N-Glycosylation Analysis of Homogenized Oral Squamous Cell Carcinoma Soft Tissue Samples by CE-LIF

Eniko Gebri¹, Kinga Hogyor², Adrienne Szabo³, Gabor Jarvas², Zuzana Demianova⁴, Andras Guttman^{2,5}

¹Department of Oral Medicine, Faculty of Dentistry, University of Debrecen, Debrecen, Hungary,

gmoki82@gmail.com

²Translational Glycomics Group, Research Institute of Biomolecular and Chemical Engineering, University of Pannonia, Veszprem, Hungary

³Department of Oral and Maxillofacial Surgery, Faculty of Dentistry, University of Debrecen, Debrecen, Hungary

⁴PreOmics, Planegg/Martinsried, Germany

⁵Horváth Csaba Memorial Laboratory of Bioseparation Sciences, Research Center for Molecular Medicine, Faculty of Medicine, Doctoral School of Molecular Medicine, University of Debrecen, Hungary

Summary

Oral squamous cell carcinoma (OSCC) is an aggressive disease with a glycoproteomically unmapped progression and a low, five-year survival rate. Besides the most commonly known risk factors of alcohol consumption, tobacco, poor oral hygiene, HPV infection, long-term immunosuppressant therapies may also increase the risk and change the therapeutic response of secondary malignancies. Alterations of protein N-glycosylation have a pivotal role in tumorigenesis and metastasis formation. Thus, our study aimed to identify novel glycobiomarkers for more precise prognosis suggesting more efficient therapeutic alternatives for oral cancers. Oral mucosal soft tissue samples were obtained by incisional biopsy from five patients with OSCC, both from the malignant and the opposite healthy gingival sides, as well as from seven age-sex matched healthy controls with the appropriate Ethical Permissions and Informed Patient Consents (DE RKEB/IKEB: 6152-2022). The collected tissues were properly homogenized, followed by N-glycan profiling of endoglycosidase released and fluorophore-labeled carbohydrates using capillary electrophoresis coupled with ultra-sensitive laser-induced fluorescent detection. Significant (p<0.05) differences have been identified between the malignant tissue samples of OSCC patients and the healthy controls, indeed between the healthy and the positive control oral mucosal samples, while there were no differences between the N-glycan profiles of the malignant tumor and the positive control samples. We can conclude that the automated sample preparation in conjunction with high-resolution CE-LIF-based glyocoanalytical method reported in this presentation proved to be an efficient and sensitive workflow for glycobiomarker-based molecular diagnostics of oral malignant lesions.