11th Conference on Dynamical Systems Applied to Biology and Natural Sciences DSABNS 2020 Trento, Italy, February 4-7, 2020

HOST CONTACT DYNAMICS SHAPES RICHNESS AND DOMINANCE OF PATHOGEN STRAINS

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The interaction among multiple microbial strains affects the spread of infectious diseases and the efficacy of interventions. Genomic tools have made it increasingly easy to observe pathogenic strains diversity, but the best interpretation of such diversity has remained difficult because of relationships with host and environmental factors. We focused on host-to-host contact behavior and use stochastic modeling and network theory to quantify its effect on strain richness and dominance [1]. We systematically compared multi-strain spread on various network models illustrating properties found in real-world examples. We then analyzed the spread of *Staphylococcus aureus* in a hospital, leveraging on a combined dataset of carriage and close proximity interactions. We found that contact dynamics has a profound impact on strain populations. Contact heterogeneities reduce strain diversity by limiting the number of circulating strains and leading few strains to dominate over the others. Conversely, strong community structure increases strain richness. In the *S. aureus* example, network structural and temporal properties could account for a large part of the variability observed in strain abundance. These results show how stochasticity and network structure affect the population ecology of pathogens and warn against interpreting observations as unambiguous evidence of epidemiological differences between strains.

References

[1] Francesco Pinotti, Éric Fleury, Didier Guillemot, Pierre-Yves Boëlle, and Chiara Poletto. *Host contact dynamics shapes richness and dominance of pathogen strains*. PLOS Computational Biology, 15(5):e1006530, May 2019.

©DSABNS ISBN: 978-989-98750-7-4