Preliminary assessment of stream bacterial community structure and function as related to trout farming in the Ecuadorian Andes

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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 standardized swabbing upon strip retrieval (n=3 per sample site; N=30 swabs in total).
- We assessed bacterial community composition with 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 MOTHUR[5]

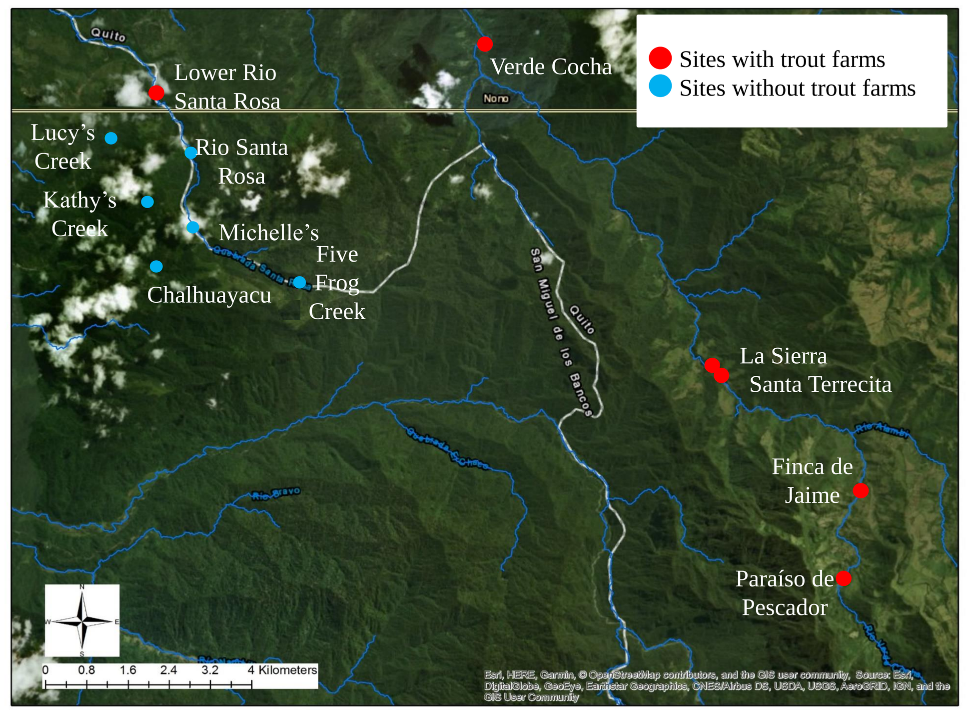

Figure 1. Sampling sites. Chalhuayacu and Santa Terrecita were not included in the analysis because the cotton strips were not recovered. Lower Rio Santa Rosa was sampled immediately upstream of the trout farm

Methods continued

- 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

- Bacterial taxonomic α diversity measures did not differ between sites with and without trout farms.

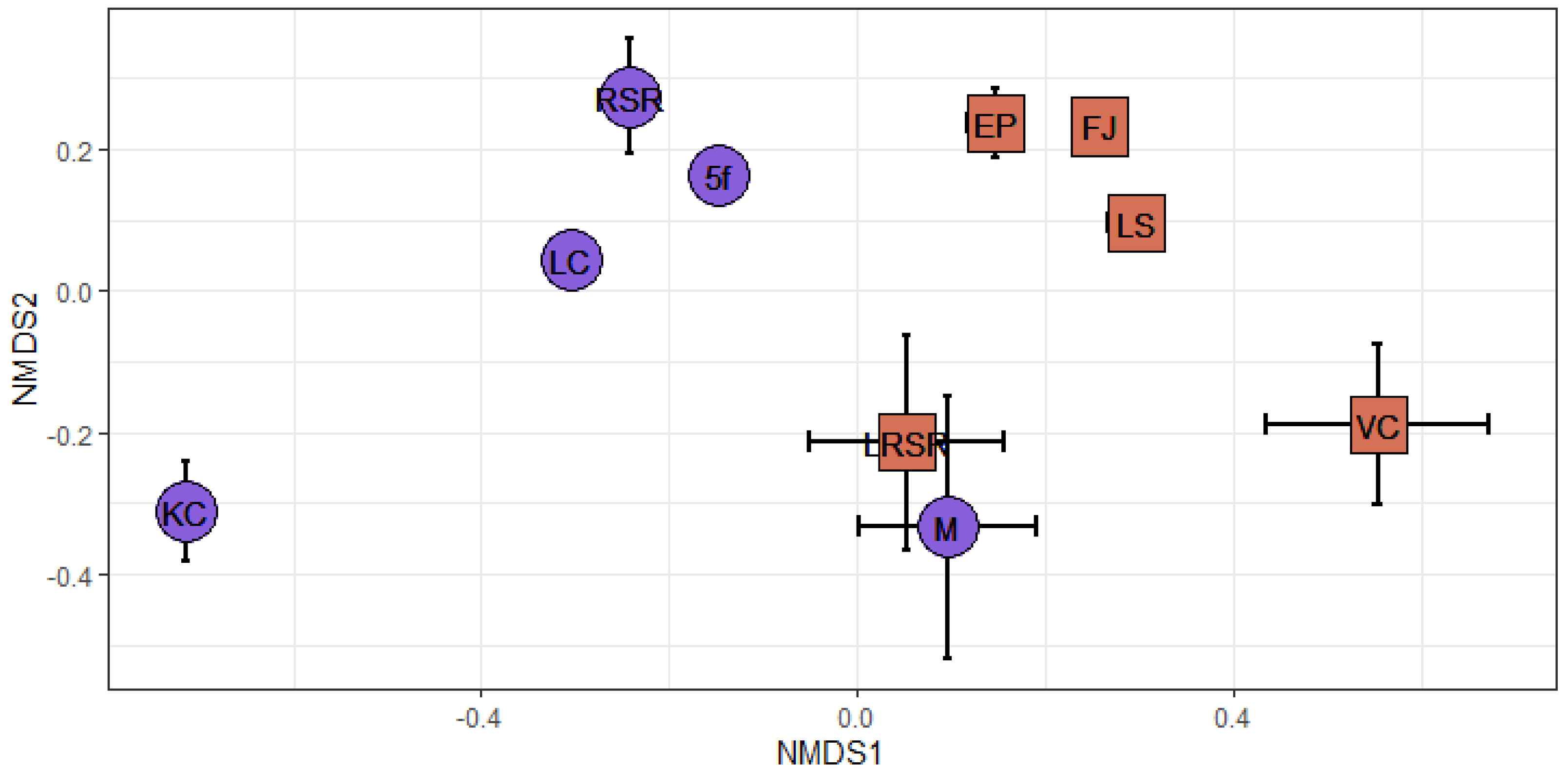

Figure 2. NMDS ordination. Stress = 10.8%. Red squares = trout farm sites, Blue circles = stream sites without trout. *note LRSR was sampled immediately above the trout farm

- NMDS ordination displayed a pattern along NMDS axis 1 indicating a potential difference in bacterial community composition related to trout farming between sites (Figure 2).
- The pattern observed in the NMDS ordination was not supported by permutation-based analysis of variance which indicated no significant effect of trout farming on bacterial community structure.

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 3. General flow-through design of trout farms in the region.

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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