

FECAL BACTERIAL DIVERSITY OF HABITUATED CHIMPANZEES (*PAN TROGLODYTES SCHWEINFURTHII*) AT MAHALE MOUNTAINS NATIONAL PARK, TANZANIA

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Although the intestinal flora of chimpanzees has not been studied, insight into this dynamic environment can be obtained through studies on their feces. We analyzed fecal samples from habituated, wild chimpanzees at Mahale Mountains National Park, Tanzania and compared microbial community profiles to determine if members of the same social group were similar. Between July and December 2007, we collected fresh fecal samples from 4 juveniles, 4 adolescents and 4 adults, including 3 parent-offspring pairs. Samples were analyzed using Terminal-Restriction Fragment Length Polymorphism (T-RFLP) of amplified 16S rRNA genes. Twelve different profiles were generated, having between 1 and 15 Terminal-Restriction Fragments (T-RFs). A total of 23 different T-RFs were produced with putative assignments corresponding to the phyla *Firmicutes* (*Clostridia*, *Bacilli* and *Lactobacilli*), *Bacteroidetes*, *Tenericutes* (*Mollicutes* Class), *Actinobacteria* and *Proteobacteria*, and to uncultured or unidentified organisms. *Firmicutes* and *Bacteroidetes* phyla and *Mollicutes* Class were the most commonly assigned. This is the first report of *Mollicutes* in wild chimpanzees. Principal Components Analysis revealed clustering of 9 of the samples. Morisita indices of community similarity ranged between 0 and 0.89. Our findings suggest that, although phylotypes are common among individuals, profiles among members of the same social group are host-specific. We conclude that factors other than social group, such as kinship and age, may influence fecal bacterial profiles of wild chimpanzees. (Funded by the National Science Foundation, Award #0238069 and #0244016).

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