Expression of mesothelin mRNA in the pancreatic juice from patients with various pancreatic diseases

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In recent analysis of gene expression in pancreatic carcinoma (PCa) using serial analysis of gene expression (SAGE) by Ryu et al., the tag for the mesothelin mRNA transcript was present in seven of eight SAGE libraries derived from PCa but not in the two SAGE libraries derived from normal pancreatic duct epithelial cells. Mesothelin mRNA expression was confirmed by *in situ* hybridization in 4 of 4 resected primary PCa and by RT-PCR in 18 of 20 PCa cell lines. Moreover, mesothelin protein expression was confirmed by immunohistochemistry in all 60 resected primary PCa tissues by Argani et al. To improve the genetic diagnosis of PCa, we evaluated mesothelin mRNA expression in pure pancreatic juices (PPJ) obtained from patients with PCa, chronic pancreatitis (CP), and intraductal papillary mucinous tumor (IPMT) by reverse-transcription PCR (RT-PCR). Two products of which the size was 308 and 226 bp were obtained by RT-PCR and the 308 bp RT-PCR product was confirmed as that derived from genomic DNA by direct DNA sequencing. Mesothelin mRNA expression was found out by RT-PCR in 7 (47%) of 15 PPJ from PCa, 5 (45%) of 11 PPJ from IPMT, and 1 (5%) of 20 PPJ from CP. Moreover, RT-PCR product (226 bp) of mesothelin mRNA in PPJ samples with PCa was stronger than that in PPJ samples with IPMT as shown in Figure. These results suggest that detection of mesothelin mRNA in the PPJ may have potential diagnostic implication for pancreatic tumor, and its quantitative analysis may be more useful for genetic diagnosis of PCa.

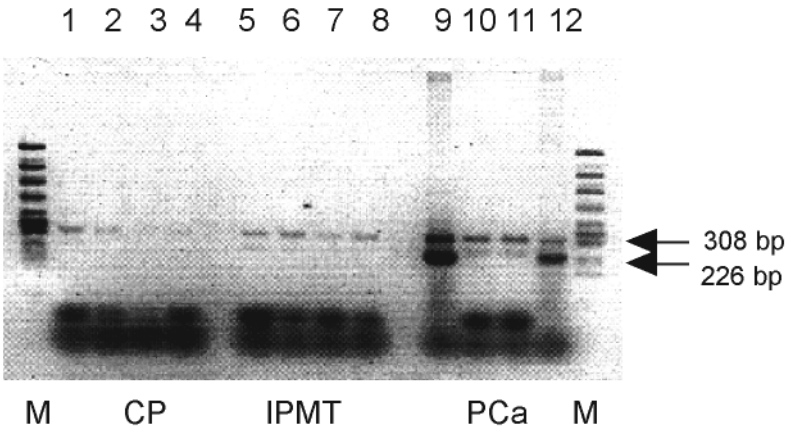

Figure Mesothelin mRNA expression in PPJ by RT-PCR from various pancreatic diseases.
M: molecular markers (ϕX174/Hinc II digest); CP: chronic pancreatitis (1~4); IPMT: intraductal papillary mucinous tumor (5~8) ; PCa: pancreatic carcinoma (9~12)