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Community assembly of the worm gut microbiome

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It has become increasingly clear that human health is strongly influenced by the bacteria that live within the gut, known collectively as the gut microbiome. This complex community varies tremendously between individuals, but understanding the sources that lead to this heterogeneity is challenging. To address this challenge, we are using a bottom-up approach to develop a predictive understanding of how the microbiome assembles and functions within a simple and experimentally tractable gut, the gut of the worm *C. elegans*. We have found that stochastic community assembly in the *C. elegans* intestine is sufficient to produce strong inter-worm heterogeneity in community composition. When worms are fed with two neutrally-competing fluorescently labeled bacterial strains, we observe stochastically-driven bimodality in community composition, where approximately half of the worms are dominated by each bacterial strain. A simple model incorporating stochastic colonization suggests that heterogeneity between worms is driven by the low rate at which bacteria successfully establish new intestinal colonies. We can increase this rate experimentally by feeding worms at high bacterial density; in these conditions the bimodality disappears. We have also characterized all pairwise interspecies competitions among a set of eleven bacterial species, illuminating the rules governing interspecies community assembly. These results demonstrate the potential importance of stochastic processes in bacterial community formation and suggest a role for *C. elegans* as a model system for ecology of host-associated communities.