A Computer-Based Integrated Analysis of Genomic Signatures in Ovarian Cancer

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Ovarian cancer is one of the deadliest gynecological cancers as a result of a lack of robust early detection methods and high rates of resistance after initial chemotherapy. Many experiments have already identified a plethora of molecular diagnostic and prognostic biomarkers in this disease, but did not carry out any extensive integrative analyses that provide insight into mechanisms of tumorigenesis. As a result, the overall goal of my project was to perform a computer-based integrative analysis of molecular aberrations in ovarian tumors. Using data downloaded from The Cancer Genome Atlas and R programming, I determined and tested the predictive potential of expression profiles for abnormal mRNA expression, miRNA expression, and DNA methylation and performed pathway enrichment analysis on these signatures. I then utilized them in conjunction with data collected from cBioPortal, DAVID, and published studies and employed a variety of statistical tests and algorithms downloaded in R to propose mechanisms of aberrant gene expression in ovarian cancer. The results generated 6 robust expression signatures, determined 48 highly predictive features of ovarian cancer, produced multiple pathways altered in this disease, and yielded a variety of processes that could possibly contribute to the abnormal expression for a large set of genes. Although mechanisms could not be identified for every gene in the gene expression signatures and the data presented in this report still remain to be experimentally validated, these results nevertheless serve as valuable insight into the molecular mechanisms of ovarian tumorigenesis and hold important implications in diagnostic, therapeutic, and prognostic applications.

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