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Exciting times for evolutionary biology

Evolutionary biologists should be proud of recent progress in their broad field. We highlight some developments in fundamental questions and the applied use of evolution.

Some argue that the biggest questions in evolution have remained the same since the field was established. Although there is some truth to this, there has been tremendous progress in the past decade or so towards answering these fundamental questions and applying the resulting understanding to diverse areas. Such progress has been driven in large part by technological developments that have enabled the generation of omics data for almost any species, combined with new analytical methods. Here, we highlight a few topics that showcase exciting developments.

One long-standing question in evolution is how individuals adapt to their environment. Answering this complex question entails understanding the genetic and evolutionary mechanisms that underlie ecologically relevant traits. The integration of genome sequencing data from several individuals of the same or related species with advances in population genetics methods has revealed interesting trends. Studies on a variety of taxa have shown that hybridization and introgression have important roles in adaptation – for example, in establishing mimetic wing patterns in *Heliconius* butterflies[1] or adaptation to desert life in North African foxes[2]. Similarly, chromosomal rearrangements such as inversions can contribute to ecologically relevant traits, as shown, for example, in sunflowers[3], Atlantic cod[4] and zokors[5]. Although genomic approaches have been used to identify genes (or even mutations) linked to ecologically relevant phenotypes, such as pigmentation in rock pocket mice, peppered moths and monkey flowers, or skeletal traits in sticklebacks[6], we also know that the regulation of gene expression frequently contributes to adaptation and divergence[7].

On a macroevolutionary scale, evolutionary biologists have long strived to understand why some clades are so much more diverse than others. Recently developed comparative methods anchored in phylogenomics have been revealing the long-term dynamics of biodiversity. Examples include how speciation, extinction and dispersal contribute to species radiations in tropical tetrapods[8]; how ecomorphological diversification affects long-term diversity of lizards and snakes[9]; and how morphological evolution and speciation rates are positively associated at broad macroevolutionary scales across vertebrates[10].

The evolution of sex has fascinated biologists for centuries. Our knowledge of the genetic determination of biological sex has until recently been restricted to a few model systems. However, the advent of long-read sequencing has enabled the discovery of sex chromosomes in many taxa, which has revealed that the sex chromosomes of some groups have remained stable for millions of years, whereas those of others have experienced marked turnover[11]. At the same time, comparative analysis of sex chromosomes in entire clades has shed light on recombination suppression and the evolutionary dynamics of specific regions of sex chromosome, such as the W and Z chromosomes in songbirds[12] or Y chromosomes in primates[13].

Perhaps one of the most challenging questions is how evolution produces new and complex traits. Comparative analyses have provided insights into the origin and evolution of novel traits in specific groups, such as eusociality in bees[14] and springboard trapping in carnivorous plants[15]. More recently, technological developments such as single-cell sequencing have enabled substantial progress towards understanding the stepwise evolution of neural systems from Placozoa to Cnidaria and Bilateria[16], as well as how new cell types and tissues contributed to the evolution of the vertebrate brain[17].

Some of the most exciting applications of evolutionary biology are in the medical arena. Viral evolution came to public attention in the COVID-19 pandemic, with attempts to predict and understand the rise of new variants. However, attempts to predict viral evolution pre-date the pandemic – for example, the evolutionary modelling used in the choice of strains for annual influenza vaccination[18]. Vaccination itself can exert selection pressure on viruses, and evolutionary modelling has been used to understand the complex interplay between vaccine escape and changes in virulence[19]. At a more fundamental level, population genetics analysis of ancient and contemporary DNA sequences has enabled us to study how bacterial and viral pathogens have evolved[20,21].

The antibiotic crisis is another topic that has brought evolution into the public eye. There is general appreciation that the overall problem is an evolutionary one, and evolutionary biology can bring specific solutions such as multidrug approaches to treatment[22] and the potential use of phages that have been coevolved to delay resistance evolution[23]. Resistance is also a major barrier to successful cancer treatment: one possible solution is evolution-informed adaptive therapy, in which reduced and intermittent dosing is used to maintain sensitive cells in the tumour rather than letting resistant cells grow unchecked. A recent study showed how such an approach may help to tackle the phenomenon of drug dependence in tumours[24]. Evolutionary models have also been used to understand the fundamental dynamics of tumour growth and development[25]. In such cases, the evolutionary principles being applied have a long history, but the actual analytical methodology has been developed only in the past few years in response to new molecular data[26], which demonstrates how advances in pure and applied evolutionary biology are progressing in tandem. We look forward to publishing further developments in these interacting strands of evolution.

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