PROGRAMME

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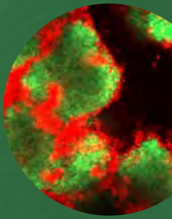
16th symposium on Bacterial Genetics and Ecology



26 - 30 June
Copenhagen · Denmark

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[O11] SEX PREDICTS GUT MICROBIOTA VARIATIONS IN WILD YELLOW BABOONS (PAPIO CYNOCEPHALUS)

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The role of gut microbiota diversity in animal ecology and conservation has become a key topic, especially since the contribution of these bacterial and fungal communities to host growth and health has been recently recognized. Most investigations in wildlife have focused on the study of extrinsic (e.g., diet, habitat) rather than intrinsic factors (e.g., sex, genetic background) affecting variation in animal gut communities. However, since male and female mammals often differ in biological traits and functional needs, sex is likely to play a major role in gut microbiota variation. Here, we evaluated if and how sex is associated with the gut microbiota richness and composition of wild yellow baboons (Papio cynocephalus) living in two habitat types, protected and unprotected forests of the Udzungwa Mountains in Tanzania. To understand whether sex and habitat type affect gut microbiota variation, we determined the sex of 34 yellow baboons (19 females and 15 males) from fecal pellets collected non-invasively using two marker genes (SRY and DDX3X). We then combined these results with amplicon sequencing datasets focusing on bacterial (V3-V4 region of the 16S rRNA gene) and fungal (ITS1-ITS2) communities of the same pellets. We found that females had gut microbiotas with a higher bacterial richness [Kruskal test; Shannon (alpha diversity): $P = 0.010$] and different composition [ANOVA; weighted Unifrac (beta diversity): $P = 0.030$] compared to males, in agreement with the strong morphological and behavioral dimorphisms shown between sexes of this species. Furthermore, forest type had a greater impact on females than males, such that the gut microbiotas of females from the two forests differed significantly in fungal composition [pairwise adonis test; Bray-Curtis: $P = 0.02$] and bacterial richness [pairwise Wilcoxon Rank Sum test; Shannon: $P = 0.023$], while those of males did not. These results indicated that the impact of habitat disturbance varied with sex, suggesting that intrinsic biological factors should be carefully considered when investigating wild animal biodiversity at any scale, and that such intraspecific variation could impact the outcome of conservation actions. However, research on the metabolic pathways, through shotgun sequencing, are encouraged to verify whether greater gut bacterial richness, such as those observed in baboon females, may translate into a greater diversity of metabolic functions.