



## PROTEOMICS IN PERIODONTAL DIAGNOSIS AND TREATMENT - A REVIEW

### Periodontology

**Dr. N. Sakthi  
Ganesh**

MDS., Senior Lecturer, RVS Dental College & Hospital, Coimbatore.

### ABSTRACT

Proteins are essential part of the metabolic pathways of living cell and its entire set with the modifications, produced by an organism or system, is considered a proteome. The onset, progression and severity of periodontal disease are mediated by various protein molecules. Periodontal proteomic markers range from salivary protein markers like Immunoglobulin G to bone remodelling protein markers. Steps involved in Proteomic analysis or protein separation, protein identification, Protein quantification, sequence analysis, bio marker diagnosis. ELISA is a technique for identifying and quantifying proteins. Antibodies against small peptides that are expected to be released by tryptic digestion of cells are specific to the protein under investigation are used in this procedure. ELISA is a technique for identifying and quantifying proteins. Antibodies against small peptides that are expected to be released by tryptic digestion of cells are specific to the protein under investigation are used in this procedure. ProtoMap enables for the detection of post-translational modification proteolysis-induced changes in gel migration. Proteomics and gene expression knowledge will help to improve periodontal disease diagnosis and therapy.

### KEYWORDS

Proteome, Genome, Immunoglobulin, ELISA, Matrix Metalloproteinases

### INTRODUCTION

Proteins are essential part of the metabolic pathways of living cell and its entire set with the modifications, produced by an organism or system, is considered a proteome. The term proteome a blend of protein and genome was coined by Marc Wilkins in 1996.[21]. In simple terms, proteomics is defined as the study of all proteins present in a particular cell or an organism in a given environment and at a specific stage in the cell cycle [24]. The onset, progression and severity of periodontal disease are mediated by various protein molecules. Periodontal tissues constitutes multi compartmental groups of interacting cells and matrices that render continuous support, attachment, proprioception and physical protection for teeth.[23]. The shift from non destructive established gingival inflammation to destructive periodontitis is characterised by alterations in molecular markers. Proteomics is a fascinating research horizon in periodontology that has the potential to be a vital tool for the early identification and prevention of periodontal pathologies that are genetically regulated.

### Type Of Proteomics

#### Structural Proteomics

Structural proteomics includes the identification of all the proteins on a genome-wide scale, determining their structure- function relationships, and describing three-dimensional structures of the proteins. The identification of all proteins on a genome wide scale, determining their structural-functional relationships, and describing three-dimensional structures are the important hurdles in structural proteomics [30].

#### Interaction Proteomics

The functions of biological systems are dependent on interactions between their components. These interactions are ultimately determined by genetic elements and selection processes [19]. Interactive proteomics focuses at physical interactions between proteins and generates disease and pathway-specific protein interaction networks. Proteins' intrinsic chemical and structural diversity, as well as their various expression levels and subcellular localisations, present unique hurdles for network investigation, necessitating the employment of a number of novel and inventive methodologies.

#### Functional Proteomics

Functional proteomics is a branch of biology that focuses on tracking and analysing the spatial and temporal features of molecular networks and fluxes in viable cells [11]. It is focused to monitor and analyse the spatial and temporal properties of the molecular networks and fluxes involved in the living cells. It concentrates on elucidation of biological functions of unknown proteins and cellular activity at molecular level.

#### Proteins Of The Periodontium

Periodontal proteomic markers range from salivary protein markers like Immunoglobulin G to bone remodeling protein markers [17].

Periodontal proteomic markers range from a wide variety of potential biomarkers like Immunoglobulins (Ig) (IgA, IgG, IgM, sIgA), by-products of tissue breakdown (collagen telopeptides, proteoglycans, osteocalcin, fibronectin fragments and bone collagen fragments), Pyridinoline cross linked carboxyl terminal telopeptide of type I collagen (pyridinoline, deoxy-pyridinoline, N-telopeptides and C-telopeptide), osteopontin, host factors that include host response cells like monocytes, Polymorphonuclear leukocytes (PMNs), macrophages, IL-1B, TNF- $\alpha$  and PGE2, host cells like immune cells, and periodontal ligament fibroblasts along with host derived enzymes like aspartate aminotransferase, acid phosphatase, elastase, cathepsin B, Matrix Metalloproteinases (MMPs) and microbial factors from Treponema denticola (T.d), Aggregatibacter actinomycetemcomitans (A.a), Porphyromonas gingivalis (P.g), Tannerella forsythia (T.f), ions like calcium, lactoferrin, platelet activating factors and hormones like cortisol [10].



Immunoglobulins (IgA, IgG, IgM, and sIgA) act as an innate defence mechanism of periodontium by interfering with adherence and metabolism of bacteria. Osteocalcin, osteonectin, and collagen telopeptidases and bone collagen are associated with local bone metabolism confined to periodontitis and systemic conditions like osteoporosis or metastatic bone cancers. Pyridinoline, deoxypyridinoline, N-telopeptides, and C-telopeptides are class of degradation molecules which are released systemically during degradation of collagen matrix and bone resorption due to post-translational modification of collagen. They have emerged as valuable proteome markers for bone turnover and are very specific for periodontal disease [16]. Osteocalcin. It is the most abundant noncollagenous protein in bone which has specific calcium binding property [20]; it is synthesized mainly by osteoblasts and thus has a dominant role in bone remodeling [5].

Osteopontin (OPN). It is noncollagenous calcium binding glycosylated phosphoprotein in bone matrix and is produced by several cells including osteoblasts, osteoclasts, and macrophages.

Osteopontin level in GCF is significantly correlated with progression of periodontal disease [18]. Interleukins and prostaglandins are important inflammatory mediators released by macrophages and PMNs by the chemoattractant effects of lipopolysaccharide present in bacterial cell wall. Protein synthesis in the functioning PDL, data have been obtained studying PDL fibroblast using immunological specific antibodies techniques. Cathepsin B, a cysteine protease whose source in GCF is mainly from macrophages, contributes to periodontal tissue destruction by proteolytic activation of neutrophil procollagenase [31]. The levels of cathepsin B were observed to increase in periodontitis. Alkaline Phosphatase (ALP) & Acid Phosphatase (ACP) are membrane-bound glycoproteins engaged in preservation of alveolar bone and renewal of the periodontal ligament. Matrix Metalloproteinases (MMPs) are Host cell-derived enzymes and are an important group of neutral proteinases implicated in the destructive process of periodontal disease that can be measured in GCF. Apart from being a disease severity indicator, MMP-8 also measures disease activity. (MMP-9) degrades collagen intercellular ground substance and may serve as a guide in periodontal treatment monitoring as its level is higher in GCF of the patients with chronic periodontitis. Neutrophils are the first line of host defence against periodontopathogenic bacteria. Hydrolytic neutral enzymes (elastase, cathepsin G, myeloperoxidase, lysozyme, hydrolases, lactoferrin, and neutrophil collagenase like MMP-8 and MMP-9) are present in neutrophilic granules [31]. Glucuronidase is a lysosomal enzyme that acts as a marker for release of primary granule from PMNs.

Aspartate Aminotransferase Enzyme (AST) is a tissue destruction biomarker released from necrotic cells in GCF and is associated with periodontitis severity [19]. Interleukins and prostaglandins are important inflammatory mediators released by macrophages and PMNs by the chemoattractant effects of lipopolysaccharide present in bacterial cell wall [2]. Fibronectin is a glycoprotein which mediates adhesion between cells. Salivary fibronectin is reduced in periodontitis as *P. gingivalis* fimbriae bind to fibronectin Platelet activating factor [PAF] is a potent phospholipid inflammatory mediator. Significant correlation was found between salivary platelet activating factor (PAF) levels and the extent of periodontal disease. Higher salivary cortisol levels were observed exerting a strong inhibitory effect on the inflammatory process and immune

### Steps Involved In Proteomics



### Methods Of Proteomic Analysis

#### Enzyme Linked Immunosorbent Assay [Elisa]

ELISA is a technique for identifying and quantifying proteins. Antibodies against small peptides that are expected to be released by tryptic digestion of cells are specific to the protein under investigation and are used in this procedure [25]. The bound primary antibodies are detected using a tagged secondary antibody. The signal is influenced by the peptide in solution interfering with the bound peptide. The signal will be maximum when no free peptide is present, and intermediate when a little level of available peptide is present, and minimal when a substantial amount of competitive peptide is present [3]. ELISA is useful in evaluating for periodontitis, reducing periodontal morbidity and increasing periodontal health.

### Mass Spectroscopy

Mass Spectroscopy is a powerful analytical tool for analysing the structure and chemical characteristics of individual molecules, as effectively as quantifying known materials and detecting novel chemicals within a sample [4]. A detector that translates the ions into electrical signals is used to detect the ions issuing from the last analyser and determine their abundance and process the detector signals that would be sent to the computer while using feedback to control the device. The most upregulated proteins in chronic periodontitis compared with controls were BP1, ITGAM, CAP37, PCMI, MMP-9, MZB1, UGT1, PLG, RAB1B, HSP90B1. The integrative data from transcriptomes and proteomics revealed MZB1 as a potent candidate for chronic periodontitis.

### Protein Topography And Migration Analysis Platform [protomap]

ProtoMap enables for the detection of post-translational modification proteolysis-induced changes in gel migration. The ProtoMap strategy is a degradomics method for screening protease substrates in complicated protein environments [26]. To isolate proteins, sodium dodecyl sulphate polyacrylamide gel electrophoresis is performed according to their relative mobility. Using bioinformatics and LC-tandem MS, the extracted protein and peptides are sorted. The data is combined via software to make a peptograph, which is a visual depiction of sodium dodecyl sulphate polyacrylamide gel electrophoresis. [7] In periodontology, it was recently confirmed that regulatory cross-talk occurs across proteases, either by direct cleavage or by targeting the appropriate inhibitors, regardless of protease type or traditional biochemical pathways [8].

### Maldi (Matrix Assisted Laser Desorption/ionization)

MALDI aids in the fast identification of proteins in specific combinations [13]. Protein identification data was collected via a 4700 proteomic analyser. A neodymium-doped yttrium aluminium garnet (Nd:YAG) laser with a 200 Hz repetition rate is deployed to acquire both MS/MS spectra data. The ones with the strongest ion signals are chosen as MS/MS precursors and external calibration with trypsin autolysis peptides [27].

### Two Dimensional Polyacrylamide Gel Electrophoresis

It is used to separate complicated protein combinations from biological specimens [15]. The targeted proteins are separated on a 12.5% SDS-polyacrylamide gel electrophoresis after equilibrium upon electrophoretic separation onto 12.5% polyacrylamide gels. Silver staining is employed to monitor the gels and determine proteins [22].

### Non Gel Based Proteome Separation Techniques

Multidimensional Liquid Chromatography (MUD-LC) in conjunction with Electrospray Ionisation MS (ESI-MS/MS) spectra, have acquired popularity as a result of the limitations of traditional proteomic approaches like not being accurate to identify minor spots and techniques like MALDI do not promote the detection of hydrophobic and basic peptides [9]. In these methods, complex protein combinations are processed in solution. One or more steps of capillary chromatography are used to fractionate the peptide mixtures which are then analysed by MS in a data-dependent manner.

### Methods Of Quantitative Proteomics

SILAC (Stable Isotope Labelling with Amino Acids)

iTRAQ™ (Isobaric Tagging For Relative and Absolute Quantification)

Chemical labelling- ICAT (Isotope Coded Affinity Tags)

SELDI-TOF (Surface Enhanced Laser Desorption/Ionisation-Time of Flight) [14]

Capillary electrophoresis (CE) [12]

### CONCLUSION

Proteomics and gene expression knowledge will help to improve periodontal disease diagnosis and therapy. Its utility in dentistry, however, will hinge on how skillfully oral healthcare providers assimilate it in and out of their practices, considering it necessitates a solid grasp of human genetics as well as the adoption of novel diagnostic and therapeutic technology. The use of proteomics and gene expression will advance the diagnosis and treatment of periodontal disease conditions, proteins being an universal component of all biological functions of the body, the scope of proteomics in health and especially the field of periodontology is expected to scale greater.

heights. An important challenge that needs to be met by research workers in periodontology is to embrace proteomics approaches when appropriate, and start to apply them to critical, unresolved questions such as the biological basis for the heterogeneity in gingival, bone, and cementum cell populations.

## REFERENCES

- Antezack A, Chaudet H, Tissot-Dupont H, Brouqui P, Monnet-Corti V. Rapid diagnosis of periodontitis, a feasibility study using MALDI-TOF mass spectrometry. *PLoS One*. 2020;15(3):e0230334
- Amar S, K. Oyaisu, L. Li, and T. Van Dyke, "Moesin: a potential LPS receptor on human monocytes," *Journal of Endotoxin Research*, vol. 7, no. 4, pp. 281–286, 2001
- Braithard O, Bishara-Shieban J, Glickstein H, Kott-Gutkowski M, Pace U, Rund DG, et al. An ELISA-based procedure for assaying proteins in digests of human leukocytes and cell lines, using specifically selected peptides and appropriate antibodies. *Proteome Sci*. 2006;4:14.
- Blonder J, Goshe MB, Moore RJ, Pasa-Tolic L, Masselon CD, Lipton MS, et al. Enrichment of integral membrane proteins for proteomic analysis using liquid chromatography-tandem mass spectrometry. *J Proteome Res*. 2002;1(4):351-60
- Bronckers A. L. J. S, Gay M, T. Dimuzio, and W. T. Butler, "Immunolocalization of  $\alpha$ -carboxylglutamic acid containing proteins in developing rat bones," *Collagen and Related Research*, vol. 5, no. 3, pp. 273–281, 1985.
- Cesareni G, A. Ceol, C. Gavrilu, L. M. Palazzi, M. Persico, and M. V. Schneider, "Comparative interactomics," *FEBS Letters*, vol. 579, no. 8, pp. 1828–1833, 2005.
- Dix MM, Simon GM, Cravatt BF. Global mapping of the topography and magnitude of proteolytic events in apoptosis. *Cell*. 2008;134(4):679-91.
- Fortelny N, Cox JH, Kappelhoff R, Starr AE, Lange PF, Pavlidis P, et al. Network analyses reveal pervasive functional regulation between proteases in the human protease web. *PLoS Biol*. 2014;12(5):e1001869
- Gevaert K, Van Damme P, Ghesquière B, Impens F, Martens L, Helsens K, et al. A la carte proteomics with an emphasis on gel-free techniques. *Proteomics*. 2007;7(16):2698-718. Ross PL, Huang YN, Marchese JN, Williamson B, Parker K, Hattan S, et al. Multiplexed protein quantitation in *Saccharomyces cerevisiae* using aminereactive isobaric tagging reagents. *Mol Cell Proteomics*. 2004;3(12):1154-69
- Giannobile WV, Beikler T, Kinney JS, Ramseier CA, Morelli T, Wong DT. Saliva as a diagnostic tool for periodontal disease: Current state and future directions. *Periodontol* 2000. 2009;50:52-64
- Godovac-Zimmermann J, Brown LR. Perspectives for mass spectrometry and functional proteomics. *Mass Spectrom Rev*. 2001;20(1):01-57.
- Grover HS, Kapoor S, Saksena N. Periodontal proteomics: Wonders never cease! *Int J Proteomics*. 2013;2013:850235.
- Groseclose MR, Massion PP, Chaurand P, Caprioli RM. High-throughput proteomic analysis of formalin-fixed paraffin-embedded tissue microarrays using MALDI imaging mass spectrometry. *Proteomics*. 2008;8(18):3715-24.
- Issaq HJ, Veenstra TD, Conrads TP, Felschow D. The SELDI-TOF MS approach to proteomics: Protein profiling and biomarker identification. *Biochem Biophys Res Commun*. 2002;292(3):587-92
- Issaq H, Veenstra T. Two-dimensional polyacrylamide gel electrophoresis (2D-PAGE): Advances and perspectives. *Biotechniques*. 2008;44(5):697-98, 700.
- Johnell O, A. Oden, C. De Laet, P. Garnero, P. D. Delmas, ' and J. A. Kanis, "Biochemical indices of bone turnover and the assessment of fracture probability," *Osteoporosis International*, vol. 13, no. 7, pp. 523–526, 2002.
- Kathariya R and A. R. Pradeep, "Salivary proteomic biomarkers for oral diseases: a review of literature," *American Overseas School of Rome*, vol. 1, pp. 43–49, 2010.
- Kido, J.-I, T. Nakamura, Y. Asahara, T. Sawa, K. Kohri, and T. Nagata, "Osteopontin in gingival crevicular fluid," *Journal of Periodontal Research*, vol. 36, no. 5, pp. 328–333, 2001.
- Lamster I. B., "Evaluation of components of gingival crevicular fluid as diagnostic tests," *Annals of Periodontology*, vol. 2, no. 1, pp. 123–137, 1997.
- Lian J. B. and C. M. Gundersen, "Osteocalcin. Biochemical considerations and clinical applications," *Clinical Orthopaedics and Related Research*, no. 226, pp. 267–291, 1988.
- Marc R. Wilkins. From Proteins to Proteomes: Large Scale Protein Identification by Two- Dimensional Electrophoresis and Amino Acid Analysis. *Nat Bio*. 1996; 14 (1): 61–65.
- May C, Brosseron F, Pfeiffer K, Fuchs K, Meyer HE, Sitek B, et al. Proteome Analysis with Classical 2D-PAGE. *Methods Mol Biol*. 2021;2228:53-62.
- Meculloch CA. Proteomics for the periodontium: current strategies and future promise. *Periodontol* 2000.2006; 40: 173-183.
- Nupursah and H. Bhutani, "Proteomics and periodontal diseases," *Indian Journal of Medical Research*, vol. 2, pp. 242–244, 2013.
- Picotti P, Bodenmiller B, Aebersold R. Proteomics meets the scientific method. *Nat Methods*. 2013;10(1):24-27.
- Simon GM, Dix MM, Cravatt BF. Comparative assessment of large-scale proteomic studies of apoptotic proteolysis. *ACS Chem Biol*. 2009;4(6):401-08
- Smirnov IP, Zhu X, Taylor T, Huang Y, Ross P, Papayanopoulos IA, et al. Suppression of alpha-cyano-4-hydroxycinnamic acid matrix clusters and reduction of chemical noise in MALDI-TOF mass spectrometry. *Anal Chem*. 2004;76(10):2958-65
- Socransky S.S and A. D. Haffajee, "Dental biofilms: difficult therapeutic targets," *Periodontology* 2000, vol. 28, no. 1, pp. 12–55, 2002
- Xu Y. Capillary electrophoresis. *Anal Chem*. 1995;67(12):463R-473R.
- Yakunin A.F, A. A. Yee, A. Savchenko, A. M. Edwards, and C. H. Arrowsmith, "Structural proteomics: a tool for genome annotation," *Current Opinion in Chemical Biology*, vol. 8, no. 1, pp. 42–48, 2004.
- Zia A, S. Khan, A. Bey, N. D. Gupta, and S. Mukhtar-UnNisar, "Oral biomarkers in the diagnosis and progression of periodontal diseases," *Biology and Medicine*, vol. 3, pp. 45–52, 2011