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Growing and maintaining a network for early career researchers through the Animal Microbiome Research Group

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Introduction

On November 10th–11th 2021, the Animal Microbiome Research Group (AMRG; formerly separate mammalian and avian microbiome research groups) hosted its second annual research meeting. This group was founded by early career researchers (ECRs) out of a desire to connect with other early career microbiome scientists—individuals who might otherwise be the only scholar to study wildlife microbiomes within their lab group, department, or institution. Connections among researchers are established during an annual virtual multi-day meeting. During these meetings, ECRs from around the world present new findings and discuss microbiome-research related topics. Connections made are then reinforced using a Slack workspace, which allows for the maintenance of a lasting network. The group's inaugural meeting and objectives have been summarized previously (Petrullo et al. 2021). Here, we provide group updates, summarize the 2021 meeting, and offer a one-year retrospective on the creation of an ECR virtual network from the participants' viewpoint.

What's new?

The 2021 meeting spanned two days and included research talks and group discussions. In contrast to the 2020 meeting, the 2021 symposium included a virtual poster session and keynote lectures from early career professors who are leaders in the field: Dr. Kevin Kohl (University of Pittsburgh, USA), Dr. Qiyun Zhu (Arizona State University, USA), and Dr. Sarah Knowles (University of Oxford, UK). Attendees had the opportunity to meet with keynote speakers in small, informal groups. As of the 2021 meeting, the formerly separate mammalian and avian microbiome research groups merged to form the more inclusive AMRG. This merger will enrich this nascent virtual network by including researchers who study a greater breadth of host systems.

Talks & Posters

Host and environmental factors shape the microbiome's composition and structure, which can affect host phenotype and fitness. Understanding these bidirectional effects is at the core of microbiome studies as highlighted by the presentations given this year.

Among host factors, host genetic variation can be linked to the gut microbiome composition as shown by Charli Davies (University of East Anglia, UK) working on the Seychelles warbler. She showed that certain alleles of the Major Histocompatibility Complex can be associated with gut microbiome compositional shifts (Davies et al., 2021). Gestation in females, which has important consequences on their physiology, is another important factor shaping the gut microbiome as illustrated by Chelsea Southworth's poster (University of Notre Dame, USA) on the effects of pregnancy in baboons.

Host diet also strongly influences the gut microbiome and is often studied alongside other factors like host evolutionary history. Dr. Elin Videvall's work (Brown University, USA) on the link between diet and gut microbiome composition in three giraffe species revealed differences among species. At a larger taxonomic scale, Sophie Teullet (University of Montpellier, France) studies the convergent adaptation to myrmecophagy in placentals and tries to reconstruct bacterial genomes and identify microbial genes that might play a role in prey digestion. Dr. Kevin Kohl (University of Pittsburgh, USA) presented results from experimental approaches demonstrating that the gut microbiome contributes to diet selection in mice (Trevelline and Kohl, 2020). Dr. Sarah Knowles (University of Oxford, UK) found seasonal shifts in the gut microbiome composition of wild wood mice (Marsh et al., 2021), likely driven by diet. She also showed that social interactions are a strong predictor of the gut microbiota (Raulo et al., 2021).

Microbiomes are partly shaped by the dispersal of microbiota between hosts, a process which can be strongly structured by host social behavior. Hanna Bensch (Linnaeus University, Sweden) demonstrated this in the form of a clear 'colony' effect on Damaraland mole rat gut microbiomes. Jonas Torfs (University of Antwerp, Belgium) presented his PhD project on the microbiome-gut-brain axis in captive bonobos where he will investigate effects of grooming. Dr. Sally Bornbusch (Smithsonian's National Zoo & Conservation Biology Institute, USA) emphasized that microbes can also be acquired from the environment by showing that wild ring-tailed lemurs harbored a greater relative abundance of soil-associated microbes than captive-environment conspecifics (Bornbusch et al., 2021). Thus, both social and environmental transmission can influence gut microbiome composition. This was reinforced by Dr. Aura Raulo (University of Turku, Finland), who reported that among wild wood mice, anaerobic taxa caused social patterns in the microbiome, while aerotolerant taxa underlay spatial patterns.

External factors also shape an individual's microbiome with consequences on host fitness, especially in the face of anthropogenic perturbations. Dr. Kevin Kohl showed that microbial communities contributed to host thermal tolerance in tadpoles subjected to temperature increase (Fontaine et al., 2021). In wild *Anolis* lizards, short-term climate warming does not have a significant effect on the gut microbiome whereas sustained drought does, as explained in Claire E. Williams's poster (University of Nevada, USA). In addition to climate change, pollutants and radiation exposure can also impact wild animals gut microbiome as illustrated by Dr. Diana Lafferty (Northern Michigan University, USA) working on wild boars in the Fukushima difficult-to-return zone, and Sameli Piirto (University of Jyväskylä, Finland) whose PhD project will investigate the effects of radionuclides exposure on great tits in Chernobyl (Ukraine).

Gut microbiomes vary over time. Empirical Dynamic Modelling has revealed a non-linear and highly chaotic dynamic of the microbiome, as summarized in Dr. Amy R. Sweeny's poster (University of Edinburgh, UK). When studying changes in the microbiome and how different factors influence this dynamic, the analysis (Björk et al., 2019) and visualization (Fink et al. 2021) of longitudinal data are important, as explained by Dr. Laura Grieneisen (University of Minnesota, USA). For instance, it is possible to study the gut microbiome's heritability as illustrated by her work on wild baboons (Grieneisen et al., 2021). Shasta Webb (University of Calgary, Canada) studies the effect of drought on the gut microbiome of wild white-faced capuchin monkeys and showed, in particular, lower microbiome richness during drought periods with microbial phyla shifts associated with rain level. Mason Stothart (University of Calgary, Canada) presented his work linking environmental variation and gut microbiome variation in feral horses (Stothart et al., 2021), and reported correlates between the microbiome and host survival. Dr. Sarah Worsley (University of East Anglia, UK) demonstrated a link between host survival and the gut microbiome composition of the Seychelles warbler's (Worsley et al., 2021). Lifetime data also offer the possibility to investigate the link between host aging and the gut microbiome. Despite being a dynamic system, the gut microbiome might stabilize with host age as suggested by Dr. Alice Risely's results (Ulm University, Germany) on the stability and repeatability of wild meerkats gut microbiome.

While 16S sequencing remains the prevailing methodology, metagenomics were more common this year. These methods require different bioinformatic tools and analytical approaches than 16S data. Dr. Qiyun Zhu (Arizona State University, USA) showcased methods created by his research group which allow for phylogeny-informed analysis of metagenomic data using the Web Of Life tree (<https://biocore.github.io/wol/>; Zhu et al., 2019) and Woltka (<https://github.com/qiyunzhu/woltka>; Zhu et al., 2021), an approach which advocates for a newly proposed unit, the Operational Genomic Unit (OGU).

For metagenomics approaches to be feasible for a wide array of host systems, we must expand the diversity of available microbial reference genomes. Additionally, we must begin to consider other types of 'omics data (e.g., transcriptomics, metabolomics) and microbiomes (e.g., oral, skin). The Earth Hologenomic Initiative (www.earthhologenome.org)—introduced by Dr. Aoife Leonard (University of Copenhagen, Denmark)—offers an ambitious solution to this problem, by seeking to collaborate with researchers from around the world to simultaneously generate a diversity of host and microbiome 'omics data.

Discussions

In addition to presentations, discussions with specific prompts are a key component of the annual AMRG meeting. Prior to the start of each discussion, conference organizers posted relevant resources in Slack. On Day 1, participants were invited to discuss microbiome data visualization. An emergent theme from these discussions was the limitation and over-reliance on visualizing complex microbiome beta diversity data in 2 dimensional ordination plots. By contrast, some attendees argued that visualizations of microbiome data would benefit from presentation of raw beta-diversity distances, and that more schematic representations of microbial relationships to the host are needed. Discussants agreed that there is not one "correct" way to visualize complex microbial systems.

On Day 2, participants were encouraged to discuss diversity, equity, and inclusion in microbiome research, namely: 1) racism in microbiome research; 2) ethics of indigenous microbiome research; 3) inclusivity in microbiome research; and 4) microbes, social equity, and human health. Initial discussions started on the equitable attribution of co-authorship and whether co-authorship is the best and most equitable reward for people who contribute to a project, particularly in cases when researchers are collaborating with people outside of academia. For many outside of academia, authorship is meaningless, and more tangible efforts such as training or funding are more valuable. Another major point of discussion centered around positionality of microbiome researchers, namely how biases can stem from ethnic, racial, socioeconomic, and language backgrounds. Actionable items that resulted from this discussion included that 1) researchers/PIs need to actively recruit students from underrepresented groups and maintain contact with them; and 2) researchers should translate their work into other languages, particularly when they work with people in different countries who speak different languages. We would also like to highlight the Microbes and Social Equity (MSE) Working Group founded by Dr. Sue Ishaq, which is composed of microbiome researchers aiming to meaningfully affect social change through microbiome research (Ishaq et al., 2021). Many members of the AMRG are also active members of the MSE group. Importantly, issues of structural inequity and discrimination are not unique to microbiome research. Actions that arose in this discussion are applicable to a wide variety of academic fields.

A growing network

The AMRG has grown over its first year. The Slack workspace, which now boasts 244 community members, is structured around 6 channels in which members can 1) introduce themselves to the AMRG, 2) circulate recently published articles, 3) advertise talks, funding opportunities, job/student postings, or journal special issues, 4) exchange advice on experimental design, lab techniques, or analytical approaches and troubleshoot problems, and 5) launch collaborative projects. Aside from public channels, the Slack workspace also allows for direct messaging, enabling researchers to connect privately.

The periods of fastest membership growth and greatest Slack engagement occurs immediately before and after annual meetings, with plateaus between meetings. An exception coincides with the publication of the first meeting summary (Petrullo et al., 2021) and subsequent re-circulation of the Slack group invitation on social media (Figure 1A). Social media appears critical for growing membership, but notably, this membership growth event did not cause an increase in the number of Slack posts, suggesting that new members do not immediately create posts in the Slack group (Figure 1B). However, this event did appear to trigger a sustained increase in member engagement (Figure 1C).

Maintaining member engagement throughout the year may require concerted posting efforts by community members to keep the workspace contents new (i.e., engagement begets engagement). For example, we see a positive correlation between the number of posts per week and the proportion of active but non-posting members (Figure 1D). Member-led workshops have recently been proposed as a way to maintain engagement in Slack. A qualitative analysis of the Slack aggregate data suggests that additional events could help sustain member engagement between annual meetings.

Conclusion

The AMRG is a growing network of ECRs studying host-microbiome relationships in the wild. The virtual home of the AMRG annual meetings and community has been valuable in an era where travel and in-person meetings are curtailed in the interest of public health. Despite a successful first year, there remains room for a growth in the diversity of methods (16S amplicon sequencing most prevalent), host systems (mammalian and avian hosts predominate), microbiome types (focus is often on gut microbiomes), and global membership seen within the AMRG group (currently heavily biased to the global north). Those interested in joining and helping to grow this vibrant virtual community can do so by visiting <https://amrg.mystrikingly.com/#join-us> or sending a direct message on Twitter (@AnimMicrobioRes).

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