predicted functions, 42 *AtRH* genes were selected for this study. These genes encode the proteins that are related to eIF4A (Boudet *et al.*, 2001) or have putative functions in stress response regulation. *Arabidopsis* T-DNA insertion mutants were selected for each gene based on their availability and genotype, with a preference for T-DNA insertions in the exon or 5' UTR regions. Seed stocks of 128 *Arabidopsis* T-DNA insertion lines corresponding to these 42 *AtRH* genes were obtained from the Arabidopsis Biological Resource Center (ABRC). Mutant and insertion information was obtained from the Salk Institute Genomic Analysis Laboratory website (http://signal.salk.edu/).

2.9.2 Screening for homozygous *Arabidopsis* T-DNA insertion lines of *AtRHs*

The genotype of each *Arabidopsis atrh* T-DNA insertion line was confirmed by PCR following the protocols suggested by ABRC (http://signal.salk.edu/tdnaprimers.2.html). Two sets of primers were used to amplify the target alleles with two gene specific primers to detect the wild-type allele or with a gene specific primer and a T-DNA left border specific primer (LB) to identify the mutant allele. Primers for genotyping were designed using the T-DNA iSect tool (http://signal.salk.edu/tdnaprimers.2.html) and were listed in Table 5. The homozygous lines were used for ELISA analysis and gene expression analysis.
Table 5  Primers used for PCR-screening of homozygous *Arabidopsis atrh* T-DNA insertion lines.

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Primer sequence (5’-3’)</th>
</tr>
</thead>
<tbody>
<tr>
<td>LB (LBb1.3)</td>
<td>ATTTTGCCGATTTCGGAAC</td>
</tr>
<tr>
<td>SALK_035421-LP</td>
<td>TCATAATGGAAGTGGCGAAG</td>
</tr>
<tr>
<td>SALK_035421-RP</td>
<td>TCTTGGTGCAACTGATGTTGC</td>
</tr>
<tr>
<td>SALK_060677-LP</td>
<td>TTCTCATCCACGGTCAAGATC</td>
</tr>
<tr>
<td>SALK_060677-RP</td>
<td>TGTACAAGAACCGTCTTCTGG</td>
</tr>
<tr>
<td>SALK_068401-LP</td>
<td>TTCTAATGTCCTTGCCATTGG</td>
</tr>
<tr>
<td>SALK_068401-RP</td>
<td>TTAAGCTTCTCCCTCAAAGGC</td>
</tr>
<tr>
<td>SALK_040389-LP</td>
<td>CTACAGGTCTGGTCAGATGG</td>
</tr>
<tr>
<td>SALK_040389-RP</td>
<td>TTAAGCTTCTCCCTCAAAGGC</td>
</tr>
<tr>
<td>SALK_106823-LP</td>
<td>TGGGTATGGCCTATAGGACCTG</td>
</tr>
<tr>
<td>SALK_106823-RP</td>
<td>TGGTGTCCTGTCTACGTTTC</td>
</tr>
</tbody>
</table>
2.9.3 Gene expression analysis of Arabidopsis T-DNA insertion lines of AtRHs

The expression of AtRH gene in different Arabidopsis T-DNA insertion lines was verified by RT-PCR with gene specific primers. cDNA was synthesized from total RNA isolated from leaf tissue of Arabidopsis T-DNA insertion mutant plants. PCR amplifications were carried out as described below (section 2.10.2).

2.10 Polymerase chain reaction (PCR)

2.10.1 Polymerase chain reaction (PCR)

PCR reactions were carried out using a thermocycler (Eppendorf) following the program guideline. For a routine PCR using Phusion® High-Fidelity DNA Polymerase, a denaturing temperature of 98°C for 30 seconds was followed by an annealing temperature of 55°C for 1 min, and primer extension was achieved at 72°C for 30 seconds per kilobase (kb) of target DNA to be amplified. These three steps were repeated for a total of 30 to 35 cycles, followed by a final extension for 5 min.

2.10.2 RT-PCR

To quantify the expression level of AtRH gene in different T-DNA insertion lines, total RNA was extracted from leaf tissue of Arabidopsis T-DNA insertion mutants and wild-type plants (WT) using the RNeasy Plant Mini Kit (Qiagen) and treated with DNase I following the manufacturer's instructions (Invitrogen). cDNA was synthesized by reverse transcription of RNA samples and used to determine the mRNA expression levels of target genes. Primers were designed within the coding region (Table 6) and target genes were amplified with annealing temperature at 60°C for 30 cycles following the same PCR procedure as section 2.10.1. Arabidopsis Actin II (Actin2) was used as an internal control.

2.10.3 Real-time quantitative RT-PCR (qRT-PCR)

Real-time qRT-PCR was conducted and analyzed with the CFX96 Real-Time PCR Detection System (Bio-Rad) following the manufacturer’s instructions. For each primer set, gel electrophoresis and melting curve analysis were carried out to ensure that only a single expected PCR product and melting temperature were generated. Each reaction
<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Primer sequence (5'-3')</th>
</tr>
</thead>
<tbody>
<tr>
<td>AtRH9-F</td>
<td>ATGATTAGCACAGTACTTCGCCGAT</td>
</tr>
<tr>
<td>AtRH9-R</td>
<td>TCAGTAAGATCTTTTACCATCGTTTG</td>
</tr>
<tr>
<td>PRH75-F</td>
<td>ATGCCTTCCCTAATGTTATCTGA</td>
</tr>
<tr>
<td>PRH75-R</td>
<td>TCAATATCTCTGGCCTCTACCA</td>
</tr>
<tr>
<td>AtRH26-F</td>
<td>ATGTCCTCGAAGTTCCCTCTCGGT</td>
</tr>
<tr>
<td>AtRH26-R</td>
<td>CTACTTGGTCTAAAGACCAGGAACG</td>
</tr>
<tr>
<td>At-Actin2-F</td>
<td>GCCATCCAAGCTGGTCTCTC</td>
</tr>
<tr>
<td>At-Actin2-R</td>
<td>GAACCACCGATCCAGACACT</td>
</tr>
</tbody>
</table>
contained 40 ng of cDNA template, 5 µM of primer mix, and 1X SsoFast™ EvaGreen® Supermix (Bio-Rad) in a total volume of 10 µl of reaction solution. qRT-PCR reactions were carried out following cycling conditions: initial incubation at 95°C for 30 seconds followed by 40 cycles of a denaturing temperature at 95°C for 5 seconds and an annealing temperature at 60°C for 5 seconds. Melting curve was recorded after 40 reaction cycles by heating from 65°C to 95°C with a ramp speed of 0.5°C every 2-5 seconds. Relative transcript abundances were calculated using CFX Manager Software (Bio-Rad). The expression of CP gene of TuMV was detected to reflect viral accumulation level using primer sets TuMV-CP-F and TuMV-CP-R. qRT-PCR analysis was also carried out to detect AtRH gene expression of the corresponding Arabidopsis T-DNA insertion lines. Gene specific primers were used for gene expression analysis. Expression of Arabidopsis Actin II was used as a reference gene to normalize the data and to calculate the relative mRNA abundance levels. For each sample analyzed, three biological replicates were included and for each biological replicate, three technical repeats were carried out. All results are shown as means of biological replicates with corresponding standard errors. The primers used for qRT-PCR were listed in Table 7.

2.11 Gateway-based cloning

The Gateway cloning technology exploits an in vitro site-specific recombination system to clone the gene of interest into an entry vector using the BP reaction. Subsequently, the gene of interest from the entry clone was subcloned into various destination vectors using the LR reaction to produce expression clones (Karimi et al., 2002). Gateway protocols rely essentially on the BP and LR Clonase® reactions (Hartley et al., 2000). PCR primers for Gateway cloning system were designed following the manufacturer’s instructions (Invitrogen). DNA fragments were amplified from cDNA of Arabidopsis leaf tissue as the template and Phusion® High-Fidelity DNA polymerase was used to construct the entry clones. A mixture of 1 µl of purified PCR product, 0.5 µl pDONR221 vector and 0.5 µl BP Clonase® (Invitrogen) was set up for BP reaction. After overnight incubation at 25°C, 2 µl of BP reaction product was transferred into 100 µl of E. coli DH10B competent cells for transformation as described. The entry clones were linearized and the insertion fragments were purified before subcloning into destination vectors.
<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Primer sequence (5'-3')</th>
</tr>
</thead>
<tbody>
<tr>
<td>At-Actin2-F</td>
<td>GCCATCCCAAGCTGTCTCTC</td>
</tr>
<tr>
<td>At-Actin2-R</td>
<td>GAACCACCGATCCAGACACT</td>
</tr>
<tr>
<td>TuMV-CP-F</td>
<td>TGGCTGATTACGAAGCTGACG</td>
</tr>
<tr>
<td>TuMV-CP-R</td>
<td>CTGCCTAAATGTGGGTTTGG</td>
</tr>
<tr>
<td>AtRH9-realtime-F</td>
<td>TCGTGCTGGAAAGAAAGGAAGCG</td>
</tr>
<tr>
<td>AtRH9-realtime-R</td>
<td>TTCCACAGCAATGCTAGGCTGAGCTG</td>
</tr>
<tr>
<td>PRH75-realtime-F</td>
<td>ATCTGGTGGTATGGAAGCTGCTG</td>
</tr>
<tr>
<td>PRH75-realtime-R</td>
<td>AGGAATGCGAGGAACCACACTGTC</td>
</tr>
</tbody>
</table>
A mixture of 1 μl of linearized entry clone plasmid, 1 μl destination vector and 0.5 μl LR Clonase® (Invitrogen) was set up for LR reaction. After overnight incubation at 25°C, 2 μl of LR reaction product was transferred into *E. coli* DH10B for transformation as described.

### 2.12 Yeast transformation

Yeast cells were transformed following the Yeast Protocols Handbook (Clontech Protocol PT3024-1). A 2 ml rich YPD medium with a yeast colony was grown overnight at 30°C with shaking, then sub-cultured into 30 ml of fresh YPD medium and continued to grow for another 3-4 h until an optical density at 600 nm (OD600) reached 0.6. Yeast cells were pelleted by centrifugation, washed in 500 μl distilled H2O and resuspended in 100 μl of freshly prepared lithium acetate (LiAc) solution (0.1 M LiAc, 10 mM Tris-HCl [PH 7.5], 1 mM EDTA). Denatured carrier DNA (10 μl) and 0.1 μg of plasmid DNA were added to 100 μl yeast competent cells and mixed well followed by the addition of 600 μl of 40% PEG 4000 (50% polyethylene glycol 4000) in LiAc solution. After incubation at 30°C for 30 min with shaking at 200 rpm, 70 μl of DMSO was added, followed by a 15 min heat shock in a 42°C water bath. Yeast cells were collected by centrifugation and resuspended in 100 μl of TE buffer (10 mM Tris-HCl [PH 7.5], 1 mM EDTA). The resuspended cells were plated on an appropriately supplemented SD medium and the plates were incubated at 30°C until colonies appeared.

### 2.13 Yeast two-hybrid assay

The Y2H assay was performed following the Clontech yeast protocols (Clontech). To perform protein-protein interaction assay, the Gateway-compatible vectors pGBKKT7-DEST (bait) and pGADT7-DEST (prey) were used (Lu *et al.*, 2010). The full-length coding regions of N1b, N1a-Pro, Vpg and CI from TuMV and the full-length coding sequences of *Arabidopsis PRH75, IMPA1, IMPA2* and *eIF(iso)4E* were introduced into vectors pGAD and pGBK, respectively. Yeast strain AH109 was co-transformed with bait and prey constructs using the LiAc transformation method (Schiestl and Gietz, 1989).

After the bait and prey constructs (in different combinations) were co-transformed into
yeast strain AH109, the yeast was plated on selection agar medium lacking leucine and tryptophan (SD/-Leu/-Trp) at 30°C for up to 5 days. The selected individual yeast transformants were grown in liquid medium and a series of diluted culture were plated onto a high-stringency selective medium lacking adenine, histidine, leucine and tryptophan (SD/-Ade/-His/-Leu/-Trp) for up to 5 days to assess positive protein-protein interactions. The interaction between TuMV VPg and Arabidopsis eIF(iso)4E expressed from pGAD-VPg and pGBK-eIF(iso)4E, respectively was used as a positive control, whereas the empty pGBK and pGAD vectors (no insert) were used in co-transformation as negative controls.

2.14 Transient expression in N. benthamiana

For transient expression analysis in N. benthamiana leaves, constructs were generated in Gateway-compatible binary vectors and transformed into Agrobacterium strain GV3101 via electroporation. Four-week-old N. benthamiana plants were used for Agrobacterium-mediated transient expression.

For agroinfiltration, Agrobacterium cultures were grown overnight in LB medium with appropriate antibiotic selection at 28°C. The Agrobacterium cells were harvested by centrifugation, and then resuspended in infiltration buffer (10 mM MgCl₂, 10 mM MES, and 150 μM acetosyringone). After incubation for 2 h at room temperature, the culture was diluted to 0.5-1.0 at OD600 and agroinfiltrated into leaf epidermal cells under gentle pressure using a syringe barrel (Sparkes et al., 2006). After agroinfiltration, the plants were maintained under normal conditions for observation.

For subcellular localization, target genes were recombined with pEarleyGate101 or pEarleyGate102 to produce transient expression vectors tagged with YFP or CFP, respectively. The corresponding vectors were transformed into Agrobacterium GV3101. Agrobacterium cultures were agroinfiltrated into N. benthamiana leaves at 0.5-1.0 of OD600. For colocalization studies of two proteins, two Agrobacterium cultures were mixed with equal volume, and 150 μl of the mixed cultures were agroinfiltrated into N. benthamiana leaves.
For BiFC assay, *Agrobacterium* cultures carrying the fusion constructs containing the N-terminal or C-terminal fragment of YFP were co-agroinfiltrated into *N. benthamiana* leaves. The reconstitution of YFP signals was monitored using a confocal microscopy 2-4 days after agroinfiltration as described (Wei et al., 2010). For protein pairs showing the YFP signals, the YFP signal and bright-field were imaged and overlaid.

2.15 Confocal microscopy

Fluorescence was visualized 2-4 days post infiltration using a Leica TCS SP2 inverted confocal microscopy (http://www.leica.com/) with an Argon-Krypton laser. Sections from agroinfiltrated leaves were excised and placed between two microscopy cover slides with a drop of water. YFP signals were imaged using a 63× water immersion objective at an excitation wavelength of 514 nm, and emissions were collected between 525 and 575 nm. Images of CFP fluorescence were obtained using the same microscopy at an excitation wavelength of 458 nm and emissions were collected between 470 and 500 nm. GFP signal was excited at 488 nm and the emitted light was captured at 505 to 525 nm. mCherry fluorescence was excited at 543 nm and the emissions were captured at 590-630 nm. Light emitted at 630-680 nm was used to record chlorophyll autofluorescence. Data for the different color channels were collected simultaneously. The samples were scanned at a resolution of 512×512 pixels. Images were collected with a charge-coupled device camera and analyzed by Leica confocal software.

2.16 Quantification of Fluorescence Resonance Energy Transfer (FRET) efficiency by acceptor photobleaching

The full-length coding regions of N1b, N1a-Pro, VPg and CI of TuMV were PCR amplified and recombined into pEarleyGate101 to produce the transient expression vectors of N1b-YFP, N1a-Pro-YFP, VPg-YFP and CI-YFP in plants, respectively. The full length coding sequence of *PRH75* was amplified and cloned into pEarleyGate102 to produce the transient expression vector of PRH75-CFP in plants. To quantify FRET efficiency, PRH75-CFP and one of N1b-YFP, N1a-Pro-YFP, VPg-YFP or CI-YFP were co-agroinfiltrated into four-week-old *N. benthamiana* leaves. Forty-eight hours after infiltration, leaf epidermal cells exhibiting coexpression of YFP- and CFP-tagged
proteins were bleached in the acceptor YFP channel with a 514-nm argon laser. The change in donor CFP fluorescence intensity was quantified by comparing pre-bleach and post-bleach images using a confocal microscopy (TCS SP2, Leica), and FRET efficiency was calculated from the formula as follows: 

\[ E = \left( \frac{\text{CFP signal after photobleaching} - \text{CFP signal before photobleaching}}{\text{CFP signal after photobleaching}} \right) \times 100 \]  

(Karpova and McNally, 2006; Song et al., 2011). The combination of PRH75-CFP and GUS-YFP was used as a negative control. Error bars represent standard deviations from nine independent FRET analysis in three independent experiments.

### 2.17 dsRNA-binding dependent fluorescence complementation (dRBFC) assay

The dRBFC assay was performed based on the system developed by our lab (Cheng et al., unpublished data). In detail, the dsRNA-binding domain of B2 of FHV (GenBank accession X77156) and the dsRNA-binding domain of VP35 of Marburg virus (MARV) (GenBank accession GQ433353) were cloned and recombined into Gateway-compatible BiFC vectors pEarleyGate201-YN or pEarleyGate201-YC (Lu et al., 2010) to produce B2-YN and VP35-YC, respectively.

For dRBFC assay, *Agrobacterium* cultures carrying B2-YN and VP35-YC constructs were agroinfiltrated into *N. benthamiana* leaves which were infected with TuMV::6K2-mCherry. The YFP signals were monitored 48 h after agroinfiltration to label the dsRNA intermediates during viral replication, highlighting the dsRNA-containing 6K2-mCherry vesicles as described (Wei et al., 2010).

### 2.18 TuMV infection assay

TuMV infection assay was carried out to test the susceptibility of *Arabidopsis atrh* T-DNA insertion lines to TuMV infection. The seedlings of *Arabidopsis* wild-type plants (WT) and selected homozygous *Arabidopsis* T-DNA insertion mutant plants were inoculated with TuMV either by mechanical inoculation or using agroinfiltration. Plants were inoculated at the five to six leaf stage of development. Virus was applied to the two oldest leaves by mechanical inoculation.

Approximately 1 g TuMV-infected leaf tissue of *N. benthamiana* was harvested as the
source of virus inoculum. The tissue was homogenized using a mortar and pestle in 10 ml inoculation buffer (50 mm potassium phosphate buffer, [pH 7.5]). Carborundum powder was lightly dusted on plant leaves intended to be inoculated. A gentle rubbing of the TuMV-containing inoculum over the leaf surface was performed to facilitate virus entry. The negative control plants were rubbed with inoculation buffer also as mock inoculations. TuMV infection assay was repeated three times for each Arabidopsis atrh T-DNA insertion line. Eight plants for each T-DNA insertion line were inoculated with the addition of four plants serving as a mock inoculation treatment. The TuMV infectious clone pCambiaTunos/GFP (TuMV-GFP) was used for agroinfiltration. Leaf tissue from TuMV-infected Arabidopsis T-DNA insertion mutants was harvested for ELISA analysis.

2.19 Triple-antibody sandwich enzyme-linked immunosorbent assay (TAS-ELISA)

After mechanical inoculation or agroinfiltration, TAS-ELISA was performed to quantify viral accumulation level of WT plants and Arabidopsis atrh T-DNA insertion mutants at the days indicated. The newly-emerged leaves of TuMV-infected mutants and WT plants were harvested for ELISA analysis. Leaf tissue was weighted and ground in ELISA sample extraction buffer, then TAS-ELISA was conducted with an ELISA kit (Agdia) following the manufacturer’s instructions. Absorbances were recorded at 405 nm with an iMark microplate reader (Bio-Rad) (Figure 3).

2.20 TRV-based virus-induced gene silencing (VIGS)

To suppress expression of AtRH9 and PRH75 in Arabidopsis by VIGS, a TRV-based vector was used. To induce silencing, Agrobacterium carrying pTRV1 vector and pTRV2-derived vector were combined in a ratio of 1:1(v/v) mixtures and agroinfiltrated into Arabidopsis seedlings. For example, pTRV1 and pTRV2-AtRH9 vectors were separately introduced into Agrobacterium and co-agroinfiltrated into Arabidopsis at the four leaf stage. Similarly, Agrobacterium carrying pTRV1 and pTRV2-PRH75 were co-agroinfiltrated to silence PRH75 in Arabidopsis. Plants co-agroinfiltrated with pTRV1 and pTRV2 empty vectors or with pTRV1 and pTRV2-PDS were used as controls. Twelve days post-infiltration, treated plants were mechanically inoculated with TuMV.
Figure 3 Methodology of triple-antibody sandwich enzyme-linked immunosorbent assay (TAS-ELISA).

Immobilized capture antibody is attached to a solid-phase surface. After adding test sample, antibody-analyte binding occurs. Enzyme-labeled analyte-specific detection antibody is added to bind to the analyte, forming the "sandwich". Then substrate is added and will produce a colored product in the presence of enzyme.
2.21 Gene structure and multiple sequence alignments

Identification and analysis of domain organization and conserved motifs of *Arabidopsis* PRH75 were performed using the specialized BLAST program for conserved domain searches at the National Center for Biotechnology Information (NCBI) protein database (http://www.ncbi.nlm.nih.gov/cdd). Multiple sequence alignments of PRH75 and DEAD-box RNA helicase (DDX) proteins from other plant species were obtained using ClustalW2 (http://www.ebi.ac.uk/Tools/clustalw2/index.html).

2.22 Statistical analysis

ELISA values and relative fold changes of TuMV accumulation were compared between *Arabidopsis atrh* T-DNA insertion mutants and WT plants using the student’s t-test. All statistical analysis were performed using Microsoft Excel software. A p-value of 0.05 or less indicates significant difference.
Chapter 3: Results

3.1 Identification of *Arabidopsis* DEAD-box RNA helicase (*AtRH*) genes essential for TuMV infection

3.1.1 Screening for homozygous T-DNA insertion lines of *AtRH* genes in *Arabidopsis*

*Arabidopsis* was used as the model host to study the involvement of *Arabidopsis* DEAD-box RNA helicase genes (*AtRH* or *RH*) in TuMV infection. Previous studies predicted that the *Arabidopsis* genome is composed of 53 *AtRH* genes (Aubourg *et al.*, 1999; Boudet *et al.*, 2001). A recent study has revealed a total of 113 putative helicase genes encoded by the *Arabidopsis* genome (Umate *et al.*, 2010). Based on the presence of the conserved DEAD helicase motif and database annotations, a dataset representing *AtRH* genes in the *Arabidopsis* genome was generated in the Arabidopsis Information Resource (TAIR) database (http://www.arabidopsis.org/) (Poole, 2007). The gene dataset was also cross-checked with the NCBI database (http://www.ncbi.nlm.nih.gov/) (Appendix I). Although a large number of DEAD-box RNA helicases had been identified as 'computer predicted putative helicases', only a few of them were experimentally confirmed to have helicase activity and their biological functions were not well characterized. To elucidate the role of *AtRH* genes associated with TuMV infection, *Arabidopsis* T-DNA insertion mutants carrying genetic lesions in the corresponding *AtRH* genes were analyzed.

*Arabidopsis* T-DNA insertion lines corresponding to 42 *AtRH* genes were selected from the TAIR database. These genes encode the proteins that are either related to eIF4A or have possible functions in PD formation or stress response regulation. Seed stocks of 128 *Arabidopsis* T-DNA insertion lines corresponding to these *AtRH* genes were ordered and obtained from ABRC (Table 8). PCR-based genotyping was carried out to screen for homozygous lines for the T-DNA insert. Based on the preliminary genotyping result, a total of 53 homozygous *Arabidopsis* T-DNA insertion lines corresponding to 26 *AtRH* genes were identified. Thirty-five *Arabidopsis* T-DNA insertion lines did not contain T-DNA inserts at the reported positions and 40 *Arabidopsis* T-DNA insertion lines were heterozygous lines. For example, only heterozygous progeny plants were recovered for
Table 8  List of *AtRH* genes and corresponding *Arabidopsis atrh* T-DNA insertion lines.

<table>
<thead>
<tr>
<th>Gene Names</th>
<th>Locus</th>
<th><em>Arabidopsis</em> T-DNA insertion lines</th>
</tr>
</thead>
<tbody>
<tr>
<td>RH1</td>
<td>AT4G15850</td>
<td>SALK_049804; SALK_049805; CS839540; SALK_049812; SALK_016796</td>
</tr>
<tr>
<td>DRH1</td>
<td>AT3G01540</td>
<td>SALK_063362; CS879140; SALK_073018; SALK_109174</td>
</tr>
<tr>
<td>RH2(eIF-4A-III)</td>
<td>AT3G19760</td>
<td>CS808417</td>
</tr>
<tr>
<td>RH3</td>
<td>AT5G26742</td>
<td>SALK_005920</td>
</tr>
<tr>
<td>RH4(eIF-4A)</td>
<td>AT3G13920</td>
<td>SALK_135778; SALK_038072; CS833761; SALK_072655; SALK_107633; SALK_48905; SALK_123728; SALK_777175</td>
</tr>
<tr>
<td>RH6</td>
<td>AT2G45810</td>
<td>CS805454; CS837992</td>
</tr>
<tr>
<td>RH8</td>
<td>AT4G00660</td>
<td>SALK_016830</td>
</tr>
<tr>
<td>RH9</td>
<td>AT3G22310</td>
<td>SALK_035421; SALK_060677; CS807388; SALK_063973</td>
</tr>
<tr>
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<td>AT5G60990</td>
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</tr>
<tr>
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<td>AT3G58510</td>
<td>SALK_122885; SALK_138586; CS81476</td>
</tr>
<tr>
<td>RH12</td>
<td>AT3G61240</td>
<td>SALK_016921; SALK_024905; SALK_111341; SALK_148563</td>
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<td>RH16</td>
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<td>SALK_066621; CS843929; CS852120</td>
</tr>
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<td>RH17</td>
<td>AT2G40700</td>
<td>SALK_076414; SALK_027066</td>
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<td>RH26</td>
<td>AT5G08610</td>
<td>SALK_025261; SALK_106823; CS846644; SALK_135761; SALK_06908; SALK_009049; CS832362</td>
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<tr>
<td>RH28</td>
<td>AT4G16630</td>
<td>SALK_012018; SALK_020556; SALK_082807</td>
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<td>RH29</td>
<td>AT1G77030</td>
<td>SALK_112020</td>
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<tr>
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<td>AT2G42520</td>
<td>SALK_099097</td>
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<tr>
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<td>RH41</td>
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<td>SALK_020125; CS843411; CS858153</td>
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<tr>
<td>RH46</td>
<td>AT5G14610</td>
<td>SALK_068359; SALK_08406; CS852203; SALK_086013; SALK_116644</td>
</tr>
<tr>
<td>Gene</td>
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<td>RH48</td>
<td>AT1G63250; SALK_013253; SALK_144751; SALK_144971</td>
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<tr>
<td>RH49</td>
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<tr>
<td>RH52</td>
<td>AT3G58570; SALK_068712; SALK_116448</td>
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<tr>
<td>RH53</td>
<td>AT3G22330; SALK_056387; SALK_065080</td>
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<tr>
<td>RH57</td>
<td>AT3G09720; SALK_019721; SALK_143440; SALK_020854; SALK_140120; CS823406</td>
<td></td>
</tr>
<tr>
<td>RH58</td>
<td>AT5G19210; CS832329</td>
<td></td>
</tr>
<tr>
<td>PRH75</td>
<td>AT5G62190; SALK_060686; SALK_068401; SALK_066279; SALK_016729; SALK_040389; SALK_040581; SALK_018195; SALK_062900</td>
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</tr>
<tr>
<td>Increased Size Exclusion Limit (ISE) (Burch-Smith and Zambryski, 2010)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ISE1(RH47)</td>
<td>AT1G12770; CS821051; CS807604; CS802911; CS843211</td>
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<tr>
<td>ISE2</td>
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</tr>
<tr>
<td>Stress Response Suppressor (STRS) (Kant et al., 2007)</td>
<td></td>
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</tr>
<tr>
<td>STRS1(RH5)</td>
<td>AT1G31970; CS815216; CS849995; CS851469; SALK_062509</td>
<td></td>
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<tr>
<td>STRS2(RH25)</td>
<td>AT5G08620; SALK_140146; SALK_028850</td>
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</tr>
<tr>
<td>elf-4A-2</td>
<td>AT1G54270; SALK_051038</td>
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</tr>
<tr>
<td>elf-4A-3</td>
<td>AT1G72730; SALK_065267</td>
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Arabidopsis mutants with T-DNA insertion in eIF4A, Increased Size Exclusion Limit (ISE) 1 and ISE2. These results were consistent with the reported embryo-defective phenotypes in homozygous Arabidopsis lines corresponding to those genes. eIF4A is required for mRNA translation and is essential for plant growth and development. Disruption of eIF4A function would cause deleterious effects in plants and its homozygote is nonviable (Huang et al., 2010). ISE1 and ISE2 are required for PD formation and embryogenesis, and their null mutants are embryo lethal (Kobayashi et al., 2007).

3.1.2 Identification of AtRH genes associated with TuMV infection

Based on the availability of homozygous T-DNA insertion lines, we further selected 41 T-DNA insertion lines corresponding to 26 AtRH genes, with a preference for T-DNA insertions in either an exon or the 5' UTR region. These homozygous mutants and WT plants in parallel were evaluated for their susceptibility to TuMV infection by conducting a TuMV infection assay (Table 9). Selected Arabidopsis T-DNA insertion lines and wild-type plants were rub-inoculated with TuMV, followed by observation of disease symptoms. Newly-emerged leaves from systemically TuMV-infected T-DNA mutant plants and wild-type plants (WT) were sampled and assayed for viral CP accumulation at 10 dpi (days post inoculation) by ELISA (Figure 4).

Among these 41 mutant lines, 18 AtRH gene mutant lines, i.e., T-DNA insertion lines of DRH1, AtRH11, AtRH16, AtRH18, AtRH20, AtRH21, AtRH24, AtRH30, AtRH31, AtRH33, AtRH37, AtRH40, AtRH41, AtRH46, AtRH53, AtRH57, STRS1, and STRS2 displayed higher CP accumulation compared to WT plants and were consistent with the enhanced severity of symptoms caused by TuMV infection. Those mutants exhibited more severe phenotypes, including stunted growth, yellowish and curled leaves, chlorotic and mosaic lesions and abnormal flower morphology. In contrast, TuMV CP accumulation in T-DNA insertion lines of AtRH9, AtRH26 and PRH75 were significantly lower than the level observed in WT plants. The attenuated symptoms in the systemically-infected plants of those mutant lines indicated that either viral replication or long-distance movement were affected. Intriguingly, ELISA results also revealed that
Table 9  List of homozygous *Arabidopsis atrh* T-DNA insertion lines for ELISA analysis.

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Locus</th>
<th><em>Arabidopsis</em> T-DNA insertion lines</th>
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<tr>
<td>RH1</td>
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<td>DRH1</td>
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<td>SALK_063362; SALK_073018</td>
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<td>RH9</td>
<td>AT3G22310</td>
<td>SALK_035421; SALK_060677</td>
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<td>RH10</td>
<td>AT5G60990</td>
<td>SALK_001503</td>
</tr>
<tr>
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<td>AT3G58510</td>
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<td>SALK_100059; CS839970</td>
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<tr>
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<td>SALK_017083; SALK_119034</td>
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<td>SALK_099097</td>
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<td>AT3G06480</td>
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<td>RH53</td>
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<td>SALK_056387</td>
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<td>RH57</td>
<td>AT3G09720</td>
<td>SALK_019721; SALK_143440</td>
</tr>
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<td>PRH75</td>
<td>AT5G62190</td>
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</tr>
<tr>
<td>STRS2</td>
<td>AT5G08620</td>
<td>SALK_028850</td>
</tr>
</tbody>
</table>
Figure 4  ELISA analysis of candidate Arabidopsis atrh T-DNA mutants.

A total of 41 homozygous Arabidopsis T-DNA insertion mutant lines corresponding to 26 AtRH genes were selected for TuMV infection assay. The Arabidopsis atrh T-DNA insertion mutants and WT plants were mechanically inoculated with TuMV. ELISA analysis was used to determine the accumulation of TuMV CP in atrh T-DNA mutants and WT plants. Extracts from newly-emerged leaves of TuMV-infected individual plants were subjected to ELISA using TuMV CP-specific antibody. The y-axis represents ELISA values at 10 days post inoculation (dpi). Error bars represent standard deviation (n ≥ 5). Asterisk indicates significant difference from WT plants (student’s t test, p<0.05).
TuMV CP levels were reduced in newly-emerged leaves of T-DNA insertion lines of AtRH1, AtRH10, AtRH12, AtRH22 and AtRH28 relative to WT plants. But the reduction did not reach significant levels. TuMV-infected wild-type Arabidopsis plants displayed symptoms such as mottle and mosaics, leaf distortion, curled bolts and stunting, leaves at late infection stages developed necrotic lesions. Compared with WT plants, only mild disease symptoms were developed on the Arabidopsis atrh9, atrh26 and prh75 mutant plants, suggesting these atrh mutants conferred partial resistance against TuMV infection. These data also supported the biological relevance of the genes AtRH9, AtRH26 and PRH75 to TuMV infection. Thus, T-DNA insertion lines of AtRH9, AtRH26 and PRH75 were selected for further analysis.

3.2 Characterization of Arabidopsis atrh9 T-DNA insertion line

3.2.1 Verification of Arabidopsis atrh9 T-DNA insertion line

Two atrh9 T-DNA insertion lines were acquired and analyzed (Figure 5A and 5B). T-DNA insertion line SALK_035421 contains a T-DNA insertion within Exon 6 of AtRH9, which recently has been confirmed to be a true knockout mutant on the basis of a Northern blot analysis (Köhler et al., 2010). At3g22310-encoded protein was previously designated Putative Mitochondrial RNA Helicase1 (PMH1), and SALK_035421 was named pmh1-1 (Matthes et al., 2007). In this thesis, SALK_035421 was designated atrh9 in consistency of the gene name AtRH9 in the AtRH family (Aubourg et al., 1999). A homozygous insertion in atrh9 was identified using two gene-specific primers (LP+RP) to detect wild-type genotype and a gene-specific primer (RP) with a T-DNA specific primer (LB) to detect T-DNA insertion genotype (Figure 5C). Loss of transcript in atrh9 was revealed by reverse transcription (RT)-PCR analysis using AtRH9-specific primers (Figure 5D). RT-PCR result was consistent with the published data (Köhler et al., 2010). Another AtRH9 T-DNA insertion line SALK_060677 with a T-DNA insertion located in the 3' untranslated region (UTR), was genotyped as a homozygous line for AtRH9 as well (Figure 5E). This mutant line is named atrh9-1. Since the insertion position of the T-DNA in this mutant was mapped to the 3' untranslated region, which suggested a likely knockdown expression, we did not test this mutant further.
A.  

AT3G22310 (AtRH9)

B.  

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Locus</th>
<th>Salk line</th>
<th>T-DNA insertion sites</th>
</tr>
</thead>
<tbody>
<tr>
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<td>Exon</td>
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<tr>
<td></td>
<td></td>
<td>SALK_060677.54.50.x</td>
<td>3’ UTR</td>
</tr>
</tbody>
</table>

C.  

D.  

E.  

[Images of gel electrophoresis and DNA sequencing results]
Figure 5  Genotyping and RT-PCR analysis of *Arabidopsis atrh9* T-DNA insertion lines.

(A) Schematic characterization of *AtRH9* and T-DNA insertion sites (triangles) in *Arabidopsis* T-DNA insertion mutants. Exons and introns are indicated by boxes and lines respectively. 5' and 3' untranslated regions are shown as open boxes.

(B) A summary of the two *Arabidopsis atrh9* T-DNA insertion lines.

(C) Screening for homozygous *atrh9* T-DNA insertion lines. PCR was conducted using genomic DNA from *atrh9* (SALK_035421) and WT plants. Two gene-specific primers (LP+RP) were used to detect wild-type genotype. A T-DNA specific primer and a gene-specific primer (LB+RP) were used to amplify a single PCR fragment which represented the pattern of homozygous genotype. WT, wild-type *Arabidopsis*; LP, left genomic primer; RP, right genomic primer; LB, Left border primer of the T-DNA insertion.

(D) RT-PCR analysis of *AtRH9* expression in *atrh9* mutants and WT plants (SALK_035421). RT-PCR was performed using cDNA derived from leaf tissues of *Arabidopsis atrh9* mutants and WT plants with *AtRH9* specific primers. *Actin2 (Actin)* gene was used as an internal control.

(E) Screening for homozygous *atrh9-1* T-DNA insertion line, SALK_060677. A single PCR product was amplified using genomic DNA from the mutant using a T-DNA specific primer and a gene-specific primer (LB+RP).
3.2.2 The accumulation of TuMV was reduced in atrh9 mutant plants

Under standard growth conditions, atrh9 mutant plants displayed no abnormal phenotypes distinguishable from Arabidopsis WT plants. To confirm the partial TuMV resistance in the atrh9 mutant plants, three-week-old atrh9 mutants and WT plants were agroinfiltrated with a GFP-tagged TuMV infectious clone (TuMV-GFP). To monitor TuMV infection in these plants, confocal microscopy was used to observe GFP fluorescence intensity. Strong signals of GFP fluorescence were observed in the newly-emerged leaves of infected WT plants, whereas only weak and scattered GFP fluorescence was detected in atrh9 mutant plants at 10 dpi (Figure 6A). Real-time RT-PCR was carried out to quantify TuMV accumulation. In the atrh9 mutant plants, TuMV viral accumulation showed a substantial decrease by 85% with respect to that in WT plants at 15 dpi (Figure 6B). In contrast to severe TuMV symptoms such as necrosis, chlorotic leaves and dwarfing developed on WT plants, atrh9 mutant plants displayed very minor symptoms, such as curled bolts (Figure 6C). Taken together, these results suggest that AtRH9 function is required for successful progression of TuMV infection.

3.2.3 Knock down of AtRH9 expression in Arabidopsis by VIGS

To further confirm the involvement of AtRH9 in TuMV infection, a TRV-based VIGS was used to silence AtRH9 expression in Arabidopsis. A cDNA fragment of AtRH9 was cloned into a pTRV2-derived vector to produce pTRV2-AtRH9. Arabidopsis wild-type seedlings were co-agroinfiltrated with the vectors pTRV2-AtRH9 and pTRV1. At 12 days post agroinfiltration, a bleaching phenotype was observed in control plants co-agroinfiltrated with pTRV2-PDS and pTRV1, indicating VIGS was established. At this time point, the TuMV infection assay was applied on AtRH9-downregulated plants (treated with pTRV2-AtRH9 and pTRV1) as well as WT plants (treated with buffer) and negative control plants (treated with empty pTRV vectors). Real-time RT-PCR was performed to evaluate AtRH9 expression and TuMV accumulation at 15 dpi (Figure 7A).
A.

TuMV-GFP  Chl  Merge

WT-TuMV

WT-Mock

atrh9-TuMV

atrh9-Mock

B.

Relative fold of TuMV accumulation

atrh9-TuMV  WT-TuMV

CP

*
Figure 6 TuMV accumulation was reduced in atrh9 mutant plants.

(A) Three-week-old Arabidopsis atrh9 mutants (SALK_035421) and WT plants were agroinfiltrated with TuMV-GFP infectious clone. Newly-emerged leaves were observed by confocal microscopy 10 days post infiltration, and representative images are shown. Mock, atrh9 mutants and WT plants were agroinfiltrated with buffer. TuMV-GFP, green fluorescence emissions; Chl, chloroplast autofluorescence. Bars, 50 µm.

(B) Relative fold changes of TuMV accumulation in atrh9 mutant plants (SALK_035421) by real-time RT-PCR at 15 dpi. RNA was extracted from newly-emerged leaves of infected individual plants at 15 dpi. Three independent experiments, each consisting of three biological replicates were carried out for quantification analysis. Each value was normalized against Actin2 transcripts in the same sample. The values are presented as means of fold change relative to WT. Error bars represent standard deviation (n=9). Asterisk indicated significant difference from WT plants (student’s t test, p<0.05).

(C) Phenotypes of TuMV-infected atrh9 mutants and WT plants. Images were taken at 15 dpi. Mock, inoculated with buffer; TuMV, inoculated with TuMV.
The severely reduced level of the \textit{AtRH9} transcript in \textit{AtRH9}-downregulated plants was coupled with partial resistance to TuMV infection (Figure 7B). Consistent with the results from TuMV infection assays on the \textit{atrh9} mutant plants, these data suggest that downregulation of \textit{AtRH9} effectively inhibits TuMV infection in \textit{Arabidopsis}.

3.2.4 Subcellular localization of \textit{Arabidopsis} AtRH9

To gain insight into the molecular function of AtRH9 required for TuMV infection, subcellular localization analysis was performed. A translational fusion of AtRH9 with YFP controlled by the CaMV 35S promoter was transiently expressed in \textit{N. benthamiana} leaf epidermal cells via agroinfiltration. Subcellular localizations of fusion proteins were monitored using a Leica TCS SP2 inverted confocal microscopy 48 h post agroinfiltration. Consistent with a previous study (Matthes \textit{et al.}, 2007), AtRH9-YFP was observed mostly in the cytoplasm (Figure 8).

3.2.5 \textit{Arabidopsis} AtRH9 interacts with TuMV NIa-Pro \textit{in planta}

To investigate if AtRH9 interacts with TuMV viral proteins \textit{in vivo}, the BiFC assay was employed. The \textit{AtRH9} gene and the coding sequence for each of the 11 TuMV viral proteins were introduced into BiFC vectors that contained DNA fragments encoding the N- or C-terminal half of YFP, respectively, and transiently co-expressed into \textit{N. benthamiana} epidermal cells by co-agroinfiltration. The YFP signal would be emitted when split fluorescent protein segments were brought together as a result of positive interaction between two tested proteins. YFP signals were detected only when AtRH9 and NIa-Pro were co-expressed, suggesting AtRH9 interacts with NIa-Pro. The interaction was apparent in both the nucleus and cytoplasm, which was consistent with the known subcellular localization of NIa-Pro (Restrepo \textit{et al.}, 1990). No YFP signal was observed in two negative control experiments (AtRH9-YC and YN, NIa-Pro-YN and YC) (Figure 9).
A.

B.
Figure 7  Knockdown of AtRH9 expression affects TuMV infection in Arabidopsis.

(A) Phenotypes of TuMV-infected AtRH9-knockdown plants, empty VIGS vector-infiltrated plants and Arabidopsis WT plants. pTRV-PDS-TuMV, wild-type Arabidopsis plants infiltrated with TRV-based VIGS vectors targeting phytoene desaturase (PDS) to silence and then inoculated with TuMV; pTRV-AtRH9-TuMV, WT infiltrated with TRV-based VIGS vectors targeting AtRH9 followed by inoculation with TuMV; pTRV-TuMV, WT infiltrated with empty TRV-based VIGS vectors and then inoculated with TuMV; WT-Mock, WT infiltrated with buffer and then inoculated with buffer; WT-TuMV, WT inoculated with TuMV. Images were taken 15 days post inoculation. TuMV, inoculated with TuMV. Mock, inoculated with buffer.

(B) Relative fold changes in TuMV accumulation and expression level of AtRH9 in AtRH9-silenced Arabidopsis plants and WT plants. RNA was extracted from leaf tissues for real-time RT-PCR analysis at 15 dpi. Three independent experiments, each consisting of three biological replicates were carried out for quantification analysis. Target genes were normalized against Actin2 transcripts in each sample. The values are presented as means of fold change relative to the WT plants. Error bars represent standard deviations.
Figure 8  Subcellular localization of *Arabidopsis* AtRH9.

Transient expression of AtRH9-YFP in *N. benthamiana* leaf epidermal cells. YFP fluorescence was observed using a confocal microscopy 48 h post agroinfiltration. DIC, differential interference contrast. Bars, 30 µm.
Figure 9  The BiFC assay for detection of the interaction between AtRH9 and TuMV NIa-Pro in planta.

*N. benthamiana* leaves were co-agroinfiltrated with constructs expressing NIa-Pro and AtRH9 fused to the N- and C- terminal half of YFP, respectively. The reconstructed YFP fluorescence was recorded 48 h post agroinfiltration using a confocal microscopy. Leaves coexpressing with AtRH9-YC and YN or NIa-Pro-YN and YC were shown as negative controls. No YFP fluorescence was detected in negative controls. DIC, differential interference contrast. Bars, 35 µm.
3.3 Characterization of *Arabidopsis atrh26* T-DNA insertion line

3.3.1 Verification of *Arabidopsis atrh26* T-DNA insertion line

To verify the homozygosity of the *atrh26* T-DNA insertion line SALK_106823, PCR-based genotyping and RT-PCR analysis were carried out. The T-DNA insertion in this mutant line was located in the promoter region of *AtRH26* (Figure 10A). Essentials of PCR genotyping as described earlier were conducted to identify the T-DNA insertion genotype (Figure 10B). PCR genotyping results were consistent in two generations. Therefore, the mutant obtained was confirmed as a homozygous T-DNA insertion line, and was named *atrh26*. RT-PCR of RNA isolated from *atrh26* leaf tissue failed to amplify the corresponding full-length *AtRH26* mRNA using gene-specific primers. This result further supports that the *atrh26* represents a homozygous knockout mutant line (Figure 10C).

3.3.2 *Arabidopsis AtRH26* is necessary for TuMV infection

*Arabidopsis atrh26* mutant plants exhibited normal growth and development under standard growth conditions (Figure 10D). The involvement of *AtRH26* in TuMV infection was evaluated by analyzing the susceptibility of *Arabidopsis atrh26* mutants to TuMV infection. After inoculation with TuMV, *atrh26* mutant plants showed mild symptoms compared with the TuMV-infected WT plants (Figure 10E).

3.3.3 Subcellular localization of *Arabidopsis AtRH26*

To localize *AtRH26*, a plant expression vector containing the coding sequence for *AtRH26* tagged with the CFP controlled by the CaMV 35S promoter was agroinfiltrated into *N. benthamiana* leaf epidermal cells. AtRH26-CFP signal was visualized by a confocal microscopy 48 h post agroinfiltration. AtRH26-CFP was found in the nucleus and cytoplasm (Figure 11).
A. AT5G08610 (AtRH26)

B. 

C. 

D. 

E. 

SALK_106823

atr26-HM WT MW

SALK_106823- AtRH26 SALK_106823- ACT2 WT- AtRH26 WT- ACT2

SALK_106823 WT

TuMV Mock TuMV Mock
Figure 10  Characterization of homozygous *Arabidopsis atrh26* T-DNA insertion line.

(A) Schematic characterization of *AtRH26* and T-DNA insertion sites (triangles) in *Arabidopsis* T-DNA insertion mutants. Exons and introns are indicated by boxes and lines, respectively. 5' and 3' untranslated regions are shown as open boxes.

(B) Genotyping of *Arabidopsis atrh26* T-DNA insertion mutants (SALK_106823). PCR was conducted using genomic DNA to amplify a single DNA fragment, which corresponds to the homozygous genotype or a single DNA product from WT plant as a control.

(C) RT-PCR analysis of the expression of *Arabidopsis AtRH26* in WT and *atrh26* T-DNA insertion line (SALK_106823). RT-PCR was performed using cDNA derived from leaf tissues of *atrh26* mutants and WT plants with *AtRH26* gene-specific primers. *Actin2 (ACT2)* gene was used as an internal control.

(D) Four-week-old of *atrh26* T-DNA insertion mutants and WT plants.

(E) *Arabidopsis atrh26* mutants and WT plants inoculated with TuMV or buffer. TuMV, inoculated with TuMV. Mock, inoculated with buffer. Photos were taken at 10 dpi.
**Figure 11**  Subcellular localization of *Arabidopsis* AtRH26.

Transient expression of AtRH26-CFP in *N. benthamiana* leaf epidermal cells. CFP fluorescence was observed using a confocal microscopy 48 h post agroinfiltration. DIC, differential interference contrast. Bars, 30 µm.
3.4 Characterization of *Arabidopsis prh75* T-DNA insertion line

In a recent published report, *PRH75* was shown to be essential for *Arabidopsis* embryo development, implying that there are no knockout T-DNA insertion mutants available for *PRH75* (Nayak *et al.*, 2013). The T-DNA insertion line SALK_040389 harbors a T-DNA insertion in the 5' UTR region of *PRH75*, 56 bp upstream from the start codon, and was named *prh75* (Figure 12A and 12B). PCR-based genotyping indicated that the mutant line was homozygous (Figure 12C). To determine if this homozygous mutant line is a knockout line, RT-PCR was conducted to examine *PRH75* expression. Although T-DNA insertion did not abolish *PRH75* expression, it indeed remarkably reduced *PRH75* expression when compared with WT plants (Figure 12D). Thus, the T-DNA insertion line *prh75* used in this study is a knockdown mutant line. The down-regulation of *PRH75* expression is likely due to position effect, since T-DNA was inserted in the 5' untranslated region. Knockdown of *PRH75* expression dose not result in any apparent change during plant growth and development, and *prh75* mutant plants are morphologically indistinguishable from wild-type plants. Another T-DNA insertion line, SALK_068401, containing a T-DNA insertion 10 bp upstream of the translation start site of PRH75 was also included in TuMV infection assay. The homozygous plants were identified by PCR analysis. PCR-based genotyping analysis showed that SALK_068401 is a homozygous T-DNA insertion line (Figure 12E). RT-PCR analysis revealed that this line is also an expression knockdown mutant line (Figure 12F). This mutant line is named *prh75-1*. The T-DNA insertion in both lines was verified by sequencing analysis of genomic DNA.

3.4.1 *PRH75* was required for TuMV infection

To determine if there is a correlation between the lack of *PRH75* and debilitation of TuMV infection, *Arabidopsis prh75* and WT plants were agroinfiltrated with TuMV-GFP. Confocal microscopy was employed to observe GFP expression levels in order to validate the susceptibility of those mutant plants to TuMV infection. Strong GFP fluorescence was observed in the newly-emerged leaves of infected WT plants whereas only weak GFP fluorescence was detected in *prh75* mutant plants at 10 dpi (Figure 13A).
A.

AT5G62190 (PRH75)

B.

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Locus</th>
<th>Salk line</th>
<th>T-DNA insertion sites</th>
</tr>
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<td>AT5G62190</td>
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<td>SALK_068401.35.25.x</td>
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</table>
Figure 12  Genotyping and RT-PCR analysis of *Arabidopsis prh75* T-DNA insertion lines.

(A) Schematic characterization of *PRH75* and T-DNA insertion sites (triangles) in *Arabidopsis* T-DNA insertion mutants. Exons and introns are indicated by boxes and lines respectively. 5' and 3' untranslated regions are shown as open boxes.

(B) A summary of two *prh75* T-DNA insertion mutant lines used in this study.

(C) Screening for the homozygous *Arabidopsis prh75* T-DNA insertion lines. PCR was conducted using genomic DNA from *prh75* (SALK_040389) and WT plants. Two gene-specific primers (LP+RP) were used to detect wild-type genotype. A T-DNA specific primer and a gene-specific primer (LB+RP) were used to amplify a single PCR product which represented the pattern of homozygous genotype. WT, wild-type *Arabidopsis*; LP, left genomic primer; RP, right genomic primer; LB, Left border primer of the T-DNA insertion.

(D) RT-PCR analysis of *PRH75* expression in *prh75* mutants (SALK_040389) and WT plants. RT-PCR was performed using cDNA derived from leaf tissues of *Arabidopsis prh75* mutants and WT plants with *PRH75* specific primers. *Actin2* (*Actin*) was used as an internal control.

(E) Screening for the homozygous *Arabidopsis prh75* T-DNA insertion line, SALK_068401. A single PCR product was amplified using genomic DNA from leaf tissues using a T-DNA specific primer and a gene-specific primer (LB+RP).

(F) RT-PCR analysis of *PRH75* expression in *prh75-1* mutants (SALK_068401) and WT plants. RT-PCR was performed using cDNA derived from leaf tissues of *prh75-1* mutants and WT plants with *PRH75* specific primers. *Actin2* (*Actin*) was used as an internal control.
TuMV accumulation in prh75 mutants and WT plants was monitored by real-time RT-PCR. TuMV viral RNA accumulation decreased significantly in prh75 mutant plants in comparison with that in WT plants at 15 dpi (Figure 13B). Consistent with the decreased TuMV accumulation, no severe TuMV-induced symptoms developed in prh75 mutant plants (Figure 13C). Therefore, knockdown of PRH75 leads to resistance to TuMV infection. Altogether, these data strongly indicate that PRH75 is essential for TuMV infection in Arabidopsis.

3.4.2 Silencing of PRH75 in Arabidopsis by VIGS confers resistance to TuMV

Given that knockout mutants are not available for PRH75, VIGS was employed to knock down the expression of PRH75 in Arabidopsis in order to further confirm its requirement for TuMV infection. A cDNA fragment of PRH75 was cloned into a pTRV2-derived vector, and Arabidopsis WT plants were co-agroinfiltrated with the resulting pTRV2-PRH75 together with pTRV1. After VIGS was established 12 days post agroinfiltration, the infiltrated plants were mechanically inoculated with TuMV. Real-time RT-PCR was performed to detect PRH75 mRNA abundance and TuMV accumulation at 15 dpi. The amount of PRH75 mRNA in treated plants was greatly reduced when compared with negative control plants which were co-agroinfiltrated with empty pTRV2 and pTRV1 vectors (Figure 14A). PRH75-knockdown Arabidopsis plants showed weak TuMV symptoms, such as curled bolts and were slightly shorter in height. In contrast, mock-treated plants (treated with buffer) and negative control plants (treated with empty pTRV vectors) were highly susceptible to TuMV and showed severe typical TuMV infection symptoms such as stunted growth and chlorosis and necrosis (Figure 14B). These data suggest that silencing of PRH75 confers resistance to TuMV infection, consistent with the results that the prh75 mutant is resistant to TuMV infection (Figure 13).
A.

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B.

![Bar chart showing relative fold of TuMV accumulation](chart.png)

Relative fold of TuMV accumulation

- prh75-TuMV: [Bar chart data]
- WT-TuMV: [Bar chart data]

- CP

* p-value
Figure 13 Relative TuMV accumulation in *prh75* mutant and wild-type plants.

(A) Confocal images of newly-emerged leaves of TuMV-infiltrated *prh75* mutants and *Arabidopsis* WT plants at 10 days post infiltration. TuMV, *prh75* mutants and WT plants agroinfiltrated with TuMV-GFP. Mock, plants agtoinfiltrated with buffer; TuMV-GFP, green fluorescence emissions; Chl, chloroplast autofluorescence. Bars, 50 µm.

(B) Real-time RT-PCR of TuMV accumulation in *prh75* mutants and WT plants. RNA was extracted from newly-emerged leaves of infected *prh75* mutants (SALK_040389) at 15 dpi. Three independent experiments, each consisting of three biological replicates, were carried out for quantification analysis. TuMV accumulation level was normalized against Actin2 transcripts in the same sample and the means of fold change was calculated relative to the TuMV level in WT plants. Error bars represent standard deviation (n=9). Asterisk indicates significant difference from WT plants (student’s t test, p<0.05).

(C) Phenotypes of TuMV-infected *prh75* mutants and WT plants. Images were taken at 15 dpi. Mock, inoculated with buffer; TuMV, inoculated with TuMV.
A.

B.
Figure 14 *PRH75*-silenced plants exhibit partial resistance to TuMV infection.

(A) Symptoms of TuMV-infected *PRH75*-silenced plants, empty VIGS vector-infiltrated plants and WT plants. pTRV-PDS-TuMV, *Arabidopsis* WT plants infiltrated with TRV-based VIGS vectors targeting *PDS* to silence and then inoculated with TuMV; pTRV-PRH75-TuMV, *Arabidopsis* WT plants infiltrated with TRV-based VIGS vectors targeting *PRH75* and then inoculated with TuMV; pTRV-TuMV, *Arabidopsis* WT plants infiltrated with empty TRV-based VIGS vectors and then inoculated with TuMV; WT-Mock, *Arabidopsis* WT plants infiltrated with buffer then inoculated with buffer; WT-TuMV, *Arabidopsis* WT plants inoculated with TuMV. Images were taken at 15 dpi. TuMV, inoculated with TuMV; Mock, inoculated with buffer.

(B) Relative fold changes of TuMV accumulation and *PRH75* expression in *PRH75*-silenced and WT plants. RNA was extracted 15 days post inoculation for real-time RT-PCR analysis. Three independent experiments, each consisting of three biological replicates, were carried out for quantification analysis. Target genes were normalized against *ActinII* transcripts in each sample. The values are presented as means of fold change relative to WT plants. Error bars represent standard deviations.
3.5 Molecular characterization of PRH75 and TuMV interactions

3.5.1 The DEAD-box RNA helicase PRH75 is conserved in many plants.

PRH75 is a DEAD-box RNA helicase that has been found in many plant species such as spinach (*Spinacia oleracea*) and mung bean (*Vigna radiate*) (Lorković *et al.*, 1997; Li *et al.*, 2001). BLASTX searches of the NCBI database revealed a number of plant proteins with sequence and structure similarities to PRH75 of *Arabidopsis*. The 12 proteins showing the highest similarity to PRH75 were from the following species: *Capsella rubella*, *Camelina sativa*, *Brassica rapa*, *Eutrema salsugineum*, *Arabis alpine*, *Brassica napus*, *Tarenaya hassleriana*, *Vitis vinifera*, *Jatropha curcas*, *Eucalyptus grandis*, *Cicer arietinum* and *Citrus clementina*. A multi-sequence alignment of corresponding motifs of PRH75 against homologs from different plant species was conducted using the CLUSTAL W program. The alignment result demonstrated that PRH75 shares all the 13 conserved motifs associated with DEAD-box RNA helicases, i.e., motif Q, I, Ia, Ib, Ic, II, III, IV, IVa, V, Va, Vb and VI (Figure 15).

The full-length cDNA of *Arabidopsis PRH75* is 2384 bp in length containing an ORF of 2016 bp which encodes a polypeptide of 671 amino acids (aa), a 94-bp 5' UTR and a 274-bp 3' UTR (Figure 16A). A conserved domain analysis of *Arabidopsis* PRH75 using the NCBI structure program (http://www.ncbi.nlm.nih.gov/Structure/index.shtml) identified the DEAD-box signature (aa 115 to 304), the helicase conserved domain (aa 376 to 441), and the GUCT domain that is considered as an RNA-binding domain at the C-terminus (aa 530 to 612) (Figure 16B).

Based on structural and functional similarity of conserved motifs, PRH75 motifs Q, I, II and VI are required for ATP binding and hydrolysis, whereas motifs Ia, Ib, Ic, IV, IVa and V are suggested to be responsible for RNA-binding (Rocak and Linder, 2004). Motifs III and Va are assumed to coordinate ATPase and unwinding activities (Tanner *et al.*, 2003) (Figure 16C). Recently, *Arabidopsis* PRH75 has been demonstrated to exhibit the capacity for RNA unwinding with RNA duplexes in an ATP-dependent manner (Nayak *et al.*, 2013).
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Figure 15  Multi-sequence alignment of PRH75 amino acid sequence with corresponding domains from different plant species.

Multiple sequences were aligned using the CLUSTAL W program. All the 13 conserved motifs of DEAD-box RNA helicase were shown in boxes with the motif acronym and a solid black line above the amino acids representing the motif. The accession numbers of the aligned protein sequences are Capsella rubella (CrDDX, XP_006279587), Camelina sativa (CsDDX, XP_010458375), Brassica rapa (BrDDX, XP_009130201), Eutrema salsugineum (EsDDX, XP_006394423), Arabis alpina (AaDDX, KFK27951), Brassica napus (BnDDX, CDX87236), Tarenaya hassleriana (ThDDX, XP_010555319), Vitis vinifera (VvDDX, XP_002269873), Jatropha curcas (JcDDX, KDP22369), Eucalyptus grandis (EgDDX, XP_010034995), Cicer arietinum (CaDDX, XP_004506292), Citrus clementina (CcDDX, XP_006421777).
Figure 16  Characterization of Arabidopsis PRH75.

(A) Schematic representation of Arabidopsis PRH75 cDNA.

(B) Schematic representation of Arabidopsis PRH75 protein. The functional domains are indicated in boxes. Conserved signatures were obtained based on the NCBI conserved domain database.

(C) Conserved motifs of Arabidopsis PRH75. The 13 characteristic motifs of DEAD-box RNA helicase are highlighted in boxes in different colors. The numbers above the boxes indicate the positions of the first amino acid of each motif.
3.5.2 PRH75 is a nuclear protein

To explore the role of PRH75 associated with TuMV infection, a transient expression assay was conducted to establish the subcellular localization of PRH75 in plant cells. PRH75 tagged with YFP (PRH75-YFP) was expressed in *N. benthamiana* leaf epidermal cells by agroinfiltration. Consistent with a previous report where PRH75 localization was found in the nucleus using a tobacco protoplast expression system (Lorković *et al.*, 1997), the YFP signal was observed predominantly in the nucleus, particularly in the nucleolar region (Figure 17). This observation indicated that PRH75 is a nuclear protein with preferred localization to the nucleolus. Upon TuMV infection, subcellular localization of PRH75 was altered. This result will be described in section 3.5.6. Distinct from many other AtRHs such as AtRH9 and AtRH26 that are localized to both the nucleus and cytoplasm, the nuclear localization of PRH75 might indicate a specific role of this protein in TuMV infection.

Plasmids containing a series of PRH75 deletion mutants were constructed to determine the region responsible for nuclear targeting. PRH75 was divided into four fragments: N-terminus (corresponding to aa 1-114), DEAD domain (aa 115-355), Helicase domain (aa 356-450) and GUCT domain (aa 451-671) (Figure 18A). The truncated PRH75 derivatives containing one or more of these fragments were fused to a modified pEarleyGate101 vector containing the GUS coding region upstream of YFP. The resulting plasmids were agroinfiltrated into *N. benthamiana* epidermal cells to express PRH75 derivatives fused with GUS-YFP. The localization pattern of truncated PRH75 derivatives indicated that the N-terminal fragment (aa 1-114) was required for nuclear targeting (Figure 18B), which is in agreement with previously published results (Lorković *et al.*, 1997).

3.5.3 PRH75 directly interacts with multiple TuMV viral replicase proteins

To examine whether *Arabidopsis* PRH75 interacts with TuMV proteins, I screened the 11 TuMV proteins using the BiFC assay. The full-length coding region for each of the 11 TuMV proteins and PRH75 were fused to N- and C- terminus of YFP, respectively. The functional reconstituted YFP signal was examined under a confocal microscopy when
Figure 17  PRH75 is localized in the nucleus.

(A) Transient expression of PRH75-YFP in *N. benthamiana* leaf epidermal cells. YFP fluorescence was observed using a confocal microscopy 48 h post agroinfiltration. DIC, differential interference contrast. Bars, 50 µm.

(B) Transient expression of PRH75-YFP with fibrillarin-CFP, a nucleolus marker protein in *N. benthamiana* leaf epidermal cells (Koroleva *et al.*, 2009). PRH75-YFP and fibrillarin-CFP were co-expressed in *N. benthamiana* leaves via agroinfiltration. Images were taken using a confocal microscopy 48 h post agroinfiltration. DIC, differential interference contrast. Bars, 15 µm.
A. Schematic diagram of truncated PRH75 proteins. The positions of the first and last amino acid residues of truncated proteins are indicated in parentheses.

B. Subcellular localization of truncated PRH75 proteins tagged with GUS-YFP in planta. Transient expression of truncated PRH75 proteins tagged with GUS-YFP in N. benthamiana leaf epidermal cells. YFP fluorescence was observed using a confocal microscopy 48 h post agroinfiltration. DIC, differential interference contrast. Bars, 30 µm.

Figure 18  Analysis of truncated PRH75 proteins.
viral fusion proteins and PRH75 fusion protein were co-expressed in plant cells following the same strategy as described previously. The results showed that PRH75 interacted with viral replicase proteins NIb, NIa-Pro, VPg and CI (Figure 19) but no detectable interactions were found with other viral proteins (Data not shown). For positive interactions, YFP signals were observed predominately in the nucleus with a small amount of signal detected in the cytoplasm. No YFP signal was detected in the negative controls (Appendix II). A targeted Y2H was performed to confirm interactions between PRH75 and TuMV viral proteins. Cotransformants of PRH75 and each viral protein were grown and selected on synthetic defined plates (SD/-Ade/-His/-Leu/-Trp). Yeast colonies co-transformed with PRH75 and each of NIb, VPg and CI, respectively, showed normal growth on the selective plates (SD/-Ade/-His/-Leu/-Trp). Controls, i.e., cotransformants of empty bait and prey vectors, PRH75 and the empty prey vector, or NIb, VPg and CI with bait only, did not grow (Figure 20). Inconsistent with the BiFC data, no positive interaction was found in yeast cells co-transformed with PRH75 and NIa-Pro.

To further confirm the interaction between PRH75 and viral proteins, a fluorescence resonance energy transfer (FRET) assay was conducted. Based on high spatial resolution, FRET analysis provides a powerful tool to detect protein-protein interactions in living cells. Translational fusion of PRH75 tagged with CFP was co-expressed with each of NIb, NIa-Pro, VPg and CI tagged with YFP in N. benthamiana leaf epidermal cells. Protein-protein interactions were examined by confocal microscopy. The change in increased intensity of CFP signal after photobleaching of YFP was determined as FRET efficiency, which indicated the positive interaction between two proteins. The results suggested a positive interaction between PRH75 and NIb with a FRET efficiency of 34.98%, as well as between PRH75 and NIa-Pro with a FRET efficiency of 37.49%. The FRET efficiency between PRH75 and VPg was 29.96% whereas between PRH75 and CI was 33.52%, respectively. The FRET efficiency between PRH75-CFP and GUS-YFP, as a negative control, was negligible (Figure 21). Taken together, PRH75 showed positive interactions with TuMV NIb, NIa-Pro, VPg and CI, respectively.
E.

Figure 19  The BiFC assay for detection of the interactions between PRH75 and TuMV viral proteins \textit{in planta}.

\textit{N. benthamiana} leaves were co-agroinfiltrated with constructs to co-express viral proteins and PRH75: (A) N1b and PRH75 fused with the N- and C- terminal moiety of YFP (YN and YC), respectively, (B) N1a-Pro-YN and PRH75-YC, (C) VPg-YN and PRH75-YC, (D) CI-YN and PRH75-YC, and (E) 6K2-YN and PRH75-YC. The reconstructed YFP fluorescence was recorded 48 h post agroinfiltration using a confocal microscopy. Bars, 50 µm.
Figure 20  The yeast two-hybrid assay for detection of the interactions between PRH75 and TuMV viral proteins.

Positive interactions between PRH75 and TuMV N1b, VPg or CI were evident in yeast. A series of 10 µl aliquots of 10x yeast dilutions co-transformed with bait and prey were spotted onto synthetic defined (SD) selection plates and incubated for 2-4 days at 30°C. Yeast cultures were plated on SD/-Leu/-Trp or SD/-Ade/-His/-Leu/-Trp dropout medium to observe yeast growth and to identify positive interactions, respectively. Co-transformation of the pGAD empty vector (prey) with pGBK-PRH75 (bait), and co-transformation of the pGBK empty vectors (bait) with pGAD-VPg (prey), pGAD-N1b (prey) and pGAD-CI (prey), respectively, were used as negative controls, and co-transformation of pGAD-VPg with pGBK-eIF(iso)4E as the positive control. Representative results were obtained in three independent experiments.
Figure 21  Quantification of FRET efficiency between PRH75 and TuMV viral proteins.

FRET efficiencies were calculated using the formula: FRET efficiency = \left\{ \frac{\text{CFP signal after photobleaching} - \text{CFP signal before photobleaching}}{\text{CFP signal after photobleaching}} \right\} \times 100. Error bars represent standard deviations for nine independent FRET analyses in three independent experiments. (A) FRET efficiency between PRH75-CFP and NIb-YFP, (B) FRET efficiency between PRH75-CFP and NIa-Pro-YFP, (C) FRET efficiency between PRH75-CFP and VPg-YFP, and (D) FRET efficiency between PRH75-CFP and CI-YFP. The combination of PRH75-CFP and GUS-YFP was used as a negative control.
3.5.4 *Arabidopsis* importin α interacts with PRH75 and TuMV viral replicase proteins

The nuclear localization of PRH75 and several potyviral replicase proteins has prompted us to look into the possibility that the nuclear transport of TuMV viral proteins is mediated by *Arabidopsis* importin α. To investigate whether *Arabidopsis* importin α is required for nucleocytoplasmic shuttle of these proteins, two isoforms of *Arabidopsis* importin α (IMPA), IMPA1 and IMPA2, were analyzed. The Y2H and BiFC assays were performed to examine the ability of IMPA1 and IMPA2 to interact with PRH75 and each of these TuMV replicase proteins.

Interactions between PRH75 and IMPA1 and IMPA2 in plant cells were identified using the BiFC assay (Figure 22). YFP fluorescence was observed in the nucleus, which is consistent with the localization pattern of PRH75. The Y2H assay confirmed that PRH75 directly interacts with *Arabidopsis* IMPA1 and IMPA2 (Figure 23).

Positive interactions were also found between IMPA1 and NIb, IMPA1 and Nla-Pro, IMPA1 and VPg, or IMPA1 and CI using the BiFC assay *in planta*. The reconstituted YFP signal was found in the nucleus and cytoplasm of plant cells co-expressing IMPA1 fused to the N-terminus of YFP with NIb, Nla-Pro, VPg and CI fused to the C-terminus of YFP, respectively (Figure 24). The Y2H assay further confirmed that IMPA1 interacted with NIb, Nla-Pro, VPg and CI (Figure 25). Taken together, these data suggest that *Arabidopsis* IMPA1 interacts with TuMV NIb, Nla-Pro, VPg and CI.

Similarly, the BiFC assay indicated the interactions of IMPA2 with NIb, Nla-Pro, VPg and CI, respectively, *in planta*. The YFP fluorescence was observed mostly in the nucleus with partially in the cytoplasm (Figure 26). The interactions between IMPA2 and NIb, Nla-Pro, VPg and CI were further confirmed by the Y2H assay. Altogether, the results showed that *Arabidopsis* IMPA2 also interacts with TuMV NIb, Nla-Pro, VPg and CI (Figure 27).

The tested interactions between PRH75, TuMV viral proteins and *Arabidopsis* IMPA1 and IMPA2 are summarized in Table 10.
A.

IMPA1-YN+PRH75-YC  DIC  Merge

B.

IMPA2-YN+PRH75-YC  DIC  Merge

Figure 22  The BiFC assay for detection of the interactions between PRH75 and *Arabidopsis* IMPA1 and IMPA2 in planta.

*N. benthamiana* leaves were co-agroinfiltrated with constructs to co-express (A) IMPA1 and PRH75 fused with the N- and C- terminal half of YFP (YN and YC), respectively, and (B) IMPA2-YN and PRH75-YC. The reconstructed YFP fluorescence was recorded 48 h post agroinfiltration using a confocal microscopy. DIC, differential interference contrast. Bars in (A), 25 µm, and in (B), 50 µm.
Figure 23 The yeast two-hybrid assay for detection of the interactions between
PRH75 and Arabidopsis IMPA1 and IMPA2.

Positive interactions were found between PRH75 and Arabidopsis IMPA1 and IMPA2 in yeast. A series of 10 µl aliquots of 10x yeast dilutions co-transformed with bait and prey were spotted onto SD selection plates and incubated for 2-4 days at 30°C. Yeast cultures were plated on SD/-Leu/-Trp or SD/-Ade/-His/-Leu/-Trp dropout medium to observe yeast growth and to identify positive interactions, respectively. Co-transformation of the pGAD empty vector (prey) with the pGBK empty vector (bait) was used as a negative control, and co-transformation of pGAD-VPg with pGBK-eIF(iso)4E as a positive control.
Figure 24  The BiFC assay for detection of the interactions between IMPA1 and TuMV viral proteins *in planta.*

*N. benthamiana* leaves were co-agroinfiltrated with constructs to co-express (A) IMPA1 and NIb fused with the N- and C- terminal half of YFP (YN and YC), respectively, (B) IMPA1-YN and NIa-Pro-YC, (C) IMPA1-YN and VPg-YC, and (D) IMPA1-YN and CI-YC. The reconstructed YFP fluorescence was recorded 48 h post agroinfiltration using a confocal microscopy. DIC, differential interference contrast. Bars in (A), 20 µm, and in (B, C, D), 50 µm.
Figure 25  The yeast two-hybrid assay for detection of the interactions between *Arabidopsis* IMPA1 and TuMV viral proteins.

Positive interactions between *Arabidopsis* IMPA1 and TuMV viral proteins Nlb, NIa-Pro, VPg or CI were detected in yeast. A series of 10 µl aliquots of 10x yeast dilutions co-transformed with bait and prey were spotted onto synthetic defined (SD) selection plates and incubated for 2-4 days at 30°C. Yeast cultures were plated on SD/-Leu/-Trp or SD/-Ade/-His/-Leu/-Trp dropout medium to observe yeast growth and to identify positive interactions, respectively. Co-transformation of the pGAD empty vector (prey) with the pGBK empty vector (bait) serves as a negative control, and co-transformation of pGAD-VPg and pGBK-eIF(iso)4E as a positive control.
Figure 26  The BiFC assay for detection of the interactions between IMPA2 and TuMV viral proteins in planta.

*N. benthamiana* leaves were co-agroinfiltrated with constructs to co-express (A) IMPA2 and NIb fused with the N- and C- terminal moiety of YFP (YN and YC), respectively, (B) IMPA2-YN and NIa-Pro-YC, (C) IMPA2-YN and VPg-YC, and (D) IMPA2-YN and CI-YC. The reconstructed YFP fluorescence was observed 48 h post agroinfiltration using a confocal microscopy. DIC, differential interference contrast. Bars, 20 µm.
Figure 27  The yeast two-hybrid assay for detection of the interactions between *Arabidopsis* IMPA2 and TuMV viral proteins.

Positive interactions between *Arabidopsis* IMPA2 and TuMV viral proteins Nib, Nla-Pro, VPg or CI were confirmed in yeast. A series of 10 µl aliquots of 10x yeast dilutions co-transformed with bait and prey were spotted onto SD selection plates and incubated for 2-4 days at 30°C. Yeast cultures were plated on SD/-Leu/-Trp or SD/-Ade/-His/-Leu/-Trp dropout medium to observe yeast growth and to identify positive interactions, respectively. Co-transformation of the pGAD empty vector (prey) with the pGBK empty vector (bait) was used as a negative control, and co-transformation of pGAD-VPg with pGBK-eIF(iso)4E as a positive control.
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3.5.5 PRH75 colocalizes with *Arabidopsis* importin α, eIF(iso)4E and TuMV viral replicase proteins

To determine if PRH75 colocalizes with IMPA1 and IMPA2, *N. benthamiana* leaves were co-agroinfiltrated with vectors expressing PRH75-CFP and IMPA1-YFP or IMPA2-YFP, respectively. At 48 h post agroinfiltration, observation was taken by a confocal microscopy and revealed that the cyan fluorescence of PRH75 predominantly overlapped the IMPA1-YFP and IMPA2-YFP fluorescence in the nucleus (Figure 28).

*Arabidopsis* eIF(iso)4E, the isoform of eIF4E, which functions as a cap-binding protein that initiates translation of mRNA (Wang and Krishnaswamy, 2012). eIF(iso)4E was reported to interact with TuMV VPg and its precursor VPg-Pro (NIa) and was required for TuMV infection (Lellis et al., 2002). When expressed alone, eIF(iso)4E was found mainly in the cytoplasm, around the nuclear membrane and in the ER network. eIF(iso)4E was redistributed to the nucleus when co-expressed with VPg-Pro (NIa) (Beauchemin et al., 2007; Beauchemin and Laliberté, 2007). The colocalization study of PRH75 with eIF(iso)4E indicated that PRH75 overlaps the localization of eIF(iso)4E in the nucleus (Figure 29).

To investigate whether the intracellular distributions of TuMV viral replicase proteins change in the presence of PRH75, we co-expressed PRH75-CFP with NIb-YFP, NIa-Pro-YFP, VPg-YFP and CI-YFP, respectively in *N. benthamiana* leaves. No different subcellular distribution patterns were found when viral protein was expressed alone or co-expressed with PRH75. These data suggested that PRH75 colocalized with TuMV viral replicase proteins in the nucleus (Figure 30).

3.5.6 Distribution of BiFC signals between PRH75 and TuMV viral replicase proteins is altered in the presence of TuMV infection

To assess whether the interactions between PRH75 and TuMV viral replicase proteins are altered during TuMV infection, the BiFC assay was carried out. Four viral proteins, NIb, NIa-Pro, VPg and CI and PRH75 were introduced into N- or C-terminal half of YFP, respectively, and co-expressed into *N. benthamiana* leaves infected with a TuMV
Figure 28  Colocalization of PRH75 and *Arabidopsis* importin α.

*N. benthamiana* leaves were co-agroinfiltrated with constructs to co-express (A) PRH75-CFP and IMPA1-YFP, (B) PRH75-CFP and IMPA2-YFP. Observations were recorded 48 h post agroinfiltration using a confocal microscopy. DIC, differential interference contrast. Bars in (A), 50 µm, and in (B) 25 µm.
Figure 29  Colocalization of PRH75 and Arabidopsis host proteins.

*N. benthamiana* leaves were co-agroinfiltrated with constructs expressing PRH75-CFP and eIF(iso)4E-YFP. Images were taken 48 h post agroinfiltration using a confocal microscopy. DIC, differential interference contrast. Bars, 30 µm.
Figure 30  Colocalization of PRH75 and TuMV viral proteins.

*N. benthamiana* leaves were co-agroinfiltrated with constructs to co-express (A-I) PRH75-CFP and Nlb-YFP, (B-I) PRH75-CFP and NIa-Pro-YFP, (C-I) PRH75-CFP and VPg-YFP, and (D-I) PRH75-CFP and CI-YFP. Transient expression of TuMV viral protein alone in *N. benthamiana*. (A-II) Nlb-YFP, (B-II) NIa-Pro-YFP, (C-II) VPg-YFP, and (D-II) CI-YFP. Images were recorded 48 h post agroinfiltration using a confocal microscopy. DIC, differential interference contrast. Bars in (A), 20 µm, in (B), 25µm, in (C), 30 µm and in (D), 50 µm.
infectious clone expressing a 6K2-mCherry fusion protein (TuMV::6K2-mCherry). The TuMV infectious clone was engineered to carry an in-frame translational fusion of 6K2-mCherry between P1 and HC-Pro. The TuMV::6K2-mCherry infectious clone can induce the formation of discrete fluorescent structures, designated as the viral vesicles. Moreover, the motility of 6K2-induced vesicle suggests that the virus movement determinant lies on 6K2 protein. dsRNA was detected within the virus-induced vesicles by staining with antibodies (Cotton et al., 2009). Further, host factors such as eIF(iso)4E (Beauchemin et al., 2007), PABP (Beauchemin and Laliberté, 2007), Hsc70-3 (Dufresne et al., 2008), eEF1A (Dufresne et al., 2008) and AtRH8 (Huang et al., 2010) were previously demonstrated to be enclosed within the 6K2-induced vesicles, indicating that TuMV 6K2 vesicles represent the sites of viral genome replication. Thus, the 6K2-mCherry induced vesicles can serve as a marker for TuMV replication complexes.

In the presence of TuMV infection, PRH75 indeed interacted with TuMV viral replicase proteins N1b, N1a-Pro, VPG and CI. Moreover, those positive interactions were colocalized with 6K2- induced vesicles (Figure 31). The colocalization of PRH75 with viral replicase proteins and 6K2-induced replication vesicles in TuMV-infected cells strongly indicated that PRH75 was translocated from the nucleus to the cytoplasm through the interactions with viral replicase proteins and PRH75 was required for successful TuMV replication.

3.5.7 PRH75 is associated with TuMV replication vesicles that are bound to chloroplasts and contain dsRNA

Previous studies have shown that 6K2-induced mobile vesicles are derived from the ER and traffic from the ER to the periphery of chloroplasts for viral replication (Wei and Wang, 2008; Wei et al., 2010). To determine if PRH75 is also transported to the chloroplast-associated 6K2 vesicles during TuMV infection, colocalization studies of PRH75-CFP and a TuMV infectious clone with a YFP fused to the viral protein marker 6K2 of the replication complex (TuMV::6K2-YFP), were performed. The infectious clone of TuMV was engineered to carry an in-frame translational fusion of 6K2-YFP between P1 and HC-Pro (Huang et al., 2010).
D.

![Image showing Figure 31](image)

**Figure 31**  The BiFC assay of interactions between PRH75 and TuMV viral proteins during TuMV infection.

Co-agroinfiltration with constructs to co-express (A) NIb and PRH75 fused with the N- and C- terminal moiety of YFP (YN and YC), respectively, into *N. benthamiana* leaves infected by TuMV::6K2-mCherry. (B) NIa-Pro-YN and PRH75-YC, (C) VPg-YN and PRH75-YC, and (D) CI-YN and PRH75-YC. DIC, differential interference contrast. Bars in (A), 30 µm; in (B-I), 30 µm, in (B-II), 20 µm; in (C-I), 30 µm, in (C-II), 20 µm and in (D), 20 µm.
N. benthamiana leaves were co-agroinfiltrated with PRH75-CFP and TuMV::6K2-YFP, and the localization of PRH75 as well as the movement of the viral vesicles were monitored by a confocal microscopy 3 days and 4 days post agroinfiltration. Indeed, the 6K2-YFP induced yellow fluorescent vesicles were observed on the outer membrane of chloroplast and closely aligned with the chloroplast in TuMV-infected N. benthamiana leaf epidermal cells. Cyan fluorescence from PRH75-CFP overlapped with the 6K2-induced vesicles at 3 days and 4 days post agroinfiltration (Figure 32). The presence of PRH75 associated with TuMV replication vesicles strongly supported the idea that PRH75 was recruited to the viral replication complexes via its binding to viral proteins and was essential for TuMV infection.

Virus replication takes places in the virus-induced vesicles that shelter viral RNA from degradation. Before replication, the viral replication complexes (VRCs) are assembled, in a process associated with intracellular membranes. The VRC contains the proteins synthesized from the viral RNA as well as host proteins to facilitate viral replication and translation (Sanfaçon, 2005). Template viral RNAs, as well as double-stranded RNA regions formed when the complementary negative-sense RNA is synthesized, are also enclosed within the vesicles. During viral replication, RNA helicases are recruited to the vesicles and considered to catalyze the separation of dsRNA. As discussed before, PRH75 colocalized and interacted with NiIb, the RNA-dependent RNA polymerase of TuMV, raising the possibility that PRH75 is recruited to the VRCs and plays a role of unwinding the viral dsRNA during replication.

To confirm that the colocalization of PRH75 matched with viral RNA replication sites, a novel strategy for localizing plant viral RNAs and VRCs in planta using an RNA-binding protein, coupled to the BiFC vectors, referred to a dsRNA-binding dependent fluorescence complementation (dRBFC) assay, has been developed (Tilsner et al., 2009) (Cheng, unpublished data). To validate the sensitivity of dsRNA detection, PRH75-CFP was co-expressed along with the dRBFC assay. The yellow fluorescence signal of the dRBFC was visualized as small, discrete aggregates distributed throughout the cytoplasm, as well as concentrated in the nucleus. The cyan fluorescence of PRH75 overlapped with the dRBFC-labelled dsRNA in the nucleus (Figure 33). In comparison with the
Figure 32  PRH75-CFP colocalized with the chloroplast-bound 6K-YFP vesicles.

*N. benthamiana* leaves were co-agroinfiltrated with constructs expressing PRH75-CFP and TuMV::6K2-YFP. (A) Images were taken 3 days post infiltration using a confocal microscopy. (B) Images were recorded 4 days post infiltration. DIC, differential interference contrast. Bars in (A), 10 µm, and in (B), 5 µm.
Figure 33  PRH75-CFP colocalized with dsRNA-containing foci.

*N. benthamiana* leaves were co-agroinfiltrated with constructs to co-express PRH75-CFP and the dRBFC assay. Observation was recorded 48 h post agroinfiltration using a confocal microscopy. DIC, differential interference contrast. Bars in (A), 30 µm, and in (B), 20 µm.
localization pattern in the absence of viral infection, coexpression of PRH75 and the dRBFC assay into *N. benthamiana* leaves infected with the TuMV infectious clone (TuMV::6K2-mCherry), resulted in observing dRBFC yellow fluorescence signals in a granular aggregation or discrete structures in the cytoplasm, resembling the described VRC during TuMV infection (Grangeon *et al.*, 2012). Since the dRBFC assay can bind both plant and viral dsRNA, dRBFC signal was also detected in the nucleus. PRH75-CFP was found to form punctate structures and colocalize with viral dsRNA in the labelled VRC (Figure 34). Collectively, these results indicated that PRH75 was recruited to VRC, namely viral dsRNA containing foci, during viral replication. In addition to unwinding the viral dsRNA intermediate, PRH75 may remain and serve other functions in the nucleus.
Figure 34 PRH75-CFP colocalized with dsRNA-containing foci in the presence of TuMV infection.

Co-agroinfiltration with constructs to co-express PRH75-CFP and the dRBFC assay into *N. benthamiana* leaves infected with TuMV::6K2-mCherry. Images were taken 48 h post agroinfiltration using a confocal microscopy. DIC, differential interference contrast. Bars in (A), 30 µm, and in (B), 10 µm.
Chapter 4: Discussion

4.1 Identification of *Arabidopsis* DEAD-box RNA helicases as host factors required for TuMV infection

In this study, a functional genomics-based screening was performed to identify *Arabidopsis* DEAD-box RNA helicases (*AtRH* or *RH*) that are required for TuMV infection. From 42 selected putative *AtRH* genes in the *Arabidopsis* genome, homozygous T-DNA insertion lines for 26 *AtRH* genes were available. In an initial screening based on symptom severity after TuMV infection, three *Arabidopsis* T-DNA insertion lines, corresponding to the genes *AtRH9*, *AtRH26* and *PRH75*, were identified as showing less susceptibility to TuMV infection than wild-type controls. Although there was some variability in symptom development among individual plants within the same genotype, *atrh9*, *atrh26* and *prh75* T-DNA mutants showed suppressed TuMV infection in comparison with wild-type plants (Figure 4). Since the preliminary BiFC experiments did not find positive interactions between *AtRH26* and TuMV viral proteins (data not shown), I selected *AtRH9* and *PRH75* for further analysis.

ELISA assays of TuMV coat protein (CP) accumulation showed remarkably reduced amounts of CP in both *atrh9* and *prh75* T-DNA mutants (Figure 4). Consistently, quantitative RT-PCR analysis of viral RNA accumulation in newly-emerged leaves of TuMV-challenged *atrh9* and *prh75* T-DNA mutants suggested that viral replication was drastically inhibited compared with that in TuMV-infected WT plants (Figures 6, 13). This conclusion was further supported by the weak green fluorescence observed from the newly-emerged leaves of *atrh9* and *prh75* T-DNA insertion mutants infected by a GFP-tagged TuMV infectious clone, indicative of a delayed viral spread relative to WT controls (Figures 6, 13). Thus, these results strongly suggest that *AtRH9* and *PRH75* are required for TuMV infection.

Both *AtRH9* and *PRH75* belong to the family of DEAD-box RNA helicase proteins that have both RNA-binding and helicase activities. As briefly discussed in Chapter 1, several *AtRHs*, for example, *AtRH8* (Huang *et al.*, 2010), *AtRH20* (Kovalev *et al.*, 2012) *AtRH2* and *AtRH5* (Kovalev and Nagy, 2014) have been found to play functional roles in viral...
infection. Here, our study has shown that AtRH9 and PRH75 are two potential host factors in the DEAD-box RNA helicase family associated with TuMV infection. The involvement of AtRH9 and PRH75 in TuMV infection and the mechanism underlying the association between DEAD-box RNA helicase and potyvirus infection, therefore became the main objective of the remainder of this thesis.

4.2 AtRH9 and its recruitment for TuMV infection

AtRH9 is a mitochondrial protein and may be involved in RNA metabolism in mitochondria as an RNA chaperon (Köhler et al., 2010). The subcellular localization of AtRH9 was visualized as punctate particles in the cytoplasm (Figure 8), consistent with the reported mitochondrial distribution (Matthes et al., 2007). It is worth noting that AtRH9 mRNA level is enhanced in response to biotic stress caused by different pathogens (Matthes et al., 2007). Likewise, AtRH9 is involved in plant-pathogen interactions but its functional role therein is currently unknown.

To explore the functional role of AtRH9 in TuMV infection, the BiFC assay was conducted to test protein-protein interactions between AtRH9 and TuMV viral proteins. This analysis revealed that AtRH9 interacts with NIa-Pro (Figure 9), a virus-encoded protease. TuMV NIa-Pro is present in the VRC and is also responsible for catalyzing the cleavage of P3/6K1, 6K1/CI, CI/6K2, 6K2/NIa, NIa/NIb, NIb/CP and the cleavage site between VPg and NIa-Pro domains in NIa protein (Li et al., 1997). However, no interaction between AtRH9 and NIa-Pro was detected by the Y2H assay (data not shown). It is possible that the interaction between AtRH9 and NIa-Pro found in the BiFC assay was either transient or mediated by one more host protein that binds to both AtRH9 and NIa-Pro and thus serves as a bridging interactor. Further study is needed to confirm the AtRH9 and NIa-Pro interaction and to elucidate the functional role played by AtRH9 in TuMV infection.

While our results demonstrate that AtRH9 is associated with TuMV infection through interaction with NIa-Pro, the biological mechanism is unclear at present. It is possible that AtRH9 may participate in the separation of RNA duplexes during viral genome
replication. Alternatively, AtRH9 is also likely to facilitate the proteolytic cleavage of TuMV polyprotein via interacting with Nia-Pro.

### 4.3 PRH75 and its roles in TuMV infection

#### 4.3.1 PRH75 is a nuclear-localized ATP-dependent DEAD-box RNA helicase

In this study, we have shown that PRH75 is a nuclear-localized DEAD-box RNA helicase in *Arabidopsis* and that it is associated with TuMV infection (Figures 17, 18). This conclusion is based on an intensive screening of *Arabidopsis atrh* T-DNA insertion lines for their susceptibility to TuMV infection. Consistent with the previous findings, the sequence analysis clearly demonstrates that PRH75 contains the conserved DEAD domain and RNA-binding domain characterized as RGG repeats at the carboxyl-terminal extension, which is also found in nucleolar fibrillarin and nucleolin (Figure 16). In addition, all the conserved domains for ATP-dependent RNA helicase activity are present in PRH75 (Figure 15). Recently, ATP-dependent RNA unwinding activity of PRH75 has been reported (Nayak et al., 2013). *Arabidopsis* PRH75 encodes an essential enzyme which is required for embryo development, thus PRH75 is referred to as an *embryo defective* gene (Nayak et al., 2013). Given the lethality of prh75 T-DNA knockout mutant, it is suggested there is no functional redundancy between PRH75 and other DEAD-box RNA helicase.

#### 4.3.2 PRH75 interacts with multiple viral proteins that are essential for TuMV replication

In this study, BiFC assays revealed a positive interaction between PRH75 and several viral proteins, including Nia-Pro, VPg, CI and Nlb, respectively (Figure 19). The intimate association between PRH75 and these viral proteins was confirmed by FRET analysis (Figure 21). However, Y2H assays only detected the positive interactions of PRH75 with Nlb, VPg, and CI, respectively, but not with Nia-Pro (Figure 20). The absence of the expected protein-protein interaction between PRH75 and Nia-Pro is probably due to weak or transient interaction intensity or lack of protein partners required for the interaction. Nonetheless, PRH75 interacts with TuMV Nia-Pro, VPg, CI and Nlb,
which represent four primary components involved in the viral replication complex (VRC) (Wei et al., 2010).

Potyviral NIa contains two nuclear localization signals (NLS) and localizes in the nucleus where NIa may induce nuclear inclusions. Mutation of NIa NLS results in a significant decrease of viral genome amplification, which indicates that nuclear localization and transport of NIa plays an essential role for viral infection (Restrepo et al., 1990; Schaad et al., 1996; Rajamäki and Valkonen, 2009). NIa contains an N-terminal VPg domain and a C-terminal NIa-Pro protease domain. NIa is processed into two functional proteins VPg and NIa-Pro, during proteolytic cleavage by the C-terminal NIa-Pro protease (Carrington and Dougherty, 1987). The nuclear localization of PRH75 supports the hypothesis that its interaction with NIa-Pro and/or VPg in the nucleus is critical for viral infection. Furthermore, two identified TuMV host factors, namely Arabidopsis PABP and eIF(iso)4E, have been found to interact and associate with TuMV VPg-Pro (NIa) in the nucleus during TuMV infection (Beauchemin et al., 2007; Beauchemin and Laliberté, 2007), providing precedent for this type of interaction. Consistently, NIa has recently been observed to interact with nucleolar fibrillain and this interaction may play a role in suppression of virus-induced gene silencing during PVA infection (Rajamäki and Valkonen, 2009).

Potyviral VPg is a multifunctional protein implicated in viral RNA replication and translation, cell-to-cell and long-distance movement, and virulence determination (Schaad et al., 1996; Schaad et al., 1997; Keller et al., 1998; Lellis et al., 2002). Potyviral VPg can be uridylylated by NIb, the RNA-dependent RNA polymerase and serve as a primer for viral RNA synthesis during replication (Puustinen and Mäkinen, 2004). Given its intrinsic structure flexibility (Grzela et al., 2008; Hébrard et al., 2009), VPg could function as a hub protein to interact with diverse viral and host proteins to regulate different functions during viral infection (Jiang and Laliberté, 2011; Rantalainen et al., 2011). The presence of VPg at the 5' end of the TuMV genome and its ability to interact with host factors eIF4E or eIF(iso)4E, which belong to the host translation machinery, strongly demonstrates that VPg is essential for viral RNA translation (Wittmann et al., 1997; Schaad et al., 2000; Lellis et al., 2002; Roudet-Tavert et al., 2007). In addition,
host proteins such as PVIP (Dunoyer et al., 2004), PABP (Dufresne et al., 2008), eEF1A (Thivierge et al., 2008) and AtRH8 (Huang et al., 2010) have also been reported to interact with VPg. The self-interaction of VPg (Guo et al., 2001) and interactions between P1 (Merits et al., 1999), HC-Pro (Roudet-Tavert et al., 2007), P3 (Merits et al., 1999), CI (Tavert-Roudet et al., 2012), Nlb (Li et al., 1997) and CP (Zilian and Maiss, 2011) have been discovered in potyviruses as well. It is worth noting that the interactome between VPg and potyviral proteins reveals the importance of co-ordinated functions with other potyviral proteins during viral infection. The ability of PRH75 to bind to VPg suggests the possibility that PRH75 may play a role in viral genome translation via interaction with VPg. Since VPg has been shown to promote viral translation by increasing the stability of viral RNA (Eskelin et al., 2011), PRH75 may be required for stabilization of viral RNA to secure efficient translation as an RNA chaperone.

Potyviral CI possesses ATPase and RNA helicase activities, which are involved in the unfolding of RNA secondary structures during viral genome replication. Mutation of conserved helicase domain residues of CI causes a significant reduction of viral RNA replication (Carrington et al., 1998). Together with VPg and Nlb, CI and host translation factors eIF(iso)4E were observed to associate with the VRC in TuMV-infected leaves (Cotton et al., 2009; Tavert-Roudet et al., 2012). It was also found that CI colocalized with dsRNA punctates in the VRC (Cotton et al., 2009) and assisted cell-to-cell transport of virions through the PD by interacting with P3N-PIPO (Wei et al., 2010). These findings have revealed a pivotal role for CI in viral genome replication, translation and intercellular movement. That is, CI not only acts as an RNA helicase to catalyse the separation of RNA duplexes but also coordinates viral RNA replication and translation by association with both viral RNA polymerase (Nlb) and eIF(iso)4E as well as to facilitate viral movement by association with P3N-PIPO. The interaction between PRH75 and CI reinforces the idea of the involvement of PRH75 in the VRC and suggested that PRH75 associated with CI and Nlb to form the protein complex which was responsible for viral genome replication. Moreover, the association of PRH75 with TuMV CI may raise the possibility that both viral helicase and cellular helicase are required for viral replication and suggest that PRH75 may work synergistically with viral helicase CI.
TuMV N\text{Ib} is a viral RNA-dependent RNA polymerase which catalyzes the synthesis of new viral genomic RNA. The N\text{Ib} protein accumulates predominantly in the nucleus as nuclear inclusions and is also recruited into the cytoplasmic membrane-bound vesicles that house the VRC during viral infection (Restrepo \textit{et al.}, 1990; Dufresne \textit{et al.}, 2008; Thivierge \textit{et al.}, 2008). Recently, N\text{Ib} has been identified to be the interacting partner of SCE1, a SUMO-conjugating enzyme by the Wang laboratory (Xiong and Wang, 2013). As a result, N\text{Ib} is SUMOylated. Silencing \textit{SCE1} could confer resistance to potyvirus infection. Thus, SUMOylation plays a crucial role in the potyvirus replication process, which may directly regulate the function of N\text{Ib} (Xiong and Wang, 2013). More recent data suggest that N\text{Ib} is predominantly SUMOylated with small ubiquitin-like modifier 3 (SUMO3), and mimicking SUMOylation of N\text{Ib} changes its partition between the nucleus and cytoplasm (Xiong \textit{et al.}, unpublished data). Intriguingly, using SCE1 as bait, the Y2H screening identified PRH75 as one of SUMO substrates in \textit{Arabidopsis} and the SUMOylation assay showed that PRH75 is SUMOylated by SUMO3 (Elrouby and Coupland, 2010). Given that N\text{Ib} and PRH75 interact with each other and both are SUMOylated, it is tempting to speculate that PRH75 is involved in N\text{Ib} SUMOylation to regulate TuMV infection. Alternatively, as SUMOylation of N\text{Ib} facilitates its cytoplasm localization and recruitment to the VRC through interacting with 6K2-VPg-Pro, it is also possible that the SUMOylated form of PRH75 allows its redistribution from the nucleus to the cytoplasm and the cytoplasmic PRH75-N\text{Ib} complex can be brought to the VRC by PRH75 or N\text{Ib} through interacting with viral replicase components essential for TuMV replication.

4.3.3 Localization of PRH75 and its recruitment to viral replication complex (VRC)

To establish the subcellular localization of the various protein complexes of PRH75 with different viral proteins during TuMV infection, the BiFC assay was conducted with co-expression of N\text{Ib}-YN, N\text{Ia}-Pro-YN, VPg-YN or CI-YN with PRH75-\text{YC}, respectively, in TuMV-infected leaves. The distribution of BiFC interacting signals between PRH75 with N\text{Ib}, N\text{Ia}-Pro, VPg or CI was observed in the nucleus as well as along with 6K2-induced vesicles in the presence of TuMV infection (Figure 31). This is in contrast with the observation that PRH75 mainly interacted with viral proteins in the nucleus in the
absence of TuMV infection (Figure 19). These results have demonstrated that the interactions of PRH75 with TuMV viral replicase proteins occur in the nucleus and in the cytoplasmic 6K2-induced vesicles during viral infection. This is consistent with the previously published data that, during viral genome replication, TuMV replicase proteins such as NIb and VPg-Pro (NIa) are localized in the cytoplasm and, to a greater extent, in the nucleus of infected cells (Restrepo et al., 1990; Li et al., 1997). Although the primary localization of PRH75 is in the nucleus, PRH75 is likely undergoing intracellular translocation from the nucleus to cytoplasm as a result of interacting with multiple viral proteins essential for viral replication in the VRC or is intercepted to join the VRC before it is targeted to the nucleus. The association of PRH75 with the viral replicase components in the nucleus and cytoplasm was further confirmed by the colocalization studies of PRH75 and TuMV NIb, NIa-Pro, VPg and CI (Figures 30).

The cytoplasmic 6K2-induced vesicles have been reported to be membrane-associated vesicular structures that contain the viral RNA and the viral and host proteins required for viral replication (Grangeon et al., 2010). The host translation machinery components such as eIF(iso)4E, PABP and eEF1A have also been shown to be present in the 6K2-induced vesicles, suggesting 6K2-induced vesicles may represent the site for viral protein synthesis as well as viral genome replication (Beauchemin et al., 2007; Beauchemin and Laliberté, 2007; Thivierge et al., 2008). Observations using confocal microscopy have identified the overlap localization pattern between PRH75 and 6K2-induced membranous vesicles along the outer chloroplast envelope (Figure 32). Furthermore, TuMV VPg-Pro (NIa), NIb and CI have been reported to be associated with viral dsRNA within the VRC (Cotton et al., 2009). Consistently, PRH75 colocalizes with dsRNA foci during viral infection which indicates the presence of PRH75 in the VRC and may play a functional during viral replication (Figure 34).

In this study, I was able to demonstrate that PRH75 colocalized with 6K2-induced vesicles and viral dsRNA (Figures 32, 34). Moreover, the intimate association with four primary components of viral replication complexes indicates that PRH75 may serve as an important host component of the VRC. Collectively, these data support a possible functional role of PRH75 in TuMV genome translation and/or replication. It is certainly
noteworthy that recruitment of PRH75 to the VRC is favourable for TuMV infection. Given the biological function of PRH75 as an efficient RNA helicase that can unwind the RNA duplexes, the emerging picture of PRH75 associated with TuMV infection is that PRH75 may alternate or remodel the secondary structure of the viral genomic RNA during viral translation or separate the viral dsRNA intermediates during the process of viral RNA replication.

4.3.4 *Arabidopsis* PRH75 is highly dynamic

It is well known that nuclear and nucleolar proteins are highly dynamic. Nucleolar proteins are in a constant flux, moving in and out of the nucleolus. As a result many of them may exhibit altered distribution patterns during interactions with different proteins or complexes, especially in response to stresses (Mayer and Grummt, 2005).

*Arabidopsis* PRH75 is predominantly localized in the nucleus, preferentially targeting to the nucleolus under normal conditions (Figure 17). In the presence of TuMV infection, PRH75 was found to be recruited to the cytoplasmic VRC (Figure 31, 32). Therefore, we speculate that the subsequent recruitment of PRH75 to the VRC may indicate a constant association with viral replicase components for TuMV genome replication under viral infection. Similarly, another DEAD-box protein, AtRH2, which is the *Arabidopsis* ortholog of the mammalian DEAD-box helicase eIF4A-III, is relocalized from the nucleoplasm to the nucleolus and splicing speckles under hypoxic stress (Koroleva *et al.*, 2009). In a recent study, it was reported that, as a component of the cytoplasmic tombusvirus VRC, AtRH2 destabilizes viral dsRNA replication intermediates and promotes bringing the 5' and 3' terminal negative-sense RNA sequences in close vicinity via long-range RNA-RNA base pairing. The newly formed RNA structure promoted by AtRH2 together with AtRH20 might facilitate the recycling of the viral replicase components for multiple rounds of positive-sense viral RNA synthesis (Kovalev and Nagy, 2014). It is not clear if PRH75 plays a similar role in TuMV infection or if there are any overlapping functions between PRH75 and AtRH2.
4.4 Nucleus, nucleolus and virus life cycle

4.4.1 The nucleolus functions as a stress sensor in response to viral infection

The notion that the nucleolus could function as a stress sensor is well documented (Boulon et al., 2010). The nucleolus is the ribosome factory where most events of ribosome biogenesis, such as ribosomal RNA synthesis, processing, and ribosome subunit assembly, take place. Apart from ribosome subunit biogenesis, the nucleolus appears to be involved in other cellular functions such as stress signalling, viral infection response and DNA repair (Mayer and Grummt, 2005).

After exposure to environmental or cellular stress, the nucleolus plays a critical role in monitoring and sensing the cellular stress signals (Olson, 2004). The nucleolar stress response includes profound alteration in the composition or organization of the nucleolus. For example, nucleolar proteins could translocate to the nucleoplasm under stress conditions. It is anticipated that the dynamic sequestration of nucleolar proteins between different sub-nuclear compartments is crucial for nucleolar stress response (Koroleva et al., 2009).

Although the relation between nucleus, nucleolus and virus infection has been a research interest in the last decade, it is still far beyond our understanding of a clear picture. However, it is well established that, during viral infection, various viral components could traffic in and out of the nucleolus or the nucleus, and some nucleolar proteins are translocated out the nucleolus or non-nucleolar proteins enter the nucleolus to fulfill their functions (Salvetti and Greco, 2014).

4.4.2 Nuclear import of TuMV viral proteins is mediated by Arabidopsis importin α

Although most RNA viruses are predominantly cytoplasmic during their life cycle, there are diverse strategies utilized by RNA viruses in which they can recruit nuclear and nucleolar components, or direct host cellular functions within the nucleus, in order to facilitate their reproductive processes, such as viral genome replication, virus assembly and intracellular trafficking (Hiscox, 2003; Weidman et al., 2003). An increasing number of studies have highlighted the importance of the functions of nucleus and nucleolus, with
special regards to some RNA virus families, namely, positive-sense, single-stranded RNA viruses belonging to the Flaviviridae, Coronaviridae and Togaviridae families. For example, members of Flaviviridae include HCV, DENV, WNV (Rice, 1996). Members of Coronaviridae include SARS-CoV and Infectious bronchitis virus (IBV) (Siddell, 1995).

Indeed, many positive-sense, single-stranded RNA viruses can interact with proteins associated with host nucleus or induce the translocation of host proteins from the nucleus. The functional relevance between nucleus or nucleolus localization of viral proteins and viral genome replication remains less well understood. However, the need of efficient trafficking of viral proteins from the cytoplasm to the nucleus has been shown to be essential for viral infection (Restrepo et al., 1990).

Despite the fact that virus-encoded proteins are usually small in size and thus could passively diffuse through the nuclear pores, active transport of viral proteins into the nucleus has been well demonstrated (Kamata et al., 2005). The localization of proteins to the nucleus or nucleolus is mediated by dedicated targeting mechanisms that recognize specific protein motifs and contribute to the efficiency of nuclear or nucleolar transport of the proteins. Most proteins that are imported to the nucleus or the nucleolus contain the nuclear localization signal (NLS) or nucleolar localization signal (NoLS). Similarly, viral NLS or NoLS have been identified within potyviral NIb and NIa (Carrington et al., 1991; Li and Carrington, 1993; Schaad et al., 1996). Furthermore, many studies have suggested that viruses can recognize and utilize the host’s nuclear import machinery to gain access to the nucleus (Krichevsky et al., 2006).

Plant nuclear import and export machinery is composed of a network of proteins that shuttle between the nucleus and the cytoplasm, allowing substrate exchange through the nuclear pore complexes (NPC) (Doye and Hurt, 1997). Among them, importin α and importin β are two of the best characterized nuclear import receptors that can bind to the substrates and translocate them into the nucleus (Goldfarb et al., 2004). In the cytoplasm, importin α could bind to proteins containing NLS or NoLS via its NLS- or NoLS-binding region. The importin α complex is then targeted and transported into the nucleus through
the nuclear pore complexes. In *Arabidopsis*, importin α is capable of mediating the nuclear import of proteins without the requirement for importin β (Krichevsky *et al*., 2006).

Our data demonstrate that two *Arabidopsis* importin α isoforms, IMPA1 and IMPA2 directly interact with TuMV NIb, NIa-Pro, VPg and CI *in vivo* and *in vitro* (Figures 24-27). Interestingly, our study also shows that PRH75 interacts with both IMPA1 and IMPA2 in the nucleus which is consistent with the colocalization result between PRH75 with IMPA1 and IMPA2 (Figures 22, 23, 28). The reason for the association between importin α, TuMV viral proteins and PRH75 is not clear. It is possible that the function of importin α is to serve as an adaptor that links TuMV viral proteins to PRH75 to form the ternary complex at the periphery of the NPC. Attempts to knockdown both *IMPA1* and *IMPA2* using VIGS were not successful (data not shown). *Arabidopsis* has nine importin α isoforms and functional redundancy is very likely (Bhattacharjee *et al*., 2008). Our study is the first to investigate and provide evidence for the functional roles of *Arabidopsis* importin α in nuclear import of TuMV viral proteins via the interaction with viral proteins.

Our finding that *Arabidopsis* IMPA1 and IMPA2 directly interact with TuMV NIb, NIa-Pro, VPg and CI is consistent with those studies reported previously. RNA silencing suppressor protein 2b of CMV is imported into the nucleus via the interaction with *Arabidopsis* importin α to counteract the RNA silencing defence in the host nucleus (Wang *et al*., 2004). HIV-encoded Rev protein, which is an essential regulator of viral gene expression, is responsible for promoting the nuclear export of unspliced and partially spliced mRNA (Dvorin and Malim, 2003). It is also a nuclear factor that could be imported into the nucleus by direct binding to human importin β (Henderson and Percipalle, 1997). Moreover, recent studies have shown that the nuclear import of HIV-1 integrase is mediated by importin α. HIV-1 replication is significantly impaired in *importin a* knockdown HeLa cells (Nitahara-Kasahara *et al*., 2007; Ao *et al*., 2010; Levin *et al*., 2010).
 Altogether, this work suggests that the association with *Arabidopsis* importin α is likely involved in the trafficking of TuMV viral proteins from the cytoplasm to the nucleus. This observation may broaden our understanding of nuclear import strategy employed by potyviruses as well as open a new investigation area for engineering antiviral strategies. However, more research attention should be paid to elucidate the mechanism underlying the nuclear import machinery during potyvirus life cycle.

### 4.5 Major findings and future directions

Although considerable effort has been made in discovering the host proteins involved in potyvirus infection, the vast majority of components are still unknown. In this study, we screened *Arabidopsis* T-DNA insertion mutants of *AtRHs* against TuMV infection and identified three mutants, *atrh9*, *atrh26* and *prh75* exhibiting reduced symptoms after TuMV infection. Among them, we found that TuMV Nlβ, Nlα-Pro, VPg and CI interact with PRH75, a nuclear-localized DEAD-box RNA helicase, in the nucleus. In TuMV-infected cells, PRH75 also associates with Nlβ, Nlα-Pro, VPg and CI that are primary components of the VRC in the cytoplasm. Moreover, PRH75 colocalized with viral dsRNA in the VRC in the presence of viral infection. Furthermore, we presented evidence that viral accumulation and replication are inhibited if *PRH75* is knocked down and concluded that PRH75 is required for TuMV infection. These findings highlight the important role of DEAD-box RNA helicases in potyvirus life cycle and will certainly shed light into the intricate relation between viruses and their hosts. Future studies should focus on unveiling the underlying molecular mechanism of the functional role DEAD-box RNA helicases play during potyvirus infection.

The involvement of nuclear RNA helicases in the viral infection process has been proposed in several independent studies. For example, RNA helicase DDX56 in the nucleolus can bind to WNV capsid protein and be recruited to the cytoplasm for viral genome replication during WNV infection (Xu *et al.*, 2011; Xu and Hobman, 2012). Nucleolin has been reported to colocalize with the NS5B protein of HCV outside the nucleolus, in the perinuclear region during HCV infection (Shimakami *et al.*, 2006; Kusakawa *et al.*, 2007).
Based on the data presented in this study, we propose a model in which PRH75 has versatile functions in TuMV infection (Figure 35). *Arabidopsis* DEAD-box RNA helicase PRH75 interacts with TuMV NiB, VPg, Nia-Pro and CI in the nucleus. The nuclear transport of viral proteins is mediated by *Arabidopsis* importin α. During TuMV infection, PRH75 is recruited to 6K2-induced viral replication complex via interacting with the important viral components NiB, VPg, Nia-Pro and CI and may assist in unwinding of viral RNA duplexes during the replication process. Downregulation of PRH75 in *Arabidopsis* impedes the viral infection. Thus, PRH75 serves as an important host factor required for TuMV infection. However, the precise function of PRH75 in potyvirus infection remains to be further explored in the future.

![Figure 35](image.png)

**Figure 35** Working model for *Arabidopsis* PRH75 associated with TuMV infection.
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## Appendices

### Appendix I: List of DEAD-box RNA helicases in *Arabidopsis*.

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Appendix II: Negative controls of the BiFC assays.

Bars, 50 µm.
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Bars, 50 µm.
CURRICULUM VITAE

Yinzi Li

Education

The University of Western Ontario
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Li, Yinzi, Zhang, Changwei, Bernards, Mark, Wang, Aiming (2010) Screening for DEAD-box RNA helicases in Arabidopsis that are required for Turnip mosaic virus (TuMV) infection. Joint Annual Meetings of the American Society of Plant Biologists and the Canadian Society of Plant Physiologists, Montréal, Canada.


Oral presentation