Introduction

- Rainbow trout (Oncorhynchus mykiss) have been repeatedly introduced into Ecuadorian streams since the 1920’s.¹
- The introduction of non-native trout can have profound effects on stream communities by means of nutrient enrichment, predation, and by competing with native taxa.²,³
- How non-native trout farming affects stream microbial communities and their associated function is largely unknown.
- We examined the association of stream bacterial community structure, organic matter decay, and environmental variables among stream sites with and without trout farms.

Methods

- Sites were chosen based upon accessibility and land-owner permissions (Figure 1).
- We deployed cotton strips at 6 trout stream sites and 6 sites without trout farms (20-29 day incubation).⁴
- Bacterial communities were collected from cotton strips via sequence data was generated through Illumina™ (MiSeq) sequencing of the 16S rRNA gene region (V4) of bacterial DNA (Microbial Systems Molecular Biology Laboratory, University of Michigan).
- Sequence data was processed in MOTHUR³.
- We assessed bacterial community composition with ANOVA (one-way analysis of variance) and β diversity between sites with and without trout farms.

Results

- Organic matter decay was assessed as percent loss of cotton strip tensile strength per degree day and utilized as a measure of stream bacterial community function.
- We compared bacterial community α diversity (richness and inverse Simpson index) and β diversity between trout stream sites and stream sites without trout using analysis of variance (ANOVA).
- We used non-metric multidimensional scaling (NMDS) to explore bacterial community structure as related to environmental variables and organic matter decay.
- We used permutation-based analysis of variance (PERMANOVA) to quantify the relationship between trout farming and bacterial community composition while accounting for stream order.
- All statistical analyses were conducted in R (version 3.4.3).

Results continued

- Stream characteristics often altered by trout farming were correlated with NMDS axis 1 (pH: r = 0.69, p < 0.001; total dissolved solids: r = 0.59, p < 0.001; dissolved oxygen: r = 0.48, p = 0.004; and percent canopy cover: r = 0.83, p < 0.001).
- Rate of organic matter decay was marginally correlated with the NMDS axis 1 (r=0.30, p=0.05).

Figure 2. NMDS ordination. Stress = 10.3%. Red squares = trout farm sites, Blue circles = stream sites without trout. *note LRSR was sampled immediately above the trout farm

Discussion

- Further investigation is warranted, increasing sites sampled and sampling across additional stream systems.
- Potential changes in bacterial community structure and function as a result of trout farming practices could have long-term effects on the ecosystem.⁶
- Bacterial community alterations of the stream could cause dysbioses between native hosts and their bacterial symbionts ultimately affecting host health.⁷,⁸

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References