# The salivary proteome in relation to oral mucositis

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**Objective**: Decreased salivary flow rate and/or changes in protein composition reported after autologous hematopoietic stem cell transplantation (ASCT) reduces the protective function of saliva. Oral mucositis (OM); inflammation of oral mucosa resulting of preparative chemotherapy for ASCT is a risk factor for systemic infections and affects patients' quality of life. In this study, a TMT-labelled proteomics experiment and a label-free quantification (LFQ) proteomics experiment were used to identify the salivary proteome in ASCT recipients and to explore whether differences in the salivary proteome occur between patients with ulcerative OM (uOM; WHO score ≥ 2) and those without (nOM).

**Methods:** In both experiments, salivary proteins were analyzed using liquid chromatography and tandem mass spectrometry. For the TMT-labelled experiment, saliva samples of 5 uOM and 5 nOM patients were pooled at different time points: baseline, 1, 2, and 3 weeks after ASCT and 3 months after ASCT. Principle component analysis was used to explore patterns between the uOM and nOM pools at different time points. For the LFQ experiment, an uOM pool (consisting of saliva from 9 uOM patients and 6 time points (same time points as TMT experiment and 12 months after ASCT)) was generated next to a nOM pool (10 nOM patients and 6 time points). Unique and up-regulated proteins of the uOM and nOM pools were further investigated with gene ontology.

**Results:** A different salivary proteome was indicated with a distinct clustering of the uOM pools at baseline, week 2 and week 3 after ASCT from the other pools. In the LFQ experiment, unique and up-regulated proteins of the uOM pool consisted of more intracellular proteins. Those proteins of the nOM pool were more involved in immune system-related processes.

**Conclusion:** The salivary proteome was suggestive of extra mucosal damage in uOM patients and extra protection in nOM patients.