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Glycoproteomics Analysis of Oral Squamous Cell Carcinoma

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Abstract

Glycosylation is one of the post-translational modification processes which play an important role in many biological processes such as protein-protein interactions and cell adhesion. Differential expression of glycosylated proteins had been found to be associated with cancer progression. However, little is known about glycosylation changes associated with oral carcinogenesis. Therefore, this study aimed to elucidate the protein glycosylation profile (N- and O-linked glycosylation) in oral squamous cell carcinoma (OSCC). Serum samples of 10 patients with oral potentially malignant disorder (OPMD), 40 patients with OSCC along with 10 healthy individuals as control group, were subjected to two-dimensional gel electrophoresis (2D-E) coupled with lectin Concanavalin A and Jacalin that specifically bind to N- and O-glycosylated proteins respectively. OPMD and OSCC glycosylated protein profiles were compared with the healthy controls using Progenesis SameSpotsv4.0 software. The glycosylated proteins of interest were then identified using mass spectrometry and database searches. In this study, several glycoproteins that exhibit tumor-specific glycosylation changes in OPMD and OSCC were identified. Among them, α1-antitrypsin (AAT), α-2-HS-glycoprotein (AHSG), apolipoprotein A-I (APOA1) and haptoglobin (HP) were detected as N-glycosylated proteins. α-2-HSglycoprotein (AHSG) and clusterin (CLU) were detected as O-glycosylated proteins. Notably, AHSG was the only glycoprotein found to have both N- and O-linked glycosylation binding sites in OPMD and OSCC. A combination of 2D-E coupled with lectin-based analysis had identified several glycoproteins that may be involved in the progression mechanism of OSCC. However, further investigation is warranted to determine their roles in OSCC.

Keywords: Oral squamous cell carcinoma, Glycoproteomics, Glycosylation, Lectin