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Emergence of elevated levels of multiple infections in spatial host-virus dynamics BRADFORD TAYLOR, Georgia Inst of Tech, CATHERINE PENINGTON, Queensland Univ of Tech, JOSHUA WEITZ, Georgia Inst of Tech —

Bacteria are subject to infection and potentially to multiple simultaneous infections by viruses. Multiply infected hosts have altered life-history traits (e.g., viral burst size) and evolutionary rates (e.g., viral recombination). Yet our understanding of multiple infections of microbes is limited to lab settings where the ratio of inoculant viruses to hosts is controlled. In contrast, rates of multiple infection in natural environments are unknown. Here, we develop an individual based model to quantify rates of multiple infections by a single viral type. We explore different dispersal regimes by varying the viral adsorption rate. High dispersal regimes lead to spatial dynamics and rates of multiple infection equivalent to predictions from mean field models. Local clustering of bacterial hosts occurs for low dispersal. Comparing to mean field, the clustering leads to increased rates of multiple infection and fatter tails in the distribution of the number of internal viruses. The emergence of increased colocalization of viruses with infected hosts leads to these deviations. We show these deviations result from the wave-like spread of viruses when invading clusters of bacteria. Our work represents a key step in understanding the population-level effects of multiple infections.

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