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A Systematic Review of the Proteomics Approach for Biomarkers and Periodontitis Diagnosis

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Abstract

We wanted to see how accurate salivary matrix metalloproteinases (MMP)-8 and -9, as well as tissue inhibitor of metalloproteinase (TIMP)-1, were at diagnosing periodontitis and differentiating periodontitis stages 1 to S3. This was a case-control study involving patients with periodontitis S1 to S3 and healthy periodontia. Saliva was collected, and clinical parameters such as plaque index, bleeding on probing, probing pocket depth, and clinical attachment level were recorded. Radiography was used to confirm the diagnosis by measuring the alveolar bone level. An enzyme-linked immunosorbent assay was used to measure salivary biomarkers. A total of 45 patients and 18 healthy subjects served as controls.

Keywords: Biomarkers • Saliva • Matrix metalloproteinases • Periodontitis

Introduction

Periodontal disease, which includes periodontitis and gingivitis, is extremely common and may affect 90% of the world's population. Gingivitis is a nonspecific inflammatory reaction to a nonspecific plaque accumulation limited to gingival tissue, with no causal destruction of periodontal tissue. Periodontitis, on the other hand, is a chronic multifactorial inflammatory disease associated with microfloral plaque biofilm, host-mediated inflammation, and loss of periodontal attachment, which is characterised by gradual destruction of periodontal tissue support.

Description

Clinical considerations are effective tools for determining the health or periodontal disease conditions of the majority of patients. However, some people are more prone to developing periodontitis and severe generalised periodontitis, as well as being less responsive to standard periodontitis treatment. Because periodontal tissues have a complex structure, a better understanding of the entire set of cellular and matrix proteins in periodontal tissue is required for future advances. Biomarkers are expected to supplement the information provided by criterion clinical parameters while also improving diagnostic accuracy [1]. Recently, researchers have been looking for biomarkers for periodontitis. Indeed, a number of genes, transcription factors, and proteins linked to periodontitis have been identified. Proteomics studies using mass spectrometry enable the discovery of proteome and clinical condition correlations. It is also appropriate for studying complex multifactorial diseases such as periodontitis.The integration of several data platforms from clinical, radiographic, and proteomics in the study of periodontitis is expected to improve periodontitis diagnosis.The current review aims to provide an in-depth examination of proteomics approaches for biomarkers and periodontitis diagnosis.

MS can also be used for protein quantification, either with stable isotope labelling or label-free quantification. To generate mass differences between peptides, proteins, or reporter ions from different samples, stable isotope labelling is used. This method can be accomplished by using stable-isotope labels such as isobaric tags for absolute and relative quantification, isotope coded affinity tags for absolute and relative quantification, mass differential tags for relative and absolute quantification, and tandem mass tags. In summary, only MS can distinguish between heavy and light proteins. Following that, quantitation is accomplished by determining the relative intensities of the heavy and light versions of the protein or peptide in the MS or MS/MS spectra [2-5].

Conclusion

Comprehensive proteomic analysis is expected to aid in the understanding of the pathogenesis of periodontal diseases, as well as the development of more precise biomarkers for diagnostic and prognostic purposes. The current task is to figure out how to combine and use the resulting data sets to benefit the patient. The studies that were reviewed primarily concentrated on expression proteomics or differential display proteomics between disease and health conditions. The assessment of biomarkers' diagnostic ability should be improved in future studies. Further research is also required to overcome proteomic profiles based on the most recent periodontal disease classification scheme.

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Conflict of Interest

There are no conflicts of interest by author.

References

1. Siegel, Rebecca. "MA MS, and Ahmedin Jemal, DVM PhD. Cancer Statistics."*A Cancer J Clin* 62 (2012): 10-29.

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2. Hu, Yueh-Chiang, Shuyuan Yeh, Shauh-Der Yeh and Erik R. Sampson, et al. "Functional domain and motif analyses of androgen receptor coregulator ARA70 and its differential expression in prostate cancer." *J Biol Chem* 279 (2004): 33438-33446.

3. Libertini, Stephen J., Clifford G. Tepper, Veronica Rodriguez and David M. Asmuth, et al. "Evidence for calpain-mediated androgen receptor cleavage as a mechanism for androgen independence." *Cancer Res* 67 (2007): 9001-9005.

4. Lin, Yu, Haisong Tan, Guopeng Yu and Ming Zhan, et al. "Molecular Mechanisms of Noncoding RNA in the Occurrence of Castration-Resistant Prostate Cancer." *Int J Mol Sci* 24 (2023): 1305.

5. Lu, Xin, James W. Horner, Erin Paul, Xiaoying Shang and Patricia Troncoso, et al. "Effective combinatorial immunotherapy for castration-resistant prostate cancer." Nature 543 (2017): 728-732.

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