

**COMPARATIVE PRIMATE VAGINAL MICROBIAL ECOLOGY**

S. Yildirim<sup>1</sup>, S. Leigh<sup>1</sup>, B.A. Wilson<sup>1</sup>, A. Rivera<sup>1</sup>, B.A. White<sup>1</sup>, M. Irwin<sup>2</sup>, T. Goldberg<sup>3</sup>, A. Salyers<sup>1</sup>, R.M. Stumpf<sup>1</sup>

<sup>1</sup>University of Illinois, Urbana-Champaign, <sup>2</sup>McGill University, <sup>3</sup>University of Wisconsin, Madison

Presenter's Email: [rstumpf@illinois.edu](mailto:rstumpf@illinois.edu)

Host-microbe interactions profoundly affect primate physiology, reproduction, health, and ultimately, evolution. Because females are central to population viability and because the reproductive tract microbiome has the potential to influence female health, fecundity and pregnancy outcomes, understanding of both the variation in primate vaginal microbial ecologies and the factors (e.g. socio-ecological, sexual, morphological, or genetic) which influence microbial variation is crucial to understanding patterns of primate host-microbe relations. To gain a preliminary understanding of primate vaginal microbial community compositions, we analyzed vaginal swab samples from four available species: yellow baboons (*Papio cynocephalus*), olive baboons (*P. anubis*), sifakas (*Propithecus diadema*), and red colobus monkeys (*Procolobus rufomitratu*s), using direct sequencing analysis of 16S rRNA gene through Titanium pyrosequencing. Sample pyrosequencing outputs were run through RDP classifier (70% bootstrap threshold) to assess the distribution of phylotypes across primate taxa and obtain an initial picture of microbial community structure and diversity. Results indicate that Firmicutes and Bacteroidetes are the most common genera across all four primate species, though a substantially greater proportion of unclassified microbes (36% vs. 0-13%) and a more diverse microbial community composition were found within the sifakas than within any of the Old World monkeys. The inclusion of additional primate species will help test hypotheses that phylogenetic, reproductive, and morphological factors can explain patterns of microbial community composition and interactions between microbes and their primate hosts. Funding provided by the University of Illinois, UIUC Institute for Genomic Biology, and the National Science Foundation (NSF # 0820709).

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