



HP-07: Deciphering Gut Microbiota Changes in Hashimoto's Disease via 16S rRNA Analysis

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Subject description: Gut microbiota research has gained global prominence, revealing its critical role in diverse health conditions, including autoimmune diseases. This study focuses on evaluating the gut microbiota composition in Hashimoto's disease, a significant autoimmune thyroid disorder.

Objectives: Our objective is to investigate the composition of gut; microbiota to determine if there is dysbiosis or alteration in Hashimoto's patients.

Methods: We recruited 20 participants diagnosed with Hashimoto's disease and 20 healthy controls. Demographic and medical information was acquired through structured questionnaires, and informed consent was obtained from all participants. Fecal samples were collected aseptically, stored at -20°C, and subjected to DNA extraction using a two-step phenol-chloroform method. The amplified V3V4 region of the 16S rRNA gene was then targeted using PCR, a recognized bacterial marker. The subsequent amplicons were purified and subsequently sequenced using the Sanger method.

Results and discussion: Our study employs bioinformatics tools to analyze raw sequencing data, enabling the identification of operational taxonomic units (OTUs) based on sequence similarity and taxonomic classifications. Statistical analyses will compare gut microbiota composition and diversity indices between the Hashimoto's disease group and healthy controls.

Conclusion: This study has the potential to offer valuable insights into the role of gut microbiota in Hashimoto's disease, fostering personalized interventions and deeper understanding of autoimmune thyroid disorders, while also suggesting promising avenues for future research.

Keywords: Gut microbiota; Hashimoto's disease; 16S rRNA gene; PCR; operational taxonomic units.