

MAR13-2012-000420

Abstract for an Invited Paper
for the MAR13 Meeting of
the American Physical Society

The statistics of genetic diversity in rapidly adapting populations.

MICHAEL DESAI, Harvard University

Evolutionary adaptation is driven by the accumulation of beneficial mutations, but the sequence-level dynamics of this process are poorly understood. The traditional view is that adaptation is dominated by rare beneficial “driver” mutations that occur sporadically and then rapidly increase in frequency until they fix (a “selective sweep”). Yet in microbial populations, multiple beneficial mutations are often present simultaneously. Selection cannot act on each mutation independently, but only on linked combinations. This means that the fate of any mutation depends on a complex interplay between its own fitness effect, the genomic background in which it arises, and the rest of the sequence variation in the population. The balance between these factors determines which mutations fix, the patterns of sequence diversity within populations, and the degree to which evolution in replicate populations will follow parallel (or divergent) trajectories at the sequence level. Earlier work has uncovered signatures of these effects, but the dynamics of genomic sequence evolution in adapting microbial populations have not yet been directly observed. In this talk, I will describe how full-genome whole-population sequencing can be used to provide a detailed view of these dynamics at high temporal resolution over 1000 generations in 40 adapting *Saccharomyces cerevisiae* populations. This data shows how patterns of sequence evolution are driven by a balance between chance interference and hitchhiking effects, which increase stochastic variation in evolutionary outcomes, and the deterministic action of selection on individual mutations, which favors parallel solutions in replicate populations.