

Gut Microbiota Dynamics in Response to Bile Duct Ligation and FK10 Intervention

Overview

This project explores the impact of bile duct ligation (BDL) and probiotic FK10 treatment on gut microbiota composition and diversity using 16S rRNA sequencing. The study evaluates microbial community responses, focusing on the abundance of Prevotellaceae and overall ecological resilience over a 14-day period in murine models.

Project Structure

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└─ gut_microbiota_project/ ─┬─ data/ # Raw and processed sequencing data ─┬─ scripts/ #
Python and shell scripts for analysis | ── qiime2_pipeline.qzv | ──
statistical_analysis.py ─┬─ results/ | ── alpha_diversity_plots/ | ──
beta_diversity_plots/ | ── taxonomic_composition/ ─┬─ summary/ | ── figures/ #
Summary figures for Prevotellaceae, PCoA plots, etc. | ── report.pdf # PDF of key
findings ── README.md # Project documentation
```

Objectives

- Assess the gut microbial composition under normal (sham) and BDL-induced cholestasis conditions.
 - Examine the effect of FK10 intervention on microbial stability.
 - Monitor the abundance of Prevotellaceae and diversity metrics over time.
 - Visualize alpha and beta diversity changes using QIIME 2 plugins.
 - Statistically compare microbial metrics across experimental groups and time points.
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Methodology

1. Data Processing

- **QIIME 2 Pipeline:**
 - Imported raw sequence reads.
 - Demultiplexed and trimmed adapters and low-quality bases.
 - Denoising and chimera filtering via DADA2 to obtain ASVs.
 - Taxonomic classification using a pre-trained Naïve Bayes classifier and Greengenes database.

2. Statistical Analysis

- **Alpha Diversity:** Shannon Entropy, Faith's Phylogenetic Diversity.
- **Beta Diversity:** Jaccard and Bray-Curtis dissimilarity indices with PCoA visualization.
- **Statistical Tests:**
 - One-way ANOVA with Tukey's post hoc test.
 - Repeated measures ANOVA for within-group changes.
 - Significance threshold: $p < 0.05$.

Key Findings

- **Prevotellaceae Resilience:** Relative abundance remained stable or increased across all experimental groups, even in BDL conditions.
 - **Alpha Diversity:** Increased diversity in BDL and FK10_BDL groups, indicating microbial adaptation rather than dysbiosis.
 - **Beta Diversity:** No strong clustering observed, suggesting overlapping microbial community structure despite specific taxonomic shifts.
 - **Effect of FK10:** Modulated microbiota composition subtly but did not prevent BDL-induced changes.
 - **Limitation:** Relative abundance metrics used; absolute quantification is recommended for follow-up studies.
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Figures

- Alpha Diversity (Shannon Index, Faith's PD)
 - Beta Diversity (PCoA plots)
 - Prevotellaceae Abundance Trends
 - Group-wise Comparative Taxonomy Charts
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Ethics Statement

This research was approved by the Institutional Review Board (IRB) at Theodor Bilharz Research Institute (TBRI), Cairo, Egypt.

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