



Conservation and the Microbiome

Research on the human microbiome, the collection of microorganisms including bacteria, Archaea, and fungi living in and on the bodies of humans, is an exciting new frontier that promises to permanently change both the way human health is understood and how humans think about themselves and their relations with other organisms. We propose that the microbiome also has significant implications for conservation biology and provides a mechanism by which biologists who focus on the human body and on ecosystems can work together and learn from one another.

The human microbiome is extraordinarily diverse. Each human has over 100 trillion microbial symbionts (Costello et al. 2009), an order of magnitude more non-human cells than human cells. Although a bacterial cell contains 1000 times less DNA than a human cell, the collective microbial genome contains roughly 100 times more genes than the human genome (Foxman & Goldberg 2010). The human microbiota is distributed in distinct ecological communities that vary spatially and temporally on and within different parts of a human's body as well as across different human hosts.

Cataloging and annotating the function of the human microbiome is the subject of active, extensive research by several well-funded international consortia in China, the European Union, and the United States (e.g., <http://nihroadmap.nih.gov.hmp>). The ability to document and explore the human microbiota is the result of new methods for sequencing nucleic acids, including genomics, proteomics, and metabolomics. These new technologies allow comprehensive surveys of the composition of microbiomes, their functional capacities, and their physiological interactions with their hosts.

Growing understanding of the microbiome is changing what it means to be human. As Turnbaugh et al. (2007: 804) state, "If humans are thought of as a composite of microbial and human cells, the human genetic landscape as an aggregate of the genes in the human genome and the microbiome, and human metabolic features as a blend of human and microbial traits, then the picture that emerges is one of a human "supraorganism." Those who study human physiology are rapidly adopting this multigenomic perspective. Animal phenotypes, including those of humans, may be better understood as the dynamic outcome of the coexistence of multiple genomes than as a single individual's genome. We are learning that physiological functions of individuals, such as digestion and immunity,

can be affected strongly by the microbiome (Dethlefsen et al. 2007). For example, the intestinal microbiome may contribute greatly to nutrient balance and to the transformation of drugs and other xenobiotics into bioactive forms (Souza et al. 2008). We are also gaining an understanding that disease can result not just from the presence of pathogens, but from the absence or altered composition of organisms in the microbiome. Variation in the structure and composition of the human microbiota is proposed as one of the correlates, if not the driver, of the increased prevalence of disorders such as obesity and asthma (Blaser & Falkow 2009).

Although a great deal of research is being conducted on the human microbiome, the professional conservation community appears to be largely unaware of these developments. We suggest that the concepts and methods used to study the human microbiome could be applied to meet conservation challenges such as captive breeding, reintroduction, invasions of non-native species, and undesirable effects of chemicals on native plants and animals.

Bringing animals into captivity and maintaining breeding populations is undertaken to protect or increase abundances of declining and rare species. Obstacles to these efforts such as callithricid wasting syndrome, which affects numerous marmoset and tamarin species, including the endangered cotton-topped tamarin (*Saguinus oedipus*) (Chalifoux et al. 1982), and helicobacter gastritis, which affects cheetahs (*Acinonyx jubatus*) in captivity, may be related to alterations of the species' microbiome as a result of changes in diet, social conditions, or medical treatment. Successful management of species in captivity may well require managing their microbiomes.

For diverse reasons, many of the numerous attempts to reintroduce species have not succeeded. A reason that generally has not been considered is that the microbiomes of reintroduced individuals may differ from those of wild individuals, which reduces the probability that reintroduced individuals will survive. Results of recent work on laboratory mice show that changes in diet lead to substantial and rapid changes in the composition of the microbiota (Faith et al. 2011). This result may provide evidence of one of the ways in which conditions in captivity before reintroduction, including controlled feeding and shifts in diet, affect an animal's microbiome and subsequent physiological function. Attention to the microbiome of animals slated for reintroduction may increase the success of reintroduction efforts.

Differences in microbiomes may affect the pattern and effects of invasions of non-native species. The interactions between non-native and native species may be affected by the transmission of microbiota among closely related species or those with similar diets (Ley et al. 2008). The historically unparalleled movement of people, domestic livestock, wild animals, plants, and microorganisms around the globe is accompanied by increases in novel interactions (Keesing et al. 2010). These movements appear to be associated with another emerging type of invasion, the transmission of infectious diseases of wild animals to humans (Jones et al. 2008). This increase in transmission may be associated with factors including changes in human and non-human microbiomes.

Many chemicals manufactured and used by humans, such as pharmaceuticals, recreational drugs, and byproducts of industrial processes and agriculture, are deposited in soil, rivers or lakes, and oceans. There has been extensive research on the effects of these chemicals on wild animals. However, there has been limited consideration of the effects of human-made chemicals on microbiomes as a possible mechanism behind the effects of these chemicals on animals. In particular, the widespread use of antibiotics as growth promoters in the agricultural industry can have a serious effect on nontarget species, including humans, via effects on members of microbiomes (Gaskins et al. 2002).

Just as conservation scientists have many exciting things to learn from the study of the human microbiome, those studying the human microbiome are borrowing from studies of ecology (Gonzalez et al. 2011) and evolution (Muegge et al. 2011) that are foundations of conservation science. Understanding of colonization and extinction dynamics may be applied to studies of microbial turnover during host ontogeny and throughout the host's life. Knowledge of colonization and extinction processes, which can be essential components of a successful conservation strategy, is necessary to understand what are now known as multigenomic organisms. Moreover, concepts that are commonly referenced by conservation biologists, such as island biogeography and metapopulation dynamics, can inform many of the research objectives of those who study microbiomes (Dethlefsen et al. 2006).

On a more practical basis, most research on animal microbiomes has been conducted on taxa that have been captive for decades or longer and hence on organisms subject to the selection processes that accompany captivity and domestication (Woodworth et al. 2002). The microbiomes of such organisms represent a small, and likely biased, sample of the diverse microbiomes yet to be discovered. It is now known that microbiome members confer novel metabolic capacities to their hosts (Hehemann et al. 2010). These capacities can be acquired in 2 ways: colonization by a new species or the development of novel metabolic traits by an existing member of the microbiome. Because microbes can

easily exchange genetic material, the functional capacities of microbiomes (and therefore of their hosts) may not be highly constrained by the small number of evolutionary processes that affect how new traits appear in monogenomic eukaryotic organisms.

We suggest the microbiome research community can learn from emerging insights in conservation biology about non-native invasive species and novel communities. Although there are many incentives for manipulating the genomes of bacteria to increase their benefits for humans, an ecological perspective argues for great caution in such work. The introduction of new genes into a given ecosystem can have unanticipated effects; thus, we can assume there will be unanticipated effects of tinkering with the ecosystems of human microbiomes and those of other species.

Humans are dramatically reshaping Earth to serve the needs of a single species, implicitly thinking *Homo sapiens* can survive on its own. The lessons emerging from studies of the human microbiome reinforce those from conservation biology. Humans must relearn that they are tightly bonded to nature and remember that survival of the human species depends on a wide range of other life forms, whether in our forests or in our mouths.

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