Macroevolution: Change above the species level

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Introduction

The basic concept of evolution – change over time – can be examined in two different time frames. The first, which considers the time period covering a few generations for a population, is microevolution. There are many examples of microevolution that are handy for teaching, such as drug resistance (NESCent 2006a) and changes in beak size of finches in the Galapagos (NESCent 2006b). Macroevolution is the study of evolution over geologic time (thousands to millions of years). It tends to be

a much more challenging idea to teach since it requires an awareness of geologic time, and relies on inferences from fossils and other records of historical events, complicated molecular analyses, and phylogenies. In general it is more difficult to grasp because it offers fewer tangible ideas. Examples of macroevolution are found in the organismal diversity all around us, but the process cannot be observed or experimentally manipulated due to the time frame involved. What scientists can do is compare the results of "natural experiments", as seen in fossils and modern organisms, and make inferences from them. The applications of macroevolution in modern life tend to be less obvious than microevolution because of the extreme time scale. One application of macroevolution is in the development of conservation plans (NESCent 2006c) because macroevolution examines the generation of new species and the decline of species – key pieces of information for effective conservation efforts.

Speciation

Speciation is a key concept in macroevolution, in which the generation of new species and loss of species are major areas of study. A basic definition of a species is "a reproductively isolated population". Although identifying extinct species from fossil evidence can be challenging, studying the concept of species is easier on a macroevolutionary scale, since the question of *when* they formed or disappeared is the focus, as opposed to *how* they arose. Fuzzy areas that create problems in defining species in microevolutionary terms, such as hybrid zones (regions in which different species come in to contact and reproduce), vanish in the face of thousands of years, leaving records of morphologically distinct species for examination. Studying extinct species is an interesting puzzle in which various incomplete bits of information are combined to build a whole picture. Typically, extinct species are defined by the morphology (structure or form) of fossils, which is compared with other fossils and the morphology of current (extant) species. The comparison can provide information about how the extinct species lived, or in cases of incomplete fossil skeletons, may provide an idea of what the missing parts may have looked like.

Phylogenetic Trees and Molecular Studies

These morphological comparisons are also used to build phylogenetic trees which demonstrate relationships between species. Extensive morphological analysis of fossils and modern birds has allowed scientists to draw phylogenetic trees demonstrating the relationship between dinosaurs and birds. Shared morphological characteristics of a particular group are called a synapomorphies, and synapomorphies are important in building accurate phylogenetic trees. Similar morphologies can be misleading, such as bat wings and bird wings, or the bodies of sharks and dolphins. These are actually examples of convergent evolution, in which independent groups evolve similar characteristics in similar environments. It is difficult to differentiate between synapomorphies and convergent evolution, so scientists rely on multiple sources of information: several morphological characteristics, behavior, physiology, environment, etc. Much of this information is missing for fossils, and it is not uncommon for phylogenetic trees to be revised when new fossil evidence is discovered. Although fossils may be set in stone, the interpretation of what they mean is not!

Sometimes phylogenetic trees can link extinct species with extant species and in these cases additional information about the validity of the tree can be drawn from **molecular comparisons** between extant groups. For example, questions about the evolution of whales were partially solved by morphological comparison of fossils with both extant and extinct species resulting in two possible phylogenetic trees; a molecular comparison between whales and other extant species provided critical information to decide between the trees. Occasionally molecular information can be gathered from preserved tissues, bones, or waste products. Insects in amber, mammoths in permafrost (NESCent 2006d), packrat middens and Neandertal bones are all examples of extinct species providing DNA samples for analysis. These samples provide exciting opportunities to examine molecular changes that may have played a role in speciation.

EvoDevo

The field of "EvoDevo", which looks at development from an evolutionary standpoint, has provided a great deal of information in recent years particularly in regard to development of complex body structures. The discovery of a set of control genes, referred to as the homeotic genes, has allowed scientists to understand how complex body plans are initially laid out in embryonic stages. The homeotic genes are a suite of genes found in animals that determine the axes of embryos, then control how embryos are divided into segments, and initiate the

development of appropriate body parts in each segment. This system is interesting because it answers so many developmental questions and also because it provides a reasonable method for development of radically different body plans. For example, additional appendages can be accounted for by duplications of segments driven by the homeotic genes. Extra appendages provide an opportunity for the evolution of new functions, such as the pinchers on this scorpion. An important aspect of homeotic genes is their universality. Versions of the homeotic genes are found in all animals and in experiments have been shown to retain their ability to direct development across species. When the gene that initiates eye development in mice is put into mutant fruit flies lacking their own homeotic gene for eye development, the mouse gene initiates the development of perfect fly eyes. This common control pathway indicates a deep, shared lineage for all animals on a macroevolutionary scale.   On a practical level, it has implications for understanding and treating birth defects and other medical problems.

Molecular biology has lead to a greater understanding of how complex body forms developed, but on a more basic level questions remain about the transitions at the cellular level: from single celled to multicellular organisms, and from prokaryote to eukaryote. These questions are very basic, and the transitions are not straightforward but are important to understand. A single cell is limited in size and capabilities, but a multicellular organism must develop complex systems to allow communication and cooperation between cells for group success. The choanoflagellates are single celled organisms that sometimes live as colonies. They are suspected to be similar to the forerunners of multicellular animals based on morphological and molecular similarities. Research in this area can help us understand how cells work together to form a single organism.

Macroevolution and Extinction

While macroevolution research provides much information on the development of new life at many levels, macroevolution is also intimately concerned with extinction, the loss of species. It has been said that all species go extinct; some just take longer than others. This extinction rate is generally balanced by speciation events. There appears to be a certain “normal” level of background extinction and this type of extinction is of critical importance to understand as we work to design effective conservation measures. Research in macroevolution trends and events can help us determine what is normal and what we need to be concerned about. This research can inform our efforts to maximize the impact of our conservation efforts. For example, research on “refugia” or areas in a region that have remained stable habitats over long periods of time can identify areas with proven conservation value. Targeting these areas can be more effective than saving larger areas of land in less stable environments.

Extinction does not always occur at a background rate. There have been at least five major extinction events in which large percentages of all living organisms became extinct. The largest mass extinction was the Permian-Triassic period (200-300 million years ago or *mya*) in which about 96% of marine species, and 70% of land species were lost. One aspect of study is determining why certain species survived, while others did not. There is some evidence that geographic distribution may play a role in survival, along with other factors such as population size. The rules of extinction may differ between species as well. Another aspect of mass extinction research is determining the factors involved. Were all mass extinctions triggered by catastrophes, such as meteor impacts or were there a number of less than catastrophic factors that added up to a catastrophic effect? Many scientists believe we are currently in a sixth mass extinction; one that is largely due to the effects of humans on the biosphere.

Radiation

In each of these mass extinction events, many ecological niches are left unoccupied. This eventually allows radiation, rapid diversification, to occur. New species evolve over a few million years - relatively short order geologically speaking - to exploit open niches. After dinosaurs were lost in the Cretaceous-Tertiary mass extinction, mammals diversified and became the dominant land species. If the current rate of extinction continues unabated and we truly experience a sixth mass extinction, it is possible that the biosphere will be altered beyond our recognition and even beyond our ability to survive. Over millions of years, new ecological systems will evolve which may originate with surviving species, but the resulting world will probably look as strange to us as the world of the dinosaurs.

The Cambrian Explosion, which occurred about 542 mya, is a famous example of radiation. Organisms diversified wildly and a wide array of fossil animals appear in a geologic moment, about 542 mya. The Cambrian Explosion may actually be a misnomer, as some scientists now suspect that the diversification began much earlier but is not well reported in the fossil record. Nevertheless, the Cambrian Explosion remains of interest because it appears to be the point at which nearly all the major animal taxa were established.

Conclusion

The concept of macroevolution is scientifically solid, as is microevolution. As with all fields in science, as one delves deeper into the literature and research the picture becomes more complicated. In macroevolution, there are ongoing discussions about the rates, causes, and methods of extinction. There is debate about what the presence or absence of a particular fossil means. Information is re-interpreted as dating techniques improve, and new fossils are discovered. This is a prime example of how science works. Knowledgeable people develop ideas, test them with new data, and make the information available to the scientific community. The community examines the ideas and tests and after often extended and vigorous debate and further testing, either rejects or accepts the ideas. Even accepted theories continue to develop over time. The core concept will remain the same, but as our knowledge increases, the details of the theory may be modified in recognition of our improved understanding. It is vital to our survival as a species to continue to increase our understanding of how evolution, both micro- and macro-, function. We are a part of the biosphere and we need to understand how the system works to ensure that we do not overwhelm and irrevocably damage it to our ultimate peril.

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