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Standing variation in spatially growing populations DIANA FUSCO, MATTI GRALKA, JONA KAYSER, OSKAR HALLATSCHEK, Univ of California - Berkeley — Patterns of genetic diversity not only reflect the evolutionary history of a species but they can also determine the evolutionary response to environmental change. For instance, the standing genetic diversity of a microbial population can be key to rescue in the face of an antibiotic attack. While genetic diversity is in general shaped by both demography and evolution, very little is understood when both factors matter, as e.g. for biofilms with pronounced spatial organization. Here, we quantitatively explore patterns of genetic diversity by using microbial colonies and well-mixed test tube populations as antipodal model systems with extreme and very little spatial structure, respectively. We find that Eden model simulations and KPZ theory can remarkably reproduce the genetic diversity in microbial colonies obtained via population sequencing. The excellent agreement allows to draw conclusions on the resilience of spatially-organized populations and to uncover new strategies to contain antibiotic resistance.

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