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Vertical distribution of microbial communities and their response to metal(loid)s along vadose zone-aquifer sediments

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Microbial community in the vadose zone has been widely investigated. However, how microbial community varies from the vadose zone to deep-subsurface aquifer are poorly understood. In this study, 12 samples from vadose zone and three aquifer sediments were collected along a 42.5 m bore at a typical agricultural land in central China. High-throughput sequencing and multivariate statistical analysis were applied to explore the underlying distributions of bacterial, archaeal and fungal communities, and their response to environmental factors. The results showed that bacterial community changed considerably at vertical scales and essential variation occurred at the third aquifer layer. Actinobacteria (19.5%), NC10 (11.0%), Alphaproteobacteria (7.7%), Gammaproteobacteria (6.9%), and Deltaproteobacteria (6.4%) were most abundant classes in the vadose zone, where Alphaproteobacteria (22.3%), Gammaproteobacteria (20.1%), Actinobacteria (17.7%) and Bacteroidia (6.9%) enriched in the aquifer sediments. Archaeal and fungal communities were relatively more homogenous, with no significant trend as a function of depth. Process analysis further indicated that Selection dominated in bacterial community, whereas stochastic process governed archaeal and fungal communities. Moreover, environment-bacteria interaction analysis revealed that metal(loid)s (especially alkali metals) rather than physiochemical variables highly shaped the bacteria community in the vadose zone-aquifer continuum, where Bacteroidetes exhibited the strongest link to the variation of metal(loid)s. This research extends our knowledge about microbial community's variation through the vadose zone to deep aquifer sediments in the studied area and similar agricultural areas.