Opinion Article

Biodiversity of protists and nematodes

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DESCRIPTION

Understanding the development of the mammalian gut microbiome, its function in digestion, health and illness, and the effects of anthropogenic change on primate biology and conservation requires documenting the natural variety of eukaryotic organisms in the nonhuman primate (NHP) stomach. Despite their ecological importance, little is known about the processes that determine the assembly and diversity of gut-associated eukaryotes in mammals. The eukaryotic assemblage of 62 individuals from 16 NHP species was assessed using an 18S rRNA gene fragment metabarcoding technique in this work. The cercopithecoids, particularly the cercopithecines, show significantly more alpha diversity than other NHP groups, according to our findings. Gut-associated protists and nematodes are common in NHPs, indicating that they have a long history of connection with NHP hosts. However, no consistent indication of phylosymbiosis or host-species specificity has been discovered. In contrast to prior observations of NHP gut bacteria, gut eukaryotes are very weakly organised by primate phylogeny, with little signal from diet. The findings of this study show that gut-associated eukaryotes provide distinct information than gut-associated bacteria and help us better comprehend the gut microbiome's organisation.

Comparative investigations of gut microbiome structure in phylogenetically similar but ecologically different host species reveal variables that control microbial community construction, structure, and stability through time. A multitude of variables influence these patterns in animals, including host gut physiology, food, phylogeny, host age, location, and social behaviour. A disproportionate concentration on bacteria has impacted our present knowledge of microbial community dynamics. This bias is due in part to the fact that eukaryotes are typically examined as parasites rather than community members, yet depending on the species and setting, they can also be beneficial or neutral. Even though eukaryotes are essential components of the gastrointestinal microbial community, the diversity and organisation of the eukaryotic microbiome across hosts is unknown. Microeukaryotes (protists and fungus) and macroeukaryotes (helminths) have a variety of effects on the gut environment. Predation, resource and niche competition, and contact with the host immune system are among ways that gut eukaryotes influence other microorganisms. Entamoeba and Blastocystis, for example, have been linked to significant changes in the gut microbiota. Larger intestinal eukaryotes can colonise with their own bacteria, which can affect the microbial population of the host. Eukaryotic species that co-colonize the same ecological niche are also regulated by bacteria in the gut. For example, *E. coli* strains inhibit the development of the opportunistic fungus *Candida albicans*. Because *Candida albicans* has been found in the guts of healthy people, antagonistic partnerships between eukaryotic and other microorganisms may help to maintain gut homeostasis.

Nonhuman primates (NHPs) are a useful model organism for studying the fundamental mechanisms that drive the ecology and development of the gut microbiome. Extant primate groups descend from several major radiations since the last common ancestor about 70 million years ago, and they are divided into four major clades (host "phylogroups" hereafter): (1) cercopithecoids (African and Asian monkeys), (2) hominoids (apes), (3) platyrrhines (Central and South American monkeys), and (4) strepsirhines (lemurs, galagos, and lorises). Wild NHPs exist in a variety of ecological and nutritional niches within and across various phylogroups, as well as in a variety of social systems ranging from solitary and pair-bonded family groups to vast, multilevel societies. Given that NHPs are our closest living relatives, knowing the gut microbiota of wild NHPs gives an essential evolutionary background.

Loss of gut microbial diversity has been reported as human populations have moved toward more urban and industrialised lifestyles, which has been associated to a number of chronic disorders. Gut eukaryotes, which have been targeted by intense antiparasitic activities during the twentieth century, are part of this loss of variety. Understanding the relationships between bacteria and eukaryotes in NHPs may provide clues to how this loss of diversity occurred.

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Using an 18S rRNA gene fragment metabarcoding technique, we evaluated 62 individual faecal samples from wild NHPs representing 16 species in this study. Five platyrrhine species from Central and South America, six cercopithecoids and two ape species from Uganda, the Central African Republic, and Ethiopia, and three lemur species from Madagascar were chosen to reflect a wide geographic range. The implications of host phylogroup on the organisation of the overall eukaryotic assemblage, the link between bacterial and eukaryotic diversity, and the distribution of specific eukaryotic species across NHP lineages are all investigated. Our findings give fresh insight on the importance of eukaryotes in microbial communities and the value of cross-species comparative research in understanding the development of the mammalian gut microbiome.