Mass spectrometry-based protein profiling of circulating exosomes for predicting the prognosis of intraductal pancreatic mucinous neoplasms

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Disclosures

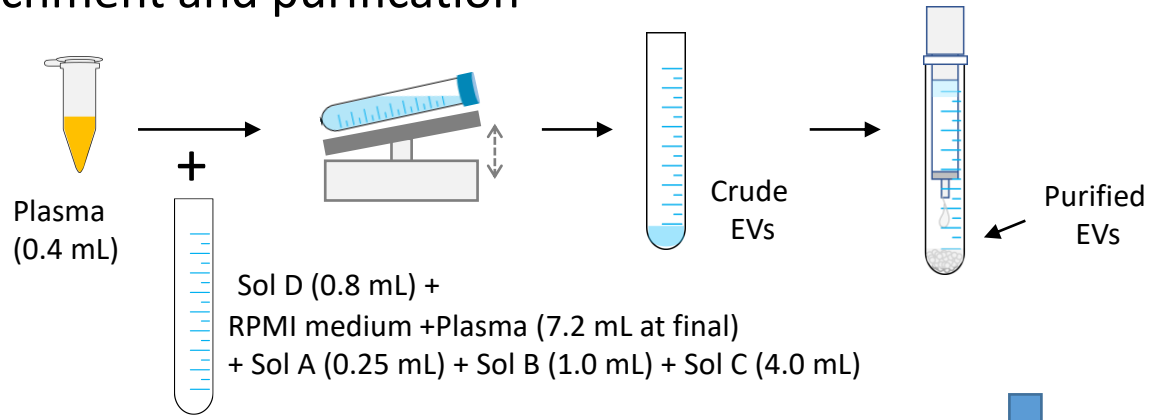
- Nothing to disclose

Background / Aims

- Current radiographic criteria-based strategies for IPMN showed limited benefit to identify patients with high-grade dysplasia or invasive cancer
- In tumor microenvironment, there are cancer cells with various genetic mutations, stromal cells, mesenchymal cells, recruited immune cells, and stromal components that can contribute the composition of tumor-associated exosome
- This study aimed to find out key exosomal proteins that distinguish IPMN from IPMN associated carcinoma

Methods: Exosomal vesicle isolation

- EV Enrichment and purification



cEV-associated protein profiling
By **Mass Spec.**

Methods

- After analyzing exosomal differentially expressed proteins(DEPs) from 6 patients enrolled in discovery session, 8 patients were enrolled and underwent proteomics analysis under blindness.

Results

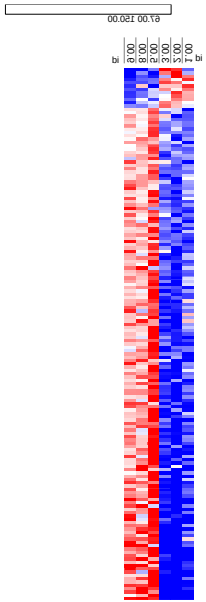
- From 400 µL plasma, 30-70 µg exosomes were isolated by ExoLutE® kit

- Size-exclusion chromatographic analysis confirmed that all isolated samples were pure enough to perform downstream quantitative proteomic analysis

Results

- LC-MS/MS for distinguishing IPMC from IPMN patients

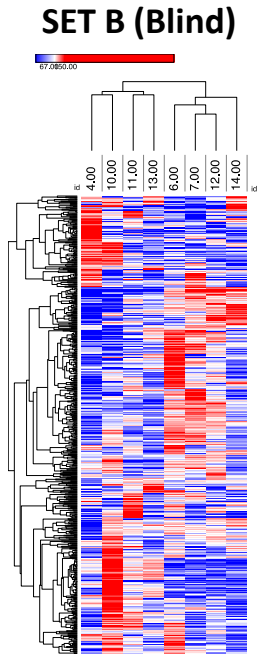
SET A (Known)



91 DEPs were identified in discovery session

Results

- LC-MS/MS for distinguishing IPMC from IPMN patients



77 DEPs were identified
from the independent clinical subset in validation cohort

By DEPs, IPMC and IPMN could be identified with 100% accuracy under blindness

9 exosomal proteins have considerable potential for predicting IPMCs from IPMNs by combinatorial analysis of proteins common to DEPs in both sessions

Conclusions

- Based on potential roles of exosomes in pathophysiology, analyzing protein component of circulating exosomes could help predict and identify IPMN with malignant potential.