Multivariant Analysis to Decipher the Human Pancreatic Cancer Proteome to Identify Novel Biomarkers and Therapeutic Targets

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Abstract

The pancreatic cancer proteome is a vital target for disease diagnosis and management. The characterization of the proteome allows for the development of personalized treatments and understanding of disease progression. In this study, we used mass spectrometry to identify and quantify proteins associated with pancreatic cancer.

Methods

We used shotgun proteomics to analyze tissue samples from 9 malignant liver metastases and their corresponding normal adjacent tissues. The tissue samples were lysed, digested, and differentially labeled with isobaric Tandem Mass Tags. The tagged peptides were then analyzed using LC-MS/MS. The data was processed using MaxQuant software.

Results

30,811 peptides and 3,960 proteins were identified from the analysis. 1,842 of them were quantified and 917 were used for multivariate analysis.

Conclusions

This project utilized a quantitative proteomics approach designed to:
1. Identify differentially expressed proteins in the human metastatic PDAC liver metastases.
2. Ascertain proteins associated with PDAC patient survival to build a predictive model for prognosis.
3. Identify potential therapeutic targets to promote patient survival.

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The tandem mass tag (TMT) methodology

Figure 1. The proteomic analysis workflow for the native sample.

Figure 2. The score plot of the native versus the normal adjacent tissue in the PrinciPal Component Analysis.

Figure 3. Characterization of PDAC Phenotypes

Figure 4. Towards a Clinical Subtyping Scheme

Figure 5. PDAC Proteome versus Survival

Concluding remarks

This analysis was looking for biomarkers potentially correlating with the patient survival days after the tumor surgery. The analysis is driven by the protein expressions. In the future, the analysis may lead to the identification of new therapeutic targets for PDAC patients.