ENVIRONMENTAL AND TEMPORAL DRIVERS OF MICROBIAL COMMUNITY DYNAMICS IN COLD-WATER AQUAPONIC SYSTEMS

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Abstract

Aquaponic systems represent an integrated and water-efficient approach to food production by combining recirculating aquaculture with hydroponic plant cultivation. The performance and stability of these systems depend not only on fish and plant interactions but also on the structure and function of associated microbial communities, which regulate nutrient cycling and water quality.

We evaluated replicated aquaponic systems based on cool/cold-water fish species, including rainbow trout (*Oncorhynchus mykiss*) and all-female yellow perch (*Perca flavescens*), for the production of lettuce (*Lactuca sativa*, Hydroponic Green Butter) and kale (*Brassica oleracea*, hybrid Winterbor). Microbial communities play a central role in the stability and performance of aquaponic systems; however, the relative importance of temporal dynamics, spatial heterogeneity, and environmental drivers remains poorly understood. In this study, we investigated microbial community structure across production cycles and system compartments using high-throughput sequencing and multivariate ecological analyses.

DNA samples were collected from key aquaponic compartments, including circulating water, rhizosphere, biodeposits, and biofilters, over three harvesting cycles, resulting in more than 200 samples for microbiome analysis. Permutational multivariate analysis of variance (PERMANOVA) revealed that microbial community composition was significantly influenced by both production cycle (p = 0.001) and system compartment (p = 0.001), with temporal dynamics emerging as the dominant driver of variation. Observed community shifts in microbial communities were closely associated with temperature and pH gradients.

These findings provide new insights into the ecological processes governing aquaponic microbiomes and highlight the importance of managing environmental conditions to enhance system stability and production performance.

Introduction

Aquaponics (AP) is the sustainable future of farming and food production. Most AP is with warm water fish and plants; our study is testing cool/cold water fishes (Yellow Perch and Rainbow Trout) and plants (Kale and Lettuce). We investigated microbial communities in each com-partment of the AP system based on combination of fish and plants.



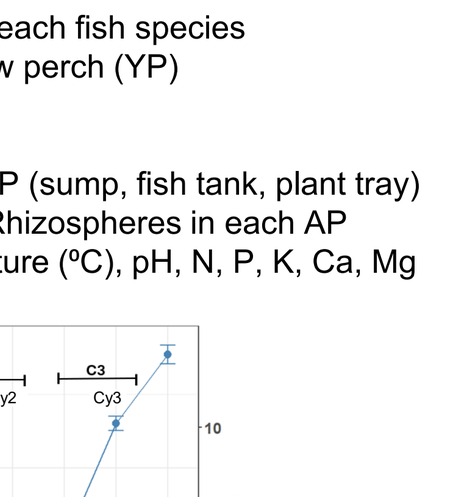


Fig. 1. Aquaponics farm set up at UNH.

Methods

Sample Collection

- 6 separate AP systems: 3 replicate AP for each fish species
  Fish: Rainbow Trout (RT) and Yellow perch (YP)
- 3 Cycles of plant harvesting
  Plant: Kale (K) and Lettuce (L)
- Water samples: 3 compartments in each AP (sump, fish tank, plant tray)
- Solid samples: Biofilter, Biodeposits, and Rhizospheres in each AP
- Physiochemical & Nutrition data: Temperature (ºC), pH, N, P, K, Ca, Mg

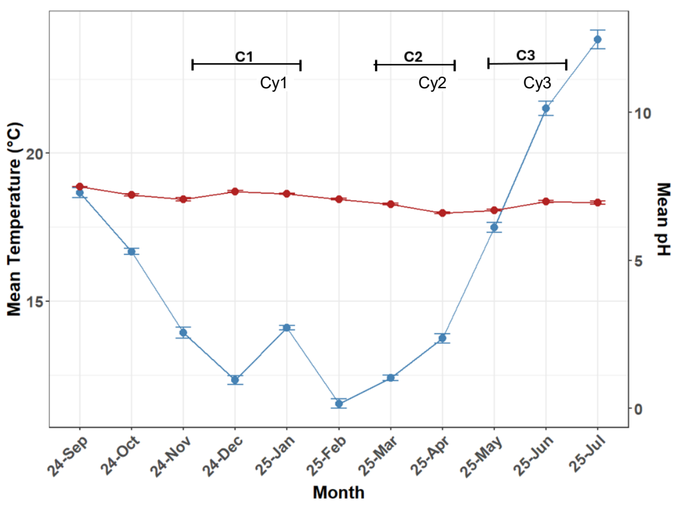


Fig. 2. Temperature and pH in 6 replicate aquaponic units at UNH during 3 experimental cycles

Laboratory & Data Analyses

- DNA extraction using Qiagen DNeasy PowerSoil Pro Kit
- DNA samples normalized to 10 ng mL^{-1} for PCR amplification
- 3 replicate PCRs to amplify the 16S rRNA target gene were pooled for sequencing analysis
- Sequencing was performed on the NovaSeq6000 platform
- Sequencing data were analyzed usingQiime2 pipeline with Silva database
- R packages were used for statistical analyses

Results

Sequencing & Taxonomy Assignment

- Unique amplicon sequence variants (ASVs) detected: 2,819 (≥0.05%)
- 1,885 ASVs were assigned to bacteria with 99% identity
- 461 OTUs at genus level (25 phyla, 49 classes, 121 orders, and 205 families)
- Rarefaction curve indicates that for all samples, the number of features saturated at about 10,000-15,000 reads

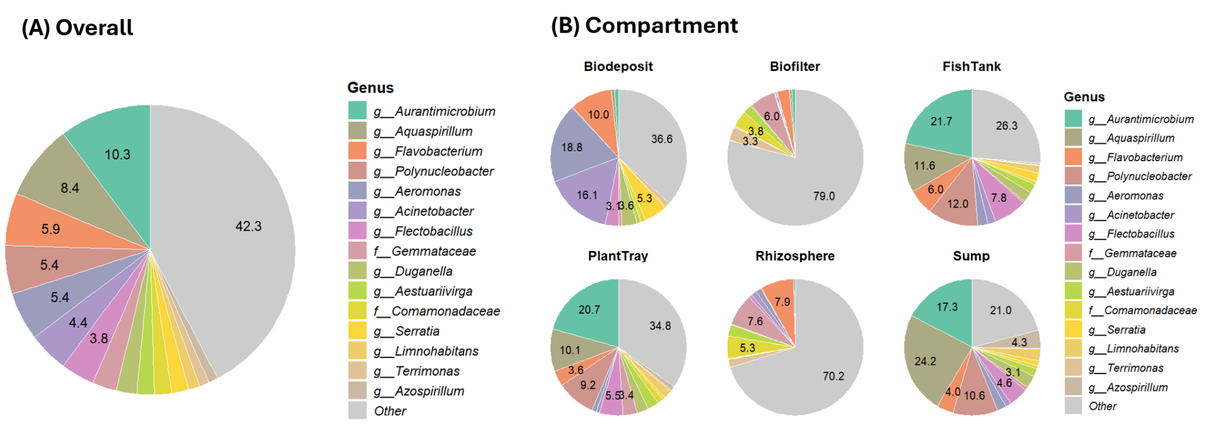


Fig. 3. Top 15 microbes and relative abundance at genus level: (A) Overall and (B) Compartment

Diversity Analysis

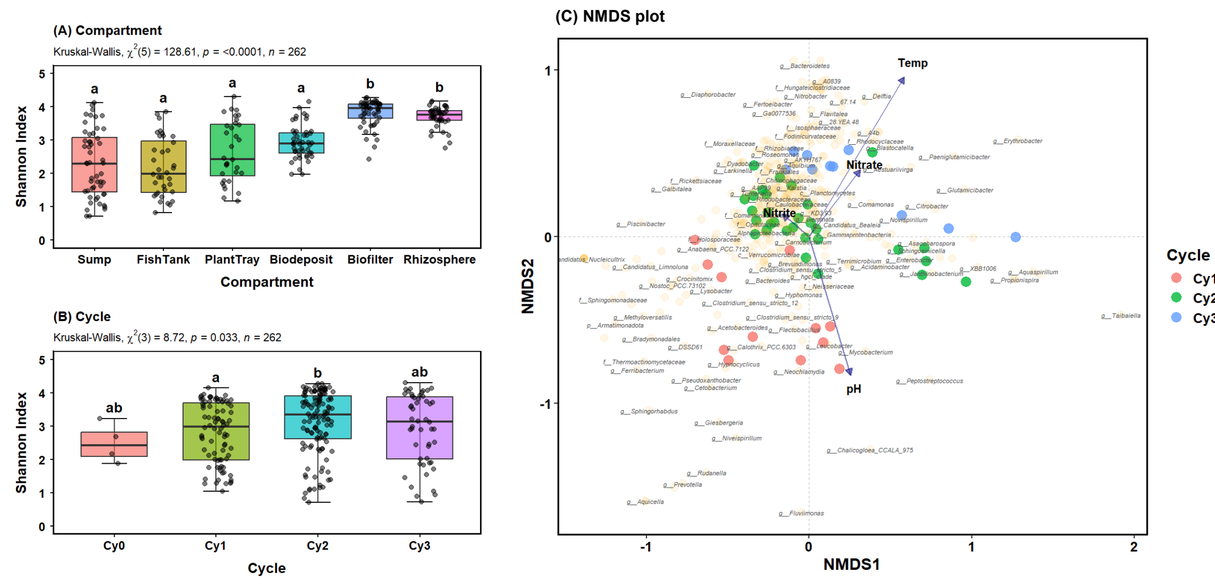


Fig. 4. Aquaponic microbiome diversity. Alpha diversity of (A) Compartment and (B) Cycle. (C) NMDS plot of microbiome communities by cycle.

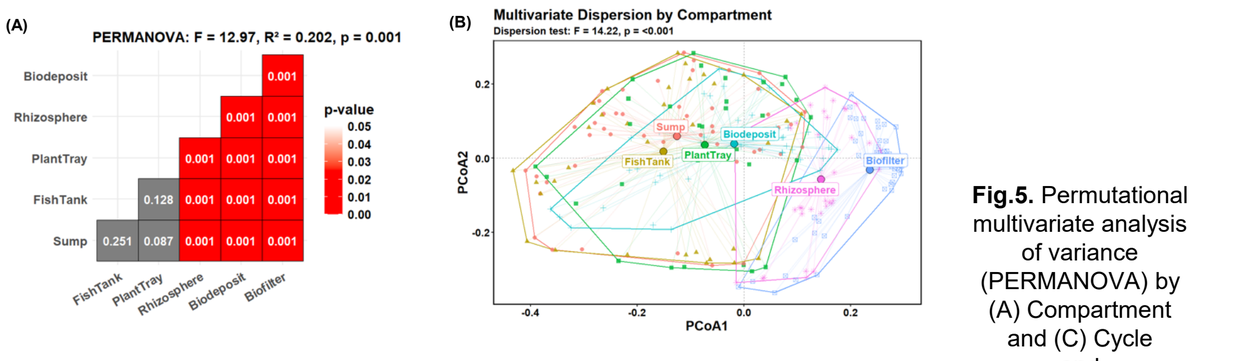


Fig.5. Permutational multivariate analysis of variance (PERMANOVA) by (A) Compartment and (C) Cycle and Multivariate Dispersion by (B) Compartment and (D) Cycle

Conclusion

- Alpha (Shannon) diversity revealed significant differences among compartments (Fig.4A) and production cycle (Fig.4B).
- NMDS ordination based on Bray-Curtis dissimilarity revealed clear shifts in microbial community composition across sampling cycles (Fig.4C).
- Environmental fitting analysis identified temperature and pH as significant drivers of microbial community structure. Temperature showed the strongest association with community variation (r^2 = 0.386, p = 0.001), followed by pH (r^2 = 0.232, p = 0.001). In contrast, nitrite (r^2 = 0.014, p = 0.723) and nitrate (r^2 = 0.079, p = 0.133) were not significantly associated with overall microbial composition (Fig.4C).
- Permutational multivariate analysis of variance (PERMANOVA) revealed that microbial community composition was significantly influenced by both production cycle (p = 0.001) and system compartment (p = 0.001). A multivariate dispersion analysis (beta-dispersion) based on PCoA ordinations showed significant difference for all test factors, except for tank (Fig.5).
- These findings suggest that spatial niche differentiation within the aquaponic system and temporal succession during system maturation were major drivers of microbial community variability.

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