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Effect on Pellicle Proteome upon Adsorption of Salivary Peptide on Hydroxyapatite and their effects on Enamel Demineralization

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Abstract

According to WHO, oral health is an important indicator of overall health. Poor oral health cause serious health problems (cardiovascular, stroke, diabetes, liver, and respiratory related), in different age groups, costing billions of dollars. So, proper oral health care management has assumed top priority. Salivary antimicrobial peptides (histatin and statherin), are part of enamel pellicle, required for the oral homeostasis. Current work focused to study the demineralization protection and pellicle proteome modulation capabilities of novel peptide constructs (single and tandem duplicate histatin constructs DR9, DR9-DR9 and histatin-statherin hybrid construct DR9-RR14). For the first time, we provided evidence that, these peptide constructs (low concentration) modulated the pellicle proteome composition as analyzed through nLC-MS. We showed that DR9, and DR9-DR9 provided enamel demineralization (Ca2+ and PO43−) protection in presence of parotid saliva pellicle. It is important work from the point-of-view of enamel protection and inhibition of pathological biofilm formation by novel salivary peptides and hence infection in the oral cavity.

Keywords

Co-Authorship Statement

All chapters were written by Rajesh Gupta and edited by Prof. Walter L. Siqueira, DDS, PhD. Prof. Siqueira provided guidance throughout the whole study, including concept of the idea, experimental design, data interpretation, statistical analyses and technical advice for all parts of the study. Yizhi Xiao, MSc, PhD, provided technical support for all the experimental parts and offered generous knowledge and consult throughout the study.

All experiments were performed by Rajesh Gupta except the followings: Paula Karina Jorge (DDS, M.Sc.) and Vinicious Augustus (DDS) prepared the enamel discs for the demineralization experiments. Eduardo Moffa (DDS, M.Sc.) and David Zuanazzi (DDS, M.Sc.) helped with the collection of parotid saliva.
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(Rajesh Gupta)
# Table of Contents

Abstract........................................................................................................................................... i
Co-Authorship Statement ................................................................................................................. ii
Acknowledgments ............................................................................................................................ iii
Table of Contents............................................................................................................................... iv
List of Tables ...................................................................................................................................... vii
List of Figures ..................................................................................................................................... ix
List of Appendices ............................................................................................................................ x
Chapter 1 .......................................................................................................................................... 1
1 Introduction ..................................................................................................................................... 1
References ......................................................................................................................................... 7
Chapter 2 .......................................................................................................................................... 14
2 Role of saliva and AEP in oral and overall health ........................................................................ 14
   2.1 Oral cavity ................................................................................................................................. 14
   2.2 Saliva ........................................................................................................................................ 15
   2.3 Salivary glands ......................................................................................................................... 16
   2.4 Salivary composition ............................................................................................................... 16
   2.5 Acquired enamel pellicle ......................................................................................................... 16
   2.6 AEP composition .................................................................................................................... 18
   2.7 AEP salivary proteins ............................................................................................................. 18
      2.7.1 AEP formation .................................................................................................................. 20
   2.8 AEP functions ......................................................................................................................... 25
      2.8.1 Enamel demineralization protection ................................................................................ 25
      2.8.2 AEP as a platform for biofilms ...................................................................................... 27
   2.9 AEP modulation ...................................................................................................................... 28
3 AEP peptide mediated enamel demineralization protection studies .......................................................... 49

3.1 Introduction ........................................................................................................................................ 49

3.2 Materials and methods .................................................................................................................... 52

3.2.1 Characterization of peptide constructs ......................................................................................... 52

3.2.2 Calculation of pI values of peptide constructs ............................................................................ 52

3.2.3 Enamel demineralization assay ..................................................................................................... 52

3.3 Results .............................................................................................................................................. 55

3.3.1 Ca$^{2+}$ and PO$_{4}^{3-}$ demineralization protection with peptide coated ............................................ 56

3.3.2 Ca$^{2+}$ and PO$_{4}^{3-}$ demineralization protection with PS coated + peptide construct coated ........... 57

3.4 Discussion ......................................................................................................................................... 58

3.5 Conclusion ......................................................................................................................................... 62

4 Modulation of AEP by incorporation of constructed peptides ......................................................... 69

4.1 Introduction ........................................................................................................................................ 69

4.2 Material and methods ....................................................................................................................... 71

4.2.1 Cleaning and acid etching of hydroxyapatite discs ..................................................................... 71

4.2.2 Saliva and peptide coating and pellicle formation on the discs ................................................ 71

4.3 Parotid salivary pellicle harvesting and protein estimation ................................................................. 72

4.4 Mass spectrometric identification of pellicle proteins ....................................................................... 73

4.4.1 Trypsin digestion and desalting procedure of pellicle proteins .................................................. 73

4.4.2 MS Analysis ................................................................................................................................... 73

4.5 Results .............................................................................................................................................. 74

4.5.1 Proteome profile of peptide-PSPL ............................................................................................... 74
4.5.2 Most abundant proteins from peptide-PSPL ........................................ 75

4.6 Peptide-PSPL proteome profile classification ........................................ 83
   4.6.1 Protein classification based on molecular functions ......................... 83
   4.6.2 Protein classification based on cellular components ........................ 83
   4.6.3 Protein classification based on biological processes ...................... 84
   4.6.4 Protein classification based on protein classes ............................... 84

4.7 Proteome profile of PS-Peptide-PSPL .................................................... 85
   4.7.1 Most abundant proteins from PS-peptide-PSPL .............................. 87

4.8 PS-Peptide-PSPL proteome profile classification .................................. 92
   4.8.1 Protein classification based on molecular functions ....................... 93
   4.8.2 Protein classification based on cellular components ...................... 93
   4.8.3 Protein classification based on biological processes ..................... 94
   4.8.4 Protein classification based on protein classes ............................. 94

4.9 Discussion .................................................................................................. 95

4.10 Conclusion ................................................................................................ 102

References .................................................................................................... 103

Chapter 5 ...................................................................................................... 110

5 Summary and conclusion ........................................................................ 110

Appendix A .................................................................................................. 112

Curriculum Vitae .......................................................................................... 113
List of Tables

Table 3-1: Sequences and other physical characteristics of histatin 3 or statherin peptide constructs……………………………………………………………………………52

Table 3-2: Means and standard deviations of Ca and PO₄ released from human dental enamel sections, coated with either control (PS) or peptide constructs………………….52

Table 3-3: Means and standard deviations of Ca and PO₄ released from human dental enamel sections, coated with control (PS) or PS coated + peptide construct coated……………53

Table 4-1: Common proteins among all the groups of peptide coated disc pellicle……70

Table 4-2: Most abundant proteins based on relative ion abundance score from control group………………………………………………………………………………………………….71

Table 4-3: Most abundant proteins based on relative ion abundance score from DR9-PSPL group………………………………………………………………………………………………72

Table 4-4: Most abundant proteins based on relative ion abundance score from DR9-DR9-PSPL group………………………………………………………………………………………………72

Table 4-5: Most abundant proteins based on relative ion abundance score from DR9-RR14-PSPL group………………………………………………………………………………………………73

Table 4-6: Values of relative ion abundance score obtained in all groups………………73

Table 4-7: Proteome profile of control (PSPL) group……………………………………75

Table 4-8: Proteome profile of DR9-DR9-PSPL group……………………………………76

Table 4-9: Proteome profile of DR9-PSPL group……………………………………………77

Table 4-10 a: Proteome profile of DR9-RR14-PSPL group…………………………………77

Table 4-10 b: Proteome profile of DR9-RR14-PSPL group…………………………………78

Table 4-11: Common proteins among all the groups of parotid saliva coated disc pellicle…82

Table 4-12: Most abundant proteins from control group……………………………………83
Table 4-13: Most abundant proteins from PS-DR9-PSPL group

Table 4-14: Most abundant proteins from PS-DR9-DR9-PSPL group

Table 4-15: Most abundant proteins from PS-DR9-RR14-PSPL group

Table 4-16: Values of ion abundance score obtained in all groups

Table 4-17: Proteome profile of control group

Table 4-18: Proteome profile of PS-DR9-PSPL group

Table 4-19: Proteome profile of PS-DR9-DR9-PSPL group

Table 4-20: Proteome profile of PS-DR9-RR14-PSPL group
List of Figures

Figure 4-1: Comparison of peptide modulated AEP proteome profile on peptide coated discs.................................................................71

Figure 4-2: Protein classification based on molecular functions..............................................79

Figure 4-3: Protein classification based on cellular components.................................80

Figure 4-4: Protein classification based on biological processes.....................................80

Figure 4-5: Protein classification based on protein classes.......................................81

Figure 4-6: Comparison of peptide modulated AEP proteome profile on parotid saliva coated discs..........................................................................................................................83

Figure 4-7: Protein classification based on molecular functions....................................89

Figure 4-8: Protein classification based on cellular components.................................89

Figure 4-9: Protein classification based on biological processes.................................90

Figure 4-10: Protein classification based on protein classes.......................................91
List of Appendices

Appendix A: .................................................................................................................. 119
Chapter 1

1 Introduction

According to World Health Organization (WHO), today oral health has become an important indicator of overall health, well-being & quality life (Sheiham 2005). It is one of the most important health management issue all over the world, but unfortunately highly neglected for various reasons including socio-economic & lack of awareness. Oral health in parts, is governed by the intricate and fragile balance of consortia of non-pathogenic and pathogenic microorganisms in the oral cavity. Poor oral health inevitably leads to the development of more serious, sometime deteriorating health complications oftentimes resulting in debilitating, and fatal health outcome. This includes direct/indirect involvement of poor oral health in precipitation of cardiovascular diseases, stroke, development of diabetes, liver problems, adverse respiratory complications, pregnancy complications & many more health problems with often extreme consequences (Health Canada, 2009; Scannapieco et al. 2003; Okuda et al. 2004). According to an estimate in Canada, oral health has become one of the major health concern economically, next to cardiovascular health in majority of population encompassing different age groups (Health Canada, 2009). According to the Canadian Institute for Health Information estimates, for the past more than two decades, total dental expenditure continues to rise by Billions of dollars, as more & more population is fast aging (Health Canada, 2009). Under such grim scenario, the proper oral health care management assumes nonetheless more importance & priority than ever before.

Oral cavity is one of the best example of diverse communities of different types of microorganisms living in peaceful co-existence. These consortia have different species of Gram-positive & Gram-negative bacteria, covering a whole multitude of cocci, bacilli, actinomycetes & other motile as well as non-motile forms (Kolenbrander and London 1993; Kolenbrander & Andersen 1986), different types of yeast, fungi & viruses as well. According to conservative estimates, based on in vitro cultivation, PCR amplification, 16S rRNA molecular typing (Paster et al. 2006; Nasidze et al. 2009; Heller et al. 2016) & pyro sequencing technology (Zaura et al. 2009), there are > 1000 different types of
microorganisms, that coexist both as planktonic form, in the saliva, as well as multi-layered, mixed species biofilms in highly specific collaborative partnership on dental & other mucosal surfaces in the mouth (Kolenbrander et al. 2010). These biofilms are formed by specific cell-cell interactions between genetically diverse microorganisms & their interactions with acquired enamel pellicle through the complicated processes of co-adhesion & co-aggregation (Kolenbrander et al. 2010). For example, intercellular interactions in Capnocytophaga gingivalis & Actinomyces israelii or between Prevotella loescheii & Streptococcus sanguinis, respectively (Bos et al. 1996).

Saliva is a complex aqueous mixture consisting of inorganic and organic components, that are derived from secretions of salivary glands, oral mucosa, the gingival fold, epithelial cells, blood cells, food, and microorganisms (Humphrey and Williamson 2001; Macarthur and Jacques 2003; Edgar et al. 2004; Huang 2004; Guo et al. 2006; Schipper et al. 2007; de Almeida Pdel et al. 2008; Siqueira et al 2008).

From the biochemical point of view, the salivary proteins represent a rich source biological information and at the same time offer unique opportunity to be of immense clinical relevance (Schipper et al. 2007).

Salivary proteome consists of thousands of salivary proteins (2300 plus proteins and peptides), that are secretory product of three major salivary glands (submandibular, sublingual, and parotid glands) and several minor salivary glands, including various non-salivary components (Dawes 2004; Bandhakavi et al. 2009; Helmerhorst and Oppenheim 2007; Siqueira et al. 2008). The salivary secretion to the tune of around ninety percent in the whole saliva is contributed by three pairs of major salivary glands (Pedersen et al. 2002). Remaining ten percent of the salivary fluid in the total saliva is contributed by minor salivary glands (estimated to be somewhere between 400-600) in the oral cavity. These minor glands are present in the oral mucosa coverings in the mouth cavity, including tongue (Lingual/Von Ebner glands), palate, cheeks, land lips (Schipper et al. 2007; Proctor and Carpenter 2007).

Some of the salivary protein secretory IgA (main salivary antibody) are present in the secretion from all major glands. There are other salivary proteins that are specific to a
particular gland (PRPs (proline-rich proteins)), that are secreted by parotid and minor salivary glands only (Dawes et al. 1963; Siqueira et al. 2008).

Saliva being one of the most crucial and vital fluids of the human body, performs multidimensional roles within the micro-environment of the oral cavity. These roles include, aid in the food digestion, and organoleptic detection of the taste and flavor of the food we eat. Additionally, saliva in the oral cavity, acts like a lubricant and antimicrobial agent. Saliva also provide protection against the acid induced teeth enamel demineralization. Besides this, one of the most important function of saliva is the formation, as well as continuous development and maturation of acquired enamel pellicle (AEP) on the enamel surface.

Enamel pellicle is principally composed of a thin organic, proteinaceous covering layer on the teeth enamel surface (Dawes et al. 1963). It is formed by highly selective adsorption of salivary proteins and peptides on to enamel surface (Hay 1967; Siqueira et al. 2007). Pellicle perform many diverse functions for example enamel surface lubrication (Tabak 1995; Douglas et al. 1991; Ramasubbu et al. 1993), enamel mineral homeostasis (Moreno et al. 1979; Hay et al. 1979; Bennick 1979), and microbial flora and biofilm modulation (Johansson et al. 2000; Gibbons and Hay 1989; Carlen et al. 1998; Gibbons 1996; Lindh et al. 2002).

The acidic proline-rich proteins and statherin, present in human parotid saliva, submandibular as well as sublingual saliva (Hay 1989; Bennick and Cannon 1978), are most important salivary proteins involved in the pellicle formation and its multidimensional functions (Hay 1973; Bennick 1987; Yao et al. 2001).

The processes of the formation of acquired enamel pellicle on enamel surface has been studied extensively for last 40 years to gain insight into the pellicle composition and structure. Hannig (1999), observed that with in one-minute exposure of the enamel surface, to the oral environment, a thin layer of enamel pellicle could be detected. Two hour period was found to be sufficient to complete pellicle formation as after 2 hours, no further increase in the protein/peptide could be observed. On the other hand, significant amount of microorganisms attach to the pellicle and initiate the formation of
biofilms/dental plaque. (Siqueira et al. 2012). The structure and architecture of the pellicle have been further probed with the help of exhaustive electron microscopic studies. The early pellicle precursor proteins selectively adsorb on to enamel surface via electrostatic interactions, resulting in the formation of a thin pellicle layer of 10-20 nm (Hannig and Joiner 2006). Within next 1.5 hours, late precursor proteins & their aggregates are selectively recruited and adsorbed to thin pellicle on the enamel surface. This process quickly leads to a mature pellicle of around 1000 nm thickness (Skjorland et al. 1995). Majority of these studies have helped to elucidate not only the detailed fine structure of pellicle the pellicle but also the pellicle thickness ranging from 30-100 nm. (Tinanoff et al. 1976; Hannig and Joiner 2006; Hannig 1989).

Various researchers have employed diverse experimental setup like hydroxyapatite (HA) discs and HA powder, with whole saliva to understand the enamel pellicle composition. Such experimental models led to the detection, identification of important and abundant pellicle proteins such as amylase, albumin, carbonic anhydrase VI, cystatins, histatins, lysozyme, proline-rich proteins (PRPs) & statherin (Hannig 1999; Li, et al. 2004; Jensen et al. 1992; Oppenheim et al. 1988, 2007; Oppenheim et al. 1986).

The current knowledge about the AEP ultrastructure is the result of various electron microscopic and AFM studies in the last more than 15 years, (Schüpbach et al. 2001; Hannig et al. 2005; Deimling et al. 2004; Siqueira et al. 2012), through ultra-microscopic examinations via AFM, TEM, and SEM. Even though, important insights about the pellicle structure and composition have been gained in last forty years, still a complete understanding of the 3-D architecture of AEP is eluding so far.

Within the last decade, the sensitive techniques of LC-ESI-MS/MS (Siqueira et al. 2007) and MALDI-TOF-MS (Vittorino et al. 2008) were employed to elucidate the pellicle proteome composition. These studies resulted in the identification of 130 proteins in the salivary pellicle composition (Siqueira et al. 2007). Out of these 130 identified proteins, 113 were found to be novel proteins. Histatins, statherin, cystatins, and PRPs, are the major constituent of pellicle making up the bulk of salivary proteins (Oppenheim et al. 1986, 1971; Hay 1975, 1973). In addition, these technical advances in the proteomic
instrumentation, resulted in the identification of 78 naturally occurring pellicle peptides, derived from 29 different in vivo pellicle proteins (Siqueira and Oppenheim 2009).

Multiple peptides identified in pellicle peptidome were the proteolytic products of statherin and histatins salivary proteins. The enamel pellicle acts as lubricant in the oral cavity, improving the speech and chewing efficiency (Tabak et al. 1982). Statherin, aPRP1, and mucins, are pellicle constituents, that are involved in these processes (Tabak 1995; Berg et al. 2004; Vukosavljevic et al. 2014). Due to lubrication properties, pellicle also play a role to protect enamel from mechanical damage (Joiner et al. 2008). Through various studies, it has been demonstrated that multiple pellicle components protect enamel from acid-induced demineralization (Hannig and Balz 2001; Cheaib and Lussi 2011; Siqueira et al. 2010).

Statherin is a salivary phosphoprotein that contain phosphorylated serine residues at 2nd and 3rd position. It has very important physical properties, crucial for proper saliva functioning. In the saliva, statherin is the highly enamel surface-active component with important lubrication function on the enamel surface. (Proctor et al. 2005; Douglas et al. 1991; Harvey et al. 2011). Additionally, statherin and aPRPs play a clinically crucial role in inhibition and prevention of crystal deposition on enamel surfaces (Hay et al. 1979). Statherin is the most important calcium phosphate precipitation inhibitor, that can display inhibitory effect at physiological concentrations (Tamaki et al. 2002). Moreover, recently our group has found that the N-terminal domain phosphate groups of statherin oligopeptides inhibit the growth of hydroxyapatite crystal (Xiao et al. 2015). Additionally, statherin quickly disappear from whole saliva due to proteolytic activity and its affinity for tooth surfaces.

Enamel pellicle contain histatins protein family members, which are secretory product of major and minor salivary glands. Histatins consists of higher amount of histidine residues (Oppenheim et al. 1986) and display significant antifungal activity against Candida albicans, the major pathogen of oral candidiasis. Histatin 1, 3 and 5 are the major members of the histatin family out of the 12 members histatin family, and account for 80% of this family (Oppenheim et al. 1988). Histatin 1, similar to statherin, contain
phosphoserine at N-terminal 2nd residue. In whole saliva, histatins is found at lower concentrations in comparison to glandular salivary secretions. This happens most likely because of salivary proteolytic activity from various proteolytic enzymes of host as well as microbial origin in the oral cavity (Siqueira et al. 2010). This results in the rapid breakdown of these salivary proteins, as soon as they are secreted into the oral cavity. Additionally, histatins are involved in multitude of processes, ranging from modulation of enamel mineralization, antibacterial activities, and saliva buffering (Castagnola et al. 2004; Groot et al. 2006).

In the light of this background, we hypothesized that novel constructs of the functional domain of histatin and statherin salivary peptides could provide protection against the acid induced enamel demineralization. This novel approach of synthetically constructing salivary peptides could possibly help us leverage and reap the immediate benefits, ahead of its time of millions of years of natural evolution, that it would otherwise follow naturally over a long period of time, as these salivary proteins could undergo evolutionary pathways that they will eventually take.

Therefore, the main aims of this study were to:

1) Investigate the demineralization protection capabilities of the novel constructs of histatin and statherin peptides functional domains compared to parotid saliva

2) Additionally, to investigate, if these novel constructs could modulate the acquired enamel pellicle proteome composition, which in turn could modulate the biofilm composition on the enamel pellicle surface.
References


Chapter 2

2 Role of saliva and AEP in oral and overall health

Saliva is one of the very versatile, heterogenous fluid of human body, very essential for the normal health and functioning of the oral cavity. It protects the teeth against the continuous mechanical, biochemical, and microbial assaults through a protective covering, salivary pellicle. Additionally, the pellicle helps with the remineralization of dental enamel apart from minor repairs of teeth and other tissues in the oral cavity against small injuries or wounds. Disturbances in the normal production of saliva not only affect the pellicle composition but also impact the oral and overall health of the individual (Sheiham 2005; Edgar et al., 2004; Dawes 2004).

Several studies have shown that there are many proteins, especially indicators of various serious pathological conditions as well as infections, that are present in both blood plasma and saliva (Humphrey and Williamson 2001; Macarthur and Jacques 2003; Edgar et al. 2004; Schipper et al. 2007; de Almeida Pdel et al. 2008; Siqueira et al. 2008; Boackle et al. 1999 and Kajisa et al. 1990). These disease markers offer very good opportunities for saliva as well as pellicle to be a very reliable, robust, and sensitive diagnostic tool for the early diagnosis of the diseases and infection.

2.1 Oral cavity

Oral cavity is one of the best example of multicultural communities of different types of microorganisms living in, harmonious, peaceful co-existence. These consortia have different species of Gram-positive & Gram-negative bacteria, covering a whole multitude of cocci, bacilli, actinomycetes & other motile as well as non-motile forms (Kolenbrander et al. 1993; Kolenbrander & Andersen 1986), including different types of yeast, fungi & viruses as well.

According to conservative estimates, based on in vitro cultivation, PCR amplification, 16 S rRNA molecular typing (Paster et al. 2006; Heller et al. 2016) & pyro sequencing technology (Zaura et al. 2009), there are > 1000 different types of microorganisms, that coexist both as planktonic form, in the saliva, as well as multi layered, mixed species
biofilms in highly specific collaborative partnership on dental & other mucosal surfaces in the mouth. These biofilms are formed by specific cell-cell interactions between genetically diverse microorganisms & their interactions with AEP through the complicated processes of co-adhesion & co-aggregation. (Kolenbrander et al. 2010).

In the oral cavity, Streptococci recognizes pellicle proteins. Most of these proteins like statherin, proline rich proteins (PRPs), salivary α-amylase, salivary agglutinin, and mucins, are part of host derived pellicle. Actinomyces attached itself to phosphorylated statherin and PRPs. On the other hand, Fusobacteria selectively and specifically attaches to statherin only, but not to PRPs (Kolenbrander et al. 2010).

2.2 Saliva

The saliva is a fluid of various structural and functional proteins, various minerals, inorganic ions, (calcium, phosphate, bicarbonates, and urea), immunoglobulins, hormones, cytokines, and other components whose abundance is dependent upon the gland from which it is secreted. Three pairs of major salivary glands, (parotid, sublingual and submandibular) and hundreds of minor salivary glands, distributed throughout the oral cavity, produce it (Thylstrup and Fejerskov 1994).

Whole saliva is a heterogenous mix fluid, (Huang 2004), that contain secretions from many source, primarily the extrinsic glands, epithelial cell secretions, and the gingival crevicular fluid. Blood capillaries, passing through the salivary glands, also contribute the entry of analytes from the blood circulation into saliva (Farnaud et al. 2010).

Whole saliva mainly consists of 99.5% water, and 0.2% inorganic substances (calcium, phosphate, bicarbonate, urea), and 0.3% proteins (Humphrey and Williamson 2001; Amerongen et al. 2004).

From human saliva, as of today, > 2300 salivary proteins have been identified using various analytical techniques (2-D PAGE, HPLC and MS) (Bandhakavi et al. 2009).

Unstimulated and stimulated saliva substantial differ in their composition. Under resting conditions, submandibular/sublingual glands contribute around 70% of the whole saliva,
whereas about 15-20% saliva comes from the parotid glands and minor salivary glands contribute around 5-8% saliva. Under stimulated conditions, the parotid gland can contribute up to 50% of the total saliva (Sreebny 2000).

### 2.3 Salivary glands

The salivary glands vary greatly in the type of secretion they produce, which corresponds to the proportion of serous to mucous cells within the respective glands. Parotid glands contain serous cells that produce a watery fluid, that is free of mucins. On the other hand, submandibular, labial, palatal, sublingual, and lingual glands, contains substantial number of mucous cells, that produces mucin rich saliva (Turner and Sugiya 2002).

### 2.4 Salivary composition

The saliva composition and amount is dictated by many variables like the circadian rhythm (Zheng et al. 2012), age (Denny et al. 1991), gender (Inoue et al. 2006), physiological status (Fábián et al. 2007), and flow rate (Sreebny 2000).

Low protein and ion concentration in the saliva, modifies the physiological properties of water into an aqueous solution of very different physical and physiological properties. These modulated properties of saliva help immensely due its multidimensional roles in lubrication, speech, food digestion, and most importantly in the pellicle formation, all of which collaborate to maintain oral health directly or indirectly (Carpenter 2012).

### 2.5 Acquired enamel pellicle

In the oral cavity, acquired enamel pellicle (AEP) is nonembryonic, extracellular, organic integument or bacteria free thin film of heterogenous proteins, that not only acts as a protective covering of the tooth enamel and modulator of bacterial biofilms, but also acts as a semipermeable membrane in caries development. (Dawes et al. 1963; Hannig and Joiner 2006).

AEP is a complex biological, multilayer, heterogeneous, 3-D architecture of specific salivary proteins fragments, small peptides, intact native proteins, glycoproteins, enzymes, mucin and their derivatives, lipids, carbohydrates & food components (Siqueira
Hay (1967) in a classical study demonstrated that the hydroxyapatite adsorbed proteins had same electrophoretic mobility whether harvested from freshly extracted teeth in vivo or salivary proteins harvested from hydroxyapatite and enamel powder in vitro. This was significant finding as to hypothesize that the pellicle that forms on tooth surfaces originates from salivary protein present in saliva.

Enamel pellicle functions as an interface between enamel surface & first layer of microorganism biofilm in the oral cavity, with diverse protective functions in the oral cavity. For example, the AEP helps in teeth lubrication, protecting enamel against mechanical damages during mastication and erosion (Hannig et al. 2004), and modulating the early microbial colonizer composition on AEP (Zahradnik et al. 1978; Lendenmann et al. 2000; Siqueira et al. 2007, 2010, 2012; Hanning & Joiner 2006; Vitorino et al. 2007).

Additionally, it acts like a semipermeable barrier helping to promote tooth remineralization, at the same time protecting acid induced teeth demineralization in the oral cavity (Hannig et al. 2007; Kosoric et al. 2007; Kosoric et al. 2010).

Interestingly, the AEP is double edged sword like a kind of necessary evil, since, not only it protects the enamel against various mechano-physical and chemical damages, but also acts as the basic platform for microbial attachment and subsequent build-up of microbial biofilms, which can augment the dental caries risk many fold (Hannig and Hannig 2009).

Despite so much importance and direct involvement of the AEP in oral physiology and pathological processes, still a complete understanding and elucidation of AEP structure, functions, and underlying physico-chemical mechanisms is lacking to great extent. The major hurdle to achieve this has been due to very small quantity formed pellicle, that could be harvested from tooth surfaces (Yao et al. 2001).
2.6 AEP composition

AEP is a complex mix of various proteins and peptides, and there have been many technical challenges in elucidating its composition. Despite these technical challenges, several researchers (Gocke et al. 2002; Li et al. 2004; Hannig et al. 2005; Hannig et al. 2009; Yao et al. 2003; Siqueira et al. 2007; Vitorino et al. 2007; Vitorino et al. 2008; Yao et al. 2001) have employed various methods and tools to gain understanding of the AEP composition.

2.7 AEP salivary proteins

The major salivary protein families associated with AEP include acidic proline rich proteins (aPRPs) (Oppenheim et al. 1971), basic PRP, amylase, MUC5B, agglutinin, cystatins (Larkin et al. 1991), histatins (Hay 1975; Oppenheim et al. 1986) and statherin (Hay 1975; Helmerhorst and Oppenheim 2007; Messana et al. 2008; Schipper et al. 2007).

Many salivary proteins, like statherin, proline-rich glycoproteins, mucins, acidic proline-rich proteins, and amylase, have been proposed to be associated with the lubricating properties of pellicle (Proctor et al. 2005; Berg et al. 2004; Hannig et al. 2007).

Previous work discovered that mature AEP proteome consists of different proteins and peptides (Siqueira et al. 2007; 2009). Siqueira et al. (2007) employed LC-ESI-MS/MS to identify the salivary protein components of in vivo AEP. Through MS following a shotgun approach, they identified 130 proteins and peptides ranging in size from >250 kDa to <5 kDa. Most of them were without any known function. About 50% were small molecular weight peptides in the in vivo formed AEP from a single subject as well as from pooled samples of number of volunteers.

Siqueira et al. (2009) in previous study discovered and identified small molecular weight salivary proteins and peptides from the in vivo AEP employing MS. They showed for the first time that 50% of AEP protein composition is made up of small proteins and peptides ranging in size from 0.8 kDa to 3.9 kDa. In all, they found that there were 78 naturally occurring peptides in AEP which originated from 29 different salivary proteins.
Zimmerman et al. (2013), for the first time did the comprehensive analysis of the proteome and peptidome composition of AEP from deciduous teeth. They identified 76 pellicle proteins and 38 naturally occurring peptides from 10 salivary proteins using MS.

Based on the possible role of these proteins in AEP development, Siqueira et al. (2007), classified these pellicle proteins into 3 major groups; Ca\textsuperscript{2+} binding proteins, PO\textsubscript{4}\textsuperscript{3–} binding proteins & proteins interacting with other salivary proteins. Pellicle proteins have also been classified according to their putative biological functions; inflammatory responses, immune defense, antimicrobial activity & remineralization potential.

Furthermore, in a recent study, Hannig et al. (2009), found that alanine amino transferase and amino transferase enzymes were present after 3 minute of pellicle formation, in active form. These enzymes, by complexing adsorbed molecules, might influence pellicle formation (Iontcheva et al. 1997) or they may influence pellicle proteins cross-linking enzymatically (Yao et al. 2000). So far, a complete role, that these active enzymes may play, in pellicle formation or its structure is yet to be elucidated.

Many different studies (electrophoretic, chromatographic, immunological) have been undertaken to investigate and elucidate the pellicle composition. Most of these studies have shown that proteins, enzymes, mucins, and glycoproteins are the major components of the pellicle (Lendenmann et al. 2000). For example, amylase, IgA, S-IgA, PRPs, mucins MG1 and MG2, albumin, carbonic anhydrase, cystatins, histatins, statherin, lactoferrin, and lysozyme, have been identified as major components of pellicle by different researches (Schüpbach et al. 2001; Li et al. 2004; Vitorino et al. 2004, Hey 1975; Oppenheim et al. 1986; Siqueira et al. 2007; Siqueira et al. 2009; Siqueira et al. 2010).

Many indirect techniques like immunological detection has immensely contributed in further identification of pellicle components and the composition of in vivo pellicle (Yao et al. 2003). The strong evidence for the presence of statherin, lysozyme, and alpha-amylase, as major components of the acquired enamel pellicle were also provided by these indirect methods of detection. (Hannig et al. 2007; Li et al. 2004).
Lately the development in analytical tools like mass spectrometry and its algorithms has given a major impetus to the high throughput discovery and characterization of salivary proteins and peptide due to its extreme sensitivity up to femtomole level. For example, Siqueira et al. (2007) for the first time identified 130 proteins pellicle through LC-ESI-MS/MS, of which 89 proteins were reproducibly present in three out of the five independent experiments, demonstrating high degree of inter sample uniformity.

Vittorino et al. (2008) employed MALDI-MS/MS to analyze human AEP and identified more than 90 pellicle peptides/proteins. Most of the identified peptide and proteins were part of statherin, histatins, cystatins basic PRPs, and aPRPs.

### 2.7.1 AEP formation

Initially, Alexander Nasmyth described it as persistent dental capsule of embryonic origin (Nasmyth 1839). Later, it was accepted that embryologic integuments are lost after teeth eruption. Dawes et al. (1963) introduced term acquired enamel pellicle to denote non-cellular, bacteria-free, protein rich membrane integument that covers the dental enamel in the oral cavity.

Pellicle formation is a highly selective process, since only a limited number of the salivary proteins are a part of AEP (Yao et al. 2003; Siqueira et al. 2007). The amino acid profiles of the saliva samples were different from the pellicle profiles, clearly indicating that pellicle was composed of selective adsorption of salivary proteins. (Siqueira et al. 2007). Phosphorylated proteins like, histatin, statherin, and acidic proline rich proteins, are the main salivary proteins, speculated to play an important role as pellicle precursor proteins. Therefore, these proteins have been extensively characterized in terms of their ability to adsorb calcium phosphate rich enamel surfaces and influencing formation of pellicle. (Yin et al. 2006; Smith and Bowen 2000).

Consensus among oral biologist is that the acquired enamel pellicle forms in two phases. In the first phase, first few layers of initial pellicle forms through non-covalent interactions of the calcium and phosphate binding proteins, with very high affinity to
hydroxyapatite (HA), adsorb the tooth surface almost instantaneously. This process occurs within few milliseconds to few minutes. (Hannig 1999).

Hannig (1999) observed that the initial stage of pellicle formation can be visualized as an electron dense basal layer observed via transmission electron microscopy. He found that the dense basal layer of the AEP starts to form within seconds, taking between 2 - 3 minutes to complete, reaching an estimated thickness of 10 - 20 nm, where it remains for about 30 minutes. A slower second phase follows the rapid first stage of AEP formation, whereby pellicle thickness increases by continuous and selective adsorption of salivary proteins from saliva.

This first phase then paves the way for a secondary slower phase, where the continuous and selective adsorption of salivary proteins and other biomolecules present in saliva continues. These two phases of protein adsorption have been observed as two distinct zones through electron microscopy, of which the first phase, adjacent to hydroxyapatite surface is primary electron dense basal layer, and the second phase is an outer globular, porous layer. (Baek et al. 2009; Lendenmann et al. 2000; Hannig 1999; Hannig et al. 2004; Hannig et al. 2005; Deimling et al. 2007). It is further speculated that mainly PRPs constitute the AEP dense basal layer, while the combination of mucins and protein aggregates constitute outer globular, porous structure.

Clasen et al. (2000), showed that pellicle thickness differences could be more likely attributed to differences in the salivary secretion from different parts of the oral cavity, as secretions from different salivary glands contain various sizes and types of proteins in varying amounts and concentrations, which differ significantly between glands Walz et al. 2006).

It was demonstrated in previous studies, that low molecular proteins present in parotid saliva, like statherin, make an initial adsorbed layer of pellicle (Proctor et al. 2005; Santos et al. 2008), which will potentially follow monolayer adsorption behavior, and adsorption will be self-limiting when the surface is saturated (Rabe et al. 2011).
Taking advantage of recent advances in ultrastructural visualization tools, most of the efforts have been geared toward the elucidation of structure in the *in vitro* and *in vivo* AEP using several techniques, like scanning electron microscopy (SEM), transmission electron microscopy (TEM) confocal laser scanning microscopy (CLSM), and atomic force microscopy (AFM) leading to in-depth understanding of AEP structure (Siqueira *et al.* 2012; Deimling *et al.* 2004, 2007; Hannig *et al.* 2004; Hannig *et al.* 2005; Schwender *et al.* 2005; Baek *et al.* 2009; Ash *et al.* 2013; Veeregowda *et al.* 2012).

Hannig & Hannig (2009), elucidated that the pellicle formation mechanism is most likely mediated through electrostatic and hydrophobic interactions during adsorption of the salivary proteins on to hydroxyapatite surface. The smaller molecular weight, surface active phosphor-serines rich proteins like histatins and statherin, have a strong affinity for the hydroxyapatite and potentially have a higher surface diffusion coefficient, which allowing them to adsorb more quickly and form the primary layers in both parotid and whole saliva in the oral cavity.

Ash *et al.* (2013) found that subsequent adsorption of late pellicle proteins depends on the attractive interactions between the proteins present in the early pellicle layer, and these attractions perhaps, can be enhanced by specific calcium mediated interactions.

Pellicle precursor proteins appear to undergo conformational changes and increase their cross-sectional area to cover the enamel surface, when they adsorb to tooth surface (Norde 1995). Santos *et al.* (2010) also observed and confirmed earlier observations that after initial protein adsorption, conformational changes occur in the pellicle structure.

During the last 40 years in many studies, a variety of electrophoretic techniques have been employed to examine salivary protein adsorbed on enamel surfaces. All these techniques resulted in the identification of different salivary protein and classification of individual members to different protein families (Al-Hashimi and Levine 1989; Kousvelari *et al.* 1980; Oppenheim *et al.* 1986).
All these studies using different techniques have firmly established that the pellicle is composed of selective adsorption of salivary proteins on to the enamel surface (Siqueira et al. 2007; Siqueira and Oppenheim 2009; Siqueira et al. 2010).

Several in vitro (Fujikawa et al. 2008; Joiner et al. 2006), in vivo (Siqueira et al 2007; Siqueira and Oppenheim 2009), and in situ (Santos et al. 2008; Deimling et al. 2007) studies have been done with an intent to gain additional insight about the pellicle structure. These studies have generated diverse, in depth understanding about the pellicle composition, formation, structure, and function.

In a previous study, Douglas et al. (1991), demonstrated that salivary statherin, due to its amphipathic nature, most likely acts as an important boundary lubricant as a constituent of the pellicle. Reeh et al. (1996) provided another piece of evidence, that the amphipathic nature of molecules was important for lubrication, as amphipathic molecules reduced friction between opposing tooth surfaces.

Several systematic approaches have been adopted to get deeper insight into pellicle formation. Various in vivo, studies where the pellicle is harvested from the enamel surface (Li et al. 2003), in situ studies, where bovine enamel, is exposed in the oral cavity (Hara et al. 2006), or in vitro studies, where different dental components are exposed to collected saliva outside oral cavity (Vitorino et al. 2004), with a view to further understand the pellicle formation process.

Many studies have been performed using the saliva incubation with hydroxyapatite plaques (Deimling et al. 2004; Smith and Bowen 2000), or hydroxyapatite powder (Vitorino et al. 2004; Lamkin et al. 2001), to simulate pellicle formation in oral cavity.

Studies have demonstrated that, statherin, acidic PRPs, and histatins, also known as pellicle precursor proteins, that show preferential, selective enamel adsorption compared to other salivary proteins (Vitorino et al. 2008; Svendsen et al. 2008).
These *in vitro* studies led to invaluable clues why some salivary proteins display differential adsorption affinities for hydroxyapatite surfaces and provide evidences which proteins may bind to enamel surfaces.

It is consensus among oral biologists, that there are 4 fundamentals steps in AEP formation: 1). Diffusion of salivary proteins towards the enamel surface, 2). Selective protein adsorption on the enamel surface, 3). Conformational changes and cross-linking of adsorbed salivary proteins, 4). Detachment of salivary protein from the pellicle and diffusion from the enamel surfaces. The protein adhesion is the outcome of Van der Waals, acid–base, and electrostatic interactions taken together. (Demodarshan *et al.* 2008).

In several studies, it has been observed that the composition of pellicle differs significantly in different locations, from where it is collected in the oral cavity. Smith and Bowen (2000), demonstrated that the overall protein composition of *in vivo* formed pellicles displayed location specific characteristics, prevailing in the different locations within oral cavity, from where the pellicles were harvested.

Amaechi *et al.* (1999), and Hannig (1999) through independent investigations of *in situ* AEP with confocal laser-scanning microscopy and transmission electron microscopy found that AEP in different areas of oral cavity differ in the thickness. Palatal site pellicle is thinner than that of buccal sites pellicle and are therefore more likely to have different pellicle composition.

Phosphoproteins contain calcium-binding domains, that may provide a region of high calcium concentration in close vicinity to the enamel surface, thus augmenting the teeth mineralization. The importance of the pellicle in preserving oral health cannot be underestimated in Xerostomia patients, suffering from dry mouth syndrome (Tabak 2006; Vissink *et al.* 2010; Turner and Ship 2007). In the absence of sufficient saliva in the oral cavity, as effective salivary pellicle cannot be produced, these patients suffer from higher incidences of dental caries and damages to the mucous membrane. (Vissink *et al.* 2010)
In last few years, different researches tried to investigate the relationship between saliva ionic composition and the pellicle structure, for which the driving force was to dissect and understand the role of calcium ions in pellicle structure. (Vassilakos et al. 1992; Tanizawa et al. 2004; Macakova et al. 2010; Kandori et al. 2008; Harding et al. 2005).

Calcium ions have been implicated to modify the attraction between enamel surfaces and salivary proteins, to which these proteins attach during pellicle formation (Hannig et al. 2009; Macakova et al. 2010).

For example, Tanizawa et al. (2004), demonstrated that pellicle formation onto hydroxyapatite surfaces was enhanced by calcium ions through calcium bridging of proteins.

Proctor et al. (2005), found that saliva calcium ion chelation resulted in a drastic loss of mechanical properties in adsorbed pellicle, indicating the pellicle structure breakdown. Therefore, investigations of physical structure of the pellicle under different calcium concentrations may help to dissect the pellicle formation mechanisms.

### 2.8 AEP functions

#### 2.8.1 Enamel demineralization protection

AEP provide protection to teeth surface from mechanical and abrasive forces. It can regulate enamel calcium phosphate demineralization and remineralization and neutralize acid produced by bacteria in the oral cavity (Amerongen et al. 2004).

AEP behaves like a semipermeable membrane, and hence by preventing demineralization and/or augmenting enamel remineralization, it helps maintain the enamel surface structure. In terms of calcium and phosphate ionic concentrations, saliva is supersaturated at pH 7.0. (Larsen and Pearce 2003).

When the salivary pH in the microenvironment of the tooth turns acidic, it is no more supersaturated with respect to calcium phosphate ions. Since the $\text{H}^+$ ions react with phosphate ($\text{PO}_4^{3-}$) or hydroxyl ions ($\text{OH}^-$) in the saliva, their concentration gets reduced in
saliva. So, the loss of calcium and phosphate ions from teeth is directly related to the loss of calcium and phosphate ions in saliva following law of mass action. It means that due to acidic pH, as the saliva becomes less saturated with calcium phosphate, the enamel hydroxyapatite starts demineralizing to counter the change in concentration of calcium phosphate ions in saliva. So, longer the tooth surface encounter acidic environment, under saturated with respect to calcium phosphate ions, the enamel start demineralizing or dissolving. Surprisingly enough, instead of acid, is water that breaks the crystal lattice bonds of hydroxyapatite structure due to loss of attraction between calcium and phosphate ions (Pearce 1988).

In the oral cavity, when bacteria encounter fermentable sugars, they produce formic acid, acetic acid, lactic acid, and propionic acid as metabolic by-products. These small chain acids, cause enamel demineralization (Garcia-Godoy and Hicks 2008).

In a recent study, Siqueira et al. (2010), provided first evidence that intact histatin peptides when adsorbed to hydroxyapatite were not only resistant to the protease degradation, but also able to protect the hydroxyapatite demineralization under acidic challenge.

Since, pellicle acts like semipermeable membrane, it controls the downward acid diffusion from biofilm to enamel surface and decelerate calcium and phosphate ion movement into and out of enamel surface. This results in slowing down the enamel demineralization in hostile low pH environments and in basic or neutral pH promotes enamel remineralization (Lussi et al. 2006, Hara et al. 2006).

Rios et al. (2008) and Meurman and Frank (1991) through independent ultramicroscopic studies demonstrated, that the acidic soft drinks induced enamel demineralization was significantly reduced by salivary pellicle.

In a previous study, Amaechi et al. (1999) showed that just one hour old in situ acquired pellicle could protect enamel surface to certain extent against the orange juice induced demineralization. Hannig et al. (2004), in another study demonstrated that even a 3-min
old \textit{in situ} pellicle could provide some protection against enamel surface demineralization induced by citric acid.

In a recent study, Hannig \textit{et al.} (2009), concluded that orange juice caused less damage than low pH carbonated beverages to the \textit{in situ} pellicle coated bovine enamel.

Hannig \textit{et al.} (2003) in previous \textit{in vivo} pellicle formation study, demonstrated, that 2 hour old AEP was as efficient as 24 hours old AEP in protecting against acid induced demineralization of the enamel surface without any statistically significant difference.

Hannig \textit{et al.} (2004) in another study demonstrated there was no significant difference, in the acidic challenge induced demineralization protection, provided by 3 minutes \textit{in situ} pellicle versus 2 hour \textit{in situ} pellicle.

\subsection*{2.8.2 AEP as a platform for biofilms}

The pellicle performs dual function of protecting tooth enamel besides providing sites for the initial attachment of bacteria to the tooth surface, which is the first step in plaque formation. Thereafter, AEP plays a major role in the interactions, that take place at the tooth-saliva interface which are important both physiologically and pathologically (Wolff and Larson 2009).

Several structural components of AEP like, mucin MG 2, fibrinogen, and PRPs acts as specific bacterial receptors (Hannig and Joiner 2006; Bonifait \textit{et al.} 2009). These pellicle proteins contain peptide sequences or epitopes on their surface, which are detected and utilized for attachment, by a variety of pili, fibrils, and fimbriae appendages on bacterial cell surfaces. Eighty percent of the early colonizers constitute Streptococcus mitis, S. soralis, and S. sanguis (Cassels \textit{et al.} 1995).

Early colonizers adhere to the pellicle through a reversible and weak binding and subsequently other bacteria attach themselves over early colonizers through irreversible attachment (Meurman and Stamatova 2007). Over a period, as biofilm start maturing, these initial colonizers are slowly replaced by anaerobic \textit{S. sobrinus}, \textit{S. mutans}, and \textit{L. actobacilli} (ten Cate 2006). These anaerobes cause the carbohydrate fermentation in
foods and produce organic acids in the oral cavity. It can reduce pH of oral cavity and ultimately leads to tooth demineralization.

On the contrary, some microbial biofilm bacteria may counter the effects of acidogenic bacteria. For example, lactic acid produced by some bacteria is metabolized by *Veillonella*. In other case, ammonia compounds are synthesized by *S. salivarius* urease, which can potentially raise the saliva pH, leading to delayed initiation of tooth demineralization process (Garcia-Godoy and Hicks 2008).

### 2.9 AEP modulation

Besides differences in secretions from different salivary glands, the circadian cycle, age, sex, diet, and general health of a person, also known to modify the salivary composition, all of which are also likely to modulate the structural differences in the pellicle samples (Castagnola *et al.* 2004).

In the oral cavity, during pellicle formation, the saliva protein adsorption behavior on dental enamel, has been shown to influenced by several dietary components (Smith and Bowen 2000; van der Mei *et al.* 2002).

Additionally, certain processed food components, like calcium in dairy products or the low pH of soft drinks, may modify the pellicle structure (Ash *et al.* 2013; Hannig *et al.* 2009; Proctor *et al.* 2005).

Besides, other nonprotein salivary components may also exert influence over the pellicle formation and structure. For example, it is thought that the use of certain oral hygiene products and/or even drinking and eating certain foods may modulate the pellicle structure. Some components of toothpaste (sodium lauryl-sulfate and sodium tri-polyphosphate) are known to dislodge certain proteins from the pellicle (Shellis *et al.* 2005; Hannig *et al.* 2009).

Comelli *et al.* (2002), observed that bacterial strains *S. thermophilus* and *Lactobacillus lactis* ssp. lactis used in the processed dairy foods integrated into an *in vitro* grown biofilm. They interfered with development of *S. sobrinus*, a cariogenic species. This
study showed, that the pellicle composition could be modulated by saliva and other components in the oral cavity. Besides, this modulation could also be achieved through food components.

Yao et al. (2001) demonstrated that under in vivo conditions, the AEP appeared to undergo extensive enzymatic changes as in vitro pellicles contained greater number of intact proteins compared to in vivo pellicles. This clearly demonstrate that under in vivo conditions AEP is a very dynamic structure, in a dynamic equilibrium with the surrounding saliva. Therefore, the AEP can be seen as dynamic protein film, that is under continuous adsorption and desorption mode in the oral cavity, and is highly sensitive to micro environmental changes in its vicinity (Rosan and Lamont 2000).

Smith and Bowen (2000), demonstrated that during in vitro pellicle formation, rinsing the hydroxyapatite disc with solutions of sucrose, xylitol, sorbitol, or milk, led to composition modulation in the pellicle. Siqueira et al. (2012) also confirmed their results and observed that when the hydroxyapatite discs were coated with different concentration solution of Sodium fluoride, this led to pellicle composition modulation.

Schupbach et al. (1996), in an interesting study found that some milk casein derivatives can displace albumin by adsorbing onto the enamel surface and get incorporated into the pellicle. Therefore, some of the dietary components may also be considered integral components of the pellicle. This has important oral implications, since the pellicle display bacterial binding receptors for several bacteria. So, any pellicle compositional modulation, that is induced by dietary modifications, can potentially change its microbial binding behavior, thus leading to changes in the biofilm composition.

Hannig et al. (2009), in an in situ study, observed that a significant amounts of the outer loose, globular layer of the AEP was removed by consumption of acidic beverages, while the basal dense layer was not affected.

Rykke and Sonju (1991), concluded that food component can modulate the pellicle composition. They found that there were significant differences between 24 hours old pellicle formed with and without intake of food and beverages.
Moreover, the proteolytic activity of proteases in saliva also results in modulated pellicle composition, and provide protein receptor sites for bacterial attachment on the pellicle (Douglas 1994).

Furthermore, in the oral cavity, enzymes from dead bacterial cells as well mucosal tissues, blood and from consumed foods can also get incorporated into the pellicle and may also modulate the pellicle structure (Lendenmann et al. 2000; Kajisa et al. 1990). But, the effects of these nonstructural external factors on the pellicle functional properties and characteristics of AEP is still unknown.

Cardenas et al. (2007), demonstrated that the resilience of the basal electron dense of pellicle layer may be attributed to Mucin MUC5B, present in pellicle. Delecrodea et al. (2015) in a recent study supported earlier studies and demonstrated that, even after acid challenges to the salivary pellicle on hydroxyapatite surface, there were certain acid resistant proteins like Cystetin-B and mucin-3A, which were still retained on the hydroxyapatite surface and could not be removed easily from the surface.

Tanizawa et al. (2004), demonstrated that Ca^{2+} ions through calcium bridging of proteins, could enhance pellicle formation onto hydroxyapatite surfaces. On the other hand, Proctor et al. (2005), found that Ca^{2+} ion chelation from saliva caused a significant reduction in the mechanical properties of salivary pellicle, indicating the potential pellicle structure breakdown.

Ash et al. (2013), found that when the calcium concentration was increased from 0-10 mM, there were significant changes in the thickness, fresh weight, protein mass, and concentration of the pellicle proteins for both parotid and whole saliva derived pellicles.
References


Chapter 3

3 AEP peptide mediated enamel demineralization protection studies

The acquired enamel pellicle is a protective covering on the enamel and other surfaces of the oral cavity, containing around 130 proteins and peptides. Around 50% of the pellicle proteins and peptides are smaller in size (<30 kDa), having posttranslational modifications. Salivary peptides are products of salivary proteins, resulting from host and bacterial origin proteases enzymatic digestion, which may either retain or enhance the functional properties of their native proteins. Statherin and histatin are the major pellicle component, highly effective in inhibiting the precipitation of primary and secondary calcium phosphate and having antimicrobial activities, respectively. Our group has identified N-terminal 9 amino acids residue peptide, DpSpSEEKFLR (DR9), from statherin, and a 14 amino acid synthetic analog of antimicrobial functional domain RKFHEKHHSHRGYR (RR14), from histatin, which are early components of in vivo pellicle, displaying a significant effect on the hydroxyapatite growth inhibition and antimicrobial activities, respectively (Xiao et al., 2015; Tayebeh et al., 2017). In the current study, we demonstrated that DR9 and its tandem duplicate DR9-DR9 peptides, exhibited significant protection against enamel demineralization, whereas DR9-RR14, the hybrid construct showed moderate protection against demineralization when compared to control.

3.1 Introduction

Several workers and studies have elucidated and reached a global consensus, that acquired enamel pellicle (AEP), is a protective, organic integument on the enamel and other surfaces in the oral cavity, consisting of around 130 proteins and peptides, through the selective adsorption of, salivary proteins and peptides, and other molecules including phosphoproteins, lipoproteins, glycoproteins, lipids and carbohydrates (Dawes et al. 1963; Vitorino et al. 2007; Siqueira et al. 2007; Hannig and Joiner 2006; Sonju 1975; Slomiany et al. 1986; Slomiany et al. 1990). The main source of these pellicle proteins and peptides, is salivary glands in the oral cavity, oral mucosa, gingival crevicular fluid,
and bacterial products (Siqueira et al. 2012; Hannig et al. 2009). Several studies have shown that pellicle proteome appears to be a derived from a subpopulation of salivary proteome through selective adsorption of salivary proteins.

The acquired enamel pellicle plays an extremely important role in the overall teeth homeostasis, by being a semipermeable membrane integument for demineralization protection, as well as to neutralize organic acids, produced as by product of bacterial metabolism (Hara et al. 2010; Siqueira et al. 2010; Siqueira et al. 2012; Zahradnik et al. 1977; Hannig et al. 2007; Kosoric et al. 2007; Kosoric et al. 2010). Pellicle also determines the early colonizers composition, that ultimately results in the microbial biofilm formation on various surfaces throughout the oral cavity. (Gibbons et al. 1988; Gibbons and Hay 1989; Li et al. 2004; Chaudhuri et al. 2007).

One of the important major component of pellicle proteins is statherin, which is highly effective in inhibiting the precipitation of primary and secondary calcium phosphate (Oppenheim et al. 2007; Schlesinger and Hay 1977) leading to supersaturation of saliva, that helps in the enamel surface remineralization. The N-terminal of statherin’s peptide contain the functional domain (Long et al. 1998; Raj et al. 1992). A naturally occurring peptide, from this N-terminal region of statherin, was identified as an early component of the pellicle (Siqueira and Oppenheim, 2009). This small peptide, called DR9, has demonstrated a significant (p<0.05) effect on the hydroxyapatite growth inhibition effect in all concentrations tested in comparison to other native statherin peptides (Xiao et al. 2010; Xiao et al. 2015).

Yang et al. (2017), constructed a statherin N-terminal bioinspired version containing first six-amino acid residues DpSpSEEK (pS corresponds to phosphorylated serine). They demonstrated that, when the peptide sequence was cysteine-labeled, DpSpSEEKC, it strongly adsorbed to HAP and induced remineralization on the demineralized tooth enamel surface. In comparison to control, this new peptide coating significantly improved the mechanical properties of the coated samples.

Salivary proteins are known to have existed for millions of years in the nature. During a period of time, over evolutionary time scale, they counter the evolutionary pressure by
duplicating the functional domains that lie within their primary structures, in an effort to improve their functional capabilities to better match the evolution. (Oppenheim et al. 2012; Troxler et al. 1997).

This protein diversity may be achieved at different hierarchical levels either at genome level through gene duplication, allelic variation, and recombination events, or at transcriptome level through alternate splicing events, and at proteome level through post-translational modifications. (Helmerhorst and Oppenheim 2007; Oppenheim et al. 2007).

Since statherin is very young protein in terms of evolutionary time scale and could not get the opportunity to evolve naturally (Oppenheim et al. 2012; Troxler et al. 1997), therefore, DR9 is the only known natural functional domain as far as the primary and secondary calcium phosphate precipitation inhibition is concerned (Xiao et al. 2015; Xiao et al. 2010). So, one possible way to test and observe the effect of evolution could be to artificially duplicate or triplicate DR9 sequence in tandem. It may result in the expected effects, we would like to see in the due course of natural evolution, thereby constructing a salivary protein with augmented dental enamel demineralization protection.

Besides functional domain multiplication, natural evolution processes over a period may also recombine the functional domains of different proteins due to gene shuffling/recombination processed to create a natural hybrid protein. Hence, another AEP protein, histatin is best candidate to be studied. Histatin has very strong activities of antimicrobial, demineralization protection, buffering, and regulation of mineral formation (Oppenheim et al. 2012; Edgerton and Koshlukova 2000; Siqueira et al. 2010; Helmerhorst et al. 2006; Vukosavljevic et al. 2012).

Histatins are known to degrade immediately in the hostile oral cavity, upon secretion from salivary glands, due to enzymatic proteolysis. Despite the degradation, histatin fragments still function like parental proteins (Helmerhorst, et al. 2007; Groot, et al. 2006, Castagnola, et al. 2004). A peptide RR14, a synthetic analog of antimicrobial functional domain RKFHEKHHSHRGYR, derived from histatin 3, was identified as member of the in vivo pellicle. It was connected with DR9 derived from statherin to create a hybrid peptide, DR9-RR14. Earlier studies have shown that the functional
domain of histatins could have the same antimicrobial effect as of the original protein. By synthetically combining RR14 with DR9, we hypothesize the creation of a novel protein with dual functionality of superior antimicrobial qualities and enhanced mineral homeostasis in one molecule. It will represent promising new molecular methodologies, with an immense potential for the oral health maintenance.

3.2 Materials and methods

3.2.1 Characterization of peptide constructs

Synthetic peptides, derived from histatin 3 or statherin (DR9, DR9-DR9 and DR9-RR14), were synthesized by China peptide, Shanghai, China. Each peptide was verified by HPLC and MS analysis for purity (> 95%) and Mᵣ values. For all the experiments, peptide solutions were prepared in water, pH 6.8, at a concentration of 1 mg/ mL. All the peptides, tested in this study, are listed along with their sequence and other physical characteristics in Table 3-1.

3.2.2 Calculation of pI values of peptide constructs

The isoelectric points (pI) of histatin 3 and statherin peptides were calculated using the online calculator developed by Gauci and coworkers using Scansite option (Azzopardi, et al. 2010). This approach let user define the specific pK values at a particular pH to calculates the pI of a given peptide. The calculation was performed in repetitive manner, till the pH, at which the net charge of peptide was zero, achieved. (Gauci, et al. 2008).

3.2.3 Enamel demineralization assay

3.2.3.1 Enamel sample preparation

Enamel sample preparation was done following the previous study by Siqueira, et al. (2010). Human permanent first molars, free of any physical defects, were cleaned, rinsed, and sectioned. After the removal of roots, the crowns were sliced vertically into 4 sections (with a 300 µm thickness each) through a diamond saw, followed by sandpaper grinding to a uniform, final thickness of 150 µm. Each section was coated with a layer of
lightcured dental adhesive (3M ESPE Scotchbond™ Universal) and nail varnish paint, leaving aside a naked, uncoated 2 mm x 150 µm window on the enamel surface.

**3.2.3.2 Enamel coating and demineralization treatment**

Enamel sections were divided randomly into 4 groups (N = 10 per group; Table 4-2) and were incubated for 2 hours with either parotid saliva (PS; 10 µg/section) at 37°C or peptide constructs (DR9/DR9-DR9/DR9-RR14 at the rate of 20 nmol/section). After incubation, the sections were gently rinsed in distilled water to remove any loosely bound parotid saliva or peptide to the exposed window (150 µm x 2mm). Then sections were submitted for demineralization assay by incubating them at 37°C in demineralization solution (2.2 mM CaCl₂, 2.2 mM NaH₂PO₄, 50 mM Acetic acid pH 4.5) for 12 days. The pH of the demineralization solution was checked every 72 hours with pH strip to ensure that the pH changes was not significant. Following experimental treatments and groups were used in this set of experiments:

<table>
<thead>
<tr>
<th>Group</th>
<th>Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>PS coated enamel section (Control)</td>
</tr>
<tr>
<td>2</td>
<td>DR9 coated enamel sections</td>
</tr>
<tr>
<td>3</td>
<td>DR9-DR9 coated enamel sections</td>
</tr>
<tr>
<td>4</td>
<td>DR9-RR14 coated enamel section</td>
</tr>
</tbody>
</table>

In another set of experiments, enamel sections were divided randomly into 4 groups (N = 10 per group; Table 4-3) and were incubated for 2 hours with PS (10 µg/section) at 37°C. After incubation, the sections were gently rinsed in distilled water to remove any loosely bound parotid saliva to the exposed window (150 µm x 2mm). After rinsing, they were again incubated with peptide (DR9/DR9-DR9/DR9-RR14 - 20 nmol/section) for 2 hours at 37°C. Following experimental treatments and groups were used in this set of experiments:
<table>
<thead>
<tr>
<th>Group</th>
<th>Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>PS coated enamel section (Control)</td>
</tr>
<tr>
<td>2</td>
<td>PS coated enamel section + DR9 coating</td>
</tr>
<tr>
<td>3</td>
<td>PS coated enamel section + DR9-DR9 coating</td>
</tr>
<tr>
<td>4</td>
<td>PS coated enamel section + DR9-RR14 coating</td>
</tr>
</tbody>
</table>

After incubation, the sections were briefly rinsed with distilled water to remove loosely bound peptide. Then sections were submitted for demineralization assay by incubating them at 37°C in demineralization solution (2.2 mM CaCl$_2$, 2.2 mM NaH$_2$PO$_4$, 50 mM Acetic acid pH 4.5) for 12 days. The pH of the demineralization solution was checked every 72 hours with pH strip to ensure that the pH changes was not significant.

### 3.2.3.3 Calcium and phosphate estimation

After 12 days in the demineralization solution, the enamel sections were removed, and the supernatant was analyzed for the calcium concentration through quantitative colorimetric calcium determination assay at 595 nm and phosphate concentration using vanadomolybdate UV-Visible spectrophotometric assay at 415 nm. All the samples were analyzed in duplicate.

### 3.2.3.4 Statistical analyses

Statistical procedures were performed with the software package Minitab 13.1. After checking for normal distribution, we subjected the data to analysis of variance (ANOVA) followed by Tukey’s test. The level of significance was set at a value of p <0.05. Means and standard deviations of calcium and phosphate released from human enamel sections first exposed to parotid saliva (control) or peptide construct or parotid saliva + pellicle peptide constructs, followed by exposure to the demineralizing solution (n = 10 per group) for 12 days. Different letter superscripts indicate statistical difference, and same letter superscripts indicate no statistical difference within the same column, according to Tukey’s test (p<0.05).
3.3 Results

Isoelectric points were calculated for each peptide construct at pH 6.8. For DR9, the statherin peptide construct, pI value was 3.62, with a net charge of -1 (at pH7.0) while for DR9-DR9, tandem repeat construct of statherin, lowest pI value of 3.44 was observed with a net charge of -2 (at pH7.0). In case of DR9-RR14 hybrid construct of statherin and histatin, intermediate pI value of 7.16 was observed with a net charge of +3 (at pH7.0). Results are summarized in Table 3-1.

Table 3-1: Sequences and other physical characteristics of histatin 3 or statherin peptide constructs.

<table>
<thead>
<tr>
<th>Amino Acid Sequence</th>
<th>Amino residues</th>
<th>Mr (kDa)</th>
<th>Net charge at pH 7.0</th>
<th>pI</th>
</tr>
</thead>
<tbody>
<tr>
<td>DSSEEKFLR (DR-9)</td>
<td>9</td>
<td>1.270</td>
<td>-1</td>
<td>3.62</td>
</tr>
<tr>
<td>DSSEEKFLRDSSEEKFLR (DR-9-DR-9)</td>
<td>18</td>
<td>2.522</td>
<td>-2</td>
<td>3.44</td>
</tr>
<tr>
<td>DSSEEKFLRRKFHEKKHHSHRGYR (DR-9-RR-14)</td>
<td>23</td>
<td>3.127</td>
<td>+3</td>
<td>7.16</td>
</tr>
</tbody>
</table>

To have further insight and functional understanding of new synthetic constructs, derived from histatin and statherin pellicle peptides, in terms of demineralization protection, when adsorbed on the salivary pellicle, we decided to test the effects of those peptides on in vitro enamel demineralization. The effect of these peptide construct on the amounts of phosphate and calcium released from the enamel specimens after 12 days in demineralization solution are summarized in Tables 3-2 and 3-3.

Table 3-2: Means and standard deviations of Ca²⁺ and PO₄³⁻ released from human dental enamel sections, coated with either control (PS) or peptide constructs.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>N</th>
<th>Ca²⁺ (mM/mm²) mean ± SD</th>
<th>PO₄³⁻ (mM/mm²) mean ± SD</th>
<th>Ca²⁺/PO₄³⁻ Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control (PS)</td>
<td>10</td>
<td>13.71±1.35[^A]</td>
<td>3.22±0.74[^A]</td>
<td>4.26</td>
</tr>
<tr>
<td>DR9-RR14</td>
<td>10</td>
<td>15.77±1.46[^A]</td>
<td>4.04±0.29[^C,D]</td>
<td>3.90</td>
</tr>
<tr>
<td>DR9-DR9</td>
<td>10</td>
<td>14.38±2.5[^A]</td>
<td>4.1±0.82[^C,D]</td>
<td>3.51</td>
</tr>
<tr>
<td>DR9</td>
<td>10</td>
<td>14.58±1.7[^A]</td>
<td>3.91±0.51[^A,C,D]</td>
<td>3.73</td>
</tr>
</tbody>
</table>
3.3.1 Ca$^{2+}$ and PO$_4^{3-}$ demineralization protection with peptide coated

In case of calcium demineralization protection, different peptide constructs (DR9, DR9-DR9, DR9-RR14), could not provide any better protection against calcium demineralization in comparison to PS control. Because, there was no statistically significant difference between different treatments, compared to parotid saliva coated control.

In case of the phosphate demineralization protection, control (PS coated only) provided better protection (lowest level of demineralized phosphate) in comparison to either of DR9-DR9 and DR9-RR14 peptide constructs as there were significant differences between control and DR9-DR9, and DR9-RR14 constructs. On the other hand, there were no statistically significant differences between Control and DR9 as well as between any of the three peptide constructs (DR9, DR9-DR9 and DR9-RR14).

The overall trend was that, for calcium and phosphate demineralization, none of the peptide construct (DR9, DR9-DR9, DR9-RR14) exhibited any significant protection when compared to control PS group (Table 4-2). Under the current experimental conditions, none of the peptide construct provided any advantage or significant demineralization protection function against calcium and phosphate from enamel surface, when directly coated on to the enamel surface.

For each of the tested group, the Ca/PO$_4$ ratio was calculated. Among the groups, a % variation of less than 7.5 percent was observed. The lowest ratio was that of DR9-DR9 coated group (3.51) while PS coated control group showed the highest ratio of 4.26.

Table 3-3: Means and standard deviations of Ca$^{2+}$ and PO$_4^{3-}$ released from human dental enamel sections, coated with control (PS) or PS coated + peptide construct coated.

<table>
<thead>
<tr>
<th>Treatment</th>
<th>N</th>
<th>Ca$^{2+}$ (mM/mm$^2$) mean ± SD</th>
<th>PO$_4^{3-}$ (mM/mm$^2$) mean ± SD</th>
<th>Ca$^{2+}$/PO$_4^{3-}$ Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control (PS)</td>
<td>10</td>
<td>14.12±1.52$^B$</td>
<td>2.10±0.28$^A$</td>
<td>6.72</td>
</tr>
<tr>
<td>PS+DR9-RR14</td>
<td>10</td>
<td>16.77±1.88$^A$</td>
<td>2.49±0.36$^A$</td>
<td>6.74</td>
</tr>
<tr>
<td>PS+DR9-DR9</td>
<td>10</td>
<td>9.93±1.58$^C$</td>
<td>1.70±0.44$^B$</td>
<td>5.84</td>
</tr>
<tr>
<td>PS +DR9</td>
<td>10</td>
<td>9.17±1.77$^C$</td>
<td>1.60±0.67$^B$</td>
<td>5.73</td>
</tr>
</tbody>
</table>
3.3.2  Ca\textsuperscript{2+} and PO\textsubscript{4}\textsuperscript{3-} demineralization protection with PS coated + peptide construct coated

The PS coated + DR9-RR14 group and control group (only PS coated) showed the highest levels of calcium and phosphate demineralization. In terms of calcium loss from the enamel sections, it was significantly different from each other. Compared to control group, both PS coated + DR9 and PS coated + DR9-DR9 groups clearly showed statistically significant reduction in the demineralization of the calcium from the enamel sections. Similarly, in comparison to PS coated + DR9-RR14 group, both PS coated + DR9 and PS coated + DR9-DR9 groups, clearly provided statistically significant protection against enamel demineralization of calcium. This imply that both these peptides, DR9 and DR9-DR9 could provide protection against calcium demineralization in comparison to both control as well as PS coated + DR9-RR14 groups. Even though both PS coated + DR9 and PS coated + DR9-DR9 groups did provide protection against demineralization of calcium, but the level of protection between these two groups was not statistically significant.

The PS coated + DR9-RR14 group and control group (PS coated) showed the highest levels of demineralization in terms of phosphate loss from the enamel sections, but were non-significantly different from each other. It means DR9-RR14 was no better than PS in protecting against phosphate mineralization from the enamel surface. Compared to control group, both PS coated + DR9 and PS coated + DR9-DR9 groups showed statistically significant reduction in the demineralization of the phosphate from the enamel sections. Similarly, in comparison to PS coated + DR9-RR14 group, both PS coated + DR9 and PS coated + DR9-DR9 groups, provided statistically significant protection against enamel demineralization of phosphate. This imply that both these peptides DR9 and DR9-DR9 could provide same level of protection against phosphate demineralization in comparison to control as well as PS coated + DR9-RR14 groups. Even though both PS coated + DR9 and PS coated + DR9-DR9 groups did provide protection against demineralization of phosphate, but the level of protection between these two groups was not statistically significant.
The calcium and phosphate demineralization results in terms of calcium and phosphate loss as well demineralization protection showed a similar trend. Overall, calcium and phosphate demineralization assay showed that compared to PS (control), PS+DR9 (Ca 9.17 ± 1.78; PO₄ 1.60 ± 0.67) and PS+DR9-DR9 (Ca 9.93 ± 1.58; PO₄ 1.70 ± 0.44) provided better protection, even though the DR9-DR9 and DR9 were non-significant from each other.

The overall trend was that, for calcium and phosphate demineralization, DR9 and DR9-DR9 peptides exhibited significant protection when compared to control PS group (Table 3-3). Under the current experimental conditions, the tandem duplication of DR9 neither did help in the augmentation of the demineralization protection function against calcium and phosphate losses from enamel surface, nor it provided any advantage, when the peptide construct coated the PS pellicle on the enamel surface.

For each of the tested group, the Ca²⁺ and PO₄³⁻ ratio was calculated. Among the groups, a % variation of less than 10 percent was observed. The lowest ratio was that of PS coated + DR9 group (5.73) while PS coated + DR9-RR14 group showed the highest ratio of 6.74.

3.4 Discussion

In this study we demonstrated, that when bound directly to the enamel surface, at lower concentration (nmol), the synthetic peptide constructs, did not provide any significant demineralization protection advantage over the control. It was contrary to the results, our group got in previous studies by either using full length histatin peptides or even using the peptide constructs at higher concentration (µg/ml) (Siqueira, et al. 2010; Tayebeh 2015 (MSc Thesis research); Tayebeh et al. 2017).

Besides tandem duplication of the functional domains, construction of salivary pellicle with augmented functionality is another potentially useful approach via hybrid molecule preparation. Tandem functional domain duplication helps in the enhancement of single functional property, the hybrid construct approach results in combining two or more different functional features in a single construct, displaying multiple functionalities. The
hybrid approach is promising strategy for novel pellicle constructs, as some of the pellicle peptides exhibit unique functionality like antimicrobial properties and or hydroxyapatite crystal inhibition properties, while other peptides display a high binding affinity for hydroxyapatite, (Vuksavljevic et al. 2011; Siqueira et al. 2012). Statherin-osteopontin (Raj et al. 1990) and cystatin-histatin (Bobek et al. 1993) hybrid constructs are best examples of such synthetic bi-functionality.

Natural functional domain of statherin, DR9, was tandem duplicated to construct DR9-DR9 as well as synthetically joined to a functional domain of histatin 3, RR14, to construct DR9-RR14 hybrid construct. Our in vitro results from this study demonstrated that at very low concentration of all constructs (nmol/disc), when peptide constructs directly coated the enamel surface, they were unable to provide any protection against acid induced demineralization as the functional differences were non-significant in comparison to control (PS only coating). Similar kind of observations were recorded by Kielbassa et al. (2005), with albumin and casein at lower concentration in terms of demineralization protection of bovine enamel. Kosoric et al. (2010) in another study demonstrated BSA concentration dependent modulation in the rate of hydroxyapatite demineralization.

This failure of peptide constructs to protect against demineralization, could be attributed to thin layer of peptide coating on enamel surface, formed as a result of monolayer formation on enamel surface because of low concentration (nmol) of the peptide. Recent studies by Tayebeh (2015; M.Sc. thesis research; Teyebeh, et al. 2017), have however, shown that all the peptides were able to provide significant demineralization protection to enamel surface against acid induced erosion, when peptides were used at higher concentration (µg/ml), possibly leading to formation of multi-layer peptide pellicle on enamel surface, that was able to not only neutralize the acid in the near vicinity of the enamel surface but also acted as semipermeable barrier, thereby further reducing the enamel demineralization.

Siqueira et al. (2010), in another study demonstrated that full length histatins provided demineralization protection to enamel surface. This protection could be attributed to high
concentration of full length peptides (mg/ml) used in that study, that might have resulted in multilayer pellicle on enamel surface, leading to acid neutralization and being semipermeable in nature, leading to demineralization protection against acid injury.

In case of DR9 and DR9-DR9, they carried a net negative charge due to presence of 2 and 4 phosphate groups respectively, which resulted in tight binding to the positively charged enamel surface. But during the acid challenge, as the pH of demineralization buffer was 4.5, which was above the pI of DR9 and DR9-DR9, it is very likely that, this might have resulted in further net negative charge on the adsorbed peptides and hence resulting in their gradual desorption from the enamel surface due to charge repulsion induced weakening of the interaction between peptide and enamel surface, leading to slight demineralization over a period of time, even though it was statistically non-significant compared to PS pellicle coating of enamel surface.

Our in vitro results from further experiments in this study demonstrated that even at very low concentration of all constructs (nmol), when peptide constructs coated the pre-coated PS pellicle enamel surface, they were able to provide some level of protection against acid induced demineralization, as the functional differences were significant in comparison to control (PS coating). Both DR9 and DR9-DR9 provided calcium and phosphate demineralization protection compared to control. DR9-RR14 did not provide any protection against calcium and phosphate demineralization. This failure to protect against demineralization by DR9-RR14 peptide could be attributed to thin layer of peptide coating on enamel surface, formed as a result of monolayer formation because of very low (nmol) peptide concentration, which was not efficient in providing a buffering action to neutralize the acidic demineralization solution as well as having very little or no semipermeable control of the pellicle in preventing the acid from coming in direct contact with the enamel surface.

Kosoric et al. (2010), suggested that BSA modifies the hydroxyapatite demineralization kinetics either by modulation of demineralization solution properties or by surface energy of hydroxyapatite. In a previous study, Juriaanse et al. (1981) demonstrated that proline rich proteins after adsorption to bovine enamel resisted the calcium and phosphate
demineralization thereby suggesting that PRP may provide protection against demineralization. We can speculate that at such lower concentration (nmol) of peptides, the charge differences due to number of phosphorylated sites, at 2nd & 3rd amino acid residues in DR9 and at 2nd, 3rd, 10th, & 11th amino acid residues in DR9-DR9 did not have much influence to provide demineralization protection. As observed in previous studies, the presence or the number of phosphorylation sites can significantly influence the adsorption of these peptide constructs to the hydroxyapatite and the process of protection against enamel demineralization as well as growth inhibition of calcium phosphate crystal under in vitro conditions, when used at high concentration. (Siqueira et al. 2010; Hunter et al. 2009; Hunter 2013; Xiao et al. 2010; Xiao et al. 2015). Apart from phosphorylation, DR9-DR9 has the lowest pI when compared to DR9 in pH 6.8, the physiological salivary pH. It can facilitate the adsorption of this peptide on to PS pellicle surface, which in turn can provide protection against demineralization (Moreno et al. 1982). It was found to be true in presence of multicomponent PS pellicle in this study, where DR9-DR9 could provide better protection against demineralization of both calcium and phosphate in comparison to control parotid saliva.

Based on the limitation of this study, it was found that the protective behavior of individual peptides was different when they were used directly to coat the enamel surface as probably at that low concentration, none of the peptide could provide any protective advantage in comparison to control parotid saliva coating.

On the other hand, DR9 and DR9-DR9 both were able to provide significant protection against demineralization of the pre-coated PS pellicle enamel sections in comparison to control PS coating, simulating the environmental conditions similar to that of in vivo formed acquired enamel pellicle. For instance, some studies have demonstrated that in the presence of other proteins the adsorption behavior of histatins changes (Yin et al. 2006). Cheaib and Lussi (2011), in other study has shown that when mixed together, casein and mucin displayed enhancement in the erosion-inhibition properties of the AEP.
3.5 Conclusion

This is the first study, through which we try to address the functional effect of those newly constructed peptides in such multi-component protein film environment. However, this study represents an initial step in the direction of getting deep insights into the possible role of these peptides in enamel protection. The basic knowledge gained from this study may provide a fundamental platform in future for the development of bioinspired peptides from histatin and statherin for therapeutic use against dental erosion and dental caries.
References


4 Modulation of AEP by incorporation of constructed peptides

4.1 Introduction

Previous work discovered that mature AEP proteome consists of around 130 different proteins, ranging in size from >250 kDa–<5 kDa, of which about 50% are small molecular weight peptides (Siqueira et al. 2007, 2009) most of them without identified biological function yet. Based on the possible role of these proteins in AEP development, they have been classified into 3 major groups; Ca binding proteins, PO₄ binding proteins and protein interacting with other salivary proteins. AEP proteins have also been classified according to their putative biological functions; inflammatory responses, immune defense, antimicrobial activity & re-mineralization capacity (Siqueira et al. 2007).

The biomolecular events in and outside the living systems, that leads to the formation of protein–protein and other biomolecule complexes involves ionic, hydrogen bonding, hydrophobic and other non-covalent weak interactions, leading to conformational changes in the proteins, resulting in the up or down regulation of their functions (Cserhati and Szogyi 1995). Due to charge in the protein molecules because of phosphorylation, as well as the presence of acidic and basic amino acid side chains, these salivary proteins interact to a different extent with mucosal as well as enamel surfaces, apart from interacting among themselves in the oral cavity (Yin et al. 2006). All these protein interactions modify (enhance or diminish) their functional properties as well as impact their stability in the oral cavity.

Cheaib et al. (2015) studied the impact of pellicle modification on early colonizers and demonstrated that casein, mucin and a casein-mucin mixture bring about pellicle modification, resulting in the significant modulation in adhesion behavior of early colonizers on the enamel pellicle.
In an earlier study, Cheaib and Lussi (2011), demonstrated that pellicle modulation by casein and a casein-mucin mixture, augmented the enamel demineralization protection capability of acquired enamel pellicle, where a mixture of casein-mucin as pellicle modulator displayed higher demineralization protection in comparison to casein alone.

Researchers in different studies (Danielsson et al. 2009; Malkoski et al. 2001; Vacca-Smith et al. 1994), found that bovine α-, β- and κ-caseins (40 kDa glycoprotein-containing fraction of κ-caseins inhibited S. mutans adhesion to saliva-coated hydroxyapatite.

In other studies, ovalbumin has been shown to reduce the in vitro acidic solution induced hydroxyapatite demineralization similar to that of casein (Hemmingway et al. 2010, 2008).

Hannig et al. (2009) found that Mucin (MUC5B), present in the basal layer of the acquired enamel pellicle, is retained on enamel surface even after 2 hours of exposure to citric acid, and concluded that it is one of the contributors to the protective properties of the pellicle.

Hannig and Joiner (2006) observed that pellicle ultrastructure changes after exposure to the acidic environment. They found that after acid exposure, the global outer layer of the pellicle gets removed, while the basal layer persists.

Hannig and Hannig (2009) in another study propounded a pellicle formation model that was based on hydrophobic and ionic interactions in addition to Van der Waals forces could ultimately result in a protein layer consisting of heterotypic complexes.

In another study, Nieuw et al. (1987), demonstrated that a 72 hour old in vitro mucin pellicle from the whole saliva provided 100 % protection against erosion under citric acid challenge.

Based on the previous research from our group, two small peptides have been derived from statherin. They contain a natural N-terminal sequence of 9 amino acid residues domain as a single unit (DR9) that has the strong inhibitory property against
hydroxyapatite crystallization and DR9-DR9 as a tandem duplicate repeat from statherin so as to artificially enhance and mimic the protein evolution (Siqueira and Oppenheim 2009; Xiao et al. 2015). Apart from that, a small domain RR14 has been derived from histatin 3, that contain 14 amino acid residues, which has got very strong antimicrobial activity (Oppenheim et al. 2012). This antimicrobial histatin domain RR14 has been synthetically combined with the statherin DR9 domain to construct a histatin-statherin hybrid domain DR9-RR14 so that the antimicrobial properties of RR14 are combined with that of hydroxyapatite crystal inhibition properties of DR9 in one construct.

4.2 Material and methods

4.2.1 Cleaning and acid etching of hydroxyapatite discs

Near enamel hydroxyapatite (HA) discs (Himed, USA) were cleaned by water bath sonication for 10 minutes once in distilled water and for 10 minutes once in 100% acetonitrile. After cleaning procedure, discs were rinsed with distilled water to remove residual acetonitrile solution. Then the discs were acid etched by submerging in 32% phosphoric acid for 30 minutes (based on pilot experiments, where previously, the acid treatment kinetics was done to standardize the time of acid treatment). After 30 minutes, the acid was removed and washed under distilled water for 1 minute. The excess water from disc surface was removed by touching the tissue paper gently to the edges of the discs and discs were dried at room temperature for 1 hour before starting the experiments.

4.2.2 Saliva and peptide coating and pellicle formation on the discs

For the first set of experiments, HA discs were incubated for 2 hours at 37°C with parotid saliva (10 ug salivary proteins/disc/well) in a total volume of 500 µl for control or with peptide solution (20 nmol/disc/well) in a total volume of 500 µl for pellicle formation in 24 well culture plates with 4 discs/treatment. After 2 hours of incubation and pellicle formation, the unbound peptide was removed from the discs by washing for 10 second in distilled water.
The pre-coated peptide discs were incubated for additional 2 hours at 37°C with 500 µl parotid saliva (10 µg salivary proteins/disc/well) for salivary pellicle formation. After 2 hours of additional incubation and pellicle formation. The discs were again briefly rinsed with distilled water for 10 second to remove any unbound saliva from disc surface.

For the second set of experiments, HA discs were incubated for 2 hours at 37°C with parotid saliva (10 µg salivary proteins/disk/well) in a total volume of 500 µl for pellicle formation in 24 well culture plates with 4 discs/treatment. After 2 hours of incubation and pellicle formation, the parotid saliva was removed from the discs and discs were briefly rinsed for 10 second in distilled water to remove unbound saliva from disc surfaces. Then these discs were incubated for additional 2 hours at 37°C in peptide solutions (DR9/DR9-DR9/DR9-RR14; 20 nmol/disc/well) in a total volume of 500 µl/disc for pellicle formation. After pellicle formation, the peptide solution was removed from the discs and rinsed for 10 second in distilled water to remove unbound peptide from disc surfaces. After this step, these discs were once again incubated with (10 µg salivary proteins/disk/well) for additional 2 hours at 37°C. After incubation, the parotid saliva was removed from the discs and discs were briefly rinsed for 10 second in distilled water to remove unbound saliva from disc surfaces.

### 4.3 Parotid salivary pellicle harvesting and protein estimation

Water bath sonication was used to harvest pellicle in 500 µl buffer B (80% acetonitrile, 0.1 % trifluoroacetic acid and 19.9% water) following 1 minute sonication. This procedure was repeated 3 times. After pellicle harvesting, the solution was centrifuged at 4°C at 10,000 x g for 10 minutes to remove hydroxyapatite residue. The supernatant pellicle solution was dried overnight in the speedvac. Next morning, the dried pellicle material was re-suspended in distilled water and used for protein estimation through micro-BCA assay using bovine serum albumin as protein standards.
4.4 Mass spectrometric identification of pellicle proteins

4.4.1 Trypsin digestion and desalting procedure of pellicle proteins

Ten µg equivalent of pellicle protein was dried and resuspended in 50 µl of denaturation solution (4 M urea, 10mM DTT, and 50mM NH4 HCO3, pH 7.8,) and incubated at room temperature for 1 hour. After incubation, the solution was diluted with the addition of 150 µL of 50 mM NH4 HCO3, pH 7.8. Afterward, the pellicle proteins were digested with 5% (w/w) trypsin for 24 hours at 37°C. After digestion, the pellicle digested material was again dried and desalted using zip-tip kit (EMD Millipore, Fisher Scientific). The purified digested sample was dried overnight and submitted for nLC-MS. In MS, each treatment was run 3 times as technical replicates. This set of experiments was repeated on three independent occasions.

4.4.2 MS Analysis

Mass spectrometric analyses were carried out with a LTQ-Velos (Thermo Scientific, San Jose, CA, USA), which allows in-line LC with the capillary-fused silica C18 column (column length 10 cm, column id 75 µm, 3 µm spherical beads, and 100 Å pore size) linked to mass spectrometer using an ESI. All samples were dried by speedVac dryer and re-suspended in 97.5% H2 O/2.4% ACN/0.1% formic acid and then subjected to RP LC-ESI-MS. The nanoflow RP-HPLC conditions were linear 65-min gradient ranging from 5 to 55% of solvent B (97.5% ACN, 0.1% formic acid) at a flow rate of 300nL/min with a maximum pressure of 280 bars. Electrospray voltage and the temperature of the ion-transfer capillary were 1.8 kV and 250°C, respectively. The resultant MS spectra were searched against human protein databases (Swiss-Prot and TrEMBL, Swiss Institute of Bioinformatics, Geneva, Switzerland, http://ca.expasy.org/sprot/) using SEQUEST and Percolator algorithms in Proteome Discoverer 1.3 software (Thermo Scientific). Search results were filtered for a False Discovery Rate of 1%, employing a decoy search strategy utilizing a reverse database.
4.5 Results

4.5.1 Proteome profile of peptide-PSPL

In first set of experiments, 4 disc/group were used with the following experimental plan:

1) Parotid saliva only, (Control) (PSPL)

2) DR9 peptide coating, followed by parotid saliva, (DR9-PSPL)

3) DR9-DR9 peptide coating, followed by parotid saliva, (DR9-DR9-PSPL), and

4) DR9-RR14 peptide coating, followed by parotid saliva, (DR9-RR14-PSPL).

Only proteins common in at least two independent experiments out of three independent repeat experiments done on separate days were considered for the further analysis. A total of 139 proteins were present in all the treatments taken together. The highest number of proteins were found in group DR9-RR14-PSPL, followed by DR9-DR9-PSPL group, which was closely followed by PSPL (control) group. Lowest number of proteins were found in group DR9-PSPL. Of the 47 proteins, 28 (59.6%) were exclusive to DR9-RR14-PSPL. Out of 34 proteins, 16 (47.1%) were exclusive to PSPL (control). For DR9-DR9-PSPL, of the 39 proteins, 20 (51.3%) were specific to this group only. Similarly, out of 19 proteins, 9 (47.4%) were specific to DR9-PSPL. Out of 139 total protein, 7 proteins (5%) were common across all groups. (Table 4-1; Figure 4-1)

**Table 4-1:** Common proteins among all the groups of peptide coated disc pellicle.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B/ Proline-rich peptide P-B/Proline-rich protein 3</td>
</tr>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6/Carbonic anhydrase VI/ Carbonic dehydratase VI/ CA-VI</td>
</tr>
<tr>
<td>P02812</td>
<td>Basic salivary proline-rich protein 2/Salivary proline-rich protein/Con1 glycoprotein</td>
</tr>
<tr>
<td>P01833</td>
<td>Polymeric immunoglobulin receptor (PIgR)/ Hepatocellular carcinoma-associated protein (TB6)</td>
</tr>
<tr>
<td>G3CIG0</td>
<td>MUC19 variant 12</td>
</tr>
<tr>
<td>Q9UKN1</td>
<td>Mucin-12</td>
</tr>
<tr>
<td>Q12955</td>
<td>Ankyrin-3</td>
</tr>
</tbody>
</table>
4.5.2 Most abundant proteins from peptide-PSPL

Based on the ion abundance score count, the 10 most abundant proteins were selected from each group of peptide-PSPL modulation experiments. (Table 4-2, 4-3, 4-4, & 4-5). In PSPL (control), the relative ion abundance score ranged from a highest of 925.17 for submaxillary gland androgen-regulated protein 3B to a lowest of 21.50 for Ig alpha-2 chain region protein.

Table 4-2: Most abundant proteins based on relative ion abundance score from control group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>925.17</td>
</tr>
<tr>
<td>P02808</td>
<td>Statherin</td>
<td>260.59</td>
</tr>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6</td>
<td>215.62</td>
</tr>
<tr>
<td>Q6NSB3</td>
<td>Alpha-amylase (Fragment)</td>
<td>175.35</td>
</tr>
<tr>
<td>Q8WX17</td>
<td>Mucin-16</td>
<td>77.81</td>
</tr>
<tr>
<td>P01833</td>
<td>Polymeric immunoglobulin receptor</td>
<td>72.27</td>
</tr>
<tr>
<td>P02812</td>
<td>Basic salivary proline-rich protein 2</td>
<td>67.13</td>
</tr>
<tr>
<td>Q7Z5P9</td>
<td>MUC19 variant 12</td>
<td>39.51</td>
</tr>
<tr>
<td>Q96Q06</td>
<td>Perilipin-4</td>
<td>30.04</td>
</tr>
</tbody>
</table>
In DR9-PSPL group, the relative ion abundance score ranged from a highest of 895.56 for submaxillary gland androgen-regulated protein 3B to a lowest of 13.67 for Ankyrin-3 protein.

**Table 4-3:** Most abundant proteins based on relative ion abundance score from DR9-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>895.56</td>
</tr>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6</td>
<td>288.18</td>
</tr>
<tr>
<td>P02812</td>
<td>Basic salivary proline-rich protein 2</td>
<td>85.23</td>
</tr>
<tr>
<td>P01833</td>
<td>Polymeric immunoglobulin receptor</td>
<td>61.98</td>
</tr>
<tr>
<td>C0JYZ2</td>
<td>Titin</td>
<td>23.88</td>
</tr>
<tr>
<td>E9PAV3</td>
<td>Nascent polypeptide-associated complex subunit alpha, muscle-specific form</td>
<td>22.60</td>
</tr>
<tr>
<td>Q7Z5P9</td>
<td>MUC19 variant 12</td>
<td>19.21</td>
</tr>
<tr>
<td>B4DSK7</td>
<td>cDNA FLJ50196, highly similar to Peroxisome proliferator-activated receptor-binding protein</td>
<td>16.99</td>
</tr>
<tr>
<td>Q9UKN1</td>
<td>Mucin-12</td>
<td>13.97</td>
</tr>
<tr>
<td>Q12955</td>
<td>Ankyrin-3</td>
<td>13.67</td>
</tr>
</tbody>
</table>

In DR9-DR9-PSPL group, the relative ion abundance score ranged from a highest of 766.95 for submaxillary gland androgen-regulated protein 3B to a lowest of 42.29 for statherin.

**Table 4-4:** Most abundant proteins based on relative ion abundance score from DR9-DR9-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>766.95</td>
</tr>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6</td>
<td>389.1</td>
</tr>
<tr>
<td>Q6NSB3</td>
<td>Alpha-amylase</td>
<td>352.09</td>
</tr>
<tr>
<td>Q8WXI7</td>
<td>Mucin-16</td>
<td>94.32</td>
</tr>
<tr>
<td>P01877</td>
<td>Ig alpha-2 chain C region</td>
<td>76.47</td>
</tr>
<tr>
<td>P01833</td>
<td>Polymeric immunoglobulin receptor</td>
<td>72.38</td>
</tr>
<tr>
<td>P02812</td>
<td>Basic salivary proline-rich protein 2</td>
<td>68.36</td>
</tr>
<tr>
<td>H6VRF8</td>
<td>Keratin 1</td>
<td>66.82</td>
</tr>
<tr>
<td>P22079</td>
<td>Lactoperoxidase</td>
<td>45.26</td>
</tr>
<tr>
<td>P02808</td>
<td>Statherin</td>
<td>42.29</td>
</tr>
</tbody>
</table>
For DR9-RR14-PSPL group, the relative ion abundance score ranged from a highest of 359.14 for carbonic anhydrase 6 to a lowest of 26.25 for Ankyrin-3.

**Table 4-5:** Most abundant proteins based on relative ion abundance score from DR9-RR14-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6</td>
<td>359.14</td>
</tr>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>278.92</td>
</tr>
<tr>
<td>Q6NSB3</td>
<td>Alpha-amylase</td>
<td>122.6</td>
</tr>
<tr>
<td>P01833</td>
<td>Polymeric immunoglobulin receptor</td>
<td>47.57</td>
</tr>
<tr>
<td>Q7Z5P9</td>
<td>MUC19 variant 12</td>
<td>44.2</td>
</tr>
<tr>
<td>Q96DA0</td>
<td>Zymogen granule protein 16 homolog B</td>
<td>39.58</td>
</tr>
<tr>
<td>P22079</td>
<td>Lactoperoxidase</td>
<td>33.7</td>
</tr>
<tr>
<td>P35527</td>
<td>Keratin, type I cytoskeletal 9</td>
<td>33.65</td>
</tr>
<tr>
<td>H6VRF8</td>
<td>Keratin 1</td>
<td>31.83</td>
</tr>
<tr>
<td>Q12955</td>
<td>Ankyrin-3</td>
<td>26.25</td>
</tr>
</tbody>
</table>

When the identified proteins (139) from all the groups (PSPL/ DR9-PSPL/ DR9-DR9-PSPL/ DR9-RR14-PSPL) were compared, it was found that there were 7 proteins, that were common across all the groups, but with differential ion abundance scores.

**Table 4-6:** Values of relative ion abundance score obtained in all peptide-PS groups.

<table>
<thead>
<tr>
<th>Common proteins</th>
<th>PSPL (Control)</th>
<th>DR9-PSPL</th>
<th>DR9-DR9-PSPL</th>
<th>DR9-RR14-PSPL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>895.56</td>
<td>925.17</td>
<td>766.95</td>
<td>278.92</td>
</tr>
<tr>
<td>Carbonic anhydrase 6</td>
<td>288.18</td>
<td>215.62</td>
<td>389.1</td>
<td>359.14</td>
</tr>
<tr>
<td>Basic salivary proline-rich protein 2</td>
<td>85.23</td>
<td>67.13</td>
<td>68.36</td>
<td>24.3</td>
</tr>
<tr>
<td>Polymeric immunoglobulin receptor</td>
<td>61.98</td>
<td>36.83</td>
<td>72.38</td>
<td>47.57</td>
</tr>
<tr>
<td>MUC19 variant 12</td>
<td>19.21</td>
<td>39.51</td>
<td>33.29</td>
<td>44.2</td>
</tr>
<tr>
<td>Mucin-12</td>
<td>16.58</td>
<td>13.97</td>
<td>16.7</td>
<td>16.42</td>
</tr>
<tr>
<td>Ankyrin-3</td>
<td>14.56</td>
<td>13.67</td>
<td>16.31</td>
<td>26.25</td>
</tr>
</tbody>
</table>

The relative abundance data of the common proteins, across all the groups, clearly showed that the protein profile as well as protein abundance was modulated by the
peptide coatings of the disc surface when compared to control group. For example, submaxillary gland androgen-regulated protein 3B, the relative abundance score for control group was 895.56 while for DR9-PSPL group, the value was 925.17. In DR9-DR9-PSPL group the value obtained for submaxillary gland androgen-regulated protein 3B was less than that of control group (766.95). Relative low abundance was also observed with DR9-RR14-PSPL group (278.92).

For carbonic anhydrase 6 protein, the relative ion abundance score for control group was 288.18, whereas for DR9 group it was lowest and less than control (215.62; 74.8%), but both in DR9-DR9-PSPL and DR9-RR14-PSPL groups, it was highest (DR9-DR9) and more than control group (389.1; 135%) and (359.14; 124.6%), respectively.

In case of basic salivary proline-rich protein 2, the relative ion abundance scores for all the groups were less than the control group. It was 85.23 in control group, whereas for DR9-PSPL and DR9-DR9-PSPL groups, it was almost similar but less than control group (67.13; 78.8%), (68.36; 80.2%), respectively. The relative ion score was lowest and less than control group in case of DR9-RR14-PSPL group (24.3; 28.5%).

For polymeric immunoglobulin receptor (PIgR), the relative ion abundance score was 61.98 in control group. For DR9-DR9-PSPL group, it was highest and more than that of control (72.38; 116.8%), while for DR9-PSPL (lowest, 36.83; 59.4%) and DR9-RR14-PSPL (47.57; 76.8%) groups, it was lower than that of control group relative ion abundance score, respectively.

In case of mucin-19 variant 12 protein, the relative ion abundance score for control group was 19.21. For all the peptide coated groups, the relative ion abundance score was more than the control with DR9-RR14-PSPL group having the highest score (44.2; 230%) in comparison to the control group, followed by DR9-PSPL group (39.51; 205.7%) and DR9-DR9-PSPL group (33.29; 173.3%) in comparison to control group, respectively.

For mucin-12, the relative ion abundance score for control group was 16.58. For DR9-PSPL group, it was less than the control group (13.97; 84.3%). In case of DR9-DR9-PSPL group, the relative ion abundance score was higher than control group (16.7;
100.7%), while DR9-RR14-PSPL group ion abundance score was lower than the control group (16.42; 99 %), respectively.

Table 4-7: Proteome profile of control (PSPL) group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q96Q06</td>
<td>Perilipin-4</td>
<td>30.04</td>
</tr>
<tr>
<td>P01877</td>
<td>Ig alpha-2 chain C region</td>
<td>21.50</td>
</tr>
<tr>
<td>Q5HYC2</td>
<td>Uncharacterized protein KIAA2026</td>
<td>20.84</td>
</tr>
<tr>
<td>Q9Y6V0</td>
<td>Protein piccolo</td>
<td>20.64</td>
</tr>
<tr>
<td>P35527</td>
<td>Keratin, type I cytoskeletal 9</td>
<td>19.25</td>
</tr>
<tr>
<td>P08493</td>
<td>Matrix Gla protein</td>
<td>18.21</td>
</tr>
<tr>
<td>Q9UKN1</td>
<td>Mucin-12</td>
<td>16.58</td>
</tr>
<tr>
<td>Q12955</td>
<td>Ankyrin-3</td>
<td>14.56</td>
</tr>
<tr>
<td>Q9NR09</td>
<td>Baculoviral IAP repeat-containing protein 6</td>
<td>14.42</td>
</tr>
<tr>
<td>Q07954</td>
<td>Prolow-density lipoprotein receptor-related protein 1</td>
<td>13.15</td>
</tr>
<tr>
<td>O75592</td>
<td>E3 ubiquitin-protein ligase MYCBP2</td>
<td>11.74</td>
</tr>
<tr>
<td>Q8WWA1</td>
<td>Transmembrane protein 40</td>
<td>11.31</td>
</tr>
<tr>
<td>Q09666</td>
<td>Neuroblast differentiation-associated protein</td>
<td>10.98</td>
</tr>
<tr>
<td>Q15751</td>
<td>Probable E3 ubiquitin-protein ligase HERC1</td>
<td>10.19</td>
</tr>
<tr>
<td>Q15772</td>
<td>Striated muscle preferentially expressed protein kinase</td>
<td>9.94</td>
</tr>
<tr>
<td>Q75MN6</td>
<td>Putative uncharacterized protein MLL3</td>
<td>9.84</td>
</tr>
<tr>
<td>Q6W4X9</td>
<td>Mucin-6</td>
<td>9.70</td>
</tr>
<tr>
<td>A1YBP1</td>
<td>Breast and ovarian cancer susceptibility protein 2 truncated variant</td>
<td>9.61</td>
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<tr>
<td>L0R8C7</td>
<td>Alternative protein PRIC285</td>
<td>7.60</td>
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<tr>
<td>Q86XX4</td>
<td>Extracellular matrix protein FRAS1</td>
<td>7.14</td>
</tr>
<tr>
<td>Q9P0K0</td>
<td>Putative zinc finger protein</td>
<td>7.06</td>
</tr>
<tr>
<td>A0A087WU78</td>
<td>Nance-Horan syndrome protein</td>
<td>7.02</td>
</tr>
<tr>
<td>Q5CZC0</td>
<td>Fibrous sheath-interacting protein 2</td>
<td>6.63</td>
</tr>
<tr>
<td>O75443</td>
<td>Alpha-pectorin</td>
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</tr>
<tr>
<td>Q59FP8</td>
<td>Neogenin</td>
<td>6.33</td>
</tr>
<tr>
<td>Q5D862</td>
<td>Filaggrin-2</td>
<td>5.71</td>
</tr>
<tr>
<td>Accession Number</td>
<td>Protein Name</td>
<td>Ion Score</td>
</tr>
<tr>
<td>------------------</td>
<td>--------------------------------------------------------</td>
<td>-----------</td>
</tr>
<tr>
<td>P02808</td>
<td>Statherin</td>
<td>42.29</td>
</tr>
<tr>
<td>Q9Y5I3</td>
<td>Protocadherin alpha-1</td>
<td>38.74</td>
</tr>
<tr>
<td>P35527</td>
<td>Keratin, type I cytoskeletal 9</td>
<td>38</td>
</tr>
<tr>
<td>G3CIG0</td>
<td>MUC19 variant 12</td>
<td>33.29</td>
</tr>
<tr>
<td>Q5T4S7</td>
<td>E3 ubiquitin-protein ligase UBR4</td>
<td>29.78</td>
</tr>
<tr>
<td>A0A0C4DGN4</td>
<td>Zymogen granule protein 16 homolog B</td>
<td>24.82</td>
</tr>
<tr>
<td>B7ZA42</td>
<td>cDNA, FLJ79056</td>
<td>20.49</td>
</tr>
<tr>
<td>Q96Q06</td>
<td>Perilipin-4</td>
<td>19.21</td>
</tr>
<tr>
<td>Q9UKN1</td>
<td>Mucin-12</td>
<td>16.7</td>
</tr>
<tr>
<td>Q14676</td>
<td>Mediator of DNA damage checkpoint protein 1</td>
<td>16.41</td>
</tr>
<tr>
<td>Q12955</td>
<td>Ankyrin-3</td>
<td>16.31</td>
</tr>
<tr>
<td>Q9Y6V0</td>
<td>Protein piccolo</td>
<td>14.35</td>
</tr>
<tr>
<td>E9PAV3</td>
<td>Nascent polyepptide-associated complex subunit alpha, muscle-specific form</td>
<td>14.13</td>
</tr>
<tr>
<td>Q86VD1</td>
<td>MORC family CW-type zinc finger protein 1</td>
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<td>H0YEF4</td>
<td>Palmitoyltransferase</td>
<td>13.17</td>
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<td>I0B0K5</td>
<td>Truncated profilaggrin</td>
<td>13.05</td>
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<tr>
<td>Q5D862</td>
<td>Filaggrin-2</td>
<td>12.86</td>
</tr>
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<td>Q5QP82</td>
<td>DDB1- and CUL4-associated factor 10</td>
<td>12.4</td>
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<td>cDNA FLJ76742, highly similar to Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2</td>
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<td>Uncharacterized protein DKFZp434B061</td>
<td>10.08</td>
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<tr>
<td>A6NKB5</td>
<td>Pecanex-like protein 2</td>
<td>9.67</td>
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<tr>
<td>F8W6X9</td>
<td>Protein sidekick-1</td>
<td>9.22</td>
</tr>
<tr>
<td>Q8WXG9</td>
<td>G-protein coupled receptor 98</td>
<td>7.19</td>
</tr>
<tr>
<td>Q02388</td>
<td>Collagen alpha-1(VII) chain</td>
<td>6.93</td>
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<tr>
<td>H0Y3R4</td>
<td>SET domain-containing protein 5</td>
<td>6.8</td>
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<td>B4DF20</td>
<td>cDNA FLJ58172, highly similar to Zinc finger protein 238</td>
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<td>L8E7G9</td>
<td>Alternative protein ZNF74</td>
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<tr>
<td>E5RJ29</td>
<td>PH and SEC7 domain-containing protein 3</td>
<td>6.35</td>
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<tr>
<td>Q9NR48</td>
<td>Histone-lysine N-methyltransferase ASH1L</td>
<td>6.32</td>
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<tr>
<td>Q96L91</td>
<td>E1A-binding protein p400</td>
<td>5.71</td>
</tr>
</tbody>
</table>

**Table 4-8:** Proteome profile of DR9-DR9-PSPL group.
Table 4-9: Proteome profile of DR9-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q12955</td>
<td>Ankyrin-3</td>
<td>13.67</td>
</tr>
<tr>
<td>Q14333</td>
<td>Facioscapulohumeral muscular dystrophy</td>
<td>9.95</td>
</tr>
<tr>
<td>Q15772</td>
<td>Striated muscle preferentially expressed protein kinase</td>
<td>9.48</td>
</tr>
<tr>
<td>Q10571</td>
<td>Probable tumor suppressor protein MN1</td>
<td>8.60</td>
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<tr>
<td>Q9H158</td>
<td>Protocadherin alpha-C1</td>
<td>8.45</td>
</tr>
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<td>B7Z7S7</td>
<td>cDNA FLJ60964, weakly similar to Homo sapiens dentin sialophosphoprotein, mRNA</td>
<td>7.35</td>
</tr>
<tr>
<td>B3KUS4</td>
<td>cDNA FLJ40508 fis, clone TESTI2045850, highly similar to AP-3 complex subunit beta-2</td>
<td>7.14</td>
</tr>
<tr>
<td>Q6W4X9</td>
<td>Mucin-6</td>
<td>6.79</td>
</tr>
<tr>
<td>E7EWQ5</td>
<td>Microtubule-associated serine/threonine-protein kinase 4</td>
<td>6.41</td>
</tr>
<tr>
<td>Q9C0F0</td>
<td>Putative Polycomb group protein ASXL3</td>
<td>6.39</td>
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</table>

Table 4-10a: Proteome profile of DR9-RR14-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q12955</td>
<td>Ankyrin-3</td>
<td>26.25</td>
</tr>
<tr>
<td>P02812</td>
<td>Basic salivary proline-rich protein 2</td>
<td>24.3</td>
</tr>
<tr>
<td>F8VV32</td>
<td>Lysozyme</td>
<td>22.08</td>
</tr>
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<td>P51587</td>
<td>Breast cancer type 2 susceptibility protein</td>
<td>18.95</td>
</tr>
<tr>
<td>Q9UGM3</td>
<td>Deleted in malignant brain tumors 1 protein</td>
<td>18.02</td>
</tr>
<tr>
<td>Q9UKN1</td>
<td>Mucin-12</td>
<td>16.42</td>
</tr>
<tr>
<td>Q96Q06</td>
<td>Perilipin-4</td>
<td>15.86</td>
</tr>
<tr>
<td>B3KW15</td>
<td>cDNA FLJ43124 fis, clone CTONG3004072</td>
<td>15.43</td>
</tr>
<tr>
<td>P13611</td>
<td>Versican core protein</td>
<td>13.7</td>
</tr>
<tr>
<td>P35908</td>
<td>Keratin, type II cytoskeletal 2 epidermal</td>
<td>13.69</td>
</tr>
<tr>
<td>Q5VST9</td>
<td>Obscurin</td>
<td>11.66</td>
</tr>
<tr>
<td>Q17R98</td>
<td>Zinc finger protein 827</td>
<td>10.99</td>
</tr>
<tr>
<td>Q86YZ3</td>
<td>Hornerin</td>
<td>9.88</td>
</tr>
<tr>
<td>O75592</td>
<td>E3 ubiquitin-protein ligase MYCBP2</td>
<td>9.59</td>
</tr>
<tr>
<td>E9PAV3</td>
<td>Nascent polypeptide-associated complex subunit α</td>
<td>9.27</td>
</tr>
<tr>
<td>Q6W4X9</td>
<td>Mucin-6</td>
<td>9.27</td>
</tr>
<tr>
<td>Q13535</td>
<td>Serine/threonine-protein kinase ATR</td>
<td>9.23</td>
</tr>
<tr>
<td>O95714</td>
<td>E3 ubiquitin-protein ligase HERC2</td>
<td>8.97</td>
</tr>
<tr>
<td>Q9H195</td>
<td>Mucin-3B</td>
<td>8.93</td>
</tr>
<tr>
<td>Q15751</td>
<td>Probable E3 ubiquitin-protein ligase HERC1</td>
<td>8.6</td>
</tr>
</tbody>
</table>
Table 4-10b: Proteome profile of DR9-RR14-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q9ULT8</td>
<td>E3 ubiquitin-protein ligase HECTD1</td>
<td>7.86</td>
</tr>
<tr>
<td>P13645</td>
<td>Keratin, type I cytoskeletal 10</td>
<td>7.79</td>
</tr>
<tr>
<td>Q9UQ35</td>
<td>Serine/arginine repetitive matrix protein 2</td>
<td>7.7</td>
</tr>
<tr>
<td>A0A024QZW7</td>
<td>Nucleoporin 153kDa, isoform CRA_a</td>
<td>7.36</td>
</tr>
<tr>
<td>A0A087WW06</td>
<td>Tetra-tricopeptide repeat protein 28</td>
<td>7.01</td>
</tr>
<tr>
<td>O15265</td>
<td>Ataxin-7</td>
<td>6.83</td>
</tr>
<tr>
<td>G3V3H7</td>
<td>A-kinase anchor protein 6</td>
<td>6.82</td>
</tr>
<tr>
<td>A6NM28</td>
<td>Zinc finger protein 92 homolog</td>
<td>6.72</td>
</tr>
<tr>
<td>Q49AJ0</td>
<td>Protein FAM135B</td>
<td>6.59</td>
</tr>
<tr>
<td>Q9UF83</td>
<td>Uncharacterized protein DKFZp434B061</td>
<td>6.57</td>
</tr>
<tr>
<td>H7BXI1</td>
<td>Extended synaptotagmin-2</td>
<td>6.49</td>
</tr>
<tr>
<td>B3KPG0</td>
<td>clone NT2R12007096, highly similar to Pleckstrin homology domain-containing family G member 1</td>
<td>6.01</td>
</tr>
<tr>
<td>P49792</td>
<td>E3 SUMO-protein ligase RanBP2</td>
<td>5.53</td>
</tr>
<tr>
<td>P08F94</td>
<td>Fibrocystin</td>
<td>5.47</td>
</tr>
<tr>
<td>P11137</td>
<td>Microtubule-associated protein 2</td>
<td>5.39</td>
</tr>
<tr>
<td>Q15772</td>
<td>Striated muscle preferentially expressed kinase</td>
<td>4.91</td>
</tr>
<tr>
<td>Q96SZ4</td>
<td>Zinc finger &amp; SCAN domain-containing protein 10</td>
<td>4.64</td>
</tr>
<tr>
<td>Q6PRX3</td>
<td>Transducin-like enhancer of split 3 splice variant 1</td>
<td>4.51</td>
</tr>
<tr>
<td>Q12955</td>
<td>Ankyrin-3</td>
<td>26.25</td>
</tr>
</tbody>
</table>

The proteome profiles of all 4 groups were clearly different from each other for majority of proteins. For instance, keratin, type I cytoskeletal 9 protein and alpha-amylase were common in control, DR9-DR9-PSPL and DR9-RR14-PSPL groups but completely absent from DR9-PSPL group. Most of the proteins were present in only two groups out of four. For example, mucin-12 and ankyrin-3 were present only in DR9-PSPL and DR9-RR14-PSPL groups and absent from control and DR9-DR9-PSPL groups. Similarly, Ig alpha-2 chain C region and statherin were present only in control and DR9-DR9-PSPL groups and absent from DR9-PSPL and DR9-RR14-PSPL groups. Likewise, zymogen granule protein 16 homolog B and keratin 1 were present in DR9-DR9-PSPL and DR9-RR14-PSPL groups, but absent from control and DR9-PSPL groups.
4.6 Peptide-PSPL proteome profile classification

Based on molecular functions, cellular components, biological functions, and protein class, the 139 pellicle proteins from Peptide-PSPL were classified as follow:

4.6.1 Protein classification based on molecular functions

By molecular functions, the proteins were grouped under binding, catalytic activity, structural molecule activity, transporter activity and others (Figure 4-2). Of the total 139 pellicle proteins, 37.5% of the proteins were involved molecular binding activities with either other or with different ion species like calcium and phosphate. 35% of the proteins were involved in different kind of catalytic activities. Only 5% proteins were involved in the transporter activity including ion transport. Around 7.5% proteins were either unknown proteins or proteins without known functions.

![Protein classification based on molecular functions in peptide-PSPL group.](image)

4.6.2 Protein classification based on cellular components

By cellular components, the proteins were grouped into cell part, extracellular region, macro molecular complex, organelles, and others (Figure 4-3). When the proteins were grouped based on the cellular components, out of 139 total pellicle proteins, 38.2% of the proteins were either part of the cellular components or associated with cellular components. Extracellular region proteins constituted 14.7% of the pellicle proteins. Around 6% of the proteins were part of the macromolecular complex with other proteins. 26.5% of the proteins were either part of the organelles or associated with the organelles. About 14.7% of the proteins were either unknown proteins or proteins without known functions.
4.6.3 Protein classification based on biological processes

Based on biological processes, the proteins were grouped under biogenesis, cellular process, immune system process, metabolic process, and others (Figure 4-4). When proteins were grouped according to biological processes, 31% of the total pellicle proteins were involved in various cellular processes, while 21.4% proteins were involved in metabolic processes. Immune system processes, comprise 3.6% of the pellicle proteins. Around 37% of the proteins were either unknown proteins or proteins with unknown functions, whereas 8.3% proteins were involved in biogenesis related activities.

4.6.4 Protein classification based on protein classes

Based on protein classes, the proteins were classified as calcium binding proteins, cell adhesion molecule, cytoskeletal proteins, immunity proteins, nucleic acid binding proteins, and others unknown or uncharacterized proteins (Figure 4-5). When the proteins
were grouped according to different classes, 1.6% of the proteins were calcium binding proteins, around 10% of the proteins were those associated with or involved in cell adhesion processes. Another ~10% proteins were either associated with cytoskeleton or part of the cytoskeletal system. About 5% of the proteins were either part of the immune system or associated with immunity. About ~10% of the pellicle proteins were either nucleic acid associated or nucleic acid binding proteins. Around 6.6% of the proteins were structural proteins. ~57% of the proteins were either unknown proteins or proteins with unknown functions.

![Protein classification based on protein classes in peptide-PSPL group.](image)

**Figure 4-5:** Protein classification based on protein classes in peptide-PSPL group.

### 4.7 Proteome profile of PS-Peptide-PSPL

In the second set of experiments, 4 disc/group were used with the following experimental plan:

1) Parotid saliva Control, (PSPL),

2) Parotid saliva coating, followed by DR9 peptide coating, followed by parotid saliva, (PS-DR9-PSPL),

3) Parotid saliva coating, followed by DR9-DR9 peptide coating, followed by parotid saliva, (PS-DR9-DR9-PSPL), and

4) Parotid saliva coating, followed by DR9-RR14 peptide coating, followed by parotid saliva, (PS-DR9-RR14-PSPL).
In the second set of pellicle modulation experiments, only those proteins were considered for the further analysis which were common in at least two independent experiments out of three independent repeat experiments done on separate days. There were in all 65 proteins from all the groups taken together. The highest number of proteins were present in PS-DR9-PSPL group, closely followed by PS-DR9-RR14-PSPL group, followed by PS-DR9-DR9-PSPL group.

Of the 12 proteins, 2 (16.7%) were exclusive to the PSPL (control) group. For PS-DR9-PSPL group, there were 20 proteins of which, 8 (40%) were exclusive to the PS-DR9-PSPL group. For PS-DR9-DR9-PSPL group, there were 15 proteins in all of which only 4 (26.7%) were exclusive to the group. In case of PS-DR9-RR14-PSPL group, there were in all 18 proteins of which 5 (27.8%) were exclusive to the group. Overall, a total of 7 proteins (~10.8%) were found to be shared among all groups (Table 4-11; Figure 4-6).

**Table 4-11:** Common proteins among all the groups of parotid saliva coated disc pellicle.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B/ Proline-rich peptide P-B/Proline-rich protein 3</td>
</tr>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6/Carbonic anhydrase VI/ Carbonic dehydratase VI/ CA-VI</td>
</tr>
<tr>
<td>P35908</td>
<td>Keratin, type II cytoskeletal 2 epidermal protein</td>
</tr>
<tr>
<td>P35527</td>
<td>Keratin, type I cytoskeletal 9</td>
</tr>
<tr>
<td>Q0KKI6</td>
<td>Immunoglobulin light chain</td>
</tr>
<tr>
<td>P13645</td>
<td>Keratin, type I cytoskeletal 10</td>
</tr>
<tr>
<td>Q9UGM3</td>
<td>Deleted in malignant brain tumors 1 protein</td>
</tr>
</tbody>
</table>
Figure 4-6: Comparison of peptide modulated AEP proteome profile on parotid saliva coated discs.

4.7.1 Most abundant proteins from PS-peptide-PSPL

Based on the relative ion abundance score count, the 10 most abundant proteins were selected from each group of PS-peptide-PSPL modulation experiments. (Table 4-12, 4-13, 4-14, & 4-15). In control, the relative ion abundance score ranged from a highest of 111.16 for keratin 1 to a lowest of 14.05 for mucin 16 protein.

Table 4-12: Most abundant proteins from control group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>H6VRF8</td>
<td>Keratin 1</td>
<td>111.16</td>
</tr>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>81.54</td>
</tr>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6</td>
<td>79.2</td>
</tr>
<tr>
<td>P35908</td>
<td>Keratin, type II cytoskeletal 2 epidermal</td>
<td>50.71</td>
</tr>
<tr>
<td>P35527</td>
<td>Keratin, type I cytoskeletal 9</td>
<td>48.36</td>
</tr>
<tr>
<td>Q0KKI6</td>
<td>Immunoglobulin light chain</td>
<td>23.78</td>
</tr>
<tr>
<td>P01833</td>
<td>Polymeric immunoglobulin receptor</td>
<td>23.15</td>
</tr>
<tr>
<td>G3CIG0</td>
<td>MUC19 variant 12</td>
<td>20.55</td>
</tr>
<tr>
<td>P13645</td>
<td>Keratin, type I cytoskeletal 10</td>
<td>18.07</td>
</tr>
<tr>
<td>B5ME49</td>
<td>Mucin-16</td>
<td>14.05</td>
</tr>
</tbody>
</table>
In PS-DR9-PSPL group, the ion abundance score ranged from a highest of 238.65 for carbonic anhydrase to a lowest of 41.32 for C1 segment protein (Fragment).

**Table 4-13:** Most abundant proteins from PS-DR9-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein Name</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6</td>
<td>238.65</td>
</tr>
<tr>
<td>H6VRF8</td>
<td>Keratin 1</td>
<td>184.2</td>
</tr>
<tr>
<td>Q0KKI6</td>
<td>Immunoglobulin light chain</td>
<td>118.2</td>
</tr>
<tr>
<td>P35908</td>
<td>Keratin, type II cytoskeletal 2 epidermal</td>
<td>95.41</td>
</tr>
<tr>
<td>P35527</td>
<td>Keratin, type I cytoskeletal 9</td>
<td>82.33</td>
</tr>
<tr>
<td>A0A075B6K9</td>
<td>Ig lambda-2 chain C regions</td>
<td>69.20</td>
</tr>
<tr>
<td>P01877</td>
<td>Ig alpha-2 chain C region</td>
<td>59.26</td>
</tr>
<tr>
<td>P13645</td>
<td>Keratin, type I cytoskeletal 10</td>
<td>58.33</td>
</tr>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>48.17</td>
</tr>
<tr>
<td>A0M8Q9</td>
<td>C1 segment protein</td>
<td>47.32</td>
</tr>
</tbody>
</table>

In PS-DR9-DR9-PSPL group, the relative ion abundance score ranged from a highest of 277.97 for carbonic anhydrase to a lowest of 38.94 for basic salivary proline-rich protein 2.

**Table 4-14:** Most abundant proteins from PS-DR9-DR9-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein description</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6</td>
<td>277.97</td>
</tr>
<tr>
<td>H6VRF8</td>
<td>Keratin 1</td>
<td>275.64</td>
</tr>
<tr>
<td>P35908</td>
<td>Keratin, type II cytoskeletal 2 epidermal</td>
<td>176.01</td>
</tr>
<tr>
<td>P13645</td>
<td>Keratin, type I cytoskeletal 10</td>
<td>160.70</td>
</tr>
<tr>
<td>Q0KKI6</td>
<td>Immunoglobulin light chain</td>
<td>124.99</td>
</tr>
<tr>
<td>Q6MZV6</td>
<td>Putative uncharacterized protein DKFZp686L19235</td>
<td>90.14</td>
</tr>
<tr>
<td>P35527</td>
<td>Keratin, type I cytoskeletal 9</td>
<td>69.69</td>
</tr>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>58.00</td>
</tr>
<tr>
<td>P12273</td>
<td>Prolactin-inducible protein</td>
<td>40.35</td>
</tr>
<tr>
<td>P02812</td>
<td>Basic salivary proline-rich protein 2</td>
<td>38.94</td>
</tr>
</tbody>
</table>

In PS-DR9-RR14-PSPL group, the relative ion abundance score ranged from a highest of 414.26 for carbonic anhydrase to a lowest of 46.89 for matrix Gla protein.
Table 4-15: Most abundant proteins from PS-DR9-RR14-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein description</th>
<th>Ion score</th>
</tr>
</thead>
<tbody>
<tr>
<td>P23280</td>
<td>Carbonic anhydrase 6</td>
<td>414.26</td>
</tr>
<tr>
<td>B7ZMD7</td>
<td>Alpha-amylase</td>
<td>390.09</td>
</tr>
<tr>
<td>Q0KK16</td>
<td>Immunoglobulin light chain</td>
<td>148.32</td>
</tr>
<tr>
<td>P02814</td>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>94.58</td>
</tr>
<tr>
<td>P35908</td>
<td>Keratin, type II cytoskeletal 2 epidermal</td>
<td>74.33</td>
</tr>
<tr>
<td>P01833</td>
<td>Polymeric immunoglobulin receptor</td>
<td>70.35</td>
</tr>
<tr>
<td>P13645</td>
<td>Keratin, type I cytoskeletal 10</td>
<td>68.69</td>
</tr>
<tr>
<td>B4E1M1</td>
<td>cDNA FLJ60391, highly similar to Lactoperoxidase</td>
<td>65.27</td>
</tr>
<tr>
<td>A0A0C4DGN4</td>
<td>Zymogen granule protein 16 homolog B</td>
<td>52.99</td>
</tr>
<tr>
<td>P08493</td>
<td>Matrix Gla protein</td>
<td>46.89</td>
</tr>
</tbody>
</table>

When the identified proteins from all the groups (PS/PS-DR9-PSPL/PS-DR9-DR9-PSPL/PS-DR9-RR14-PSPL) were compared, it was found that there were 7 proteins, that were common across all the groups, but with differential relative ion abundance scores.

Table 4-16: Values of ion abundance score obtained in all PS-peptide-PSPL groups.

<table>
<thead>
<tr>
<th>Common Proteins</th>
<th>PSPL (Control)</th>
<th>PS-DR9-PSPL</th>
<th>PS-DR9-DR9-PSPL</th>
<th>PS-DR9-RR14-PSPL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Submaxillary gland androgen-regulated protein 3B</td>
<td>81.54</td>
<td>48.17</td>
<td>58.00</td>
<td>94.58</td>
</tr>
<tr>
<td>Carbonic anhydrase 6</td>
<td>79.2</td>
<td>238.7</td>
<td>277.97</td>
<td>414.26</td>
</tr>
<tr>
<td>Keratin, type II cytoskeletal 2 epidermal protein</td>
<td>51.71</td>
<td>95.41</td>
<td>176.01</td>
<td>74.33</td>
</tr>
<tr>
<td>Keratin, type I cytoskeletal 9</td>
<td>48.4</td>
<td>82.33</td>
<td>69.69</td>
<td>46.61</td>
</tr>
<tr>
<td>Immunoglobulin light chain</td>
<td>23.8</td>
<td>118.2</td>
<td>124.99</td>
<td>148.32</td>
</tr>
<tr>
<td>Keratin, type I cytoskeletal 10</td>
<td>18.1</td>
<td>58.33</td>
<td>160.7</td>
<td>68.69</td>
</tr>
<tr>
<td>Deleted in malignant brain tumors 1 protein</td>
<td>6.72</td>
<td>25.74</td>
<td>28.48</td>
<td>35.44</td>
</tr>
</tbody>
</table>

The relative ionic abundance data of the common proteins across all the groups, clearly showed that the protein profile as well as abundance was modulated by the peptide coatings on the PS pellicle coated surface, in comparison to control group. For example, in case of submaxillary gland androgen-regulated protein 3B, the relative ion abundance score for control was 81.54. For both, PS-DR9-PSPL and PS-DR9-DR9-PSPL groups, it was lowest and less than that of control group (48.17; 59.1%) and (58.0; 71.13%),
respectively. The score was highest for PS-DR9-RR14-PSPL coated disc (94.58; 116%), compared to control.

For carbonic anhydrase 6 protein, the ion abundance score for control was 79.2, whereas for PS-DR9-PSPL, PS-DR9-DR9-PSPL groups it was higher and more than control (238.7; 301.4%), (277.97; 351%) and highest for PS-DR9-RR14-PSPL (414.26; 523.1%) in comparison to control, respectively.

In case of keratin, type II cytoskeletal 2 epidermal protein, the ion abundance score for all the treatments was more than the control. It was 51.71 in control, whereas for PS-DR9-PSPL, PS-DR9-RR14-PSPL it was higher than control (95.41; 184.5 %) and (74.33; 143.7%) and highest for PS-DR9-DR9-PSPL group (176.01; 340.4%), respectively compared to control.

For keratin, type I cytoskeletal 9 protein, the ion abundance score was 48.4 in control. For PS-DR9-RR14-PSPL group, it was lowest and less than that of control (46.61; 96.3%). Ion scores for PS-DR9-PSPL (highest) was followed by PS-DR9-DR9-PSPL, (82.33; 170.1%) and (69.69; 144 %) respectively, were higher than that of control.

In case of immunoglobulin light chain protein, the ion abundance score for control was 23.8. For all the peptide coated groups, the ion score was more than the control with DR9-RR14-PSPL group having the highest ion score (148.32; 623.2%), followed by PS-DR9-DR9-PSPL group (124.99; 525.2%) and PS-DR9-PSPL group (118.2; 496.6%) of the control, respectively.

For keratin type I cytoskeletal 10 protein, the ion abundance score for control was 18.1. In comparison to PS control, the ion abundance score was highest for PS-DR9-DR9-PSPL group (160.7; 887.9%) followed by PS-DR9-RR14-PSPL (68.69; 379.5%), and followed by PS-DR9-PSPL (58.33; 322.3 %), respectively, and was more than the control.

In case of deleted in malignant brain tumors 1 protein, the control had an ion abundance count of 6.72. Compared to control, ion abundance count was higher in all the groups
with PS-DR9-RR14-PSPL group being the highest (35.44; 527.4%), followed by PS-DR9-DR9-PSPL (28.48; 423.8%) and lowest PS-DR9-PSPL group (25.74; 383%), respectively.

**Table 4-17**: Proteome profile of control group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein description</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q59ED1</td>
<td>Cubilin variant</td>
<td>10.31</td>
</tr>
<tr>
<td>Q9UGM3</td>
<td>Deleted in malignant brain tumors 1 protein</td>
<td>6.72</td>
</tr>
</tbody>
</table>

**Table 4-18**: Proteome profile of PS-DR9-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein description</th>
<th>Ion Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>P01833</td>
<td>Polymeric immunoglobulin receptor</td>
<td>44.71</td>
</tr>
<tr>
<td>P22079</td>
<td>Lactoperoxidase</td>
<td>43.66</td>
</tr>
<tr>
<td>A0A0C4DGN4</td>
<td>Zymogen granule protein 16 homolog B</td>
<td>40.92</td>
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<tr>
<td>P61626</td>
<td>Lysozyme C</td>
<td>40.05</td>
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<tr>
<td>A2KBC1</td>
<td>Anti-(ED-B) scFV</td>
<td>38.52</td>
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<tr>
<td>Q9UGM3</td>
<td>Deleted in malignant brain tumors 1 protein SV=2</td>
<td>25.74</td>
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<tr>
<td>P09228</td>
<td>Cystatin-SA</td>
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<tr>
<td>P01034</td>
<td>Cystatin-C</td>
<td>16.02</td>
</tr>
<tr>
<td>P12273</td>
<td>Prolactin-inducible protein</td>
<td>14.07</td>
</tr>
<tr>
<td>E9PKG6</td>
<td>Nucleobindin-2</td>
<td>8.96</td>
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**Table 4-19**: Proteome profile of PS-DR9-DR9-PSPL group.

<table>
<thead>
<tr>
<th>Accession Number</th>
<th>Protein description</th>
<th>Ion Score</th>
</tr>
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<tbody>
<tr>
<td>A0A087X2C0</td>
<td>Ig mu chain C region</td>
<td>28.98</td>
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<tr>
<td>Q9UGM3</td>
<td>Deleted in malignant brain tumors 1 protein</td>
<td>28.48</td>
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<td>A0A0C4DGN4</td>
<td>Zymogen granule protein 16 homolog B</td>
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<tr>
<td>C9JEV0</td>
<td>Zinc-alpha-2-glycoprotein</td>
<td>14.22</td>
</tr>
<tr>
<td>A8K739</td>
<td>cDNA FLJ77339</td>
<td>10.32</td>
</tr>
</tbody>
</table>

**Table 4-20**: Proteome profile of PS-DR9-RR14-PSPL group.

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<th>Protein description</th>
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<td>P35527</td>
<td>Keratin, type I cytoskeletal 9</td>
<td>46.61</td>
</tr>
<tr>
<td>A8K739</td>
<td>cDNA FLJ77339</td>
<td>36.07</td>
</tr>
<tr>
<td>Q9UGM3</td>
<td>Deleted in malignant brain tumors 1 protein</td>
<td>35.44</td>
</tr>
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<td>P01034</td>
<td>Cystatin-C</td>
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</tr>
<tr>
<td>P12273</td>
<td>Prolactin-inducible protein</td>
<td>21.22</td>
</tr>
<tr>
<td>B4DI70</td>
<td>cDNA highly similar to Galectin-3-binding protein</td>
<td>16.13</td>
</tr>
<tr>
<td>P10909</td>
<td>Clusterin</td>
<td>13.62</td>
</tr>
<tr>
<td>----------</td>
<td>---------------</td>
<td>-------</td>
</tr>
<tr>
<td>G3CIG0</td>
<td>MUC19 variant 12</td>
<td>6.32</td>
</tr>
</tbody>
</table>

The proteome profiles of all the 4 groups (control and 3 PS-peptide-PS pellicle), were clearly different from each other. For instance, alpha-amylase (Fragment) was absent in control, PS-DR9-PSPL, and PS-DR9-DR9-PSPL and present in PS-DR9-RR14-PSPL group only. Mucin-16 protein was present in control only and was absent in all other groups. Lysozyme C was present only in PS-DR9-PSPL and absent from all other groups, including control. Cystatin-SA was present only in PS-DR9-PSPL and from all other groups whereas cystatin-C was present in PS-DR9-PSPL and PS-DR9-RR14-PSPL groups and absent in control as well as PS-DR9-DR9-PSPL. On the contrary, prolactin-inducible protein and zymogen granule protein 16 homolog B were absent in control and present in all the peptide groups. Keratin I was absent in PS-DR9-RR14-PSPL but present in all other groups. Similarly, MUC 19 variant 12 protein was present in control and PS-DR9-RR14-PSPL and absent from PS-DR9-PSPL and PS-DR9-DR9-PSPL groups.

There were some proteins like keratin type II cytoskeletal 2 epidermal, keratin type I cytoskeletal 10, keratin type I cytoskeletal 9, submaxillary gland androgen-regulated protein 3B, carbonic anhydrase 6, immunoglobulin light chain (Fragment) and deleted in malignant brain tumors 1 protein, that were present in all the groups, irrespective of presence or absence of peptides on the PS pellicle surface.

**4.8 PS-Peptide-PSPL proteome profile classification**

Based on molecular functions, cellular components, biological functions and protein class, the 65 pellicle proteins from PS-peptide-PSPL were classified as follow:
4.8.1  Protein classification based on molecular functions

By molecular functions, the proteins were grouped under binding, catalytic activity, structural molecule activity, transporter activity and others (Figure 4-7).

![Protein classification based on molecular functions](image)

**Figure 4-7:** Protein classification based on molecular functions in PS-peptide-PSPL group.

Of the total 65 pellicle proteins, 23.8% of the proteins were involved in molecular binding activities with either other proteins or with different ion species like Ca and Phosphate. About 43% of the proteins were involved in different kind of catalytic activities. 19% of the proteins had structural molecule activity. Around 14% proteins were either unknown proteins or proteins without known functions.

4.8.2  Protein classification based on cellular components

By cellular components, the proteins were grouped into cell part, extracellular region, macro molecular complex, organelles, and others. (Figure 4-8).

![Protein classification based on cellular components](image)

**Figure 4-8:** Protein classification based on cellular components in PS-peptide-PSPL group.
When the proteins were grouped based on the cellular components, out of 65 total pellicle proteins, 17.6% of the proteins were either part of the cellular components or associated with cellular components. Extracellular region proteins constituted 23.5% of the pellicle proteins. About 17.6% of the proteins were part of macromolecular complex with other proteins. 20% of the proteins were either part of organelle system or associated with organelles. Around 23.5% proteins were either unknown proteins or proteins without known functions.

### 4.8.3 Protein classification based on biological processes

Based on biological processes, the proteins were grouped under biogenesis, cellular process, immune system process, and metabolic process.

![Pie chart showing protein classification based on biological processes](image)

**Figure 4-9**: Protein classification based on biological processes in PS-peptide-PSPL group.

When proteins were grouped according to biological processes, 12% of the proteins were involved in the biogenesis related processes and 17% of the total pellicle proteins were involved in various cellular processes, while 21.3% proteins were involved in metabolic processes. Immune system processes, comprise 10.6% of the pellicle proteins. Around 45% of the proteins were either unknown proteins or proteins with unknown functions.

### 4.8.4 Protein classification based on protein classes

Based on protein class, the proteins were classified calcium binding proteins, cell adhesion molecule, cytoskeletal proteins, immunity proteins, and others.
When the proteins were grouped according to different classes, 4.2% of the proteins were calcium binding proteins, around 4.2% of the proteins were those associated with or involved in cell adhesion processes. Another 12.5% proteins were either associated with cytoskeleton or part of the cytoskeletal system. About 4.2 % of the proteins were either part of the immune system or associated with immunity. About 17% of the proteins were structural proteins. ~54% of the proteins were either unknown proteins or proteins with unknow functions.

4.9 Discussion

In the current study, the peptide pellicle was allowed to accumulate on the surface of hydroxyapatite discs, and then the saliva pellicle was accumulated on top of peptide pellicle. We found that this resulted in the different profile of majority of salivary proteins that constituted the pellicle in all the peptide groups in comparison to control where no peptide was used. Only ~4% of the proteins, out of a total of 139 proteins were found to be common across all the treatments. Another interesting aspect observed was that 45-60% of the proteins were specific to each treatment, according to the peptide used in the treatment. This further indicates that peptide coating of the disc surface was responsible for the modulation as well as specificity of the proteins to each group. This can be explained by the fact that all the three peptides (DR9/DR9-DR9/DR9-RR14) carried different net charges at pH 7 and had different pI values. Peptide having different net charges interact differently to the same pool of parotid saliva proteins. Due to the presence of seven histidine, three arginine and three lysine residues, histatin 5 has a got very high positive charge (Yin et al. 2006). The adsorption of such proteins, with low
affinity, to hydroxyapatite, can be augmented through their interaction with other strongly bound proteins to the dental enamel. Besides electrostatic interactions, an increase in entropy drives the protein adsorption to dental enamel surface. Moreover, histatins, statherin, and acidic proline-rich proteins (aPRPs), comprise the basal layer of the enamel pellicle. These proteins modulate the ionic concentration of calcium and phosphate in the oral cavity and are thought to exert control over the dental enamel erosion. (Siqueira et al. 2007).

In the process of enamel erosion, the proteomic composition of the pellicle play an important role. High-molecular-weight glycoproteins, salivary mucins (MUC5B) are one of the main pellicle components, and constitute 7 to 26% of total salivary proteins in the pellicle (Slomiany et al. 1996). In our study, we also found that mucins in different isoforms was present in PS pellicle under different peptide treatments.

Perinpanayagam, et al. (1995), did the characterization of low molecular peptides from parotid saliva. They concluded that these peptides are the result of post translation proteolysis of the parotid salivary antimicrobial proteins. They also estimated that these small peptides are present in nanomole (nM) concentration in the parotid saliva. Whether these levels are sufficient to exert any biological effect is open to speculation. Therefore, the rationale for using 20 nmol concentration in our experiments was based on the nanomole concentration of these peptides in the parotid saliva. We wanted to test if these levels of salivary peptides are sufficient to exert any biological effect in terms of demineralization protection as well as pellicle modulation. What we found that these peptides (DR9/DR9-DR9/DR9-RR14) at 20 nmol concentration could exert their biological effect in terms of the modulation of pellicle composition.

Since the MUC5B, a high-molecular-weight mucin, has around 6 x affinity to hydroxyapatite, compared to MUC7, a low-molecular weight mucin, the MUC5B adsorbs to the tooth surface and contributes to the formation of the acquired enamel pellicle by quickly adsorbing to enamel surface. (Tabak 1990). In this study, we found that different isoforms of mucin were part of the pellicle, the binding of which was selectively modulated by the peptides in case of PS-peptide-PSPL where mucin -16 and 19 isoforms
were present in control but absent in both PS-DR9-PS and PS-DR9-DR9-PS treatment and only mucin-19 was detected in PS-DR9-RR14-PS treatment, whereas in peptide-PSPL the mucin isoforms were present in all the treatments to different extent based on their ionic abundance scores. This clearly showed that the peptides were modulating the proteomic composition of the pellicle in a very selective manner depending upon whether they were present directly on the surface of hydroxyapatite or on the surface of PS pellicle.

Low-molecular-weight salivary proteins, histatins, are synthesized and secreted in the oral cavity by the parotid and other minor salivary glands. (Siqueira et al. 2008; Oppenheim et al. 1986).

Three main types of histatins (1, 3, and 5), have been detected as the components enamel pellicle. (Siqueira et al. 2010). Being multifunctional proteins in nature, besides the fungicidal activity, (Xu et al. 1991) these proteins display significant protective activity against demineralization challenges as well (Siqueira et al. 2010). Histatin and statherin phosphoproteins have been shown to display acid demineralization protection against acid challenges (Siqueira et al. 2010; Li et al. 2004). Phosphorylated proteins have been speculated to display more affinity to hydroxyapatite, therefore, phosphorylated histatin 1 and statherin provide higher protection in comparison to non-phosphorylated residues. (Siqueira et al. 2012, Richardson et al. 1993).

Apart from the phosphoproteins, another high molecular weight acidic, hydrophilic protein albumin, has been implicated to play a role in demineralization protection. (Hemingway et al. 2010).

Salivary protein statherin is most potent inhibitor of both primary and secondary calcium phosphate precipitation, and histatin-1 displayed the least inhibition. Tamaki et al. (2002), found that only statherin was able to effectively inhibit calcium phosphate spontaneous precipitation at physiological concentrations.

Yin et al. (2003) found that only histatin 1 contained N-terminal phosphorylated serine, among all the histatins, which greatly increased its hydroxyapatite binding affinity.
Due to the technical limitations imposed by the instrument, for MS analysis, the protease digestion of the proteins and peptides bigger than 5 kDa becomes a necessity. Siqueira and Oppenheim (2009), in LC-ESI MS/MS mediated salivary proteomic profiling of the human pellicle proteome, identified 78 natural peptides (with a MW range of 767 – 3981 Da) that originated from 29 different proteins without any prior proteolytic treatment. Siqueira and Oppenheim (2009), by avoiding trypsinization, demonstrated that naturally occurring salivary peptides in the enamel pellicle can be identified.

Yao et al. (2000) proposed that statherin, histatins and proline-rich proteins (PRPs) are thought to initiate pellicle formation, which in turn, through transglutaminase enzyme follow cross-linking via covalent bonds between c-amide groups of a specific glutamine and an e-amino group of a specific lysine of adsorbed salivary proteins, leading to their complex formation with each other. (Bradway et al. 1992; Yao et al. 1999; Hannig et al. 2008).

Yao et al. (2000) observed that under in vitro conditions, transglutaminase catalyzed acidic PRP-1 and statherin cross-link. They also observed that under in vitro conditions the PRPs is involved in cross-linking with histatins salivary proteins as well.

Lendenmann et al. (2000) observed that IgA is the component of enamel pellicle and has been observed in the saliva as well (Lee et al. 2007).

IgA is implicated to promote some specific bacterial clearance, which was also observed in the gut (Mantis et al. 2011), besides neutralizing certain viruses in the oral cavity (McNabb and Tomasi, 1981). These protective immunological properties of the pellicle are very important for overall health protection, and maintenance of the normal functioning of oral cavity.

Salivary proteins statherin, agglutinins, PRPs, histatins and cystatins can help in aggregation of bacterial cells, thereby reducing their adherence and colonization on the enamel pellicle surface. This can significantly control and modulate the quality of biofilms in the oral cavity (Humphrey and Williamson, 2001). In this study, we also found that polymeric immunoglobulin receptor protein, Ig alpha-2 chain C region,
immunoproteins, and statherin, were part of Peptide-PSPL proteome, thus confirming earlier observations by Lendenmann et al. (2000).

In addition to immunoglobulin light chain, Ig alpha-2 C region proteins, PRP, polymeric immunoglobulin receptor protein, Ig lambda-2 chain C regions and cystatins were part of PS-Peptide-PSPL proteome, supporting the earlier observations of Lendenmann et al. (2000). Presence of these proteins in the pellicle further strengthen and support the important role of overall oral health protection, normal functioning of the oral cavity, in addition to the modulation of colonization and biofilm formation in the oral cavity, that is played by pellicle (Mantis et al. 2011; McNabb and Tomasi, 1981; Humphrey and Williamson, 2001).

Different enzymological, electrophoretic, immunological and mass spectrometer methods have been employed to detect amylase in the enamel pellicle. Amylase has been shown to present both in vitro enamel pellicles (Rølla et al. 1983; Siqueira et al. 2012) as well as in situ pellicles as a major component of pellicle (Carlen et al. 1998; Siquiera et al. 2007; Siqueira and Oppenheim 2009; Deimling et al. 2004). In this study, we also found that alpha-amylase was one of the major component of pellicle in both types of pellicle (peptide-PSPL and PS-Peptide-PSPL), thus supporting previous studies. Apart from alpha-amylase, carbonic anhydrase 6, lactoperoxidase were found to be present in the peptide-PSPL.

Among acquired enamel pellicle proteins, lysozyme is one of the main enzymatic protein (Siqueira et al. 2007; Li et al. 2004). Lysozyme has been found in an active form both in the in situ enamel pellicles (Li et al. 2004), as well as in the in vitro experimental pellicles (Hennig et al 2005; Siqueira et al. 2009). In this study, the lysozyme was identified in the pellicle modulated by DR9-RR14 peptide coated disc only. In case of PS-DR9-PSPL, the lysozyme was detected, thereby supporting previous studies in relation to presence of lysozyme in the in vitro pellicle. It is speculated, that presence of other two peptide coating on the HA surface (DR9 and DR9-DR9), could have modified the surface electrochemistry of HA surface, that might have led to nonadherence and hence integration of lysozyme into in vitro pellicle. In case of PS-DR9 coating, the
presence of multiprotein PS coating on HA surface might have changed the surface electrochemistry in a way, that preferentially favored lysozyme over the DR9 in the pellicle.

Tellefson and Germaine, (1986) and Cimasoni et al. (1987) found that lysozyme specifically binds to certain bacteria and may help them not only to aggregate but also in bacterial adherence to the enamel pellicle. On the other hand, in a contrasting study, Roger et al. (1994) showed that lysozyme inhibited the adsorption of Streptococcus to saliva-coated hydroxyapatite.

It has been demonstrated, that peroxidase adsorb irreversibly and retain the enzymatically active conformation, to human enamel, when saliva was incubated with enamel powder (Tenovuo et al. 1977; Hennig et al. 2005). Pruitt and Adamson (1977), showed that 75% of activity of the immobilized enzyme in the pellicle was retained. In this study, we also identified the peroxidase, thus confirming the previous observations regarding presence of peroxidase in the in vitro pellicle. We identified lactoperoxidase in DR9-RR14 PSPL and PS-DR9-RR14-PSPL. This can very well be explained by the selective interaction of DR9-RR14 with peroxidase both in presence and absence of salivary pellicle on the disc surface.

Leinonen et al. (1999), employed immunostaining antibody techniques, to detect carbonic anhydrase VI (CA VI) in in situ formed enamel pellicles. In another study, Li et al. (2004) detected CA II in the in situ enamel pellicle, by employing monoclonal antibodies. In this study, we also found, that CA was present in the in vitro pellicle.

PRPs are one of the major constituent of enamel pellicle and they represent around one-third of the salivary proteins (Bennick, 1987; Hay et al. 1988; Gibbons and Hay 1989). These proteins adsorb on to the enamel surface and incorporated as an integral part of the enamel pellicle due to their negatively charged amino acid. (Lamkin et al. 1996). In this study, we also found that PRPs were present in PS saliva control and all the peptide coated discs (DR9, DR9-DR9, DR9-RR14).
Through general consensus, it is accepted that, enzymes adsorb into the pellicle in a selective fashion similar to other salivary proteins, since only a fraction of enzymes present in saliva has been identified in the enamel pellicle (Yao et al. 2003; Hay, 1967).

Pruitt et al. (1969), proposed the idea that salivary proteins could compete for adsorption and inhibit certain enzymes from immobilization in the pellicle. From a clinical viewpoint, the main objective would be to modulate the pellicle composition, which plays a crucial role in the attachment of bacteria, for the biofilm establishment, that will be harmless, non-cariogenic and ecologically stable. Basically, this forms the basis of our hypothesis that salivary peptides can modulate the pellicle composition. We found in this study that when peptides were used for coating the disc surface, they did selectively modulate and inhibit adsorption of certain enzymes (alpha-amylase), which was absent from the peptide treated pellicle (DR9 peptide coating) in comparison to the control.

On the other hand, carbonic anhydrase was one such enzyme, the adsorption of which was not affected by presence or absence of the peptides, but the extent of its presence in the pellicle was differential according to different ionic abundance count across the treatments in both the Peptide-PSPL as well as PS-peptide-PSPL.

In case of peptide coating of disc surface, it is speculated that there was possible uniform charge due to homo-molecular layer of peptide, and hence there was direct interaction between the peptide layer (different surface electrochemistry for each peptide) and the PSPL proteins, resulting in increasing trend of ion abundance. On the contrary in case of PS-Peptide-PSPL, the ion abundance trend was irregular. This can be possibly attributed to the influence and competition of the disc surface PSPL on the adsorption of specific peptide, possibly due to surface charge interactions of PSPL proteins and peptide with 2nd layer of PSPL proteins. This in turn influenced the further differential binding of second layer of PSPL on the peptide layer.

The adsorption behavior of a single salivary protein can be significantly different than one that can be observed if that protein is present in a mixture of different proteins (Yin et al. 2006). In this study, we observed that there was indeed difference in the behavior of salivary peptides in absence and presence of mixture of different salivary proteins.
4.10 Conclusion

Overall, this study provided direct evidence that salivary peptides at nanomole concentration are capable of exerting and involved in the modulation of the pellicle proteome composition as well as protein abundance based on their ion count, possibly through the modification in the protein-protein interactions. This modulation both in proteome profile and abundance of proteins is influenced, in parts due to presence and absence of PSPL proteins on the hydroxyapatite surface as was observed in terms of lower number of pellicle proteins recovered from PS-peptide-PSPL in comparison to peptide-PSPL. This is initial step in the direction of further understanding the actual molecular mechanism of how the protein-protein interactions bring about the pellicle proteome modulation to pave the way for dental caries and other oral healthcare management in the future.
References


40.


Chapter 5

5 Summary and conclusion

1. Under the current experimental conditions, the direct coating of HA surface with peptide constructs (DR9, DR9-DR9, DR9-RR14) at low concentrations of the peptides (20 nmol), did not provide any advantage or significant demineralization protection against calcium and phosphate losses from enamel surface compared to control.

2. When the PS pre-coated HA disc were coated with peptide constructs (DR9, DR9-DR9, DR9-RR14), DR9 and DR9-DR9 peptides exhibited similar and significant level of calcium and phosphate demineralization protection, compared to control.

3. At lower concentration, DR9-DR9, did not provide any advantage over DR9, over demineralization protection against calcium and phosphate losses from enamel surface.

4. At lower concentration, the peptide DR9-RR14 did not provide any protection against calcium and phosphate demineralization.

5. In the peptide mediated pellicle proteome modulation experiments, out of 139 proteins identified in all the groups from peptide coated discs, (PS/ DR9-PSPL/ DR9-DR9-PSPL/ DR9-RR14-PSPL), interestingly, 45-60% of the proteins were specific to each group according to the peptide used. Only 7 proteins (~4%), were common across all the groups, but with differential ion abundance scores.

6. The proteome profiles of all 4 groups were clearly different from each other for majority of proteins, since most of the proteins were present in only two groups out of four.

From the current study, it can be concluded that DR9 (single & tandem repeat construct) provided significant enamel demineralization protection. Additionally, all the tested peptide constructs (DR9, DR9-DR9, DR9-RR14) modulated the enamel pellicle proteome composition. Overall, this study, provided direct evidence, that salivary
peptides at nanomolar concentration are capable of exerting and involved in the modulation of the pellicle biological functions.
Appendix A

Abbreviations

µg  Microgram
µl  Microliter
µm  Micrometer
2-D PAGE  2-dimensional poly acrylamide gel electrophoresis
3-D  Three dimensional
AEP  Acquired enamel pellicle
AFM  Atomic force microscopy
aPRPs  Acidic proline rich proteins
BSA  Bovine serum albumin
Buffer B  80% acetonitrile, 0.1 % trifluoroacetic acid and 19.9% water
°C  Degree Celsius
CA  Carbonic anhydrase
Ca and PO$_4^-$  Calcium and phosphate
CaCl$_2$  Calcium chloride
PSPL  Parotid saliva pellicle
DR9-PSPL  Parotid saliva pellicle on top of DR9 coating
DR9-DR9-PSPL  Parotid saliva pellicle on top of DR9-DR9 coating
DR9-RR14-PSPL  Parotid saliva pellicle on top of DR9-RR14 coating
PS-DR9-PSPL  Parotid saliva pellicle on top of PS-DR9 coating
PS-DR9-DR9-PSPL  Parotid saliva pellicle on top of PS-DR9-DR9 coating
PS-DR9-RR14-PSPL  Parotid saliva pellicle on top of PS-DR9-RR14 coating
DTT  Dithiothreitol
HA  Hydroxyapatite
HPLC  High performance liquid chromatography
kDa  Kilo Dalton
LC-ESI-MS/MS  Liquid chromatography-electron spray ionization-tandem mass spectrometry
MALDI-TOF-MS  Matrix assisted lased desorption ionization-time of flight-mass spectrometry
micro-BCA  micro-BiCinconinic Acid protein estimation assay
mM  Millimolar
NaH$_2$PO$_4$  Ammonium dihydrogen phosphate
NH$_4$ HCO$_3$  Ammonium bicarbonate
nLC-ESI-MS  Nano liquid chromatography-electron spray ionization- mass spectrometry
RP-HPLC  Reverse phase high performance liquid hromatography
nM  Nano mole
PCR  Polymerase chain reaction
pH  Hydrogen ion concentration
pI  Isoelectric point
PRPs  Proline-rich proteins
PS  Parotid saliva
SEM  Scanning electron microscopy
TEM  Tunneling electron microscopy
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