

CEvNS rate to the standard model prediction, they found it to be consistent. They used this result to set stringent new limits on nonstandard neutrino interactions.

Other neutrino experiments planned and running are continuing the search for new physics. One major target of interest is the so-called sterile neutrino (7), a hypothetical fourth neutrino that may be mixed with the other three, but has no other known interactions. Several experiments are being carried out to look for a telltale disappearance of neutrinos from nuclear reactors or radioactive neutrino sources at very short distances. Meanwhile, the Fermi National Accelerator Laboratory (Fermilab), in Batavia, Illinois, is building out its Short-Baseline Neutrino Program, a suite of three detectors at distances of 100 to 600 m along a beam of neutrinos.

Although a discovery of sterile neutrinos would represent a major paradigm shift in particle physics, physicists are still working out the kinks from the first time neutrinos broke the standard model. New experiments, like the Deep Underground Neutrino Experiment (DUNE), are expected to come online in the next 7 to 10 years. DUNE, which will send a beam of neutrinos from Fermilab to a detector located in a decommissioned gold mine in South Dakota, is designed to make precision measurements of several neutrino oscillation parameters. Their main quarry is something known as the CP phase, a number that controls the degree to which the symmetry between matter and antimatter is violated. Many models tie this CP phase to another CP phase that operates at a much higher energy scale, one that was present in the first moments after the Big Bang. Through a proposed process known as leptogenesis, an asymmetry in primordial neutrino interactions causes a slight enhancement of matter over antimatter (8). Because matter and antimatter have a tendency to annihilate one another, this tiny excess would be all that survives to become the stuff of today's universe.

Such existential questions are the heady stuff of neutrino physics. With a lively experimental program planned and underway, the next 25 years may bring equally lofty answers, and with them more fascinating new questions as well. ■

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Bacteria shed by domestic animals contribute to the spread of antibiotic resistance.

ENVIRONMENT

Microbial mass movements

Wastewater, tourism, and trade are moving microbes around the globe at an unprecedented scale

By Yong-Guan Zhu,¹ Michael Gillings,² Pascal Simonet,³ Dov Stekel,⁴ Steve Banwart,⁵ Josep Penuelas^{6,7}

For several billion years, microorganisms and the genes they carry have mainly been moved by physical forces such as air and water currents. These forces generated biogeographic patterns for microorganisms that are similar to those of animals and plants (1). In the past 100 years, humans have changed these dynamics by transporting large numbers of cells to new locations through waste disposal, tourism, and global transport and by modifying selection pressures at those locations. As a consequence, we are in the midst of a substantial alteration to microbial biogeography. This has the potential to change ecosystem services and biogeochemistry in unpredictable ways.

DISSEMINATION THROUGH WASTEWATER

Disposal of sewage increases the dissemination of both microorganisms and genes

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(see the figure) (2). Globally, some 359,000 km² of croplands depend on irrigation with urban wastewater, 80% of which undergoes little or no treatment (3). Use of wastewater or manure in agriculture contaminates fruits, vegetables, and farm animals that are then distributed globally (4).

Wastewater carries high densities of microorganisms and their cargo genes. It also contains pollutants with biological effects, including metals, antibiotics, and disinfectants (5). These compounds act as selective agents and stimulate bacterial stress response systems that increase mutation rates in the co-dispersed bacteria. This allows bacterial cells to respond dynamically to changing environments by generating novel variability, conferring adaptive advantages on at least a subset of cells arriving at a new location.

Coselection on different cargo genes amplifies this effect. For example, diverse genes for resistance to metals and disinfectants are often clustered next to multiple antibiotic resistance genes on the same genetic element. Exposure to selective agents maintains these clusters of resistance determinants (2), greatly increasing the probability of selection at a destination and improving the chances of recruitment after dispersal.

THE EXAMPLE OF CLASS 1 INTEGRONS

For a sense of the scale of these effects, consider the clinical class 1 integron. This DNA element acquires foreign genes from the environment and has played a central role in spreading antibiotic resistance between bacterial pathogens. DNA sequencing data show

that it had a single origin, in a single cell, in the early 20th century (6). Derivatives of this original element can now be found in diverse bacterial species, resident in many different vertebrate hosts, and on every continent.

Millions to billions of copies of this element now exist in every gram of feces from humans and domestic animals; up to 10²³ copies are shed into the environment every day (see the figure) (7, 8). This remarkable increase in abundance and distribution has been driven by antibiotic selection, increases in human population, and dissemination via global transport.

THE ROLE OF HUMAN AND MATERIAL MOVEMENT

Humans and animals now move around the globe on an unprecedented scale, and this movement actively transports and enriches a specific subset of microorganisms. Humans and agricultural animals now comprise 35 times as much biomass as wild terrestrial mammals (9). The bacteria shed in feces, therefore, mainly represent the gut microbiota of humans, cattle, sheep, goats, pigs, and chickens. These specific gut microorganisms have vastly increased in both abundance and distribution, particularly in the last century. Efficiency of dispersal is enhanced by the 1.2 billion international tourist movements per year, as evidenced by the rapid spread of bacterial clones and antibiotic resistance genes between continents (10).

Humans also promote dispersal of microbial cells via mass movement of materials. Ballast water from commercial shipping moves diverse microorganisms around the globe. An estimated 100 million metric tons of ballast water is discharged each year into U.S. ports alone, giving some indication of the volumes involved (11). Human activities now move more soil,

sand, and rock than all natural processes combined. Natural fluvial erosion is 21 gigatons (Gt) per year, much lower than the 75 Gt per year eroded by agriculture (12). This erosion transports very large numbers of bacteria, given that soil can contain more than a billion microbial cells per gram. Movements on this scale have consequences for human health, agriculture, and ecosystem functions, such as increasing the spread of human pathogens and threatening sustainable food productivity.

CHANGES TO BIOGEOCHEMICAL CYCLES

Because human activities are changing the distribution and abundance of microorganisms, the resultant changes in microbial ecosystems will affect biogeochemical cycles driven by microbial activity (13). Knowledge of the connections between microbial biodiversity and landscape-scale biogeochemical processes, as well as below-ground ecosystems, will be essential to predict the magnitude and direction of these changes (14).

Linking the rapidly expanding databases generated by environmental genomics with biogeochemical models could reveal changes in nutrient cycles. This fusion of genomics and Earth system science is a first step to understanding how the biochemical functions of microorganisms could be altered, temporally and spatially, by global change (15). Human manipulation of carbon and nitrogen cycles influences the natural fixation of nitrogen into biologically available forms and has changed the rates of both natural and anthropogenic emissions of carbon dioxide and methane. The dynamics of the microbial nitrogen cycle are being perturbed by industrial nitrogen fixation, while warming of wetlands and thawing permafrost release large quantities of microbially generated methane.

UNLOCKING THE COMPLEXITY

Current evidence suggests that human activity is having the same effects on the otherwise invisible microbial world as it is on the world of larger organisms: increasing homogeneity, extinctions of endemic organisms, and instability in ecosystem processes. Complex feedbacks between microbial activities, dispersal of cells and genes, natural selection, and the interactions between physical, chemical, geological, and human processes need to be modeled to help predict future changes in the biosphere. Such a fusion of biological and geochemical data sets would help to elucidate the global operations of complex, multigene microbial phenotypes. Current models cannot predict these activities, which are centrally important to biogeochemistry and human health.

There is a recent growing trend for monitoring the environmental dissemination of genes, particularly those that confer phenotypes of direct relevance to human and animal health. Much of this work has focused on the clusters of resistance genes that have been assembled under the aegis of human selection pressure (2). Realization of the global extent of pollution with these xenogenetic elements (7), and the organisms that carry them, should stimulate questions at a much more global scale. Investigations into microbial invasions, microbial extinctions, and perturbations to microbial ecosystems are a high priority. In particular, monitoring of and improvements in waste water and manure treatments are critical. Microorganisms usually perform their essential ecosystem services invisibly, but we ignore them at our peril. ■

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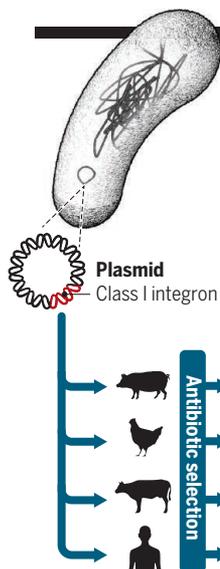
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Global change for microbes

The clinical class I integron illustrates how human activities affect the abundance and distribution of genes and microorganisms. Driven by antibiotic selection, it has colonized different bacteria, vertebrate hosts, and continents. Its spectacular rise in abundance has been driven by antibiotic selection. Large numbers of integron copies are now being shed back into the environment, driving the spread of antibiotic resistance. See supplementary materials for data sources.



| | COPIES PER GRAM FECES | GRAMS OF FECES PER DAY | SIZE OF POPULATION | TOTAL COPIES RELEASED PER DAY |
|--------------------------------|-----------------------------------|------------------------|-----------------------|------------------------------------|
| Antibiotic selection (Pig) | 10 ⁸ –10 ¹¹ | 570 | 1 × 10 ⁹ | 10 ¹⁹ –10 ²³ |
| Antibiotic selection (Chicken) | 10 ⁸ –10 ¹⁰ | 20 | 1 × 10 ¹⁰ | 10 ¹⁹ –10 ²¹ |
| Antibiotic selection (Cow) | 10 ⁶ –10 ⁷ | 3000 | 1.4 × 10 ⁹ | 10 ¹⁹ –10 ²⁰ |
| Antibiotic selection (Human) | 10 ⁶ –10 ⁷ | 160 | 7.6 × 10 ⁹ | 10 ¹⁸ –10 ¹⁹ |

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