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Dr. Samraat Pawar Reader

The Editor
PLOS Computational Biology

Dear Editor,

We are submitting a manuscript titled *The role of competition vs cooperation in microbial community coalescence*, for consideration an article in *PLOS Computational Biology*.

Microbial communities play a critical role in biological systems, mediating processes ranging from animal development and host health (1; 2) to natural ecosystem functioning (3). Understanding how these complex communities assemble, function, and persist is a major new frontier in biology (4).

Entire, distinct microbial communities are often displaced over space and come into contact with each other, merging to form a new community, a phenomenon that has been termed community coalescence (5). Although coalescence commonly occurs and is an important means of microbial community formation, our ability to predict the outcomes of such events based on the properties of the parent communities remains limited. While recent theoretical work has begun to elucidate the role of competition in coalescence (6; 7), that of cooperation, the other key interaction type commonly seen in microbial communities, remains unclear. Here, using a general consumer-resource model, extensive simulations, and novel metrics that link community structure to coalescence success, we provide new insights into the combined effects of competitive and cooperative interactions on the outcomes of coalescence events. In particular, we show that species from less competitive parent communities, which have maximized resource partitioning, tend to dominate the new community after coalescence, regardless of their cooperativeness. However, counter-intuitively, when competition in both parent communities is significantly weaker than cooperation, the more cooperative one is at a disadvantage during coalescence because multi-species invasions are able to easily disrupt established metabolite cross-feeding links.

Encounters between microbial communities are frequent in nature, and mixing of microbial communities is gaining popularity for bio-engineering, soil restoration, faecal microbiota transplantation, and the use of probiotics (8; 9). Therefore, the novel insights into mechanisms underlying microbial community coalescence that our study provides are likely to be of interest to a broad audience. Furthermore, our mathematical model and simulation framework is general, and will stimulate further research in multiple new directions, towards a deeper understanding of microbial community coalescence.

We suggest the following potential reviewers for our manuscript:

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We confirm that this manuscript is not under consideration for publication in any other journal and we declare no conflicts of interest.

Yours sincerely,

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