Few genes are associated with the capability of pancreatic ductal adenocarcinoma cells to grow in the liver of nude rats.

Abstract:

Owing to aggressiveness and chemoresistance, pancreatic ductal adenocarcinoma (PDAC) is characterised by a poor prognosis. To address this disease-specific dilemma we aimed to establish animal models, which can be used for identifying new specific tumor markers, as well as serving as tools for potential therapeutic approaches. From a panel of sixteen pancreatic cancer cell lines, two human (Suit2-007 and Suit2-013) and a rat (ASML) cell line were selected for their properties to grow in the liver of male RNU rats and mimic liver metastasis of PDAC. For better monitoring of metastatic tumor growth in vivo, all three pancreatic cancer cell lines were stably transfected with eGFP and luciferase marker genes. In addition, the mRNA expression profile of 13 human PDAC cell lines was analyzed by BeadChip array analysis. Only 33 genes and 5 signaling pathways were identified as significantly associated with the ability of the cell lines to grow initially and/or consistently in rat liver. Only a minority of these genes (osteopontin, matrix metalloproteinase-1 and insulin-like growth factor 1) has been intensively studied and shown to be closely related to cancer progression. The function of the remaining 30 genes ranges from moderate to poorly investigated, and their function in cancer progression is still unclear. The
ensuing three pancreatic cancer liver metastasis models vary in their aggressiveness and macroscopic growth. They will be used for preclinical evaluation of new therapeutic approaches aiming at the genes identified.