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ECOLOGY

Fishing for answers

By Christian Jørgensen and Katja Enberg

One hallmark of the Anthropocene is a rapid change in the ways our bipedal species affects the wild inhabitants on Earth. Emerging evidence on many fronts suggests that human-induced environmental change can lead to marked evolution on decadal or even shorter time scales. One eye-opening study from 2002 simulated intensive fishing and reported a twofold difference in body weight after just four generations of selectively harvesting either small or large individuals (1). Merely documenting that rapid evolution takes place, however, falls short of deciphering how it occurs at a mechanistic level—a prerequisite for predicting evolution in other cases. On page 487 of this issue, Therkildsen et al. (2) show that genomic changes manifested during the original 2002 experiment partly aligned with variation along a natural gradient in the wild, but that strong selection also quickly eroded genetic variance.

Behind the many documented facets of contemporary global change—species invasions, land-use modifications, climate change—lie untold stories of new and strong selection pressures (3). “New selection pressure” is a gentler way of saying that individuals die sooner or reproduce less. Other individuals that better tackle the new environment pass on their heritable traits; thus, the population evolves and perhaps persists. This is how the ancestors of existing species have outlived every environmental challenge until now. The current rate of human-driven ecological changes, however, raises a key question: Is evolution fast enough to keep up, or will these strong selection pressures curtail biodiversity?

A first approach to understanding evolutionary change is phenotype-centric and starts from knowledge of how organisms function in their environment (for example, physiology, behavior, and ecology). The challenge here is to decipher how phenotypes with certain heritable traits survive or reproduce better than alternative phenotypes. Therkildsen et al. studied the Atlantic silverside, a fish species that exists along a latitudinal diversity gradient wherein clever experiments have demonstrated advantages of fast growth in northern populations driven by a short productive season (4). By contrast, south-
ern fish grow more slowly because summers are longer and winters milder.

The phenotype-centric approach assumes that when phenotypic traits are selected, corresponding changes at the molecular level follow suit (5). This mechanism is easiest to grasp for continuous traits—phenotypes that display a range of presentations, such as body height or growth rate—as these are often influenced by the joint effects of perhaps hundreds of genes. If there is, for example, a selective advantage of fast growth, then individuals having more of the gene variants (alleles) for fast growth also produce more offspring, and alleles for fast growth will accumulate.

The breathtaking diversity of life suggests that genomic constraints on the path of evolution are less restrictive if genes can be recombined and reshuffled over many generations. But with the current rate of anthropogenic change, evolution happens over just a few generations. When evolution approaches maximum rates, or when only a few genes in specific pathways are involved (6), it begins to matter where the genes are physically positioned on chromosomes and whether the genes affect multiple nodes in the complex biochemical network of a cell. Thus, scientists require a second, DNA-centric approach that views evolution from the bottom up (from genes to organisms). This perspective adds a focus on the effects of distinct alleles and their interactions, which can make evolutionary trajectories deviate from those predicted by phenotype-centric methods. Under strong selection, certain alleles might confer substantial benefits to their bearers and, over a few generations, spread through the population like a brushfire (a so-called selective sweep). Another gene that happens to reside in a nearby chromosomal location can hitchhike to fame, and its effects on the organism can influence the evolutionary outcome.

The genomic changes in the 2002 silverside study are of interest because selection was strong and evolution rapid. Large fish were removed from two populations (Down1 and Down2), and after four generations, the fish were markedly smaller. The opposite happened when small fish were harvested; and when harvesting was random, no change in body size occurred.

Therkildsen et al. pulled the fish from 2002 out of the freezer and searched their genomes for changes in genetic markers that accompanied the evolved size differences. In all of the experimental populations, thousands of genetic markers spread over nearly every chromosome changed in frequency. These results support the phenotype-centric view of polygenic evolution and are not surprising for a trait such as growth, which depends on multiple physiological processes. There was also strong evidence that attributes of the physical DNA molecule altered evolutionary outcomes. In the Down2 experimental tank, one individual had a chromosome variant typical of slow-growing fish from the southern range of this species’ distribution in the wild. This variant swept through the Down2 experimental population near-total dominance, and all of the alleles on this large chromosomal segment were inherited by the fourth generation. This observation is well explained by the DNA-centric view of evolution but would come as a surprise to a researcher solely relying on phenotype-centric methods.

Therkildsen et al. also demonstrated how maintaining genetic diversity might be crucial to conserving species diversity. Rapid evolution of growth was made possible in part by preexisting growth differences throughout the species’ natural range. Alleles that became common in fast-growing laboratory populations were shared by northern, fast-growing fish in the wild, and populations that evolved a slow-growth phenotype accumulated southern-type alleles. Without the broad array of alternative alleles in the starting populations, the rate of evolution would have been orders of magnitude slower because new genetic material would have had to arise from random mutations.

It is worrisome how quickly alleles disappeared during the short experiment. Alleles that strongly increased in frequency in one population did not necessarily change in parallel populations subjected to the same treatment. Thus, several genomic configurations yielded similar phenotypes (7), and different alleles were lost in different populations. Such chance events are typical of small populations. However, genetic variance eroded even faster in the selected silverside lines because it was similar individuals that survived and bred. This suggests that conservationists who assess a population as threatened because of its small size should extend this concern to somewhat larger populations that were recently or are currently under strong selection. 

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MICROBIOLOGY

Walk on the wildling side

Wild microbiota in inbred mice is a new tool for preclinical studies of human disease

By Samuel Philip Nobs1 and Eran Elinav2,3

Animal models are an important tool in investigating molecular mechanisms of disease pathogenesis and in developing therapeutic approaches for human disease. In many instances, though, success in preclinical experiments cannot be translated into the human setting (1). One potential explanation for this discrepancy between animal model and human experimental outcomes may involve the microbiota, a large ecosystem of bacteria, fungi, protozoa, and viruses that colonize mucosal surfaces in the human body, particularly the gastrointestinal tract (2). Differences in microbiota diversity, resilience, and presence of pathogens between laboratory animals and other “wild” mammals may lead to a limited reproducibility of animal experimentation when attempted in different localities or when used as models of human disease (3). On page 461 of this issue, Rosshart et al. (4) generate a more physiologically relevant preclinical mouse model by combining the diversity of the microbiota found in wild mice with the genetic uniformity of laboratory animals.

It has been suggested that the microbiota is of major importance for human health, regulating the development of many diseases, such as obesity, asthma, inflammatory bowel disease, and cancer (5). Interindividual differences in the microbiota may explain some phenotypic variability in humans, such as responses to food (6), cancer immunotherapy (7, 8), or drugs (9). The microbiota has been shown to influence multiple organ systems, including the immune system (5), and its manipulation or the manipulation of its metabolic products is considered a promising avenue for therapy of human disease (10). Rosshart et al. created “wildling” mice by inverse germ-free rederivation, trans-