Abstract Submitted
for the MAR16 Meeting of
The American Physical Society

Adapting populations in space: clonal interference and genetic diversity DANIEL WEISSMAN, Emory University, NICK BARTON, IST Austria — Most species inhabit ranges much larger than the scales over which individuals interact. How does this spatial structure interact with adaptive evolution? We consider a simple model of a spatially-extended, adapting population and show that, while clonal interference severely limits the adaptation of purely asexual populations, even rare recombination is enough to allow adaptation at rates approaching those of well-mixed populations. We also find that the genetic hitchhiking produced by the adaptive alleles sweeping through the population has strange effects on the patterns of genetic diversity. In large spatial ranges, even low rates of adaptation cause all individuals in the population to rapidly trace their ancestry back to individuals living in a small region in the center of the range. The probability of fixation of an allele is thus strongly dependent on the alleles spatial location, with alleles from the center favored. Surprisingly, these effects are seen genome-wide (instead of being localized to the regions of the genome undergoing the sweeps). The spatial concentration of ancestry produces a power-law dependence of relatedness on distance, so that even individuals sampled far apart are likely to be fairly closely related, masking the underlying spatial structure.

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Date submitted: 05 Nov 2015

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