

Summary Report

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

Objective

This study aimed to evaluate how **bile duct ligation (BDL)** and **FK10 probiotic treatment** affect gut microbiota composition and diversity over a 14-day period in mice. Special focus was placed on the abundance and resilience of the bacterial family **Prevotellaceae** under different physiological and intervention conditions.

Experimental Groups

- **SHAM** - Healthy control
 - **Sham_FK10** - Healthy mice treated with FK10
 - **BDL** - Mice with induced cholestasis
 - **FK10_BDL** - BDL mice treated with FK10
 - **BDL+UDCA** - BDL mice treated with ursodeoxycholic acid (UDCA)
 - **UK** - Untreated control reference group
-

Methods Overview

- **Data Source:** 16S rRNA gene sequencing
 - **Software Tools:** QIIME 2, DADA2, Naïve Bayes Classifier
 - **Reference Database:** Greengenes
 - **Analysis Metrics:**
 - **Alpha Diversity:** Shannon Entropy, Faith's Phylogenetic Diversity
 - **Beta Diversity:** Jaccard, Bray-Curtis (PCoA plots)
 - **Statistics:**
 - One-way ANOVA + Tukey's post hoc
 - Repeated Measures ANOVA ($p < 0.05$)
-

Key Findings

Prevotellaceae Abundance

- **Maintained or Increased** across all groups, contradicting expectations of depletion under cholestasis.
- Day 1 → Day 14 changes:
 - SHAM: 41% → 47%
 - BDL: 42% → 53%
 - FK10_BDL: 34% → 36%
 - Sham_FK10: 28% → 42%
 - UK: 31% → 43%

Microbial Resilience

- No signs of overt dysbiosis.
- Prevotellaceae, known for SCFA production, likely contributed to microbial stability.

▮ Diversity Metrics

- **Alpha Diversity:**

- Increased in BDL and FK10_BDL groups, suggesting adaptation and proliferation of non-dominant taxa.
- Transient increases followed by stabilization in FK10_BDL.

- **Beta Diversity:**

- PCoA plots revealed **no distinct clustering** by group or time point.
 - Indicates overlapping microbial community structures.
-

▮ Interpretation

- FK10 has subtle microbiota-modulatory effects but **does not prevent BDL-induced microbial shifts**.
 - BDL alters microbial community dynamics without collapsing overall structure.
 - The gut environment remained **permissive for SCFA-producing bacteria**, particularly Prevotellaceae.
 - Observed shifts reflect **ecological adaptation**, not pathology.
-

▮ Limitations

- Data based on **relative abundance**; absolute quantification (e.g., qPCR) is needed for more conclusive insights.
 - Short study duration (14 days) may not capture long-term dynamics.
-

▮ Conclusion

This study challenges the notion that cholestasis necessarily leads to gut dysbiosis. Instead, the microbial ecosystem, particularly Prevotellaceae, displayed resilience and dynamic adaptation. While FK10 influenced baseline diversity, it did not significantly counteract BDL effects. These findings offer important insights into host-microbiota interactions under hepatic stress and open avenues for future probiotic-based interventions.

▮ Citation

Reham Wael, Dr. Marwa Amer, Dr. Rehab Abdallah (2025).
Gut Microbiota Dynamics in Response to Bile Duct Ligation and FK10 Intervention.
Misr University for Science and Technology & Theodor Bilharz Research Institute.