ed with recombinant ectodomains of the epitope NC16a of the BP180 antigen and carboxy-terminal domains of BP230 antigen were used. All ELISAs were performed according to the manufacturer’s instructions. Values greater than 8.7 U/ml were considered positive. Histopathological and DIF results were considered as the gold standard. Global validation of the test results was established by calculating the sensitivity, specificity and both the positive and negative predictive values.

**Results.** Sixty-four patients were enrolled (M:F=1:4). Ages ranged from 40 to 82 years (mean 61 years). There were 30 patients with MMP, 16 patients with OLP, 14 affected by PV, 3 lichenoid dysplasia and 1 erythema multiforme. ELISA sensitivity and specificity was respectively 47 and 79%. PPV percentage was 67% while NPV was 83%.

**Conclusions.** In suspected oral MPP, both ELISA tests and histopathological + DIF have to be performed because of ELISA low sensitivity. Although BP180 and BP230 are the major target antigens in patients with MMP limited to the oral cavity, they are not the only. This aspect may explain the low sensitivity rate of ELISA in oral MMP when used as the sole diagnostic support.

**References**


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**Proteomic identification of salivary biomarkers in 20 patients with Oral Squamous Cell Carcinoma**

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**Objectives.** Saliva has been proposed as a potential diagnostic fluid combined with proteomic analysis. The aim of this study is to assess the proteomic salivary profile using SELDI-TOF-MS technology in patients with Oral Squamous Cell Carcinoma (OSCC), grouped in relation to the TNM staging and compared with healthy subjects.

**Methods.** In this secondary hospital based case-control study, patients with confirmed histopathological diagnosis of primary untreated OSCC as “cases” and healthy age- and sex-matched subjects as “controls” were consecutively enrolled, after informed consent. Saliva (5 mL) was collected by spitting directly into a clean 15 mL conical tube, aliquoted and stored at -80°C until use. SELDI-TOF Q10 ProteinChip system was used to screen for differentially expressed proteins in the saliva samples according to the manufacturer’s instructions (BioRad Inc.). Univariate statistics and ROC plot were used for data analysis.

**Results.** Twenty cases (6 M, 14 F; middle age 66.8 yy) and 20 controls (8 M, 12 F, middle age 61.9 yy) were included. In cases, seven were early-EsOSCC (3 stage I and 4 stage II) and 13 were late-LsOSCC (7 stage III and 6 stage IV). Proteomic analysis showed significant statistical differences in peptide profile in control vs OSCC and in EsOSCC vs LsOSCC samples (p<0.05). The differentiated pattern between overall OSCC and controls consisted of one peptide peak (8940-ROC-1), between EsOSCC and controls of four peptide peaks (7096-ROC 0.93; 12712–ROC 0.89; 8086 – ROC 0.93 and 11002 – ROC 0.93) and between LsOSCC and EsOSCC of one peptide peak (6026-ROC 0.80).

**Conclusions.** Although with limitation of the small sample size, this first study suggests that saliva contains proteomic signatures that could serve as biomarkers for OSCC at different stages. Once validated on a large clinical cohort, oral fluid proteomic based on SELDI-TOF-MS technology may be extensively used as a promising new non-invasive tool for early diagnosis in oral cancer patients.

**References**