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Summary

SINGLE CELL TRANSCRIPTOMIC ANALYSES IMPLICATE AN IMMUNOSUPPRESSIVE TUMOR MICROENVIRONMENT IN PANCREATIC CANCER LIVER METASTASIS

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Pancreas

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Single-cell RNA sequencing of matched primary pancreatic tumors and liver metastases from four patients reveals distinct cellular compositions and identifies specific stromal and immune cell subtypes critical to the metastatic microenvironment.

KEY POINTS

- Epithelial cancer cells showed distinct transcriptomic profiles in liver metastases with clearly defined evolutionary routes from primary tumors
- Specific cell subtypes were identified as critical to the pro-tumor metastatic microenvironment including RGS5+ cancer-associated fibroblasts, CCL18+ lipid-associated macrophages, S100A8+ neutrophils, and FOXP3+ regulatory T cells
- Four new biomarkers associated with PDAC metastasis and poor prognosis were identified: LITAF, SPRR1B, KLK7, and LGALS9
- Cellular interactome analysis revealed that lack of tumor-immune cell interaction in metastatic tissues contributes to immunosuppressive microenvironment formation
- The authors suggest this first single-cell analysis of matched PDAC primary and metastatic tissues may inform design of novel targeted therapies

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