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Dear Editor,

Please find enclosed the manuscript "Multi-strain disease dynamics on metapopulation networks" which we would like to have considered for publication in *PLOS Computational Biology* as a research article in response to the **PLOS Cross-Journal Call for Papers on the Mathematical Modelling of Infectious Disease Dynamics**. In particular, we believe this work directly addresses "The role of population movement on various scales in altering the spread of disease" as well as "Disease modelling and forecasting in both local and global contexts."

Strain structure is ubiquitous among the most widespread diseases in the world today, and has been the subject of extensive epidemiological research over the past decades. Likewise, there has been extensive research on networks of interconnected populations, termed metapopulations, especially within the ecological literature. Surprisingly, however, there have been few attempts to link these two areas of research, despite a need for better understanding and control of pathogen spread.

Here, we use a mathematical model combining multi-strain disease dynamics and meta-population network structure to show that there can be dramatic effects on the temporal dynamics of pathogen prevalence when migration is allowed between populations. We explore several simple network structures and evince some remarkably simple and consistent patterns relating the dynamics of origin and destination populations. We additionally perform simulations to note the effect on larger metapopulation networks. In summary, we find that, when populations are linked, the dynamics of destination populations are significantly influenced by the dynamics of origin populations, with migration having the potential to reduce disease prevalence or even change the dynamical regime in the desitnation population. Generalizing to larger networks, we see a significant effect of network structure on total disease prevalence as well, with more heterogeneity in degree (the number of other populations a given population is connected to) leading to increased prevalence and decreased immunity in the metapopulation as a whole.

This work provides a general framework linking two well-established areas of ecological theory: metapopulations and multi-strain disease dynamics. We believe the insights expounded on in our work will instigate further research into the structures of real-world metapopulations, and, in particular the role of network structures on endemic disease dynamics. This framework will prove particularly useful to researchers of systems with high migration rates, such as in the context of mobile species in fragmented landscapes or the movements of livestock between growing facilities, but we believe the generality of our theoretical approach will prove broadly interesting to the readership of *PLOS Computational Biology*.

Thank you for the attention dedicated to our work.

Sincerely,

Matthew J. Michalska-Smith, Kimberly VanderWaal,
Montserrat Torremorell, Cesar Corzo,
and Meggan E Craft