A Top-Down Approach to Discriminate Adaptive Landscape Topology

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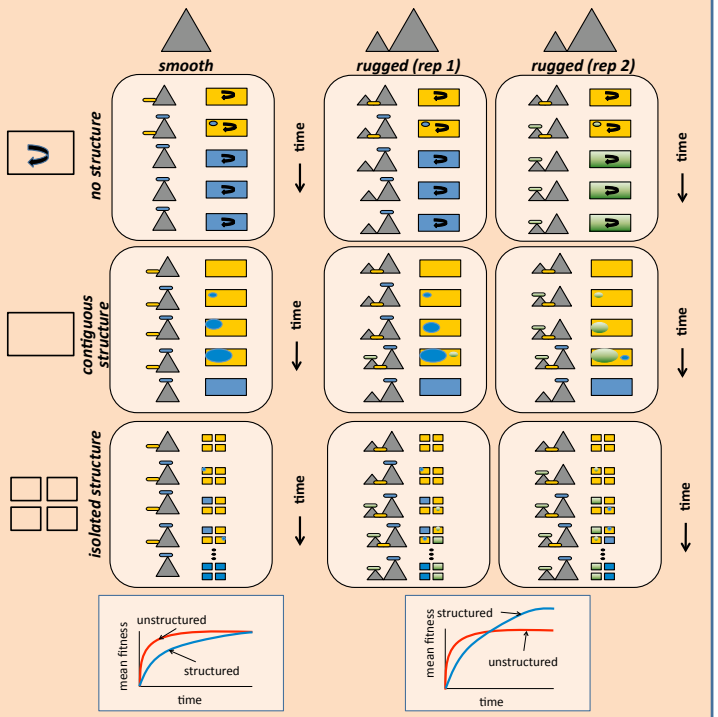
Smooth or Rugged?

Sewall Wright's landscape metaphor enjoys widespread use within evolutionary biology. Because of the astronomical number of possible genotypes, the landscape topology of even the simplest organism has been elusive. For example, does the landscape contain just one peak (smooth) or are there multiple peaks (rugged)? How does an evolving population move in its landscape? We are interested in designing in vitro experiments that can address some of these questions. One approach is to focus on a very small area of the landscape by assessing fitness directly from a set of genotypes. Here we take a different approach. To discriminate different topologies, we look for patterns of changes in fitness between populations with different degrees of population structure.

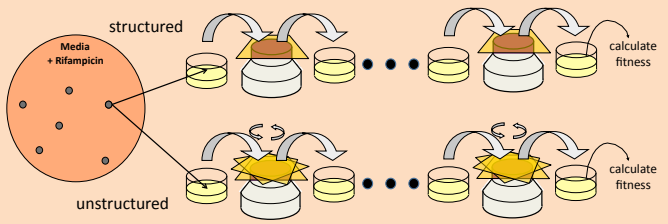
Theoretical Predictions



The three different colors (orange, blue and green) in the schematic represent three different genotypes. There are two types of structure illustrated above: genotype structure (columns) and physical structure (rows). For our experimental design, we will use different degrees of physical structure to infer genotype structures. A population in an unstructured environment in a *smooth* landscape will find the optimal solution relatively quickly (with the more fit genotype sweeping through the population). A structured population will generally reach the same fitness but more slowly. Different replicate populations in a *rugged* landscape with an unstructured environment will find different locally optimum solutions (2 replicates shown). With physical structure the population will more likely hit a higher mean fitness than in an unstructured physical environment.

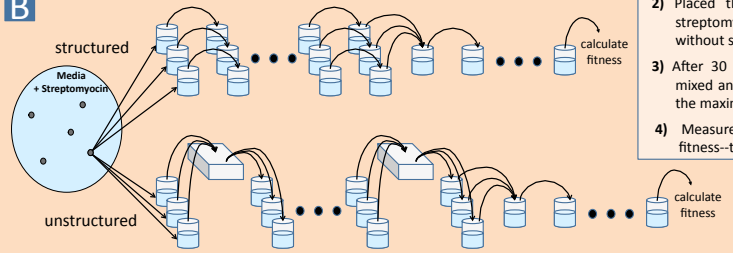
Experiments

A



1) Obtained two rifampicin-resistant strains of *E. coli*
2) Placed each strain in one of two rifampicin-free environments: one with structure (local dispersal) and one without structure (global dispersal)
3) Tracked the average fitness (on plates) in each treatment

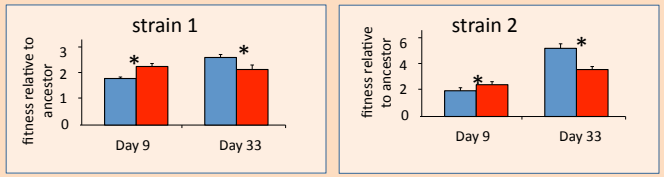
B



1) Obtained one streptomycin-resistant strain of *E. coli*
2) Placed the strain in one of two environments with streptomycin: one with structure (no mixing) and one without structure (mixing microtiter wells every transfer)
3) After 30 transfers, all wells from each treatment were mixed and propagated in one well for one week to allow the maximally fit genotype to displace the others
4) Measured absorbance in a spectrometer as a proxy for fitness--the growth rate of the evolved strain

Results and Discussion

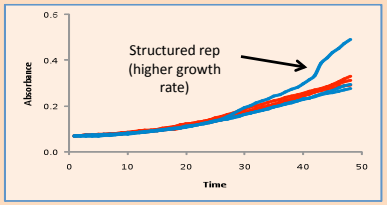
A



The results were consistent with the landscape being rugged rather than smooth. In experiment *A*, the structured treatment had a higher mean fitness on day 9, but the unstructured treatment had a higher mean fitness by day 33. On both days the differences were significant. For *B*, the results were not significant but they were suggestive of a rugged landscape. Further work is being done with this experiment.

structured
unstructured

B



Future directions There are several other experiments that we will be running in the near future. We will increase the scale of experiment *B* considerably by increasing the number of subpopulations and by increasing the number of transfers. We will also vary the structured environments with several different aminoglycoside antibiotics. We will evolve our bacteria in the heterogeneous environments before returning the bacteria to a homogeneous environment (i.e., just the streptomyocin environment). When returned to a homogeneous environment, we will check whether scattering in genotype space results in a higher ending fitness point. We will also investigate the genetic basis for the mean fitness differences among populations.