they are calibrated, and little information exists about vegetation in semi-arid ecosystems compared with other regions. Similarly, the pathways for CO_2 once it has been absorbed into semi-arid vegetation remain poorly understood[10,11], so there are few solid data from which to assess the stability of the CO_2 sink in such ecosystems. More broadly, semi-arid systems are vulnerable to a range of factors that are difficult to model, such as overgrazing, fire, flooding and chronic soil erosion[10,11], many of which are linked to human activity. These processes must somehow be accounted for, both in models and in policies for land use and conservation, if the invaluable function of semi-arid ecosystems as a global CO_2 sink is to be managed and maintained.

Nevertheless, Poulter *et al.* make a key contribution in highlighting the crucial, and hitherto often overlooked, role of such ecosystems in the global carbon cycle, and in identifying several important processes, which should markedly improve our understanding of future atmospheric CO_2 levels. Let us hope that their research stimulates more work on the ground to better understand and manage these fragile but essential ecosystems. ■

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MICROBIOLOGY

Barriers to the spread of resistance

Despite identifying abundant genes capable of conferring antibiotic resistance in soil microorganisms, a study finds that few are shared by human pathogens and that there is little transfer of the genes within the soil communities. **SEE LETTER P.612**

MORTEN O. A. SOMMER

Antibiotic resistance is complicating the treatment of many bacterial infections, leading to increasing mortality and health-care costs across the globe. Pathogens frequently acquire resistance to antibiotics from other sources, and soil-dwelling bacteria are considered an important reservoir of resistance genes. In this issue, Forsberg *et al.*[1] (page 612) identify nearly 3,000 genes conferring antibiotic resistance from the soil, and find that only a minute fraction of these genes is shared with human pathogens. Furthermore, their data suggest that it is the mobilization of and selection for such genes, rather than their supply, that limits their transfer among soil bacteria and with other bacteria, including human pathogens.

The genome sequencing of thousands of bacterial pathogens has shown that antibiotic-resistance genes are often acquired by pathogens from other sources through horizontal gene transfer[2]. This process allows even distantly related bacteria to transfer genes through the action of viruses (bacteriophages) or conjugative plasmids (small DNA molecules separate from chromosomal DNA that have the machinery to facilitate transfer between bacteria), or through uptake of free-floating DNA in the environment. All of these mechanisms are known to contribute to the emergence of antibiotic resistance in human pathogens, yet the origin of most clinically relevant resistance genes remains elusive. Accordingly, research efforts are directed at addressing this question through the elucidation of antibiotic-resistance genes harboured by different microbial communities[3].

Several soil bacteria can produce antibiotics, and these bacteria also have the necessary genes to confer immunity against the toxins they produce. Accordingly, it has been proposed[2] that these antibiotic producers could be an origin of antibiotic-resistance genes. Subsequent research has also pointed to other soil microbes that might serve as sources of resistance genes, including bacteria that can subsist on antibiotics[4]. Yet, in spite of substantial research in this area, only a few studies have demonstrated a link between resistance genes in the soil and resistance genes in human pathogens[5].

Forsberg and colleagues deployed functional metagenomics to study soil microbial communities and characterize genes that confer antibiotic resistance on a non-resistant strain of the bacterium *Escherichia coli*. They identified nearly 3,000 resistance-conferring genes,

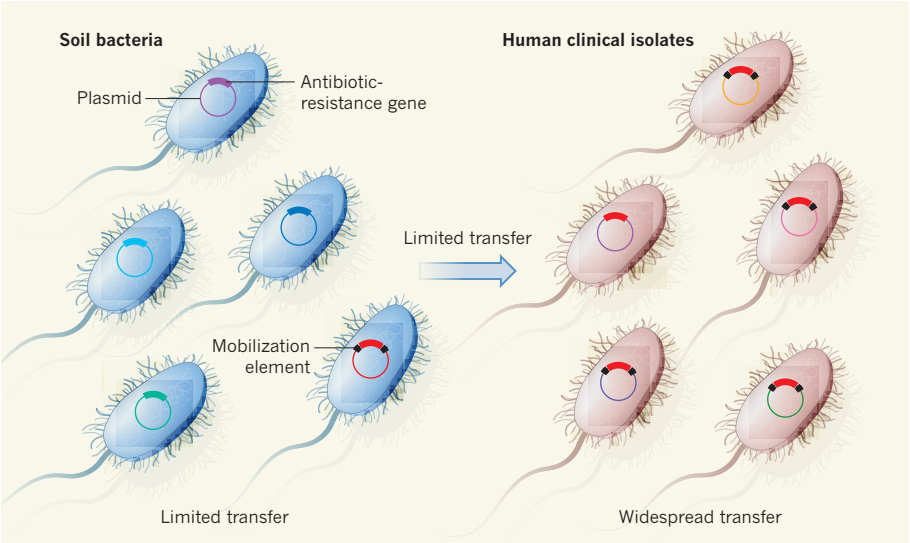

Figure 1 | Limited transfer. Forsberg and colleagues' metagenomic analysis of soil microorganisms[1] identified around 3,000 genes capable of conferring antibiotic resistance, but found that less than 0.1% of these genes have been identified as associated with antibiotic resistance in bacteria isolated from human patients. They also show that fewer resistance genes in the soil bacteria are flanked by mobilization elements than those in pathogens, suggesting that there is limited transfer of these genes within the soil community and from the soil to other bacteria.

which is a number comparable to all currently known antibiotic-resistance genes[6]. Thus, this study shows clearly that an extraordinary diversity of antibiotic-resistance genes exists in nature, as suggested by previous analysis of soil microbial communities[7].

An earlier study[5] from the group presenting the current paper reported the first case of the transfer of several drug-resistance genes between innocuous soil bacteria and human pathogens, highlighting that transfer of genes between such bacteria is possible. But that study included bacterial-enrichment steps that prevent quantification of the extent of such transfer. In the present study, the authors used a method that did not require enrichment and which allowed them to quantify the extent of antibiotic-resistance genes that are shared between soil bacteria and previously characterized bacteria.

They found that only around 0.1% of the identified resistance genes from soil are highly similar (greater than 99% nucleotide identity) to previously detected resistance genes, indicating that there is only limited overlap between the resistance genes of soil bacteria and other bacteria, including those that cause infections in humans (Fig. 1). Although this low overlap does not exclude the possibility of soil bacteria acting as an origin of antibiotic-resistance genes that cause clinical problems, it does demonstrate that only a minute fraction of resistance genes from soil bacteria have been transferred to human pathogens.

Forsberg *et al.* also investigated whether the limited overlap might result from limited transfer of antibiotic-resistance genes within the soil microbial community. If this is the case, specific resistance genes should be stably associated with specific phylogenetic divisions. The authors show that this is correct and conclude that the resistance-gene pool of different soil communities is closely linked to the phylogenetic architecture of those communities. The authors were not able to resolve the phylogenetic architecture beyond the phylum level, and so horizontal transfer of genes within a specific phylum cannot entirely be ruled out. However, they show that soil bacteria, in contrast to human pathogens, have a much lower number of mobilization elements flanking their resistance genes, which supports their hypothesis of limited transfer of resistance genes between soil bacteria. These results are consistent with the hypothesis that there is limited selection for antibiotic resistance within the soil microbiota compared to the selection for antibiotic resistance in human pathogens.

These findings fuel the ongoing question of what is the function of antibiotic-resistance genes in their natural hosts. For instance, the MFS transporter proteins identified by the authors as conferring resistance to a wide range of antibiotic classes may not actually function as antibiotic-resistance proteins in their hosts, but rather in different processes, such as the transport of other small molecules that may be more abundant than antibiotics in the soil. Similarly, the identified β-lactamase enzymes might serve as cell-wall remodelling enzymes in their natural hosts. The apparent paucity of mobilization elements flanking these genes would suggest that selection for and transfer of resistance functions in the soil is not as strong as in other environments.

Irrespective of the function of these genes in their natural hosts, Forsberg and colleagues' study demonstrates that the soil microbiota harbours an extraordinary diversity of genes that have the potential to confer antibiotic resistance in human pathogens such as *E. coli*. Their findings also suggest that it may not be the availability of genes encoding proteins capable of conferring antibiotic resistance that limits the spread of resistance, but rather the mobilization and transfer of these genes. Functional metagenomic studies of soils that have been exposed to inhibitory concentrations of antibiotics should be performed to test whether this increases the extent of resistance-gene mobilization. ■

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MATERIALS SCIENCE

Energy storage wrapped up

Cables and wires are used to conduct electricity, but can they also store energy? The answer is a resounding 'yes', if they are encased by a supercapacitor device — a finding that might open up many applications.

YURY GOGOTSI

Electrical cables entangle the world, supplying electricity to buildings, machines and electronic devices. The systems currently used to store electrical energy are separate from the cables, and are bulky contraptions often consisting of assemblies of 'supercapacitor' devices. Reporting in *Advanced Materials*, Yu and Thomas[1] describe coaxial cables consisting of a copper core surrounded by a supercapacitor sheath, which can both transmit and store electricity.

Energy storage in supercapacitors can involve two mechanisms[2]: the formation of a double layer of ions adsorbed on oppositely charged electrode surfaces; and pseudocapacitance, in which fast electrochemical reactions occur at the surface of an electrochemically active material, such as manganese dioxide. Because pseudocapacitance occurs on a large electrode surface, it always takes place alongside double-layer capacitance.

In supercapacitors, charge is stored only at surfaces, and so — unlike in batteries — its availability is not limited by diffusion processes, allowing high power to be achieved[3]. Similarly, because charging and discharging do not involve a bulk-phase transformation, as they do in batteries, supercapacitors are much more reversible (less energy is lost during a charge–discharge cycle) and have a longer cycle life[2] (up to a million charge–discharge cycles). These properties are desirable for energy-storing cables.

To add capacitive storage to conventional wires, Yu and Thomas effectively wrapped a supercapacitor around a core conductor wire (Fig. 1). They began by growing nanowires of insulating copper oxide perpendicular to the surface of a copper wire, and then coated these nanowires with a gold–palladium alloy, which acts as a current collector for the supercapacitor. An electrochemically active coating of manganese oxide was then deposited on top of the alloy. The resulting brush-like architecture leads to a 100-fold increase in surface area compared with the bare copper wire; a large surface area is crucial for capacitive energy storage. The nanowires serve as a sheath covering the copper wire, and form the first electrode of the supercapacitor.

To construct the rest of the device, the authors coated this electrode with a solid electrolyte (a material that conducts ions, but not electrons, and which electrically connects