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Exploring microbiome in gastric cancer microenvironment: a novel diagnostic strategy

Mun-Seong Ik[1], Yu Yeuni[2], and Yun Hak Kim[3,4*]

[1] *Interdisplinary of Genomic Data Science, School of Medicine, Pusan National University*
[2] *Biomedical Research Institute, School of Medicine, Pusan National University*
[3] *Department of Anatomy, School of Medicine, Pusan National University*
[4] *Department of Biomedical informatics, School of Medicine, Pusan National University*
**Corresponding author: yunhak10510@pusan.ac.kr*

The intricate interplay between the metabolic processes of the intestinal microbiome and its host constitutes a pivotal component of overall health. This interaction is partially facilitated through the secretion of microbial-derived metabolites that gain access to the circulatory system. Moreover, the intestinal microbiome exerts a significant influence on a range of gastrointestinal diseases. In this study, our primary aim is to identify microbiota that could potentially impact the development of gastric cancer.

DNA sequencing data from 431 patients diagnosed with gastric cancer, obtained from The Cancer Genome Atlas (TCGA), were subjected to analysis. This dataset comprised 395 primary tumor samples and 36 solid tissue normal samples. A total of 1,993 genera were annotated using Kraken2. Subsequently, we conducted analyses of alpha and beta diversity and identified the relative abundance of genera and phyla. A differential abundance analysis was conducted using ALDEx2 to identify genera that exhibit significant differences between primary tumor and solid tissue normal. We identified only 25 genera statistically significant. Using these genera, we conducted a Kaplan-Meier survival analysis with primary cancer samples, categorizing them into two groups based on the median fraction. Five genera from 25 genera showed significant association with survival rate. Subsequently, a correlation analysis was executed between the five strains and immune cells(naïve B cell, CD8+ central memory T cell, Macrophage M1) which are estimated from RNA sequencing utilizing the XCELL algorithm. The findings from this analysis demonstrated a significant relationship between *Legionella, Methylomicrobium* bacteria and immune cells.

Legionella and *Methylomicrobium* have been identified as potential diagnostic and prognostic markers associated with gastric cancer. This study provides novel insights and holds promise for advancements in the diagnosis of gastric cancer by elucidating the intricate interplay between the microbiome and the disease.