Big Data Analytics: Identification of Novel Cancer Progression Gene Signatures for Precision/ Personalized Medicine

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Precision and personalized medicine are emerging approaches for cancer therapeutics. By characterizing patients' risk for adverse developments such as tumor progression, specialized treatment plans can be tailored to individual patients. However, most current biomarkers are lacking in performance level, limiting their clinical application in precision/personalized medicine. To identify better biomarkers suitable for precision medicine, a novel discovery pipeline analyzing gene expression profiling, cancer survival gene screens, and clinical data in a large cohort of cancer patients was used. The rationale behind this methodology is that highly-expressed cancer survival genes are better candidates for biomarkers of disease progression. By using this approach, 22 genes were identified as a progression gene signature (PGS) in lung adenocarcinoma (LUAD) and designated as LUAD-PGS. Further analyses using pair-wise comparison of receiver operating characteristic (ROC) curves and risk score calculations revealed that LUAD-PGS significantly outperformed current biomarkers in accurately predicting patient risk for tumor progression. Implementing the same working pipeline, novel PGSs were identified in other cancers with higher performance levels than existing biomarkers. Taken together, the results from this study demonstrate the utility of the new biomarker discovery pipeline developed herein in identifying novel PGSs that more accurately predict patient risk of cancer progression, thereby meeting a need in precision medicine.

Awards Won:

Fourth Award of $500