

Between and within group variation in the gut microbiome of a black-and-white colobus monkey

Eva C. Wikberg¹, Diana Christie², Pascale Sicotte¹, Nelson Ting²

¹ Department of Anthropology and Archaeology, University of Calgary; ² Department of Anthropology and Institute of Ecology and Evolution, University of Oregon

Background

The gut microbial community is associated with host health and nutrition. Similarities in the gut microbiome is often linked to group membership, but the relative contributions of habitat, diet, proximity, and social contact are still unclear. The aim of this study is to investigate the link between group membership and the gut microbiome in female *Colobus vellerosus* (white-thighed colobus) at Boabeng-Fiema, Ghana. This population inhabits a mosaic forest fragment and shows facultative female dispersal.



Study questions

How is similarity of the gut microbial composition affected by:

1. Habitat usage?
2. Group membership and female immigration status?
3. Recent group fission?

Methods

- Subjects: 43 females in 6 groups with neighboring home ranges (BS, DA, NP, RT, SP, WW: Fig. 1.).
- Ranging data: Hourly recorded location points between May and Aug 2007.
- Demographic data: Natal, founder (i.e., established new group), or immigrant status (regardless of time in current group) from 7 years of data.
- Microbiome data:
 - 16S rRNA library preparation and sequencing on an Illumina NextSeq platform.
 - Quality filtering and assembly using a custom pipeline.
 - 87,600 reads/sample and identification of 2,958 operational taxonomic units (OTUs).
 - Beta-diversity measured using Bray-Curtis dissimilarity.

Results

1. Habitat use

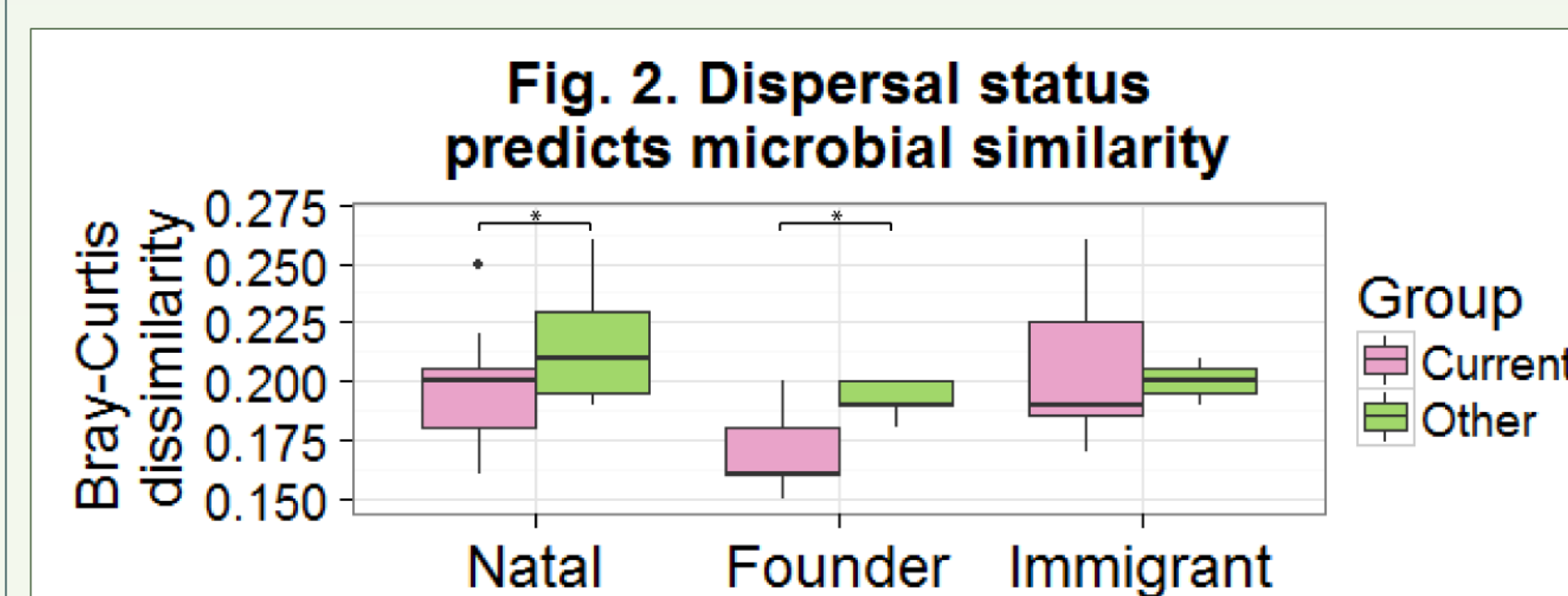
All groups use primary and secondary forest, but the percentage of time spent in the primary forest varies (range: 9-87%). Habitat use has a small but significant effect on microbial similarity (Table 1, N=43, PERMANOVA).

Variable	F	R ²	p
% time in primary forest	2.08	0.05	<0.01
% time 50m of settlement	1.89	0.04	<0.01
% time in lowest forest strata (ground or bushes)	2.27	0.05	<0.01
Read depth	1.21	0.03	0.10

2. Group membership & immigration status

Group membership predicts microbial similarity (N=43, partial Mantel test controlling for R-values, $r=0.26$, $p<0.001$).

Natal and founder, but not immigrant females, have more similar microbiomes to females in their current group than to females in other groups (Fig. 2., N=28, Wilcoxon).



3. Group fission (DA & NP sampled 9 mo post fission)

Microbiomes are more similar within than between sister groups (N=14, permutation test, observed mean Bray-Curtis dissimilarity index: 0.17, 95% CI: 0.18-0.19).

Females have more similar microbiomes to females in the other sister group than to females in other groups (Fig. 3., N=14, Wilcoxon).

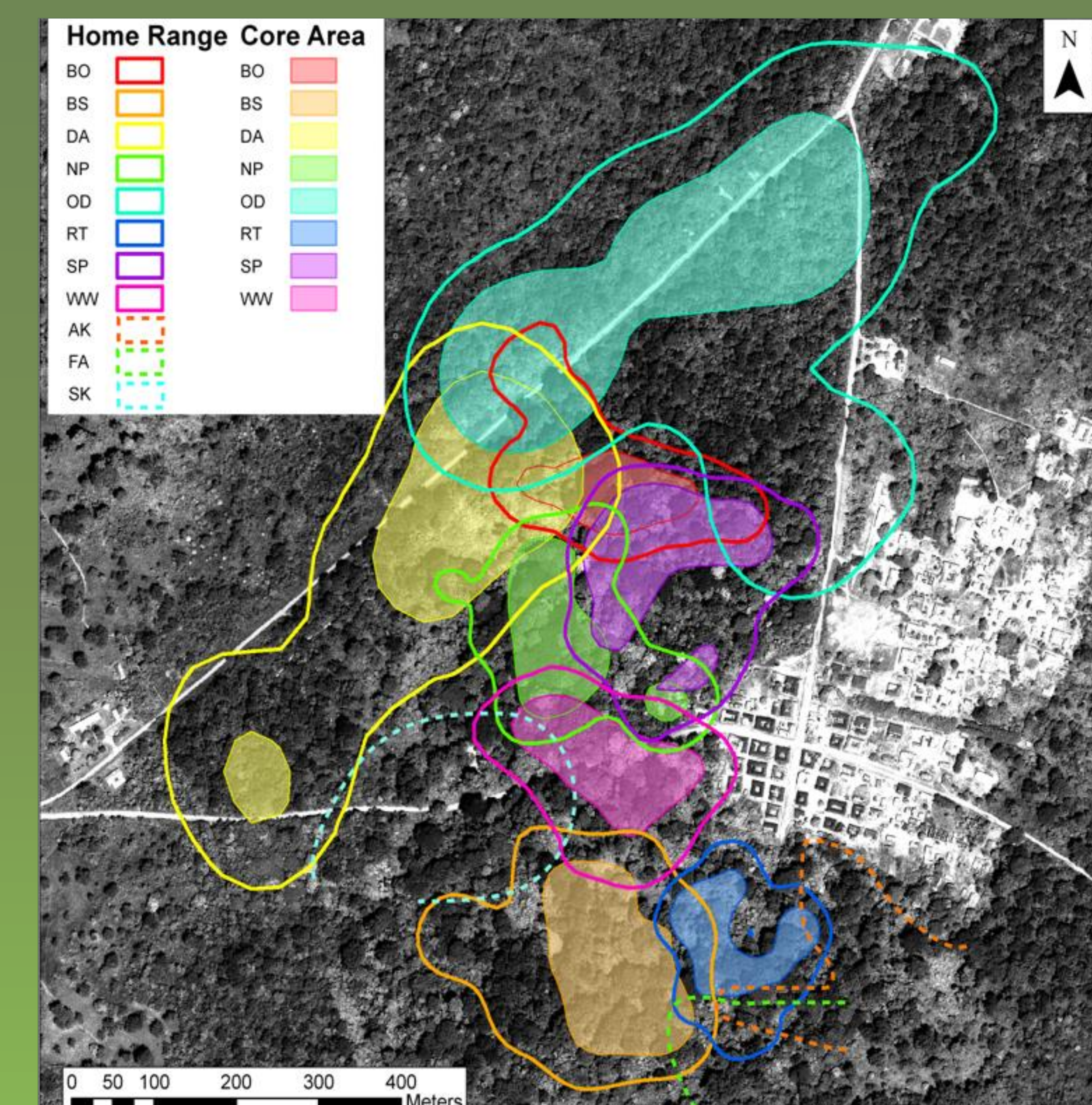
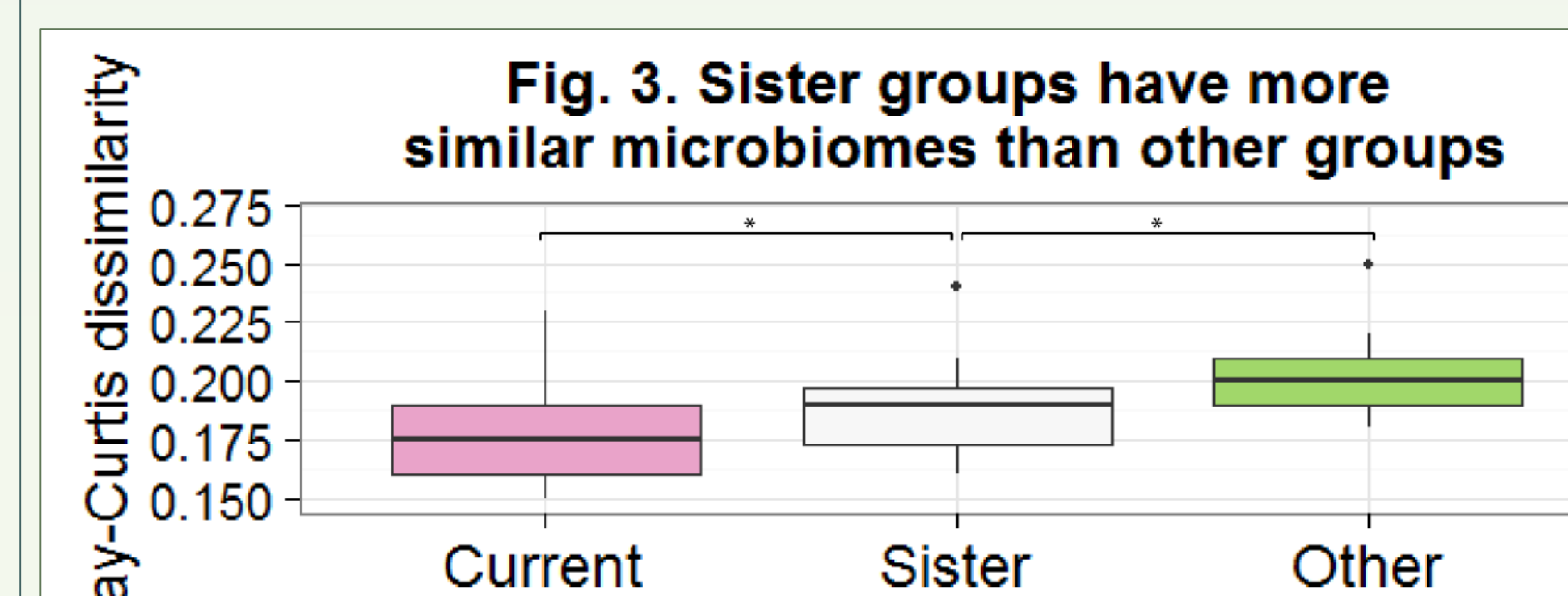


Fig. 1. Home ranges of all colobus groups in the main forest fragment of Boabeng-Fiema. Dashed lines indicate partial home ranges of non-study groups.

Conclusions

1. Groups have distinct microbiomes that are partly associated with differential habitat use.
2. Natal and founder females, but not immigrant females, have more similar microbiomes to females in their current group than in other groups.
3. Sister groups' microbiomes are distinguishable but still more similar to each other than to other groups.

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