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# Integrative Translational Staging System With Clinical Parameters Provides Precision Strategies For Resectable Pancreatic Cancer.

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**Background** : Even though the 8th edition AJCC cancer staging system for pancreatic cancer has validated major clinicopathologic factors in multiple clinical cohorts, there is still an unmet need for integrative consideration using multi-omics data to stratify the patients with pancreatic cancer elaborately.

**Methods** : We performed a comprehensive analysis and profiling using genomic, transcriptomic, and proteomic data from TCGA-PAAD and other translational cohorts (4 cohorts, n=340). Molecular features and major subtypes were analyzed mutually with clinical and pathologic factors, especially the 8th AJCC staging system.

**Results** : Aggressive molecular subtypes, basal-like and squamous subtype, were significantly associated with a higher nodal stage, but tumor size didn't show a clear association with molecular features. The activated stroma of the pancreatic cancer microenvironment was significantly correlated with poor differentiation and large tumor size. The mutational pattern of KRAS and several transcriptomic pathways, such as epithelial-mesenchymal transition and DNA repair, were differently presented in each clinical stage from the 8th AJCC TNM staging system. The optimal algorithm was identified to show significantly higher performance for the prediction for cancer relapse and cancer-specific survival in discovery and validation cohorts. The in-silico prediction for molecular target agents and immunotherapy was performed for final clusters from the optimal stratification system revealed from the integrative analysis.

**Conclusions** : Our comprehensive multi-omics analysis reveals clear needs for the combination of clinical staging and molecular profiling and provides crucial evidence for precision strategy in patients with resectable pancreatic cancer.

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