Mapping the gut microbiome in patients with small intestinal neuroendocrine tumors

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Background

- Carcinoid syndrome (CS): a debilitating endocrine complication of metastatic small intestinal neuroendocrine tumors (SI-NETs)
- Little progress in uncovering drivers and treatment options
- Microbiome research has uncovered novel treatment targets in other cancers
- Enterochromaffin cells communicate with bowel content, including microbial species and their secreted molecules

Aim

- To map the gut microbiome of SI-NET patients and its association with CS

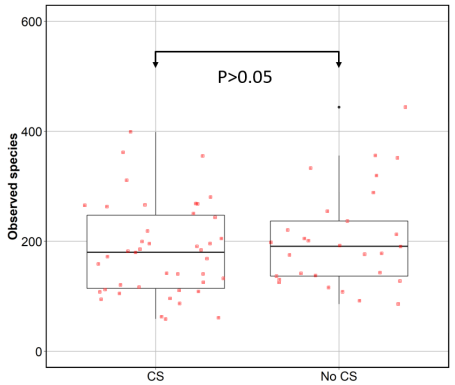
Methods

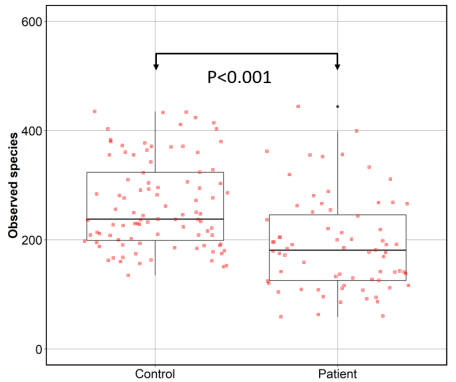
- Collection of fecal samples of SI-NET patients and controls
- Questionnaires and electronic health records
- Microbiome analysis through 16S sequencing

Results

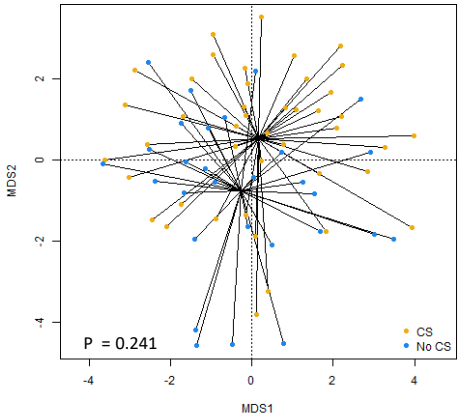
- 87 patients (53 with the CS), 95 controls
- CS vs no CS
  - Similar microbial richness and distribution
  - No differentially abundant species
- SI-NET patients vs controls
  - Patients had a less rich and diverse microbiome
  - Different microbial distribution
  - 14 species more abundant in patients
  - 28 species more abundant in controls

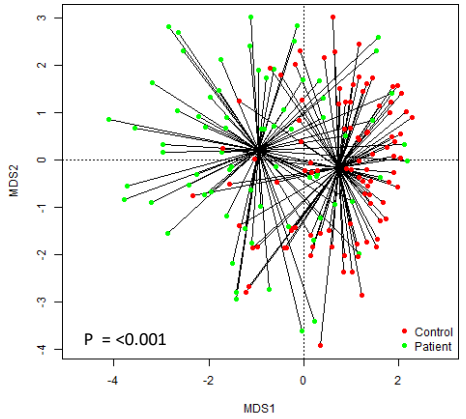
α-diversity: comparison of the microbial diversity within groups



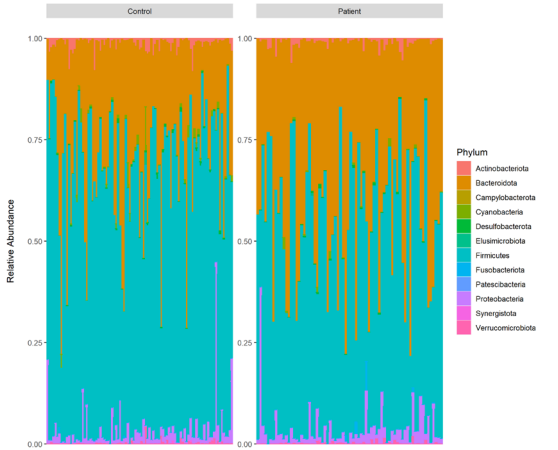


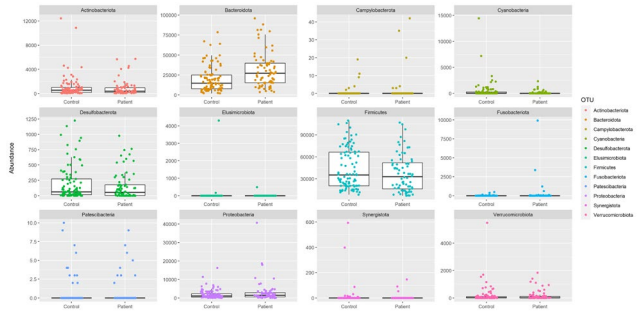
β-diversity: comparison of the microbial diversity between groups





Distribution of phyla





Conclusions

- **No association** between the gut microbiome and the presence of **CS** was found
- The gut microbiome of **SI-NET** patients **was different** from that of **controls**
- Potentially **oncogenic** and **protective bacteria** were **identified**
- Current efforts focus on a SI-NET microbial signature, metagenomics and metabolomics

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