Long-term evolution is 'surprisingly predictable,' experiment shows

March 18 2013, by Bjorn Carey

Dr. Michael Palmer, left, and Professor Marcus Feldman, with co-author Arnav Moudgil (not pictured), found that the long-term evolutionary dynamics were surprisingly predictable in a model of protein folding and binding.

(Phys.org) —A protein-folding simulation shows that the debated theory of long-term evolution is not only possible, but that the outcomes are predictable. The Stanford experiment provides a framework for testing evolutionary outcomes in living organisms.

Two birds are vying for food. One bird's beak is shaped, by virtue of a random mutation, such that it's slightly more adept at cracking seeds. This sets the bird on the road toward acquiring more food, a better chance of scoring a mate and, most important, passing on its genetic endowment.

This individual's success is an example of short-term evolution, the widely accepted Darwinian process of natural selection by which individual organisms that have better adapted to their surroundings prevail.

In recent years, however, some scientists have argued that natural selection occurs not just at the individual organism level, but also between lineages over the course of many generations. In a new study, Stanford biologists have demonstrated that not only is this long-term evolution possible, but that long-term evolutionary outcomes can be surprisingly predictable.

The group set up a computer simulation in which 128 lineages of proteins continuously folded into new shapes, competing to bind with other molecules, called ligands, in each new configuration. The better each protein could attach itself to the ligands, the more ligands it would scoop up, and the higher its fitness – that is, its average number of "offspring" – would be. The simulation was run for 10,000 generations.

Although the chaos of 128 lineages – a total of more than 16,000 individual proteins – mutating over thousands of generations might seem unpredictable, and that it would be nearly impossible for the same thing to happen twice, it's actually the opposite.

"Even though things look complicated, the possible evolutionary trajectories are quite constrained," said lead author Michael Palmer, a computational biologist at Stanford. "There are only a few viable mutations at any point, which makes the dynamics predictable and repeatable, even over the long term."

The study, co-authored by Marcus Feldman, a biology professor at Stanford, and Stanford research biologist Arnav Moudgil, was recently published in the *Journal of the Royal Society Interface*.

In some experiments, the lineages that consistently came out on top in the long term were not initially the best adapted at binding to ligands. "The immediate fitness is not the only important thing," Palmer said. "Yes, a lineage does have to survive in the short term. But just as important is how it is able to adapt to new and potentially variable environments over the longer term."

A good example of this scenario is Darwin's famous finches. It's thought that individuals – perhaps just a single pair of birds – from a South American species ended up on the Galápagos Islands about 1 million years ago. Today their descendants have diversified into about 15 modern species. Some eat seeds, some eat insects, or flowers. Some eat ticks, or even drink the blood of other birds.

"If there was some catastrophe that removed one of those food sources, it might wipe out one or more of the 15 species, but the rest of the lineage – the descendants of that initial pair of birds – would persist," Palmer said. "Now say there was a competing lineage that was great at cracking seeds, but unable to evolve to other diets due to some prior genetic constraint. The same catastrophe could wipe it out."

The finding, and others like it, could represent a significant shift in viewpoint for biologists. For one thing, it means that in certain situations, scientists should look beyond the details at the level of the individual organism, as the evolutionary dynamics can be accurately understood as lineage selection.

It also has implications on a species' genomic architecture, or how a genome is organized on the lineage level. While a lineage's genome might primarily select for a particular set of traits in order for individuals to survive in the short term, in order to out-compete other lineages, it must also be able to adapt to new conditions over the long term.

"An individual can have a lucky mutation that produces an immediate adaptation," said Palmer. "Or a lineage can have a lucky mutation that happens to position it to adapt to the range of environments it will experience over the next thousand generations. A single mutation can have a distinct short-term and long-term fitness."

The authors believe that the work can be replicated in microorganisms, and are now hoping that microbiologists will apply the new metrics of selection in vitro.

"There is already some evidence in vitro that there is a lot of constraint on evolutionary trajectories," Palmer said, "and we think we've come up with a good framework to quantify evolutionary predictability and long-term fitness."

More information: Paper: rsif.royalsocietypublishing.or … 130026.full.pdf+html

Provided by Stanford University