POSTER - RNA AND TRANSCRIPTOMICS

DIFFERENTIAL EXPRESSION ANALYSIS IN CLEAR CELL OVARIAN CANCER DATA

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Clear cell ovarian carcinoma (OCCC) is a rare and aggressive histological subtype of epithelial ovarian cancer, accounting for approximately 5 to 10% of cases of this neoplasm. It is characterized by a highly chemoresistant phenotype, highlighting the urgent need to identify more effective therapeutic approaches. Unlike other ovarian cancer subtypes, OCCC presents a distinct molecular profile, frequently associated with mutations in the ARID1A, PIK3CA, and PTEN genes, as well as alterations in the Hippo pathway and HIF-1α signaling, suggesting specific mechanisms of oncogenesis and tumor progression. The scarcity of effective therapies for this subtype underscores the need for a deeper understanding of its molecular biology in order to enable the development of new therapeutic strategies. In this study, we performed a differential expression analysis using RNA-seq data from the Genotype-Tissue Expression (GTEx) project as controls and from patients with gene expression profiles of epithelial ovarian cancer (PRJNA783540), both available in public databases. Data processing included normalization, filtering, and statistical analysis using the DESeq2 package, considering an adjusted p-value threshold of < 0.05. Preliminary results showed that differentially expressed mRNAs are linked to pathways involved in hypoxia response, chromosome segregation,

xenobiotic response, and tissue metabolism. On the other hand, lncRNAs were mainly associated with the regulation of lipase and phospholipase activity. These findings suggest a complex molecular profile in OCCC, where hypoxia promotes cell survival and treatment resistance, xenobiotic response emerges as a key mechanism of chemotherapy resistance, and lncRNAs regulating lipases and phospholipases indicate a dependence on lipid metabolism for tumor maintenance. These combined factors make OCCC a particularly challenging cancer, but also open avenues for new therapeutic strategies, including the modulation of lipid metabolism and resistance mechanisms. Experimental validation and correlation with clinical data will be essential to elucidate the impact of these molecular signatures on disease progression and the development of personalized treatments for patients with OCCC.

Palavras-chave: keywords: ovarian cancer; clear cell carcinoma; gene expression; rna-seq; biomarkers.