What can whole genome sequencing reveal about animal sociality?

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Evolution of sociality

• Difficult to understand evolution of sociality

• Kin selection theory predicts that individuals tend to bias their affiliative behaviours towards close relatives

• Challenging to accurately estimate dyadic relatedness
Kinship estimation

- Pedigree estimates probabilities of sharing alleles from common ancestors
- Pedigrees provide limited information
- Realized relatedness may strongly differ within categories
- Variation resulting from recombination events during meiosis
Realized relatedness

- Calculate length and number of DNA segments that are identical-by-descent (IBD) to assess realized relatedness
Macaca mulatta

- Multifemale, multimale groups consisting of kin and nonkin
- Female philopatry, male dispersal
- Extensive female family groups that hang out together continuously
- Females mate with different males in consecutive years
- Many maternal or paternal half-siblings, but full siblings rare
Study population

- Cayo Santiago, Puerto Rico
- 409 animals from India introduced in 1938
- Demographic data since 1956, genetic data since 1992
- Pedigree data limited to three generations
Whole genome sequencing

Sample preparation (n = 880)

Sample collection (blood, tissue) ➔ DNA extraction ➔ Preparation for sequencing

Data processing

Mapping of reads to ref-genome

Variant calling

Imputation of missing variants

IBD calculation
## Whole genome sequencing

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| Sample collection (blood, tissue) | DNA extraction | Preparation for sequencing |

### Sequencing

| (PCR amplification) | Library preparation | Illumina sequencing 20x or 6x coverage |
# Whole genome sequencing

## Sample preparation (n = 880)

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1. Quantify variation in IBD within and between kin classes using whole genome sequencing data (WGS)

- ongoing work -
IBD vs. pedigree

1. High variability within kin classes
2. Overlap between kin classes

→ relatedness is continuous!

n = 2854
1. IBD segments

half-siblings       aunt/uncle-niece/nephew

1 \[\rightarrow\] 2

3 \[\rightarrow\] 4 \[\rightarrow\] 6, 8

5 \[\rightarrow\] 4 \[\rightarrow\] 6, 8

r = 0.25
1. IBD segments

half-siblings

aunt/uncle-niece/nephew

r = 0.25
1. IBD segments

- **half-siblings**
- **aunt/uncle-niece/nephew**

The graph shows the distribution of IBD (Identity by Descent) segments measured in centimorgans (cM). The y-axis represents the sum of IBD segments >4cM. The x-axis is not explicitly labeled but likely represents different categories or subtypes of relationships.

Key observations:
- The green bars indicate segments >20cM, followed by darker shades for 12-20cM, 8-12cM, and 4-8cM.
- The data suggests a decline in longer segments as the relationship becomes more distant, with a notable increase in shorter segments for more distant relatives.

Detailed analysis of the graph would require specific values or additional context provided in the accompanying text or slides.
2. Determine whether social preferences are predicted by gradient of IBD

- future work -
2. Kin recognition and kin bias

- Kin recognition basis for kin bias to evolve
- Maternal kin use familiarity
- Paternal kin may use phenotype matching: similar behavioural and/or physical traits
- Previous studies: rates of social interactions between kin increases with increasing pedigree relatedness
- What does realized genetic variation contribute to kin recognition and kin bias?
2. Predictions

- Available data: social preference and perception of kin cues
- Amount of IBD shared will predict kin bias within and between kin classes
- Paternal kin will mainly follow gradient in IBD (a/d)
- Maternal kin are primarily influenced by social constrains (c)
Conclusion

• IBD based on WGS data reveals variation in relatedness within and between kin classes

• Novel way to understand role of relatedness in evolution of sociality in animals
Acknowledgements

supervisor
Anja Widdig

collectors
Vladimir M. Jovanovic, Noah Snyder-Mackler, Katja Nowick, Michael Montague, Harald Ringbauer, Jenny Tung

further collaborators
Stefanie Bley, Lauren Brent, Constance Dubuc, Peter Fröhlich, James Higham, Yilei Huang, Xiaowen Jia, Anahita Kazem, Toni Krüger, Lars Kulik, Tara Mandalaywala, Dana Pfefferle, Michael Platt, Brigitte Schlögl, Lydia Schmidt, Erin Siracusa, Hendrikje Westphal