Abstract II

Burning mouth syndrome (BMS) is a chronic pain disorder characterized by severe burning sensation in normal looking oral mucosa. Diagnosis of BMS remains to be a challenge to oral healthcare professionals because the method for definite diagnosis is still uncertain. In this study, a quantitative saliva proteomic analysis was performed in order to identify target proteins in BMS patients' saliva that may be used as biomarkers for simple, non-invasive detection of the disease. By using isobaric tags for relative and absolute quantitation labeling and liquid chromatography-tandem mass spectrometry to quantify 1130 saliva proteins between BMS patients and healthy control subjects, we found that 50 proteins were significantly changed in the BMS patients when compared to the healthy control subjects ($p \leq 0.05$, 39 up-regulated and 11 down-regulated). Four candidates, alpha-enolase, interleukin-18 (IL-18), kallikrein-13 (KLK13), and cathepsin G, were selected for further validation. Based on enzyme-linked immunosorbent assay measurements, three potential biomarkers, alpha-enolase, IL-18, and KLK13, were successfully validated. The fold changes for alpha-enolase, IL-18, and KLK13 were determined as 3.6, 2.9, and 2.2 (burning mouth syndrome vs. control), and corresponding receiver operating characteristic values were determined as 0.78, 0.83, and 0.68, respectively. Our findings indicate that testing of the identified protein biomarkers in saliva might be a valuable clinical tool for BMS detection. Further validation studies of the identified biomarkers or additional candidate biomarkers are needed to achieve a multi-marker prediction model for improved detection of BMS with high sensitivity and specificity.