From one gene pool to two

Evolution changes allele frequencies across generations. Speciation produces new species from pre-existing ones; evolutionary change does not always result in speciation.

1. DEFINE THE BIOLOGICAL BOUNDARY

For sexually reproducing organisms, the biological species concept groups populations that can interbreed naturally and produce viable, fertile offspring. Reproductive isolation prevents effective gene flow between groups. Looking different, or living far apart, is not enough to establish a new species.

2. ALLOPATRIC SPECIATION: GEOGRAPHICAL SEPARATION

A. A BARRIER REDUCES GENE FLOW

A river, mountain barrier or colonisation of an isolated island separates populations. Whether a barrier works depends on the organism's ability to disperse and breed.

B. THE SEPARATED GENE POOLS DIVERGE

New mutations, genetic drift and different selection pressures can change allele frequencies independently. Differences can accumulate across generations.

C. REPRODUCTIVE ISOLATION EVOLVES

If the groups meet again, they may no longer exchange genes successfully: mating may not occur, or hybrids may have reduced viability or fertility.

3. SEPARATION IS A START, NOT A GUARANTEE

If populations reconnect before reproductive barriers evolve, gene flow may resume. Geographical isolation does not automatically mean speciation has occurred.

Species and allopatric divergence: OpenStax, Biology 2e 18.2.
Reproductive isolation as a process: University of Minnesota, Speciation.

Scope: Cambridge Biology 9700, section 17.3, outcomes 1-3, p. 44.

Different gene pools, same area

Sympatric speciation occurs without an initial geographical barrier. Ecological differences or mating behaviour can restrict gene flow within the same geographical area.

1. TWO WAYS TO REDUCE INTERBREEDING

ECOLOGICAL SEPARATION

Groups use different resources or breeding habitats. If they mate in those habitats, individuals encounter and breed mainly within their own group.

BEHAVIOURAL SEPARATION

Differences in courtship signals and mate preferences cause individuals to mate mainly with others sharing the same signals.

Example mechanisms: insects mating on different host plants; birds responding to different courtship songs. These are illustrations, not proof of completed speciation.

2. LINK ISOLATION TO GENETIC DIVERGENCE

Reduced interbreeding limits the mixing of alleles. Selection may favour different traits in different niches, while mutation and drift also contribute to divergence. Reproductive barriers can strengthen over time; a habitat preference alone does not demonstrate that two species exist.

3. REPRODUCTIVE BARRIERS CAN ACT AT TWO STAGES

Before fertilisation: different habitats, breeding times or courtship signals can prevent mating; incompatible gametes may prevent fertilisation.
After fertilisation: a hybrid may fail to develop normally or may survive but be infertile.

Shared outcome: the groups maintain distinct gene pools. The key contrast is how isolation starts, not whether natural selection is present.

Mating barriers and sympatric speciation: University of Minnesota, Speciation.
Ecological and behavioural separation: Cambridge 9700, 17.3.3.

Scope: Cambridge Biology 9700, section 17.3, outcomes 1-3, p. 44.

Read the evidence for ancestry

Related species inherit DNA from a common ancestor. Comparing corresponding sequences helps infer relationships, especially when many independent regions support the same pattern.

1. ALIGN CORRESPONDING DNA REGIONS

A	ATGCCATTGAAC
B	ATGCCACTGAAC
C	ACGTCATCGAAT

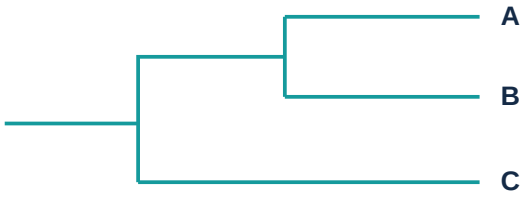
Differences in 12 aligned bases

A-B: 1

A-C: 4

B-C: 5

A and B are most similar in this artificial example. This supports a closer relationship, but a short fragment alone is weak evidence. Compare homologous regions and use much more sequence data.



Assume C is an independently identified outgroup. A and B share the more recent branching point. Branch lengths here do not measure time or change.

2. INTERPRET SIMILARITY CAUTIOUSLY

Fewer differences often indicate a more recent common ancestor, but mutation rates vary and a site can change more than once. One gene may give an incomplete picture. A tree is a testable hypothesis about ancestry, not a ranking from primitive to advanced.

3. USE OTHER EVIDENCE AS SUPPORTING CONTEXT

Protein amino acid sequences can also be compared. Homologous structures share an inherited underlying pattern, even when functions differ. Fossils document past forms and change through time, but preservation is incomplete. Similar function alone may reflect convergent evolution rather than close ancestry.

Core: DNA evidence; fossils, proteins and anatomy provide supporting context.

DNA-to-tree method: HHMI BioInteractive, Creating Phylogenetic Trees.
Sequence interpretation: OpenStax, Determining Evolutionary Relationships.
Fossils and comparative anatomy: OpenStax, Biology 2e 18.1.

Scope: Cambridge Biology 9700, section 17.3, outcomes 1-3, p. 44.