

Gut Microbiome and Dietary Composition of Common Loons (*Gavia immer*): Disease Ecology and Seasonal Patterns

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Key finding: ecological season, not cause of death, drives the Common Loon gut microbiome.



Introduction

The gut microbiome plays a central role in avian health, contributing to digestion, immune regulation, and disease susceptibility. The Common Loon (*Gavia immer*) is a sentinel species for aquatic ecosystem health that migrates between freshwater breeding lakes and marine wintering grounds, yet its gut microbiome has never been characterized. Lead toxicosis is the leading cause of disease-associated mortality in northeastern loons, and in other taxa, lead exposure is associated with gut dysbiosis and disrupted commensal communities. Using amplicon-based metabarcoding (16S rRNA V4) of archived gastrointestinal samples from necropsy submissions in New Hampshire and Maine (2021–2024), we characterize bacterial community composition across disease status, cause of death, and ecological season. This study leverages expertise in wildlife disease ecology, molecular ecology, and employs a multi-disciplinary and multi-institutional collaboration.

Objectives

1. Characterize the gut bacterial microbiome (16S rRNA) of Common Loons in New England, establishing a baseline community composition across disease status and ecological season.
2. Determine whether cause of mortality leaves a detectable signature in gut microbial community composition, with emphasis on lead toxicosis versus trauma as a post-mortem surveillance tool.
3. Evaluate whether ecological season — reflecting the freshwater breeding to marine wintering migration — structures gut bacterial community composition independent of disease status.

Methods

Samples n=35 gastrointestinal tract samples from Common Loons submitted to wildlife rehabilitation and diagnostic centers in NH and ME (2021–2024). Groups: Diseased (n=14), Trauma (n=14), Marine (n=5). Ecological seasons: Breeding (n=15), Freshwater Non-breeding (n=6), Saltwater (n=6).

Sequencing & Processing 16S rRNA V4 region (515F/806R primers) · DADA2 amplicon denoising · SILVA 138 taxonomy classifier · QIIME2 amplicon-2024.5 · Rarefaction depth: 8,000 reads/sample

Custom Metabarcoding Pipeline for Wildlife & One Health Research Developed as part of a UNH–Tufts University collaboration, this 15-script modular Python pipeline provides an accessible, reproducible metabarcoding workflow for wildlife and One Health scientists across New England and beyond — lowering the barrier to entry for microbiome and dietary metabarcoding in wildlife disease ecology

Statistics PERMANOVA (999 permutations, seed=42) · Pairwise comparisons between all group pairs · Benjamini-Hochberg FDR correction

Conclusions

Gut bacterial community structure in Common Loons is significantly restructured across ecological seasons. Breeding birds show distinct community composition from Saltwater non-breeding birds across all four beta diversity metrics (BC q=0.003, Jac q=0.039, WUF q=0.042, UWF q=0.015), consistent with the ecological dietary transition during migration.

Disease status leaves a detectable signature in gut community composition. Jaccard beta diversity differed significantly between diseased vs. trauma (DvT) loons (q=0.013), indicating species-level turnover without corresponding changes in richness or abundance-weighted composition, suggesting qualitative rather than quantitative community reorganization.

Enterococcus enrichment tracks ecological season, not cause of death. Every bird with *Enterococcus* >20% was Saltwater non-breeding (median 45.9%, n=6), vs. near-absent in Breeding and Freshwater non-breeding birds, spanning Lead, PI, and Trauma deaths. The apparent Lead elevation reflects a single Saltwater Lead bird — reinforcing rather than weakening the absence of a Lead-specific signature, and likely a major driver of the seasonal community separation.

Limitations. Small subgroup sizes (n = 4–6) limit cause-of-death inference; findings are exploratory.

Diet and eukaryote communities do not explain microbiome differences. MiFish presence/absence PERMANOVA was non-significant (p=0.512), suggesting the DvT microbiome signal is driven by disease physiology rather than dietary differences. This study provides the first characterization of the Common Loon gut microbiome and demonstrates that post-mortem amplicon sequencing of archived necropsy samples is a viable tool for wildlife disease surveillance.

Further directions include expanded sample sizes to determine whether these findings scale across broader loon populations and geographic ranges, with increased N.

References

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Figure 1 — Beta Diversity PCoA (Ecological Season)

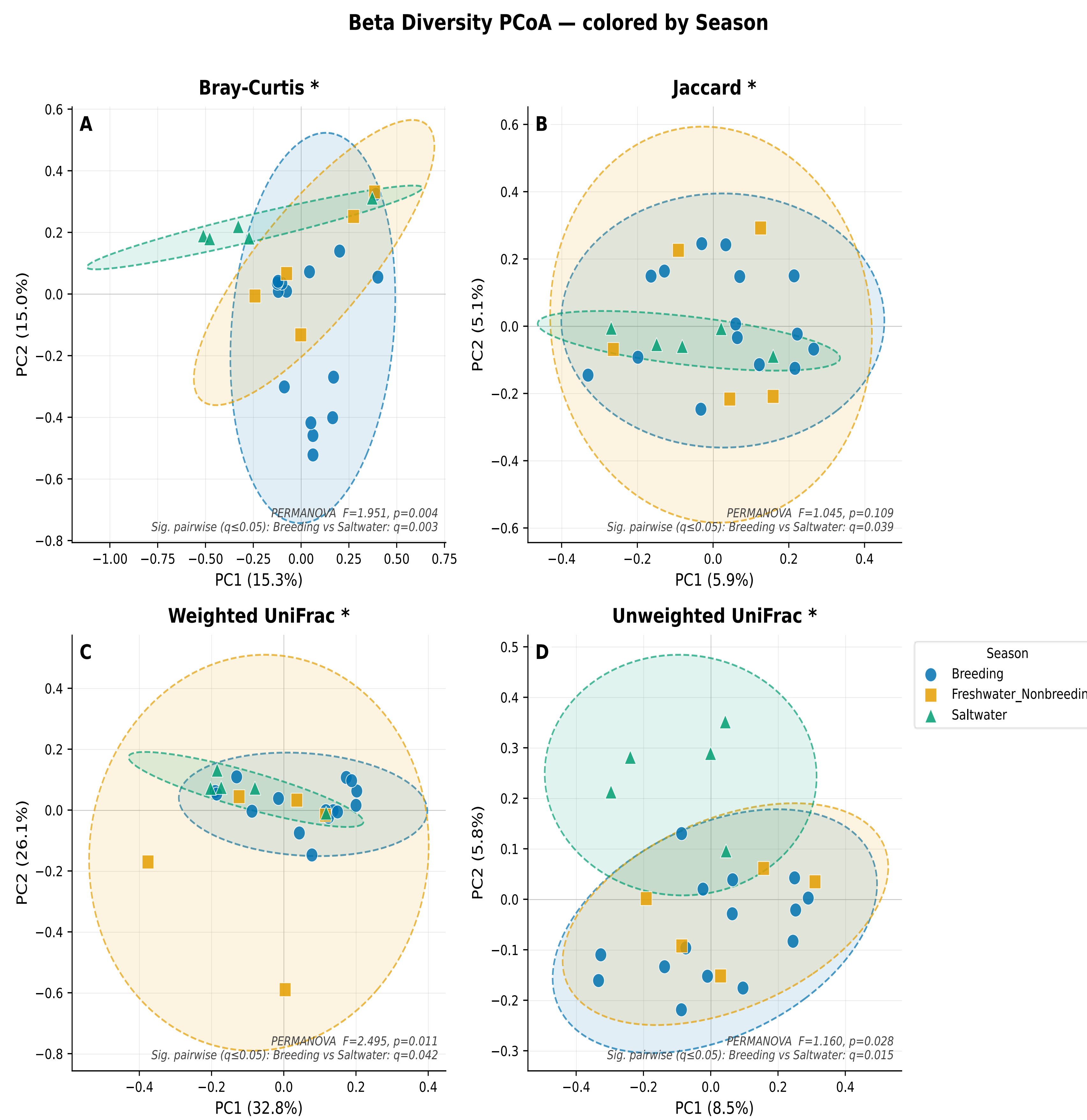


Figure 2 — Genus-Level Relative Abundance (Ecological Season)

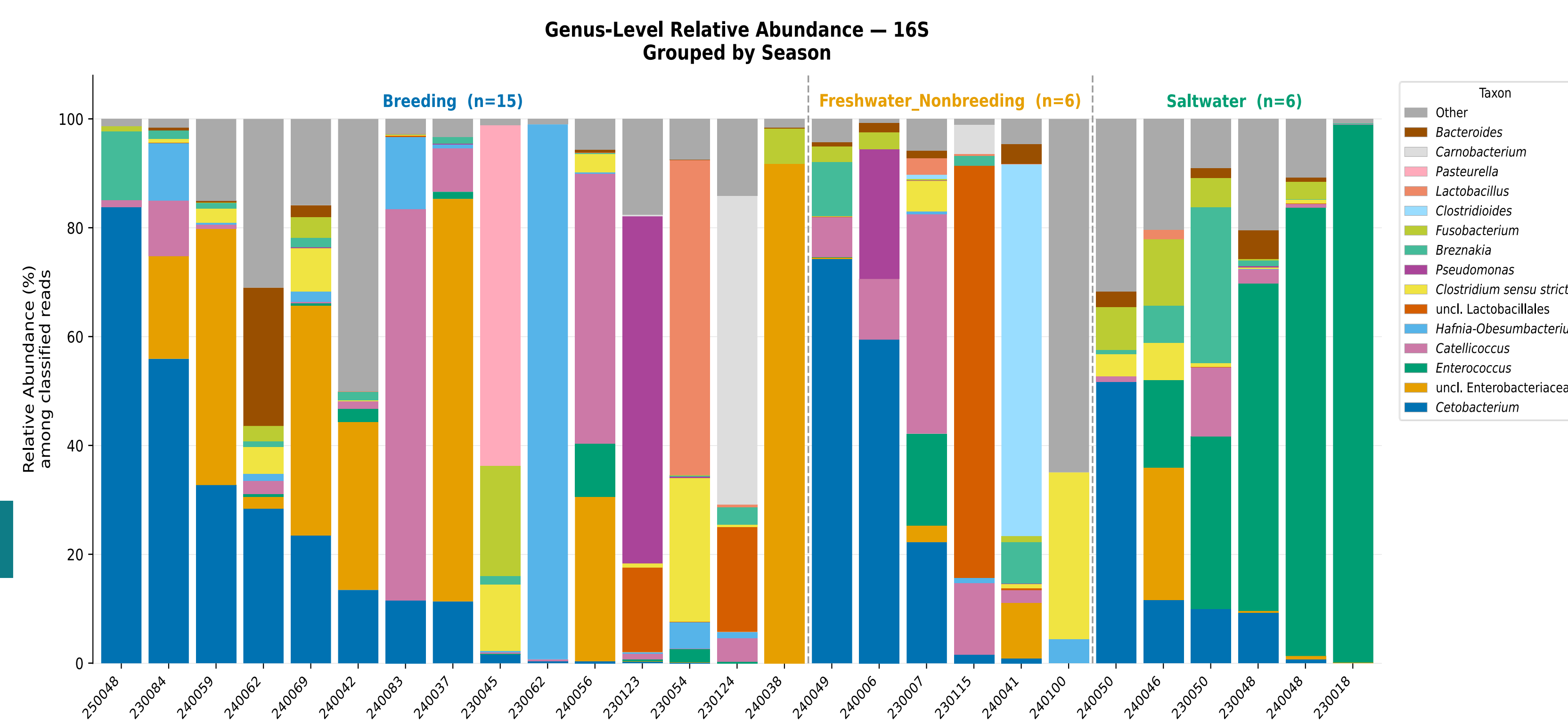


Figure 3 — Beta Diversity PCoA (Diseased vs. Trauma)

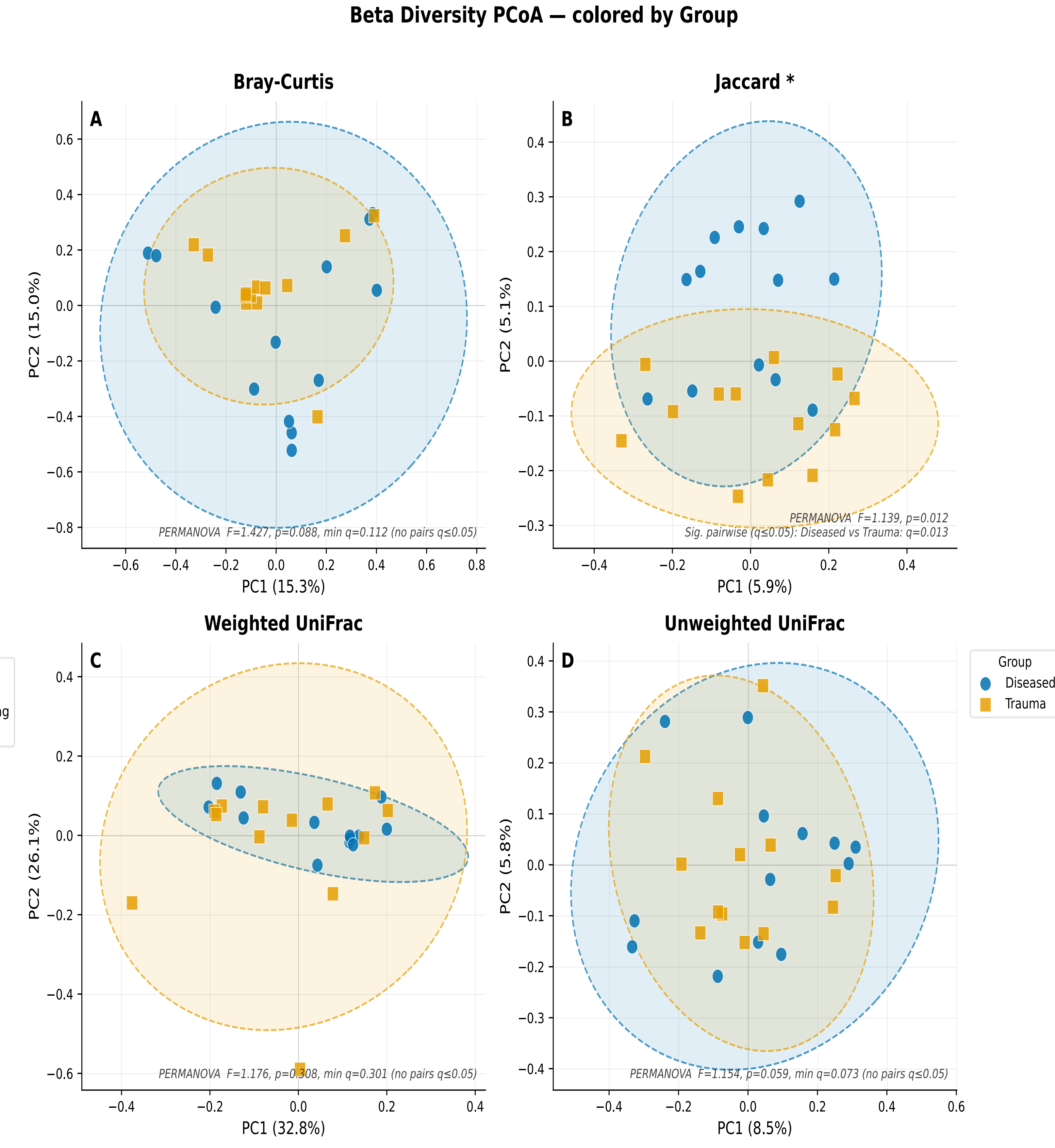


Figure 4 — Genus-Level Relative Abundance (Cause of Death)

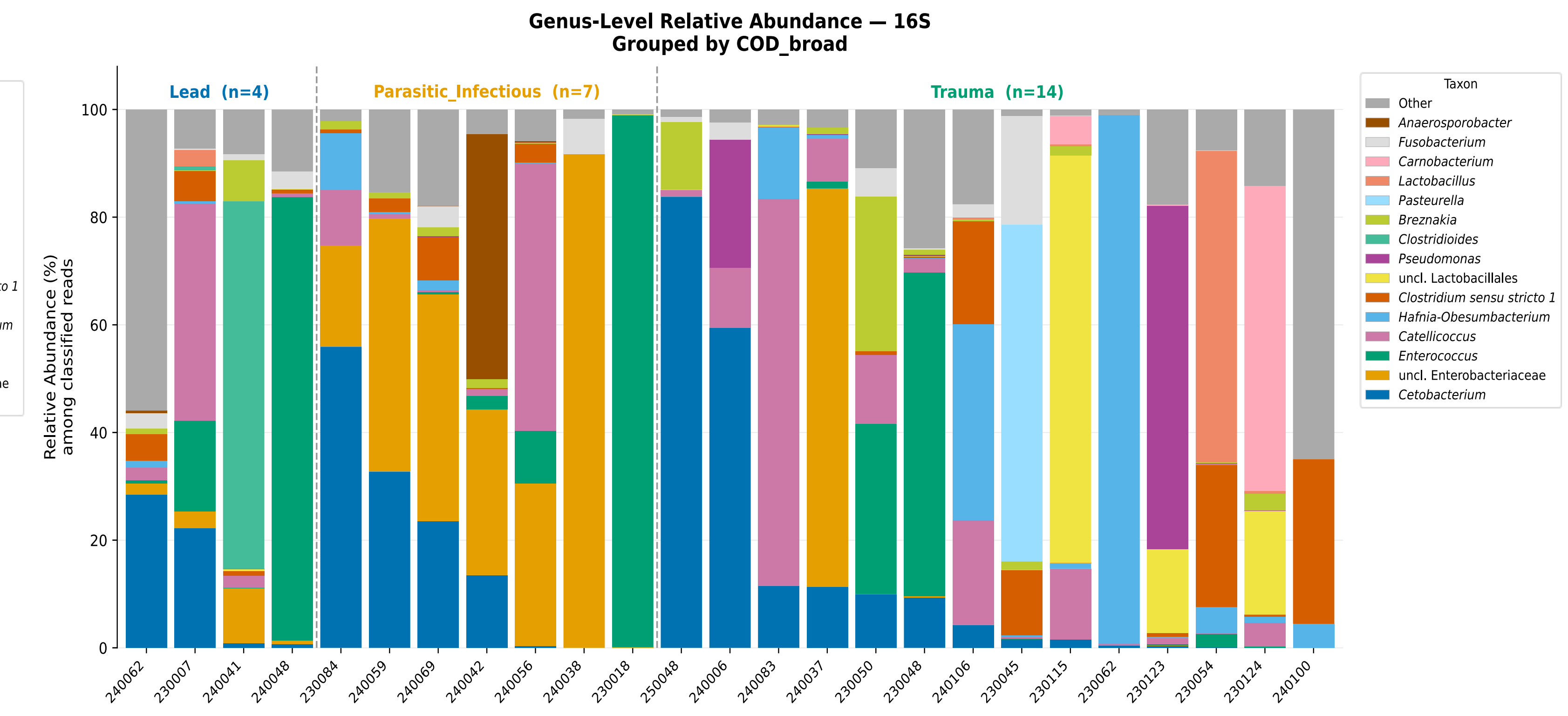


Figure 4. Within each cause-of-death group, elevated Enterococcus reflects saltwater individuals (cf. Fig. 2); season, not cause of death, is the driver.