Human Impacts on Dissemination of Microbial Cells and Genes in the Biosphere

This is the author's version of the work. It is posted here by emission of the AAAS for personal use, not for redistribution. The definitive version was published in Science Journal.


Yong-Guan Zhu¹, Michael Gillings², Pascal Simonet³, Dov Stekel⁴, Steve Banwart⁵ and Josep Penuelas⁶,⁷

¹ Key Lab of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen 361021, China; ² Department of Biological Sciences, Macquarie University, Sydney, NSW 2109, Australia; ³ Environmental Microbial Genomics Group, Université de Lyon, 69134, France; ⁴ School of Biosciences, University of Nottingham, Nottingham NG7 2RD, United Kingdom; ⁵ Department of Geography, The University of Sheffield, Sheffield S10 2TN, United Kingdom; ⁶ CSIC, Global Ecology Unit, CREAF- CSIC-UAB, Bellaterra, 08193 Barcelona, Catalonia, Spain; ⁷ CREAF, Cerdanyola del Vallès, 08193 Barcelona, Catalonia, Spain

Corresponding Authors:

Y.G. Zhu
Address: Key Lab of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen 361021, China
Email: ygzhu@iue.ac.cn

M.R. Gillings
Department of Biological Sciences, Macquarie University, Sydney, NSW 2109, Australia
Email: michael.gillings@mq.edu.au
For several billion years, microorganisms and the genes they carry have primarily been moved by physical forces such as air and water currents. Three general drivers have influenced their spread: opportunity for dispersal; stochastics (numbers of foreign cells arriving at a location); and recruitment (persistence of cells at the new location, often driven by local selection). These forces have historically generated biogeographic patterns for microorganisms that are similar to those of animals and plants (1). Humans have significantly changed these dynamics. We perturb microbial populations by transporting large numbers of cells to new locations, and by modifying selection pressures at those locations. As a consequence, we are substantially altering microbial biogeography.

To give a sense of the scale of these effects, we can use one example, 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, sometime in the early 20th Century (2). 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 occur in every gram of feces from humans and domestic animals (Figure 1). This spectacular increase in abundance and distribution has been driven by antibiotic selection, increases in population, and dissemination via global transport. The numbers of class 1 integrons released in waste streams mean that this DNA element has become a significant pollutant across wide geographic areas, with up to $10^{23}$ copies being shed into the environment every day (Figure 1) (3, 4).

The increasing abundance and distribution of the class 1 integron is just one example of the genes and bacterial hosts now being disseminated by human activity. Key drivers for increased dissemination of microorganisms include waste disposal, global transport and tourism. Disposal of sewage increases the dissemination of both microorganisms and genes (Figure 1) (5). Some 35.9 Mha of croplands are dependent on irrigation with urban wastewater, 80% of which undergoes little, or no treatment (6). Use of wastewater or manure in agriculture contaminates fruits, vegetables and farm animals, that are then distributed globally via the food-supply chain (7).
Wastewater carries high densities of microorganisms and their cargo genes. It also contains significant concentrations of compounds with biological effects, including metals, antibiotics and disinfectants (8). The simultaneous dispersal of microorganisms and selective agents increases mutation rates in these microbial populations, enhancing their evolvability. This allows them to respond dynamically to changing environments by generating de novo variability, which in turn is likely to confer adaptive advantages on at least a subset of cells arriving at a new location. Co-selection on different cargo genes amplifies this effect. For example, diverse genes for resistance to metals and disinfectants are often closely linked to multiple antibiotic-resistance genes on the same genetic element. Exposure to selective agents maintains these clusters of resistance determinants (5), greatly increasing the probability of selection at a destination, and improving the chances of recruitment after dispersal.

Humans and animals now move on an unprecedented scale, and this movement actively transports and enriches a specific subset of microorganisms. Humans and agricultural animals now comprise 35-fold more biomass than wild terrestrial mammals (9), so the bacteria shed in feces 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, evidenced by the rapid spread of bacterial clones and genes conferring antibiotic resistance 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 tonnes of ballast water is discharged each year into US 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 Gt/y, much lower than the 75 Gt/y eroded by agriculture (12). This erosion transports vast numbers of microorganisms, especially in soil.

Understanding how human activities cause systematic changes in ecosystems is increasingly important, particularly in regard to our effects on biogeochemistry driven by microorganisms (13). Such studies involve a concerted effort to link the distribution and composition of biodiversity with biogeochemical processes at landscape scales and with belowground ecosystem functions (14).
Linking the rapidly expanding databases generated by environmental genomics with the construction of biogeochemical models is increasingly important. 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). In particular, fixation of atmospheric nitrogen into biologically available forms, and global carbon dioxide and methane emissions are strongly affected by human activity. The dynamics of the microbial nitrogen cycle will be perturbed by industrial nitrogen fixation, while warming of wetlands and thawing of permafrost will release large quantities of microbially generated methane.

There are complex feedbacks between microbial activities, dispersal of cells and genes, natural selection, and the interactions between physical, chemical, geological and human processes. Understanding these is a grand challenge for this century. Progress can only be made by forming new, interdisciplinary research teams that can manage and interpret the enormous data sets required. These data sets can then be applied to the complex, multi-gene phenotypes that are centrally important to global biogeochemistry and human health.

There is a growing, and recent 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 (5). Realization of the global extent of pollution with these xenogenetic elements (3), and the organisms that carry them, should now stimulate much more global questions. Investigations into microbial invasions, microbial extinctions, and perturbations to microbial ecosystems are now a high priority. In particular, monitoring 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.

References


**ACKNOWLEDGMENTS**

This research was supported by the Natural Science Foundation of China (41571130063), Chinese Academy of Sciences (XDB15020302 and XDB15020402), the Australian Research Council (DP130103839), and the European Research Council Synergy Grant ERC-2013-726 SyG-610028 IMBALANCE-P.