OI0362 Functional analysis of interferon-γ and tumor necrosis factor α polymorphisms in lichen planus

FUNCTIONAL ANALYSIS OF INTERFERON-g AND TUMOR NECROSIS FACTOR a POLYMORPHISMS IN LICHEN PLANUS

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Objectives: Th1 cytokines are apparently overexpressed in oral lichen planus (OLP), but OLP patients with and without hepatitis C virus (HCV) infection showed a different genetic cytokine background, suggesting distinct pathogenetic mechanisms. The aim of the study was to correlate the in situ expression of interferon-g (IFN-g) and tumor necrosis factor a (TNF-a), using a real-time polymerase chain reaction (PCR) technique, with the respective genetic polymorphisms.

Methods: The study enrolled 25 patients (15 without and 10 with HCV infection) with histologically confirmed OLP and 21 healthy patients undergoing tooth extraction. Specimens of total RNA from the oral bioptic samples were extracted using a standardized system. Gene expression of IFN-g,TNF-a, and CD14 were evaluated by means of real-time PCR (ABI Prism 7700; Applied Biosystems, Foster City, CA, USA) using SYBRGreen as the detection method. Cytokine genotyping was performed in OLP patients by a sequence-specific polymerase chain reaction (PCR-SSP) assay as previously reported (Carrozzo et al., 2007). For statistical analysis, the Spearman rank correlation coefficient has been used. Results: The IFN-g UTR 5644 genotype showed a significant correlation with in situ expression just in patients without HCV infection (P ¼ .027), whereas no correlation was found in HCV-positive OLP patients. TNF-a in situ expression showed no correlation with genetic polymorphisms, regardless of the HCV status.

Conclusions: The present investigation confirms that increased expression of IFN-g seen in OLP tissue can be genetically driven in patients without HCV infection. It is likely that the limited sample size has influenced the apparent negative result of TNF-a.