

Proteomics based approach to evaluate the differential expression of a set of proteins in head and neck squamous cell carcinoma treated with radiotherapy



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Biography

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Abstract

Head and neck squamous cell carcinoma (HNSCC) has been reported to rank seventh in terms of incidence and sixth in terms of mortality, worldwide, according to the Globocan 2018 report. It is the second most prevalent form of cancer in the Indian male population. Radiotherapy, with concomitant chemotherapy, is the standard treatment for HNSCC. The survival rates of HNSCC patients have remained suboptimal due to development of resistance to treatment, thus, necessitating the need for early identification of patients who are likely to develop resistance. There is little data on the use of biomarkers to assess early response to treatment. Therefore, we decided to explore the differential expression of proteins at different time points of radiotherapy and their correlation with patient outcomes. Serum samples were obtained from oropharyngeal and laryngeal cancer patients who had undergone curative chemo-radiotherapy and whose outcomes were well documented. The samples were categorized into two groups i.e. good and poor responders based on the patient outcome. Peptides obtained by in solution reduction, alkylation and trypsin digestion, were labelled with iTRAQ and subjected to nLC-MS/MS. Targeted mass spectrometry was used for further validation of the target proteins. To our conclusion, proteins belonging to apoptotic pathways, ECM organization, and oncogenic MAP signaling pathways were found to be differentially regulated. On further validation, these identified proteins can provide novel leads for translational research and clinical management.

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