Investigating gut microbial communities in two species of rhinoceros

Candace L. WILLIAMS^{1,2}, Christopher W. TUBBS¹

¹Reproductive Physiology, San Diego Zoo Global-Institute for Conservation Research, Escondido, CA, USA ²Institute for Genomics, Biocomputing & Biotechnology, Mississippi State University, Mississippi State, MS, USA

Dietary phytoestrogens have been suspected to play a role in the reduced fertility of captive-born southern white rhinoceros (Ceratotherium cimum cimum; SWR), as wild SWRs consume lower levels of phytoestrogens and have a greater reproductive success in comparison with their captive counterparts. Interestingly, other rhino species, such as the greater one-horned rhinoceros (Rhinoceros unicornis; GOHR), consume similar diets without any evidence of reproductive failure. Although the relationship between diet and SWR infertility is known, little is understood about the physiological mechanism. Specifically, information related to microbial phytoestrogen metabolism in the SWR gastrointestinal tract (GIT) is lacking, as members of the GIT microbiota of other species have displayed phytoestrogen metabolism, but no study of the rhinoceros has occurred to date. Following 16S rRNA next-generation sequencing, we found that SWR and GOHR gut microbiotas were represented by 18 phyla, with five phyla found at > 1.0 % relative sequence abundance. For the SWR and GOHR, the Bacteroidetes (56 ± 1.1 %; 30 ± 1.8 %) and the Firmicutes (30 ± 1.1 %; 55 ± 2.2 %) dominated, accompanied by the Lentisphaerae (6.4 ± 0.36 %; 4.8 ± 0.44 %), the Verrucomicrobia $(0.80 \pm 0.38 \%; 3.6 \pm 2.0\%)$, and the Spirochaetae $(1.1 \pm 0.095 \%; 1.8 \pm 0.45 \%)$, all significantly different with respect to rhino species (P < 0.05). Bacterial community composition (Jaccard) and structure (Bray-Curtis) differed significantly with respect to rhino species as observed by three-dimensional nonmetric multi-dimensional scaling, and communities were also significantly different at the phylum, family, and operational taxonomic unit level (all levels, P <0.001). Further analyses are currently underway to determine which microorganisms may be involved in phytoestrogen metabolism. Together, information regarding GIT microbiota and diet estrogenicity associated with both SWR and GOHR would provide a better understanding of the role phytoestrogens play in captive-born SWR infertility.