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Diversity and spatial scaling of the soil metagenome

F. Monroy[1,2], T.M. Bezemer[2], W.H. van der Putten[2,3]
[1]Universidade de Vigo, Ecoloxía e Bioloxía Animal, Vigo, Spain
[2]Netherlands Institute of Ecology, Heteren, Netherlands
[3]Wageningen University, Nematology, Wageningen, Netherlands

Introduction: Microorganisms constitute the main source of biodiversity on Earth and soils are considered to harbour most of this diversity. However, our knowledge about the rules governing diversity patterns comes mainly from the study of aboveground multicellular, conspicuous organisms. Whether soil microorganisms show biogeographical patterns and how these patterns influence their diversity are main questions in ecology. Considering the wide range of methods available to assess the diversity of microorganisms -from the use of selective-culture conditions to single-gene analyses and metagenomics- we discuss which diversity patterns are soundly supported and which ones might be revolutionized by the use of metagenomic data.
Material/Methods: We focused on the bacterial communities of temperate semi-natural grasslands in southern UK, where the occurrence of different diversity patterns was assessed by PCR-DGGE analysis of 16S rRNA.
Results: In the studied grasslands, 1) the presence/absence of bacterial taxa was related to variation in soil chemistry and plant community composition; 2) independently of the environmental factors, the similarity of bacterial communities decreased with geographic distance in grasslands separated between 1 and ~200 km, and 3) the diversity of bacteria was much lower at the cm scale than expected if the abundances of the different taxa were randomly distributed.
Discussion/Conclusions: The results support the view that variation in community composition in response to environmental factors is a common pattern in microorganisms. The choice between different screening methodologies or their combination will probably affect the precision rather than the ability to recognize the pattern itself. On the other hand, the distance effect on community similarity is a striking result for microorganisms, considering their expected dispersion abilities and the relatively short range of distances covered. The observed variation among community similarities suggests that the estimation of distance effects may be limited by the number of taxa detected with our methodology. Metagenomic data would overcome this limitation, probably showing that the distance-decay in community similarity is more common than thought. Moreover, as we showed, this pattern may be associated with the occurrence of strong bacterial interactions at very small spatial scales. A systematic validation of the idea that local processes are major determinants of microbial biogeographical patterns is waiting for the potential of metagenomics to provide extensive information on the communities of bacteria and other soil microorganisms.

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Influence of soil aggregate size on microbial community composition

S. Jennings[1], G. Kowalchuk[1], T. Urich[2]
[1]Netherlands Institute of Ecology, Microbial Ecology, Heteren, Netherlands
[2]University of Vienna, Vienna, Austria

Recent inventories of microbial diversity have shown that soils support an enormous quantity and diversity of micro-organisms. A number of explanations have been raised to explain this incredibly high level of diversity, but the importance of soil structure in the maintenance of soil biodiversity has been largely overlooked. Indeed, the majority of studies have necessarily focused on composite soil samples and large soil volumes (>0.5 g), thereby neglecting the highly structured and heterogeneous nature of soil. However, microbial populations in soil may be spatially separated in many cases, with soil aggregates potentially serving as distinct islands habitats. To investigate the heterogeneity of soil communities at a more relevant scale, we therefore addressed microbial community structure and function via two different approaches, (1) parallel examination of microbial community structure and function of different soil aggregate size classes through meta-transcriptomics, and (2) community analysis of individual soil aggregates. Freshly sampled soil (4 cores, top 5 cm) was quickly dry fractionated (4mm, 2mm, 0.8mm, 0.25mm and 0.053mm sieves), the total RNA content was extracted, cDNA synthesized and pyrosequenced. In addition, individual aggregates (6-180 mg) were picked for subsequent DNA extraction and community analysis. Metatranscriptomic analysis, supplemented with qPCR of the different aggregate size classes showed differences in community structure between fraction classes. Furthermore, we observed that individual soil aggregates often supported highly disparate microbial communities. Taken