بسم اللہ الرحمن الرحیم

Intestinal bacteria are potential biomarkers for gastric cancer

استاد مربوطه: دکتر پورسینا

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Contents

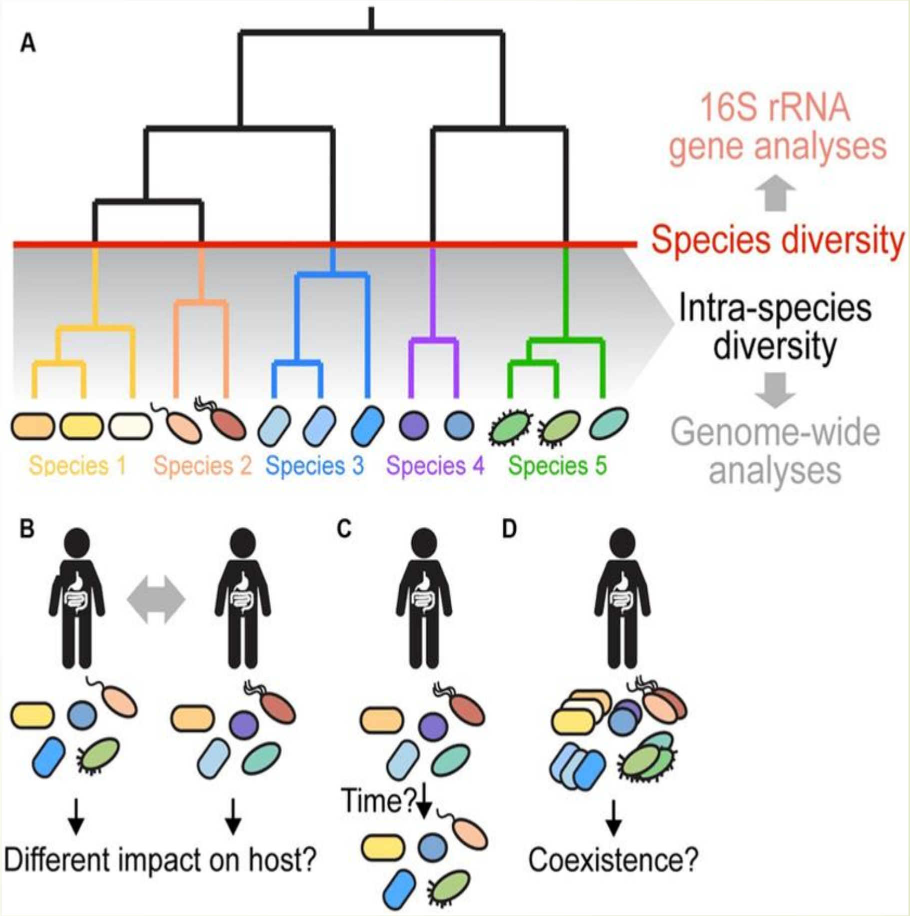
Introduction

- Gastric cancer is a common malignant tumor
- Recent studies have shown that bacterial load and microbial diversity are higher in patients with gastric cancer
- Some microorganisms producing various short-chain fatty acids (SCFAs)
- The possible role of *Desulfovibrio* in gastric cancer was assessed with H2S-treated HT-29 cell

16S sequencing for diversity

- Total fecal genome DNA was extracted

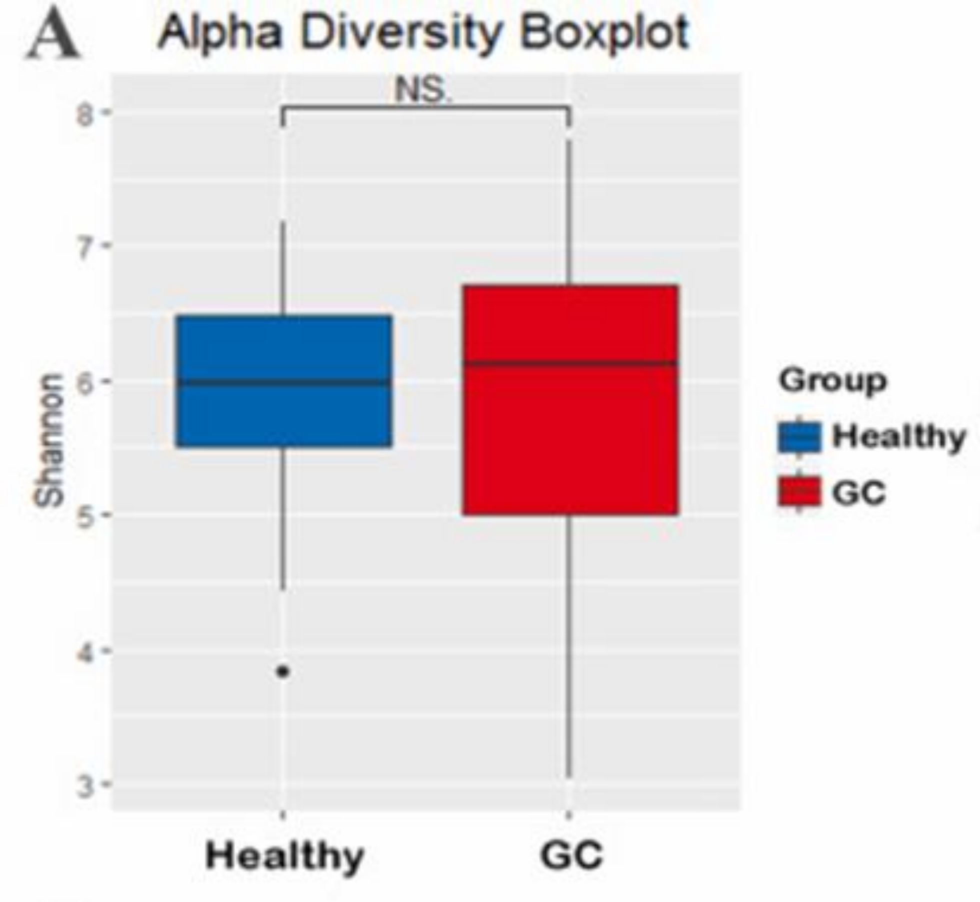
- Operational taxonomic unit or OTU is considered as the **basic unit used in numerical taxonomy**



The comparison of fecal microbiota shows that gastric cancer patients had lower between-sample microbial **diversities** than healthy people

The comparison of fecal microbiota

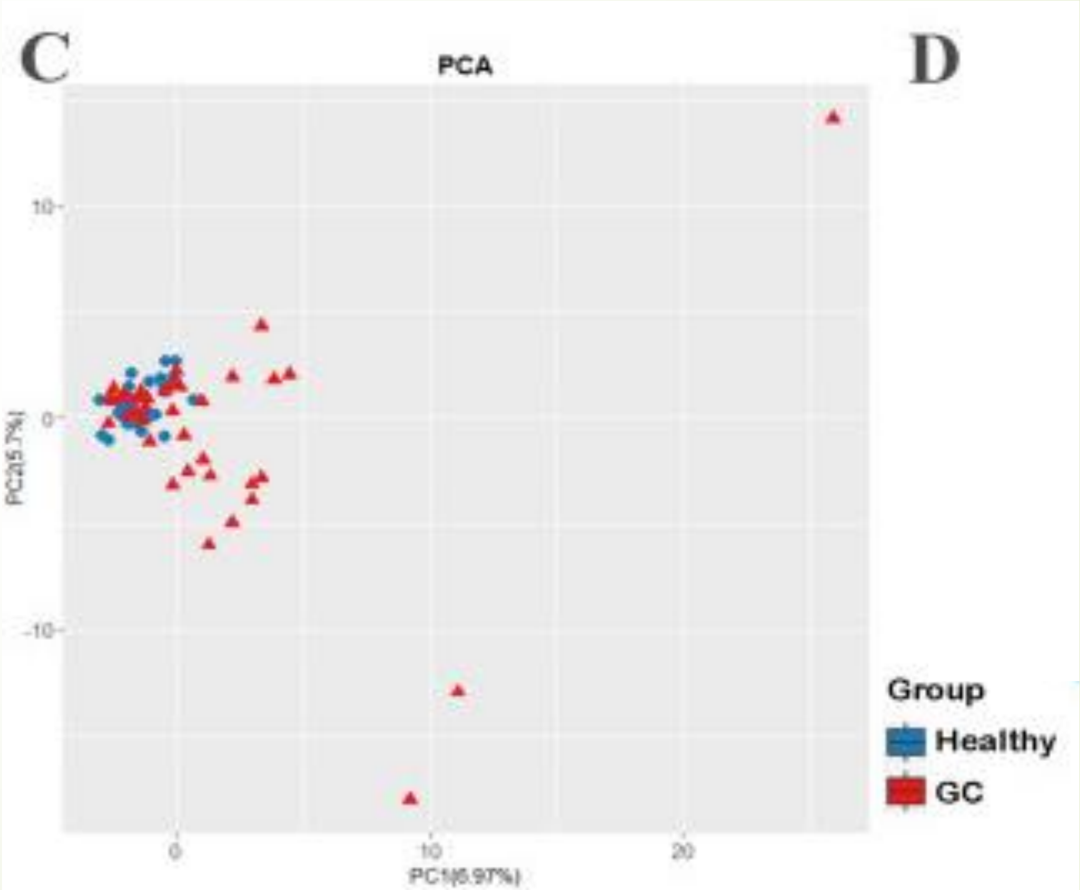
- no significant distinguishment in the within-sample diversity between gastric cancer patients and healthy people and the data of other indices further verified this conclusion



The comparison of fecal microbiota

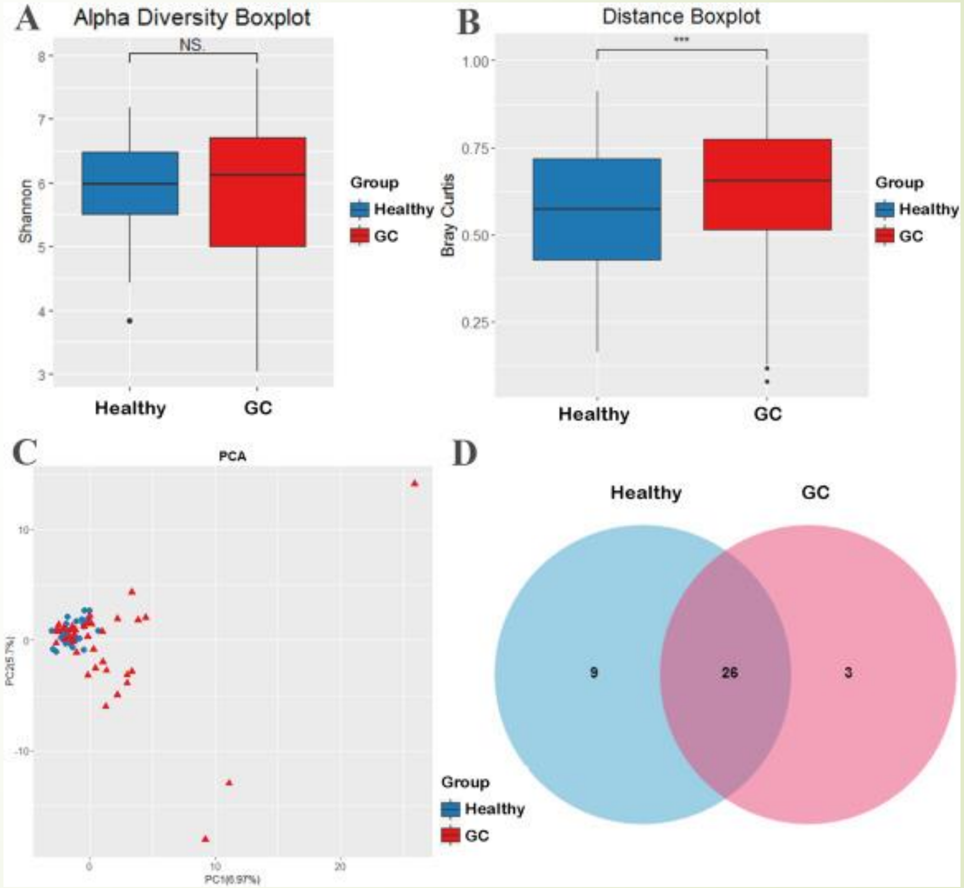
- principal component analysis (PCA) of the fecal microbiota obtained from gastric cancer patients showed more dispersed distributions than those of normal controls.

(Principal components analysis)



The comparison of fecal microbiota

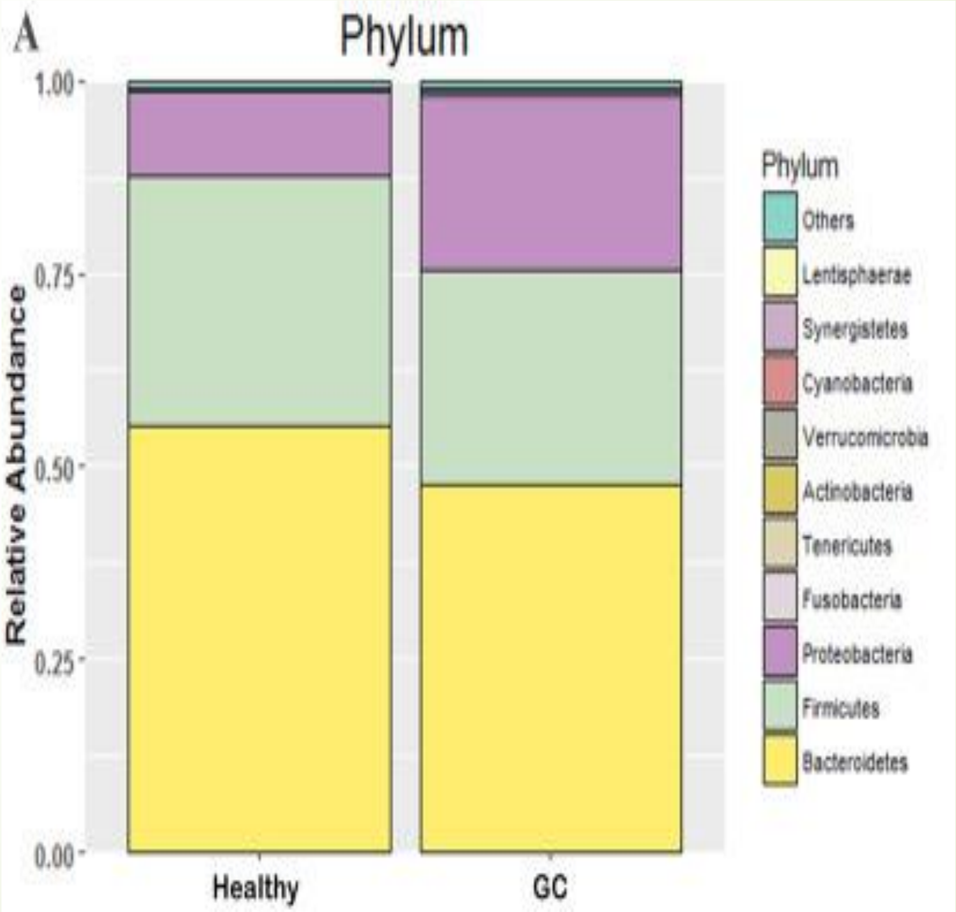
- no shift in fecal microbes between normal control individuals and gastric cancer patients
- between-sample diversities increased significantly in the intestinal microbiota of patients with gastric cancer.



Bacterial **variation** in the intestinal microbiota of gastric cancer patients

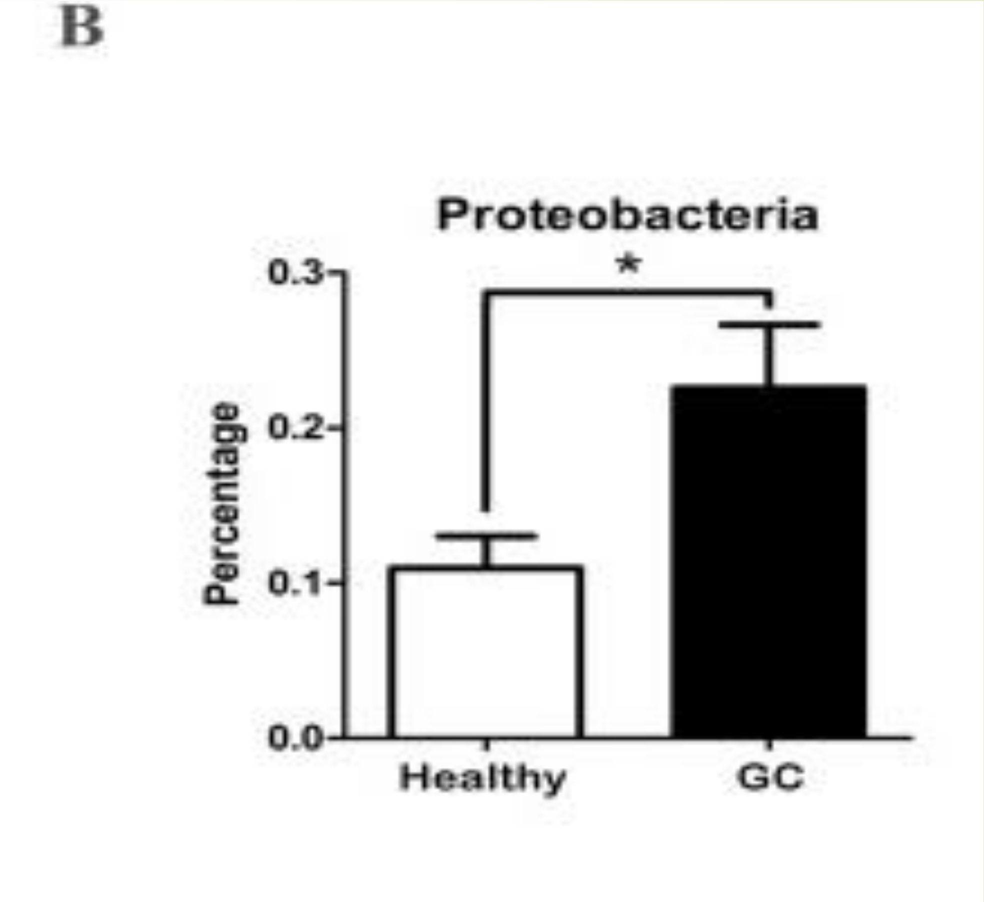
Bacterial variation

- At the phylum level, Bacteroidetes, Firmicutes and Proteobacteria constituted more than 95% of the total bacterial mass of all samples
- Bacteroidetes, Firmicutes contents did not differ significantly between the gastric cancer patients and healthy people.



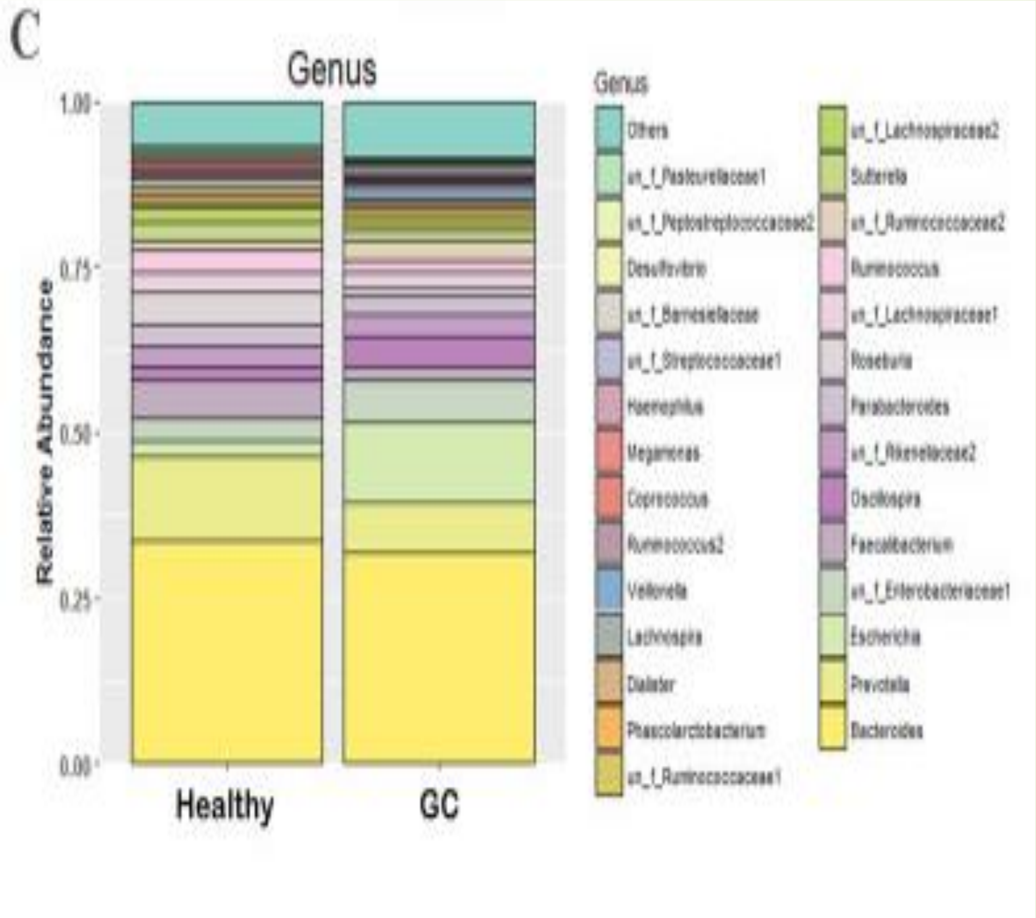
Bacterial variation

- Proteobacteria showed a significant difference between the two groups(enriched in the stools of GC)



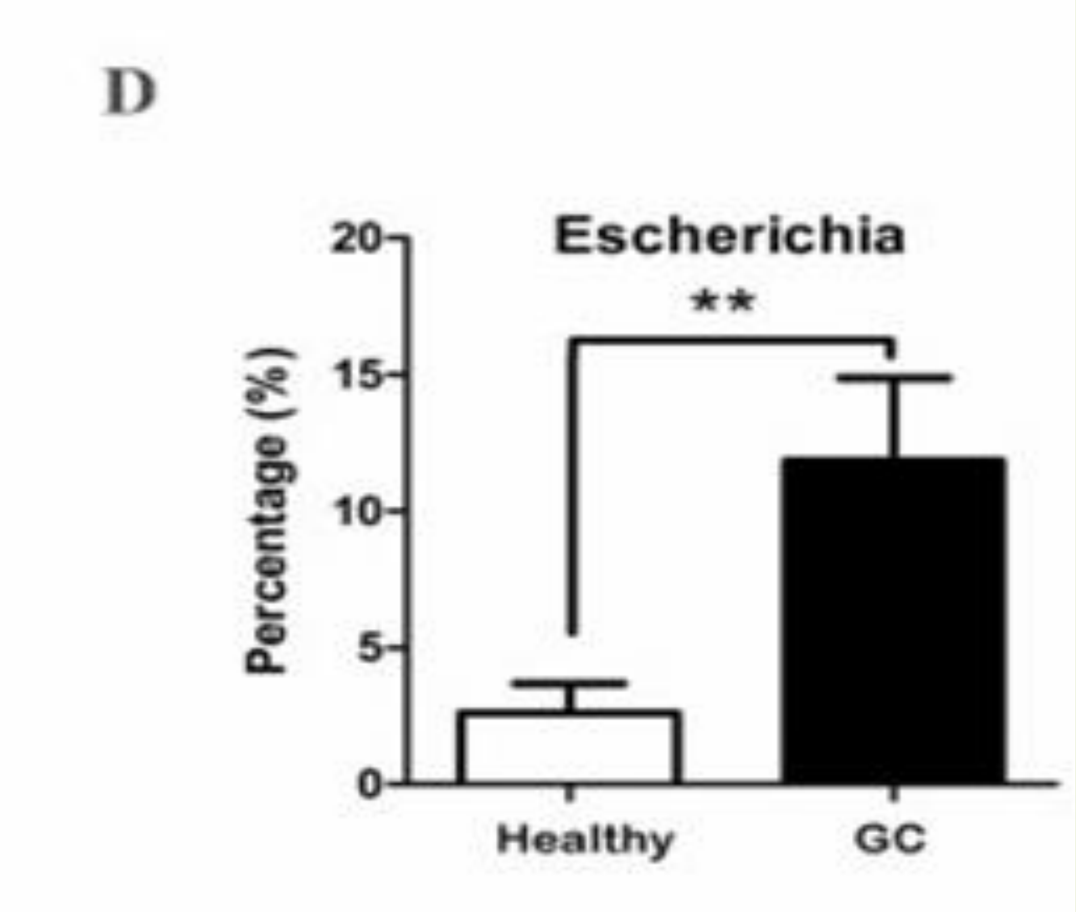
Bacterial variation

- The genus *Bacteroides* was the most abundant genus in both gastric cancer patients and healthy people
- no significant difference in content between the two groups



Bacterial variation

- In those genera with relatively high abundance, *Escherichia, Roseburia* and *Desulfovibrio* were found to have significant content variation in the feces of gastric cancer patients in comparison to that of healthy controls.

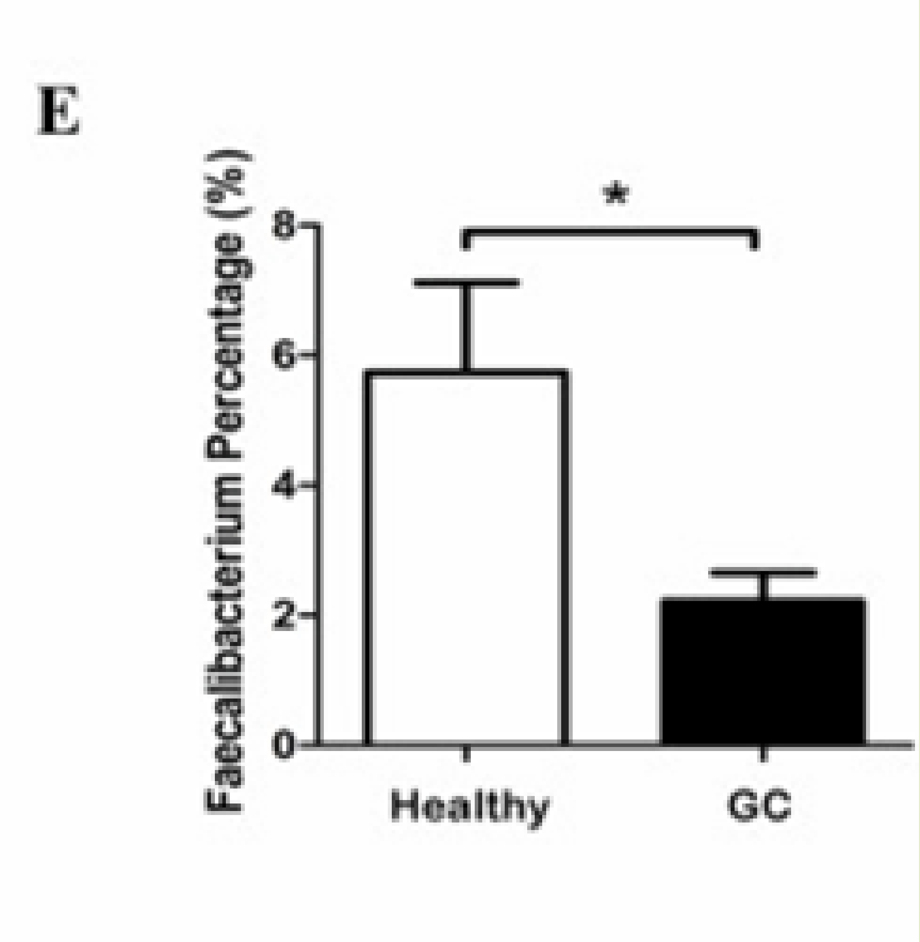


Bacterial variation

- Other genera with significant differences between the two groups.
- Among the bacteria with a content of more than 1% of all intestinal bacteria the facultative anaerobic (aerotolerant) bacteria were *Enterobacteriaceae, Escherichia* and *Streptococcaceae*, and all were elevated in the intestine of gastric cancer patients.

Bacterial variation

- The abundance of most obligate anaerobic bacteria decreased significantly in the intestine of tumor patients
- The content of oxygen-sensitive *Faecalibacterium* decreased by 61.4%, suggesting an oxygen-dependent shift in the intestinal microbiota of gastric cancer patients.

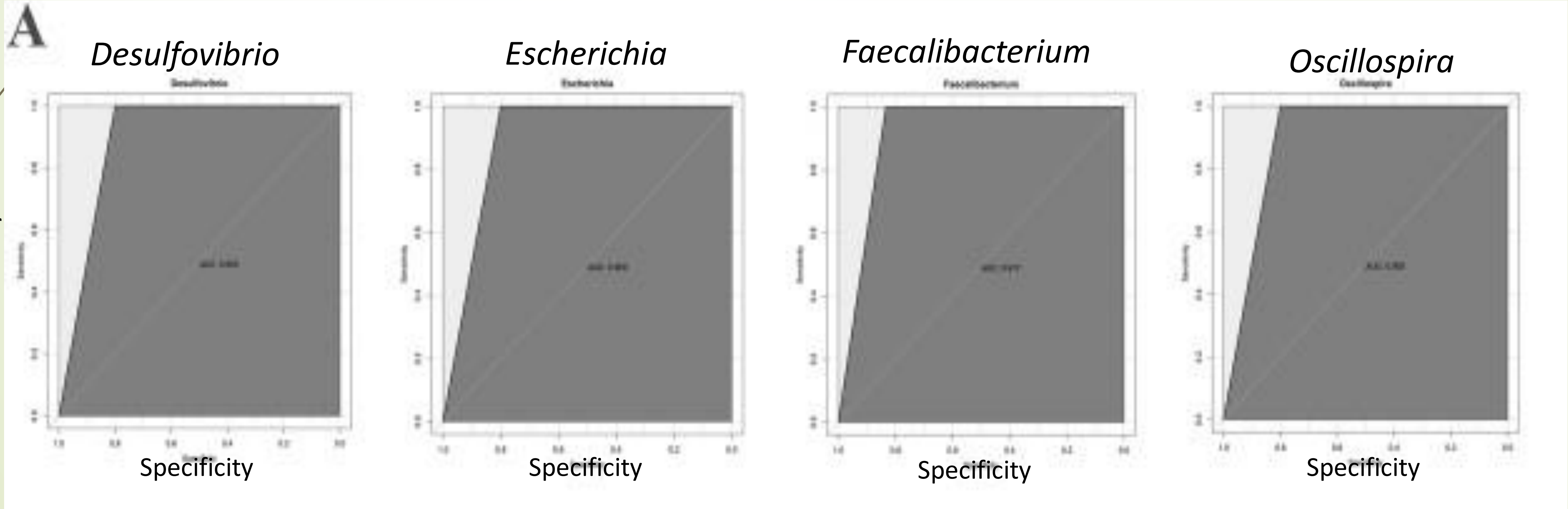


Differential bacteria can be used to **predict gastric cancer**, and *desulfovibrio* is especially enriched in stage IV gastric cancer

Differential bacteria can be used to predict gastric cancer

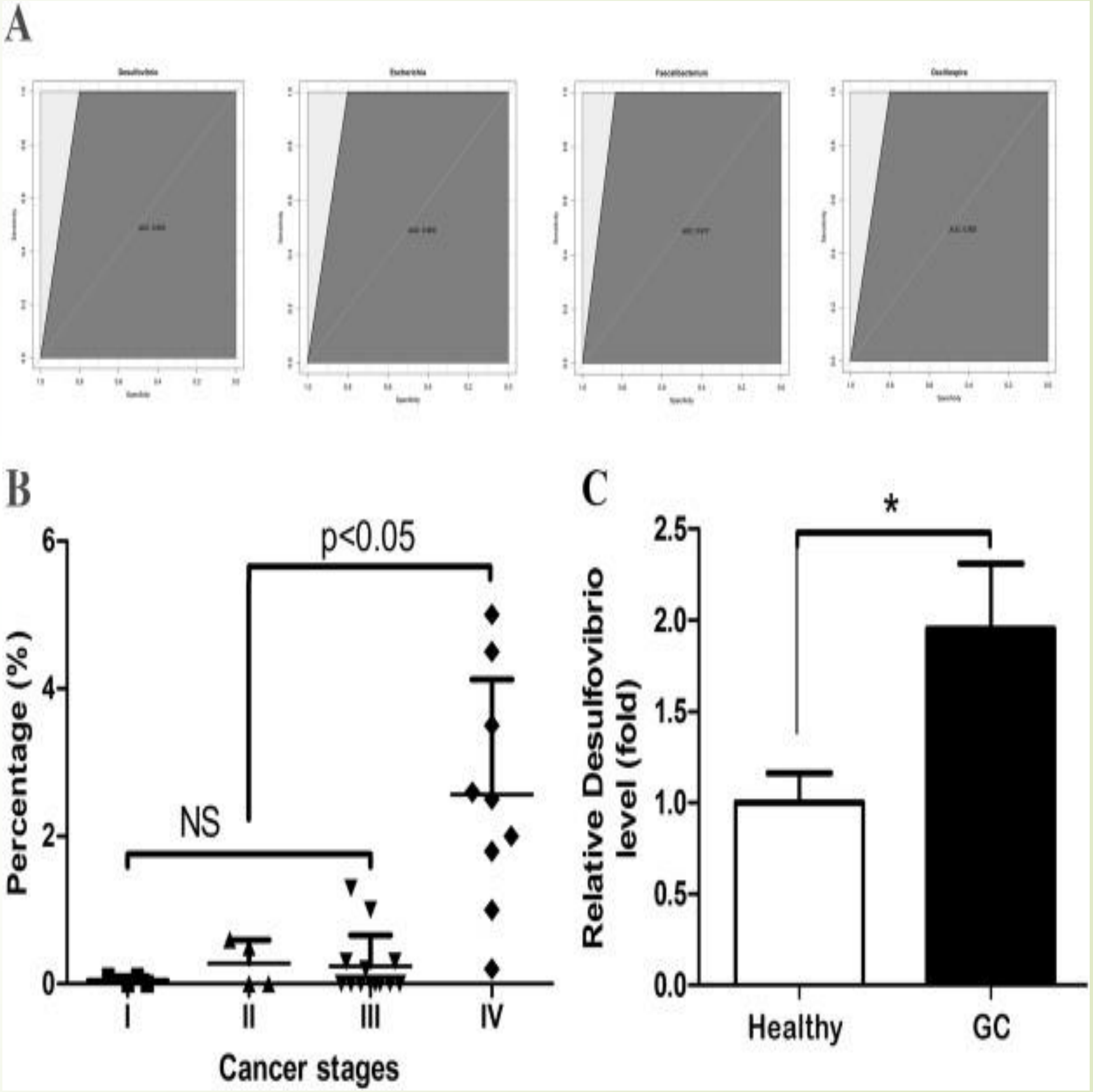
- changes in *Escherichia, Faecalibacterium* and *Oscillospira* have been reported in a large number in many diseases.
- *Desulfovibrio* was found to be significantly enriched in the feces of gastric cancer patients.

- The results showed that the differential bacteria *Desulfovibrio, Escherichia, Faecalibacterium*, and *Oscillospira* can be used as biomarkers to distinguish disease and healthy groups with the highest precision of 90% or above.

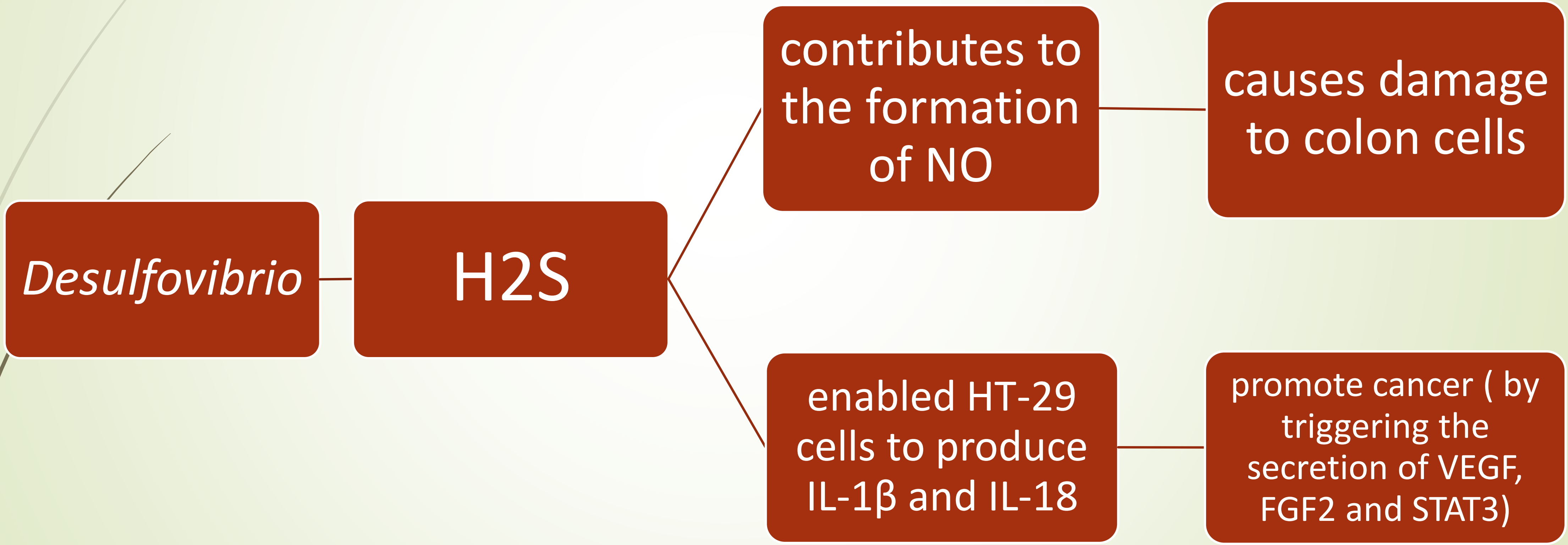


Differential bacteria can be used to predict gastric cancer

The distinct distribution of *Desulfovibrio* in healthy individuals and gastric cancer patients was verified by qPCR detection.



The effect of *Desulfovibrio* on the immune system



Desulfovibrio

H2S

contributes to the formation of NO

causes damage to colon cells

enabled HT-29 cells to produce IL-1β and IL-18

promote cancer (by triggering the secretion of VEGF, FGF2 and STAT3)

Enzyme-linked immunosorbent assay (ELISA)

was detected with ELISA :

- IL-1β
- H_2S
- IL-18

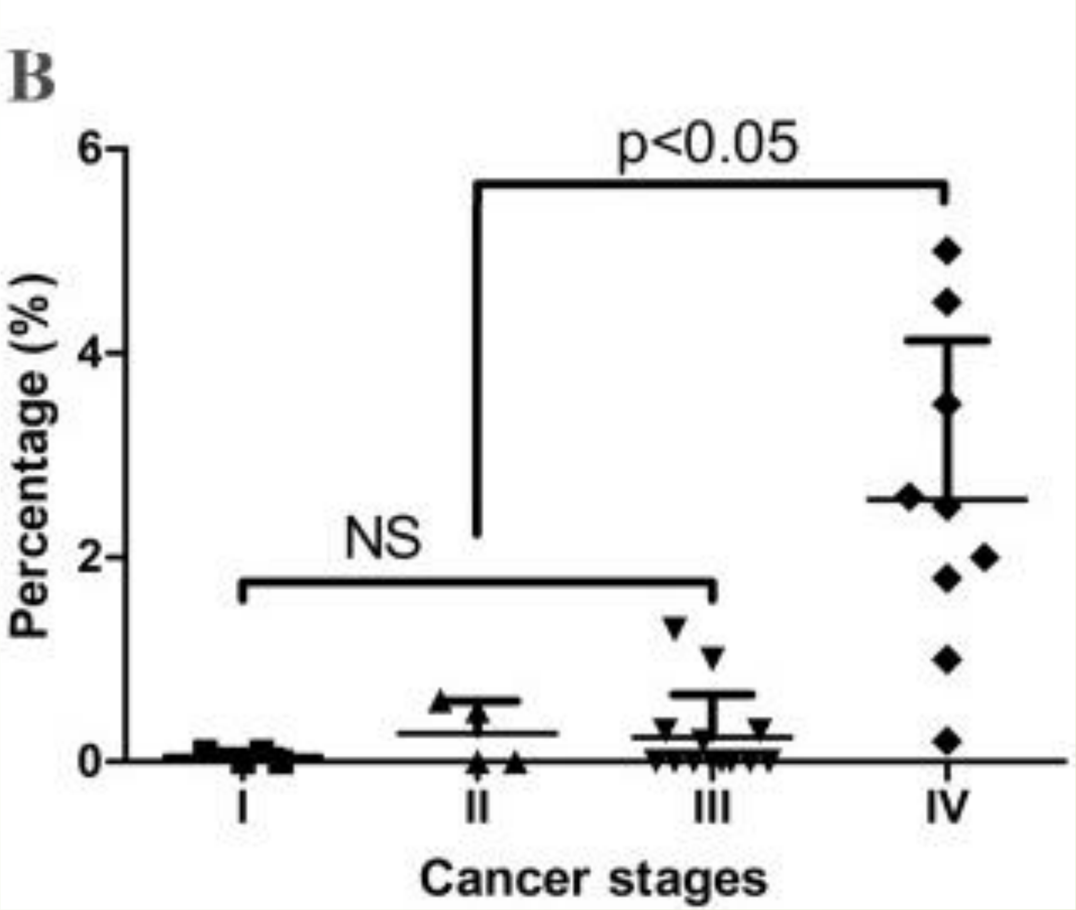
reverse transcription and quantitative PCR

Was detected with RT-QPCR:

- Total cellular RNA extraction
- human IL-1β
- human IL-18
- total bacteria
- genus Desulfovibrio 16S rRNA

Differential bacteria can be used to predict gastric cancer

- The patients with stage IV gastric cancer had more *Desulfovibrio* than those with stage I, II and III gastric cancer.



Differential bacteria can be used to predict gastric cancer

- the amount of *Escherichia, Veillonella* and *Roseburia* were not significantly different among the gastric cancer patients with different stages.
- almost all of the hosts whose fecal *Desulfovibrio* contents were higher than 1% were gastric cancer patients.
- people with higher *Desulfovibrio* contents were all patients with stage IV gastric cancer.

Reference

- Liu S, Dai J, Lan X, Fan B, Dong T, Zhang Y, Han M, Intestinal bacteria are potential biomarkers and therapeutic targets for gastric cancer, Microbial Pathogenesis (2021), doi: https://doi.org/10.1016/j.micpath.2021.104747