Ecology

Global soil map pinpoints key sites for conservation

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A map of Earth reveals hotspots of soil biodiversity and regions to target for conservation. Many of these areas are currently unprotected, which suggests that it is time to rethink our soil management and conservation priorities. **See p.693**

The growing interest in soil biodiversity has produced a wealth of information about the variability in soil organisms and their role in the functioning of soil ecosystems[1,2]. Global surveys are available that provide such data for bacteria, fungi and macrofauna[3], nematode worms[4] and earthworms[5]. Guerra *et al.*[6] complement these findings on page 693 with a worldwide survey that includes an analysis of 615 soil samples from 151 locations, representing all continents.

The strength of Guerra and colleagues' approach lies in the multifaceted character of the soil sampling undertaken. This included gathering measures of soil biodiversity – by monitoring organisms such as bacteria, fungi, protozoa and invertebrates – and assessing soil-ecosystem functioning in terms of processes such as carbon and nutrient cycling, positive plant–microorganism interactions, water-holding capacity and natural resistance to soil-borne diseases.

By applying advanced statistical and modelling techniques, the authors constructed an integrated framework to map soil biodiversity and functioning along worldwide environmental gradients of climate, vegetation and altitude. The approach was ambitious, given the immense task of capturing soil biodiversity. Soil harbours a wide variety of soil-dwelling organisms[1,2], which display all kinds of feeding modes, such as herbivory, microbivory, omnivory and predatory behaviours. Together, the organisms form highly complex food webs[7]. The soil food web brings together biodiversity and function, because these trophic interactions (who eats whom) represent a web of pathways of ingestion, processing and excretion of organic and inorganic materials, which are activities thought to make a major contribution to the global cycling of carbon and nutrients[8].

Guerra and colleagues created their comprehensive picture of soil biodiversity by assessing two metrics: species diversity at a particular location (known as alpha diversity) and the extent to which the species composition at a location differs from that at other locations (referred to as dissimilarity), which can be interpreted as a measure of uniqueness. These metrics are connected to soil processes and environmental conditions. The outcome gives a mixed picture, with contrasting results in terms of the key factors identified. For example, soil pH was found to be important for microbial diversity, whereas soil organic matter (the carbon and nitrogen contents) was associated with faunal diversity. Varied patterns also exist for aspects of soil ecosystem functioning. The pH is crucial for carbon storage, water retention and pest control, whereas temperature correlates with soil organic matter decomposition and nutrients, and seasonal precipitation is linked to positive plant–microbe interactions.

Hotspots of biodiversity were found in temperate and Mediterranean regions and in alpine tundra. By contrast, the hotspots of species uniqueness occur mostly in the tropics and drylands. The hotspots for biodiversity, uniqueness and soil-ecosystem processes are not clearly correlated with each other.

The results raise several questions. For example, why do hotspots of diversity occur in temperate regions, and why are unique soil communities a particular characteristic of the tropics and drylands? The findings also prompt the question of how soil ecosystem functions might benefit from biodiversity. Indeed, the results might chime with the idea that some ecosystem processes depend on only a few groups of organisms, such as in the case of nitrogen cycling through nitrification, and that other processes depend on the activity of many species[9]. High levels of back-up components (redundancy) might be available for some processes, such as soil respiration.

Another factor that might affect the relationship between biodiversity and ecosystem function is spatial variation in the physical packing of soil and the gaps between soil particles, which can result in heterogeneous distributions of water, air, organic matter and nutrients. Such soil heterogeneity means that only a small proportion of all possible trophic interactions actually take place, which might then obscure the identification of possible specific relationships between soil organisms and soil processing[7].

To show that their framework has potential applications, Guerra and colleagues defined priority regions for nature conservation on the basis of high levels of soil biodiversity and ecosystem function (Fig. 1). The alarming finding that most of these priority areas are not currently under any sort of conservation protection should indicate the need to rethink our priorities in terms of national and international conservation planning. The authors also showed that their modelling framework can be used in analyses of different future scenarios, for example to identify regions particularly sensitive to climate change in terms of predicted losses in soil biodiversity and function.

The framework might also have potential for broader application in efforts to counteract

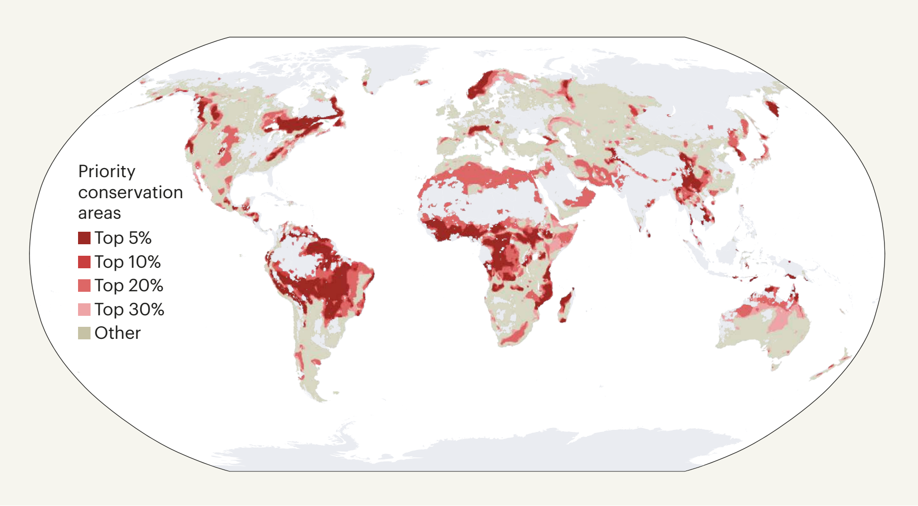

Figure 1 | Priority areas for soil conservation. Guerra *et al.*[6] assessed soil biodiversity and ecosystem functions at 615 sites around the world, enabling them to identify areas requiring protection. (Figure based on Fig. 2a of ref. 6.)

climate change. The "4 per 1000" Initiative (which aims to increase carbon storage in soil by 0.4% annually), launched at the 21st Conference of the Parties in Paris (http://4p1000.org), and the latest report of the Intergovernmental Panel on Climate Change indicate that soils have the potential to store annually a substantial amount of carbon – on a scale relevant in comparison to the emission of carbon dioxide through human activities[10]. Achieving this high storage goal, and, in particular, deciding where and how to focus our efforts (see go.nature.com/3chahft), requires an understanding of underlying biological processes in the soil[11,12].

The fate of carbon that enters the soil, that is, whether it is emitted or stored, depends on the diversity and function of the soil microbial community. Bacteria produce compounds that 'glue' soil particles together, thereby forming aggregates in which carbon is stored. Fungi incorporate more carbon in their biomass than the amount they release through respiration, and this carbon is trapped in soil aggregates as recalcitrant 'necromass' (dead biomass)[13]. Guerra and colleagues' map shows, in a spatially explicit way, carbon storage together with the diversity of the soil organisms involved. This information will surely help efforts to discover and understand the soil microbial and environmental conditions under which carbon storage takes place, and how that might be optimized.

A next step in developing future versions of this map should be to gather data representing other locations, so as to capture further soil types, forms of land use and climates. The Global Soil Biodiversity Observatory, an initiative that aims to monitor and forecast the status of soil biodiversity and soil health (go.nature.com/3ea7tgc), might contribute to future efforts to monitor soil biodiversity and to the further development of this highly useful soil biodiversity map of the world.

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1. Johnson, N. *et al.* (eds) *Global Soil Biodiversity Atlas* (EU, 2016).
2. FAO *et al. State of Knowledge of Soil Biodiversity — Status, Challenges and Potentialities* (FAO, 2020).
3. Cameron, E. K. *et al. Nature Ecol. Evol.* **2**, 1042–1043 (2018).
4. van den Hoogen, J. *et al. Nature* **572**, 194–198 (2019).
5. Phillips, H. R. P. *et al. Science* **366**, 480–485 (2019).
6. Guerra, C. A. *et al. Nature* **610**, 693–698 (2022).
7. Moore, J. C. & de Ruiter, P. C. *Energetic Food Webs: An Analysis of Real and Model Ecosystems* (Oxford Univ. Press, 2012).
8. Wolters V. *et al. Bioscience* **50**, 1089–1098 (2000).
9. Schimel, J. P. & Schaeffer, S. M. *Front. Microbiol.* **3**, 348 (2012).
10. IPCC. In *Climate Change 2022: Mitigation of Climate Change. Contribution of Working Group III to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change Impacts, Adaptation, and Vulnerability: Summary for Policymakers* (eds Shukla, P. R. *et al.*) 50 (Cambridge Univ. Press, 2022).
11. Chenu, C. *et al. Soil Till. Res.* **188**, 41–52 (2019).
12. Liang, C., Schimel, J. P. & Jastrow, J. D. *Nature Microbiol.* **2**, 17105 (2017).
13. Hannula, S. E. & Morriën, E. *Geoderma* **413**, 115767 (2022).

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Microbiology

Mystery find of microbial DNA elements called Borgs

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Microorganisms store some genetic information on non-chromosomal elements. The emergence of a surprising version of these elements shifts our understanding of their diversity and potential roles. **See p.731**

Most microorganisms have a single chromosome that harbours almost all of their genetic information[1,2]. Extra genomic information is frequently encoded in non-chromosomal DNA segments called extrachromosomal elements (ECEs), which exist in the form of structures such as plasmids that consist of DNA in a linear or circular form. Al-Shayeb *et al.*[3] report on page 731 the discovery of unusually large ECEs containing numerous and diverse genes that encode proteins involved in metabolic activity. The authors hypothesize that these ECEs increase the capacity of their microbial hosts to consume the greenhouse gas methane.

The authors discovered 19 types of large ECE when analysing samples, such as of wetland soil, underground (sediment-associated) water and discharges from mines, taken from sites in the United States. The cells that are thought to host the ECEs are from the genus *Methanoperedens*, a group of archaea – unicellular microorganisms that are evolutionarily distinct from bacteria (Fig. 1). These ECEs are inferred to replicate in *Methanoperedens* cells, and have, like most ECEs, a tendency to acquire genetic information from other organisms and their environment. To highlight this ability to assimilate genes, especially from their *Methanoperedens* host, Al-Shayeb and colleagues named these ECEs Borgs, after a group of aliens in the science-fiction franchise Star Trek – creatures that assimilated thousands of species from across the Galaxy.

Most of the recovered Borg sequences are partial representations of these ECEs, but there are four complete sequences, which share a common genome organization. The sequences were inferred to be linear and to range in size from 662 to 918 kilobase pairs of DNA.

Most of the Borg-encoded proteins corresponded to unknown hypothetical proteins, but approximately 21% matched archaeal proteins, most of which (on the basis of gene- and protein-sequence similarity and other characteristics) were assigned to *Methanoperedens*. Al-Shayeb and colleagues ruled out the idea that these sequences represent previously unknown archaeal genomes, because of their near-complete lack of characteristic archaeal genes – marker genes or genes encoding components (ribosomal proteins) of the machinery that makes proteins. The authors conclude that these novel sequences cannot exist independently in microbes, and must be bona fide ECEs. The abundance ratios between Borgs and their potential hosts ranged from 2:1 to 8:1, suggesting that *Methanoperedens* cells can harbour multiple copies of the same Borg. Interestingly, several samples with relatively high abundances of *Methanoperedens* lacked Borgs, supporting the idea that these ECEs are associated only with specific types of *Methanoperedens* host.

Borgs are probably not chromosomes. Neither do they qualify as viruses, because of their lack of sequences encoding recognizable proteins needed for the construction of a protective viral coat, which is essential to encase the viral genetic material and to help viruses to infect cells[4]. Thus, these large ECEs probably represent plasmids. Plasmids in the form of bacterial or archaeal DNA molecules are, in most cases, smaller than their host's chromosome(s) and generally dispensable, and they typically encode proteins that provide functions which give their host an advantage under specific conditions[5,6]. All of these criteria might apply to Borgs, and, therefore, on the basis of their large size, Borgs can be classified as ECEs called megaplasmids.

Numerous bacteria and archaea harbour megaplasmids. These large ECEs have greater