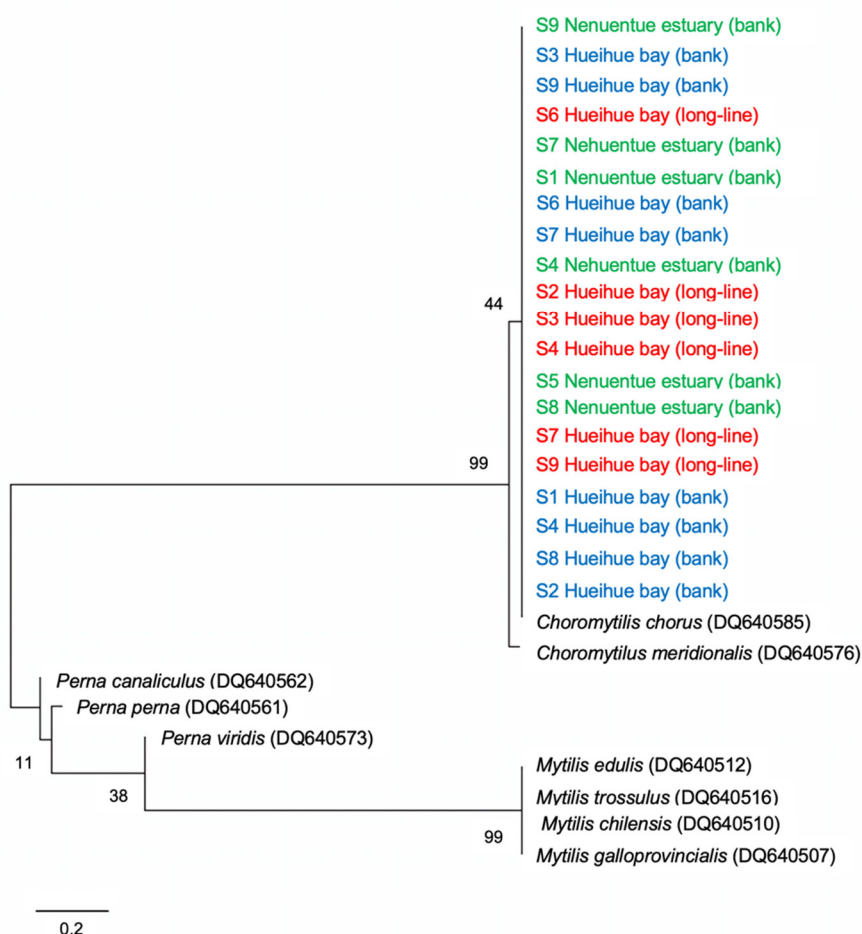


Article

# 16S rRNA–Based Analysis Reveals Differences in the Bacterial Community Present in Tissues of *Choromytilus chorus* (Mytilidae, Bivalvia) Grown in an Estuary and a Bay in Southern Chile



**Supplementary Figure 1.** Maximum Likelihood phylogenetic tree built with ITS sequences from the collected mussel tissues samples and representative members of Mytilidae family deposited in GenBank database from NCBI. The accession number in GenBank are presented within parentheses. The bar represents 20% divergence and a bootstrap of 1,000 repetitions was used. In green: tissue samples of *Choromytilus chorus* specimens collected from natural bank in Nehuentue Estuary; In blue: tissue samples of *C. chorus* specimens collected from natural bank in Hueihue Bay; In red: tissue samples of *C. chorus* specimens collected from long-line system in Hueihue Bay.