Zoogeography Lesson 13



#### Journal club topics:

Title and references	Student
New developments in the field of genomic technologies and their relevance to conservation management. https://doi.org/10.1007/s10592-021-01415-5	
Chapter 7, case study: The Hawaiian Islands	Emelie
Life history, climate and biogeography interactively affect worldwide genetic diversity of plant and animal populations. https://www.nature.com/articles/s41467-021-20958-2	
Animal invaders threaten protected areas worldwide. https://doi.org/10.1038/s41467-020-16719-2	
Urbanization and agricultural intensification destabilize animal communities differently than diversity loss. https://doi.org/10.1038/s41467-020-16240-6	
Low level of anthropization linked to harsh vertebrate biodiversity declines in Amazonia https://doi.org/10.1038/s41467-022-30842-2	
Factors shaping the abundance and diversity of the gut archaeome across the animal kingdom https://doi.org/10.1038/s41467-022-31038-4	

The final biogeographical step towards the appearance of a new species occurs when hybrids between the two independent populations are found only along a narrow zone where the two populations meet.

although continued interbreeding within this zone can produce a population of hybrids, these hybrids cannot compete elsewhere with either of the pure parent populations.

Nevertheless, 25% of plant species and 10% of animal species are known to hybridize, and the number of cases known in animals is growing rapidly.

where a species has been extending its range and, in the process, has had to adapt to new environments, we can see the resulting pattern of evolutionary change laid out on the landscape as a pattern of biogeography.

In a few cases, the end-products of that process have come into contact and demonstrated the extent of the genetic change by refusing to mate with one another: they have evolved into separate species, known as **ring species**.

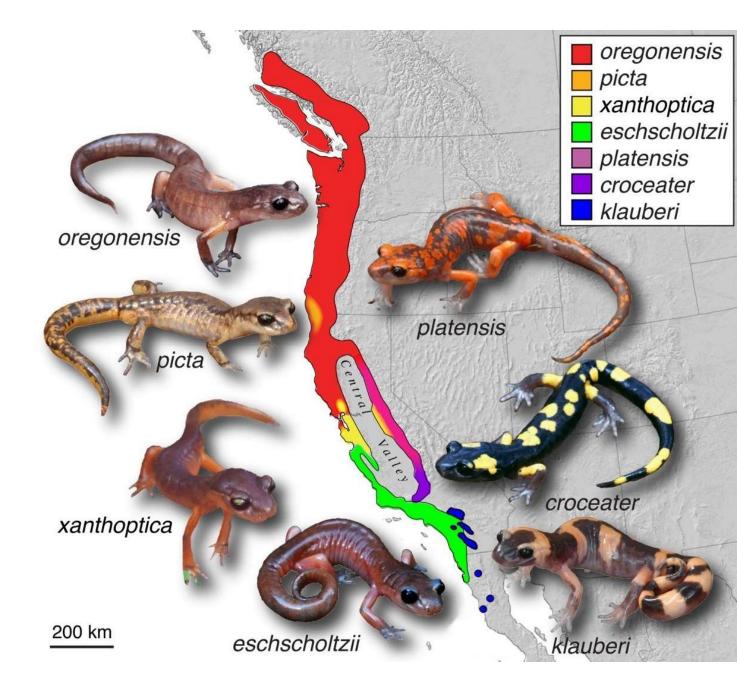
*Ensatina oregonensis* living in Washington State and Oregon, which spread into northern California,

where it formed the new species *Ensatina eschscholtzii*.

As this species continued to spread southward, encircling the hot lowlands of the San Joaquin Valley, it developed populations with different genetic constitutions.

One result of this was that the populations had different colour patterns.

because these populations were able to interbreed with one another, they were recognized as separate subspecies of the single species E. eschscholtzii (E. e. picta, E. e. platensis etc.).



There is no general rule as to the length of time that it will take for the descendants of one original species to diverge so far from one another in their genetic constitution that they have become separate species.

The most important factor in determining the rate of genetic change is the speed at which the environment changes. If it changes rapidly, the organism must also change rapidly or else become liable to extinction.

But the rate at which an organism can respond is also dependent on population size.

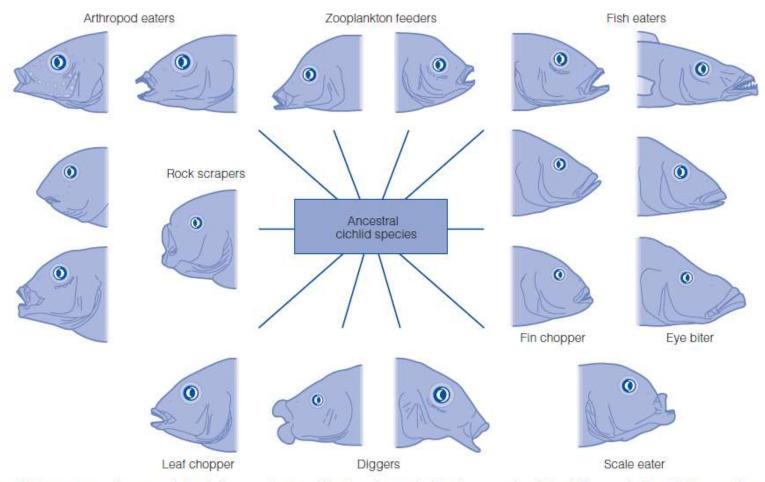
In a <u>small population</u>, the random effect of genetic drift may by chance produce a new mixture of genetic characteristics that match the new requirements of the environment.

This is less likely to happen in a <u>larger population</u>, where the sheer size of the gene pool makes rapid evolutionary change of this kind less likely.

## Sympatry versus Allopatry

In all the examples considered so far, it has been assumed that the divergence between the populations as they evolved into separate species took place in isolation from one another, a situation known as **allopatric speciation** (from Ancient Greek  $\ddot{\alpha}\lambda\lambda\sigma\varsigma$  (állos) 'other', and  $\pi\alpha\tau\rho\iota\varsigma$  (patrís) 'fatherland').

new species can also arise by **sympatric speciation**, within the area of distribution of the ancestral species.



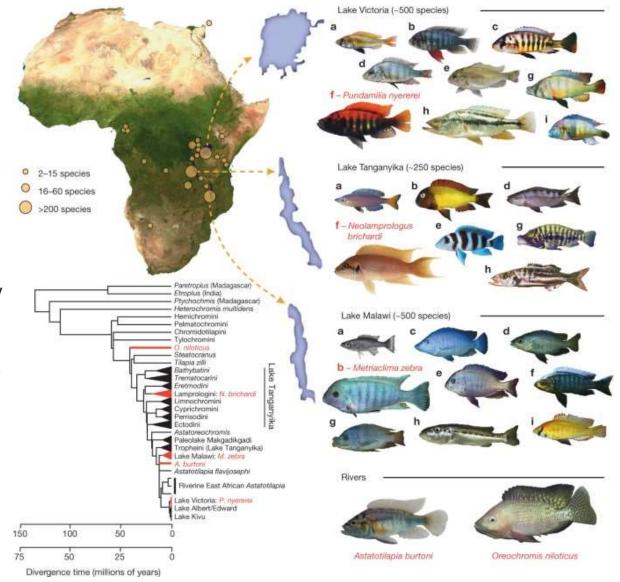
**Figure 6.3** A selection of the different shapes of head and mouth that have evolved for different feeding habits in the cichlid fishes in Lake Malawi. Adapted from Fryer and Iles [7].

- Genetic mechanisms for post-mating isolation are frequently weak or absent in these fishes

- they are mainly brightly coloured and it is present evident dimorphism.

- The waters of the lake contain suspended particles that absorb particular wavelengths of light. As a result, blue colours that are clearly visible in the surface waters become increasingly unclear at greater depths, where red colours instead are more visible.

- in fish that live close to the surface, where blue is more visible, the fish themselves are blue and their visual pigment is more sensitive to that colour. In those that live at greater depths, where red is more visible, the fish are red and their visual pigment is more sensitive to that colour.

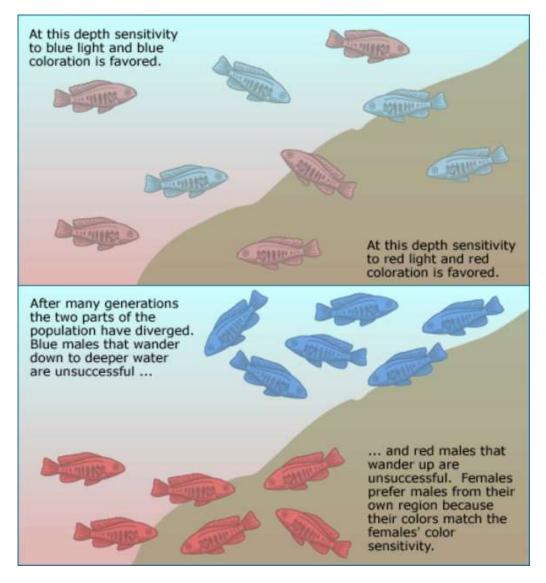


https://doi.org/10.1038/nature13726

As long as the rate of change in the relative visibility of the colours changes gradually with depth, these differences in the environment and in the genetics and mating preferences of the fish are sufficient **to keep the** different **populations genetically separate**.

where there is a more rapid change in relative visibility, so that the two populations encounter each other more frequently, they **interbreed** with one another, forming a single population within which **both types of visual pigment are to be found.** 

This type of evolutionary change, associated with differences in the sensory systems and behaviour, has been called **sensory drive** 



The fish need good visibility in order for the females to be able to see the colour of male that they prefer, but recent changes in their environments are making this more and more difficult.

Because of increasing human activity around Lake Victoria, nutrients and silt are draining into the lake from surrounding farmland, together with sewage from urban settlements,

causing turbidity and poor light penetration in the waters.

Human activity could thus bring the diversification of fish in this lake to a halt

### Darwin's finches



Figure 6.5 Galápagos ground finches with beaks of different size: from left to right, *Geospiza magnirostris*, *Geospiza fortis*, *Geospiza fuliginosa* and *Geospiza difficilis*.

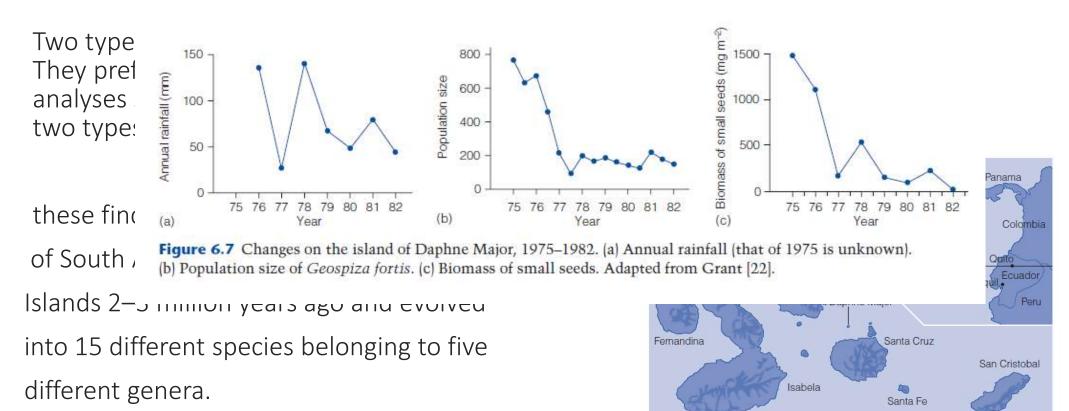
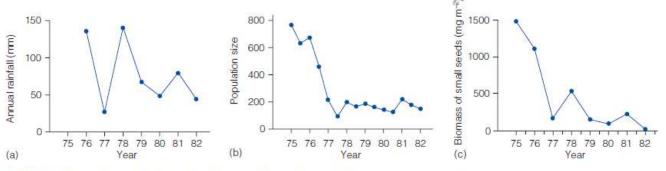


Figure 6.4 Map of the Galápagos Islands.

50 km



**Figure 6.7** Changes on the island of Daphne Major, 1975–1982. (a) Annual rainfall (that of 1975 is unknown). (b) Population size of *Geospiza fortis*. (c) Biomass of small seeds. Adapted from Grant [22].

1983: the year of the strongest 20th-century El Niño event; the rainfall was 10 times the previously known maximum. The island was drenched, and its plants grew rampantly – by June, the total mass of seeds was almost 12 times greater than in the previous year.

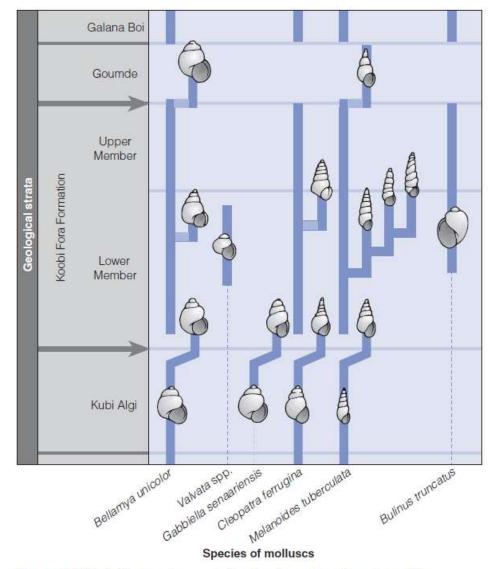
This time, small soft seeds predominated – they formed up to 80% of the total mass of seeds, up to 10 times more than the previous maximum.

By June, there were more than 2000 ground finches on the island, the numbers of *G. fortis* having increased by more than four times.

984 there was only 53 mm of rain, and in 1985 only 4 mm.

Now there was a new episode of drastic selection, but in the opposite direction from that which had followed the drought of 1973. Now it was selecting smaller birds, with smaller beaks, more suited to eating the plentiful smaller seeds.

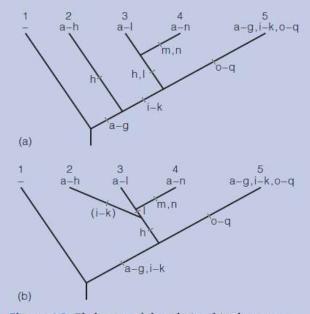
the periods of change took place in several lineages at about the <u>same time</u> suggests that they were the <u>result of</u> <u>external events</u> that affected all of them, rather than resulting from some inherent evolutionary mechanism



**Figure 6.8** Evolutionary changes in fossil gastropod molluscs in northern Kenya. The arrows indicate the levels at which sudden evolutionary changes took place simultaneously in several different species. From Dowdeswell [23].

#### **Cladistics and parsimony**

First of all, Hennig tried to identify a group of taxa that were all related to one another, sharing a common ancestor and including all its descendants. Such a lineage is known as a **clade**. He then treated the process of evolutionary change in this clade as a series of branching events, or 'dichotomies', at each of which a single group divides into two daughter groups. At each dichotomy, known as a *node*, one or more of the characteristics of the group changes from the original ancestral or **plesiomorphic** state into a derived or **apomorphic** state. The plesiomorphic characters are recognized by comparison with an *outgroup*, which is closely related to the lineage being studied but not a part of it. The evolutionary history of the group can then be portrayed as a branching **cladogram**. Thus, in Figure 6.9, characters a–g evolved after the divergence between group 1, which is the outgroup, and groups 2–5. They are therefore derived, or apomorphic, relative to the characters of group 1 (in which these characters have remained primitive, or plesiomorphic), but plesiomorphic for groups 2–5. Other new, apomorphic characters then evolved at different points within the evolutionary history of groups 2–6 and can therefore be used to analyse their patterns of relationship.



**Figure 6.9** Cladogram of the relationships between five groups, using characteristics a to q. The positions at which characters were lost are shown in brackets.

# Willi Hennig:



In constructing a cladogram, the characters shown by the different taxa are listed, and the taxa are then arranged so that those that show a similar set of characters are placed in adjacent positions on the branching 'tree'. As far as possible, it is assumed that each apomorphic evolutionary event only occurred once in the history of each group of related taxa (a concept known as economy of hypothesis, or **parsimony**), and the taxa are arranged on the cladogram in such a way as to minimize the number of parallelisms. For example, in Figure 6.9 it is most parsimonious to believe that character h, which is absent in group 5, has evolved twice, because that involves the assumption of only that single additional evolutionary event (Figure 6.9a). The alternative is to transfer the origin of group 2 to near the base of groups 3–4, with the consequent need to assume that characters i-k had been lost in the evolution of group 2 (shown in brackets) - an assumption of three additional evolutionary events, instead of only one (Figure 6.9b).



