



Discussion

Microbiomes, metagenomics, and primate conservation: New strategies, tools, and applications



R.M. Stumpf^{a,b,*}, A. Gomez^c, K.R. Amato^d, C.J. Yeoman^e, J.D. Polk^b, B.A. Wilson^a, K.E. Nelson^c, B.A. White^a, S.R. Leigh^f

^a C.R. Woese Institute for Genomic Biology, University of Illinois at Urbana Champaign, IL 61801, USA

^b Department of Anthropology, University of Illinois at Urbana Champaign, IL 61801, USA

^c Department of Human Biology, J. Craig Venter Institute, La Jolla, CA 92037, USA

^d Department of Anthropology, Northwestern University, Evanston, USA

^e Department of Animal and Range Sciences, Montana State University, Bozeman, MT 59717, USA

^f Department of Anthropology, University of Colorado, Boulder, CO 80309, USA

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ABSTRACT

Conservation strategies require multifaceted approaches to monitor and protect primate populations, many of which are rapidly declining around the world. We propose that microbial ecology and next-generation microbiome analyses offer valuable perspectives and tools for investigating and monitoring primate health and improving conservation efforts. The microbial communities inhabiting primates and other taxa profoundly affect host health, nutrition, physiology, and immune systems, through relationships that range from commensal and mutualistic to pathogenic. Recent advances in DNA sequencing now make it feasible and economically viable to identify microbiomes among and within hosts. Herein, we highlight several examples in which microbial analyses of primates can aid conservation approaches that are broadly applicable across other taxa. First, we highlight evidence for clear spatial variation (e.g. biogeographic niche specificity, both within the anatomical regions of the host body, as well as in the geographic location of the host) and temporal (e.g. seasonal, ontogenetic) patterns in microbial distribution. We emphasize that microbial communities are sensitive to alterations in the external environment and that microbial diversity correlates with habitat quality, imposing direct health consequences. Incorporating microbial host and biogeographic variation holds great potential for forest corridor assessments and for reintroduction efforts. Finally, microbial pathogens transmitted between humans and wild primate populations carry both direct and indirect conservation implications. Principally, we argue that phylogenetic analyses of infectious pathogens (e.g., Ebola, dengue, *Borellia*, and *Treponema*) can aid our understanding of modes of disease transmission and aid conservation disease abatement efforts. The application of microbial analyses to conservation is currently in its infancy but holds enormous potential. To date, no conservation policy or legislation includes microbiome assessments. Integrating new understanding of the patterns of microbial diversity and early signs of impending microbial disruption offer valuable tools for informing conservation strategies and monitoring and promoting primate (including human) health.

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1. Introduction

The world's primates currently face enormous ecological pressures (Cowlshaw and Dunbar, 2000; Estrada, 2013; Benchimol and Peres, 2014). Many species are critically endangered, and populations are declining rapidly (Walsh et al., 2003). Primate conservation is a complex and multifaceted challenge. Contributing factors are linked to the

rapidly expanding human population and anthropogenic activities, such as logging, large-scale agriculture, and cattle ranching (Estrada, 2013). Tropical range countries of West Africa, Indonesia, and South America hold some of the highest levels of plant and animal biodiversity, yet are also experiencing some of the highest rates of deforestation (Fig. 1). These changes in the tropics are catastrophic for primate biodiversity, as these ranges represent their primary habitat, leading to adverse conservation outcomes.

Current wildlife conservation strategies include establishing national parks and protected areas, anti-logging and anti-poaching regulations, incentives for local conservation, captive breeding and reintroduction

* Corresponding author at: Carl R. Woese Institute for Genomic Biology, The University of Illinois, 1206 West Gregory Avenue, Urbana, IL 61801, USA.
E-mail address: rstumpf@illinois.edu (R.M. Stumpf).

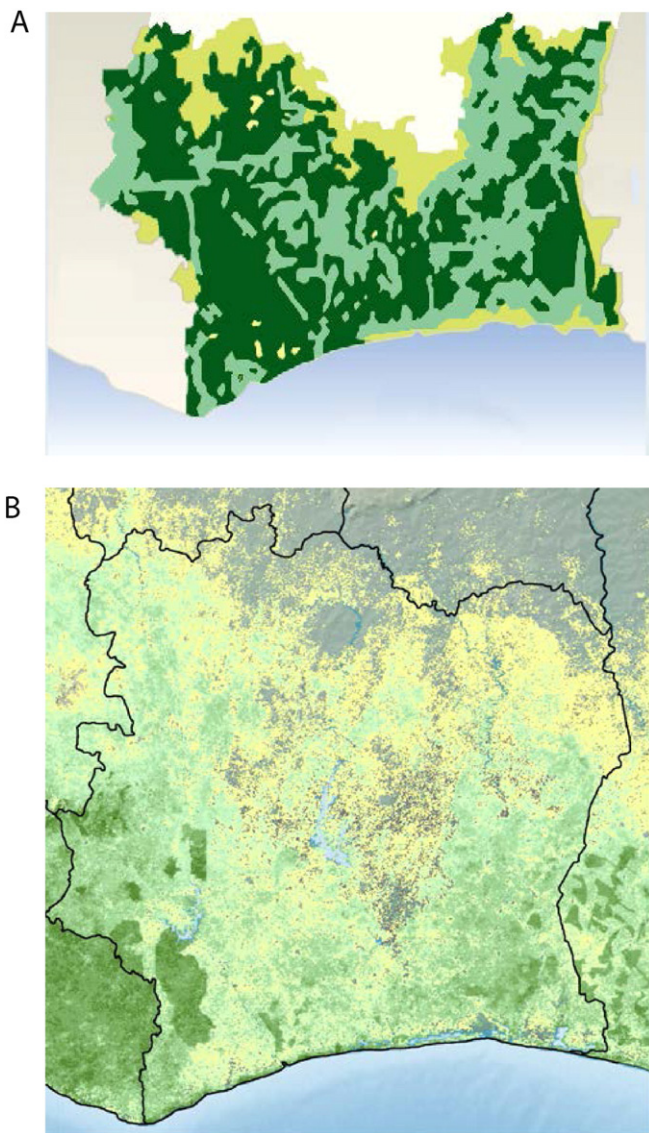


Fig. 1. Rapid reduction in the forest cover of Côte d'Ivoire from 1955 (A) through 2010 (B), largely due to Western interests. Dark green indicate more continuous forest cover, yellow is open country. Continuous forest remains only in very limited, protected areas such as the Taï Forest. Image A is from (<http://www.grida.no/>); B is modified from data at www.fao.org.

programs. More recently, the application of tools such as geographic information systems (GIS) and camera traps to conservation challenges holds great potential for understanding patterns of habitat variation, usage, and population densities. However, these strategies had mixed results. Increasingly, effective conservation strategies require integrated solutions at the macro- and micro-ecological levels.

Analyses of primate microbiomes are emerging as a suite of novel tools that have great potential for supporting conservation efforts. The primate body hosts trillions of microbial cells (Savage, 1977; Gill, et al. 2006; Peterson et al., 2009; Qin et al., 2010; Bianconi et al., 2013). These microbial communities are genetically diverse, varying considerably by individual, location in or on the body, host age, phase in life history, and by host species (Ley et al., 2008; Costello et al., 2009; Kim et al., 2009; Yildirim et al., 2010; Ravel et al., 2011; Aagaard et al., 2012; Faust et al., 2012; HMPC, 2012; Li et al., 2012; Yatsunenko et al., 2012; Stumpf et al., 2013; Swartz et al., 2014). Microbial communities also vary by host diet and habitat and are sensitive to alterations in the external environment (Amato et al., 2013; Gomez et al., 2015, 2016; Barelli et al., 2015).

Relationships between microbial communities and their primate hosts are critically important. Microbes profoundly affect primate health through interactions that range from commensal and mutualistic to pathogenic (Dethlefsen et al., 2006). In light of these interdependent relationships, host and their associated microbes are now considered more appropriately to be a 'supraorganism' or 'holobiont' (Rosenberg et al., 2010; Zilber-Rosenberg and Rosenberg, 2008; Singh et al., 2013), consisting of a single unit subject to evolutionary selection (Zilber-Rosenberg and Rosenberg, 2008; Yeoman et al., 2011).

We propose that microbial analyses offer valuable insight into primate health, nutrition, behavior, life history, and disease, with significant potential for informing primate conservation decisions. Recent advances in DNA sequencing now make it feasible and economically viable to conduct metagenomic analyses for assessing the community of microbes (bacteria, archaea, fungi, protists, and viruses) from a particular host or environment (Gill et al., 2006). By permitting rapid identification of microbial communities one can examine and compare microbiomes across a vast number of hosts, habitats, and species. Below, we suggest several ways in which the application of metagenomic analyses and a greater understanding of microbial ecology could contribute to effective conservation of primates and other taxa. We commence with an overview of the implications of the gut microbiome for host health and nutrition, and discuss the role of microbe–host interactions in a changing environment, in captive care, and in reintroductions. We also provide an overview of microbial applications for understanding host dispersal and conservation hotspots and investigate the potential of microbial phylogenetic analyses for understanding disease transmission and wildlife trafficking. Finally, we conclude with suggestions for future directions.

1.1. Microbes and host health

Primate hosts rely on microbes to conduct important metabolic and immune functions (Hooper et al., 2012; LeBlanc et al., 2013; Lee and Mazmanian, 2010; Lozupone et al., 2012; Tremaroli and Bäckhed, 2012; Yatsunenko et al., 2012). For example, much evidence supports the significant impact of the gastrointestinal GI tract microbiome on host health and nutrition (e.g., Ley et al., 2008; Muegge et al., 2011; Kau et al., 2011; Flint et al., 2012; Amato et al., 2013; Foster and McVey Neufeld, 2013; Gomez et al., 2015, 2016). Microbes conduct critical functions for the host by producing vitamins important for health and reproduction, (e.g., folate, B6, and B12 necessary for brain growth Moran et al., 2008), and synthesizing hormone-like molecules, which provide metabolic and reproductive regulation through modulation of signal transduction pathways, gene expression and splicing (Bäckhed et al., 2005; Blaser, 2006; Dethlefsen et al., 2007; Dominguez-Bello et al., 2010; Hehemann et al., 2010; Heijtz et al., 2011; Hooper et al., 2012; Mazmanian et al., 2008; Brownlie and Johnson, 2009; Costello et al., 2009; Round and Mazmanian, 2009).

Digestion and nutritional benefits, in particular, are strongly affected by the host microbiome (Stevens and Hume, 1998; Samuel et al., 2008; Sekirov et al., 2010; Grenham et al., 2011). For example, gut microbes in the large intestine play a significant role in increasing nutrient availability (Turnbaugh et al., 2006), largely by breaking down resistant fibers and starches, modulating nutrient absorption, and producing short chain fatty acids (SCFAs, e.g., acetate, propionate, and butyrate), an important source for host energy (Macfarlane and Macfarlane, 2003; Samuel et al., 2008). In humans, for example, SCFAs contributed by gut microbes provide 6–10% of the daily energy supply and nutrition (Stevens and Hume, 1998), whereas in more folivorous primates, such as gorilla, SCFAs produced by gut microbes during fermentation produce up to 57% of host daily energetic needs (Popovich et al., 1997).

In addition to augmenting host nutritional status, the microbiome is essential for host protection, contributing to the maturation and modulation of host immunity and barrier function by influencing innate and adaptive immune defenses (Rakoff-Nahoum et al., 2004; Bäckhed et al. 2004; Blaser, 2006; Dominguez-Bello et al., 2010; Dethlefsen

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