

Salivary proteome of aphthous stomatitis reveals the participation of vitamin metabolism, nutrients, and bacteria

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Abstract

There are currently no preventative options for recurrent aphthous stomatitis, and the only available treatments are palliative. This is partly due to a poor understanding of its etiopathogenesis. In this case-control study, we characterized the salivary proteome of patients with recurrent aphthous stomatitis in the presence and absence of lesions. Through mass spectrometry-based proteomics and bioinformatics tools, we identified that the presence of oral ulcers is associated with several specific biological processes, including the metabolic pathways of vitamin B9, B12, nitrogen, selenium, and the bacterium *Neisseria meningitidis*. These changes occurred only in the presence of clinically visible lesions, and there were no relevant differences between patients in anatomical regions unaffected by ulcers. Additionally, using western blot and ELISA assays, we verified that carbonic anhydrase 1 (CA1) and hemoglobin subunit beta (HBB) proteins are highly expressed during the ulcerative and remission phases of recurrent aphthous stomatitis. Our results cumulatively support saliva as an indicator of the pathophysiological changes, which occur during the clinical course of lesions. From a clinical perspective, we suggest that recurrent aphthous stomatitis is a condition triggered by temporary biological changes in people with lesions. © 2021, The Author(s).