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Spatial Expansions of Microorganisms in Structured and Continuous Environments

The spread of populations into new, previously unoccupied territory is a frequently occurring phenomenon which - despite its transient nature - determines the genetic diversity and thus affects the long term fate of the population. Favorable two-dimensional environments punctuated by finite-sized regions of poor growth, i.e., obstacles such as lakes or mountains interrupting a land mass favorable for species, can arise in many spatial expansions, but have thus far received little systematic attention. We address this problem (complementary to populations subject to spatial bottlenecks) via a combined experimental and theoretical approach that focuses on the shape of the population front in simplified geometries and its consequences on the population's genetic diversity.

In one experimental model system bacteriophage T7 spreads on an *Escherichia coli* lawn, consisting of regions of susceptible and resistant bacteria, with the latter representing regions of poor growth for the phage. An inkjet printing assay allows us to create environments with a single well-controlled obstacle and to quantitatively study how obstacles deform the phage front. We find that a simple model based on an 'argument of least time' describes the observed transient perturbations of the front semi-quantitatively and a reaction-diffusion model based on the Fisher equation suggests where the small quantitative deviations between model and experiment originate from. The character of the transient perturbations suggest that the fate of alleles at the front are determined by their spatial position in the front relative to the region of poor growth. This effect of 'selection by geometry' is illustrated by a range expansion of *E. coli* on agar plates with obstacles and three different fluorescent labels and addressed in more detail using stochastic simulations

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Hosted by Berenike Maier