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Drs Neufeld, Stein, and Watanabe, Editors-in-Chief
Members of the Editorial Board, *ISME J*

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Dear colleagues,

Enclosed please find our manuscript entitled "*Competitive hierarchies, antibiosis, and the distribution of bacterial life history traits in a microbiome*" for publication consideration as an Article for *ISME J*.

While microbiome research is now integrated with nearly every field in biology, from medicine to crop protection and ecology to evolutionary biology, we still have a limited understanding of the nature of the interactions (antagonistic or otherwise) that occur between microbes that co-occur in nature. In particular, although microbiomes are being manipulated for 'growth-promotion' in crop plant systems, the basic biology, particularly the role that interactions among constituent microbes play in establishing a resident microbiome, is poorly known. Without studies that measure how microbial traits mediate their interactions within microbiomes, we risk relying on a weak ecological foundation for understanding of population and community-level dynamics within host-associated microbiomes.

In our enclosed manuscript, rather than leaning on laboratory strains, we provide a systematic description of the link between microbial traits and competitive outcomes using strains directly isolated from leaves of a native host plant. By linking independent measures of canonical resource usage traits with a systematic comparison of competitive outcomes in spatial microcosms, our study uncovers strong competitive asymmetries between two major *Pseudomonas* sp. clades that predominate within a plant microbiome that has been studied extensively by our group from a variety of perspectives.

Further, we find that the underlying patterns of trait variance and covariance differ between bacterial clades, with separate axes of variation underlying competitive ability in each clade. Finally, the particular distribution of antibiosis and resistance traits discovered in this community predicts indirect facilitation of relatively weaker *P. syringae* competitors by 'keystone' *P. fluorescens* strains. Not only can *P. fluorescens* out-compete *P. syringae* in spatial microenvironments by way of spatial pre-emption and antibiosis, but they can potentially ensure that the surviving *P. syringae* genotypes are relatively weaker competitors via the indirect effects of antibiosis.

We conducted our study on bacterial strains derived from a native herbaceous plant, *Cardamine cordifolia*—a mustard that is closely related to *Arabidopsis thaliana*. Given the important literature on interactions between *Arabidopsis* and the phytopathogen *P. syringae*, our work helps establish precedent for leaf-derived *P. fluorescens* to be strong and dominant competitors within this and potentially other widespread *Pseudomonas*-rich plant systems. This is a new role for *P. fluorescens*, and the remarkable variety of patterns of antibiosis we report represents a tremendous resource for the community to dissect. Finally, harnessing the biotic or antibiotic properties of such *P. fluorescens* to shift community assembly towards certain outcomes (e.g., to bulwark against establishment of phytopathogenic *P. syringae*) would represent a boon for the field of microbiome engineering.

In summary, our manuscript lays a solid ecological foundation for mechanistic tests of how broadly important microbial taxa assemble within the context of a native plant microbiome. Given the broad implications of our results, the simplicity and directness of our empirical and analytical approach, we believe that this work is well-suited to the broad readership of *ISME J*.

Sincerely,

A handwritten signature in black ink, appearing to read "Noah Whiteman".

Noah K. Whiteman, Ph.D.

A handwritten signature in black ink, appearing to read "Parris Humphrey".

Parris T. Humphrey, Ph.D.