MICROBIAL ASSOCIATIONS AND SPATIAL PROXIMITY PREDICT NORTH AMERICAN MOOSE (ALCES ALCES) GASTROINTESTINAL COMMUNITY COMPOSITION[1]

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ABSTRACT

Microbial communities are increasingly recognized as crucial for animal health. However, our understanding of how microbial communities are structured across wildlife populations is poor. Mechanisms such as interspecific associations are important in structuring free-living communities, but we still lack an understanding of how important interspecific associations are in structuring gut microbial communities in comparison to other factors such as host characteristics or spatial proximity of hosts. Here we ask how gut microbial communities are structured in a population of North American moose (*Alces alces*). We identify key microbial interspecific associations within the moose gut and quantify how important they are relative to key host characteristics, such as body condition, for predicting microbial community composition. We sampled gut microbial communities from 55 moose in a population experiencing decline due to a myriad of factors, including pathogens and malnutrition. We examined microbial community dynamics in this population utilizing novel graphical network models that can explicitly incorporate spatial information. We found that interspecific associations were the most important mechanism structuring gut microbial communities in moose and detected both positive and negative associations. Models only accounting for associations between microbes had higher predictive value compared to models including moose sex, evidence of previous pathogen exposure, or body condition. Adding spatial information on moose location further strengthened our model and allowed us to predict microbe occurrences with ~90% accuracy. Collectively, our results suggest that microbial interspecific associations coupled with host spatial proximity are vital in shaping gut microbial communities in a large herbivore. In this case, previous pathogen exposure and moose body condition were not as important in predicting gut microbial community composition. The approach applied here can be used to quantify interspecific associations and gain a more nuanced understanding of the spatial and host factors shaping microbial communities in non-model hosts.

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