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ABSTRACT BOOK

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Sex and habitat are associated with gut bacterial and fungal variations in wild yellow baboons (*Papio cynocephalus*)

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Variations in richness and composition of mammal gut bacteria and fungi have mainly been related to diet, lifestyle, and habitat; however, less is known about the effect of sex on non-human primate gut microbiota. To understand the association of sex and habitat with microbiota diversity, we non-invasively collected and analyzed faecal samples from 40 yellow baboons (*Papio cynocephalus*) living in well-protected and disturbed forests of the Udzungwa Mountains in Tanzania. Sex determination has been performed using the marker genes: SRY (Sex-determining Region Y) and DDX3X (DEAD-Box Helicase 3-X Linked). Molecular investigations resulted in 34 individuals sexed, including 19 females and 15 males, belonging to 5 social groups. Combining these results with two amplicon-sequencing datasets focusing on bacterial (16S rRNA gene, V1-V3 region) and fungal (ITS1-ITS2) gut communities, we found a significantly higher bacterial richness in baboon females compared to males. No significant difference in observed fungal richness was detected between sexes; however, beta diversity estimates (Bray-Curtis dissimilarity) indicated that fungal and bacterial composition was significantly different between males and females. This was true in both protected and fragmented forest types. Although the sample size is relatively small, our results highlight the relevant contribution of an intrinsic factor shaping the variation of both bacterial and fungal communities in wild non-human primates.