

## New research finds major activation themes in denture-stomatitis

July 16 2010

Today during the 88th General Session & Exhibition of the International Association for Dental Research, in Barcelona, Spain, S. Offenbacher will present an abstract titled "Mucosal Gene Expression and Salivary Proteomic Analysis of Candidiasis-Associated Denture-Stomatitis."

The goal of the study was to compare whole-transcriptome, mucosal gene expression in Candida albicans (a parasitic fungus that can infect the mouth) associated chronic denture stomatitis to that of healthy oral mucosa and perform proteomic analyses of potential salivary biomarkers. Denture stomatitis is a condition in which the mucosa underneath a denture becomes inflamed and sometimes painful.

In this study, oral palatal biopsies were obtained from 17 healthy and 15 *C. albicans*-infected stomatitis subjects for whole-transcriptome analyses using Affymetrix arrays. The presence of *C. albicans* was confirmed by cytology and cultivable methods and the clinical severity of the stomatitis and denture fit evaluated by the Newton and Kapur Classifications.

A false discovery rate (FDR) of 2-fold including key cytokines [IL1F6, IL1B], chemokines [CXCL1, CCL10, IL8] as well as markers of epithelial suppression and neutrophil recruitment/ activation. Seventy-one genes were down-regulated >2-fold including epithelial adhesion molecules and keratins. Five of the 6 most significant gene ontology pathways involve inflammation and activation of the immune response with CD28 and CTLA signaling of Tcells. There was strong up-



regulation of TLR2, CD14, MYD88, IKKA and NFKB as the dominant toll-like receptor signaling pathway. Six extracellular protein genes upregulated in stomatitis were confirmed within the saliva using proteomic methods.

Neutrophil recruitment activation, epithelial suppression, TLR2 pathway up-regulation, T cell activation and bone resorption appear as major activation themes in stomatitis.

Provided by International & American Association for Dental Research

Citation: New research finds major activation themes in denture-stomatitis (2010, July 16) retrieved 28 April 2024 from <u>https://medicalxpress.com/news/2010-07-major-themes-denture-stomatitis.html</u>

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