“Bacterial Community Dynamics and Variability in Shallow Aquifers”

The shallow, terrestrial subsurface plays an important role in sustaining life above ground. Globally, subsurface environments are becoming increasingly threatened by anthropogenic sources of contamination and disturbance. The Oak Ridge Reservation (ORR), located in Oak Ridge, Tennessee, played an important role in the development of nuclear weapons during World War II. In the process, soils, sediments and groundwater underlying the reservation became contaminated with radioactive and hazardous wastes. Strategies to remediate polluted subsurface environments such as Oak Ridge have included natural attenuation by resident microbes such as bacteria. Such studies would be aided by a thorough understanding of the natural variability of microbial diversity over space and time in uncontaminated environments. We examined the microbial community diversity and variability in both contaminated and non-contaminated sites of the ORR via ss-rRNA paired-end sequencing. An initial in-situ spatio-temporal survey of non-contaminated groundwater was conducted in order to understand how diversity and richness change overtime in an undisturbed aquifer. Moreover, different models were used to estimate possible causal relationships between geochemical parameters and population distribution. Additionally, surrogate sediment samplers were filled with native sediment to assess the diversity of the attached bacterial fraction. Communities observed in the attached fraction were a subset of groundwater communities, although the dominant fractions of each were distinct. After initial assessment, in-vitro groundwater was used as both a nutrient and microbial source for bioreactors filled with glass beads of various sizes in order to understand the potential effects of pore space and particle size on community dynamics. Potential viability and activity rates of resident microbes in both contaminated and non-contaminated groundwater and cored sediments were assessed using PMA-Seq and other complementary methods. Collectively, results show that 1) microbial communities in groundwater are highly dynamic over short time-scales, 2) corresponding changes in geochemistry are mostly weakly related to changes in community structure (except perhaps after a disturbance or stress period), 3) community assembly may be affected by pore space volume, 4) PMA-viable populations differ between solid and aqueous fractions, 5) viable populations may not always be highly metabolically active, and 6) traditional estimates of largely abundant populations may be influenced by the presence of DNA from non-viable members, resulting in less abundant populations being unmeasured or underestimated. The results of this study have implications for sampling and appropriate estimations of microbial populations in situ as well as the inherent variability in an uncontaminated shallow aquifer.

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