

XPRESS PRESENTATION - OMICS

EVALUATION OF GENES FROM MEMBRANE TRANSPORTERS AS POSSIBLE PREDICTORS OF RESPONSE TO CHEMOTHERAPY TREATMENT IN PATIENTS WITH CERVICAL CANCER

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Cervical cancer (CC) is the leading cause of female morbidity and cancer deaths worldwide. Approximately 70% of patients are diagnosed with locally advanced CC and may progress to metastases. Although chemotherapy treatment is considered adequate, the survival rate remains unsatisfactory. Membrane transporters are a large group of proteins responsible for the maintenance of proper amounts of molecules inside and outside the cells. They

can play a vital role in determining intracellular drug concentrations and cell metabolism. Among them, we can highlight the ATPase transporter family, involved in crucial pathways for the invasion, migration and metastasis of tumor cells. The solute transport protein (SLC) groups also stand out among transporters for playing critical roles in the movement of cytotoxic agents across the neoplastic cell membrane. The potential to determine the efficacy and even the toxicity of chemotherapy gives these transporters a promising role as prognostic biomarkers for cervical cancer. The present study aims to identify possible ATPase transporter and SLC genes that present a correlation between their differential expression pattern and the manifestation of resistance to chemoradiotherapy treatment in patients with cervical cancer, leading to more accurate decision-making and more effective therapy. RNA samples from non-stem cells from 21 responders (R) and 10 non-responders (NR) patients were sequenced using RNA-Seq and then analyzed for differential gene expression (DEGs). Preliminary results demonstrate two large groups of genes with antagonistic differential expression profiles. The first group, composed mainly of the SLC35 and ATP13 families, had overexpressed genes in NR compared to R. The second group, mostly represented by the SLC25 and ATP6 family, was overexpressed in R compared to NR. The data obtained demonstrate that both groups are promising predictors of response to chemoradiotherapy. The diversity of biochemical functions of the SLC and ATPase transporter families, involved in mechanisms of processes such as cell metabolism, cell proliferation, apoptosis, and intracellular drug flow, make them a potential prognostic tool for cervical cancer.