

Salivary protein profile as a tool for patient stratification in peri-implantitis

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Introduction

Dental implants are one of the most frequently used treatment options for tooth replacement. Approximately 30% of patients with dental implants develop peri-implantitis, which is an oral inflammatory disease¹⁻⁴. Our goal was to examine a group of patients with different degrees of periodontal disease including peri-implantitis and use protein profiles to stratify them.

Methods

Oral health from 71 patients was examined and unstimulated whole saliva was collected and processed according the standard operating procedure described by Rosa and colleagues (2016)⁵. Total protein profile analyzed by capillary electrophoresis and bioinformatics analysis was performed to determine which proteins are identified and related to disease conditions. The study consisted of 17 patients without oral disease, 31 patient with soft tissue conditions (gingivitis and/or mucositis) and 23 patients with hard tissue conditions (periodontitis and/or peri-implantitis). The total protein profiles for each patient were obtained by capillary electrophoresis. The bioinformatics tools used to analyze the results were: OralCard⁵, UniProt⁶ and AgBase⁷ to access the biological function of proteins in most different molecular weight ranges.

Results

The different salivary total protein profiles for each individual in different study conditions were compared (Fig.1a). The protein molecular weight ranges which best identify each of the study groups were identified. An example of the most different protein profiles corresponding to each study condition correspond to 30-50kDa and 60-80kDa (Fig.1b). There are 6 proteins exclusive for soft tissue conditions and 5 proteins exclusive of hard tissue conditions in molecular weight range of 30-50kDa (Fig. 2a). In molecular weight range 60-70kDa there are two proteins exclusive of soft tissue conditions and 1 of hard tissue conditions (Fig. 2b). For both groups of profiles Table I details the proteins corresponding the that molecular weight range and which are involved in immune processes.

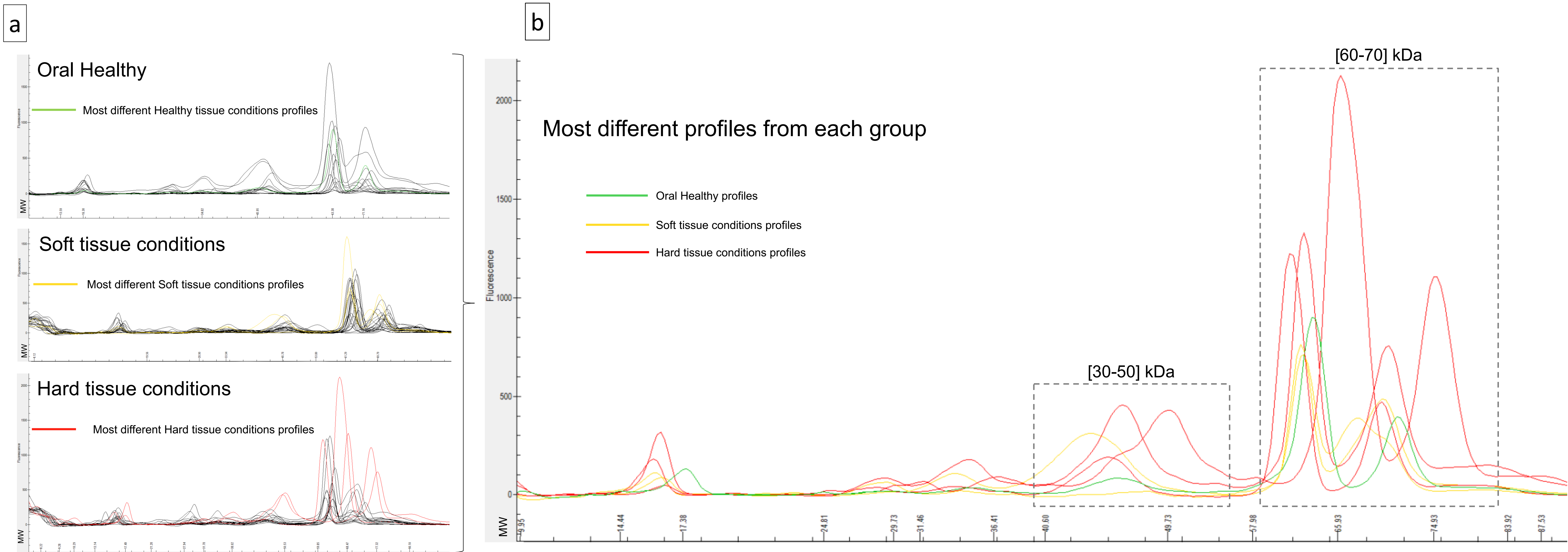


Fig. 1 - Capillary electrophoresis - Protein profiling analysis between each condition for every individual in the study (a). MW ranges which allow the discrimination of proteins characterizing each study condition (b).

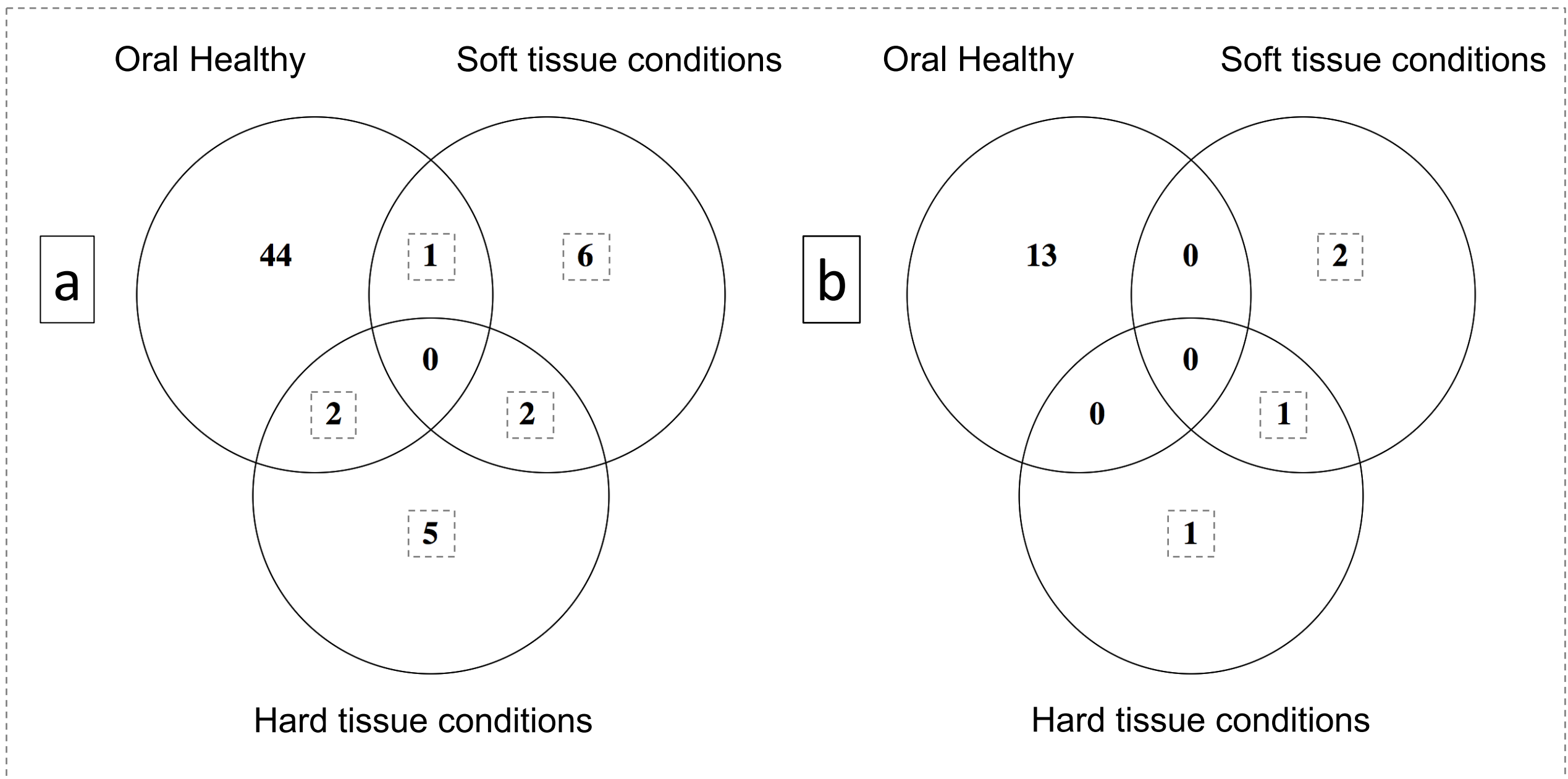


Fig2. Proteins in each MW range (a - [30-50]kDa | b - [60-80]kDa) are related with each study group.

Conclusion

For each MW range the main proteins which allow for the distinction between soft and hard tissue condition were identified. Future quantification of these proteins in saliva will be useful as prognostic markers for peri-implantitis.

References:

1. Al-Radha, A. S. D., Pal, A., Petteimerides, A. P., & Jenkinson, H. F. (2012). Molecular analysis of microbiota associated with peri-implant diseases. *Journal of dentistry*, 40(11), 989-998.
2. Albrektsson T, Isidor F. Consensus report of session IV. In: Lang NP, Karring T (eds). Proceedings of the 1st European Workshop on Periodontology. London: Quintessence, 1994: 365-369.
3. Al-Sabbagh, M. (2014). *Complications in Implant Dentistry. An Issue of Dental Clinics of North America* (Vol. 59, No. 1). Elsevier Health Sciences.
4. Saliva as a diagnostic tool for periodontal disease: current state and future directions WV Giannobile, T Beikler, JS Kinney, CA Ramseier- Periodontology 2000, 2009
5. Rosa, N., Marques, J., Esteves, E., Fernandes, M., Mendes, V. M., Afonso, A., ... & Barros, M. (2016). Protein Quality Assessment on Saliva Samples for Biobanking Purposes. *Biopreservation and biobanking*.
6. The UniProt Consortium, UniProt: the universal protein knowledgebase, *Nucleic Acids Res.* 45 (2017) D158-D169.
7. AgBase: McCarthy FM, Gresham CR, Buza TJ, Chouvarine P, Pillai LR, Kumar R, Ozkan S, Wang H, Manda P, Arick T, Bridges SM, Burgess SC. (2010) "AgBase: supporting functional modeling in agricultural organisms." *Nucleic Acids Res.* 2010 Nov 12.