Prognostic Impact of Gene Expression Profile in Squamous Cell Carcinoma and Adenocarcinoma of Cervix

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Background: Cervical cancer is the second cause of cancer-related deaths among women in developing countries. Locally advanced disease is frequently seen, with high rate of failure treatment. Most common histological types are squamous cell (SCC) and adenocarcinoma (AC). The treatment is same for both histologies (concurrent chemoradiation). However, different studies suggest a worse prognosis for AC. Therefore, it is important characterize the biological behavior of the neoplasm for personalize treatment.

Objectives: To characterize a global expression profile between SCC and AC and correlate with clinical outcome after standard treatment in both histological types.

Methods: A group of 32 cervical tumor of patients with locally advanced cervical cancer were included in present study, each patient was followed up clinically during the protocol. Genome-wide expression profile by high-density expression microarray; and class prediction was performed (8 AC; 24 SSC). The profiles were validated by qRT-PCR and immunohistochemistry.

Results: Through the study of group analysis ($p < 0.05$), found 2,780 genes that reveal two molecular groups with correspondence to histological types. The molecular profile with $V < 0.0001$ were grouped with cluster of 63 genes allow clearly observe both groups. The P2RY2, IRF6, S100A2, CALML3 genes confirm our results by qRT-PCR and immunohistochemistry. Finally, the response to standard treatment was evaluated, and show no significant differences between both groups.

Conclusion: The results were a gene expression profile that correlates with each histological type in this cohort. Molecular differences have greater involvement in cellular functions and apparently have no influence on outcome treatment. It is necessary to evaluate a greater number of cases to identify a possible group of genes associated with a worse prognosis.

References: