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# Microbiome Markers Of Pancreatic Cancer Based On Bacteria-Derived Extracellular Vesicles Acquired From Blood Samples: A Retrospective Propensity Score Matching Analysis

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**Background** : Novel biomarkers for early diagnosis of pancreatic cancer (PC) are necessary to improve prognosis.

**Methods** : We aimed to discover candidate biomarkers by identifying compositional differences of microbiome between patients with PC (n = 38) and healthy controls (n = 52), using microbial extracellular vesicles (EVs) acquired from blood samples. Composition analysis was performed using 16S rRNA gene analysis and bacteria-derived EVs. Statistically significant differences in microbial compositions were used to construct PC prediction models after propensity score matching analysis to reduce other possible biases.

**Results** : Between-group differences in microbial compositions were identified at the phylum and genus levels. At the phylum level, three species (Verrucomicrobia, Deferribacteres, and Bacteroidetes) were more abundant and one species (Actinobacteria) was less abundant in PC patients. At the genus level, four species (Stenotrophomonas, Sphingomonas, Propionibacterium, and Corynebacterium) were less abundant and six species (Ruminococcaceae UCG-014, Lachnospiraceae NK4A136 group, Akkermansia, Turicibacter, Ruminiclostridium, and Lachnospiraceae UCG-001) were more abundant in PC patients. Using the best combination of these microbiome markers, we constructed a PC prediction model that yielded a high area under the receiver operating characteristic curve (0.966 and 1.000, at the phylum and genus level, respectively).

**Conclusions** : These microbiome markers, which altered microbial compositions, are therefore candidate biomarkers for early diagnosis of PC.

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