Analysis of blood microbiome in patients with gastric cancer

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Background

- Gastric cancer (GC) is one of the most common cancers in the world and third leading cause of cancer-related death.
- Microbiome is associated with various diseases as well as with GC.
- Bacterial DNA corresponds to various states of human health.

Aim

To perform a microbiome analysis and identify possible circulating biomarkers for GC.

Methods

- 35 GC patients and 43 Controls.
- DNA extracting from blood plasma.
- The V1–V2 region of the bacterial 16S rRNA sequencing on a Illumina MiSeq, using 27F and 338R primers.
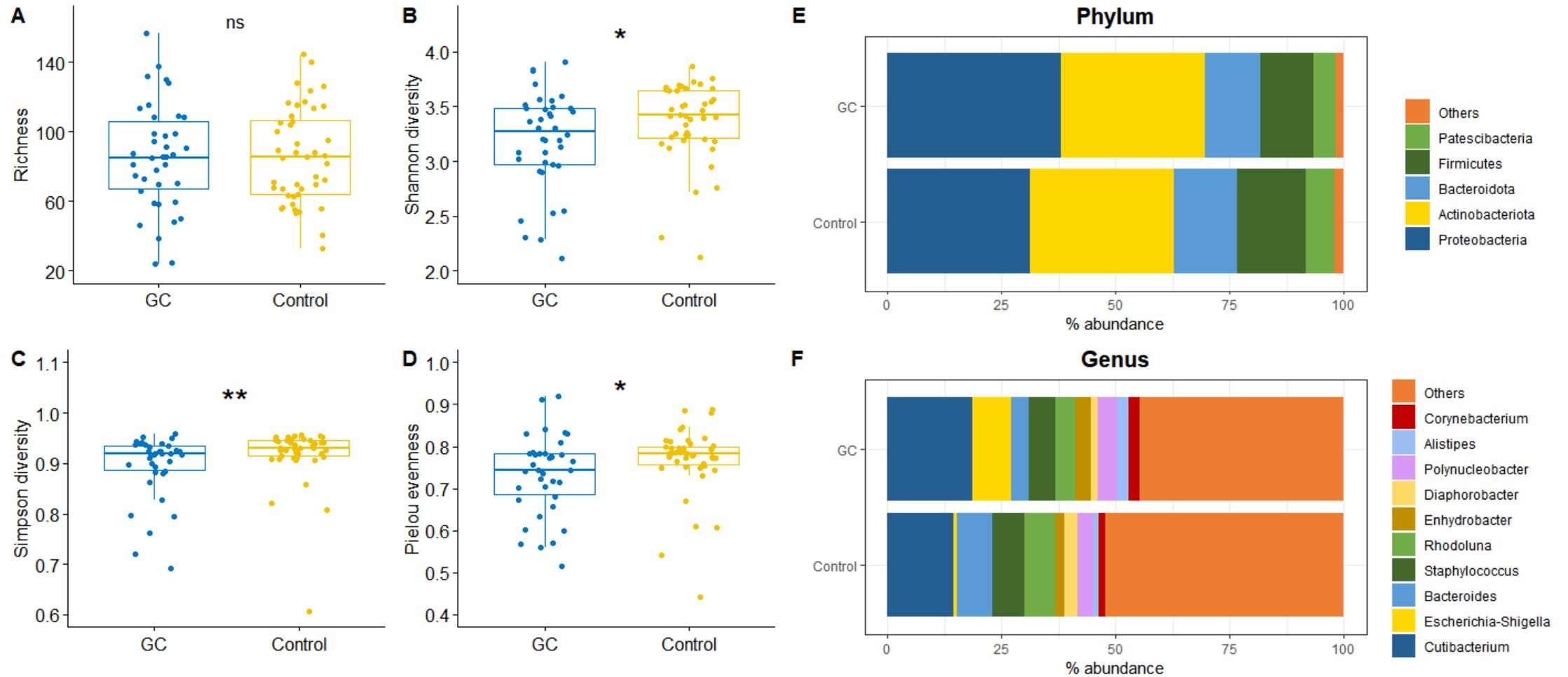- Bioinformatic and statistical analysis.

Research Results (1)

Figure 1. Comparison of plasma microbiome among healthy controls (Controls) and patients with gastric cancer (GC). (A-D) alpha diversity. (E,F) Barplots of the taxonomic profiles. $**P < 0.01$, $*P < 0.05$, ns- not significant.

Research Results (2)

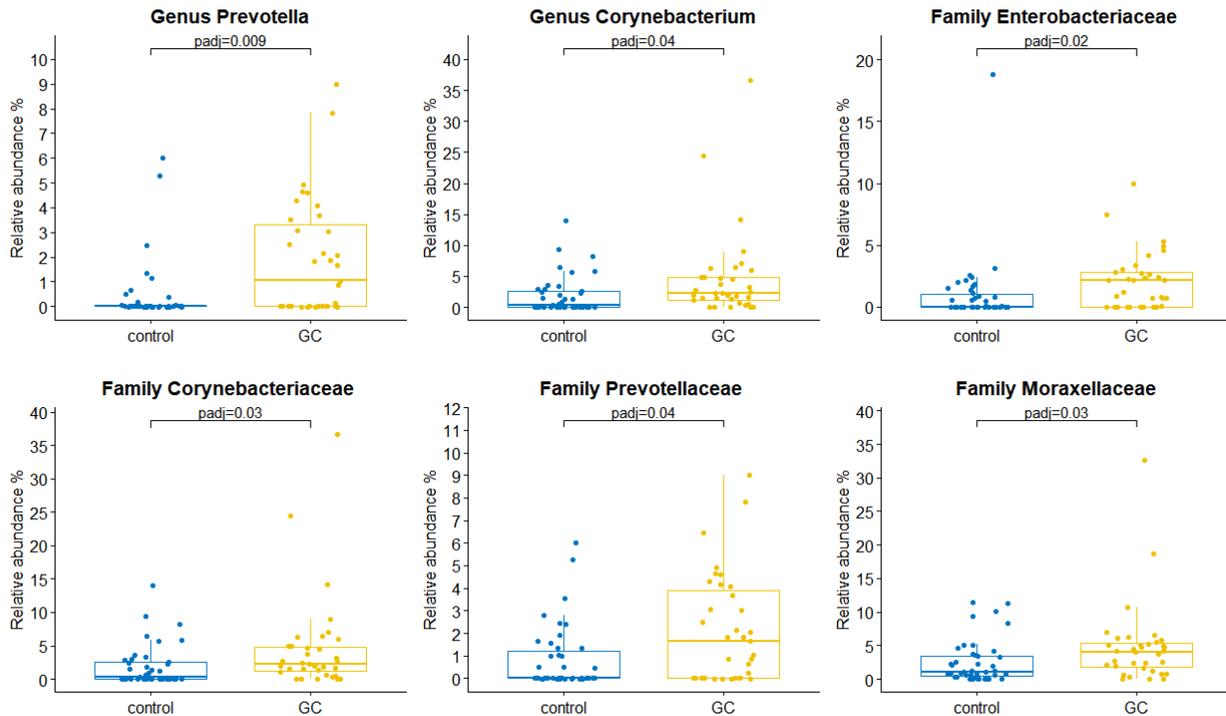Differential abundance analysis (GC vs Controls, Mann-Whitney U test, FDR) :

Figure 2. Boxplots of significantly different bacterial genera and families between control and GC groups.

Association with clinical data:

g. Prevotella
- intestinal tumour growing type
- absence of metastases (M0)
- absence or a small number of cancer cells in the lymph nodes (N0-N1)
- larger tumor (T3-T4)

g. Corynebacterium
- diffuse tumour growing type
- low cell differentiation (G3)

f. Enterobacteriaceae
- diffuse tumour growing type
- present of metastases (M0)
- absence or a small number of cancer cells in the lymph nodes (N0-N1)
- low cell differentiation (G3)

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Conclusions

1. Global circulating microbiome profile of GC patients differs from that of the control group.
2. GC patients' blood microbiome are less diverse as controls.
3. *Prevotella, Corynebacterium, Corynebacteriaceae, Prevotellaceae, Moraxellaceae,* and *Enterobacteriaceae* could presumably be used as clinical biomarkers of GC.