Molecular characterization of pancreatic cytology for improving diagnostic and clinical yield in pancreatic adenocarcinoma

Pancreatic adenocarcinoma -PDAC- ranks among the ones with the worst prognosis. In PDAC therapeutic strategies are largely ineffective and it frequently poses diagnostic challenges. The majority of patients present with late disease and only 20% have surgically resectable tumours. The median overall survival associated with the current chemotherapy is less than 1 year. Moreover, diagnosis can be difficult: benign conditions can mimic malignancy on imaging studies, limiting the utility of these techniques and biopsy acquisition presents a challenge for endoscopists, often resulting in small and limited tissue specimens. The most effective diagnostic procedure is based on cytological material obtained during echoendoscopic evaluation of the pancreas with Fine Needle Aspiration –FNA-_technique. FNA is at present the standard of care in obtaining pathological material. More importantly, this is often the only tumor material available for further characterization of the neoplastic lesion. However this cytological sample is considered to have limited potential for more extensive molecular characterization. These diagnostic challenges highlight the need and the aim of this project for more accurate pathological and molecular characterization of PDAC. This aim can be reached through:1)Improving the quality, the quantity and the processing of the cytologic sampling obtained during echoendoscopy in order to extend the diagnostic potential of this material; 2)Utilizing cytological material to identify a specific set of genes that can molecularly characterize the tumor sample and contribute to differential diagnosis of selected neoplastic diseases of the pancreas; 3)Establishing protocols for in vitro culturing the neoplastic cells obtained by FNA and generate potential clinically relevant data; 4)Characterizing the genomic profile of PDAC with a comprehensive panel of genes utilizing NGS in order to identify molecular signatures that could permit a better selection of appropriate chemotherapeutic approach.

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