HUMB1060 Evolution of man

Lecture 1 Evolution and taxonomy

Aims

Welcome to the human evolution course. We, the course organisers, hope that you will find it both interesting and enjoyable - but unfortunately before you can really get to grips with the stuff you will need some background theory. That's what today's lecture is all about.

The course is about human evolution. This means that at some stage, preferably fairly early on, you need to have some idea about evolution and it will also be helpful to have some idea about what we mean by "human". The first part of this lecture is an introduction to the central ideas of evolution, and the second half is about how we group animals, so we all know what we are talking about. Discussion about how similar and how different humans are from other animals takes up a lot of the course.

Evolution - change through time

The word "evolution" simply means change through time. It doesn't imply a direction, nor does it imply improvement, merely change In this context evolution refers to the observation that the animals in the world have not always been the same as those that we see around us today. How do we know that this is true?

Evidence - history

We know that distributions of animals change. We have historical records of bears in England 1,000 years ago, and wolves in Scotland in the seventeenth century. Our ancestors hunted wild boar. We find bones in caves including lemming and reindeer with no historical record of either being present here. We have records and stuffed dodos: we have film sequences of the Tasmanian wolf only 50 years old, but there are none around today.

Evidence - fossils and middens

When we look at piles of sediment that have accumulated, in a cave or a rubbish heap for example, we find that the bones present in the top layers are the most similar to what we find today: chicken and rabbit bones would indicate that the rubbish is newer than Roman, because the Romans introduced both species into Britain. These bones just look like - old bones. As you dig deeper bones start to become 'mineralised'. The colour changes and the bones become heavier as the calcium and various other chemicals are dissolved away and replaced by other minerals from the surrounding earth. These bones are older, and it is in these layers that we start to find (in the UK) animals such as hippopotamuses and lions. In a very large column of sediment, the bones found in the lower layers become completely different from those found today: very large cats and elephant like creatures, or whatever.

Clearly, when these sediments were laid down, the fauna was quite different from today: animals were similar, and the range of animals was similar, but the actual animals themselves were noticeably different in form.

In other places, there are rocks that look rather like solidified sediment. We assume that these are columns of sediment that have become solidified over a very long period of time due to various geological processes. These rocks contain very bizarre animals very unlike anything seen today. Sometimes, giant lizard like creatures are common. At other sites, only fish are found even though the current location is miles from the nearest water.

Dating techniques

You may have noticed that I have avoided talking about ages. I've used terms such as "old" and "very old". This is because techniques for dating rocks, fossils and bones accurately are relatively new.

The earliest method of dating is "stratigraphic dating". This follows on directly from the column of sediment. Anything nearer the top is younger than anything further down. This gives you an

idea of the relative ages of rocks, and by estimating the rate of deposition of sediment you can attempt to calculate an absolute age It's not terribly accurate, but it is very intuitive. There aren't any deposits of sediment that cover the whole age of the earth continuously, so that you need to look at the change in the fossils in one deposit, and match them with fossils in other deposits to attempt to build up a full picture.

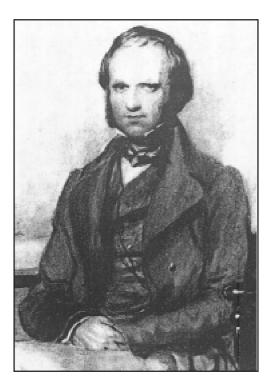
EPOCH	SYSTEM	STRATUM	TYPICAL FOSSILS	-	
QUATERNARY.	13. RECENT		- the second	Irish Elk.	
TERTIARY	II. MIOCENE.		13 RA		
CAINOZOIC.	10. Eocene			Mastodon.	
	9. Cretaceous			1. Univalve (Cerithium). 2. Conifer (Sequoia).	
SECONDARY of Mesozoic.	8. JURASSIC OF OOLITIC		10.	1. Nummulite. 2. Univalve (Natica).	
				 Pearl Mussel (Inoceranius). Ammonite, new form (Turrilites). Bivalve (Pacten). Ammonite, new form (Handtes). 	
	7. TRIASSIC			 Bivalve (Pholadomya). Bivalve (Trigonia). Cycad (Mantellia). Univalve (Nerinica). 	
	6. PERMIAN			 Fish-lizard (Ichthyosaur). Ammonite. Sea-lily (Encrinus). Labyrinthodom. Footprints of Labyrinthoden. 	
PRIMARY or PAL4:0201C and E0201C.	5. Carboniferou	s		1. Bivalve (Bakemellia). 2. Lampshell (Productus). 3. Ganoid (Pateoniscus). 1. Precursors of Animonites (Gonialite).	
	4 Devonian .		5	 Club-moss (Lepidolenieron). Club-moss (Lepidolenieron). Horsetail Plants (Calamite). Ganoid Fish (Pterichthys). 	
				Lampshells { 1. Strophomena. 2. Lingula, 3. Pentamerus. Trilobite 4. Calymene.	
	3. SILURIAN .		2	Senweed (Oldhamia).	
	2. CAMBRIAN . I. LAURENTIAN			Eozoon Canadense 3),	
	eteenth-century illustration		and shows some of the fossils Clodd, 1888. Story of Creation	and shows some of the fossils associated with each period. (From E. Clodd, 1888. Story of Creation. Longmans Green & Co., London.)	

With the discovery of radioactive decay, other more precise dating techniques have become possible. The best known is radioaction dating which works well on organic material and relies on the proportions of a radioactive and non-radioactive form of carbon. For older materials, other radioactive isotopes can be used: potassium, uranium etc. Each series covers a different time scale, and is useful in particular geological circumstances. None are without their problems, but they can give much better estimates of absolute ages than stratigraphy alone. There are also other techniques based on thermo-luminescence, or magnetic field reversals that can be used. Used together, these have provided a widely accepted set of dates for various rock layers and fossil animals.

Controlling Change

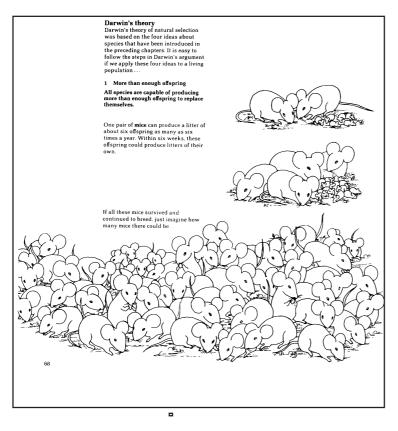
Problems with random change

As I emphasised at the beginning of this lecture. Evolution doesn't imply improvement, or any sort of direction itself. Merely change. However, from our examination of the fossil record, it is clear that animals and plants have become a great deal more sophisticated over the years, and it certainly seems that more recent variations have a tendency of replacing earlier versions. Very many varieties no longer exist - indeed the average "life span" for a species seems to be of the order of a few million years. From various mathematical considerations, it seems highly unlikely that all this change can occur purely by chance. Fortunately, Charles Darwin came up with a



There is a grandeur in this view of life, with its several powers, having been originally breathed by the Creator into a few forms or into one; and that, whilst this planet has gone cycling on according to the fixed law of gravity, from so simple a beginning endless forms most beautiful and most wonderful have been, and are being *evolved*.

Charles Darwin: The Origin of Species



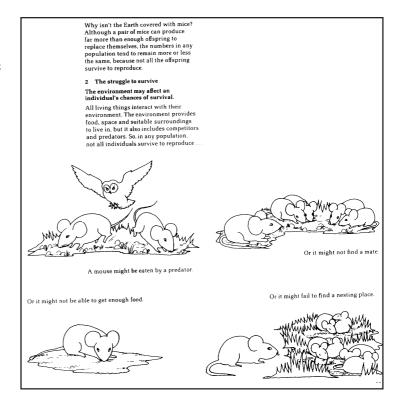
mechanism that explains the apparent direction of evolution extraordinarily well, although he only used the term once, on the last page of 'Origin of the Species'

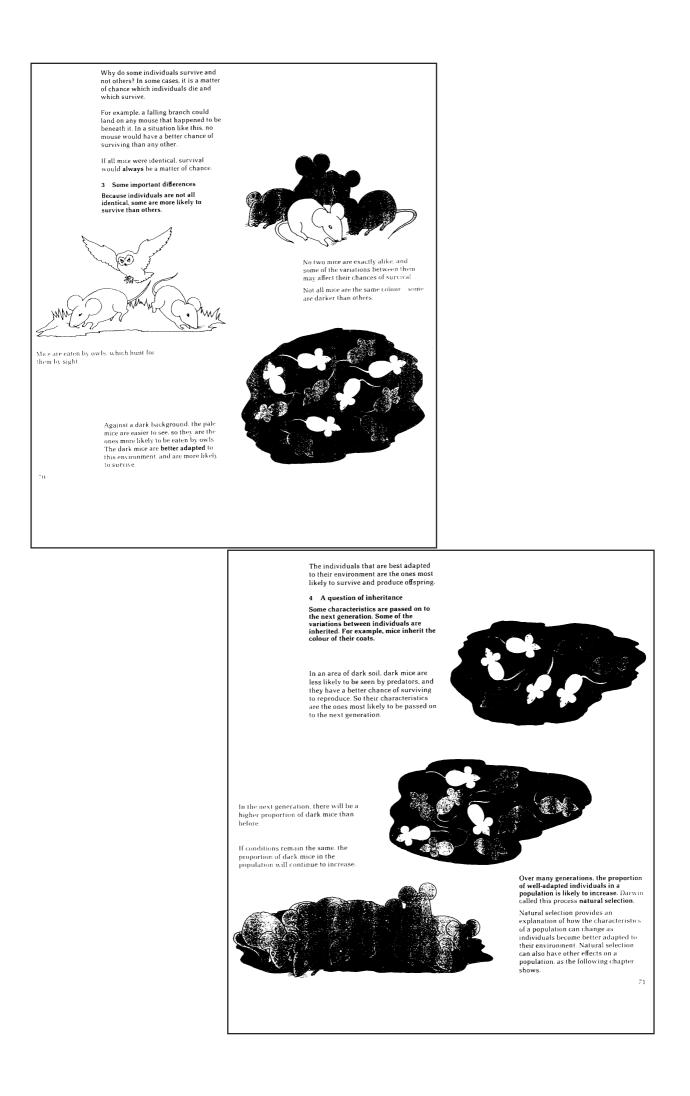
Natural selection

The Darwinian argument, "Evolution by natural selection", is extremely clever, and nowadays seems almost self-evident or even circular: who but the fittest would you expect to survive?. It is based on empirical observations of natural history and is

supported by a wealth of evidence.

However, it is now thought that although a large proportion of genetic diversity can be ascribed to natural selection, random genetic drift plays an important non-directed role since certain features show variation without any fitness change. In addition with the discovery of entities like retroviruses that incorporate their DNA into the host genome, it is clear that there are other mechanisms that act directly at a genetic level.





Classification

Classification is simply the ordering of organisms into groups, and giving them names. Before anyone was particularly bothered about evolution, this tended to be a very simple exercise: we'll put all animals that swim in one group (fish & whales); flying animals in another (bats & birds); and the ones that climb trees (monkeys & squirrels). Linnaeus expanded on this a little by using more than one characteristic in his groupings and thus the binomial naming of genus+species we use today (man, for example is *Homo sapiens*), but nevertheless, there was always dispute about how to produce a "natural" grouping

When evolution became accepted, it became clear that the obvious way of grouping organisms was by their evolutionary relationship - a huge family tree, if you like, showing how the various animals have descended from common ancestors and grouped accordingly.

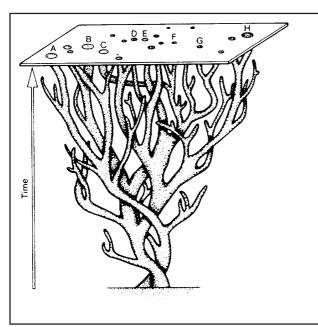
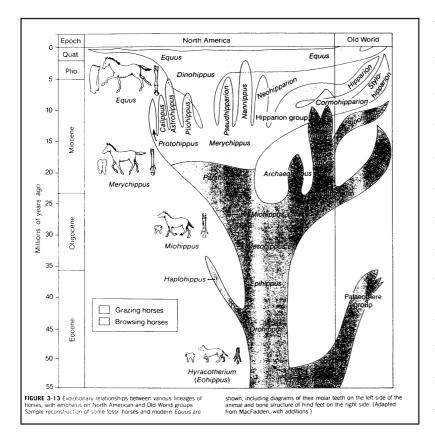


FIGURE 11-7 Diagram of a phylogenetic tree of related populations shown as continuous branches undergoing evolutionary changes through time. Some populations have become extinct, and others have merged or diverged to produce new and different forms. If we consider time as the vertical axis in this illustration, distances along the x and y axes might indicate measurements of different genetic traits. Thus, the differences between some populations, such as A and H at the present time level (top of figure), may be sufficiently great to warrant separate taxonomic designations, whereas others (e.g., D and E) may not yet be taxonomically distinct. Note also that there may be convergences between two separate lineages (e.g., B and C) in respect to the measured traits, which can conceal their evolutionary separation. (Adapted from Levin.)

Phylogenetic reconstruction

This, then, is the goal. But how do we achieve it? The best/easiest way is to look at the fossil record and find all the ancestral groups. This is precisely what has been done for horses.



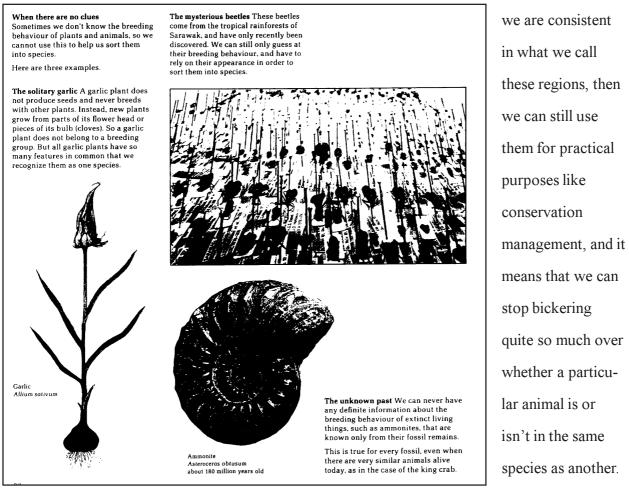
Unfortunately, this is normally not possible because for most animals, there are either just not enough fossils available for this sort of analysis or too many different survivors, making an impenetrable bush instead of a neat tree. There are other problems too. Although a family tree is a natural way of grouping organisms, we still need to decide on what we are going to use as the smallest group. The answer to

this (usually), is the species, but this begs the question:

What is a species?

Generally, a species is defined as a sexually interbreeding (or potentially interbreeding) group of individuals normally separated from other species by the absence of genetic exchange. This is the species concept". This is fine, in theory, but in practice, there are problems Group A can mate with group B and produce offspring. Group B can mate with group C and produce offspring, but group A and group C can't mate. In addition it doesn't help define what a species is for fossil animals where mating can't be observed. And finally, it is no help for defining species in organisms that don't reproduce sexually. A number of other species definitions have been postulated to overcome these problems, but none of them are perfect.

My personal view is that the concept of a species is a completely arbitrary construct that humans have created. Organisms can be thought of as a continuum of genetic variation, and we use species as a way of naming regions in that continuum for our own convenience. The size of these regions is roughly consistent, but there is definitely overlap at the edges, or even gaps. As long as

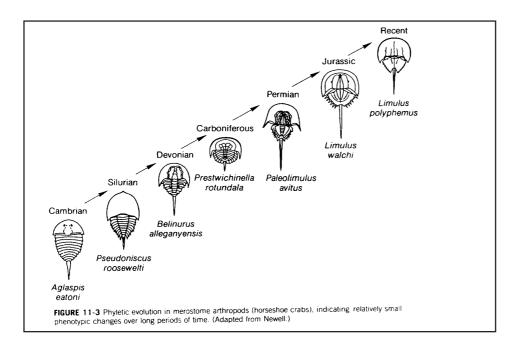


The concept of a

species is OK, just remember that it tends to be fuzzy round the edges.

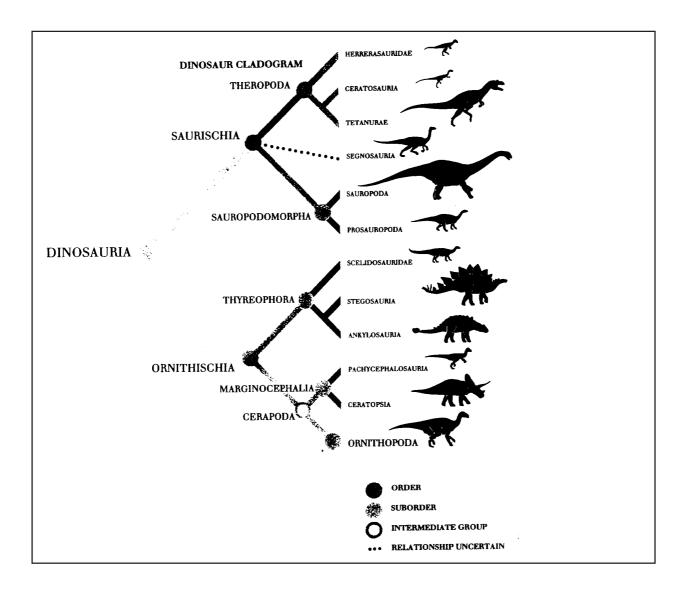
Practical Reconstruction of the family tree

Firstly, evolution (change over time) doesn't have to lead to a branching pattern. A single group can change gradually without splitting into two distinct groups. This process is called Anagenesis.



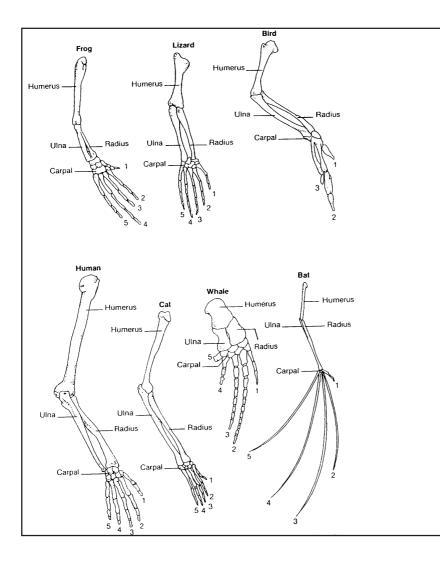
However, the much more interesting problem is the reconstruction of the branching pattern, where species split into two or more groups. This is called Cladogenesis and is what gives us our family tree.

Determination of phylogenetic trees is difficult in practice because the common ancestors are usually long extinct and the fossil record is inadequate. However, the relationship can be inferred



by looking at common, inherited characteristics: the more morphological, embryological, behavioural, physiological, biochemical, genetic and chromosomal inherited characteristics that organisms have in common, the more likely they are to have descended from a common ancestor. Studying things in common gives us a phenetic classification. Merely sharing common features is not enough since they may derive from different evolutionary causes:.

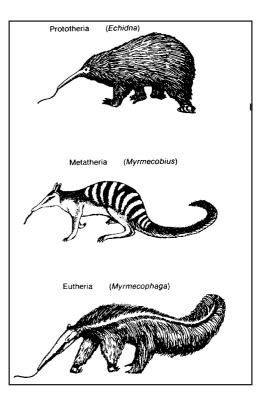
1. Homology



This is what we want, the best classification. The feature is shared because it derives directly from a common ancestor. For example the bony features of the forelimbs in vertebrates.

2. Parallelism

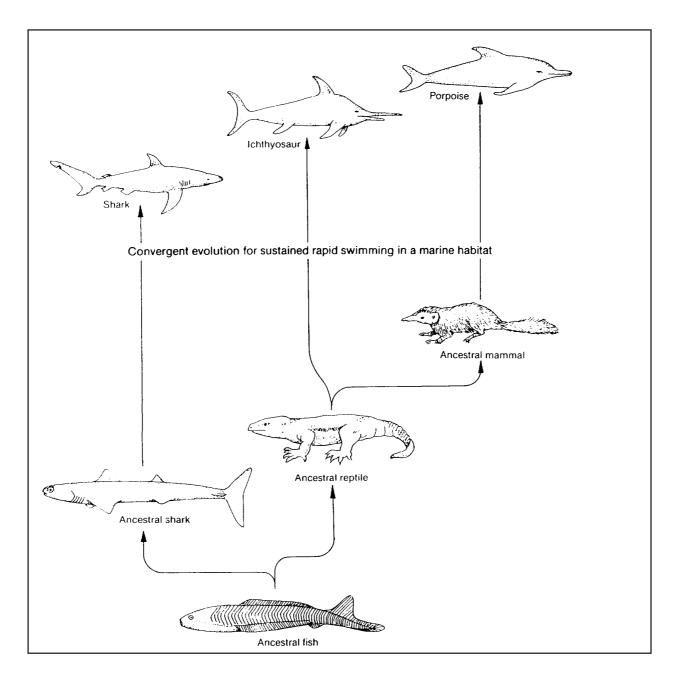
The similar feature occurs in different species, but it is not present in their immediate common ancestor. For example, anteater-like features in various different mammalian lineages These shared features are very much functional adaptations.



3.Convergence

Similar to parallelism, but the ancestral lineages differed for a considerable period of time. For example vertebrate and octopus eyes, or the hydrodynamic morphology of marine predators from the widely separated fish, reptile and mammalian classes

In Practice



Obviously, homologies are what we need to consider to reconstruct phylogenies. However, they are not always easily separated from the other two. Consider the convergence example: the shape of the pectoral fins in these animals is very similar due to convergence. However, there is a great deal of homology there two. Especially between the reptile and the mammal due to a common

land vertebrate ancestor.

Problems

Taxonomy isn't only for evolutionary reconstruction. We need fairly stable names and grouping for practical purposes such as conservation. Groupings make animals easier to remember and identify, and we don't want it all to change every time someone decides that actually humans are closer related to chimpanzees than chimps are related to gorillas. This means that official naming schemes tend to lag somewhat behind the current thrust of research. There is quite a bureaucracy preventing everyone from renaming animals at a whim, and there are international efforts to try and maintain some consistency. Even so, there are generally several alternative classification schemes around for groups of animals that seem to last about 5 years until the next big name in a particular field writes the latest review paper on that specific taxonomy. A good text book will tell you which scheme it is using, and a really good textbook will list several alternatives so you can make up your own mind.

Summary

1. Evolution happens. There is very good evidence for change in the life forms that inhabit the earth over long periods of time.

2. Charles Darwin's theory about the origin of species through natural selection explains the apparent direction of evolutionary change extremely well. It is probably one of the most widely accepted theories in modern biology.

3. For practical purposes, we need to group animals. Animals that can interbreed are grouped as species. Species are grouped in a tree structure that more or less attempts to mimic the evolutionary process. We attempt to use the interbreeding idea for extant animals, but for fossil forms we use similarity in shape.

4. Unfortunately, every scientist has their own personal preference when it comes to classification. That's life!