

Collapse of beneficial microbial communities and deterioration of soil health: a cause for reduced crop productivity

Microbial diversity has profound effects on ecosystem functions. Decomposition of organic matter, nutrient cycling, bioremediation of toxics and pollutants, and both the spread and control of infectious diseases are some key roles of soil microbes in the ecosystems. They determine plant growth. However, the relationships between microbial functioning and sustenance of plant growth are still poorly understood. In the last two decades, there has been a decline in the yields of major crops in Asia despite the use of recommended cultural practices¹. The reduced crop productivity in conventional agriculture has been explained to have been caused by the indiscriminate use of chemical inputs (fertilizers and agrochemicals) and intensive cropping, which have made the soil sick¹. This correspondence illustrates that the collapse of beneficial soil microbial communities under conventional agriculture hampers the delicate positive interactions within and between aboveground and belowground biotic communities, resulting in reduced crop productivity.

Conventional tillage significantly reduces the diversity of bacteria by reducing both substrate richness and evenness². Therefore, bacterial community assemblages under the tillage have more similar structures than those under zero tillage. However, conservation tillage and legume-based crop rotations in wheat have been observed to support the diversity of soil microbial communities and may affect the sustainability of agroecosystems².

Plant species identity is a factor influencing microbial community composition³. This is because there are strong interactions between aboveground and belowground biotic communities, as revealed by correlations between bacterial metabolic and plant taxonomic diversities⁴. Plant species and soil type are two important characteristics affecting the structure of the total bacterial community⁵. Soil C/N ratio is most often associated with changes in microbial community composition⁶. Human alteration of soil microbial communities via the alteration of plant community composition and diversity has been observed, which is mediated in part by changes in

soil C quality⁶. Moreover, 16S rRNA gene and phospholipid fatty acid analyses have revealed shifts in the total microbial community in response to the different management regimes, indicating that deliberate management of soils can have a considerable impact on microbial community structure and function in tropical soils⁷. Applications of chemical fertilizers and agrochemicals lower the soil microbial diversity⁸. Soil bacteria are more sensitive to chemical N fertilizer application during the plant growth cycle⁹.

It is well known that phytotoxins such as phenolics, flavonoids and alkaloids are released from plants to the soil. They are known as allelopathic compounds. To make an agroecosystem sustainable these compounds should be removed, a role which is played by the evolving microbial communities with changing functionality for biodegradation. However, temporal changes in bacterial functionality have been observed to disappear in the conventional cultivation with chemical inputs⁸. This leads to the accumulation of allelopathic compounds, resulting in reduced crop productivity. In contrast, organic farming is generally characterized by elevated microbiological parameters⁶, due to incorporation of a wide range of microbial communities via organic manures.

Chemical fertilizers and herbicide application in conventional agriculture also affect negatively the potential for top-down control of aboveground pests¹⁰, possibly due to reduced microbial diversity. They also change interactions within and between below- and aboveground components, ultimately promoting negative environmental impacts of agriculture by reducing internal biological cycles and pest control. On the contrary, organic farming fosters microbial and faunal decomposers and this propagates into the aboveground system via generalist predators, thereby increasing biological control¹⁰.

Land degradation reflected by yield decline, and diseases and pests under conventional agriculture is a common global problem. As described above, it is mainly caused by the depletion of beneficial microbial communities due to con-

tinuous use of chemical inputs and intensive cropping. The degraded lands are rehabilitated using crop rotation or converting into organic farming systems. These are medium to long-term options with relatively high cost. Handling of organic fertilizers in organic farming is also a difficult job. Therefore, less bulky, short-term and low-cost biofertilizing methods are now being tested to replenish the beneficial microbial communities in degraded as well as conventional croplands. One such group of biofertilizers is the biofilmed biofertilizers (BBs), which contain beneficial microbial communities with biofertilizing and biocontrolling capabilities¹¹. The BBs are now being experimented with rice, tea, maize, etc. in Sri Lanka with initial successes, and will be shortly tested with wheat and rice in Australia.

1. Narwal, S. S., In *Allelopathy: A Physiological Process with Ecological Implications* (eds Reigosa, M. J., Pedrol, N. and González, L.), Springer, The Netherlands, 2006, pp. 537–564.
2. Lupwayi, N. Z., Rice, W. A. and Clayton, G. W., *Soil Biol. Biochem.*, 1998, **30**, 1733–1741.
3. Carney, K. M. and Matson, P. A., *Microb. Ecol.*, 2006, **52**, 226–238.
4. He, X. Y. *et al.*, *Plant Soil*, 2008, **307**, 123–134.
5. Garbeva, P., Van Elsas, J. D. and Van Veen, J. A., *Plant Soil*, 2008, **302**, 19–32.
6. Truu, M., Truu, J. and Ivask, M., *Eur. J. Soil Biol.*, 2008, **44**, 231–237.
7. Bossio, D. A. *et al.*, *Microb. Ecol.*, 2005, **49**, 50–62.
8. Papatheodorou, E. M., Efthimiadou, E. and Stamou, G. P., *Eur. J. Soil Biol.*, 2008, **44**, 429–436.
9. Crecchio, C. *et al.*, *Soil Biol. Biochem.*, 2007, **39**, 1391–1400.
10. Birkhofer, K. *et al.*, *Soil Biol. Biochem.*, 2008, **40**, 2297–2308.
11. Seneviratne, G., Kécskés, M. and Kennedy, I. R., In *Efficient Nutrient Use in Rice Production in Vietnam Achieved Using Inoculant Biofertilizers* (eds Kennedy, I. R. *et al.*), ACIAR Proceedings, No. 130, Australia, 2008, pp. 126–130.

GAMINI SENEVIRATNE

*Institute of Fundamental Studies,
Hantana Road, Kandy,
Sri Lanka
e-mail: gaminis@ifs.ac.lk*