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Assignment:

Give account of the Evidence of evolution and it's application

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CHAPTER 1.0

INTRODUCTION

Evolution is a biologic process,but it is also significant to geology. Evolution, theory in biology postulating that the various types of plants, animals, and other living things on Earth have their origin in other preexisting types and that the distinguishable differences are due to modifications in successive generations. The theory of evolution is one of the fundamental keystones of modern biological theory, anatomy, molecular biology, biography, fossil and direct observation.

Evolution is conveniently refer to as the biologic equivalent of the continuing changes that have occurred and continue to occur on the earth.

Evolution is change in the heritable characteristics of biological populations over successive generations. These characteristics are the expressions of genes, which are passed on from parent to offspring during reproduction. Variation tends to exist within any given population as a result of genetic mutation and recombination. Evolution occurs when evolutionary processes such as natural selection (including sexual selection) and genetic drift act on this variation, resulting in certain characteristics becoming more common or more rare within a population.

The 19th-century English naturalist Charles Darwin argued that organisms come about by evolution, and he provided a scientific explanation, essentially correct but incomplete, of how evolution occurs and why it is that organisms have features—such as wings, eyes, and kidneys—clearly structured to serve specific functions. Natural selection was the fundamental concept in his explanation. Natural selection occurs because individuals having more-useful traits, such as more-acute vision or swifter legs, survive better and produce more progeny than individuals with less-favorable traits. Genetics, a science born in the 20th century, reveals in detail how natural selection works and led to the development of the modern theory of evolution. Beginning in the 1960s, a related scientific discipline, molecular biology, enormously advanced knowledge of biological evolution and made it possible to investigate detailed problems that had seemed completely out of reach only a short time previously—for example, how similar the genes of

humans and chimpanzees might be (they differ in about 1–2 percent of the units that make up the genes).

1.1Evidence of evolution

Evidence for evolution, anatomy, molecular biology, biography, fossil and direct observation.

Key points:

- Evidence for evolution comes from many different areas of biology:

- Anatomy. Species may share similar physical features because the feature was present in a common ancestor (homologous structures).

- Molecular biology. DNA and the genetic code reflect the shared ancestry of life.

DNA comparisons can show how related species are.

- Bio-geography. The global distribution of organisms and the unique features of island species reflect evolution and geological change.

- Fossils. Fossils document the existence of now-extinct past species that are related to present-day species.

- Direct observation. We can directly observe small-scale evolution in organisms with short life cycles (e.g., pesticide- resistant insects).

Evolution is a key unifying principle in biology. As Theodosius Dobzhansky once said, "Nothing in biology makes sense except in the light of of evolution.

But what, exactly, are the features of biology that make more sense through the lens of evolution? To put it another way, what are the indications or traces that show evolution has taken place in the past and is still happening today?

Biologist sometimes define evolution base on scales.

1.1.2 scales of evolution

- Macro-evolution, which refers to large-scale changes that occur over extended time periods,such as the formation of new species and groups.

- Micro-evolution, which refers to small-scale changes that affect just one or a few genes and happen in populations over shorter timescales.

- Micro-evolution and macro-evolution aren't really two different processes. They're the same process.

Evolution - occurring on different timescales. Micro-evolutionary processes occurring over thousands or millions of years can add up to large-scale changes that define new species or group.

Anatomy and embryology.

Darwin thought of evolution as "descent with modification," a process in which species change and give rise to new species over many generations. He proposed that the evolutionary history of life forms a branching tree with many levels, in which all species can be traced back to an ancient common ancestor.

In this tree model, more closely related groups of species have more recent common ancestors, and each group will tend to share features that were present in its last common ancestor. We can use this idea to "work backwards" and figure out how organisms are related based on their shared features.

Homologous features

If two or more species share a unique physical feature, such as a complex bone structure or a body plan, they may all have inherited this feature from a common ancestor. Physical features shared due to evolutionary history (a common ancestor).

To give one classic example, the forelimbs of whales, humans, birds, and dogs look pretty different on the outside. That's because they're adapted to function in different environments. However, if you look at the bone structure of the forelimbs, you'll find that the pattern of bones is very similar across species. It's unlikely that such similar structures would have evolved independently in each species, and more likely that the basic layout of bones was already present in a common.

Some homologous structures can be seen only in embryos. For instance, all vertebrate embryos (including humans) have gill slits and a tail during early development. The developmental patterns of these species become more different later on (which is why your embryonic tail is now your tailbone, and your gill slits have turned into your jaw and inner ear).

Sometimes, organisms have structures that are homologous to important structures in other organisms but that have lost their major ancestral function. These structures, which are often reduced in size, are known as vestigial structures. Examples of vestigial structures include the tailbone of humans (a vestigial tail), the hind leg bones.

Analogous features

Not all physical features that look alike are marks of common ancestry. Instead, some physical similarities are analogous: they evolved independently in different organisms because the organisms lived in similar environments or experienced similar selective pressures.

This process is called convergent evolution. (To converge means to come together, like two lines meeting at a point.)

For example, two distantly related species that live in the Arctic, the arctic fox and the ptarmigan (a bird), both undergo seasonal changes of color from dark to snowy white. This shared feature doesn't reflect common ancestry - i.e., it's unlikely that the last common ancestor of the fox and ptarmigan changed color with the seasons, Instead, this feature was favored separately in both species due to similar selective pressures. That is, the genetically

determined ability to switch to light coloration in winter helped both foxes and ptarmigans survive.

MOLECULAR BIOLOGY

Like structural homologies, similarities between biological molecules can reflect shared evolutionary ancestry. At the most basic level, all living organisms share:

• The same genetic material (DNA)

• The same, or highly similar, genetic codes

• The same basic process of gene expression(transcription and translation)

• The same molecular building blocks, such as amino acids

These shared features suggest that all living things are descended from a

common ancestor, and that this ancestor had DNA as its genetic material, used the genetic code, and expressed its genes by transcription and translation.

Present-day organisms all share these features because they were "inherited" from the ancestor (and because any big changes in this basic machinery would have broken the basic functionality of cells).

Although they're great for establishing the common origins of life, features like having DNA or carrying out transcription and translation are not so useful for figuring out how related particular organisms are. If we want to determine which organisms in a group are most closely related, we need to use different types of molecular features, such as the nucleotide sequences of genes

HOMOLOGOUS GENE

Biologists often compare the sequences of related genes found in different species (often called homologous or orthologous genes) to figure out how those species are evolutionarily related to one another.

The basic idea behind this approach is that two species have the "same" gene because they inherited it from a common ancestor. For instance,humans, cows, chickens, and chimpanzees all have a gene that encodes the hormone insulin, because this gene was already present in their last common ancestor.

In general, the more DNA differences in homologous genes (or amino acid differences in the proteins they encode) between two species, the more distantly the species are related. For instance,human and chimpanzee insulin proteins are much more similar (about 98% identical) than human and chicken insulin proteins (about 64% identical), reflecting that humans and chimpanzees are more closely

BIO-GEOGRAPHY

The geographic distribution of organisms on Earth follows patterns that are best explained by evolution, in combination with the movement of tectonic plates over geological time. For example, broad groupings of organisms that had already evolved before the breakup of the super continent Pangaea (about 200 million years ago) tend to be distributed worldwide. In contrast, broad groupings that evolved after the breakup tend to appear uniquely in smaller regions of Earth.

For instance, there are unique groups of plants and animals on northern and southern continents that can be traced to the split of Pangaea into two super continents (Laurasia in the north, Gondwana in the south)

FOSSIL RECORD

Fossils are the preserved remains of previously living organisms or their traces, dating from the distant past. The fossil record is not, alas, complete

or unbroken: most organisms never fossilize, and even the organisms that do fossilize are rare unique insights into evolution over long timescales.

Fossils document the existence of now-extinct species, showing that different organisms have lived on Earth during different periods of the planet's history.

They can also help scientists control the mosquito populations (and reduce malaria) in these regions.

CHAPTER 2.0

EVOLUTIONARY PRINCIPLES AND THEIR PRACTICAL APPLICATION

Evolutionary principles are now routinely incorporated into medicine and agriculture. Examples include the design of treatments that slow the evolution of resistance by weeds, pests, and pathogens, and the design of breeding programs that maximize crop yield or quality. Evolutionary principles are also increasingly incorporated into conservation biology, natural resource management, and environmental science. Examples include the protection of small and isolated populations from inbreeding depression, the identification of key traits involved in adaptation to climate change, the design of harvesting regimes that minimize unwanted life-history evolution, and the setting of conservation priorities based on populations, species, or communities that harbor the greatest evolutionary diversity and potential. The adoption of evolutionary principles has proceeded somewhat independently in these different fields, even though the underlying fundamental concepts are the same. We explore these fundamental concepts under four main themes: variation, selection, connectivity, and eco-evolutionary dynamics. Within each theme, we present several key evolutionary principles and illustrate their use in addressing applied problems.

Variation

Phenotypic variation determines how organisms interact with their environment and respond to the resulting selection pressures. This variation can come in the form of genetic differences, individual phenotypic plasticity (potential for an organism to produce different phenotypes in different environments), epigenetic changes (gene expression regulated by modification of DNA or histones), maternal effects (phenotype of the mother influences the phenotype of her offspring), and several other forms of non-genetic inheritance (Bonduriansky and Day 2009). Understanding the origins, nature, and maintenance of this variation provides an important

foundation for predicting and interpreting responses to changing environmental conditions.

Phenotypes matter

Modern genetic tools have revolutionized the information available to biologists, but this has caused an increasing tendency to forget that phenotypes, rather than just genotypes, matter (Houle 2010). Phenotypes matter because they are the direct interface with the environment, which is critical in two major respects. First, selection acts directly on phenotypes, with genetic change potentially occurring as an indirect consequence. Second, phenotypes have ecological effects, for example, on population dynamics, on community structure, and on ecosystem function (see section on Eco-evolutionary dynamics). An understanding of phenotypes therefore should precede an understanding of genotypes.

Additional compelling reasons exist to study phenotypes. First, adaptation to a given set of environmental conditions will usually involve many genes, as well as interactions among them (more details are given in the following paragraphs), and so examining only a few genes will not be sufficient for understanding adaptive potential or evolutionary responses. Second, phenotypic variation is structured not only by genes, but also by nongenetic effects. As a result, populations that are phenotypically different for a given trait might be genetically similar with respect to that trait, whereas groups that are phenotypically similar for a given trait might be genetically different with respect to that trait (Conover and Schultz 1995). In addition, adaptive responses to changing conditions can be genetic ('adaptation' in the strict sense), nongenetic (e.g., plasticity), or some combination of the two. For instance, the effect of a given genotype can differ between environments, yielding a genotype-by-environment interaction. A recent example at the genomic level is the demonstration that a particular allele can have opposite phenotypic effects in different Eucalyptus nitens populations (Southerton et al. 2010). Phenotypic traits should thus be considered as 'reaction norms,' which depict the phenotypes expressed by a given genotype (or population or species) across a range of different environmental conditions (Stearns 1989; Gluckman et al. 2009b; Fig. 2). Importantly, these reaction norms can

evolve in response to selection (Stearns and Koella 1986; Olsen et al. 2004; Lande 2009; Crispo et al. 2010

Different phenotypic traits will differ in their relevance to both fitness and ecological processes. An important task is therefore to identify 'key' traits or trait complexes – in broad analogy with the search for limiting factors in ecology (Sih and Gleeson 1995). A standard approach is to measure a set of phenotypic traits (e.g., body size and shape) and to relate variation in these traits to (i) some measure of fitness, such as survival, fecundity, or lifetime reproductive success (Lande and Arnold 1983; Brodie et al. 1995); and (ii) some ecological response (e.g., population growth rate, community richness, and nutrient cycling). These methods can identify traits under strong selection and traits that might have large ecological effects.

Non-genetic changes can be very important – especially on short time scales.

Organisms poorly suited for their local environment can respond adaptively by altering their location to better suit their phenotype (e.g., habitat choice) or by altering their phenotype to better suit their location (e.g., plasticity or evolution). For the former, individuals often avoid newly disturbed areas (e.g., Frid and Dill 2002) and can select areas for which their phenotypes are better suited (review: Edelaar et al. 2008). In many cases, however, such movement is not feasible or sufficient, and so populations must respond in situ. In this latter case, the quickest route to adaptive change will often be individual phenotypic plasticity, particularly behavioral plasticity, or maternal effects (Stearns 1989; Price et al. 2003; West-Eberhard 2003; Ghalambor et al. 2007; Räsänen and Kruuk 2007; Sih et al. 2011).

Congruent with this suggestion, a meta-analysis of phenotypic change in natural populations experiencing environmental change concluded that plasticity was probably very important (Hendry et al. 2008). As a specific example, populations of many species experiencing climate warming now reproduce at earlier dates (Parmesan and Yohe 2003), and a large part of this change reflects individuals responding plastically to increased temperature (Gienapp et al. 2008). This does not mean that genetic change does not contribute to these phenological shifts (Bradshaw and Holzapfel 2008) – merely that plasticity certainly does.

Phenotypic plasticity is not, however, a panacea – because it is subject to a number of limits and costs (DeWitt 1998). Hence, most phenotypic responses to environmental change will ultimately involve both plastic and genetic contributions (Dieckmann and Heino 2007; Visser 2008; Phillimore et al. 2010; Sih et al. 2011; Fig. 3). Variation in humans and domesticated organisms provides nice examples. For instance, lightly pigmented human skin becomes darker under greater exposure to sun, and hemoglobin levels rise at high elevations. At the same time, adaptive genetic differences are present in these same traits: human populations from areas with more sun exposure have genetically darker skin (Jablonski 2004) and human populations living at high elevation have evolved several mechanisms to increase oxygen uptake and transport (Beall 2006). From a reaction-norm perspective, phenotypic variation in these traits reflects both genetic and plastic effects, along with possible genetic variation in this plasticity. These ideas are considered daily in agriculture, where production or quality are maximized by simultaneously seeking the best genetic strains, creating the best environmental conditions (fertilizer, water, pesticides, and herbicides), and finding the best match between genetic strains and environmental conditions.

Selection

Natural selection is the engine that converts variation into evolutionary change. Selection occurs when particular phenotypes/genotypes have higher fitness than others. In well-adapted populations, selection may be relatively weak because most individuals will be near a local fitness peak. As environments change, however, maladaptation is expected to increase and the result can be strong selection and contemporary evolution.

Selection and adaptation can occur at multiple levels

Evolution by natural selection can occur at any level of biological organization, so long as the requisite ingredients are in place: heritable

variation among entities that differ in fitness (Keller 1999). These entities can be species, populations (groups), families, individuals, genes, or alleles. Sometimes selection acts in different directions at different levels, for example, traits that improve individual fitness can arise at the expense of overall population fitness. The tension between levels of selection can play out in a number of ways depending on selection and variation present at each level. These factors often combine in ways that make individual-level selection the most influential for evolution, but this does not mean that the other levels should be ignored.

The relevance of higher-level selection is particularly clear in agriculture and natural resource management. In these contexts, humans often strive to maximize yield, but this can run counter to selection for increased individual competitiveness (Donald 1968; Denison et al. 2003). For instance, competition among individual plants favors larger root systems and larger leaves, but productivity at the population level is maximized at intermediate root and leaf sizes (Schieving and Poorter 1999; Zhang et al. 1999). Cognizance of these trade-offs can improve the design of breeding programs and cultivation methods for evolutionary improvements in yield (Donald 1968; Harper 1977; Denison et al. 2003; Denison 2011). In fisheries, the frequent evolution of smaller size or earlier maturation under intensive harvesting leads to the evolution of life histories that can decrease yield (Conover and Munch 2002; Olsen et al. 2004). The challenge is to design harvest programs that slow, avert, or reverse this yield-impairing evolution (Law and Grey 1989).

Selection overwhelms drift

Populations frequently differ from each other in a number of phenotypic traits and genes. If these differences are the result of genetic drift, they indicate restricted gene flow but little else. If the differences are adaptive, however, they are more likely to (i) trigger protection in conservation efforts (Waples 1991; Smith et al. 1993; Moritz 1994), (ii) influence productivity in agricultural settings (Denison et al. 2003), and (iii) suggest ways to combat pathogens or invasive species. At one level are inferences about whether populations are adaptively divergent in general (i.e., local adaptation). At

another level are inferences about whether and why particular phenotypic differences or changes are adaptive.

Human activities impose particularly strong selection

Humans cause dramatic environmental changes and should therefore impose particularly strong selection. Especially obvious are the many examples of bacteria evolving resistance to antibiotics (Palumbi 2001). As noted by Bergstrom and Feldgarden (2007): 'The evolution of resistance to a clinical antibiotic occurs with near certainty after several years of widespread use'. Human viruses, such as HIV, also evolve resistance to a variety of treatments (Little et al. 2002), as does cancer in response to chemotherapy (Pepper et al. 2009). Insects that are vectors of human diseases, particularly mosquitoes, frequently evolve resistance to insecticides (Hemingway and Ranson 2000; Raymond et al. 2001). Agriculture is rife with analogous situations. Heap (1997) reports '183 herbicide-resistant weed biotypes (124 different species) in 42 countries'. Whalon et al. (2008) list 7747 cases of resistance evolution to 331 compounds in 553 pest arthropod species.