EDITORIAL

Ecology and metagenomics of soil microorganisms

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Microorganisms are essential for the formation and biogenesis of soil, maintenance of soil structure and fertility and the biogeochemical cycling processes, as well as for other ecosystem functions, that are essential for plant growth and bioremediation. Understanding the factors that determine the growth, activity and diversity of soil microbial communities, their control by soil physicochemical characteristics and their interactions with other soil inhabitants is therefore essential for sustainable management of soil ecosystem function, and prediction of the impact of environmental change. This Thematic Issue brings together articles derived from two important international conferences on soil microbial ecology and on the application and exploitation of modern molecular methods in ecological studies.

The meeting on Ecology of Soil Microorganisms: Microbes as Important Drivers of Soil Processes was held in Prague, Czech Republic on 27 April–1 May 2011. The meeting was organized as a specialized soil conference providing an interdisciplinary platform for microbiologists, ecologists and soil biogeochemists. It demonstrated the power of the novel tools used in microbial ecology including, among many others, next-generation sequencing and stable isotope methods, but also showed that new methodologies can only deliver important knowledge when combined with classical studies on individual microorganisms, *in situ* chemical and biochemical analyses or ecosystem integration and modelling. The programme addressed both fundamental questions of soil microbiology and major current issues: the functioning of agricultural soils under different management strategies, the role of forest soils in global biogeochemical cycles and the global human-induced effects on soils and their microbiota. The sessions on global change effects, agricultural soils and microbe-catalysed biogeochemical processes attracted particular attention. The meeting was supported by FEMS and ISME.

The Soil Metagenomics 2010 symposium, which took place in Braunschweig, Germany between 8 and 10 December 2010, was initiated by the Johann Heinrich von Thünen Institute (vTI), Federal Research Center for Rural Areas, Forestry and Fisheries and mainly supported by the German Science Foundation (DFG). The objective was to assess the implications of next-generation, high-throughput, nucleic acid sequencing technologies for research in microbial diversity and soil ecology. From the introduction of cultivation-independent, nucleic acid analyses in the 1980s, the speed of DNA sequencing increased until the year 2000 by only approximately one to two orders of magnitude, from fewer than 100 to 1000 kbp per day per sequencing machine. During the following decade, however, until 2010, the speed of sequencing increased logarithmically one-million-fold, and further increases are expected during the years to come. This increase in information eradicates previous restrictions of limited datasets and, consequently, has changed research strategies in many fundamental and applied areas. For example, it has influenced how we explore microbial habitats at spatial scales from micrometres to global biogeography, how we manage microbial activities for sustainable agriculture in the future and how we search for beneficial products made by yet-to-be-cultivated soil microorganisms. While biochemistry and molecular genetics were important add-on disciplines for soil microbial ecologists in previous decades, bioinformatics is now crucial for efficient handling and analysis of large datasets to unveil hidden information.

The Thematic Issue begins with three MiniReviews, on the impact of global change on the soil nitrogen cycle, on soil fungi and on limitations of metagenomics specific to soil microbial ecology. These MiniReviews are followed by 10 research papers arising from the Ecology of Soil Microorganisms meeting. Articles on the role of surfactants produced by soil pseudomonads and on microbial communities in spoil heaps and associated with land use change are followed by several papers on soil fungi, including mycorrhizal fungi. These articles link with two papers on plant–microbe interactions, which are followed by two studies of soil biodegradation, of jet fuel and chlorophenols. The final three research articles arose from the Soil Metagenomics meeting, comprising a stable isotope probing analysis of toluene-degrading soil microorganisms and two articles on metagenomic-driven gene discovery.

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