

Establishing a virtual network in mammalian microbiome research

1 | INTRODUCTION

On November 12th–13th 2020, we organized a 2-day mammalian microbiome virtual seminar in which almost 80 early career researchers participated from across the world (Figure 1a). The meeting led to presentations of forefront research on the study of captive and wild mammal microbiomes and stimulating discussions covering a broad range of topics. Highlights also included short breakout room sessions in which participants introduced themselves and long breakout room sessions in which participants discussed emerging topics in microbiome research. Microbiome research is a relatively recent field of study, and even more so when focusing on wild mammals. Contrary to studies in laboratories with balanced experimental design, we often face variation in many socio-ecological correlates during sample collection in natural populations, triggering the need for different methods and statistical tools to analyze the data. This research field is developing rapidly but it remains hard to stay up to date on the burgeoning methods. Moreover, microbiome researchers in evolution, ecology, and anthropology departments are often the only one or one of a few to work on the microbiome in their group, and it remains challenging to find colleagues to talk to about specific methodological issues. The aim of the meeting was to create a dynamic research community of early career scientists—mostly graduate students and post-doctoral researchers (Figure 1b)—interested in ecology, evolution, and the microbiome that are able to interact, share papers and research, and discuss methods. We further created a Slack workspace to organize the meeting and to facilitate future interactions after the meeting concluded.

2 | TALKS

A large motivation for organizing this seminar was to bring together researchers working on similar concepts but disparate systems or locations, and in this regard the program of talks was successful. Thirteen early career researchers presented their work over four sessions. Although each presenter worked on a distinct host system or dataset, the sessions had overarching themes of *diet & ecology*, *aging & fitness*, *development*, and *methodological approaches* (Figure 1c).

In our diet & ecology section, exciting work was presented that addressed enduring questions for wild microbiome studies such as how important is host phylogeny compared to environmental factors in driving gut microbiota communities? Dr. Liz Mallott (Northwestern

University) and colleagues found that diet composition drove distinct community composition in the gut microbiome for eight species of platyrrhine monkeys in Ecuador. Connie Rojas (Michigan State University) investigated the relative importance of host phylogenetic versus sociological and environmental factors for predicting gut microbiome structure in spotted hyenas and other African mammals. These talks highlighted in particular the value of long-term studies. Tatiana Murillo Corrales (German Primate Center) presented her work from longitudinal data from wild red-fronted lemurs exploring short-term fluctuations in bacterial taxa of the gut according to season and dietary shifts. Work from Sierra Gilman (University of Washington) posed the question of whether the structure of the gut itself influenced gut microbiome composition using data from American black bears, a species with a relatively simple gastrointestinal (GI) tract. She showed that gut microbiome composition of the jejunum and caecum did not differ substantially, which was a unique perspective given most studies are limited to fecal or colon samples. Ahmad Ud Din (Southwest Medical University, Luzhou, Sichuan, China) rounded out the session by exploring the concept of probiotics as an option to circumvent dysbiosis effects of conventional disease therapies.

In addition to being a dynamic community which responds to ecological factors, the microbiome is likely to play a large role in shaping life history traits and fitness. These effects can be difficult to assess in natural populations, but two talks in this area highlighted exciting insights into the area. Mauna Dasari (University of Notre Dame) presented validation of a “microbiome clock” as a noninvasive measure of aging in wild baboons, and further showed that behavior and early life experience can alter the rate at which a microbiome ages. Dr. Laura Grieneisen (University of Minnesota) estimated the heritability of the gut microbiome from the same study species and found that microbial heritability estimates are temporally dynamic, similar across primate taxa, and require longitudinal sampling to accurately be estimated. Throughout ecological & life history-adjacent topics, a recurring concept was that longitudinal data from diverse host groups and timepoints is important to understand exactly what is driving microbiota community composition. Dr. Amy Sweeny (University of Edinburgh) presented a methodological talk highlighting a generalized linear mixed-effects model approach to wild mammalian microbiota analysis. Using pilot data from wild Soay sheep, she showed that this approach can help to deal with complex simultaneous drivers of microbiota composition in natural populations.

Speakers in the development session presented novel avenues of research characterizing the maturation trajectory and its

contamination by host DNA. Combining culturing with culture-independent techniques was suggested, and groups discussed interesting evolutionary questions related to developmental programming (e.g., milk and reproductive tract microbiomes) and communication (e.g., scent gland microbiome) that can be addressed by studying these non-gut communities.

The discussion segment of the second day of the seminar began with breakout sessions focused largely on methods in microbiome research. First, groups discussed (4) the coming (and perhaps already here) omics revolution. Individuals shared their least and most effective lab protocols. Next, the breakout groups engaged in (5) a debate on normalization methods and the properties of microbiome data that make analysis difficult. Groups discussed which normalization methods they have used and if they have been successful. Finally, (6) the discussion portion of the seminar concluded with groups considering the use of mixed models to analyze microbiome count data. Groups discussed the incorporation of fixed and random effects into models, as well as the underlying distributions of microbiome count data that may necessitate nonparametric approaches.


4 | CONCLUSION

Webinars present some advantages over in-person conferences, since it becomes possible to interact with colleagues from all over the world without much logistical and financial constraint. Ultimately, it allows meetings to be more frequent and more inclusive, and can expose researchers to a community of scientists from more diverse

backgrounds. We encourage early career researchers to organize similar events in their own field, especially during this period of social distancing and isolation, where professional interactions are limited. We are currently administering a Slack workspace to facilitate networking, collaboration, and the organization of future meetings and discussion groups. Early career researchers working on animal microbiomes are welcome to join this workspace by contacting one of the authors/organizers.

DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

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