EXPRESSION OF TRANSGLUTAMINASE GENES IN PATIENTS WITH CHRONIC PERIODONTITIS

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Aim. Gingival epithelium play a key role in the protection of oral tissues from microbial challenge, especially during the periodontal disease. Oral mucosal epithelial cells (i.e. oral keratinocytes) actively participate in immune responses and in?ammation by secreting a variety of cytokines, chemokines, growth factors and neuropeptides and that responses is related to periodontal pathogenesis. Transglutaminase 1 (TG1) is primarily expressed in stratified squamous epithelia, in which the ordered expression of specialized genes is associated with proliferation and terminal differentiation of keratinocytes. TG1 is also involved in cell envelope formation by cross-linking of precursor proteins, such as loricrin and involucrin. This study was aimed to evaluate levels of mRNA transcripts of different forms of transglutaminase in the human gingival tissues from patients with chronic periodontitis and relative controls.

Materials and methods. This study included 22 patients with chronic periodontitis (CP) and 22 healthy controls. For each patient, the values of Probing Depth, Clinical Attachment Level and Bleeding on Probing were recorded. Gingival specimens obtained from patients and healthy subjects were fixed with neutral buffered formalin for 24 h and then the sagittal sections (5 µm thick) were made from the specimens and stained with hematoxylin and eosin. Gene expression of transglutaminase1, transglutaminase2, transglutaminase3 and metalloprotease2 was evaluated by Real-time PCR, while that of Factor XIIIA and metalloprotease9 by RT-PCR. The level protein were evaluated by western blot analysis.

Results. The values of all the clinical parametres were significantly higher in the CP group than in the healthy control group ($p<0.05$). In the CP group the mRNA expression of transglutaminase1 and transglutaminase3 was significantly decreased in comparison with healthy control group. A slight unsignificant changes of transglutaminase2 gene expression was observed in samples from CP patients in comparison to controls. We showed also that protein contents of both TG1 and TG3 were reduced in gingival tissues from patients in comparison to normal samples, whereas no significant differences were observed in TG2 expression in samples from normal and periodontal tissues.

Conclusions. This study demonstrates that different types of TGs are expressed in the human gingival tissues and alterations of mRNA transcript and expression levels. In this study, for the first time we reported the reduced expression of TG1 associated with altered structure of gingival tissues in course of periodontal diseases. These observations suggest that transglutaminase gene expression may be modified in response to chronic injury in the damaged gingival and emphasize the key role of these enzymes in gingival remodelling/healing and adaptive processes. This change is potentially capable of exerting a considerable influence on disease activity and treatment outcomes, especially for the role of this mediators during the regeneration process. Further studies aimed at identifying the molecular mechanisms responsible for these changes and their reversibility may have a significant impact on our understanding of the complex processes involved in periodontal disease.