Complexity of molecular alterations impacts pancreatic cancer prognosis.

Individualized cancer treatment (e.g., targeted therapy) based on molecular alterations has emerged as an important strategy to improve the current standard-of-care chemotherapy. A large number of studies have demonstrated the importance of biomarkers not only in predicting prognosis but more importantly in predicting the response towards therapies. For example, amplification or mutation status of the two biomarkers HER2 (human epidermal growth factor 2) and BRCA (breast cancer) can be used to decide on a specific targeted therapy in breast cancer. However, no biomarkers with a similar clinical impact have been identified in pancreatic ductal adenocarcinoma. Although many genome-wide and proteome-based high-throughput studies have identified candidate genes or proteins as promising biomarkers, none of them were eventually transferred into the clinical setting. Notably, the most reliable markers for predicting prognosis are still the tumor stage and grade and biomarkers for therapy response remain undefined. One reason lies in the lack of systemic approaches to analyze the complexity of dominating cancer pathways and the impact of such signal complexity on prognosis and therapy response.