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Bacterial community structure in aquifers corresponds to stratigraphy

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So far, groundwater microbiology with respect to different host rocks has not been well described in the literature. However, factors influencing the communities would be of interest to provide a tool for mapping groundwater paths. The Thuringian Basin (Germany) studied here, contains formations of the Permian (Zechstein) and also Triassic period of Buntsandstein, Muschelkalk and Keuper, all of which can be found to crop out at the surface in different regions. We analyzed the bacterial community of nine natural springs and sixteen groundwater wells of the respective rock formations as well as core material from the Zechstein salts. For that we sampled in a mine 3 differnet salt rock samples (carnallitite, halite and sylvinitite).

To validate the different approaches, similar rock formations were compared and a consistent microbial community for Buntsandstein could be verified. Similary, for Zechstein, the presence of halophiles was seen with cultivation, isolation directly from the rock material and also in groundwater with DNA-dependent approaches. A higher overlap between sandstone- and limestone-derived communities was visible as if compared to the salt formations.

Principal component analysis confirmed formation specific patterns for Muschelkalk, Buntsandstein and Zechstein for the bacterial taxa present, with some overlaps. Bacilli and Gammaproteobacteria were the major groups, with the genera Pseudomonas, Marinomonas, Bacillus, Marinobacter and Pseudoalteromonas representing the communities. The bacteria are well adapted to their respective environment with survival strategies including a wide range of salinity which makes them suitable as tracers for fluid movement below the ground.

The results indicate the usefulness and robustness of the approach taken here to investigate aquifer community structures in dependence of the stratigraphy of the groundwater reservoir.