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Advantages of the metagenomic approach for soil exploration: reply from Vogel *et al.*

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We read with interest the comments on our Editorial (TerraGenome: a consortium for the sequencing of a whole-soil metagenome. *Nature Rev. Microbiol.* **7**, 252 (2009))[1] by Singh and colleagues (Soil genomics. *Nature Rev. Microbiol.* **7**, 3 Aug 2009 (doi:10.1038/nrmicro2119-c1)) and Baveye (To sequence or not to sequence the whole-soil metagenome? *Nature Rev. Microbiol.* **7**, 16 Sep 2009 (doi:10.1038.nrmicro2119-c2). Indeed, the soil metagenome is viewed increasingly as being crucial for biosphere function and human interdependence, and therefore the debate about methods for its exploration is warming up.

The Terragenome international consortium initiative (http://www.terragenome.org/) will help coordinate efforts to fully explore and exploit the soil metagenome[1]. Although approaches vary, none is excluded even if global environmental DNA extraction techniques provide the highest (and most economically advantageous) genomic diversity. The tremendous quantity of genomic data extracted from the soil metagenome requires improved sequence analysis and better resources for function prediction. These resources are being supplied in part by initiatives to increase the number of individual microorganisms that are sequenced and studied in terms of their ecosystem function and physiological characteristics (for example, the Genomic Encyclopedia of Bacteria and Archaea project (http://www.jgi.doe.gov/programs/GEBA/)). This information is essential to provide a scaffold for metagenomic studies, although the diversity of organisms studied in such initiatives is considerably less than that found in any one soil from which DNA has been extracted for metagenome analysis, for targeted sequencing or for the production of clone libraries.

New technologies are necessary to understand the biological complexity of soil and the extensive diversity of the microbiota present, especially the initial descriptive challenge from which functional and systems insights will be obtained. This is particularly relevant as the majority of the microorganisms in soil cannot yet be grown in the laboratory. A range of high-throughput and sophisticated molecular techniques have been developed to facilitate the analysis of soil biodiversity, including soil metagenomics for direct analysis and exploration of soil-extracted microbial-community DNA. This is the study and exploration of the collective genomes of all organisms present in a particular soil sample[2] and for the first time makes the prospect of completely sequencing a soil metagenome realistic.

Owing to the enormity and complexity of the challenge of organizing this activity, so far only limited resources have been directed towards the sequencing of a soil metagenome, compared with those devoted to the human microbiome[3] or marine environments[4]. The deep metagenomic exploration of soil can provide information for the better management of this resource and for using informed approaches to ensure its functionality. To do this, the detail and range of microbial diversity should be described. We need to understand the extent of strain and species variation in soil and the fraction of the soil community that is active under a given condition. As well as determining the key functions of the community, we need to identify the dominant and rare community members (for example, bacteria, archaea, fungi, viruses and protists), determine their relative contributions to ecosystem functions and evaluate how the microbial community, as well as the physical and chemical composition of soils, varies at microscopic and macroscopic scales and over time. These data are useful for assessing and developing approaches to mitigate the effects of perturbations such as climate change, land-use change and anthropogenic inputs (including pollutants and fertilizers) on the composition, activity and function of the soil community.

A coordinated approach for the study and assessment of soil biological diversity will push the boundaries of our knowledge. The lack of detailed knowledge of the world beneath our feet is alarming. This ignorance is a product of the small physical scale of the biota present, the magnitude of their diversity in space and time and, until recently, the lack of suitable analytical methods. Sequencing the soil metagenome is the first step to providing this information. Combined with other data, it will have considerable economic and environmental value, providing insights into the ecology of microorganisms that are beneficial to or threaten crop production, enhancing food security through the development of sustainable agricultural practices and ensuring the quality and provision of ecosystem services. The soil microbial community is also well known as a key resource for novel biocatalysts involved in either biosynthetic or biodegradation processes, including those that can be used for new drug discovery approaches[5–7], the degradation of human-made polluting compounds[8–10], the improvement of indispensable bioprocesses in the biotransformation industry, the production of biofuels[11] and the fundamentals of biodiversity and spatial complexity[12]. Soil metagenomics can only improve these activities, and the technological advances offered will provide fundamental data that will aid in sustaining the terrestrial environment.

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