

Upstream aquatic history and seasonality shape microbial community composition in a small mountainous river

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Riverine microorganisms play critical roles in major biogeochemical processes and catalyze many ecosystem services essential for sustaining life, yet we understand little about the mechanisms determining their composition. Microbial communities are modified and re-assembled in a fluvial system during transit from land to the ocean. The potential effects of upstream assembly and resistant time may shape downstream microbial community composition within aquatic networks, generating complex patterns of ecological succession. Here, we reconstructed the microbial succession along a land-freshwater-estuary continuum within a small mountainous river, the Gaoping River, with a high sediment yield ($3600 \text{ gm}^{-2}\text{yr}^{-1}$) and distinct wet season in southwestern Taiwan. We characterized hydrological seasonality and differentiated the total and reactive community by sequencing both 16 rRNA genes and their transcripts. Our analyses yielded diverse community compositions with a total of 38,679 ASVs, which were taxonomically assigned to 87 phyla have been recovered, while their abundances showed a highly skewed distribution pattern among sites and seasons. For example, ASVs affiliated with Comamonadaceae, known to have heterotrophic denitrification capability, were more abundant in downstream sites. In the middle course, the dominant ASVs were affiliated with different strains under the genus *Thiobacillus*, while those dominant ASVs were absent in upstream sites. Moreover, both microbial community compositions and geochemical features varied spatiotemporally and demonstrated a pattern of gradual change along the watershed, and a proportion of microbes co-occurred in soils, suspension particles, and riverbeds. Furthermore, parts of bacterial order were correlated regionally with nutrient and chemical concentrations. By examining the divergence and convergence between DNA and RNA-based microbial assemblages along the continuum and across seasons, we found that during the period of low-water level the similarity between total and reactive community compositions seemed to be greater than samples collected during the period of high-water level. Therefore, we inferred temporal shifts in the relative importance of assembly processes, with species selection dominant in spring and winter, and mass effects becoming stronger in summer, especially downstream sites. Overall, the current results consider the upstream history and hydrological seasonality as the deterministic factors controlling microbial community