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A Cell-of-Origin Signature for Informing Pancreatic Ductal Adenocarcinoma Treatment

Pancreatic ductal adenocarcinoma (PDAC) is projected to become the second leading cause of cancer-related deaths in the United States by 2030. Despite advances in cancer research, the 5-year survival rate for patients with PDAC remains only 9%, largely due to late-stage diagnosis and limited effectiveness of current therapies.

While PDAC has been categorized into multiple molecular subtypes based on patterns of gene expression, these classification systems are not routinely used to guide clinical treatment. One major challenge is the limited understanding of the biological mechanisms that drive distinct molecular subtypes. In addition, there remains a lack of consensus regarding both the number of PDAC subtypes and the specific gene signatures that define them. Establishing a more biologically grounded and clinically relevant molecular classification system may improve the development of targeted therapies for distinct subtypes of the disease.

The Attardi lab at Stanford has designed a novel approach to identify gene expression profiles that that classify PDACs into specific subtypes based on different cell types of origin. Building on this framework, transcriptomic data from patient tumors can be analyzed to determine whether they are enriched for these gene expression signatures, enabling more precise molecular classification of the disease. Linking specific PDAC subtypes to their responses to different drugs could help improve early detection and drive more personalized and effective treatment options for patients with pancreatic cancer.

Stage of Development: *In vivo*

Applications

- Diagnosis and treatment of pancreatic ductal adenocarcinoma

Advantages

- Reliable
  - Cell-of-origin signatures independently showed significant associations with patient survival outcomes across multiple data sets
- Better than existing approaches
  - Molecular signatures derived from mouse models reflect cell biology that cannot be achieved with bioinformatics

Innovators

- Laura Attardi
- Christina Curtis
- Brittany Flowers
- Hang Xu
- Jose Seoane Fernandez

Licensing Contact

Imelda Oropeza

Senior Licensing Manager, Physcial Sciences

Email