PROTEOMICS IN HEAD NECK CANCER WITH INVASIVE PHENOTYPE

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The regional lymph nodes play a pivotal role in diagnosis, staging and management of head and neck squamous cell carcinomas. Despite their importance, detailed understanding of the probable mechanisms of lymphatic metastases has not been completely achieved. The aim of the present study was to analyze proteome profiling patterns in metastatic and normal tissues pools from patients with oral or larynx squamous cell carcinomas using two-dimensional electrophoresis and MALDI-TOF/TOF (Matrix-Assisted Laser Desorption Ionisation-Time Of Flight) mass spectrometry. Twenty metastatic and fifteen normal lymph nodes were analyzed. We could distinguish normal and metastatic pools by visual and computational analysis based on the proteome profiling patterns. A set of tumor-associated proteins were found to be significantly increased in their expression levels in lymph node metastatic compared with normal lymph nodes. These proteins, including HSP27, vimentin and cytokeratin 19, are involved in cell cycle, signaling pathways, cytoskeleton organization and biogenesis, apoptosis and cell differentiation. The present findings demonstrated the rich protein information that can be produced by means of proteomics analysis, which may be the basis for rational designs of diagnostic and therapeutic methods in cancer.