Identification of malignancy factors by analyzing cystic tumors of the pancreas.

AIM: The diversity in the aggressiveness of cystic tumors of the pancreas - ranging from the usually benign serous cystadenoma to lesions of variable degrees of malignancy - was utilized for the identification of molecular factors that are involved in the occurrence of malignancy.

METHODS: We analyzed the transcript profiles of different cystic tumor types. The results were confirmed at the protein level by immunohistochemistry. Also, functional studies with siRNA silencing were performed. RESULTS: Expression variations at the RNA and protein level were identified that are closely correlated with the degree of malignancy. Besides, all tumors could be classified effectively by this means. Many of the identified factors had not previously been known to be associated with malignant cystic lesions. siRNA silencing of the gene with the most prominent variation - the anti-apoptotic factor FASTK (Fas-activated serine/threonine kinase) - revealed a regulative effect on several genes known to be relevant to the development of tumors.

CONCLUSION: By a molecular analysis of rare types of pancreatic cancer, which are less frequent in terms of disease, variations could be identified that could be critical for the regulation of malignancy and thus relevant to the treatment of also the majority of pancreatic tumors.