BIOZONE

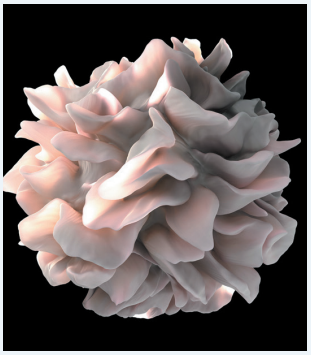
# AP BIOLOGY

SAMPLE PACKET
FOR CLASSROOM TRIAL

UNIT 2

# Cell Structure and Function

## Learning Objectives



### Developing understanding

**CONTENT:** This unit explores cells as the units of life. How do cells contribute to the organization of life and provide the environment in which organelles can function? Cells and cellular organelles have membranes that enable them to establish and maintain an internal environment and control exchanges with the external cellular environment. The maintenance of internal and external cellular environments is called homeostasis. An understanding of the principles of cellular homeostasis is important to understanding the material in the units that follow.

**SKILLS:** This unit emphasizes skills in explaining the relationships between structure and function of organelles and cellular components on the subcellular and cellular levels. You should become proficient in describing data, making calculations, and analyzing different types of data.

### 2.1 Cell structure: subcellular components ..... activities 16 - 21

☐ 1. Describe the structure and/or function of subcellular components and organelles to include ribosomes, rough and smooth endoplasmic reticulum (ER), the Golgi complex, mitochondria, lysosomes, vacuoles, and chloroplasts.

### 2.2 Cell structure and function..... activities 16 - 21

☐ 2. Explain how subcellular components and organelles contribute to cell function with reference to ER, mitochondria, lysosomes, and vacuoles.

☐ 3. With reference to membrane infolding in prokaryotes, and chloroplasts and mitochondria in eukaryotes, describe the structural features of a cell that allow organisms to capture, store, and use energy.

### 2.3 Cell size ..... activities 22 - 25

☐ 4. Explain the effect of surface area-to-volume ratios on the exchange of materials between cells or organisms and the environment. Describe the strategies and specializations of organisms that increase the efficiency of these exchanges.

### 2.4 Plasma membranes..... activity 26

☐ 5. Describe the components of the plasma (cell) membrane, including phospholipids and proteins, and their roles in maintaining the internal environment of the cell. Describe the fluid mosaic model of membrane structure and explain how this model explains membrane behavior.

### 2.5 Membrane permeability ..... activities 27 - 28

☐ 6. Explain how the selective permeability of cell membranes is a direct consequence of membrane structure. Which molecules pass freely across the membrane and which move across through channel and carrier proteins?

☐ 7. With respect to prokaryotes, plants, and fungi, describe the role of the cell wall in maintaining cell structure and function.

### 2.6 Membrane transport ..... activities 29, 34 - 36

☐ 8. Describe the mechanisms that organisms use to maintain solute and water balance, including the distinction between passive and active transport.

☐ 9. Describe how organisms transport large molecules across the plasma membrane. Include reference to how selective permeability allows for the formation of concentration gradients across the membrane, and how endocytosis and exocytosis enable movement of materials into and out of the cell using energy.

### 2.7 Facilitated diffusion ..... activity 29

☐ 10. Using examples, explain the role of membrane proteins in the facilitated diffusion of large polar molecules and ions across the plasma membrane. Contrast facilitated diffusion with active transport processes, which also involve membrane proteins, but require the expenditure of energy (e.g. the $Na^+/K^+$ ion pump, which maintains membrane potential).

### 2.8 Tonicity and osmoregulation..... activities 29 - 33

☐ 11. Explain how external environments can be hypotonic, hypertonic, or isotonic to the internal environment of the cell. Explain the components of water potential and use water potential to explain the movement of water into and out of cells by osmosis.

☐ 12. Using examples, explain the role of osmoregulation in the health and survival or organisms. Examples could include the contractile vacuoles of protists and the vacuoles of plants. Determine the solute potential (osmolarity) and water potential of plant cells (e.g. potato cells) through investigation and calculation ($\psi_s = -iCRT$).

### 2.9 Mechanisms of transport ..... activities 29, 34 - 36

☐ 13. Summarize the passive and active transport processes that enable ions and other molecules to move across membranes. Include reference to diffusion osmosis, facilitated diffusion, primary active transport (e.g. the $Na^+/K^+$ pump) and secondary active transport (e.g. the $Na^+$/glucose co-transporter), endocytosis, and exocytosis.

### 2.10 Compartmentalizaton..... activity 37

☐ 14. Describe the membrane-bound structures of eukaryotic cells and explain their role in providing cellular compartments within which specific reaction sequences can occur. Explain how the process of compartmentalization improves the efficiency of cellular functions.

### 2.11 Origins of cell compartments ..... activity 38

☐ 15. Describe similarities and/or differences in compartmentalization in prokaryotic and eukaryotic cells and comment of the significance of these similarities/differences. Outline the endosymbiotic theory for the origin of cellular organelles in eukaryotes and describe the evidence for it.

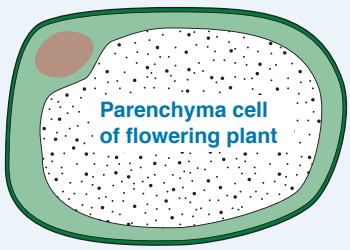
☐ 16. Describe the relationship between the functions of eukaryotic cellular organelles (specifically chloroplasts and mitochondria) and their free-living ancestral counterparts.

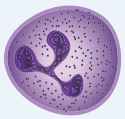
# 22 Cell Sizes

**Key Question**: How do different types of cells vary in size?

Different types of cells have different sizes. Eukaryotic cells are much larger than prokaryotic cells, but even they vary widely in size. Cells also have different shapes. Many have no fixed shape, but others have shapes approximating spheres, e.g. *Streptococcus,* cylinders, e.g. *E. coli*, or rectangular prisms, e.g. plant cells. The volume of these cells can then be estimated using the appropriate formula for their shape.

## Typical sizes of cells and viruses

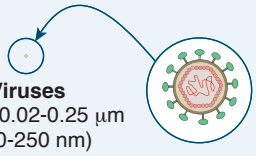


Human white blood cell

**Eukaryotic cells**
(e.g. plant and animal cells)
**Size**: 10-100 μm diameter.
Cellular organelles may be up to 10 μm.

**Prokaryotic cells**
**Size**: Typically 2-10 μm length, 0.2-2 μm diameter.
Upper limit 30 μm long.



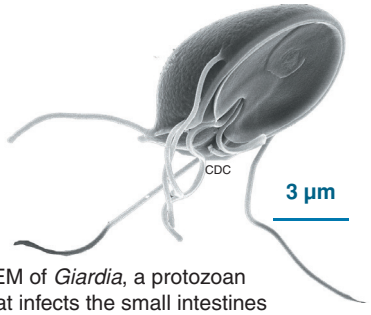
**Viruses**
**Size**: 0.02-0.25 μm (20-250 nm)

| Unit of length (international system) | | |
|---|---|---|
| **Unit** | **Meters** | **Equivalent** |
| 1 meter (m) | 1 m | = 1000 millimeters |
| 1 millimeter (mm) | $10^{-3}$ m | = 1000 micrometers |
| 1 micrometer (μm) | $10^{-6}$ m | = 1000 nanometers |
| 1 nanometer (nm) | $10^{-9}$ m | = 1000 picometers |

Micrometers are sometimes referred to as microns. Smaller structures are usually measured in nanometers (nm) e.g. molecules (1 nm) and plasma membrane thickness (10 nm).

1.0 mm

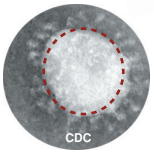
*Daphnia* is a small crustacean found as part of the zooplankton of lakes and ponds.




SEM of *Giardia*, a protozoan that infects the small intestines of many vertebrate groups.

50 μm

*Paramecium* is a protozoan commonly found in ponds.

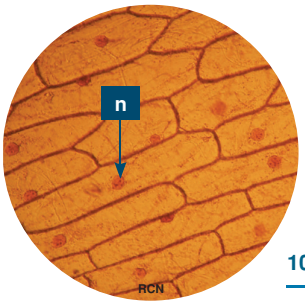



*Coronavirus* is the virus responsible for SARS.

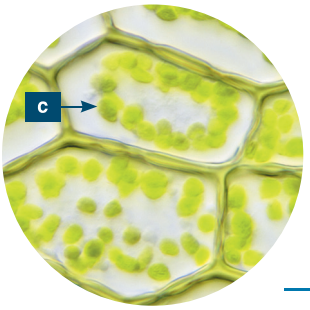
10 nm

10 μm


*Salmonella* is a bacterium found in many environments and causes food poisoning in humans.




Onion epidermal cells: the nucleus (n) is just visible.

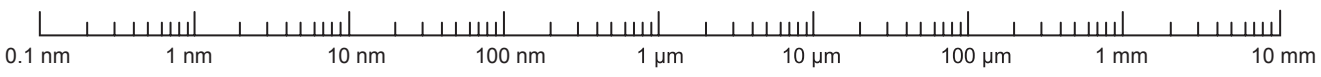



Mosses are low growing primitive plants. In these cells, the chloroplasts (c) can be seen, mostly around the cell edges.

1. Using the measurement scales provided on each of the photographs above, determine the longest dimension (length or diameter) of the cell/animal/organelle indicated in μm and mm. Do not include cilia or flagella. Attach your working:

| | | | | | |
|---|---|---|---|---|---|
| (a) *Daphnia*: | _____ μm | _____ mm | (e) Chloroplast: | _____ μm | _____ mm |
| (b) *Giardia*: | _____ μm | _____ mm | (f) *Paramecium*: | _____ μm | _____ mm |
| (c) Nucleus | _____ μm | _____ mm | (g) *Salmonella*: | _____ μm | _____ mm |
| (d) *Elodea* leaf cell: | _____ μm | _____ mm | (h) *Coronavirus*: | _____ μm | _____ mm |

2. Mark and label the examples above on the log scale below according to their size:







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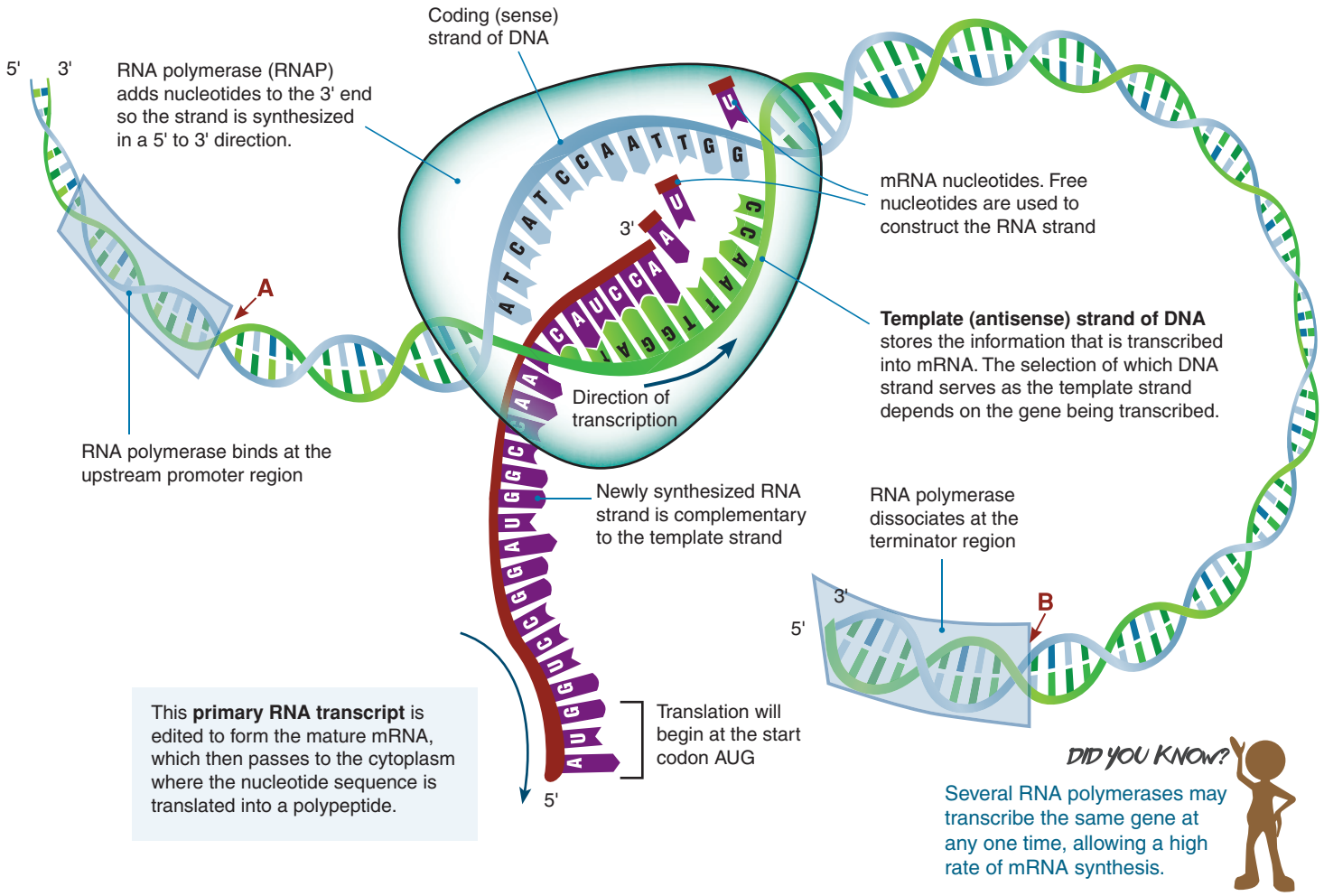
# 116 Transcription in Eukaryotes

**Key Question**: What is the purpose of transcription, where does it occur, and what are the key steps in the process?

Transcription is the first stage of gene expression. It takes place in the nucleus and is carried out by the enzyme RNA polymerase, which rewrites the DNA into a primary RNA transcript using a single template strand of DNA. The protein-coding portion of a gene is bounded by an upstream start (promoter) region and a downstream terminator region. These regions control transcription by telling RNA polymerase where to start and stop transcription. In eukaryotes, non protein-coding sections called **introns** must first be removed and the remaining **exons** spliced together to form the mature mRNA before the gene can be translated into a protein. This editing process also occurs in the nucleus.

## Transcription is carried out by RNA polymerase (RNAP)




**DID YOU KNOW?**

Several RNA polymerases may transcribe the same gene at any one time, allowing a high rate of mRNA synthesis.

1. (a) Name the enzyme responsible for transcribing the DNA: _____

   (b) What strand of DNA does this enzyme use? _____

   (c) Is the code on this strand the same as or complementary to the RNA being formed: _____

   (d) Which nucleotide base replaces thymine in mRNA? _____

   (e) Explain what is represented by points **A** and **B** on the diagram: _____

   _____

2. (a) In which direction is the RNA strand synthesized? _____

   (b) Explain why this is the case: _____

   _____

3. (a) Why is AUG called the start codon? _____

   (b) What would the three letter code be on the DNA coding strand? _____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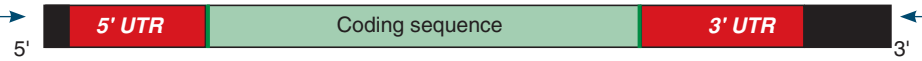
# 117 mRNA Processing in Eukaryotes

**Key Question**: How is the primary transcript modified after transcription and what do the modifications achieve?

Once a gene is transcribed, the primary transcript is modified to produce the mRNA strand that will be translated in the cytoplasm. Modifications to the 5' and 3' ends of the transcript enable the mRNA to exit the nucleus and remain stable long enough to be translated. Other post transcriptional modifications remove non-protein coding intronic DNA and splice exons in different combinations to produce different protein end products.

## Primary RNA is modified by the addition of caps and tails

**CAP**
A guanine nucleotide cap at the 5' end of the primary transcript stops degradation during transport from the nucleus and helps in the first phase of translation.




**POLY-A TAIL**
Adenosine nucleotides are added to the primary transcript. These poly-A tails aid nuclear export, translation, and stability of the mRNA.

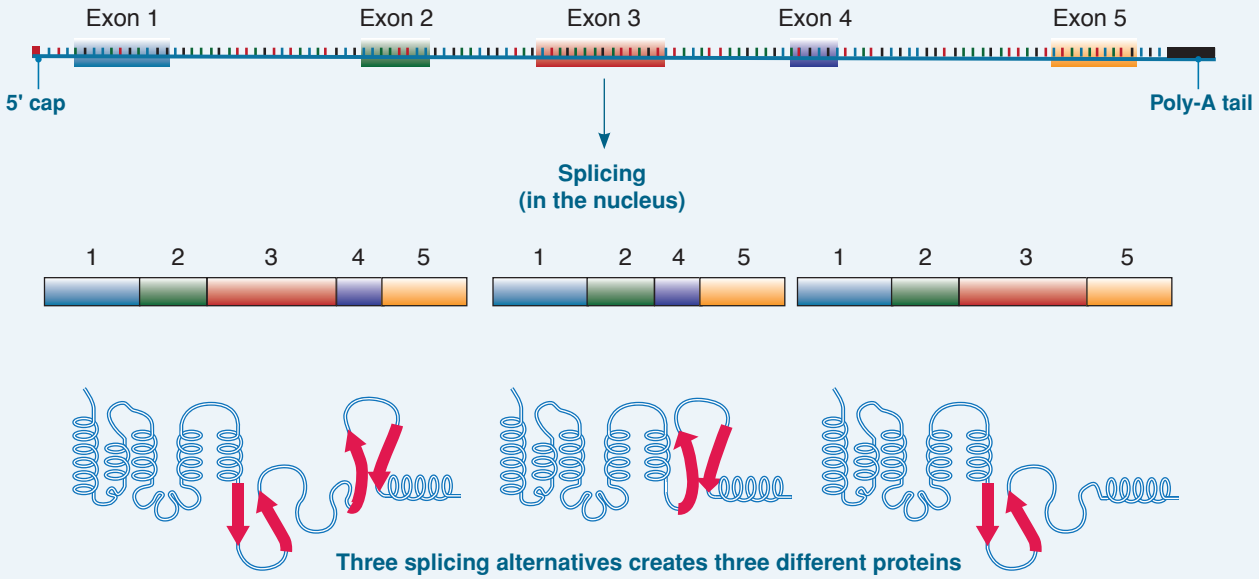
After transcription, the primary RNA transcript is modified by enzymes to create 'caps' and 'tails'. These modifications are part of the untranslated region (UTR) at each end of a gene. They stabilize the RNA, protect it from degradation, and help its transport through the nuclear pore. They are also important in translation although they are not translated themselves. The START and STOP points of translation are marked by darker green lines.

## Modification after transcription

- As you have seen earlier, introns are removed from the primary mRNA transcript and the exons are spliced together. However, exons can be spliced together in different ways to create variations in the translated proteins. Exon splicing occurs in the nucleus, either during or immediately after transcription.
- In mammals, the most common method of alternative splicing involves exon skipping, in which not all exons are spliced into the final mRNA (below).

**DID YOU KNOW?**

Human DNA contains 25,000 genes, but produces up to 1 million different proteins. Modifications after transcription and translation allow several proteins to be produced from just one gene.




Three splicing alternatives creates three different proteins

1. Explain the purpose of the caps and tail on mRNA? _____

_____

2. (a) What happens to the intronic sequences in DNA after transcription? _____

   (b) What is one possible fate for these introns? _____

3. Explain how so many proteins can be produced from a much smaller number of genes: _____

_____

_____

4. If a human produces 1 million proteins, but human DNA codes for only 25,000 genes, on average how many proteins are produced per gene?

_____

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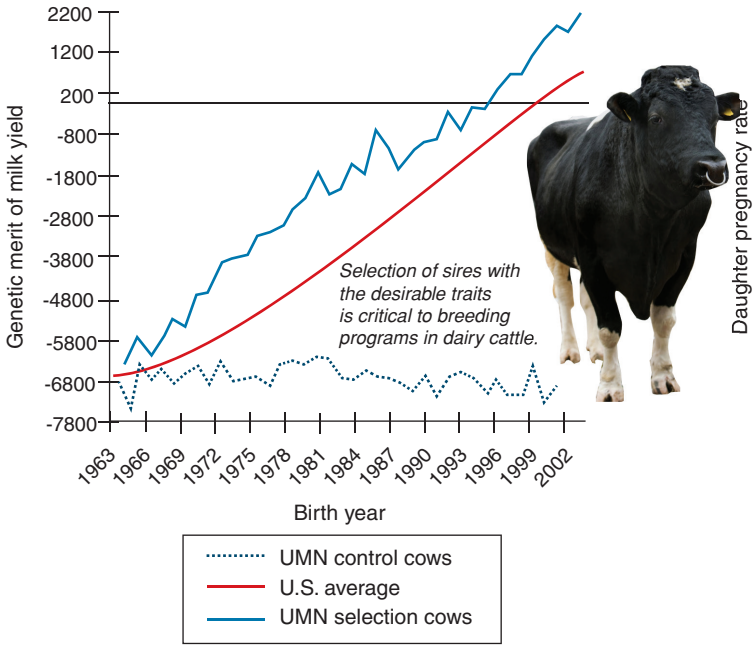
# 155 Selection and Population Change

**Key Question**: How is selective breeding able to produce rapid change in the phenotypic characteristics of a population?

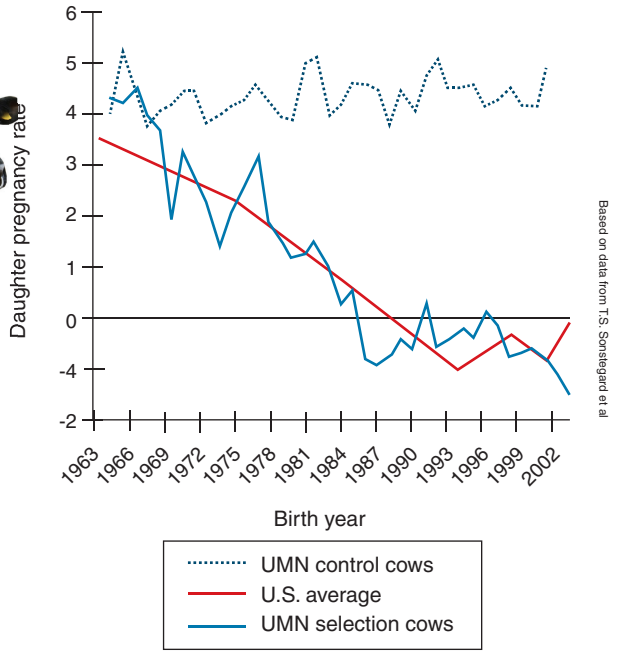
Humans may create the selection pressure for evolutionary change by choosing and breeding together individuals with particular traits. The example of milk yield in Holstein cows illustrates how humans have directly influenced the genetic makeup of Holstein cattle with respect to milk production and fertility. Since the 1960s, the University of Minnesota has maintained a Holstein cattle herd in which there has been no selection. They also maintain a herd that was selected for increased milk production between 1965 and 1985. They compared the genetic merit of milk yield in these groups to that of the USA Holstein average. Note that selective breeding is the term usually used in livestock improvement.

**Gain in genetic merit of milk yield**




Milk production in the University of Minnesota (UMN) herd subjected to selective breeding increased in line with the U.S. average production. In real terms, milk production per cow per milking season increased by 3740 kg since 1964. The herd with no selection remained effectively constant for milk production.

**Fertility in holstein cows**




Along with increased milk production there has been a distinct decrease in fertility. The fertility of the University of Minnesota (UMN) herd that was not subjected to selection remained constant while the fertility of the herd selected for milk production decreased with the U.S. fertility average.

1. (a) Describe the relationship between milk yield and fertility on Holstein cows: _____

   _____

   (b) What does this suggest about where the genes for milk production and fertility are carried? _____

   _____

   _____

2. What limits might this place on maximum milk yield? _____

   _____

3. Why is sire selection important in selective breeding, even if the characters involved are expressed only in the female?

   _____

4. Natural selection is the mechanism by which organisms with favorable traits become proportionally more common in the population. How does artificial selection mimic natural selection? How does the example of the Holstein cattle show that reproductive success is a compromise between many competing traits?

   _____

   _____

   _____

   _____

   _____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# 174 What Can Highly Conserved Proteins Tell Us?

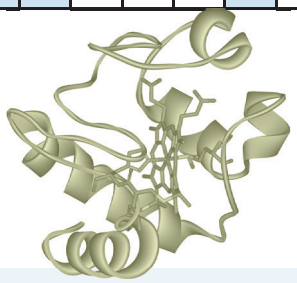
**Key Question**: What are highly conserved proteins and what can they tell us about evolutionary relationships?

Some proteins are common in many different species. These proteins are called highly conserved proteins, meaning they change (mutate) very little over time. This is because they have critical roles in the organism (e.g. in cellular respiration) and mutations are likely to be lethal. Evidence indicates that highly conserved proteins are homologous and have been derived from a common ancestor. Because they are highly conserved, changes in the amino acid sequence are likely to represent major divergences between groups during the course of evolution. Examples of highly conserved proteins are cytochrome c, a respiratory protein (below) and the Pax-6 protein (bottom).

## Cytochrome *c* compared between species

| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Human | | Gly | Asp | Val | Glu | Lys | Gly | Lys | Lys | Ile | Phe | Ile | Met | Lys | Cys | Ser | Gln | Cys | His | Thr | Val | Glu | Lys |
| Pig | | | | | | | | | | | | Val | Gln | | | Ala | | | | | | | |
| Chicken | | | | Ile | | | | | | Val | | Val | Gln | | | Ala | | | | | | | |
| Dogfish | | | | | | | | | | Val | | Val | Gln | | | Ala | | | | | | | Asn |
| Drosophila | << | | | | | | | | | Leu | | Val | Gln | Arg | | Ala | | | | | | | Ala |
| Wheat | << | | Asn | Pro | Asp | Ala | | Ala | | | | Lys | Thr | Arg | | Ala | | | | | | Asp | Ala |
| Yeast | << | | Ser | Ala | Lys | | | Ala | Thr | Leu | | Lys | Thr | Arg | | Glu | Leu | | | | | | |

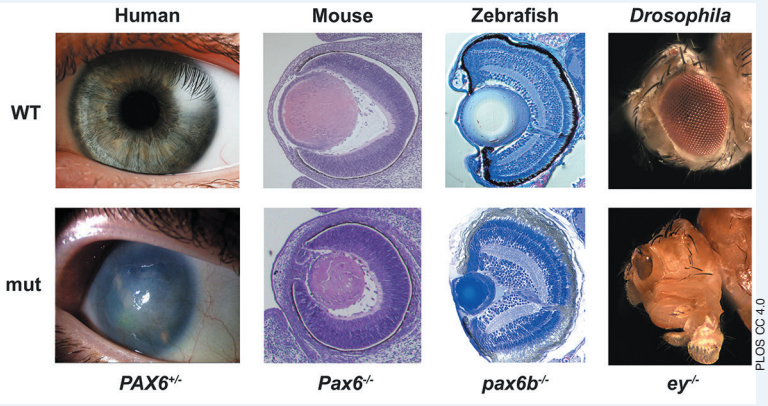
Cytochrome C (right) is a respiratory protein located in the electron transport chain in mitochondria. Highly conserved proteins, such as cytochrome c, change very little over time and between species because they carry out important roles and if they changed too much they may no longer function properly.



The table above shows the N-terminal 22 amino acid residues of human cytochrome c, with corresponding sequences from other organisms aligned beneath. Sequences are aligned to give the most position matches. A shaded square indicates no change. In every case, the cytochrome's heme group is attached to the Cys-14 and Cys-17. In *Drosophila*, wheat, and yeast, arrows indicate that several amino acids precede the sequence shown.

## The Pax-6 protein provides evidence for evolution

- The Pax-6 gene belongs to a family of master genes that regulate the formation of a number of organs, including the eye, during embryonic development.
- The Pax-6 gene produces the Pax-6 protein, which acts as a transcription factor to control the expression of other genes.
- Scientists know the role of Pax-6 in eye development because they created a knockout model in mice where the Pax-6 gene is not expressed. The knockout model is eyeless or has very underdeveloped eyes.
- The Pax-6 gene is so highly conserved that the gene from one species can be inserted into another species, and still produce a normal eye.
- This suggests the Pax-6 proteins are homologous, and the gene has been inherited from a common ancestor.




The images above show the effect of a non-functional Pax-6 gene. In all cases, a non-functional gene leads to non-functional eyes. In the case of the *Drosophila* the eye is missing. Experiments have shown that Pax-6 genes work across species. When a mouse Pax-6 gene was inserted into fly DNA and turned on in the fly's legs, the fly developed morphologically normal eyes on its legs!

1. Use the cytochrome c table above to answer the following:

(a) Which two organisms in the table are most distantly related? Explain your answer: _____

_____

_____

(b) Which two organisms in the table are most closely related? Explain your answer: _____

_____

_____

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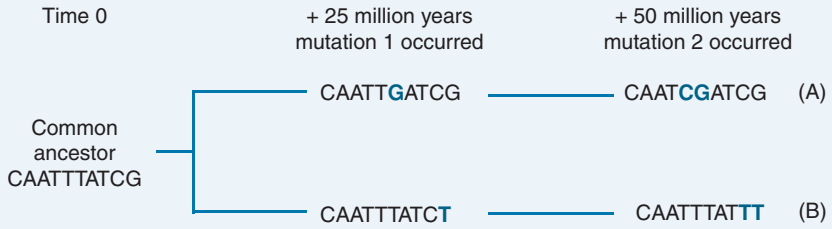
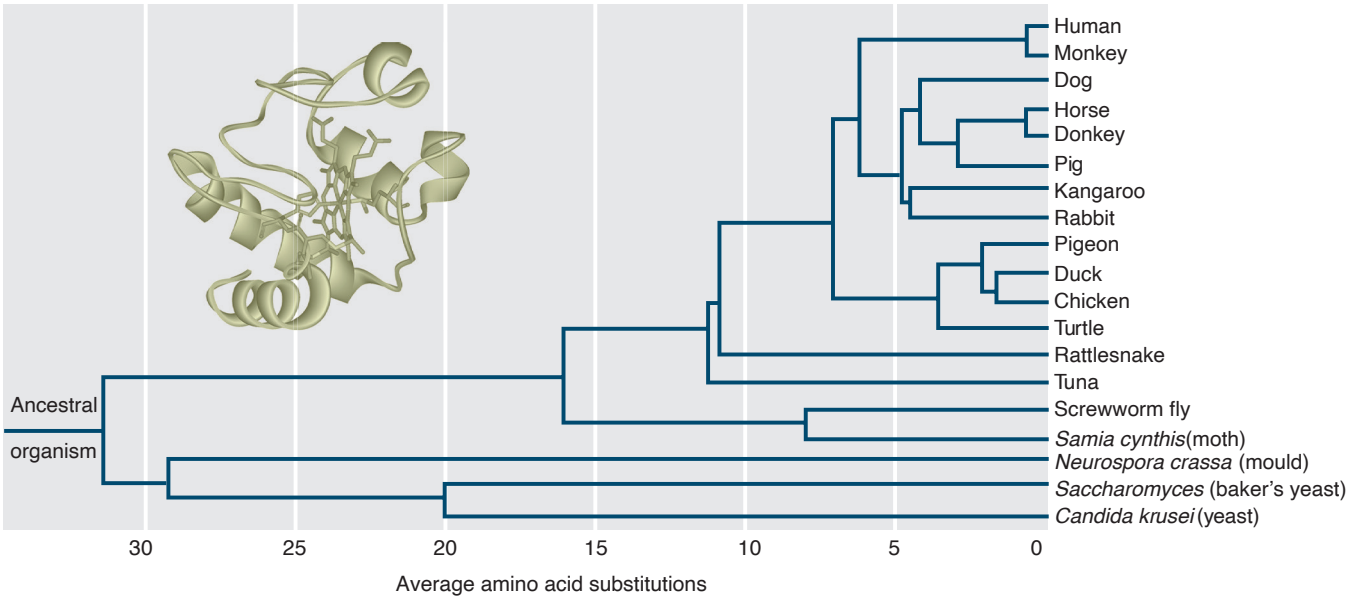
## Cytochrome *c* and phylogeny

Because conserved proteins are found across many species they can be used to create a phylogeny showing species relationships based on their mutations. The molecular clock hypothesis states that mutations occur at a relatively constant rate for any given gene. The genetic difference between any two species can indicate when two species last shared a common ancestor and can be used to construct a phylogenetic tree. The molecular clock for each species, and each protein, may run at different rates, so molecular clock data is calibrated with other evidence (e.g. morphological) to confirm phylogeny. Molecular clock calculations are carried out on DNA or amino acid sequences.

In this hypothetical example, the DNA sequence for a gene in two species (A and B) alive today differs by four bases. The mutation rate for the gene is approximately one base per 25 million years. Based on this rate, it can be determined that the common ancestor for these two species lived 50 million years ago.




2. For cytochrome *c*, suggest why amino acids 14 and 17 are unchanged in all the organisms shown in the table: _____

3. (a) Describe the role of the Pax-6 gene: _____

(b) What evidence is there that the Pax-6 protein is highly conserved? _____

4. (a) Describe a limitation of using molecular clocks to establish phylogeny: _____

(b) Why are highly conserved proteins good for constructing phylogenies? _____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# 176 Gene Duplication and Evolution

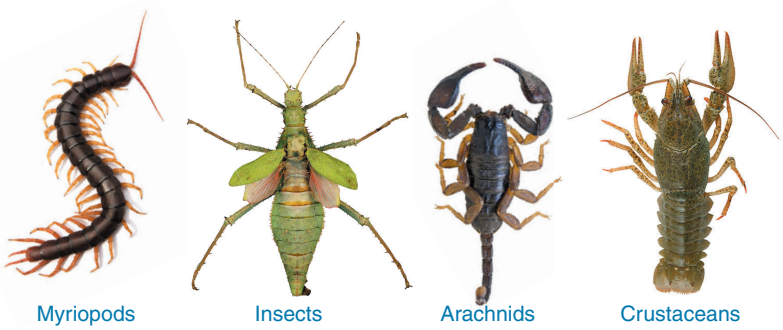
**Key Question**: What do genomic comparisons reveal about the evolution and diversification of arthropod taxa?

Evolutionary developmental biology (or *evo-devo*) is a rapidly advancing area of evolutionary biology that examines how changes to developmental processes can result in the novel features we see appearing in evolutionary radiations.

Genomic comparisons among arthropod taxa have been important in revealing how the duplication and mutation of the genes regulating development have been involved in the evolution of novel structures and body plans. In particular, it explains how new characteristics in taxa can appear with apparent suddenness.

## Evolution: you work with what you've got!

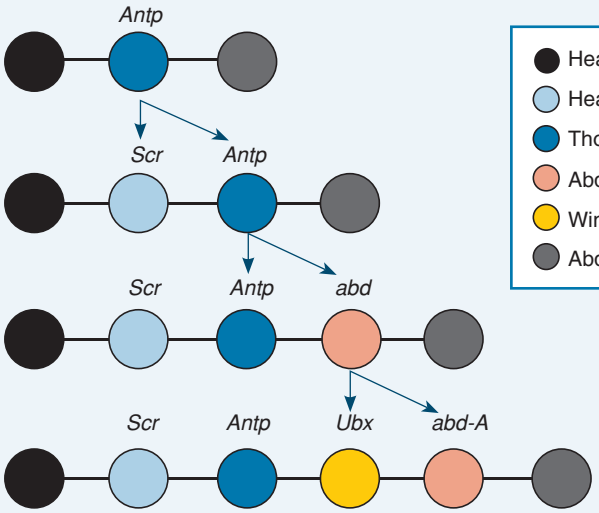
- Genomic studies have revealed the role of developmental genes in the evolution of novel forms and structures, and given valuable insight into the genetic mechanisms underlying evolutionary radiations.
- Arthropods, annelids, and vertebrates, all have highly modular bodies, i.e. the body is made up of repeating units. In arthropods, changes to individual segments through duplication and modification of genes has seen the evolution of a diverse range of body forms.
- For example, a gene involved in the development of appendages in arthropods can be duplicated and the duplicate gene modified. This produces modifications to some appendages, enabling a new set of functions without having to modify all other the appendages.

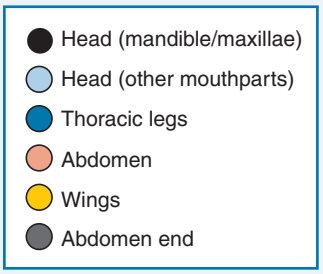


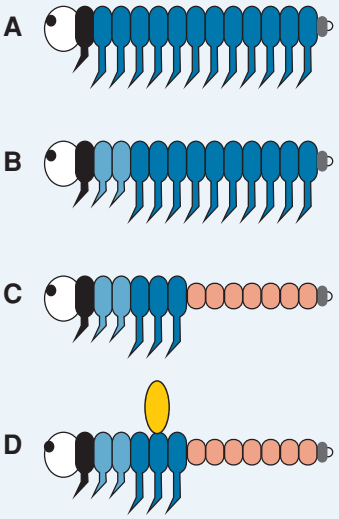
Myriopods Insects Arachnids Crustaceans

Evolution works with what is already present, and 'new' structures are just modifications of pre-existing structures. Segmental modifications produce a large amount of morphological variation in arthropods.

## Developmental genes and arthropods




By looking at the DNA sequences in a series of genes we can piece together the order in which genes were duplicated and modified. The sequence above shows the order in which genes that are expressed in various parts of an arthropod appeared, starting with the original antennapedia (Antp) gene, which controls the development of appendages near the head.

We can identify which body segments the genes are expressed in and so work out the order in which body segments were modified. Above we start with a primitive arthropod (**A**). Three genes control development of the head, the middle segments, and the tail. Subsequent duplication and modification of genes produces an arthropod resembling a centipede (**B**), then a primitive wingless insect (**C**), and finally a modern winged insect (**D**).

1. Using the information above, explain how comparisons of developmental genes among different taxa can provide evidence for how different organisms are related and their evolutionary history:

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# 186 Constructing Phylogenies Using Cladistics

**Key Question**: What are cladograms and how are shared derived characters used to construct them?

A **cladogram** is a phylogenetic tree constructed using a taxonomic tool called cladistics. Cladistics groups organisms on the basis of their **shared derived characters** (features arising in an ancestor and shared by all its descendants) and ignores features that are not the result of shared ancestry. A clade, or branch on the tree, includes a common ancestor and all its descendants (i.e. it is monophyletic). Increasingly, cladistic methods rely on molecular data (e.g. DNA sequences) to determine phylogenies. Highly conserved DNA sequences are used because changes are likely to signal a significant evolutionary divergence. Cladograms may not always agree completely with phylogenies constructed using traditional methods but similarities in the trees indicate that the proposed relationships are likely to be correct.

## Derived vs ancestral characters

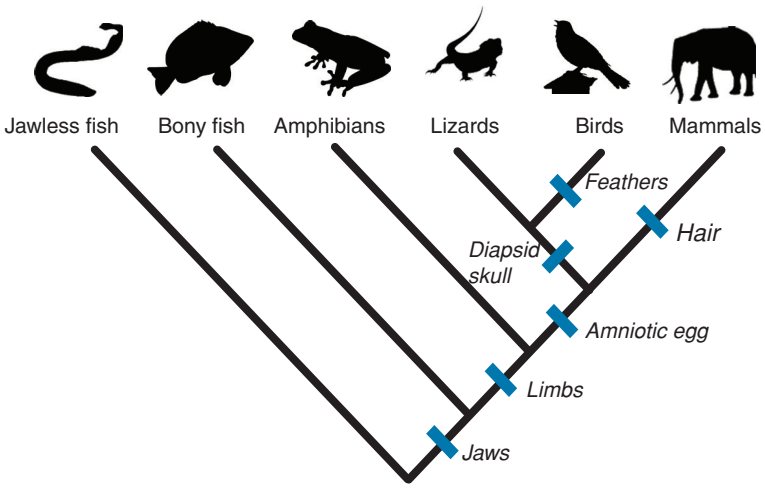
When constructing cladograms, shared derived characters are used to separate the clades (branches on the tree). Using ancestral characters (those that arise in a species that is ancestral to more than one group) would result in distantly related organisms being grouped together and would not help to determine the evolutionary relationships within a clade. Whether or not a character is derived depends on the taxonomic level being considered. For example, a backbone is an ancestral character for mammals, but a derived character for vertebrates. Production of milk is a derived character shared by all mammals but no other taxa.

*The backbone in a mammal, e.g. rat, is an ancestral character common to all vertebrate taxa. However, the production of milk from mammary glands is a derived character, shared by all mammals but no other taxa.*

## Constructing a simple cladogram

- A table listing the features for comparison allows us to identify where we should make branches in the cladogram. An **outgroup** (one which is known to have no or little relationship to the other taxa in the table) is used as a basis for comparison.
- The table (right) lists features shared by selected taxa. The outgroup (jawless fish) shares just one feature (vertebral column), so it gives a reference for comparison and the first branch of the cladogram. As the number of taxa in the table increases, the number of possible trees that could be drawn increases exponentially.
- Several different cladograms can be constructed from the same data. To determine the most likely relationships, the rule of **parsimony** is used. Parsimony assumes that the tree with the simplest explanation (the least number of evolutionary events) is most likely to show the correct (or most plausible) evolutionary relationship.
- A possible cladogram for the data in the table is shown on the right. Its construction assumed that six evolutionary events took place (labeled as blue bars on the cladogram). If other cladograms were constructed, but involved more evolutionary events, the one shown would be assumed to be correct because it is the most parsimonious.
- Parsimony can lead to some confusion. Some evolutionary events have occurred multiple times. An example is the evolution of the four chambered heart, which occurred separately in both birds and mammals. The use of fossil evidence and DNA analysis can help to solve problems like this.

| Comparative features | Jawless fish (outgroup) | Bony fish | Amphibians | Lizards | Birds | Mammals |
|---|---|---|---|---|---|---|
| | **Taxa** | | | | | |
| Vertebral column | ✔ | ✔ | ✔ | ✔ | ✔ | ✔ |
| Jaws | ✘ | ✔ | ✔ | ✔ | ✔ | ✔ |
| Four supporting limbs | ✘ | ✘ | ✔ | ✔ | ✔ | ✔ |
| Amniotic egg | ✘ | ✘ | ✘ | ✔ | ✔ | ✔ |
| Diapsid skull | ✘ | ✘ | ✘ | ✔ | ✔ | ✘ |
| Feathers | ✘ | ✘ | ✘ | ✘ | ✔ | ✘ |
| Hair | ✘ | ✘ | ✘ | ✘ | ✘ | ✔ |





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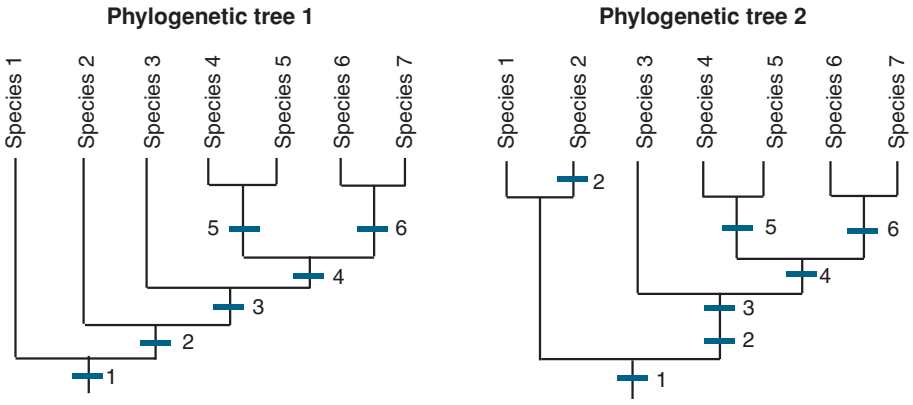
1. (a) Distinguish between a shared derived characteristic and a shared ancestral characteristic: _____

(b) Why are ancestral characters not useful in constructing evolutionary histories? _____

2. What assumption is made when applying the rule of parsimony in constructing a cladogram? _____

3. Two possible phylogenetic trees constructed from the same character table are shown below. The numbers next to a blue bar represent an evolutionary event.




(a) Which tree is more likely to be correct?

_____

(b) State your reason:

_____

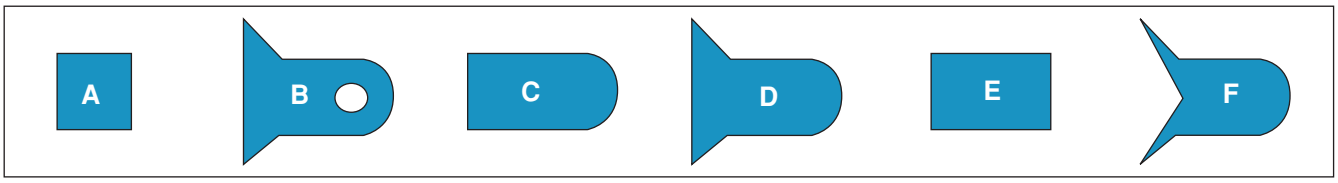
_____

_____

(c) Identify the event which has occurred twice in phylogenetic tree 2: _____

4. A phylogenetic tree is a hypothesis for an evolutionary history. How could you test it? _____

5. Use the shapes below to construct a cladogram that shows their phylogenetic relationships (hint: A is the outgroup).





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# 194 Sympatric Speciation

**Key Question**: What mechanisms are involved in speciation when there is no geographical separation?

In sympatric (same place) speciation, a new species evolves from a single ancestral species while inhabiting the same geographic region. Sympatric speciation is rarer than allopatric speciation, although it is not uncommon in plants which form polyploids. There are two situations in which sympatric speciation is thought to occur. These are described below.

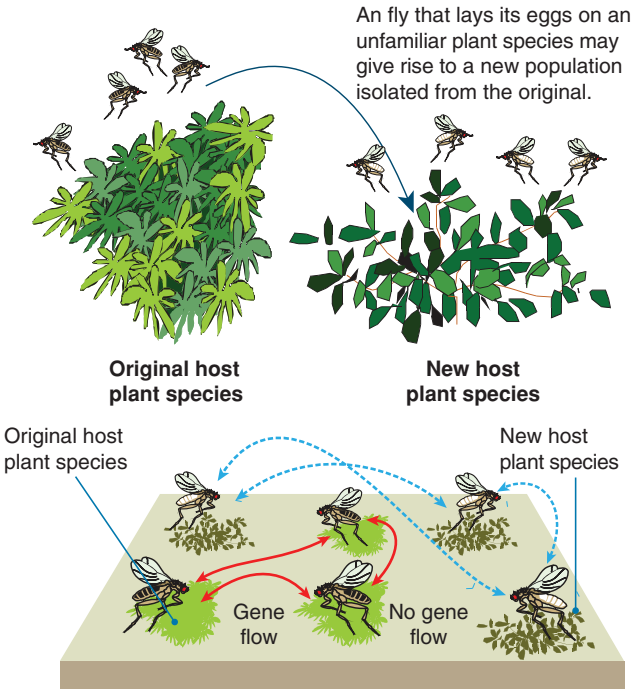
## Speciation through niche differentiation

### Niche isolation

There are many microhabitats within a heterogeneous environment (one that is not the same everywhere). Some individuals in a population may preferentially occupy to occupy one particular microhabitat, only rarely coming in contact with those that select other microhabitats. Some organisms become so dependent on the resources offered by their particular microhabitat that they never interact with others of their species in different microhabitats.

### Reproductive isolation

Sub-populations, which have remained genetically isolated because of their microhabitat preferences, become reproductively isolated. They have become new species with subtle differences in behavior, structure, and physiology. Gene flow (via sexual reproduction) is limited to organisms that share similar microhabitat preferences (as shown right).
**Example**: Some host-specific phytophagous insects (insects that feed on plants) lay eggs on plants identical to the species they themselves hatched on. Host plant preference leads to isolation despite the populations being sympatric.

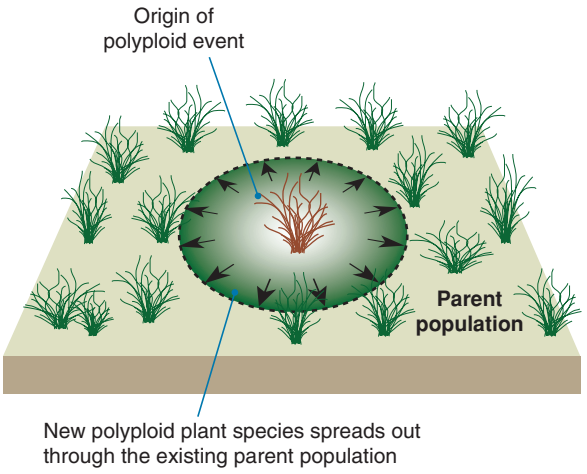



## Instant speciation by polyploidy

Polyploidy may result in the formation of a new species without isolation from the parent species. This event, occurring during meiosis, produces sudden reproductive isolation for the new group. Because the sex-determining mechanism is disturbed, animals are rarely able to achieve new species status this way (they are sterile). Many plants, on the other hand, are able to reproduce vegetatively, or self pollinate. This ability to reproduce on their own enables such polyploid plants to produce a breeding population.

### Speciation by allopolyploidy

This type of polyploidy usually arises from the doubling of chromosomes in a hybrid between two different species. The doubling often makes the hybrid fertile. **Examples**: Modern wheat. Swedes are a polyploid species formed from a hybrid between a type of cabbage and a type of turnip.




1. Use the diagram above to explain how niche differentiation can result in speciation: _____

2. What is the mechanism for instant speciation? Explain why it is more common in plants than in animals: _____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## Sympatric speciation in apple maggot flies

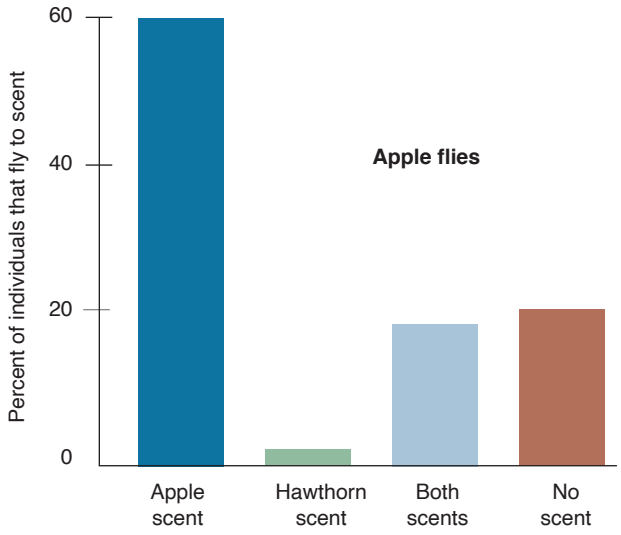
Apple maggot flies are native to North America. They infest the fruit of apple trees, laying eggs in the fruit, which develop into maggots that burrow into and eat the fruit. However, apple trees are not native to North America and were introduced less than 300 years ago.

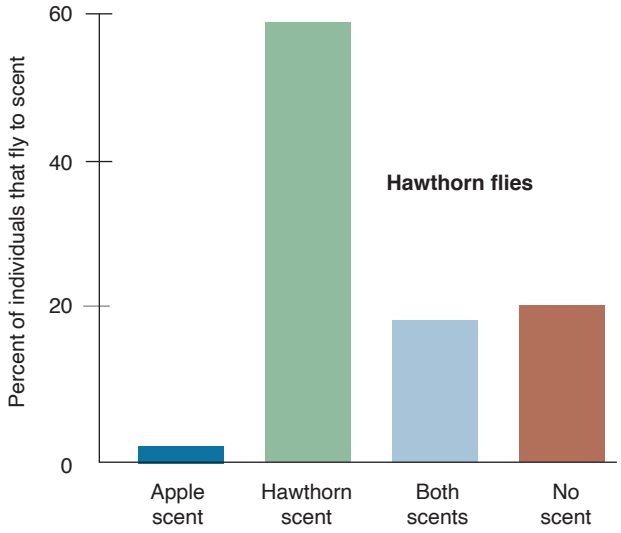
Joseph Berger, Bugwood.org

Research found that apple maggot flies also infest the fruit of native hawthorns. More importantly, flies that develop from maggots infesting hawthorns mated and laid eggs on hawthorns (hawthorn flies). Flies that develop from maggots that infested apples preferred to mate and lay eggs on apples (apple flies). Only 6% of matings took place between flies from different fruits.

Other experiments show the flies discriminate between scents on a genetic basis and have alleles associated with attraction to hawthorn or apple scent.

This separation of individuals by preference of apples or hawthorns has been a consequence of the introduction of apple trees. Although the flies are morphologically and genetically the same, their behavior has separated them into different populations on the pathway to speciation.




3. What plant did the apple maggot fly infest before apple trees were introduced to North America?

4. What kind of natural selection is occurring in the apple maggot fly? _____

5. (a) Explain the mechanisms that are causing this selection to occur: _____

   (b) How might these mechanisms affect the future evolution of the apple maggot fly? _____

6. Apple fruits tend to drop earlier in the season that hawthorn fruits. How might this enhance the separation of apple flies and hawthorn flies?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