

From the Mountain to the Valley - Drivers of Groundwater Prokaryotic Communities along an Alpine River Corridor

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Abstract

Rivers extend into the underlying groundwater which represents the unseen freshwater majority. Understanding microbial community composition and dynamics of shallow groundwater and lotic ecosystems is thus crucial, due to their potential impact on ecosystem processes and functioning.

A 300 km section of the Mur river valley, from 2000 m.a.s.l. in the Austrian alps to the flats (200 m.a.s.l.) at the Slovenian border, was followed, analyzing river water from 14 stations and groundwater from 45 wells in early summer and late autumn. The active (RNA derived) and total prokaryotic communities were characterized using high-throughput gene amplicon sequencing. Key physico-chemical parameters and stress indicators were recorded. The groundwater microbiome is analyzed regarding its composition, change with land use, and difference to the river. Community composition and species turnover differed significantly. At high altitudes, dispersal limitation was the main driver of groundwater community assembly, whereas in the lowland, homogeneous selection explained the larger share. Land use was a key determinant of the groundwater microbiome composition. The alpine region was more diverse in prokaryotic taxa, with some early diverging archaeal lineages being highly abundant. This dataset shows a longitudinal change in prokaryotic communities that is dependent on regional differences affected by geomorphology and land use.

Keywords

community assembly, diversity, hydrological exchange

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Conflicts of interest

The authors have declared that no competing interests exist.