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## **Ecogenomics of Microbes**

## TITLE Diversification and coherence in a species of pelagic freshwater bacteria

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In many prokaryotic genera a clustered phylogeny is observed, comparably to the occurrence of species in sexually reproducing organisms. Yet, the diversity within bacterial species can be vast compared to what is known from macroorganisms, implying the coexistence of various closely related genotypes within a single habitat. Two major questions can be addressed. (i) What is the ecophysiological relevance of the diversity observed within lineages/species and (ii) what are the driving forces providing coherence within species?

Polynucleobacter is a particularly interesting taxon for studying these issues in freshwaters due to its cosmopolitan distribution and high global abundance. Polynucleobacter asymbioticus, prevalent in dystrophic ponds in the Austrian Alps, was selected for polyphasic investigations, including the targeted isolation of strains from different sites, genetic analysis (multi locus sequence typing and genome sequencing) in the context of geographic structure and physiological testing.

Overall, genetic variability occurs most notably in genomic islands, to some of which specific functions could be assigned and demonstrated in ecophysiological experiments. Interspecies genome comparisons provide evidence for recent exchanges of genomic islands across species boundaries. The variability resulting from the presence of different genomic islands might provide fine scale niche differentiation and thus, enable the coexistence of numerous closely related genotypes. On the other hand, analysis of the core genomes indicate high recombination rates between conspecific strains, not significantly reduced by the geographic separation of the respective habitats. This may indicate that homologous recombination is the main factor providing genetic coherence within the species.