

Poster 013 Expression analysis of PLVAP in hepatocellular carcinoma patient samples

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Background

Hepatocellular carcinoma (HCC) is a very prevalent tumor worldwide and the most common primary liver tumor. It is characterized by a high mortality and morbidity. Although several treatment methods are available, treatment options are limited due to underlying liver cirrhosis or late diagnosis. To further improve diagnosis and therapeutic approaches, it is urgent to have a better understanding of key aspects of HCC development.

Methods and Results:

Multiple HCC datasets were combined for a comprehensive bioinformatic analysis using two independent analysis methods, Lasso regression and SVM-RFE. Seven differentially expressed genes were identified (CLEC4M, ECM1, DBH, CFP, NAT2, CXCL14, PLVAP) and screened for their diagnostic and prognostic potential. A correlation analysis, determining the relationship between gene expression and common biomarkers was added. For one of the targets, PLVAP, we found a correlation to overall survival (OS) of HCC patients, indicating its potential diagnostic relevance. Finally, we investigated the protein expression of PLVAP in HCC tissue specimens (n=20) provided by the HTCR/Biobank. The cell morphology was analyzed using Hematoxylin-Eosin staining and target specific expression was done using immunofluorescence (IF) staining. PLVAP is reported to be highly expressed in endothelial cells with a moderate correlation with vascular endothelial biomarkers CD31, CD34, CD105, and VEGFR2. This was confirmed by strong PLVAP detection in cells of vascular structures, which are known to be lined by endothelial cells. Expression profile of PLVAP was then correlated with corresponding clinical information to assess its prognostic potential, revealing an inverse correlation between PLVAP expression and HCC patients T stage.

Conclusion:

Our study identified several genes in HCC data sets with potential value as prognostic markers. For one, PLVAP, we found an inverse correlation in its expression to the clinically relevant T staging of HCC patients indicating its possible relevance during tumor growth and a possible diagnostic value. Further work aims to confirm this observation in an increased set of HCC samples as well as by adding endothelial-specific staining.