AB072. P044. Analyses of aberrant methylation of tumor suppressive miRNAs in the patients with pancreaticobiliary diseases in bile juice

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Backgrounds: Dysregulation of miRNA is associated with carcinogenesis of various cancers. However, there have been no reports about epigenetic abnormalities of tumor suppressive miRNA using the samples other than pancreatic tissues in the patients with pancreatic cancer (PC). In this study, we tried to examine methylation of tumor suppressive miRNAs in the patients with pancreaticobiliary diseases in order to detect miRNAs specific for PC in bile juice.

Methods: Bile juice was collected by endoscopically or percutaneously in 26 patients with PC, nine patients with biliary tract cancer (BTC), and ten patients with benign pancreaticobiliary diseases (BD). DNA was extracted from bile juice, treated with sodium bisulfite, and amplified by PCR. Next, sequencing analyses were performed by next generation sequencer and methylation rate were evaluated in 16 tumor suppressive miRNAs.

Results: Moderate to high methylation was observed in eight miRNAs (miR-30a-3p, 34a, 34bc, 96, 126, 141, 200a, and 200bc). In miR-34a and 34bc, methylation rate of miRNA in the patients with BTC was significantly higher than that with PC and BD. On the other hand, in miR-126, methylation rate of miRNA in the patients with BD was significantly higher than that with PC and BTC. However, methylation rate of miRNA in the patients with PC was not significantly higher than that with other pancreaticobiliary diseases.

Conclusions: Methylation analyses of miRNAs in bile juice were supposed to be useful for differentiation of pancreaticobiliary diseases. Further investigation is necessary for detecting tumor suppressive miRNA specific for PC.

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