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Serum MALDI Profiling for Pancreatic Ductal Adenocarcinoma Biomarkers Discovery: A Pilot Study

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Context The available biomarkers for diagnosing pancreatic cancer, like CA 19-9, lack in sensitivity and specificity for an early detection requiring additional efforts to better understand the molecular basis of this pathology and to find novel strategies for a more accurate patient's screening. Recent advances in quantitative proteomics based on non-invasive approaches have stimulated their clinical applications founded on the analysis of biological fluids like serum. **Objective** To detect substances able to differentiate pancreatic cancer patients from healthy subjects. **Methods** Ten sera from histologically proven pancreatic ductal adenocarcinoma patients and 10 from healthy controls comparable for sex and age were analyzed in order to evaluate the small proteins and peptides which could discriminate the two classes. In order to reduce the dynamic range, the high abundant protein components of serum were removed and the MALDI profiling was adopted for the detection of differentially changed species possibly related to the tumor onset. After acquisition, spectra were processed by ClinProTools for statistics (Wilcoxon test $P<0.05$, PCA analysis and $AUC>0.800$). **Results:** MALDI profiling allowed to detect 82 peaks in the acquisition range of 1.5-35 kDa which underwent statistical analysis. The comparison between pathological and control samples revealed a high discrimination power as indicated by the presence of 35 significantly changed peaks (10 over- and 25 under-expressed in cancer) with AUC not lower than 0.872. In addition, several peaks were found strongly represented exclusively in one of the classes suggesting the presence of proteins and peptides which characterize one of the two states, only. **Conclusions** These preliminary results suggest the potentiality of this approach to discriminate pancreatic cancer patients and controls. The next step will consist on their validation, by increasing the number of analyzed samples, and identification of molecules characterizing the changed peaks associating them to their histological pattern.