~~With~~Thanks to new genomic and epigenomic screening methods, understanding of pancreatic cancer has ~~been~~increased greatly ~~improved~~ in recent years. Comprehensive pancreatic cancer genome studies have indicated that there is an association between most of the genetic alterations and particular core signaling pathways, including genes with a high ~~frequent mutate genes.~~frequency of mutation. Histological precursors ~~for~~ of pancreatic cancer ~~of pancreas, namely,~~ including pancreatic intraepithelial neoplasia, mucinous cystic neoplasms, and intraductal papillary mucinous neoplasms, ~~are~~have been well ~~known following morphological~~characterized by morphologic studies. ~~In addition, recent genome~~Recent genomic screening methods have shown that each of these precursor lesions ~~were~~is associated with specific ~~molecule~~molecular alterations. In ~~the~~ familial cases of pancreatic cancer, ~~multiple~~several causative genes ~~responsible were~~have been identified. Furthermore, epigenetic changes are considered to play an important role in ~~progressing~~the progression of pancreatic cancer. Some tumor ~~suppression~~suppressor genes are reported to be silenced due to aberrant hypermethylation of the promoter CpG island ~~hypermethylation.~~. Several ~~of~~ genetically ~~modified~~ engineered mouse models ~~were created, and provided a tool~~have been developed, which ~~is~~are reliable ~~to identify~~tools for identifying molecules ~~mainly~~that are involved ~~with~~in the development or progression of pancreatic cancer.