Eukaryote Organisms

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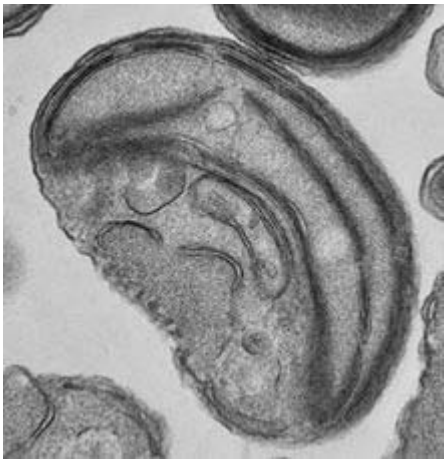
Chapter 1

Eukaryote

Eukaryotes Temporal range: Proterozoic – Recent

Ostreococcus is the smallest known free living eukaryote, with an average size of 0.8 μm.
Scientific classification
Domain: **Eukaryota** Whittaker & Margulis,1978
Kingdoms
Animalia – Animals
Fungi
Amoebozoa
Plantae – Plants
Chromalveolata
Rhizaria
Excavata
Alternative phylogeny

- ***Unikonta***
  - **Opisthokonta**

        - Metazoa
        - Mesomycetozoa
        - Choanozoa
        - Eumycota
    - Amoebozoa
- ***Bikonta***
    - Apusozoa
    - Rhizaria
    - Excavata
    - Archaeplastida
    - Chromalveolata

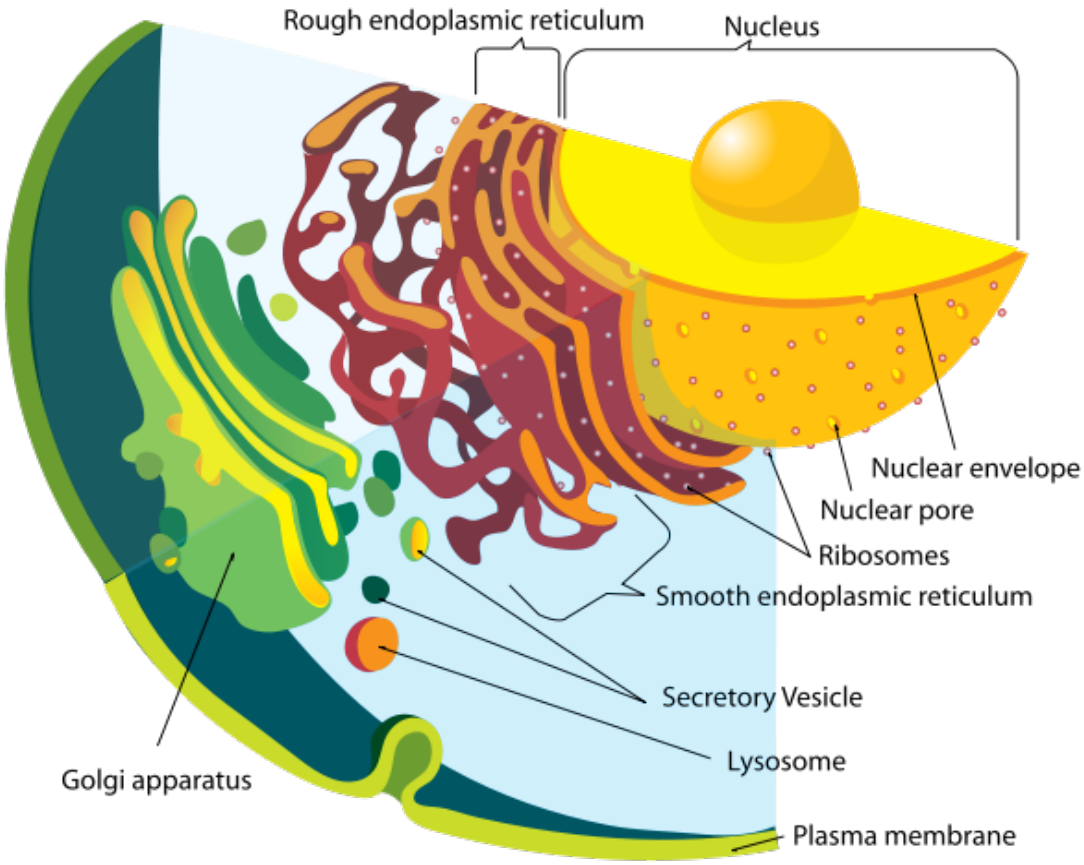
A **eukaryote** is an organism whose cells contain complex structures enclosed within membranes. The defining membrane-bound structure that sets eukaryotic cells apart from prokaryotic cells is the nucleus, or nuclear envelope, within which the genetic material is carried. The presence of a nucleus gives eukaryotes their name, which comes from the Greek ευ (*eu*, "good") and κάρυον (*karyon*, "nut" or "kernel"). Most eukaryotic cells also contain other membrane-bound organelles such as mitochondria, chloroplasts and the Golgi apparatus. All species of large complex organisms are eukaryotes, including animals, plants and fungi, although most species of eukaryotic protists are microorganisms.

Cell division in eukaryotes is different from that in organisms without a nucleus (prokaryotes). It involves separating the duplicated chromosomes, through movements directed by microtubules. There are two types of division processes. In mitosis, one cell divides to produce two genetically identical cells. In meiosis, which is required in sexual reproduction, one diploid cell (having two instances of each chromosome, one from each parent) undergoes recombination of each pair of parental chromosomes, and then two stages of cell division, resulting in four haploid cells (gametes). Each gamete has just one complement of chromosomes, each a unique mix of the corresponding pair of parental chromosomes.

Eukaryotes appear to be monophyletic, and so make up one of the three domains of life. The two other domains, Bacteria and Archaea, are prokaryotes and have none of the above features. Eukaryotes represent a tiny minority of all living things; even in a human body there are 10 times more microbes than human cells.

Cell features

Eukaryotic cells are typically much larger than those of prokaryotes. They have a variety of internal membranes and structures, called organelles, and a cytoskeleton composed of microtubules, microfilaments, and intermediate filaments, which play an important role in defining the cell's organization and shape. Eukaryotic DNA is divided into several linear bundles called chromosomes, which are separated by a microtubular spindle during nuclear division.



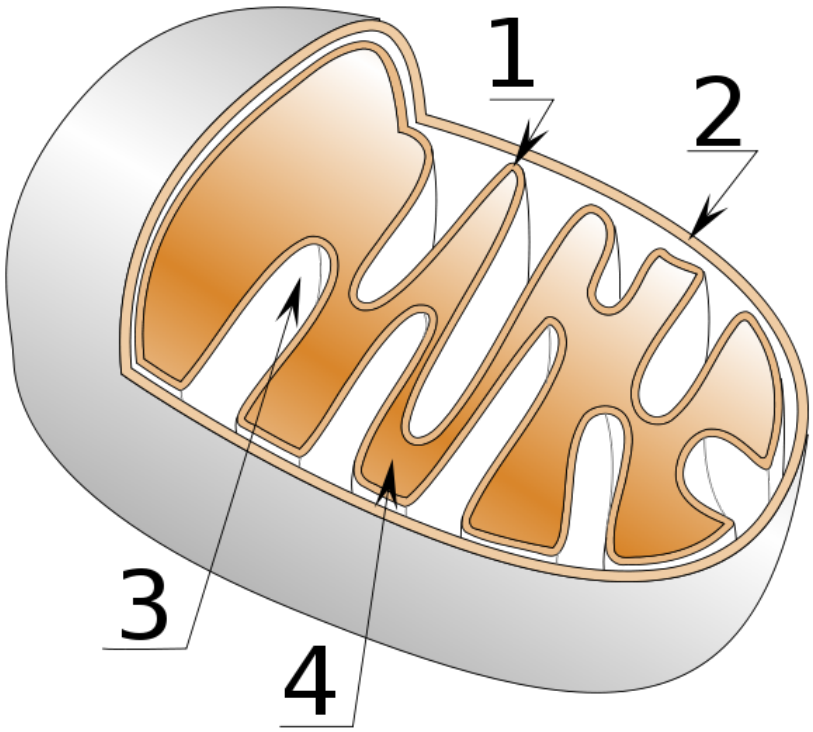
Detail of the endomembrane system and its components

Internal membrane

Eukaryotic cells include a variety of membrane-bound structures, collectively referred to as the endomembrane system. Simple compartments, called vesicles or vacuoles, can form by budding off other membranes. Many cells ingest food and other materials through a process of endocytosis, where the outer membrane invaginates and then pinches off to form a vesicle. It is probable that most other membrane-bound organelles are ultimately derived from such vesicles.

The nucleus is surrounded by a double membrane (commonly referred to as a nuclear envelope), with pores that allow material to move in and out. Various tube- and sheet-like extensions of the nuclear membrane form what is called the endoplasmic reticulum or ER, which is involved in protein transport and maturation. It includes the rough ER where ribosomes are attached to synthesize proteins, which enter the interior space or lumen. Subsequently, they generally enter vesicles, which bud off from the smooth ER. In most eukaryotes, these protein-carrying vesicles are released and further modified in stacks of flattened vesicles, called Golgi bodies or dictyosomes.

Vesicles may be specialized for various purposes. For instance, lysosomes contain enzymes that break down the contents of food vacuoles, and peroxisomes are used to break down peroxide, which is toxic otherwise. Many protozoa have contractile vacuoles, which collect and expel excess water, and extrusomes, which expel material used to deflect predators or capture prey. In multicellular organisms, hormones are often produced in vesicles. In higher plants, most of a cell's volume is taken up by a central vacuole, which primarily maintains its osmotic pressure.



Mitochondria structure:
1) Inner membrane
2) Outer membrane
3) Crista
4) Matrix

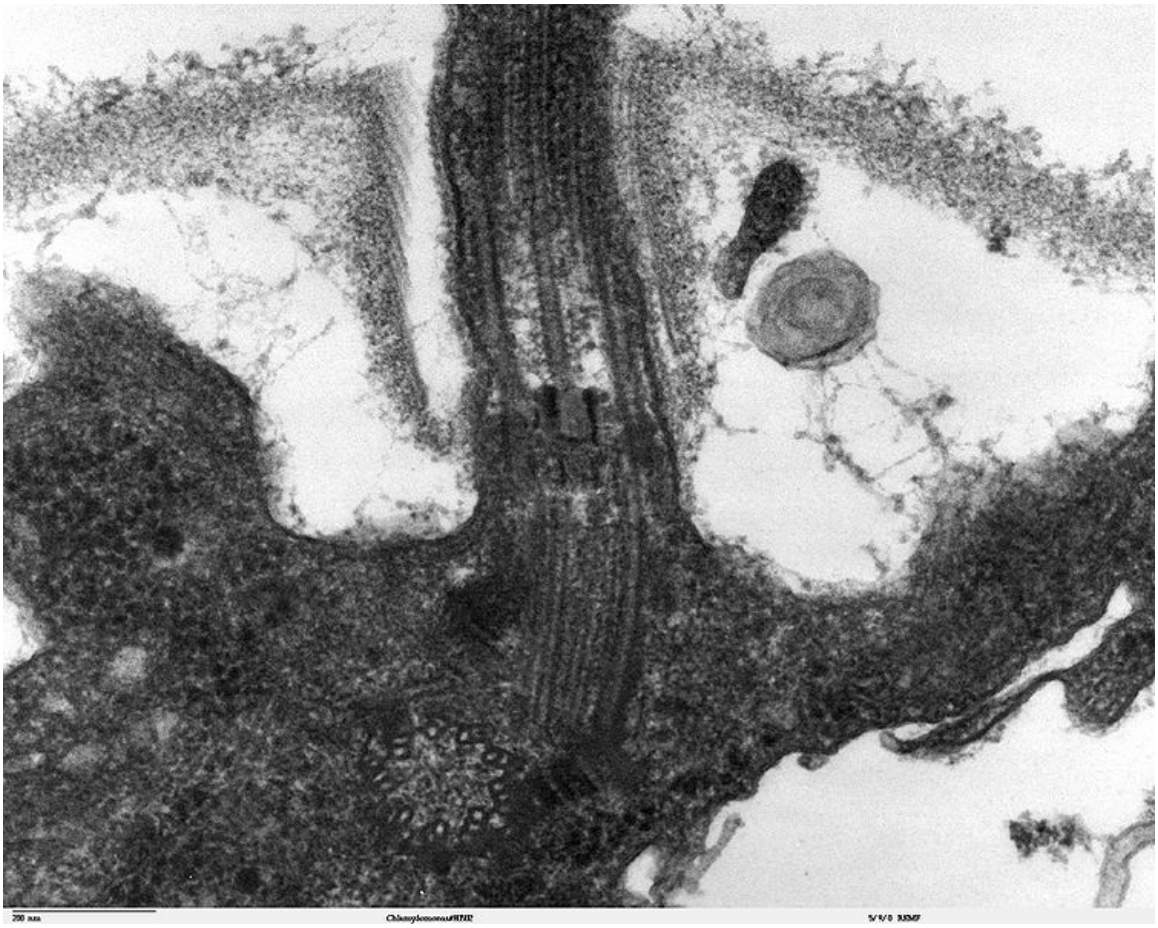
Mitochondria and plastids

Mitochondria are organelles found in nearly all eukaryotes. They are surrounded by two membranes (each a phospholipid bi-layer), the inner of which is folded into invaginations called cristae, where aerobic respiration takes place. Mitochondria contain their own DNA. They are now generally held to have developed from endosymbiotic prokaryotes, probably proteobacteria. The few protozoa that lack mitochondria have been found to contain mitochondrion-derived organelles, such as hydrogenosomes and mitosomes.

Plants and various groups of algae also have plastids. Again, these have their own DNA and developed from endosymbiotes, in this case cyanobacteria. They usually take the form of chloroplasts, which like cyanobacteria contain chlorophyll and produce organic compounds (such as glucose) through photosynthesis. Others are involved in storing food. Although plastids likely had a single origin, not all plastid-containing groups are closely related. Instead, some eukaryotes have obtained them from others through secondary endosymbiosis or ingestion.

Endosymbiotic origins have also been proposed for the nucleus, for which see below, and for eukaryotic flagella, supposed to have developed from spirochaetes. This is not generally accepted, both from a lack of cytological evidence and difficulty in reconciling this with cellular reproduction.

Cytoskeletal structures



Longitudinal section through the flagellum of *Chlamydomonas reinhardtii*

Many eukaryotes have long slender motile cytoplasmic projections, called flagella, or similar structures called cilia. Flagella and cilia are sometimes referred to as undulipodia, and are variously involved in movement, feeding, and sensation. They are composed mainly of tubulin. These are entirely distinct from prokaryotic flagella. They are

supported by a bundle of microtubules arising from a basal body, also called a kinetosome or centriole, characteristically arranged as nine doublets surrounding two singlets. Flagella also may have hairs, or mastigonemes, and scales connecting membranes and internal rods. Their interior is continuous with the cell's cytoplasm.

Microfilamental structures composed by actin and actin binding proteins, e.g., α-actinin, fimbrin, filamin are present in submembraneous cortical layers and bundles, as well. Motor proteins of microtubules, e.g., dynein or kinesin and actin, e.g., myosins provide dynamic character of the network.

Centrioles are often present even in cells and groups that do not have flagella. They generally occur in groups of one or two, called kinetids, that give rise to various microtubular roots. These form a primary component of the cytoskeletal structure, and are often assembled over the course of several cell divisions, with one flagellum retained from the parent and the other derived from it. Centrioles may also be associated in the formation of a spindle during nuclear division.

Significance of cytoskeletal structures is underlined in determination of shape of the cells, as well as their being essential components of migratory responses like chemotaxis and chemokinesis. Some protists have various other microtubule-supported organelles. These include the radiolaria and heliozoa, which produce axopodia used in flotation or to capture prey, and the haptophytes, which have a peculiar flagellum-like organelle called the haptonema. An animal cell is a form of Eukaryotic cell that makes up many tissues in animals.

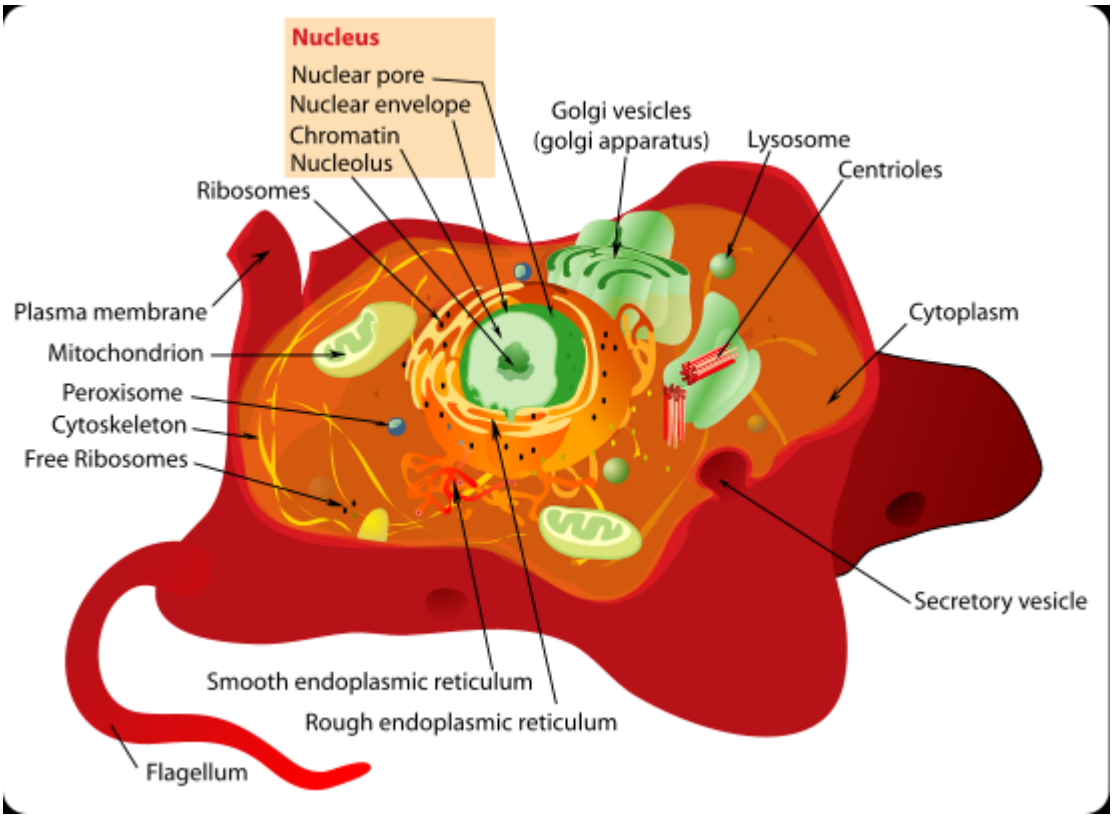
Plant cell wall

Plant cells have a cell wall, a fairly rigid layer outside the cell membrane, providing the cell with structural support, protection, and a filtering mechanism. The cell wall also prevents over-expansion when water enters the cell. The major carbohydrates making up the primary cell wall of land plants are cellulose, hemicellulose, and pectin. The cellulose microfibrils are linked via hemicellulosic tethers to form the cellulose-hemicellulose network, which is embedded in the pectin matrix. The most common hemicellulose in the primary cell wall is xyloglucan.

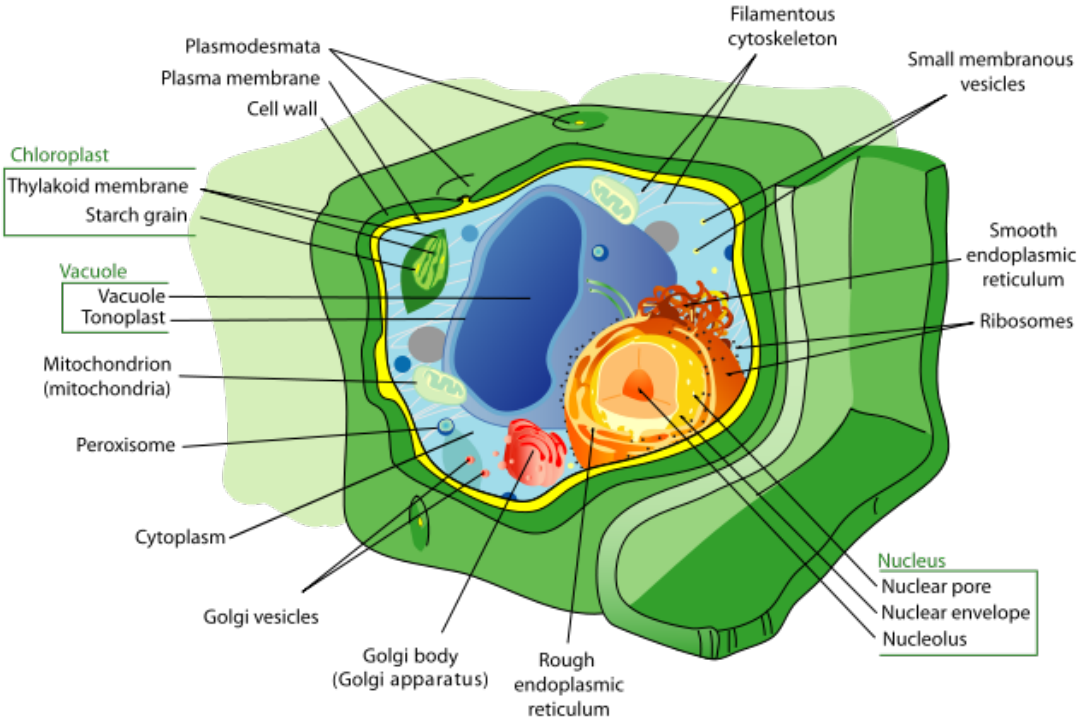
Differences among eukaryotic cells

There are many different types of eukaryotic cells, though animals and plants are the most familiar eukaryotes, and thus provide an excellent starting point for understanding eukaryotic structure. Fungi and many protists have some substantial differences, however.

Animal cell



Structure of a typical animal cell



Structure of a typical plant cell

An **animal cell** is a form of eukaryotic cell that makes up many tissues in animals. The animal cell is distinct from other eukaryotes, most notably plant cells, as they lack cell walls and chloroplasts, and they have smaller vacuoles. Due to the lack of a rigid cell wall, animal cells can adopt a variety of shapes, and a phagocytic cell can even engulf other structures.

There are many different cell types. For instance, there are approximately 210 distinct cell types in the adult human body.

Plant cell

Plant cells are quite different from the cells of the other eukaryotic organisms. Their distinctive features are:

- A large central vacuole (enclosed by a membrane, the tonoplast), which maintains the cell's turgor and controls movement of molecules between the cytosol and sap
- A primary cell wall containing cellulose, hemicellulose and pectin, deposited by the protoplast on the outside of the cell membrane; this contrasts with the cell walls of fungi, which contain chitin, and the cell envelopes of prokaryotes, in which peptidoglycans are the main structural molecules

- The plasmodesmata, linking pores in the cell wall that allow each plant cell to communicate with other adjacent cells; this is different from the functionally analogous system of gap junctions between animal cells.
- Plastids, especially chloroplasts that contain chlorophyll, the pigment that gives plants their green color and allows them to perform photosynthesis
- Higher plants, including conifers and flowering plants (Angiospermae) lack the flagellae and centrioles that are present in animal cells.

Fungal cell

Fungal cells are most similar to animal cells, with the following exceptions:

- A cell wall that contains chitin
- Less definition between cells; the hyphae of higher fungi have porous partitions called septa, which allow the passage of cytoplasm, organelles, and, sometimes, nuclei. Primitive fungi have few or no septa, so each organism is essentially a giant multinucleate supercell; these fungi are described as coenocytic.
- Only the most primitive fungi, chytrids, have flagella.

Other eukaryotic cells

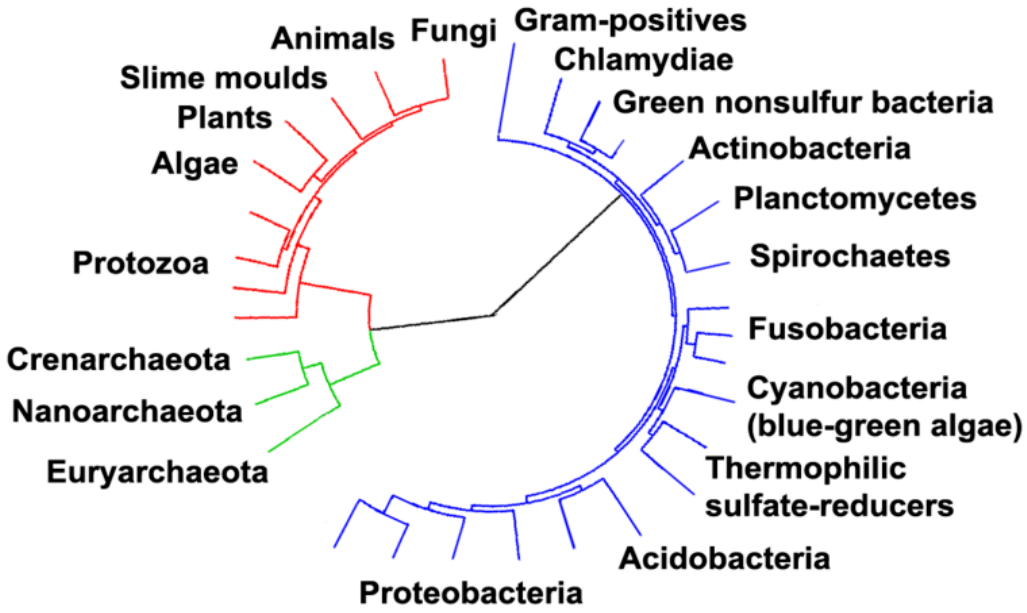
Eukaryotes are a very diverse group, and their cell structures are equally diverse. Many have cell walls; many do not. Many have chloroplasts, derived from primary, secondary, or even tertiary endosymbiosis; and many do not. Some groups have unique structures, such as the cyanelles of the glaucophytes, the haptonema of the haptophytes, or the ejectisomes of the cryptomonads. Other structures, such as pseudopods, are found in various eukaryote groups in different forms, such as the lobose amoebozoans or the reticulose foraminiferans.

Reproduction

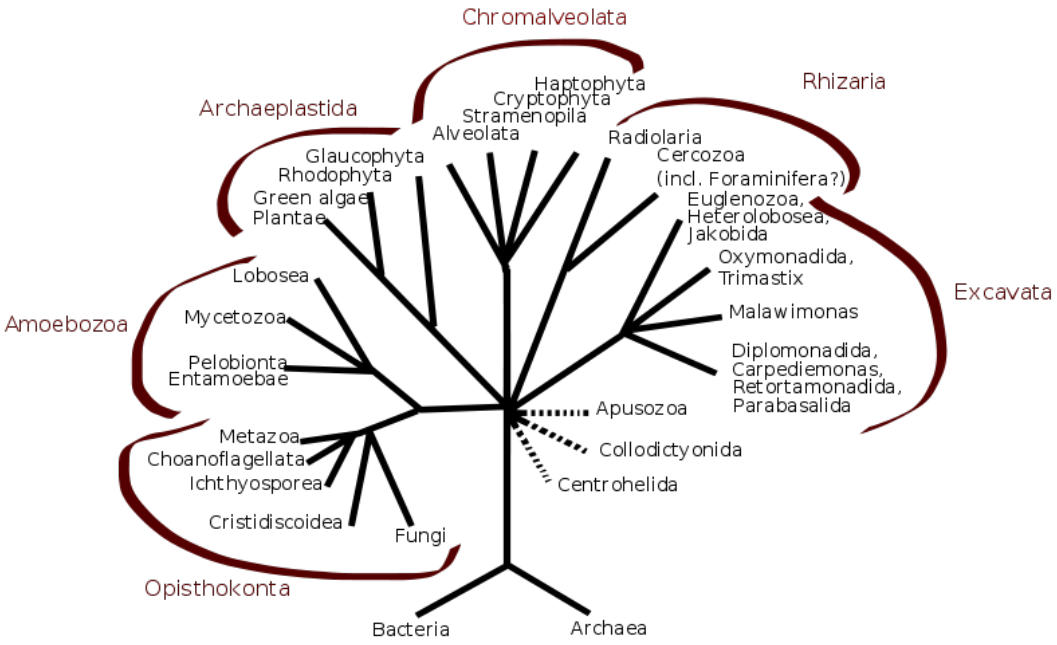
Nuclear division is often coordinated with cell division. This generally takes place by mitosis, a process that allows each daughter nucleus to receive one copy of each chromosome. In most eukaryotes, there is also a process of sexual reproduction, typically involving an alternation between haploid generations, wherein only one copy of each chromosome is present, and diploid generations, wherein two are present, occurring through nuclear fusion (syngamy) and meiosis. There is considerable variation in this pattern, however.

Eukaryotes have a smaller surface area to volume ratio than prokaryotes, and thus have lower metabolic rates and longer generation times. In some multicellular organisms, cells specialized for metabolism will have enlarged surface areas, such as intestinal vili.

Origin and evolution



Phylogenetic tree showing the relationship between the eukaryotes and other forms of life. Eukaryotes are colored red, archaea green and bacteria blue.



One hypothesis of eukaryotic relationships

The origin of the eukaryotic cell was a milestone in the evolution of life, since they include all complex cells and almost all multi-cellular organisms. The timing of this series of events is hard to determine; Knoll (2006) suggests they developed approximately 1.6–2.1 billion years ago. Some acritarchs are known from at least 1650 million years ago, and the possible alga *Grypania* has been found as far back as 2100 million years ago.

Fossils that are clearly related to modern groups start appearing around 1.2 billion years ago, in the form of a red alga, though recent work suggests the existence of fossilized filamentous algae in the Vindhya basin dating back to 1.6 to 1.7 billion years ago.

Biomarkers suggest that at least stem eukaryotes arose even earlier. The presence of steranes in Australian shales indicates that eukaryotes were present 2.7 billion years ago.

Phylogeny

rRNA trees constructed during the 1980s and 1990s left most eukaryotes in an unresolved "crown" group (not technically a true crown), which was usually divided by the form of the mitochondrial cristae. The few groups that lack mitochondria branched separately, and so the absence was believed to be primitive; but this is now considered an artifact of long-branch attraction, and they are known to have lost them secondarily.

Six supergroup/kingdom model

A classification produced in 2005 for the International Society of Protistologists, which reflected the consensus of the time, divided the eukaryotes into six supposedly monophyletic 'supergroups'. Although the published classification deliberately did not use formal taxonomic ranks, other sources have treated each of the six as a separate Kingdom.

Excavata	Various flagellate protozoa
Amoebozoa	Most lobose amoeboids and slime moulds
Opisthokonta	Animals, fungi, choanoflagellates, etc.
Rhizaria	Foraminifera, Radiolaria, and various other amoeboid protozoa
Chromalveolata	Stramenopiles (or Heterokonta), Haptophyta, Cryptophyta (or cryptomonads), and Alveolata
Archaeplastida (or Primoplantae)	Land plants, green algae, red algae, and glaucophytes

However, in the same year (2005), doubts were expressed as to whether some of these supergroups were monophyletic, particularly the Chromalveolata, and a review in 2006 noted the lack of evidence for several of the supposed six supergroups.

As of 2010, there is widespread agreement that the Rhizaria belong with the Stramenopiles and the Alveolata, in a clade dubbed the SAR supergroup, so that Rhizara is not one of the main eukaryote groups; also that the Amoeboza and Opisthokonta are each monophyletic and form a clade, often called the unikonts. Beyond this, there does not appear to be a consensus.

Relationship to Archaea

Eukaryotes are more closely related to Archaea than Bacteria, at least in terms of nuclear DNA and genetic machinery, and one controversial idea is to place them with Archaea in the clade Neomura. However, in other respects, such as membrane composition, eukaryotes are similar to Bacteria. Three main explanations for this have been proposed:

- Eukaryotes resulted from the complete fusion of two or more cells, wherein the cytoplasm formed from a eubacterium, and the nucleus from an archaeon, from a virus, or from a pre-cell.
- Eukaryotes developed from Archaea, and acquired their eubacterial characteristics from the proto-mitochondrion.
- Eukaryotes and Archaea developed separately from a modified eubacterium.

There is also the Kronocyte theory for the origin of the Eukaryotic cell. This postulates that a primitive Eukaryotic cell emerged from the pre-DNA world but retained the earlier RNA based chemistry from which all modern life emerged. This primitive cell is called the Kronocyte. According to this hypothesis an RNA based Kronocyte coexisted with the DNA based Archaea (and probably eubacteria) and became the modern eukaryotic cell after a number of major endosymbioses—the first was the incorporation of an Archaea that introduced DNA metabolism and the nucleus, then the incorporation of an alphaproteobacter that became the mitochondria (and photosynthetic bacteria found in today's plants as chloroplasts). The Kronocyte hypothesis explains the large number of genes that are today only found in Eukaryotes but not in Archaea or Bacteria.

Endomembrane system and mitochondria

The origins of the endomembrane system and mitochondria are also unclear. The **phagotrophic hypothesis** proposes that eukaryotic-type membranes lacking a cell wall originated first, with the development of endocytosis, whereas mitochondria were acquired by ingestion as endosymbionts. The **syntrophic hypothesis** proposes that the proto-eukaryote relied on the proto-mitochondrion for food, and so ultimately grew to surround it. Here the membranes originated after the engulfment of the mitochondrion, in part thanks to mitochondrial genes (the hydrogen hypothesis is one particular version).

In a study using genomes to construct supertrees, Pisani *et al.* (2007) suggest that, along with evidence that there was never a mitochondrion-less eukaryote, eukaryotes evolved from a syntrophy between an archaea closely related to Thermoplasmatales and an α-proteobacterium, likely a symbiosis driven by sulfur or hydrogen. The mitochondrion and its genome is a remnant of the α-proteobacterial endosymbiont.

Chapter 2

Chromalveolate

Chromalveolate

Clockwise from top-left: a haptophyte, some diatoms, a water mold, a cryptomonad, and *Macrocystis*, a phaeophyte

Scientific classification	
Domain:	Eukarya
(unranked)	Bikonta
(unranked):	Corticata
Kingdom:	**Chromalveolata***

Phyla

- Heterokontophyta
- Haptophyta
- Cryptophyta
- **Alveolata** (Superphylum)
  - Ciliophora
  - Apicomplexa

- Dinoflagellata

Chromalveolata is a eukaryote supergroup first proposed by Thomas Cavalier-Smith as a refinement of his kingdom Chromista, which was first put forward in 1981. Chromalveolata was proposed to represent the result of a single secondary endosymbiosis between a line descending from a bikont and a red alga that became the progenitor of chlorophyll c containing plastids. In a major classification produced in 2005, Chromalveolata was regarded as one of the six major groups within the eukaryotes. However this has been increasingly challenged. Thus two papers published in 2008 have phylogenetic trees in which the chromalveolates are split up.

Groups and classification

Historically, many chromalveolates were considered plants, because of their cell walls, photosynthetic ability, and in some cases their morphological resemblance to the land plants (Embryophyta). However, when the five-kingdom system took prevalence over the animal-plant dichotomy, most chromalveolates were put into the kingdom Protista, with the water molds and slime nets put into the kingdom Fungi, and the brown algae staying in the plant kingdom.

In 2005, in a classification reflecting the consensus at the time, the Chromalveolata were regarded as one of the six major clades of eukaryotes. Although not given a formal taxonomic status in this classification, elsewhere the group has been treated as a Kingdom. The Chromalveolata were divided into four major subgroups:

- Cryptophyta
- Haptophyta
- Stramenopiles (or Heterokontophyta)
- Alveolata

Other groups which may be included within, or related to, chromalveolates, are:

- Telonemia

Though several groups, such as the ciliates and the water molds, have lost the ability to photosynthesize, most are autotrophic. All photosynthetic chromalveolates use chlorophylls *a* and *c*, and many use accessory pigments. Chromalveolates share similar glyceraldehyde 3-phosphate dehydrogenase proteins.

However, as early as 2005, doubts were being expressed as to whether the Chromalveolata was monophyletic, and a review in 2006 noted the lack of evidence for several of the supposed six major eukaryote groups, including the Chromalveolata. As of 2010 there seems to be an emerging consensus that the group is not monophyletic. The four original subgroups fall into two categories, one comprising the Cryptophyta and the Haptophyta, the other the Stramenopiles and the Alveolata.

Halvaria

Analyses in 2007 and 2008 agree that the Stramenopiles and the Alveolata are related, forming a reduced chromalveolate clade.

Hacrobia

The Haptophyta and Cryptophyta are related in these analyses, forming a clade which has been called 'Hacrobia'.

Position of SAR and Hacrobia

The Hacrobia appear to be more closely related to the Archaeplastida (plants in the very broad sense), being a sister group in one analysis, and actually nested inside this group in another. (Earlier, Cavalier-Smith had suggested a clade called Corticata for the grouping of *all* the chromalveolates and the Archaeplastida.) The SAR supergroup and the Archaeplastida/Hacrobia combination are grouped in the bikonts, which all appear to descend from a heterotrophic eukaryote with two flagella.

Morphology

Chromalveolates, unlike other groups with multicellular representatives, do not have very many common morphological characteristics. Each major subgroup has certain unique features, including the alveoli of the Alveolata, the haptonema of the Haptophyta, the ejectisome of the Crytophyta, and the two different flagella of the Heterokontophyta. However, none of these features are present in all of the groups.

The only common chromalveolate features are these:

- The shared origin of chloroplasts, as mentioned above
- Presence of cellulose in most cell walls

Since this is such a diverse group, it is difficult to summarize shared chromalveolate characteristics.

Ecological role

A potato plant infected with *Phytophthora infestans*.

Many chromalveolates affect our ecosystem in enormous ways. Some of these organisms can be very harmful. Dinoflagellates produce red tides which can devastate fish populations and intoxicate oyster harvests. Apicomplexans are some of the most successful specific parasites to animals. Water molds cause several plant diseases. In fact, it was a water mold, *Phytophthora infestans*, that caused the Irish potato famine.

A Californian kelp forest.

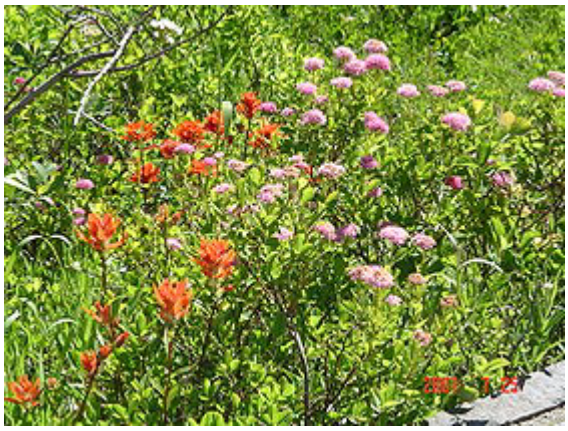
However, many chromalveolates are vital members of our ecosystem. Diatoms are one of the major photosynthetic producers, and as such produce much of the oxygen we breathe, and also take in much of the carbon dioxide from the atmosphere. Brown algae, most specifically kelps, create underwater "forest" habitats for many marine creatures, and provide a large portion of the diet of coastal communities.

Chromalveolates also provide many products that we use. The algin in brown algae is used as a food thickener, most famously in ice cream. The siliceous shells of diatoms have many uses, such as in reflective paint, in toothpaste, or as a filter, in what is known as diatomaceous earth.

Chapter 3

Archaeplastida

Archaeplastida
Temporal range: Mesoproterozoic–Recent
Had'n
Archean
Proterozoic
Pha.



Indian paintbrush and wild huckleberry

Scientific classification	
Domain:	Eukaryota
(unranked):	**Archaeplastida** Adl *et al.* 2005

Subgroups

- Red algae
- Glaucophytes

- Plantae (land plants and green algae)

The **Archaeplastida** (or **Plantae** *sensu lato*) are a major group of eukaryotes, comprising the red and green algae and the land plants, together with a small group called the glaucophytes. The plastids (chloroplasts) of all of these organisms are surrounded by two membranes, suggesting they developed directly from endosymbiotic cyanobacteria. In all other groups, plastids are surrounded by three or four membranes, suggesting they were acquired secondarily from red or green algae.

Although many studies have suggested that the Archaeplastida form a monophyletic group, a 2009 paper argues that they are in fact paraphyletic. The enrichment of novel red algal genes in a recent study demonstrates a strong signal for Plantae (Archaeplastida) monophyly and an equally strong signal of gene sharing history between the red/green algae and other lineages, thus shedding lights on the complexity of eukaryote evolution.

The cells of the Archaeplastida typically lack centrioles and have mitochondria with flat cristae. There is usually a cell wall including cellulose, and food is stored in the form of starch. However, these characters are also shared with other eukaryotes. The main evidence the Archaeplastida form a monophyletic group comes from genetic studies, which indicate that their plastids probably had a single origin. This evidence is disputed.

The archaeplastidans fall into two main evolutionary lines. The red algae are pigmented with chlorophyll *a* and phycobiliproteins, like most cyanobacteria. The green algae and land plants – together known as Viridiplantae (Latin for "green plants") or Chloroplastida – are pigmented with chlorophylls *a* and *b*, but lack phycobiliproteins. The glaucophytes have typical cyanobacterial pigments, and are unusual in retaining a cell wall within their plastids (called cyanelles).

Taxonomy

The consensus in 2005, when the group consisting of the glaucophytes, red and green algae and land plants was named 'Archaeoplastida', was that it was a clade, i.e. was monophyletic. Many studies published since this date have provided evidence which is in agreement. On the other hand, other studies have suggested that the group is paraphyletic. To date, the situation appears unresolved, but a strong signal for Plantae (Archaeplastida) monophyly has been demonstrated in a recent study (with an enrichment of red algal genes). The assumption made here is that Archaeplastida is a valid clade.

Various names have been given to the group. Some authors have simply referred to the group as plants or Plantae. However, the name Plantae is ambiguous, since it has also been applied to less inclusive clades, such as Viridiplantae and embryophytes. To distinguish, the larger group is sometimes known as Plantae *sensu lato* ("plants in the broad sense").

To avoid ambiguity, other names have been proposed. Primoplantae, which appeared in 2004, seems to be the first new name suggested for this group.

Another name that has been applied to this node is Plastida, defined as the clade sharing "plastids of primary (direct prokaryote) origin [as] in *Magnolia virginiana* Linnaeus 1753".

The name Archaeplastida was proposed in 2005 by a large international group of authors (Adl et al.) who aimed to produce a classification for the eukaryotes which took into account morphology, biochemistry and phylogenetics, and which had "some stability in the near term." They rejected the use of formal taxonomic ranks in favour of a hierarchical arrangement where the clade names do not signify rank. Thus the phylum name 'Glaucophyta' and the class name 'Rhodophyceae' appear at the same level in their classification. The divisions proposed for the Archaeplastida are shown below in both tabular and diagrammatic form.

Archaeplastida:

- Glaucophyta Skuja 1954 (Glaucocystophyta Kies and Kremer 1986) – glaucophytes

  Glaucophytes are a small group of freshwater single-celled algae. Their chloroplasts, called *cyanelles*, have a peptidoglycan layer, making them more similar to cyanobacteria than those of the remaining Archaeplastida.

- Rhodophyceae Thuret 1855, emend. Rabenhorst 1863, emend. Adl et al. 2005 (Rhodophyta Wettstein 1901) – red algae

  Red algae form one of the largest groups of algae. Most are seaweeds, being multicellular and marine. Their red colour comes from phycobiliproteins, used as accessory pigments in light capture for photosynthesis.

- Chloroplastida Adl et al. 2005 (Viridiplantae Cavalier-Smith 1981; Chlorobionta Jeffrey 1982, emend. Bremer 1985, emend. Lewis and McCourt 2004; Chlorobiota Kendrick and Crane 1997)

  Chloroplastida is the term chosen by Adl et al. for the group made up of the green algae and land plants (embryophytes). Except where lost secondarily, all have chloroplasts without a peptidoglycan layer and lack phycobiliproteins.

  - Chlorophyta Pascher 1914, emend. Lewis and Mc Court 2004 – green algae (part)

  Adl et al. employ a narrow definition of the Chlorophyta; other sources include the Chlorodendrales and Prasinophytae, which may themselves be combined.

  - Ulvophyceae Mattox and Stewart 1984

- Trebouxiophyceae Friedl 1995 (Pleurastrophyceae Mattox et al. 1984; Microthamniales Melkonian 1990)
- Chlorophyceae Christensen 1994

- Chlorodendrales Fritsch 1917 – green algae (part)
- Prasinophytae Cavalier-Smith 1998, emend. Lewis and McCourt 2004 – green algae (part)
- *Mesostigma* Lauterborn 1894, emend. McCourt in Adl et al. 2005 (Mesostigmata Turmel, Otis, and Lemieux 2002)
- Charophyta Karol et al. 2001, emend. Lewis and McCourt 2004 (Charophyceae Smith 1938, emend. Mattox and Stewart 1984) – green algae (part) and land plants

Charophyta *sensu lato*, as used by Adl et al., is a monophyletic group which is made up of some green algae, including the stoneworts (Charophyta *sensu stricto*), as well as the land plants (embryophytes).

Morphology

All archaeplastidans have plastids (chloroplasts) that carry out photosynthesis and are believed to be derived from captured cyanobacteria. In glaucophytes, perhaps the most primitive members of the group, the chloroplast is called a *cyanelle* and shares several features with cyanobacteria, including a peptidoglycan cell wall, that are not retained in other members of the group. The resemblance of cyanelles to cyanobacteria supports the endosymbiotic theory.

The cells of most archaeplastidans have walls, commonly but not always made of cellulose.

The Archaeplastida vary widely in the degree of their cell organization, from isolated cells to filaments to colonies to multi-celled organisms. The earliest were unicellular, and many groups remain so today. Multicellularity evolved separately in several groups, including red algae, ulvophyte green algae, and in the green algae that gave rise to stoneworts and land plants.

Endosymbiosis

Because the ancestral archaeplastidan is hypothesized to have acquired its chloroplasts directly by engulfing cyanobacteria, the event is known as a *primary endosymbiosis* (as reflected in the name chosen for the group 'Archaeplastida' i.e. 'ancient plastid'). Evidence for primary endosymbosis includes the presence of a double membrane around the chloroplasts; one membrane belonged to the bacterium, and the other to the eukaryote that captured it. Over time, many genes from the chloroplast have been transferred to the nucleus of the host cell. The presence of such genes in the nuclei of eukaryotes without chloroplasts suggests this transfer happened early in the evolution of the group.

Other eukaryotes with chloroplasts appear to have gained them by engulfing a single-celled archaeplastidan with its own bacterially-derived chloroplasts. Because these events involve endosymbiosis of cells that have their own endosymbionts, the process is called *secondary endosymbiosis*. The chloroplasts of such eukaryotes are typically surrounded by more than two membranes, reflecting a history of multiple engulfment. The chloroplasts of euglenids and chlorarachniophytes appear to be captured green algae, whereas those of other photosynthetic eukaryotes, such as heterokont algae, cryptophytes, haptophytes, and dinoflagellates, appear to be captured red algae.

Fossil record

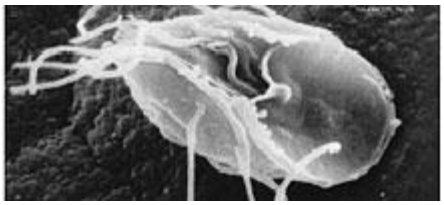
Perhaps the most ancient remains of Archaeplastida are microfossils from the Roper group in northern Australia. The structure of these single-celled fossils resembles that of modern green algae. They date to the Mesoproterozoic Era, about 1500 to 1300 Ma (million years ago) These fossils are consistent with a molecular clock study that calculated that this clade diverged about 1500 Ma. The oldest fossil that can be assigned to a specific modern group is the red alga *Bangiomorpha*, from 1200 Ma.

In the late Neoproterozoic Era, algal fossils became more numerous and diverse. Eventually, in the Paleozoic Era, plants emerged onto land, and have continued to flourish up to the present.

Chapter 4

Excavate, Opisthokont and Rhizaria

Excavate

Excavates

Giardia lamblia, a parasitic diplomonad
Scientific classification
Domain: Eukaryota
(unranked): Bikonta
Kingdom: **Excavata** (Cavalier-Smith) Simpson, 2003
Phyla
Metamonada
Loukozoa
Euglenozoa
Percolozoa

The **excavates** are a major kingdom of unicellular eukaryotes, often known as **Excavata**. The phylogenetic category Excavata, proposed by Cavalier-Smith in 2002, contains a

variety of free-living and symbiotic forms, and also includes some important parasites of humans.

Characteristics

Many excavates lack 'classical' mitochondria - these organisms are often referred to as 'amitochondriate', although most, perhaps all, retain a mitochondrial organelle in greatly modified form. Others have mitochondria with tubular, discoidal, or in some cases, laminar cristae. Most excavates have two, four, or more flagella and many have a conspicuous ventral feeding groove with a characteristic ultrastructure, supported by microtubules. However, various groups that lack these traits may be considered excavates based on genetic evidence (primarily phylogenetic trees of molecular sequences).

The closest that the excavates come to multicellularity are the acrasid slime moulds. Like other cellular slime moulds, they live most of their life as single cells, but will sometimes assemble into a larger cluster.

Subgroups

Excavates are classified into four major subgroups at the phylum/superphylum level. These are shown in the table below.

Superphylum	Phylum	Representative genera	Description
Discoba	Euglenozoa	e.g. *Euglena*, *Trypanosoma*	Many important parasites, one large group with plastids (chloroplasts)
	Percolozoa (Heterolobosea)	e.g. *Naegleria*, *Acrasis*	Most alternate between flagellate and amoeboid forms
	Jakobida	e.g. *Jakoba*, *Reclinomonas*	Free-living, sometimes loricate flagellates, with very gene-rich mitochondrial genomes
Metamonada	Preaxostyla	e.g. Oxymonads, *Trimastix*	Amitochontriate flagellates, either free-living (*Trimastix*) or living in the hindguts of insects
	Fornicata	e.g. *Giardia*, *Carpediemonas*	Amitochondriate, mostly symbiotes and parasites of animals.
	Parabasalia	e.g. *Trichomonas*	Amitochondriate flagellates, generally intestinal commensals of insects. Some human pathogens.

Heterolobosea (Percolozoa) and Euglenozoa appear to be particularly close relatives, and are united by the presence of discoid cristae within the mitochondria (Superphylum **Discicristata**). More recently a close relationship has been shown between Discicristata

and Jakobida. Most jakobids have tubular cristae, like most other protists, while the metamonads are unusual in having lost classical mitochondria—instead they have 'hydrogenosomes', 'mitosomes' or uncharacterised organelles. In addition to the groups mentioned in the table above, the genus *Malawimonas* is generally considered to be a member of Excavata owing to its typical excavate morphology, and phylogenetic affinity to excavate groups in some molecular phylogenies. However, its position among excavates remains elusive.

Excavate relationships are still uncertain; it is possible that they are not a monophyletic group. The monophyly of the excavates is far from clear, although it seems like there are several clades within the excavates which are monophyletic.

Certain excavates are often considered among the most primitive eukaryotes, based partly on their placement in many evolutionary trees. This could encourage proposals that excavates are a paraphyletic grade that includes the ancestors of other living eukaryotes. However, the placement of certain excavates as 'early branches' may be an analysis artifact caused by long branch attraction, as has been seen with some other groups, for example, microsporidia.

Opisthokont

Opisthokont
Temporal range: Neoproterozoic–Recent
Had'n
Archean
Proterozoic
Pha.
Scientific classification
Domain: Eukaryota
(unranked): Unikonta
(unranked): **Opisthokonta**

The **opisthokonts** (Greek: ὀπίσθιος (*opísthios*) = "rear, posterior" + κοντός (*kontós*) = "pole" i.e. "flagellum") are a broad group of eukaryotes, including both the animal and fungus kingdoms, together with the eukaryotic microorganisms that are sometimes grouped in the paraphyletic phylum Choanozoa (previously assigned to the protist "kingdom"). Both genetic and ultrastructural studies strongly support that opisthokonts form a monophyletic group.

"Opisthokonta" and "Fungi/Metazoa group" are sometimes considered synonymous.

Flagella

One common characteristic is that flagellate cells, such as most animal sperm and chytrid spores, propel themselves with a single **posterior** flagellum. This gives the groups its name.

In contrast, flagellate cells in other eukaryote groups propel themselves with one or more **anterior** flagella.

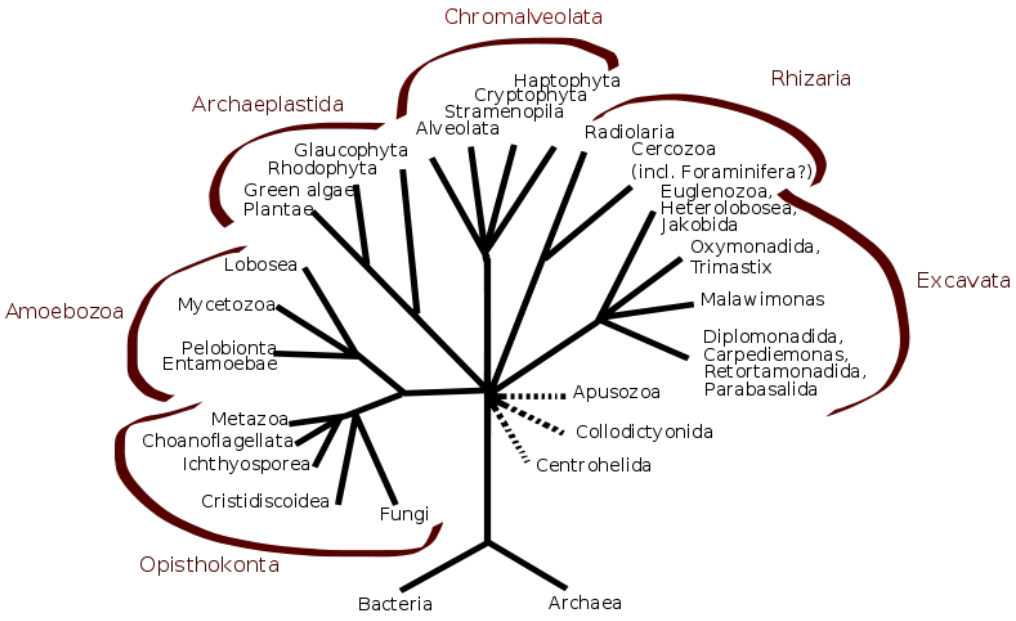
History

The close relationship between animals and fungi was suggested by Cavalier-Smith in 1987, who used the informal name opisthokonta (the formal name has been used for the chytrids), and was confirmed by later genetic studies.

Early phylogenies placed them near the plants and other groups that have mitochondria with flat cristae, but this character varies.

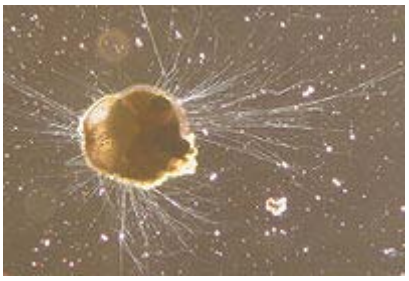
Cavalier-Smith and Stechmann argue that the uniciliate eukaryotes such as opisthokonts and Amoebozoa, collectively called unikonts, split off from the other biciliate eukaryotes, called bikonts, shortly after they evolved.

Taxonomy



One hypothesis of eukaryote relationships

Rhizaria

Rhizaria **Temporal range: Neoproterozoic - Recent**

Live *Ammonia tepida* (Foraminifera)
Scientific classification
Domain: Eukaryota
(unranked): Bikonta
Supergroup: **Rhizaria** Cavalier-Smith, 2002
Phyla
Cercozoa Retaria Foraminifera Radiolaria

The **Rhizaria** are a species-rich supergroup of unicellular eukaryotes. This supergroup was proposed by Cavalier-Smith in 2002. They vary considerably in form, but for the most part they are amoeboids with filose, reticulose, or microtubule-supported pseudopods. Many produce shells or skeletons, which may be quite complex in structure, and these make up the vast majority of protozoan fossils. Nearly all have mitochondria with tubular cristae.

Groups

There are three main groups of Rhizaria:

- Cercozoa - Various amoebae and flagellates, usually with filose pseudopods and common in soil
- Foraminifera - Amoeboids with reticulose pseudopods, common as marine benthos

- Radiolaria - Amoeboids with axopods, common as marine plankton

A few other groups may be included in the Cercozoa, but on some trees appear closer to the Foraminifera. These are the Phytomyxea and Ascetosporea, parasites of plants and animals respectively, and the peculiar amoeba *Gromia*. The different groups of Rhizaria are considered close relatives based mainly on genetic similarities, and have been regarded as an extension of the Cercozoa. The name Rhizaria for the expanded group was introduced by Cavalier-Smith in 2002, who also included the centrohelids and Apusozoa.

Evolutionary relationship

Rhizaria is part of the bikont clade, which also comprises the Archaeplastida, the Chromalveolata, the Excavata, and some smaller, unresolved groups such as the Apusozoa and the Centrohelida. As bikonts, they all descend from a heterotrophic eukaryote with two flagella.

Historically, many rhizarians were considered animals, with their motility and heterotrophy as justification. However, when the five-kingdom system took prevalence over the animal-plant dichotomy, the rhizarians were put into the kingdom Protista. Then, after Woese published his three-domain system, because of the paraphyly of the kingdom Monera, taxonomists turned their attention to the eukaryote domain, and the inherent paraphyly of Protista. After much debate, which continues to this day, Rhizaria emerged as a monophyletic group.

Chapter 5

Fungus

Fungi Temporal range: Early Devonian–Recent	
	
Clockwise from top left: *Amanita muscaria*, a basidiomycete; *Sarcoscypha coccinea*, an ascomycete; bread covered in mold; a chytrid; a *Penicillium* conidiophore.	
Scientific classification	
Domain:	Eukaryota
(unranked):	Opisthokonta
Kingdom:	**Fungi** (L., 1753) R.T. Moore, 1980
Subkingdoms/Phyla/Subphyla	
Blastocladiomycota Chytridiomycota Glomeromycota	

Microsporidia
Neocallimastigomycota

Dikarya (inc. Deuteromycota)

Ascomycota
Pezizomycotina
Saccharomycotina
Taphrinomycotina
Basidiomycota
Agaricomycotina
Pucciniomycotina
Ustilaginomycotina

Subphyla Incertae sedis

Entomophthoromycotina
Kickxellomycotina
Mucoromycotina
Zoopagomycotina

A **fungus** is a member of a large group of eukaryotic organisms that includes microorganisms such as yeasts and molds (British English: moulds), as well as the more familiar mushrooms. These organisms are classified as a kingdom, **Fungi**, which is separate from plants, animals, and bacteria. One major difference is that fungal cells have cell walls that contain chitin, unlike the cell walls of plants, which contain cellulose. These and other differences show that the fungi form a single group of related organisms, named the *Eumycota* (*true fungi* or *Eumycetes*), that share a common ancestor (a *monophyletic group*). This fungal group is distinct from the structurally similar myxomycetes (slime molds) and oomycetes (water molds). The discipline of biology devoted to the study of fungi is known as mycology, which is often regarded as a branch of botany, even though genetic studies have shown that fungi are more closely related to animals than to plants.

Abundant worldwide, most fungi are inconspicuous because of the small size of their structures, and their cryptic lifestyles in soil, on dead matter, and as symbionts of plants, animals, or other fungi. They may become noticeable when fruiting, either as mushrooms or molds. Fungi perform an essential role in the decomposition of organic matter and have fundamental roles in nutrient cycling and exchange. They have long been used as a direct source of food, such as mushrooms and truffles, as a leavening agent for bread, and in fermentation of various food products, such as wine, beer, and soy sauce. Since the 1940s, fungi have been used for the production of antibiotics, and, more recently, various enzymes produced by fungi are used industrially and in detergents. Fungi are also used as biological pesticides to control weeds, plant diseases and insect pests. Many species produce bioactive compounds called mycotoxins, such as alkaloids and polyketides, that are toxic to animals including humans. The fruiting structures of a few species contain

psychotropic compounds and are consumed recreationally or in traditional spiritual ceremonies. Fungi can break down manufactured materials and buildings, and become significant pathogens of humans and other animals. Losses of crops due to fungal diseases (e.g. rice blast disease) or food spoilage can have a large impact on human food supplies and local economies.

The fungus kingdom encompasses an enormous diversity of taxa with varied ecologies, life cycle strategies, and morphologies ranging from single-celled aquatic chytrids to large mushrooms. However, little is known of the true biodiversity of Kingdom Fungi, which has been estimated at around 1.5 million species, with about 5% of these having been formally classified. Ever since the pioneering 18th and 19th century taxonomical works of Carl Linnaeus, Christian Hendrik Persoon, and Elias Magnus Fries, fungi have been classified according to their morphology (e.g., characteristics such as spore color or microscopic features) or physiology. Advances in molecular genetics have opened the way for DNA analysis to be incorporated into taxonomy, which has sometimes challenged the historical groupings based on morphology and other traits. Phylogenetic studies published in the last decade have helped reshape the classification of Kingdom Fungi, which is divided into one subkingdom, seven phyla, and ten subphyla.

Etymology

The English word *fungus* is directly adopted from the Latin *fungus* (mushroom), used in the writings of Horace and Pliny. This in turn is derived from the Greek word *sphongos*/σφογγος ("sponge"), which refers to the macroscopic structures and morphology of mushrooms and molds; the root is also used in other languages, such as the German *Schwamm* ("sponge"), *Schimmel* ("mold"), and the French *champignon* and the Spanish *champiñon* (which both mean "mushroom"). The use of the word *mycology*, which is derived from the Greek *mykes*/μύκης (mushroom) and *logos*/λόγος (discourse), to denote the scientific study of fungi is thought to have originated in 1836 with English naturalist Miles Joseph Berkeley's publication *The English Flora of Sir James Edward Smith, Vol. 5*.

Characteristics

Before the introduction of molecular methods for phylogenetic analysis, taxonomists considered fungi to be members of the Plant Kingdom because of similarities in lifestyle: both fungi and plants are mainly immobile, and have similarities in general morphology and growth habitat. Like plants, fungi often grow in soil, and in the case of mushrooms form conspicuous fruiting bodies, which sometimes bear resemblance to plants such as mosses. The fungi are now considered a separate kingdom, distinct from both plants and animals, from which they appear to have diverged around one billion years ago. Some morphological, biochemical, and genetic features are shared with other organisms, while others are unique to the fungi, clearly separating them from the other kingdoms:

Shared features:

- With other eukaryotes: As other eukaryotes, fungal cells contain membrane-bound nuclei with chromosomes that contain DNA with noncoding regions called introns and coding regions called exons. In addition, fungi possess membrane-bound cytoplasmic organelles such as mitochondria, sterol-containing membranes, and ribosomes of the 80S type. They have a characteristic range of soluble carbohydrates and storage compounds, including sugar alcohols (e.g., mannitol), disaccharides, (e.g., trehalose), and polysaccharides (e.g., glycogen, which is also found in animals).
- With animals: Fungi lack chloroplasts and are heterotrophic organisms, requiring preformed organic compounds as energy sources.
- With plants: Fungi possess a cell wall and vacuoles. They reproduce by both sexual and asexual means, and like basal plant groups (such as ferns and mosses) produce spores. Similar to mosses and algae, fungi typically have haploid nuclei.
- With euglenoids and bacteria: Higher fungi, euglenoids, and some bacteria produce the amino acid L-lysine in specific biosynthesis steps, called the α-aminoadipate pathway.
- The cells of most fungi grow as tubular, elongated, and thread-like (filamentous) structures and are called hyphae, which may contain multiple nuclei and extend at their tips. Each tip contains a set of aggregated vesicles—cellular structures consisting of proteins, lipids, and other organic molecules—called Spitzenkörper. Both fungi and oomycetes grow as filamentous hyphal cells. In contrast, similar-looking organisms, such as filamentous green algae, grow by repeated cell division within a chain of cells.
- In common with some plant and animal species, more than 60 fungal species display the phenomenon of bioluminescence.

Unique features:

- Some species grow as single-celled yeasts that reproduce by budding or binary fission. Dimorphic fungi can switch between a yeast phase and a hyphal phase in response to environmental conditions.
- The fungal cell wall is composed of glucans and chitin; while the former compounds are also found in plants and the latter in the exoskeleton of arthropods, fungi are the only organisms that combine these two structural molecules in their cell wall. In contrast to plants and the oomycetes, fungal cell walls do not contain cellulose.

Omphalotus nidiformis, a bioluminescent mushroom

Most fungi lack an efficient system for long-distance transport of water and nutrients, such as the xylem and phloem in many plants. To overcome these limitations, some fungi, such as *Armillaria*, form rhizomorphs, that resemble and perform functions similar to the roots of plants. Another characteristic shared with plants includes a biosynthetic pathway for producing terpenes that uses mevalonic acid and pyrophosphate as chemical building blocks. However, plants have an additional terpene pathway in their chloroplasts, a structure fungi do not possess. Fungi produce several secondary metabolites that are similar or identical in structure to those made by plants. Many of the plant and fungal enzymes that make these compounds differ from each other in sequence and other characteristics, which indicates separate origins and evolution of these enzymes in the fungi and plants.

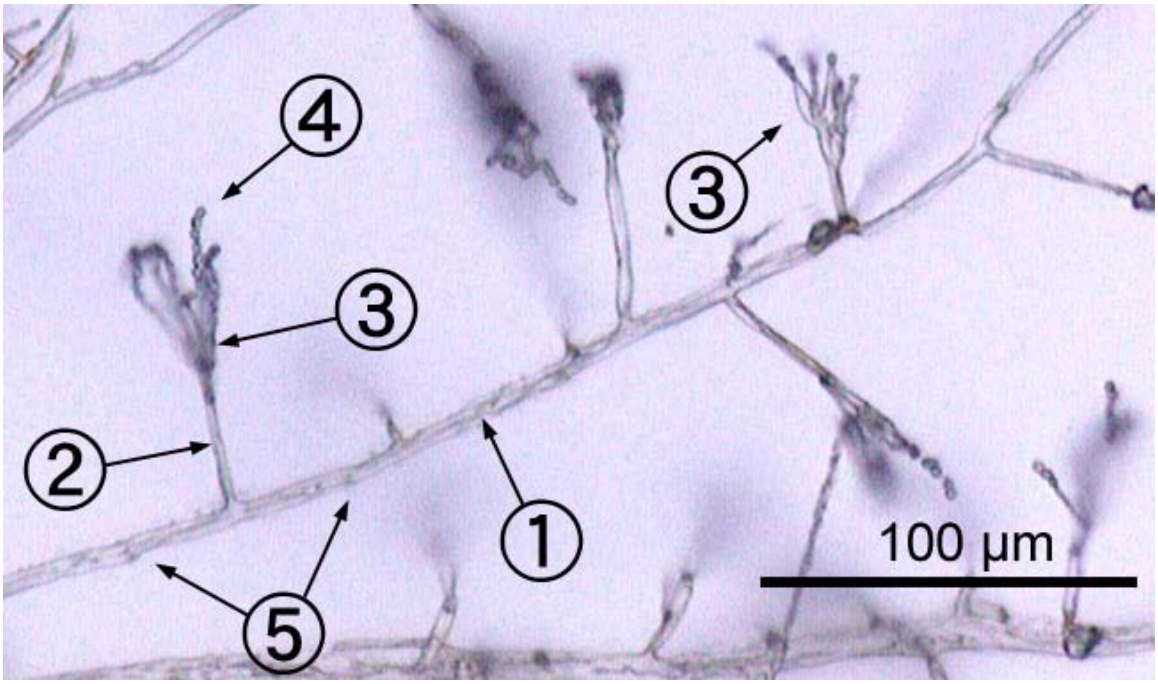
Diversity

Fungi have a worldwide distribution, and grow in a wide range of habitats, including extreme environments such as deserts or areas with high salt concentrations or ionizing radiation, as well as in deep sea sediments. Some can survive the intense UV and cosmic radiation encountered during space travel. Most grow in terrestrial environments, though several species live partly or solely in aquatic habitats, such as the chytrid fungus *Batrachochytrium dendrobatidis*, a parasite that has been responsible for a worldwide decline in amphibian populations. This organism spends part of its life cycle as a motile zoospore, enabling it to propel itself through water and enter its amphibian host. Other examples of aquatic fungi include those living in hydrothermal areas of the ocean.

Around 100,000 species of fungi have been formally described by taxonomists, but the global biodiversity of the fungus kingdom is not fully understood. On the basis of observations of the ratio of the number of fungal species to the number of plant species in selected environments, the fungal kingdom has been estimated to contain about 1.5 million species. In mycology, species have historically been distinguished by a variety of methods and concepts. Classification based on morphological characteristics, such as the size and shape of spores or fruiting structures, has traditionally dominated fungal taxonomy. Species may also be distinguished by their biochemical and physiological characteristics, such as their ability to metabolize certain biochemicals, or their reaction to chemical tests. The biological species concept discriminates species based on their ability to mate. The application of molecular tools, such as DNA sequencing and phylogenetic analysis, to study diversity has greatly enhanced the resolution and added robustness to estimates of genetic diversity within various taxonomic groups.

Morphology

Microscopic structures



An environmental isolate of *Penicillium*
1. hypha 2. conidiophore 3. phialide 4. conidia 5. septa

Most fungi grow as hyphae, which are cylindrical, thread-like structures 2–10 µm in diameter and up to several centimeters in length. Hyphae grow at their tips (apices); new hyphae are typically formed by emergence of new tips along existing hyphae by a process called *branching*, or occasionally growing hyphal tips bifurcate (fork) giving rise to two parallel-growing hyphae. The combination of apical growth and branching/forking leads to the development of a mycelium, an interconnected network of hyphae. Hyphae can be either septate or coenocytic: septate hyphae are divided into compartments separated by cross walls (internal cell walls, called septa, that are formed at right angles to the cell wall giving the hypha its shape), with each compartment containing one or more nuclei; coenocytic hyphae are not compartmentalized. Septa have pores that allow cytoplasm, organelles, and sometimes nuclei to pass through; an example is the dolipore septum in the fungi of the phylum Basidiomycota. Coenocytic hyphae are essentially multinucleate supercells.

Many species have developed specialized hyphal structures for nutrient uptake from living hosts; examples include haustoria in plant-parasitic species of most fungal phyla, and arbuscules of several mycorrhizal fungi, which penetrate into the host cells to consume nutrients.

Although fungi are opisthokonts—a grouping of evolutionarily related organisms broadly characterized by a single posterior flagellum—all phyla except for the chytrids have lost

their posterior flagella. Fungi are unusual among the eukaryotes in having a cell wall that, in addition to glucans (e.g., β-1,3-glucan) and other typical components, also contains the biopolymer chitin.

Macroscopic structures

Armillaria solidipes

Fungal mycelia can become visible to the naked eye, for example, on various surfaces and substrates, such as damp walls and on spoiled food, where they are commonly called molds. Mycelia grown on solid agar media in laboratory petri dishes are usually referred to as colonies. These colonies can exhibit growth shapes and colors (due to spores or pigmentation) that can be used as diagnostic features in the identification of species or groups. Some individual fungal colonies can reach extraordinary dimensions and ages as in the case of a clonal colony of *Armillaria solidipes*, which extends over an area of more than 900 ha (3.5 square miles), with an estimated age of nearly 9,000 years.

The apothecium—a specialized structure important in sexual reproduction in the ascomycetes—is a cup-shaped fruiting body that holds the hymenium, a layer of tissue containing the spore-bearing cells. The fruiting bodies of the basidiomycetes (basidiocarps) and some ascomycetes can sometimes grow very large, and many are well-known as mushrooms.

Growth and physiology

The growth of fungi as hyphae on or in solid substrates or as single cells in aquatic environments is adapted for the efficient extraction of nutrients, because these growth forms have high surface area to volume ratios. Hyphae are specifically adapted for growth on solid surfaces, and to invade substrates and tissues. They can exert large penetrative mechanical forces; for example, the plant pathogen *Magnaporthe grisea* forms a structure called an appressorium which evolved to puncture plant tissues. The pressure generated by the appressorium, directed against the plant epidermis, can exceed 8 megapascals (1,200 psi). The filamentous fungus *Paecilomyces lilacinus* uses a similar structure to penetrate the eggs of nematodes.

Mold covering a decaying peach. The frames were taken approximately 12 hours apart over a period of six days.

The mechanical pressure exerted by the appressorium is generated from physiological processes that increase intracellular turgor by producing osmolytes such as glycerol. Morphological adaptations such as these are complemented by hydrolytic enzymes secreted into the environment to digest large organic molecules—such as polysaccharides, proteins, lipids, and other organic substrates—into smaller molecules that may then be absorbed as nutrients. The vast majority of filamentous fungi grow in a polar fashion—i.e., by extension into one direction—by elongation at the tip (apex) of the hypha. Alternative forms of fungal growth include intercalary extension (i.e., by longitudinal expansion of hyphal compartments that are below the apex) as in the case of some endophytic fungi, or growth by volume expansion during the development of mushroom stipes and other large organs. Growth of fungi as multicellular structures consisting of somatic and reproductive cells—a feature independently evolved in animals and plants—has several functions, including the development of fruiting bodies for dissemination of sexual spores and biofilms for substrate colonization and intercellular communication.

Traditionally, the fungi are considered heterotrophs, organisms that rely solely on carbon fixed by other organisms for metabolism. Fungi have evolved a high degree of metabolic versatility that allows them to use a diverse range of organic substrates for growth, including simple compounds such as nitrate, ammonia, acetate, or ethanol. For some

species it has been shown that the pigment melanin may play a role in extracting energy from ionizing radiation, such as gamma radiation; however, this form of "radiotrophic" growth has only been described for a few species, the effects on growth rates are small, and the underlying biophysical and biochemical processes are not known. The authors speculate that this process might bear similarity to CO_2 fixation via visible light, but instead utilizing ionizing radiation as a source of energy.

Reproduction

Polyporus squamosus

Fungal reproduction is complex, reflecting the differences in lifestyles and genetic makeup within this kingdom of organisms. It is estimated that a third of all fungi reproduce by different modes of propagation; for example, reproduction may occur in two well-differentiated stages within the life cycle of a species, the teleomorph and the anamorph. Environmental conditions trigger genetically determined developmental states that lead to the creation of specialized structures for sexual or asexual reproduction. These structures aid reproduction by efficiently dispersing spores or spore-containing propagules.

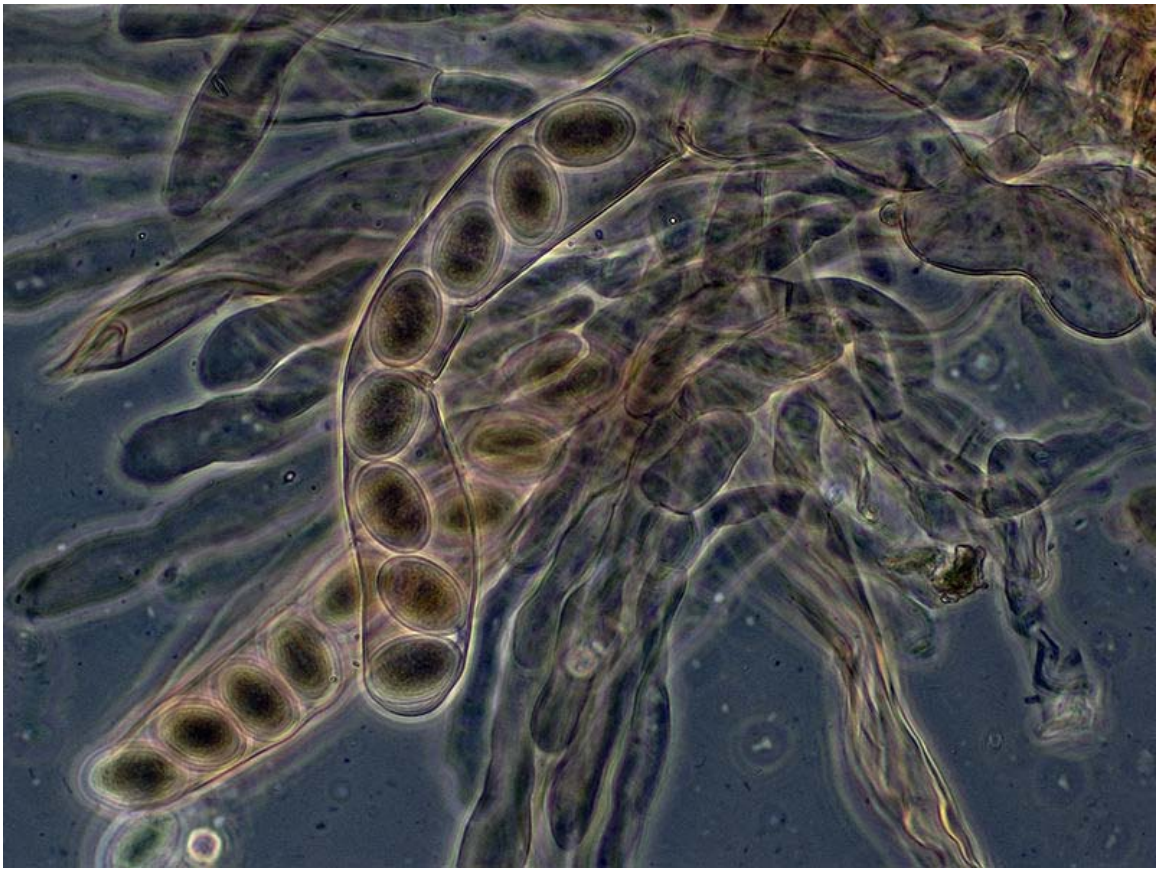
Asexual reproduction

Asexual reproduction via vegetative spores (conidia) or through mycelial fragmentation is common; it maintains clonal populations adapted to a specific niche, and allows more rapid dispersal than sexual reproduction. The "Fungi imperfecti" (fungi lacking the perfect or sexual stage) or Deuteromycota comprise all the species which lack an observable sexual cycle.

Sexual reproduction

Sexual reproduction with meiosis exists in all fungal phyla (with the exception of the Glomeromycota). It differs in many aspects from sexual reproduction in animals or plants. Differences also exist between fungal groups and can be used to discriminate species by morphological differences in sexual structures and reproductive strategies. Mating experiments between fungal isolates may identify species on the basis of biological species concepts. The major fungal groupings have initially been delineated based on the morphology of their sexual structures and spores; for example, the spore-containing structures, asci and basidia, can be used in the identification of ascomycetes and basidiomycetes, respectively. Some species may allow mating only between individuals of opposite mating type, while others can mate and sexually reproduce with any other individual or itself. Species of the former mating system are called heterothallic, and of the latter homothallic.

Most fungi have both an haploid and diploid stage in their life cycles. In sexually reproducing fungi, compatible individuals may combine by fusing their hyphae together into an interconnected network; this process, anastomosis, is required for the initiation of the sexual cycle. Ascomycetes and basidiomycetes go through a dikaryotic stage, in which the nuclei inherited from the two parents do not combine immediately after cell fusion, but remain separate in the hyphal cells.



The 8-spored asci of *Morchella elata*, viewed with phase contrast microscopy

In ascomycetes, dikaryotic hyphae of the hymenium (the spore-bearing tissue layer) form a characteristic *hook* at the hyphal septum. During cell division, formation of the hook ensures proper distribution of the newly divided nuclei into the apical and basal hyphal compartments. An ascus (plural *asci*) is then formed, in which karyogamy (nuclear fusion) occurs. Asci are embedded in an ascocarp, or fruiting body. Karyogamy in the asci is followed immediately by meiosis and the production of ascospores. After dispersal, the ascospores may germinate and form a new haploid mycelium.

Sexual reproduction in basidiomycetes is similar to that of the ascomycetes. Compatible haploid hyphae fuse to produce a dikaryotic mycelium. However, the dikaryotic phase is more extensive in the basidiomycetes, often also present in the vegetatively growing mycelium. A specialized anatomical structure, called a clamp connection, is formed at each hyphal septum. As with the structurally similar hook in the ascomycetes, the clamp connection in the basidiomycetes is required for controlled transfer of nuclei during cell division, to maintain the dikaryotic stage with two genetically different nuclei in each hyphal compartment. A basidiocarp is formed in which club-like structures known as basidia generate haploid basidiospores after karyogamy and meiosis. The most commonly known basidiocarps are mushrooms, but they may also take other forms.

In glomeromycetes (formerly zygomycetes), haploid hyphae of two individuals fuse, forming a gametangium, a specialized cell structure that becomes a fertile gamete-producing cell. The gametangium develops into a zygospore, a thick-walled spore formed by the union of gametes. When the zygospore germinates, it undergoes meiosis, generating new haploid hyphae, which may then form asexual sporangiospores. These sporangiospores allow the fungus to rapidly disperse and germinate into new genetically identical haploid fungal mycelia.

Spore dispersal

Both asexual and sexual spores or sporangiospores are often actively dispersed by forcible ejection from their reproductive structures. This ejection ensures exit of the spores from the reproductive structures as well as travelling through the air over long distances.

The bird's nest fungus *Cyathus stercoreus*

Specialized mechanical and physiological mechanisms, as well as spore surface structures (such as hydrophobins), enable efficient spore ejection. For example, the structure of the spore-bearing cells in some ascomycete species is such that the buildup of substances affecting cell volume and fluid balance enables the explosive discharge of spores into the air. The forcible discharge of single spores termed *ballistospores* involves

formation of a small drop of water (Buller's drop), which upon contact with the spore leads to its projectile release with an initial acceleration of more than 10,000 g; the net result is that the spore is ejected 0.01–0.02 cm, sufficient distance for it to fall through the gills or pores into the air below. Other fungi, like the puffballs, rely on alternative mechanisms for spore release, such as external mechanical forces. The bird's nest fungi use the force of falling water drops to liberate the spores from cup-shaped fruiting bodies. Another strategy is seen in the stinkhorns, a group of fungi with lively colors and putrid odor that attract insects to disperse their spores.

Other sexual processes

Besides regular sexual reproduction with meiosis, certain fungi, such as those in the genera *Penicillium* and *Aspergillus*, may exchange genetic material via parasexual processes, initiated by anastomosis between hyphae and plasmogamy of fungal cells. The frequency and relative importance of parasexual events is unclear and may be lower than other sexual processes. It is known to play a role in intraspecific hybridization and is likely required for hybridization between species, which has been associated with major events in fungal evolution.

Evolution

In contrast to plants and animals, the early fossil record of the fungi is meager. Factors that likely contribute to the under-representation of fungal species among fossils include the nature of fungal fruiting bodies, which are soft, fleshy, and easily degradable tissues and the microscopic dimensions of most fungal structures, which therefore are not readily evident. Fungal fossils are difficult to distinguish from those of other microbes, and are most easily identified when they resemble extant fungi. Often recovered from a permineralized plant or animal host, these samples are typically studied by making thin-section preparations that can be examined with light microscopy or transmission electron microscopy. Compression fossils are studied by dissolving the surrounding matrix with acid and then using light or scanning electron microscopy to examine surface details.

The earliest fossils possessing features typical of fungi date to the Proterozoic eon, some 1,430 million years ago (Ma); these multicellular benthic organisms had filamentous structures with septa, and were capable of anastomosis. More recent studies (2009) estimate the arrival of fungal organisms at about 760–1060 Ma on the basis of comparisons of the rate of evolution in closely related groups. For much of the Paleozoic Era (542–251 Ma), the fungi appear to have been aquatic and consisted of organisms similar to the extant Chytrids in having flagellum-bearing spores. The evolutionary adaptation from an aquatic to a terrestrial lifestyle necessitated a diversification of ecological strategies for obtaining nutrients, including parasitism, saprobism, and the development of mutualistic relationships such as mycorrhiza and lichenization. Recent (2009) studies suggest that the ancestral ecological state of the Ascomycota was saprobism, and that independent lichenization events have occurred multiple times.

The fungi probably colonized the land during the Cambrian (542–488.3 Ma), long before land plants. Fossilized hyphae and spores recovered from the Ordovician of Wisconsin (460 Ma) resemble modern-day Glomerales, and existed at a time when the land flora likely consisted of only non-vascular bryophyte-like plants. Prototaxites, which was probably a fungus or lichen, would have been the tallest organism of the late Silurian. Fungal fossils do not become common and uncontroversial until the early Devonian (416–359.2 Ma), when they are abundant in the Rhynie chert, mostly as Zygomycota and Chytridiomycota. At about this same time, approximately 400 Ma, the Ascomycota and Basidiomycota diverged, and all modern classes of fungi were present by the Late Carboniferous (Pennsylvanian, 318.1–299 Ma).

Lichen-like fossils have been found in the Doushantuo Formation in southern China dating back to 635–551 Ma. Lichens were a component of the early terrestrial ecosystems, and the estimated age of the oldest terrestrial lichen fossil is 400 Ma; this date corresponds to the age of the oldest known sporocarp fossil, a *Paleopyrenomycites* species found in the Rhynie Chert. The oldest fossil with microscopic features resembling modern-day basidiomycetes is *Palaeoancistrus*, found permineralized with a fern from the Pennsylvanian. Rare in the fossil record are the homobasidiomycetes (a taxon roughly equivalent to the mushroom-producing species of the agaricomycetes). Two amber-preserved specimens provide evidence that the earliest known mushroom-forming fungi (the extinct species *Archaeomarasmius legletti*) appeared during the mid-Cretaceous, 90 Ma.

Some time after the Permian-Triassic extinction event (251.4 Ma), a fungal spike (originally thought to be an extraordinary abundance of fungal spores in sediments) formed, suggesting that fungi were the dominant life form at this time, representing nearly 100% of the available fossil record for this period. However, the relative proportion of fungal spores relative to spores formed by algal species is difficult to assess, the spike did not appear worldwide, and in many places it did not fall on the Permian-Triassic boundary.

Taxonomy

Although commonly included in botany curricula and textbooks, fungi are more closely related to animals than to plants and are placed with the animals in the monophyletic group of opisthokonts. Analyses using molecular phylogenetics support a monophyletic origin of the Fungi. The taxonomy of the Fungi is in a state of constant flux, especially due to recent research based on DNA comparisons. These current phylogenetic analyses often overturn classifications based on older and sometimes less discriminative methods based on morphological features and biological species concepts obtained from experimental matings.

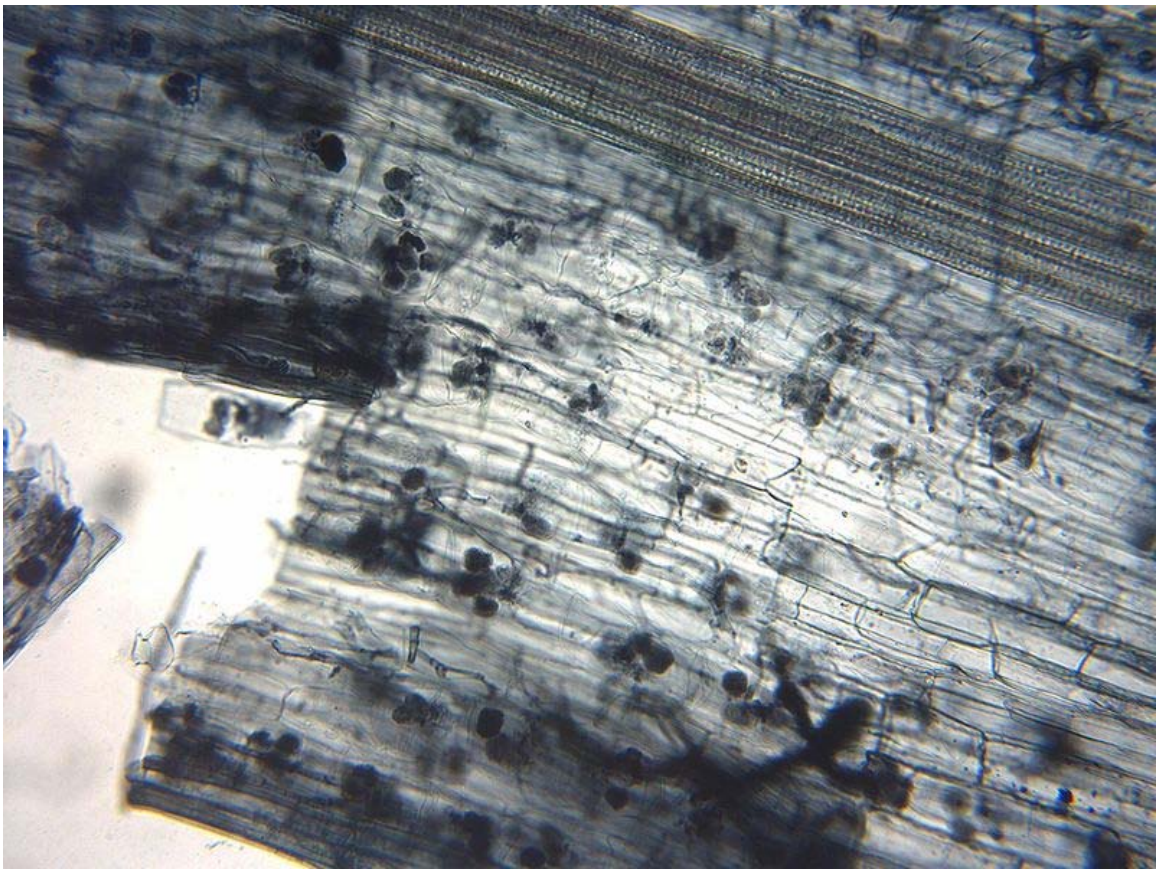
There is no unique generally accepted system at the higher taxonomic levels and there are frequent name changes at every level, from species upwards. Efforts among researchers are now underway to establish and encourage usage of a unified and more consistent nomenclature. Fungal species can also have multiple scientific names depending on their

life cycle and mode (sexual or asexual) of reproduction. Web sites such as Index Fungorum and ITIS list current names of fungal species (with cross-references to older synonyms).

The 2007 classification of Kingdom Fungi is the result of a large-scale collaborative research effort involving dozens of mycologists and other scientists working on fungal taxonomy. It recognizes seven phyla, two of which—the Ascomycota and the Basidiomycota—are contained within a branch representing subkingdom Dikarya. The below cladogram depicts the major fungal taxa and their relationship to opisthokont and unikont organisms. The lengths of the branches in this tree are not proportional to evolutionary distances.

Taxonomic groups

The major phyla (sometimes called divisions) of fungi have been classified mainly on the basis of characteristics of their sexual reproductive structures. Currently, seven phyla are proposed: Microsporidia, Chytridiomycota, Blastocladiomycota, Neocallimastigomycota, Glomeromycota, Ascomycota, and Basidiomycota.



Arbuscular mycorrhiza seen under microscope. Flax root cortical cells containing paired arbuscules.

Phylogenetic analysis has demonstrated that the Microsporidia, unicellular parasites of animals and protists, are fairly recent and highly derived endobiotic fungi (living within the tissue of another species). One 2006 study concludes that the Microsporidia are a sister group to the true fungi, that is, they are each other's closest evolutionary relative. Hibbett and colleagues suggest that this analysis does not clash with their classification of the Fungi, and although the Microsporidia are elevated to phylum status, it is acknowledged that further analysis is required to clarify evolutionary relationships within this group.

The Chytridiomycota are commonly known as chytrids. These fungi are distributed worldwide. Chytrids produce zoospores that are capable of active movement through aqueous phases with a single flagellum, leading early taxonomists to classify them as protists. Molecular phylogenies, inferred from rRNA sequences in ribosomes, suggest that the Chytrids are a basal group divergent from the other fungal phyla, consisting of four major clades with suggestive evidence for paraphyly or possibly polyphyly.

The Blastocladiomycota were previously considered a taxonomic clade within the Chytridiomycota. Recent molecular data and ultrastructural characteristics, however, place the Blastocladiomycota as a sister clade to the Zygomycota, Glomeromycota, and Dikarya (Ascomycota and Basidiomycota). The blastocladiomycetes are saprotrophs, feeding on decomposing organic matter, and they are parasites of all eukaryotic groups. Unlike their close relatives, the chytrids, which mostly exhibit zygotic meiosis, the blastocladiomycetes undergo sporic meiosis.

The Neocallimastigomycota were earlier placed in the phylum Chytridomycota. Members of this small phylum are anaerobic organisms, living in the digestive system of larger herbivorous mammals and possibly in other terrestrial and aquatic environments. They lack mitochondria but contain hydrogenosomes of mitochondrial origin. As the related chrytrids, neocallimastigomycetes form zoospores that are posteriorly uniflagellate or polyflagellate.

Members of the Glomeromycota form arbuscular mycorrhizae, a form of symbiosis where fungal hyphae invade plant root cells and both species benefit from the resulting increased supply of nutrients. All known Glomeromycota species reproduce asexually. The symbiotic association between the Glomeromycota and plants is ancient, with evidence dating to 400 million years ago. Formerly part of the Zygomycota (commonly known as 'sugar' and 'pin' molds), the Glomeromycota were elevated to phylum status in 2001 and now replace the older phylum Zygomycota. Fungi that were placed in the Zygomycota are now being reassigned to the Glomeromycota, or the subphyla incertae sedis Mucoromycotina, Kickxellomycotina, the Zoopagomycotina and the Entomophthoromycotina. Some well-known examples of fungi formerly in the Zygomycota include black bread mold (*Rhizopus stolonifer*), and *Pilobolus* species, capable of ejecting spores several meters through the air. Medically relevant genera include *Mucor*, *Rhizomucor*, and *Rhizopus*.

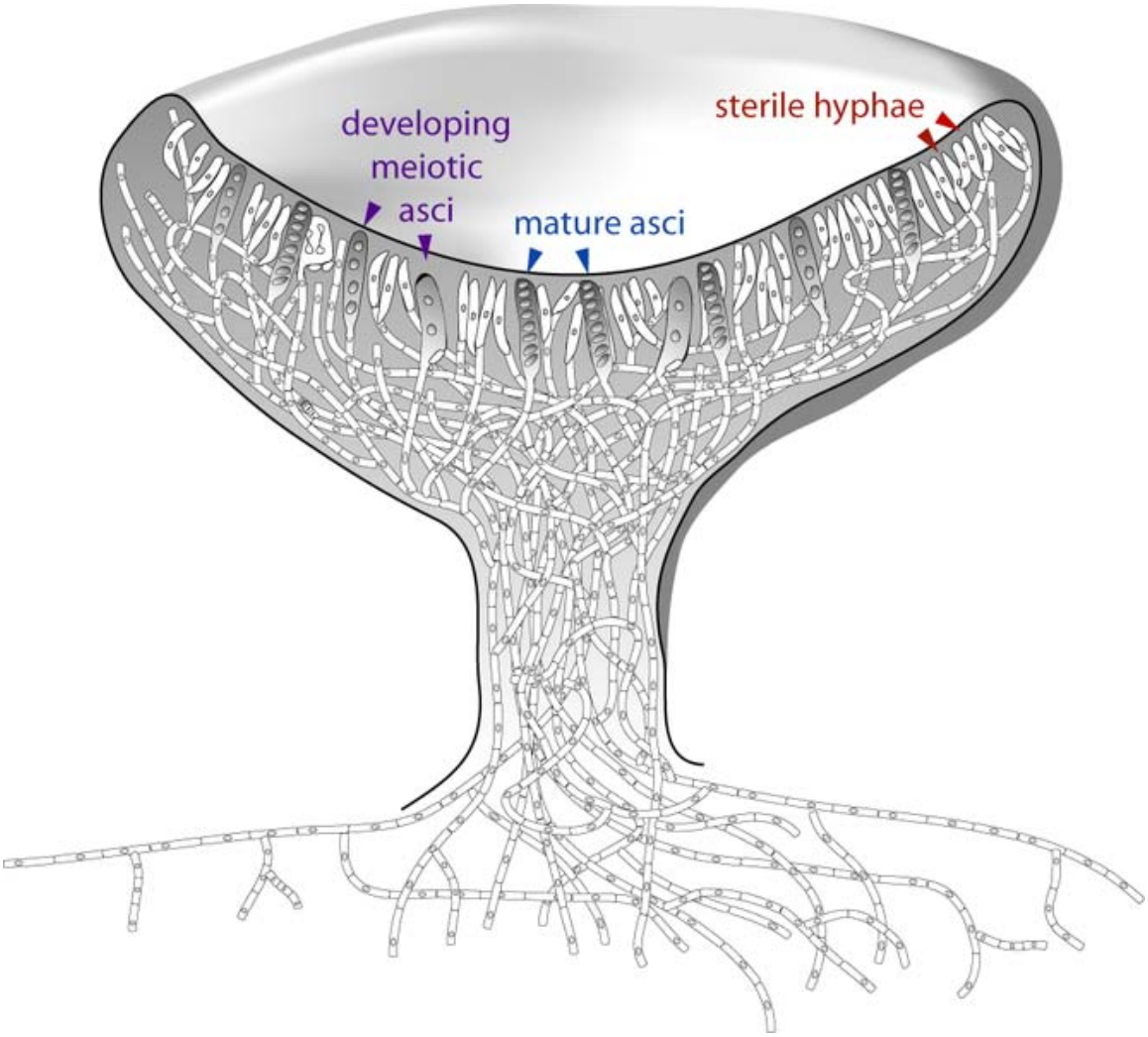


Diagram of an apothecium (the typical cup-like reproductive structure of Ascomycetes) showing sterile tissues as well as developing and mature asci.

The Ascomycota, commonly known as sac fungi or ascomycetes, constitute the largest taxonomic group within the Eumycota. These fungi form meiotic spores called ascospores, which are enclosed in a special sac-like structure called an ascus. This phylum includes morels, a few mushrooms and truffles, single-celled yeasts (e.g., of the genera *Saccharomyces*, *Kluyveromyces*, *Pichia*, and *Candida*), and many filamentous fungi living as saprotrophs, parasites, and mutualistic symbionts. Prominent and important genera of filamentous ascomycetes include *Aspergillus*, *Penicillium*, *Fusarium*, and *Claviceps*. Many ascomycete species have only been observed undergoing asexual reproduction (called anamorphic species), but analysis of molecular data has often been able to identify their closest teleomorphs in the Ascomycota. Because the products of meiosis are retained within the sac-like ascus, ascomycetes have been used for elucidating principles of genetics and heredity (e.g. *Neurospora crassa*).

Members of the Basidiomycota, commonly known as the club fungi or basidiomycetes, produce meiospores called basidiospores on club-like stalks called basidia. Most common mushrooms belong to this group, as well as rust and smut fungi, which are major pathogens of grains. Other important basidiomycetes include the maize pathogen *Ustilago maydis*, human commensal species of the genus *Malassezia*, and the opportunistic human pathogen, *Cryptococcus neoformans*.

Fungus-like organisms

Because of similarities in morphology and lifestyle, the slime molds (myxomycetes) and water molds (oomycetes) were formerly classified in the kingdom Fungi. Unlike true fungi the cell walls of these organisms contain cellulose and lack chitin. Myxomycetes are unikonts like fungi, but are grouped in the Amoebozoa. Oomycetes are diploid bikonts, grouped in the Chromalveolate kingdom. Neither water molds nor slime molds are closely related to the true fungi, and, therefore, taxonomists no longer group them in the kingdom Fungi. Nonetheless, studies of the oomycetes and myxomycetes are still often included in mycology textbooks and primary research literature.

The nucleariids, currently grouped in the Choanozoa, may be a sister group to the eumycete clade, and as such could be included in an expanded fungal kingdom.

Ecology

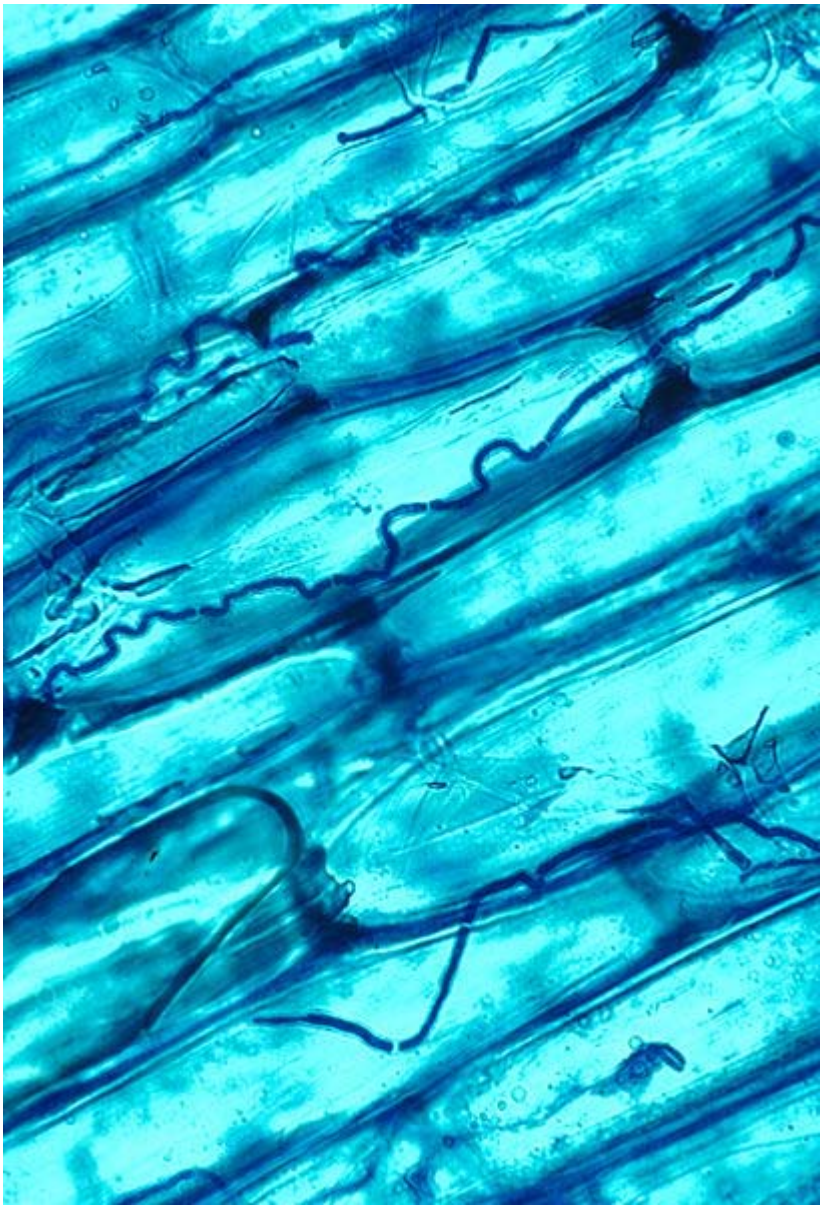
Although often inconspicuous, fungi occur in every environment on Earth and play very important roles in most ecosystems. Along with bacteria, fungi are the major decomposers in most terrestrial (and some aquatic) ecosystems, and therefore play a critical role in biogeochemical cycles and in many food webs. As decomposers, they play an essential role in nutrient cycling, especially as saprotrophs and symbionts, degrading organic matter to inorganic molecules, which can then re-enter anabolic metabolic pathways in plants or other organisms.

Symbiosis

Many fungi have important symbiotic relationships with organisms from most if not all Kingdoms. These interactions can be mutualistic or antagonistic in nature, or in the case of commensal fungi are of no apparent benefit or detriment to the host.

With plants

Mycorrhizal symbiosis between plants and fungi is one of the most well-known plant–fungus associations and is of significant importance for plant growth and persistence in many ecosystems; over 90% of all plant species engage in mycorrhizal relationships with fungi and are dependent upon this relationship for survival.



The dark filaments are hyphae of the endophytic fungus *Neotyphodium coenophialum* in the intercellular spaces of tall fescue leaf sheath tissue

The mycorrhizal symbiosis is ancient, dating to at least 400 million years ago. It often increases the plant's uptake of inorganic compounds, such as nitrate and phosphate from soils having low concentrations of these key plant nutrients. The fungal partners may also mediate plant-to-plant transfer of carbohydrates and other nutrients. Such mycorrhizal communities are called "common mycorrhizal networks". A special case of mycorrhiza is myco-heterotrophy, whereby the plant parasitizes the fungus, obtaining all of its nutrients from its fungal symbiont. Some fungal species inhabit the tissues inside roots, stems, and leaves, in which case they are called endophytes. Similar to mycorrhiza, endophytic colonization by fungi may benefit both symbionts; for example, endophytes of grasses

impart to their host increased resistance to herbivores and other environmental stresses and receive food and shelter from the plant in return.

With algae and cyanobacteria

The lichen *Lobaria pulmonaria*, a symbiosis of fungal, algal, and cyanobacterial species

Lichens are formed by a symbiotic relationship between algae or cyanobacteria (referred to in lichen terminology as "photobionts") and fungi (mostly various species of ascomycetes and a few basidiomycetes), in which individual photobiont cells are embedded in a tissue formed by the fungus. Lichens occur in every ecosystem on all continents, play a key role in soil formation and the initiation of biological succession, and are the dominating life forms in extreme environments, including polar, alpine, and semiarid desert regions. They are able to grow on inhospitable surfaces, including bare soil, rocks, tree bark, wood, shells, barnacles and leaves. As in mycorrhizas, the photobiont provides sugars and other carbohydrates via photosynthesis, while the fungus provides minerals and water. The functions of both symbiotic organisms are so closely intertwined that they function almost as a single organism; in most cases the resulting organism differs greatly from the individual components. Lichenization is a common mode of nutrition; around 20% of fungi—between 17,500 and 20,000 described species—are lichenized. Characteristics common to most lichens include obtaining organic carbon by photosynthesis, slow growth, small size, long life, long-lasting

(seasonal) vegetative reproductive structures, mineral nutrition obtained largely from airborne sources, and greater tolerance of desiccation than most other photosynthetic organisms in the same habitat.

With insects

Many insects also engage in mutualistic relationships with fungi. Several groups of ants cultivate fungi in the order Agaricales as their primary food source, while ambrosia beetles cultivate various species of fungi in the bark of trees that they infest. Similarly, females of several wood wasp species (genus *Sirex*) inject their eggs together with spores of the wood-rotting fungus *Amylostereum areolatum* into the sapwood of pine trees; the growth of the fungus provides ideal nutritional conditions for the development of the wasp larvae. Termites on the African savannah are also known to cultivate fungi, and yeasts of the genera *Candida* and *Lachancea* inhabit the gut of a wide range of insects, including neuropterans, beetles, and cockroaches; it is not known whether these fungi benefit their hosts.

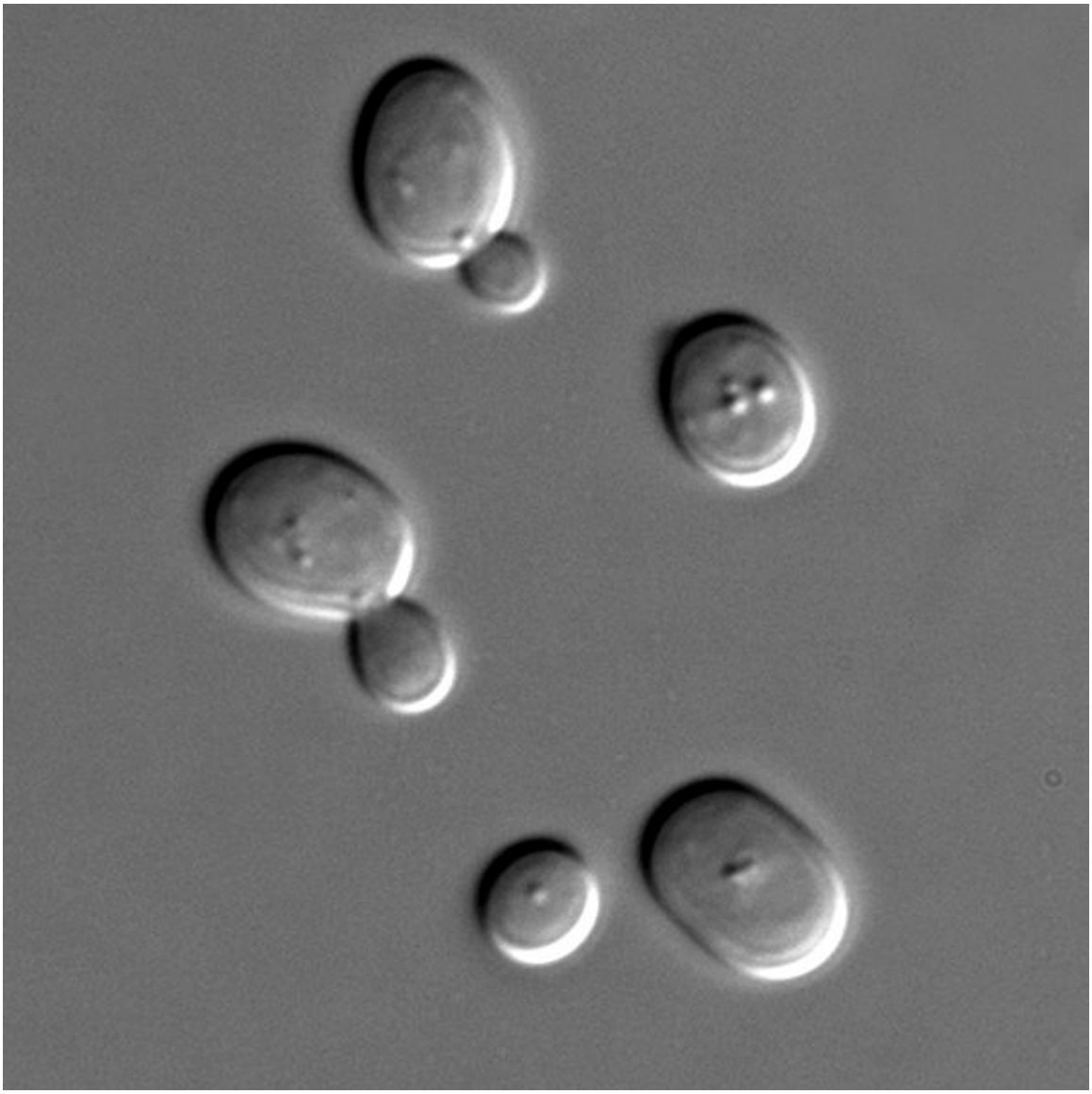
As pathogens and parasites

The plant pathogen *Aecidium magellanicum* causes calafate rust, seen here on a *Berberis* shrub in Chile.

Many fungi are parasites on plants, animals (including humans), and other fungi. Serious pathogens of many cultivated plants causing extensive damage and losses to agriculture and forestry include the rice blast fungus *Magnaporthe oryzae*, tree pathogens such as *Ophiostoma ulmi* and *Ophiostoma novo-ulmi* causing Dutch elm disease, and *Cryphonectria parasitica* responsible for chestnut blight, and plant pathogens in the genera *Fusarium*, *Ustilago*, *Alternaria*, and *Cochliobolus*. Some carnivorous fungi, like *Paecilomyces lilacinus*, are predators of nematodes, which they capture using an array of specialized structures such as constricting rings or adhesive nets.

Some fungi can cause serious diseases in humans, several of which may be fatal if untreated. These include aspergilloses, candidoses, coccidioidomycosis, cryptococcosis, histoplasmosis, mycetomas, and paracoccidioidomycosis. Furthermore, persons with immuno-deficiencies are particularly susceptible to disease by genera such as *Aspergillus*, *Candida*, *Cryptoccocus*, *Histoplasma*, and *Pneumocystis*. Other fungi can attack eyes, nails, hair, and especially skin, the so-called dermatophytic and keratinophilic fungi, and cause local infections such as ringworm and athlete's foot. Fungal spores are also a cause of allergies, and fungi from different taxonomic groups can evoke allergic reactions.

Human use



Saccharomyces cerevisiae cells shown with DIC microscopy.

The human use of fungi for food preparation or preservation and other purposes is extensive and has a long history. Mushroom farming and mushroom gathering are large industries in many countries. The study of the historical uses and sociological impact of fungi is known as ethnomycology. Because of the capacity of this group to produce an enormous range of natural products with antimicrobial or other biological activities, many species have long been used or are being developed for industrial production of antibiotics, vitamins, and anti-cancer and cholesterol-lowering drugs. More recently, methods have been developed for genetic engineering of fungi, enabling metabolic engineering of fungal species. For example, genetic modification of yeast species—which are easy to grow at fast rates in large fermentation vessels—has opened up ways of

pharmaceutical production that are potentially more efficient than production by the original source organisms.

Drugs

Many species produce metabolites that are major sources of pharmacologically active drugs. Particularly important are the antibiotics, including the penicillins, a structurally related group of β-lactam antibiotics that are synthesized from small peptides. Although naturally occurring penicillins such as penicillin G (produced by *Penicillium chrysogenum*) have a relatively narrow spectrum of biological activity, a wide range of other penicillins can be produced by chemical modification of the natural penicillins. Modern penicillins are semisynthetic compounds, obtained initially from fermentation cultures, but then structurally altered for specific desirable properties. Other antibiotics produced by fungi include: ciclosporin, commonly used as an immunosuppressant during transplant surgery; and fusidic acid, used to help control infection from methicillin-resistant *Staphylococcus aureus* bacteria. Widespread use of these antibiotics for the treatment of bacterial diseases, such as tuberculosis, syphilis, leprosy, and many others began in the early 20th century and continues to play a major part in anti-bacterial chemotherapy. In nature, antibiotics of fungal or bacterial origin appear to play a dual role: at high concentrations they act as chemical defense against competition with other microorganisms in species-rich environments, such as the rhizosphere, and at low concentrations as quorum-sensing molecules for intra- or interspecies signaling.

Other drugs produced by fungi include griseofulvin isolated from *Penicillium griseofulvum*, used to treat fungal infections, and statins (HMG-CoA reductase inhibitors), used to inhibit cholesterol synthesis. Examples of statins found in fungi include mevastatin from *Penicillium citrinum* and lovastatin from *Aspergillus terreus* and the oyster mushroom.

Cultured foods

Baker's yeast or *Saccharomyces cerevisiae*, a single-celled fungus, is used to make bread and other wheat-based products, such as pizza dough and dumplings. Yeast species of the genus *Saccharomyces* are also used to produce alcoholic beverages through fermentation. Shoyu koji mold (*Aspergillus oryzae*) is an essential ingredient in brewing Shoyu (soy sauce) and sake, and the preparation of miso, while *Rhizopus* species are used for making tempeh. Several of these fungi are domesticated species that were bred or selected according to their capacity to ferment food without producing harmful mycotoxins, which are produced by very closely related *Aspergilli*. Quorn, a meat substitute, is made from *Fusarium venenatum*.

Medicinal use

The medicinal fungi *Ganoderma lucidum* (left) and *Cordyceps sinensis* (right).

Certain mushrooms enjoy usage as therapeutics in folk medicines, such as Traditional Chinese medicine. Notable medicinal mushrooms with a well-documented history of use include *Agaricus subrufescens*, *Ganoderma lucidum*, and *Cordyceps sinensis*. Research has identified compounds produced by these and other fungi that have inhibitory biological effects against viruses and cancer cells. Specific metabolites, such as polysaccharide-K, ergotamine, and β-lactam antibiotics, are routinely used in clinical medicine. The shiitake mushroom is a source of lentinan, a clinical drug approved for use in cancer treatments in several countries, including Japan. In Europe and Japan, polysaccharide-K (brand name Krestin), a chemical derived from *Trametes versicolor*, is an approved adjuvant for cancer therapy.

Edible and poisonous species

Amanita phalloides accounts for the majority of fatal mushroom poisonings worldwide.

Edible mushrooms are well-known examples of fungi. Many are commercially raised, but others must be harvested from the wild. *Agaricus bisporus*, sold as button mushrooms when small or Portobello mushrooms when larger, is a commonly eaten species, used in salads, soups, and many other dishes. Many Asian fungi are commercially grown and have increased in popularity in the West. They are often available fresh in grocery stores and markets, including straw mushrooms (*Volvariella volvacea*), oyster mushrooms (*Pleurotus ostreatus*), shiitakes (*Lentinula edodes*), and enokitake (*Flammulina* spp.).

There are many more mushroom species that are harvested from the wild for personal consumption or commercial sale. Milk mushrooms, morels, chanterelles, truffles, black

trumpets, and *porcini* mushrooms (*Boletus edulis*) (also known as king boletes) demand a high price on the market. They are often used in gourmet dishes.

Certain types of cheeses require inoculation of milk curds with fungal species that impart a unique flavor and texture to the cheese. Examples include the blue color in cheeses such as Stilton or Roquefort, which are made by inoculation with *Penicillium roqueforti*. Molds used in cheese production are non-toxic and are thus safe for human consumption; however, mycotoxins (e.g., aflatoxins, roquefortine C, patulin, or others) may accumulate because of growth of other fungi during cheese ripening or storage.

Stilton cheese veined with *Penicillium roqueforti*

Many mushroom species are poisonous to humans, with toxicities ranging from slight digestive problems or allergic reactions as well as hallucinations to severe organ failures and death. Genera with mushrooms containing deadly toxins include *Conocybe*, *Galerina*, *Lepiota*, and most infamously, *Amanita*. The latter genus includes the destroying angel *(A. virosa)* and the death cap *(A. phalloides)*, the most common cause of deadly mushroom poisoning. The false morel (*Gyromitra esculenta*) is occasionally considered a delicacy when cooked, yet can be highly toxic when eaten raw. *Tricholoma equestre* was considered edible until being implicated in serious poisonings causing rhabdomyolysis. Fly agaric mushrooms (*Amanita muscaria*) also cause occasional non-

fatal poisonings, mostly as a result of ingestion for use as a recreational drug for its hallucinogenic properties. Historically, fly agaric was used by different peoples in Europe and Asia and its present usage for religious or shamanic purposes is reported from some ethnic groups such as the Koryak people of north-eastern Siberia.

As it is difficult to accurately identify a safe mushroom without proper training and knowledge, it is often advised to assume that a wild mushroom is poisonous and not to consume it.

Pest control

Grasshoppers killed by *Beauveria bassiana*

In agriculture, fungi may be useful if they actively compete for nutrients and space with pathogenic microorganisms such as bacteria or other fungi via the competitive exclusion principle, or if they are parasites of these pathogens. For example, certain species may be used to eliminate or suppress the growth of harmful plant pathogens, such as insects, mites, weeds, nematodes and other fungi that cause diseases of important crop plants. This has generated strong interest in practical applications that use these fungi in the biological control of these agricultural pests. Entomopathogenic fungi can be used as biopesticides, as they actively kill insects. Examples that have been used as biological insecticides are *Beauveria bassiana*, *Metarhizium* spp, *Hirsutella* spp, *Paecilomyces* (*Isaria*) spp, and *Lecanicillium lecanii*. Endophytic fungi of grasses of the genus *Neotyphodium*, such as *N. coenophialum*, produce alkaloids that are toxic to a range of invertebrate and vertebrate herbivores. These alkaloids protect grass plants from herbivory, but several endophyte alkaloids can poison grazing animals, such as cattle and sheep. Infecting cultivars of pasture or forage grasses with *Neotyphodium* endophytes is one approach being used in grass breeding programs; the fungal strains are selected for producing only alkaloids that increase resistance to herbivores such as insects, while being non-toxic to livestock.

Bioremediation

Certain fungi, in particular "white rot" fungi, can degrade insecticides, herbicides, pentachlorophenol, creosote, coal tars, and heavy fuels and turn them into carbon dioxide, water, and basic elements. Fungi have been shown to biomineralize uranium oxides, suggesting they may have application in the bioremediation of radioactively polluted sites.

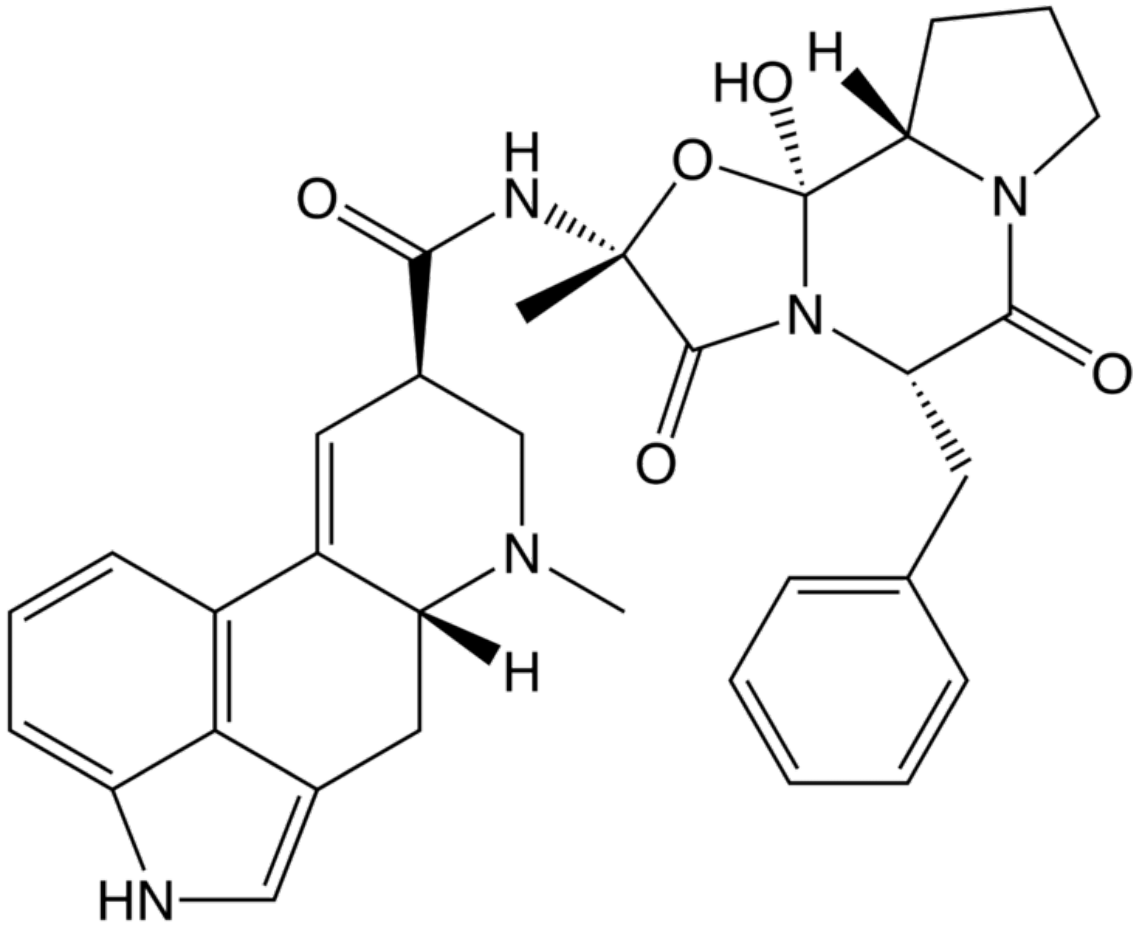
Model organisms

Several pivotal discoveries in biology were made by researchers using fungi as model organisms, that is, fungi that grow and sexually reproduce rapidly in the laboratory. For example, the one gene-one enzyme hypothesis was formulated by scientists who used the bread mold *Neurospora crassa* to test their biochemical theories. Other important model fungi are *Aspergillus nidulans* and the yeasts, *Saccaromyces cerevisiae* and *Schizosaccharomyces pombe*, each of which has a long history of use to investigate issues in eukaryotic cell biology and genetics, such as cell cycle regulation, chromatin structure, and gene regulation. Other fungal models have more recently emerged that each address specific biological questions relevant to medicine, plant pathology, and industrial uses; examples include *Candida albicans*, a dimorphic, opportunistic human pathogen, *Magnaporthe grisea*, a plant pathogen, and *Pichia pastoris*, a yeast widely used for eukaryotic protein expression.

Others

Fungi are used extensively to produce industrial chemicals like citric, gluconic, lactic, and malic acids, and industrial enzymes, such as lipases used in biological detergents, cellulases used in making cellulosic ethanol and stonewashed jeans, and amylases, invertases, proteases and xylanases. Several species, most notably *Psilocybin mushrooms* (colloquially known as *magic mushrooms*), are ingested for their psychedelic properties, both recreationally and religiously.

Mycotoxins



Ergotamine, a major mycotoxin produced by *Claviceps* species, which if ingested can cause gangrene, convulsions, and hallucinations

Many fungi produce biologically active compounds, several of which are toxic to animals or plants and are therefore called mycotoxins. Of particular relevance to humans are mycotoxins produced by molds causing food spoilage, and poisonous mushrooms. Particularly infamous are the lethal amatoxins in some *Amanita* mushrooms, and ergot alkaloids, which have a long history of causing serious epidemics of ergotism (St Anthony's Fire) in people consuming rye or related cereals contaminated with sclerotia of the ergot fungus, *Claviceps purpurea*. Other notable mycotoxins include the aflatoxins, which are insidious liver toxins and highly carcinogenic metabolites produced by certain *Aspergillus* species often growing in or on grains and nuts consumed by humans, ochratoxins, patulin, and trichothecenes (e.g., T-2 mycotoxin) and fumonisins, which have significant impact on human food supplies or animal livestock.

Mycotoxins are secondary metabolites (or natural products), and research has established the existence of biochemical pathways solely for the purpose of producing mycotoxins and other natural products in fungi. Mycotoxins may provide fitness benefits in terms of

physiological adaptation, competition with other microbes and fungi, and protection from consumption (fungivory).

Mycology

Mycology is the branch of biology concerned with the systematic study of fungi, including their genetic and biochemical properties, their taxonomy, and their use to humans as a source of medicine, food, and psychotropic substances consumed for religious purposes, as well as their dangers, such as poisoning or infection. The field of phytopathology, the study of plant diseases, is closely related because many plant pathogens are fungi.

Use of fungi by humans dates back to prehistory; Ötzi the Iceman, a well-preserved mummy of a 5,300 year old Neolithic man found frozen in the Austrian Alps, carried two species of polypore mushrooms that may have been used as tinder (*Fomes fomentarius*), or for medicinal purposes (*Piptoporus betulinus*). Ancient peoples have used fungi as food sources–often unknowingly–for millennia, in the preparation of leavened bread and fermented juices. Some of the oldest written records contain references to the destruction of crops that were probably caused by pathogenic fungi.

History

Mycology is a relatively new science that became systematic after the development of the microscope in the 16th century. Although fungal spores were first observed by Giambattista della Porta in 1588, the seminal work in the development of mycology is considered to be the publication of Pier Antonio Micheli's 1729 work *Nova plantarum genera*. Micheli not only observed spores, but showed that under the proper conditions, they could be induced into growing into the same species of fungi from which they originated. Extending the use of the binomial system of nomenclature introduced by Carl Linnaeus in his *Species plantarum* (1753), the Dutch Christian Hendrik Persoon (1761–1836) established the first classification of mushrooms with such skill so as to be considered a founder of modern mycology. Later, Elias Magnus Fries (1794–1878) further elaborated the classification of fungi, using spore color and various microscopic characteristics, methods still used by taxonomists today. Other notable early contributors to mycology in the 17th–19th and early 20th centuries include Miles Joseph Berkeley, August Carl Joseph Corda, Anton de Bary, the brothers Louis René and Charles Tulasne, Arthur H. R. Buller, Curtis G. Lloyd, and Pier Andrea Saccardo. The 20th century has seen a modernization of mycology that has come from advances in biochemistry, genetics, molecular biology, and biotechnology. The use of DNA sequencing technologies and phylogenetic analysis has provided new insights into fungal relationships and biodiversity, and has challenged traditional morphology-based groupings in fungal taxonomy.

Chapter 6

Protist

Protist **Temporal range: Neoproterozoic - Recent**

Scientific classification
Domain: **Eukarya**
Kingdom: **Protista*** Haeckel, 1866
Typical phyla

- **Chromalveolata**
  - Heterokontophyta
  - Haptophyta
  - Cryptophyta (cryptomonads)
  - **Alveolata**
    - Dinoflagellata
    - Apicomplexa
    - Ciliophora (ciliates)

- **Excavata**
  - Euglenozoa
  - Percolozoa
  - Metamonada
- **Rhizaria**
  - Radiolaria
  - Foraminifera
  - Cercozoa
- **Archaeplastida (in part)**
  - Rhodophyta (red algae)
  - Glaucophyta (basal archaeplastids)
- **Unikonta (in part)**
  - Amoebozoa
  - Choanozoa

Protists are a diverse group of eukaryotic microorganisms. Historically, protists were treated as the kingdom **Protista**, which includes mostly unicellular organisms that do not fit into the other kingdoms, but this group is contested in modern taxonomy. Instead, it is "better regarded as a loose grouping of 30 or 40 disparate phyla with diverse combinations of trophic modes, mechanisms of motility, cell coverings and life cycles."

The protists do not have much in common besides a relatively simple organization—either they are unicellular, or they are multicellular without specialized tissues. This simple cellular organization distinguishes the protists from other eukaryotes, such as fungi, animals and plants.

The term *protista* was first used by Ernst Haeckel in 1866. Protists were traditionally subdivided into several groups based on similarities to the "higher" kingdoms: the one-celled animal-like protozoa, the plant-like protophyta (mostly one-celled algae), and the fungus-like slime molds and water molds. Because these groups often overlap, they have been replaced by phylogenetic-based classifications. However, they are still useful as informal names for describing the morphology and ecology of protists.

Protists live in almost any environment that contains liquid water. Many protists, such as the algae, are photosynthetic and are vital primary producers in ecosystems, particularly in the ocean as part of the plankton. Other protists, such as the Kinetoplastids and Apicomplexa, are responsible for a range of serious human diseases, such as malaria and sleeping sickness.

Classification

Historical classifications

The first division of the protists from other organisms came in the 1830s, when the German biologist Georg A. Goldfuss introduced the word *protozoa* to refer to organisms such as ciliates and corals. This group was expanded in 1845 to include all "unicellular animals", such as Foraminifera and amoebae. The formal taxonomic category *Protoctista* was first proposed in the early 1860s by John Hogg, who argued that the protists should include what he saw as primitive unicellular forms of both plants and animals. He defined the Protoctista as a "fourth kingdom of nature", in addition to the then-traditional kingdoms of plants, animals and minerals. The kingdom of minerals was later removed from taxonomy by Ernst Haeckel, leaving plants, animals, and the protists as a “kingdom of primitive forms”.

Herbert Copeland resurrected Hogg's label almost a century later, arguing that "Protoctista" literally meant "first established beings", Copeland complained that Haeckel's term *protista* included anucleated microbes such as bacteria. Copeland's use of the term *protoctista* did not. In contrast, Copeland's term included nucleated eukaryotes such as diatoms, green algae and fungi. This classification was the basis for Whittaker's later definition of Fungi, Animalia, Plantae and Protista as the four kingdoms of life. The kingdom Protista was later modified to separate prokaryotes into the separate kingdom of Monera, leaving the protists as a group of eukaryotic microorganisms. These five kingdoms remained the accepted classification until the development of molecular phylogenetics in the late 20th century, when it became apparent that neither protists nor monera were single groups of related organisms (they were not monophyletic groups).

Modern classifications

Currently, the term *protist* is used to refer to unicellular eukaryotes that either exist as independent cells, or if they occur in colonies, do not show differentiation into tissues. The term *protozoa* is used to refer to heterotrophic species of protists that do not form filaments. These terms are not used in current taxonomy, and are retained only as convenient ways to refer to these organisms.

The taxonomy of protists is still changing. Newer classifications attempt to present monophyletic groups based on ultrastructure, biochemistry, and genetics. Because the protists as a whole are paraphyletic, such systems often split up or abandon the kingdom, instead treating the protist groups as separate lines of eukaryotes. The recent scheme by Adl *et al.* (2005) is an example that does not bother with formal ranks (phylum, class, etc.) and instead lists organisms in hierarchical lists. This is intended to make the classification more stable in the long term and easier to update. Some of the main groups of protists, which may be treated as phyla, are listed in the taxobox at right. Many are thought to be monophyletic, though there is still uncertainty. For instance, the excavates are probably not monophyletic and the chromalveolates are probably only monophyletic if the haptophytes and cryptomonads are excluded.

Metabolism

Nutrition in some different types of protists is variable. In flagellates, for example, filter feeding may sometimes occur where the flagella find the prey. Other protists can engulf bacteria and digest them internally, by extending their cell membrane around the food material to form a food vacuole. This is then taken into the cell via endocytosis (usually phagocytosis; sometimes pinocytosis).

Nutritional types in protist metabolism

Nutritional type	Source of energy	Source of carbon	Examples
Phototrophs	Sunlight	Organic compounds or carbon fixation	Algae, Dinoflagellates or Euglena
Organotrophs	Organic compounds	Organic compounds	Apicomplexa, Trypanosomes or Amoebae

Reproduction

Some protists reproduce sexually (conjugation), while others reproduce asexually (binary fission).

Some species, for example *Plasmodium falciparum*, have extremely complex life cycles that involve multiple forms of the organism, some of which reproduce sexually and others asexually. However, it is unclear how frequently sexual reproduction causes genetic exchange between different strains of *Plasmodium* in nature and most populations of parasitic protists may be clonal lines that rarely exchange genes with other members of their species.

Role as pathogens

Some protists are significant pathogens of both animals and plants; for example *Plasmodium falciparum*, which causes malaria in humans, and *Phytophthora infestans*, which causes potato blight. A more thorough understanding of protist biology may allow these diseases to be treated more efficiently.

Researchers from the Agricultural Research Service are taking advantage of protists as pathogens in an effort to control red imported fire ant (*Solenopsis invicta*) populations in Argentina. With the help of spore-producing protists such as *Kneallhazia solenopsae* the red fire ant populations can be reduced by 53-100%. Researchers have also found a way to infect phorid flies with the protist without harming the flies. This is important because the flies act as a vector to infect the red fire ant population with the pathogenic protist.

Chapter 7

Animal

Animals Temporal range: Ediacaran - Recent

Scientific classification

Domain:	Eukarya
(unranked)	Opisthokonta
(unranked)	Holozoa
(unranked)	Filozoa

Kingdom: **Animalia**
Linnaeus, 1758

Phyla

- **Subkingdom Parazoa**
  - Porifera
  - Placozoa
- **Subkingdom Eumetazoa**
  - **Radiata (unranked)**
    - Ctenophora
    - Cnidaria
  - **Bilateria (unranked)**
    - Orthonectida
    - Rhombozoa
    - Acoelomorpha
    - Chaetognatha
    - **Superphylum Deuterostomia**
      - Chordata
      - Hemichordata
      - Echinodermata
      - Xenoturbellida
      - Vetulicolia †
    - **Protostomia (unranked)**
      - **Superphylum Ecdysozoa**
        - Kinorhyncha
        - Loricifera
        - Priapulida
        - Nematoda
        - Nematomorpha
        - Lobopodia
        - Onychophora
        - Tardigrada
        - Arthropoda
      - **Superphylum Platyzoa**
        - Platyhelminthes
        - Gastrotricha
        - Rotifera
        - Acanthocephala
        - Gnathostomulida
        - Micrognathozoa
        - Cycliophora
      - **Superphylum Lophotrochozoa**
        - Sipuncula
        - Hyolitha †
        - Nemertea
        - Phoronida
        - Bryozoa

- Entoprocta
- Brachiopoda
- Mollusca
- Annelida
- Echiura

Animals are a major group of multicellular, eukaryotic organisms of the kingdom **Animalia** or **Metazoa**. Their body plan eventually becomes fixed as they develop, although some undergo a process of metamorphosis later on in their life. Most animals are motile, meaning they can move spontaneously and independently. All animals are also heterotrophs, meaning they must ingest other organisms for sustenance.

Most known animal phyla appeared in the fossil record as marine species during the Cambrian explosion, about 542 million years ago.

Etymology

The word "animal" comes from the Latin word *animalis*, meaning "having breath". In everyday colloquial usage, the word usually refers to non-human animals. Frequently, only closer relatives of humans such as mammals and other vertebrates are meant in colloquial use. The biological definition of the word refers to all members of the kingdom Animalia, encompassing creatures as diverse as sponges, jellyfish, insects and humans.

Characteristics

Animals have several characteristics that set them apart from other living things. Animals are eukaryotic and mostly multicellular, which separates them from bacteria and most protists. They are heterotrophic, generally digesting food in an internal chamber, which separates them from plants and algae. They are also distinguished from plants, algae, and fungi by lacking rigid cell walls. All animals are motile, if only at certain life stages. In most animals, embryos pass through a blastula stage, which is a characteristic exclusive to animals.

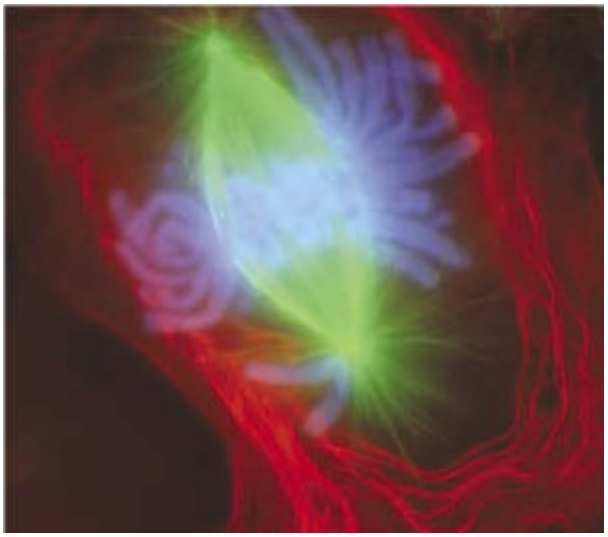
Structure

With a few exceptions, most notably the sponges (Phylum Porifera) and Placozoa, animals have bodies differentiated into separate tissues. These include muscles, which are able to contract and control locomotion, and nerve tissues, which send and process signals. Typically, there is also an internal digestive chamber, with one or two openings. Animals with this sort of organization are called metazoans, or eumetazoans when the former is used for animals in general.

All animals have eukaryotic cells, surrounded by a characteristic extracellular matrix composed of collagen and elastic glycoproteins. This may be calcified to form structures like shells , bones, and spicules. During development, it forms a relatively flexible

framework upon which cells can move about and be reorganized, making complex structures possible. In contrast, other multicellular organisms, like plants and fungi, have cells held in place by cell walls, and so develop by progressive growth. Also, unique to animal cells are the following intercellular junctions: tight junctions, gap junctions, and desmosomes.

Reproduction and development



A newt lung cell stained with fluorescent dyes undergoing mitosis, specifically early anaphase

Nearly all animals undergo some form of sexual reproduction. They have a few specialized reproductive cells, which undergo meiosis to produce smaller, motile spermatozoa or larger, non-motile ova. These fuse to form zygotes, which develop into new individuals.

Many animals are also capable of asexual reproduction. This may take place through parthenogenesis, where fertile eggs are produced without mating, budding, or fragmentation.

A zygote initially develops into a hollow sphere, called a blastula, which undergoes rearrangement and differentiation. In sponges, blastula larvae swim to a new location and develop into a new sponge. In most other groups, the blastula undergoes more complicated rearrangement. It first invaginates to form a gastrula with a digestive chamber, and two separate germ layers — an external ectoderm and an internal endoderm. In most cases, a mesoderm also develops between them. These germ layers then differentiate to form tissues and organs.

Food and energy sourcing

All animals are heterotrophs, meaning that they feed directly or indirectly on other living things. They are often further subdivided into groups such as carnivores, herbivores, omnivores, and parasites.

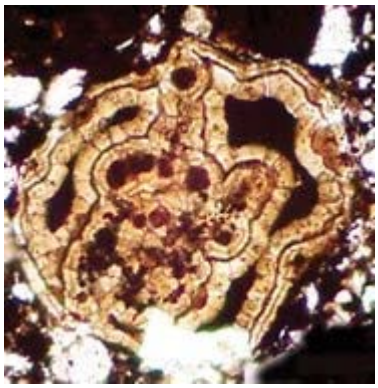
Predation is a biological interaction where a predator (a heterotroph that is hunting) feeds on its prey (the organism that is attacked). Predators may or may not kill their prey prior to feeding on them, but the act of predation always results in the death of the prey. The other main category of consumption is detritivory, the consumption of dead organic matter. It can at times be difficult to separate the two feeding behaviours, for example, where parasitic species prey on a host organism and then lay their eggs on it for their offs pring to feed on its decaying corpse. Selective pressures imposed on one another has led to an evolutionary arms race between prey and predator, resulting in various antipredator adaptations.

Most animals feed indirectly from the energy of sunlight. Plants use this energy to convert sunlight into simple sugars using a process known as photosynthesis. Starting with the molecules carbon dioxide (CO_2) and water (H_2O), photosynthesis converts the energy of sunlight into chemical energy stored in the bonds of glucose ($C_6H_{12}O_6$) and releases oxygen (O_2). These sugars are then used as the building blocks which allow the plant to grow. When animals eat these plants (or eat other animals which have eaten plants), the sugars produced by the plant are used by the animal. They are either used directly to help the animal grow, or broken down, releasing stored solar energy, and giving the animal the energy required for motion. This process is known as glycolysis.

Animals living close to hydrothermal vents and cold seeps on the ocean floor are not dependent on the energy of sunlight. Instead chemosynthetic archaea and bacteria form the base of the food chain.

Origin and fossil record

Dunkleosteus was a gigantic, 10-foot-long (3.0 m) prehistoric fish.



Vernanimalcula guizhouena is a fossil believed by some to represent the earliest known member of the *Bilateria*.

Animals are generally considered to have evolved from a flagellated eukaryote. Their closest known living relatives are the choanoflagellates, collared flagellates that have a morphology similar to the choanocytes of certain sponges. Molecular studies place animals in a supergroup called the opisthokonts, which also include the choanoflagellates, fungi and a few small parasitic protists. The name comes from the posterior location of the flagellum in motile cells, such as most animal spermatozoa, whereas other eukaryotes tend to have anterior flagella.

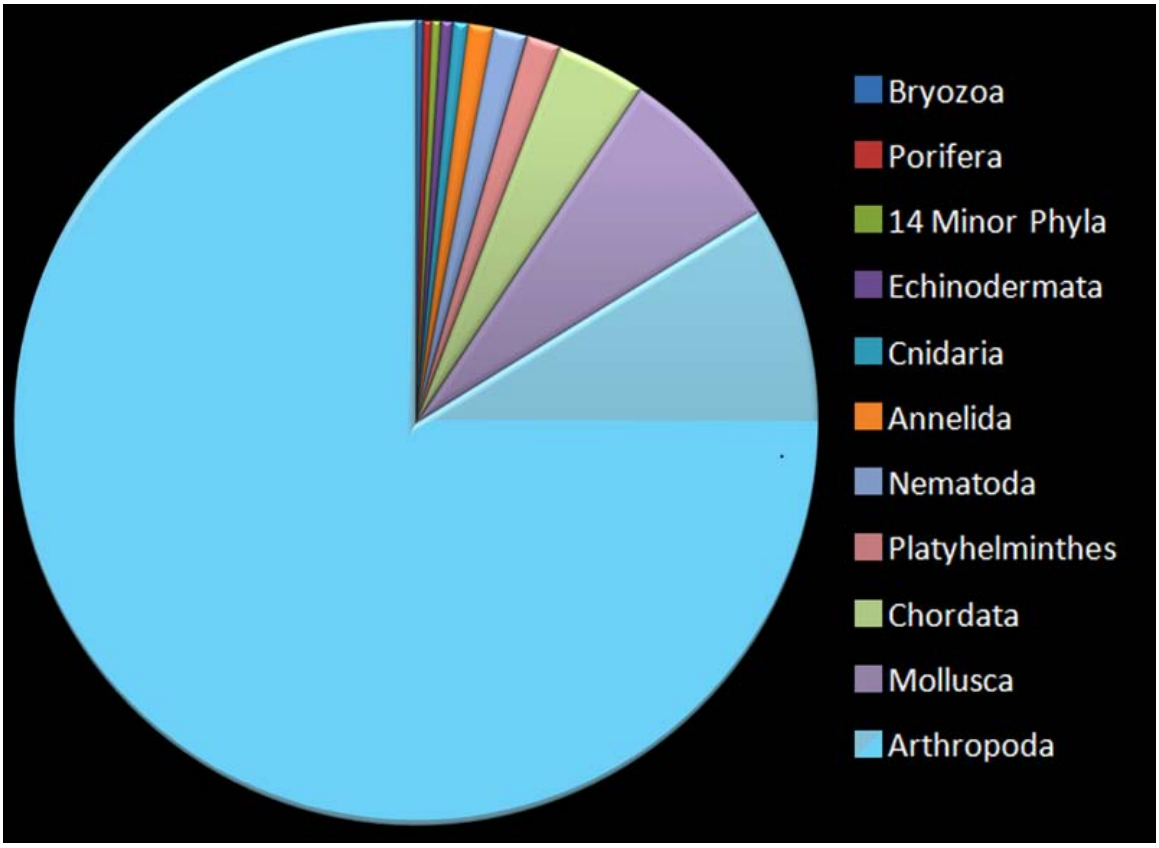
The first fossils that might represent animals appear in the Trezona Formation at Trezona Bore, West Central Flinders, South Australia. These fossils are interpreted as being early sponges. They were found in 665-million-year-old rock.

The next oldest possible animal fossils are found towards the end of the Precambrian, around 610 million years ago, and are known as the Ediacaran or Vendian biota. These are difficult to relate to later fossils, however. Some may represent precursors of modern phyla, but they may be separate groups, and it is possible they are not really animals at all.

Aside from them, most known animal phyla make a more or less simultaneous appearance during the Cambrian period, about 542 million years ago. It is still disputed whether this event, called the Cambrian explosion, represents a rapid divergence between different groups or a change in conditions that made fossilization possible.

Some paleontologists suggest that animals appeared much earlier than the Cambrian explosion, possibly as early as 1 billion years ago. Trace fossils such as tracks and burrows found in the Tonian era indicate the presence of triploblastic worms, like metazoans, roughly as large (about 5 mm wide) and complex as earthworms. During the beginning of the Tonian period around 1 billion years ago, there was a decrease in Stromatolite diversity, which may indicate the appearance of grazing animals, since Stromatolites diversity increased when grazing animals went extinct at the End Permian and End Ordovician extinction events, and decreased shortly after the grazer populations recovered. However the discovery that tracks very similar to these early trace fossils are produced today by the giant single-celled protist *Gromia sphaerica* casts doubt on their interpretation as evidence of early animal evolution.

Groups of animals



The relative number of species contributed to the total by each phylum of animals.

Porifera, Radiata and basal Bilateria

Orange elephant ear sponge, *Agelas clathrodes*, in foreground. Two corals in the background: a sea fan, *Iciligorgia schrammi*, and a sea rod, *Plexaurella nutans*.

The sponges (Porifera) were long thought to have diverged from other animals early. They lack the complex organization found in most other phyla. Their cells are differentiated, but in most cases not organized into distinct tissues. Sponges typically feed by drawing in water through pores. Archaeocyatha, which have fused skeletons, may represent sponges or a separate phylum. However, a phylogenomic study in 2008 of 150 genes in 29 animals across 21 phyla revealed that it is the Ctenophora or comb jellies which are the basal lineage of animals, at least among those 21 phyla. The authors speculate that sponges—or at least those lines of sponges they investigated—are not so primitive, but may instead be secondarily simplified.

Among the other phyla, the Ctenophora and the Cnidaria, which includes sea anemones, corals, and jellyfish, are radially symmetric and have digestive chambers with a single opening, which serves as both the mouth and the anus. Both have distinct tissues, but they are not organized into organs. There are only two main germ layers, the ectoderm and endoderm, with only scattered cells between them. As such, these animals are sometimes called diploblastic. The tiny placozoans are similar, but they do not have a permanent digestive chamber.

The remaining animals form a monophyletic group called the Bilateria. For the most part, they are bilaterally symmetric, and often have a specialized head with feeding and sensory organs. The body is triploblastic, i.e. all three germ layers are well-developed, and tissues form distinct organs. The digestive chamber has two openings, a mouth and an anus, and there is also an internal body cavity called a coelom or pseudocoelom. There are exceptions to each of these characteristics, however — for instance adult echinoderms are radially symmetric, and certain parasitic worms have extremely simplified body structures.

Genetic studies have considerably changed our understanding of the relationships within the Bilateria. Most appear to belong to two major lineages: the deuterostomes and the protostomes, the latter of which includes the Ecdysozoa, Platyzoa, and Lophotrochozoa. In addition, there are a few small groups of bilaterians with relatively similar structure that appear to have diverged before these major groups. These include the Acoelomorpha, Rhombozoa, and Orthonectida. The Myxozoa, single-celled parasites that were originally considered Protozoa, are now believed to have developed from the Medusozoa as well.

Deuterostomes

Superb Fairy-wren, *Malurus cyaneus*

Deuterostomes differ from the other Bilateria, called protostomes, in several ways. In both cases there is a complete digestive tract. However, in protostomes, the initial opening (the archenteron) develops into the mouth, and an anus forms separately. In deuterostomes this is reversed. In most protostomes, cells simply fill in the interior of the gastrula to form the mesoderm, called schizocoelous development, but in deuterostomes, it forms through invagination of the endoderm, called enterocoelic pouching. Deuterostomes also have a dorsal, rather than a ventral, nerve chord and their embryos undergo different cleavage.

All this suggests the deuterostomes and protostomes are separate, monophyletic lineages. The main phyla of deuterostomes are the Echinodermata and Chordata. The former are radially symmetric and exclusively marine, such as starfish, sea urchins, and sea cucumbers. The latter are dominated by the vertebrates, animals with backbones. These include fish, amphibians, reptiles, birds, and mammals.

In addition to these, the deuterostomes also include the Hemichordata, or acorn worms. Although they are not especially prominent today, the important fossil graptolites may belong to this group.

The Chaetognatha or arrow worms may also be deuterostomes, but more recent studies suggest protostome affinities.

Ecdysozoa

Yellow-winged darter, *Sympetrum flaveolum*

The Ecdysozoa are protostomes, named after the common trait of growth by moulting or ecdysis. The largest animal phylum belongs here, the Arthropoda, including insects, spiders, crabs, and their kin. All these organisms have a body divided into repeating segments, typically with paired appendages. Two smaller phyla, the Onychophora and Tardigrada, are close relatives of the arthropods and share these traits.

The ecdysozoans also include the Nematoda or roundworms, perhaps the second largest animal phylum. Roundworms are typically microscopic, and occur in nearly every environment where there is water. A number are important parasites. Smaller phyla related to them are the Nematomorpha or horsehair worms, and the Kinorhyncha, Priapulida, and Loricifera. These groups have a reduced coelom, called a pseudocoelom.

The remaining two groups of protostomes are sometimes grouped together as the Spiralia, since in both embryos develop with spiral cleavage.

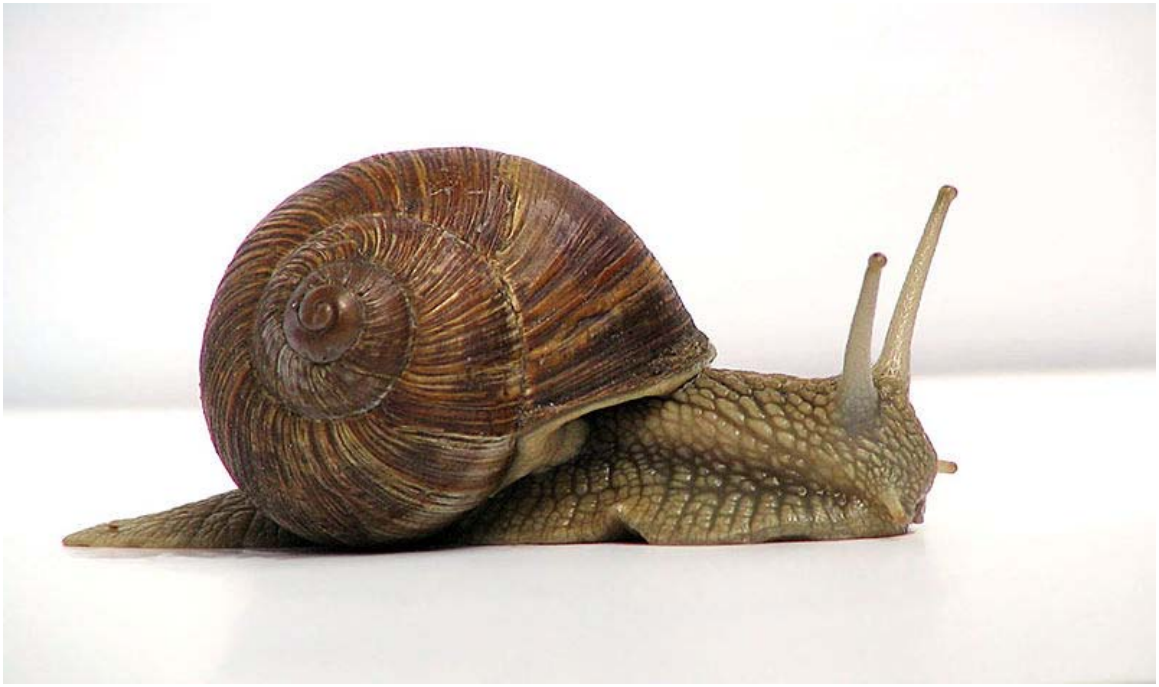
Platyzoa

Pseudobiceros bedfordi, (Bedford's flatworm)

The Platyzoa include the phylum Platyhelminthes, the flatworms. These were originally considered some of the most primitive Bilateria, but it now appears they developed from more complex ancestors. A number of parasites are included in this group, such as the flukes and tapeworms. Flatworms are acoelomates, lacking a body cavity, as are their closest relatives, the microscopic Gastrotricha.

The other platyzoan phyla are mostly microscopic and pseudocoelomate. The most prominent are the Rotifera or rotifers, which are common in aqueous environments. They also include the Acanthocephala or spiny-headed worms, the Gnathostomulida, Micrognathozoa, and possibly the Cycliophora. These groups share the presence of complex jaws, from which they are called the Gnathifera.

Lophotrochozoa



Roman snail, *Helix pomatia*

The Lophotrochozoa include two of the most successful animal phyla, the Mollusca and Annelida. The former, which is the second-largest animal phylum by number of described species, includes animals such as snails, clams, and squids, and the latter comprises the segmented worms, such as earthworms and leeches. These two groups have long been considered close relatives because of the common presence of trochophore larvae, but the annelids were considered closer to the arthropods because they are both segmented. Now, this is generally considered convergent evolution, owing to many morphological and genetic differences between the two phyla.

The Lophotrochozoa also include the Nemertea or ribbon worms, the Sipuncula, and several phyla that have a ring of ciliated tentacles around the mouth, called a lophophore. These were traditionally grouped together as the lophophorates. but it now appears that the lophophorate group may be paraphyletic, with some closer to the nemerteans and some to the molluscs and annelids. They include the Brachiopoda or lamp shells, which are prominent in the fossil record, the Entoprocta, the Phoronida, and possibly the Bryozoa or moss animals.

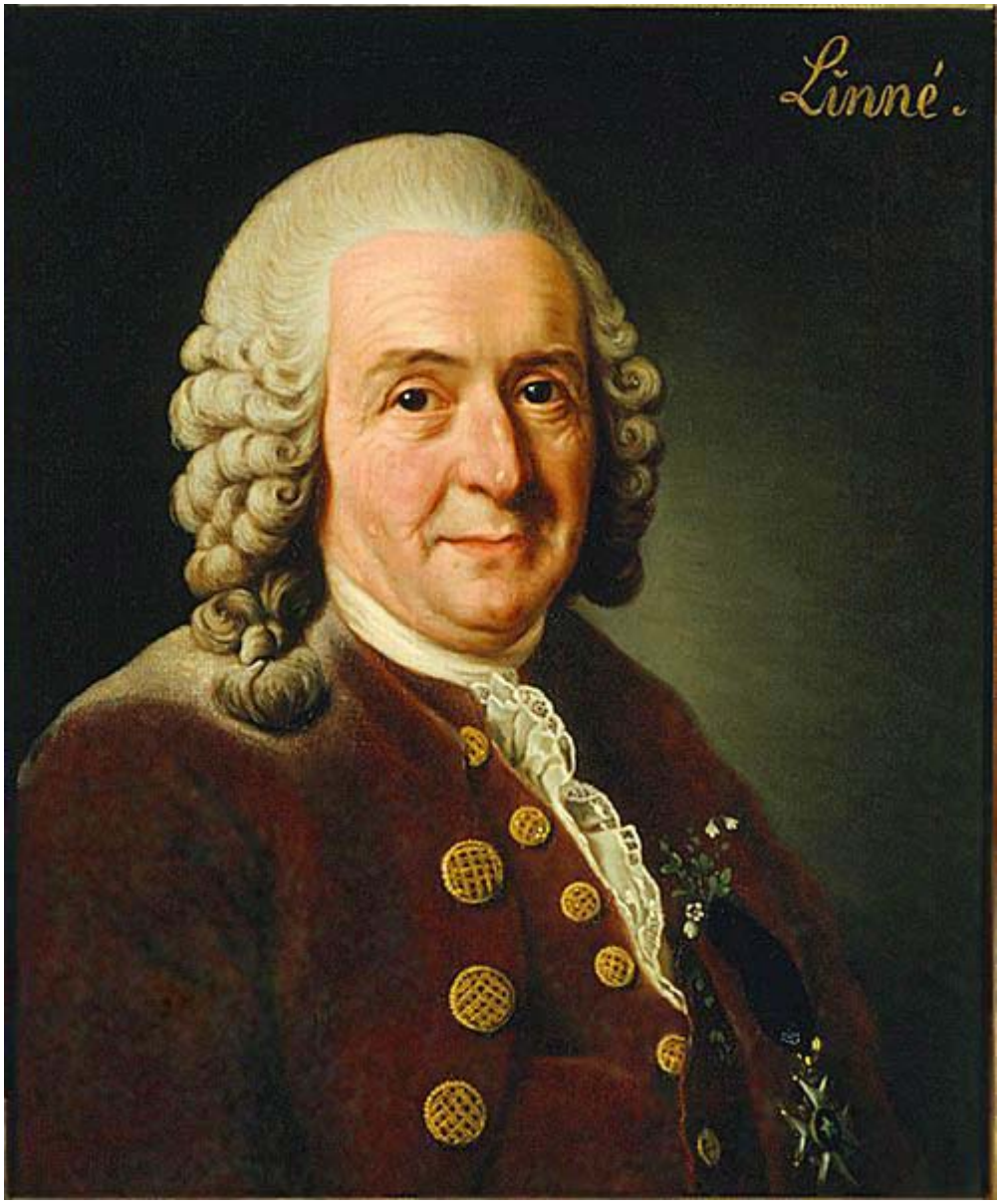
Model organisms

Because of the great diversity found in animals, it is more economical for scientists to study a small number of chosen species so that connections can be drawn from their work and conclusions extrapolated about how animals function in general. Because they are easy to keep and breed, the fruit fly *Drosophila melanogaster* and the nematode

Caenorhabditis elegans have long been the most intensively studied metazoan model organisms, and were among the first life-forms to be genetically sequenced. This was facilitated by the severely reduced state of their genomes, but as many genes, introns, and linkages lost, these ecdysozoans can teach us little about the origins of animals in general. The extent of this type of evolution within the superphylum will be revealed by the crustacean, annelid, and molluscan genome projects currently in progress. Analysis of the starlet sea anemone genome has emphasised the importance of sponges, placozoans, and choanoflagellates, also being sequenced, in explaining the arrival of 1500 ancestral genes unique to the Eumetazoa.

An analysis of the homoscleromorph sponge *Oscarella carmela* also suggests that the last common ancestor of sponges and the eumetazoan animals was more complex than previously assumed.

Other model organisms belonging to the animal kingdom include the mouse (*Mus musculus*) and zebrafish (*Danio rerio*).



Carolus Linnaeus, known as the father of modern taxonomy

History of classification

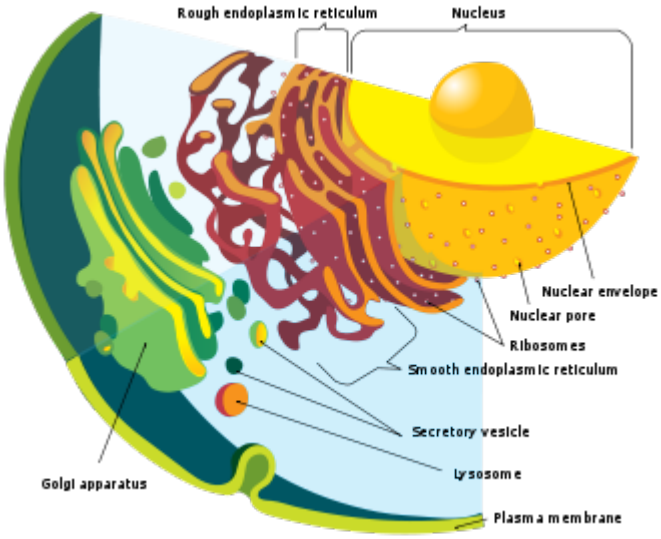
Aristotle divided the living world between animals and plants, and this was followed by Carolus Linnaeus (Carl von Linné), in the first hierarchical classification. Since then biologists have begun emphasizing evolutionary relationships, and so these groups have been restricted somewhat. For instance, microscopic protozoa were originally considered animals because they move, but are now treated separately.

In Linnaeus's original scheme, the animals were one of three kingdoms, divided into the classes of Vermes, Insecta, Pisces, Amphibia, Reptila, Aves, and Mammalia. Since then the last five have all been subsumed into a single phylum, the Chordata, whereas the

various other forms have been separated out. The above lists represent our current understanding of the group, though there is some variation from source to source.

Chapter 8

Endomembrane System



Detail of the endomembrane system and its components

The **endomembrane system** is composed of the different membranes that are suspended in the cytoplasm within a eukaryotic cell. These membranes divide the cell into functional and structural compartments, or organelles. In eukaryotes the organelles of the endomembrane system include: the nuclear envelope, the endoplasmic reticulum, the Golgi apparatus, lysosomes, vacuoles, vesicles, and the cell membrane. The system is defined more accurately as the set of membranes that form a single functional and developmental unit, either being connected together directly, or exchanging material through vesicle transport. Importantly, the endomembrane system does not include the membranes of mitochondria ,chloroplasts or peroxisomes.

The nuclear envelope is a membrane containing two layers, that encompasses the contents of the nucleus. The endoplasmic reticulum (ER) is a synthesis and transport organelle that branches into the cytoplasm in plant and animal cells. The Golgi apparatus is a series of multiple compartments where molecules are packaged for delivery to other cell components or for secretion from the cell. Vacuoles, which are found in both plant and animal cells (though much bigger in plant cells), are responsible for maintaining the shape and structure of the cell as well as storing waste products. A vesicle is a relatively small, membrane-enclosed sac that stores or transports substances. The plasma membrane, also referred to as the cell membrane, is a protective barrier that regulates what enters and leaves the cell. There is also an organelle known as the spitzenkörper that is only found in fungi, and is connected with hyphal tip growth.

In prokaryotes endomembranes are rare, although in many photosynthetic bacteria the plasma membrane is highly folded and most of the cell cytoplasm is filled with layers of light-gathering membrane. These light-gathering membranes may even form enclosed structures called chlorosomes in green sulfur bacteria.

The organelles of the endomembrane system are related through direct contact or by the transfer of membrane segments as vesicles. Despite these relationships, the various membranes are not identical in structure and function. The thickness, molecular composition, and metabolic behavior of a membrane are not fixed, they may be modified several times during the membrane's life. One unifying characteristic the membranes share is a lipid bilayer, with proteins attached to either side or traversing them.

History of the concept

Most lipids are synthesized in yeast either in the endoplasmic reticulum, lipid particles, or the mitochondrion, with little or no lipid synthesis occurring in the plasma membrane or nuclear membrane. Sphingolipid biosynthesis begins in the endoplasmic reticulum, but is completed in the Golgi apparatus. The situation is similar on mammals, with the exception of the first few steps in ether lipid biosynthesis, which occur in peroxisomes. The various membranes that enclose the other subcellular organelles must therefore be constructed by transfer of lipids from these sites of synthesis. However, although it is clear that lipid transport is a central process in organelle biogenesis, the mechanisms by which lipids are transported through cells remain poorly understood.

The first proposal that the membranes within cells form a single system that exchanges material between its components was by Morré and Mollenhauer in 1974. This proposal was made as a way of explaining how the various lipid membranes are assembled in the cell, with these membranes being assembled through *lipid flow* from the sites of lipid synthesis. The idea of lipid flow through a continuous system of membranes and vesicles was an alternative to the various membranes being independent entities that are formed from transport of free lipid components, such as fatty acids and sterols, through the cytosol. Importantly, the transport of lipids through the cytosol and lipid flow through a continuous endomembrane system are not mutually exclusive processes and both may occur in cells.

Components of the system

Nuclear envelope

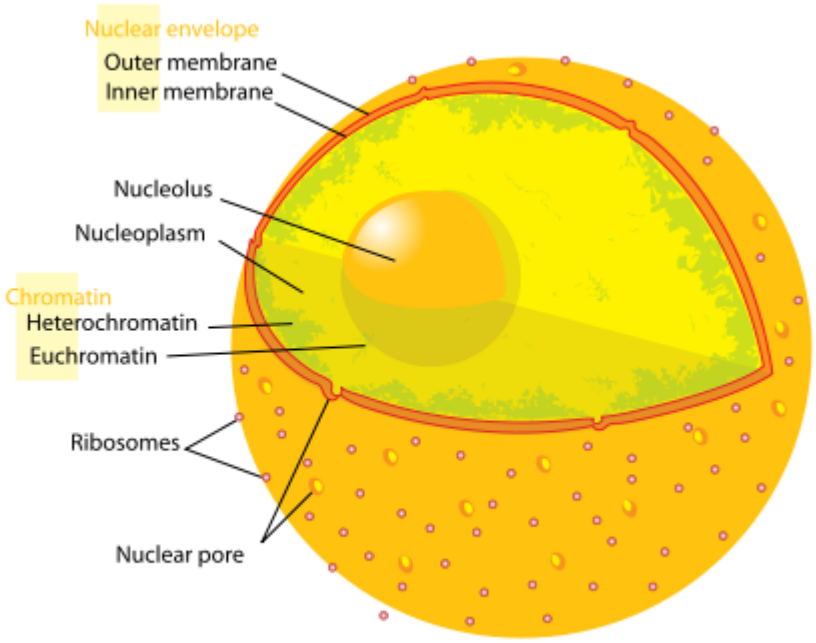


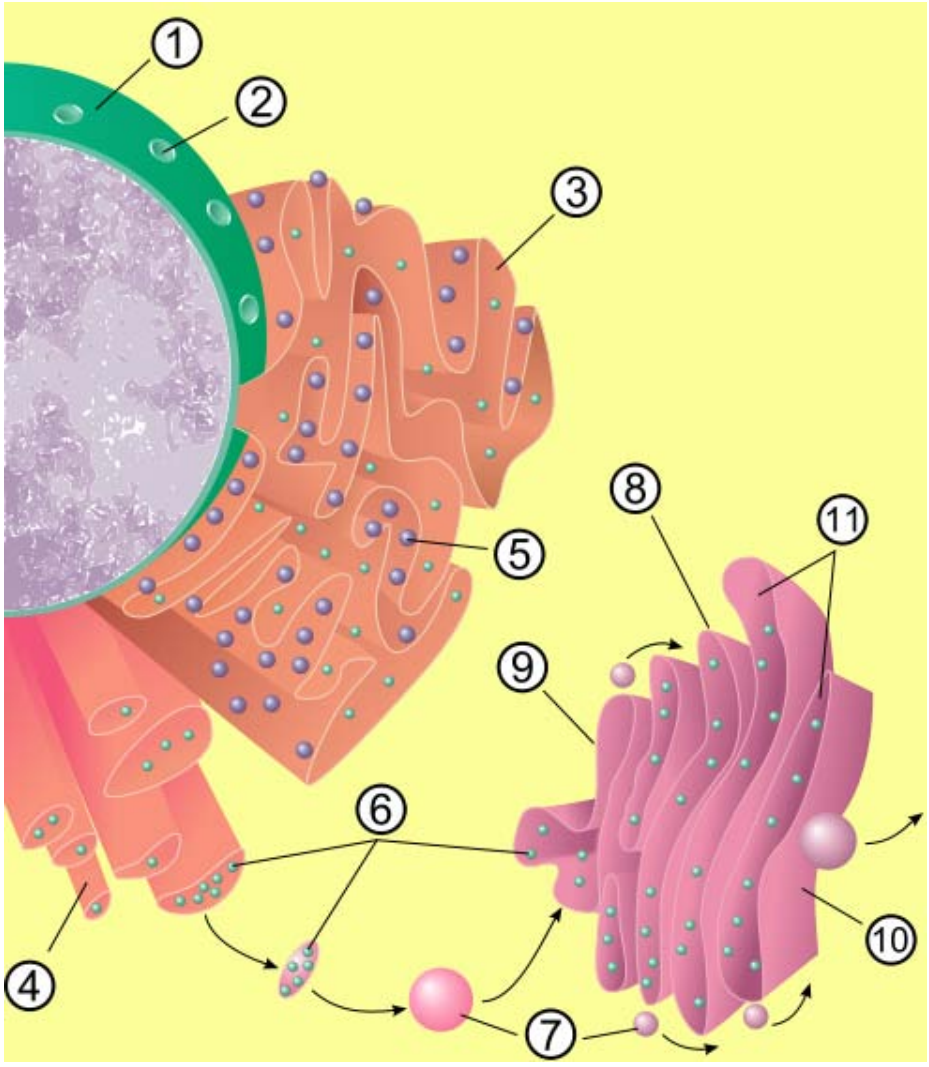
Diagram of the nucleus with the nuclear envelope shown as the orange portion.

The nuclear envelope encloses the nucleus, separating its contents from the cytoplasm. It has two membranes, each a lipid bilayer with associated proteins. The outer nuclear membrane is constant with the rough endoplasmic reticulum membrane, and like that structure, features ribosomes attached to the surface. The outer membrane is also constant with the inner nuclear membrane since the two layers are fused together at numerous tiny holes called nuclear pores that perforate the nuclear envelope. These pores are about 120 nm in diameter and regulate the passage of molecules between the nucleus and cytoplasm, permitting some to pass through the membrane, but not others. Since the nuclear pores are located in an area of high traffic, they play an important role in the physiology of cells. The space between the outer and inner membranes is called the perinuclear space and is joined with the lumen of the rough ER.

The nuclear envelopes structure is determined by a network of intermediate filaments (protein filaments). This network is organized into lining similar to mesh called the nuclear lamina, which binds to chromatin, integral membrane proteins, and other nuclear components along the inner surface of the nucleus. The nuclear lamina is thought to help materials inside the nucleus reach the nuclear pores and in the disintegration of the nuclear envelope during mitosis and its reassembly at the end of the process.

The nuclear pores are highly efficient at selectively allowing the passage of materials to and from the nucleus, because the nuclear envelope has a considerable amount of traffic. RNA and ribosomal subunits must be continually transferred from the nucleus to the cytoplasm. Histones, gene regulatory proteins, DNA and RNA polymerases, and other substances essential for nuclear activities must be imported from the cytoplasm. The nuclear envelope of a typical mammalian cell contains 3000–4000 pore complexes. If the cell is synthesizing DNA each pore complex needs to transport about 100 histone molecules per minute. If the cell is growing rapidly, each complex also needs to transport about 6 newly assembled large and small ribosomal subunits per minute from the nucleus to the cytosol, where they are used to synthesize proteins.

Endoplasmic reticulum



1 Nucleus **2** Nuclear pore **3** Rough endoplasmic reticulum (RER) **4** Smooth endoplasmic reticulum (SER) **5** Ribosome on the rough ER **6** Proteins that are transported **7** Transport vesicle **8** Golgi apparatus **9** Cis face of the Golgi apparatus **10** Trans face of the Golgi apparatus **11** Cisternae of the Golgi apparatus

The endoplasmic reticulum (ER) is a membranous synthesis and transport organelle that is an extension of the nuclear envelope. More than half the total membrane in eukaryotic cells is accounted for by the ER. The ER is made up of flattened sacs and branching tubules that are thought to interconnect, so that the ER membrane forms a continuous sheet enclosing a single internal space. This highly convoluted space is called the ER lumen and is also referred to as the ER cisternal space. The lumen takes up about ten percent of the entire cell volume. The endoplasmic reticulum membrane allows molecules to be selectively transferred between the lumen and the cytoplasm, and since it is connected to the nuclear envelope, it provides a channel between the nucleus and the cytoplasm.

The ER has a central role in producing, processing, and transporting biochemical compounds for use inside and outside of the cell. Its membrane is the site of production of all the transmembrane proteins and lipids for most of the cell's organelles, including the ER itself, the Golgi apparatus, lysosomes, endosomes, mitochondria, peroxisomes, secretory vesicles, and the plasma membrane. Furthermore, almost all of the proteins that will exit the cell, plus those destined for the lumen of the ER, Golgi apparatus, or lysosomes, are originally delivered to the ER lumen. Consequently, many of the proteins found in the cisternal space of the endoplasmic reticulum lumen are there only temporarily as they pass on their way to other locations. Other proteins, however, constantly remain in the lumen and are known as endoplasmic reticulum resident proteins. These special proteins contain a specialized retention signal made up of a specific sequence of amino acids that enables them to be retained by the organelle. An example of an important endoplasmic reticulum resident protein is the chaperon protein known as BiP which identifies other proteins that have been improperly built or processed and keeps them from being sent to their final destinations.

There are two distinct, though connected, regions of ER that differ in structure and function: smooth ER and rough ER. The rough endoplasmic reticulum is so named because the cytoplasmic surface is covered with ribosomes, giving it a bumpy appearance when viewed through an electron microscope. The smooth ER appears smooth since its cytoplasmic surface lacks ribosomes.

Functions of the smooth ER

In the great majority of cells, smooth ER regions are scarce and are often partly smooth and partly rough. They are sometimes called transitional ER because they contain ER exit sites from which transport vesicles carrying newly synthesized proteins and lipids bud off for transport to the Golgi apparatus. In certain specialized cells, however, the smooth ER is abundant and has additional functions. The smooth ER of theses specialized cells function in diverse metabolic processes, including synthesis of lipids, metabolism of carbohydrates, and detoxification of drugs and poisons.

Enzymes of the smooth ER are vital to the synthesis of lipids, including oils, phospholipids, and steroids. Sex hormones of vertebrates and the steroid hormones

secreted by the adrenal glands are among the steroids produced by the smooth ER in animal cells. The cells that synthesis these hormones are rich in smooth ER.

Liver cells are another example of specialized cells that contain an abundance of smooth ER. These cells provide an example of the role of smooth ER in carbohydrate metabolism. Liver cells store carbohydrates in the form of glycogen. The hydrolysis of glycogen leads to the release of glucose from the liver cells, which is important in the regulation of sugar concentration in the blood. However, glycogen hydrolysis requires glucose phosphate, an ionic form of the sugar that can not exit the cell. An enzyme of the liver cell's smooth ER removes the phosphate from the glucose, so that it can then leave the cell.

Enzymes of the smooth ER can also help detoxify drugs and poisons. Detoxification usually involves the addition of a hydroxyl group to a drug, making the drug more soluble and thus easier to purge from the body. One extensively studied detoxification reaction is carried out by the cytochrome P450 family of enzymes, which catalyze water-insoluble drugs or metabolites that would otherwise accumulate to toxic levels in cell membrane.

Muscle cells have another specialized function of smooth ER. The ER membrane pumps calcium ions from the cytosol into the cisternal space. When a muscle cell becomes stimulated by a nerve impulse, calcium goes back across the ER membrane into the cytosol and generates the contraction of the muscle cell.

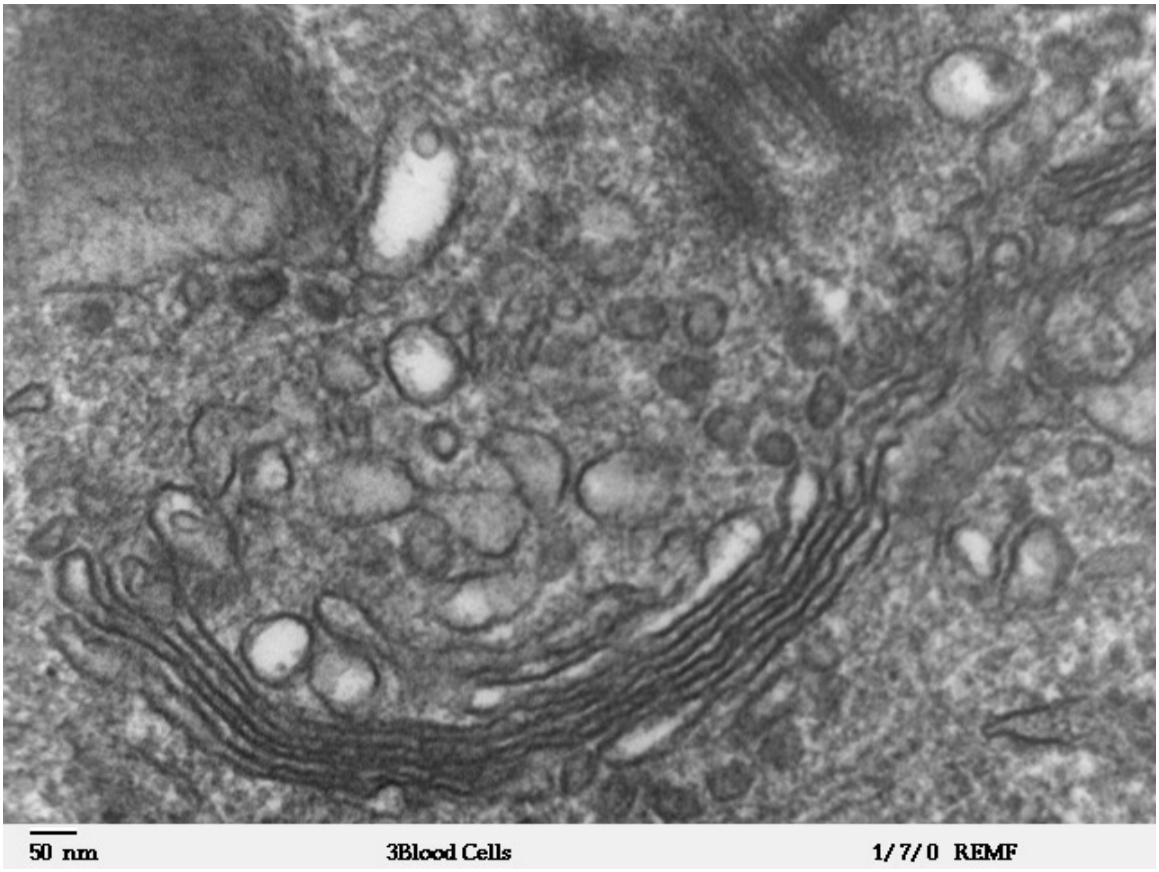
Functions of the rough ER

Many types of cells export proteins produced by ribosomes attached to the rough ER. The ribosomes assemble amino acids into protein units, which are carried into the rough ER for further adjustments. These proteins may be either transmembrane proteins, which become embedded in the membrane of the endoplasmic reticulum, or water-soluble proteins, which are able to pass through the membrane into the lumen. Those that reach the inside of the endoplasmic reticulum are folded into the correct three-dimensional conformation. Chemicals, such as carbohydrates or sugars, are added, then the endoplasmic reticulum either transports the completed proteins, called secretory proteins, to areas of the cell where they are needed, or they are sent to the Golgi apparatus for further processing and modification.

Once secretory proteins are formed, the ER membrane separates them from the proteins that will remain in the cytosol. Secretory proteins depart from the ER enfolded in the membranes of vesicles that bud like bubbles from the transitional ER. These vesicles in transit to another part of the cell are called transport vesicles. An alternative mechanism for transport of lipids and proteins out of the ER are through lipid transfer proteins at regions called membrane contact sites where the ER becomes closely and stably associated with the membranes of other organelles, such as the plasma membrane, Golgi or lysosomes.

In addition to making secretory proteins, the rough ER makes membranes that grows in place from the addition of proteins and phospholipids. As polypeptides intended to be membrane proteins grow from the ribosomes, they are inserted into the ER membrane itself and are kept there by their hydrophobic portions. The rough ER also produces its own membrane phospholipids; enzymes built into the ER membrane assemble phospholipids. The ER membrane expands and can be transferred by transport vesicles to other components of the endomembrane system.

Golgi apparatus



Micrograph of Golgi apparatus, visible as a stack of semicircular black rings near the bottom. Numerous circular vesicles can be seen in proximity to the organelle

The Golgi apparatus (also known as the Golgi body and the Golgi complex) is composed of interconnected sacs called cisternae. Its shape can be related to that of a stack of pancakes. The number of these stacks varies with the specific function of the cell. The Golgi apparatus is used by the cell for further protein modification. The section of the Golgi apparatus that receives the vesicles from the ER is known as the cis face, and is usually near the ER. The opposite end of the Golgi apparatus is called the trans face, this is where the modified compounds leave. The trans face is usually facing the plasma membrane, which is where most of the substances the Golgi apparatus modifies are sent.

Vesicles sent off by the ER containing proteins are further altered at the golgi apparatus and then prepared for secretion from the cell or transport to other parts of the cell. Various things can happen to the proteins on their journey through the enzyme covered space of the Golgi apparatus. The modification and synthesis of the carbohydrate portions of glycoproteins is common in protein processing. The Golgi apparatus removes and substitutes sugar monomers, producing a large variety of oligosaccharides. In addition to modifying proteins, the golgi also manufactures macromolecules itself. In plant cells, the Golgi produces pectins and other polysaccharides needed by the plant structure.

Once the modification process is completed the golgi apparatus sorts the products of its processing and sends them to various parts of the cell. Molecular identification labels or tags are added by the golgi enzymes to help with this. After everything is organized, the golgi apparatus sends off its products by budding vesicles from its trans face.

Vacuoles

Vacuoles, like vesicles, are membrane-bounded sacs within the cell. They are larger than vesicles and their specific function varies. The operations of vacuoles are different for plant and animal vacuoles.

In plant cells, vacuoles cover anywhere from 30% to 90% of the total cell volume. Most mature plant cells contain one large central vacuole encompassed by a membrane called the tonoplast. Vacuoles of plant cells act as storage compartments for the nutrients and waste of a cell. The solution that these molecules are stored in is called the cell sap. Pigments that color the cell are sometime located in the cell sap. Vacuoles can also increase the size of the cell, which elongates as water is added, and they control the turgor pressure (the osmotic pressure that keeps the cell wall from caving in). Like lysosomes of animal cells, vacuoles have an acidic pH and contain hydrolytic enzymes. The pH of vacuoles enables them to perform homeostatic procedures in the cell. For example, when the pH in the cells environment drops, the H+ surging into the cytosol can be transferred to a vacuole in order to keep the cytosol's pH constant.

In animals, vacuoles serve in exocytosis and endocytosis processes. Endocytosis refers to when particles are taken into the cell. The material to be taken in is surrounded by the plasma membrane, and then transferred to a vacuole. There are two types of endocytosis, phagocytosis (cell eating) and pinocytosis (cell drinking). In phagocytosis, cells engulf large particles such as bacteria. Pinocytosis is the same process, except the substances being ingested are in the fluid form.

Vesicles

Vesicles are small membrane-enclosed transport units that can transfer molecules between different compartments. Most vesicles transfer the membranes assembled in the endoplasmic reticulum to the Golgi apparatus, and then from the Golgi apparatus to various locations.

There are various types of vesicles each with a different protein configuration. Most are formed from specific regions of membranes. When a vesicle buds off from a membrane it contains specific proteins on its cytosolic surface. Each membrane a vesicle travels to contains a marker on its cytosolic surface. This marker corresponds with the proteins on the vesicle traveling to the membrane. Once the vesicle finds the membrane, they fuse.

There are three well known types of vesicles. They are clathrin-coated, COPI-coated, and COPII-coated vesicles. Each performs different functions in the cell. For example, clathrin-coated vesicles transport substances between the golgi apparatus and the plasma membrane. COPI- and COPPII-coated vesicles are frequently used for transportation between the ER and the golgi apparatus.

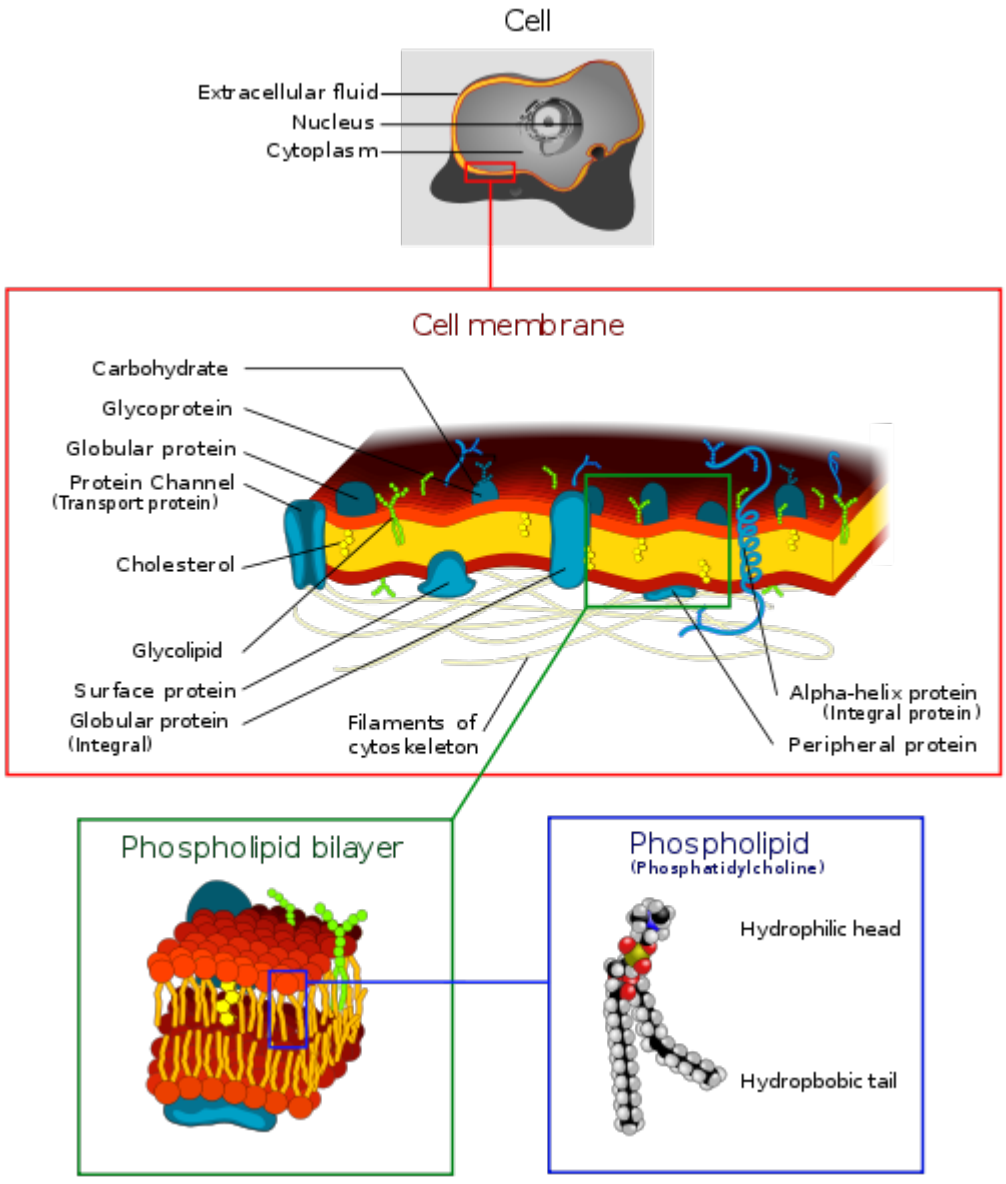
Lysosomes

Lysosomes are organelles that contain hydrolytic enzymes that are used for intracellular digestion. The main functions of a lysosome are to process molecules taken in by the cell and to recycle worn out cell parts. The enzymes inside of lysosomes are acid hydrolases which require an acidic environment for optimal performance. Lysosomes provide such an environment by maintaining a pH of 5.0 inside of the organelle. If a lysosome were to rupture, the enzymes released would not be very active because of the cytosol's neutral pH. However, if numerous lysosomes leaked the cell could be destroyed from autodigestion.

Lysosomes carry out intracellular digestion by fusing with a vacuole and releasing their enzymes into the vacuole. Through this process, sugars, amino acids, and other monomers pass into the cytosol and become nutrients for the cell. Lysosomes also use their hydrolytic enzymes to recycle the cell's obsolete organelles in a process called autophagy. The lysosome engulfs another organelle and uses its enzymes to take apart the ingested material. The resulting organic monomers are then returned to the cytosol for reuse. The last function of a lysosome is to digest the cell itself through autolysis.

Spitzenkörper

The spitzenkörper is a component of the endomembrane system found only in fungi, and is associated with hyphal tip growth. It is a phase-dark body that is composed of an aggregation of membrane-bound vesicles containing cell wall components, serving as a point of assemblage and release of such components intermediate between the Golgi and the cell membrane. The spitzenkörper is motile and generates new hyphal tip growth as it moves forward.



Detailed illustration of the plasma membrane. Including the structure of a phospholipid.

Plasma membrane

The plasma membrane is a phospholipid bilayer membrane that separates the cell from its environment and regulates the transport of molecules and signals into and out of the cell. Embedded in the membrane are proteins that perform the functions of the plasma membrane. The plasma membrane is not a fixed or rigid structure, the molecules that compose the membrane are capable of lateral movement. This movement and the multiple components of the membrane are why it is referred to as a fluid mosaic. Smaller molecules such as carbon dioxide, water, and oxygen can pass through the plasma membrane freely by diffusion or osmosis. Larger molecules needed by the cell are assisted by proteins through active transport.

The plasma membrane of a cell has multiple functions. These include transporting nutrients into the cell, allowing waste to leave, preventing materials from entering the cell, averting needed materials from leaving the cell, maintaining the pH of the cytosol, and preserving the osmotic pressure of the cytosol. Transport proteins which allow some materials to pass through but not others are used for these functions. These proteins use ATP hydrolysis to pump materials against their concentration gradients.

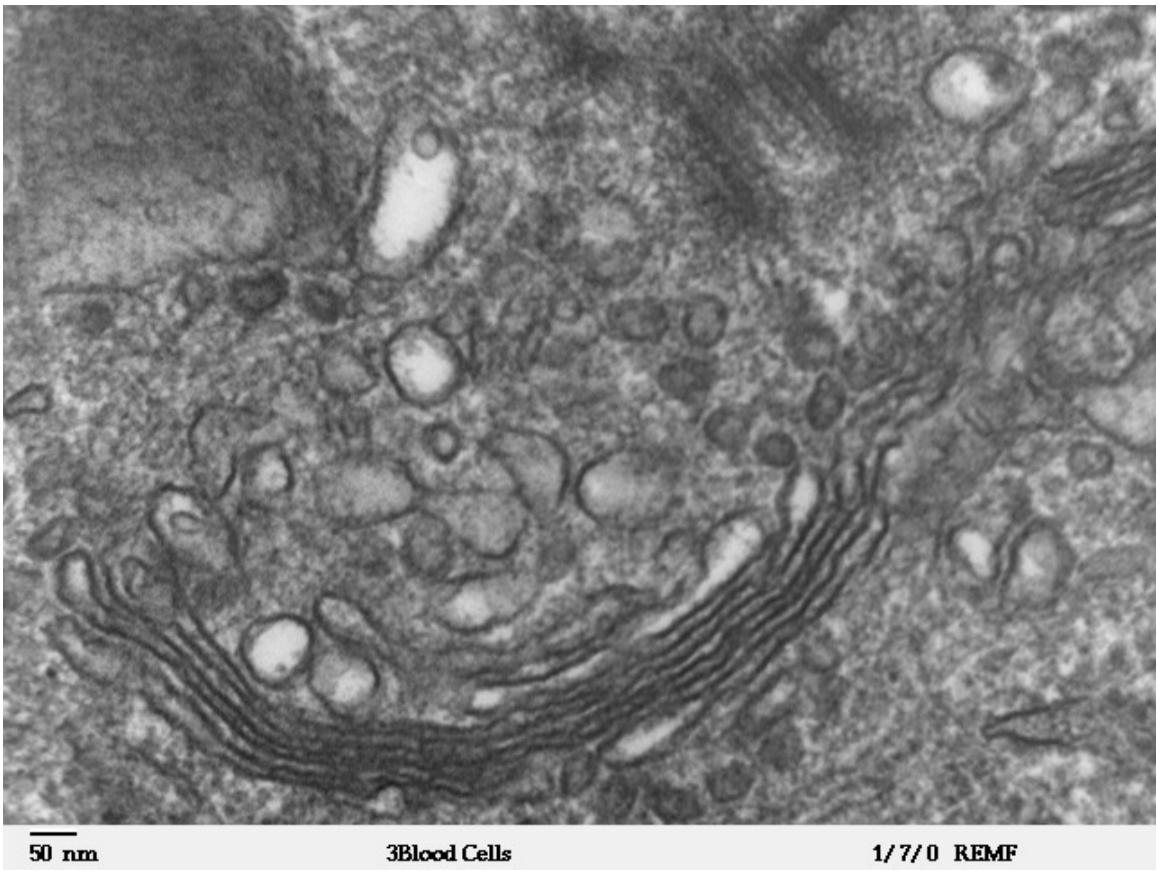
In addition to these universal functions, the plasma membrane has a more specific role in multicellular organisms. Glycoproteins on the membrane assist the cell in recognizing other cells, in order to exchange metabolites and form tissues. Other proteins on the plasma membrane allow attachment to the cytoskeleton and extracellular matrix; a function that maintains cell shape and fixes the location of membrane proteins. Enzymes that catalyze reactions are also found on the plasma membrane. Receptor proteins on the membrane have a shape that matches with a chemical messenger, resulting in various cellular responses.

Evolution

The Golgi, ER, and lysosomes are likely to have evolved as a result of the plasma membrane going through invagination. An increase in the overall volume of a cell would require the plasma membrane to fold in order to maintain a constant surface area to volume ratio. These folds may have led to the specialization of internal membranes to maintain communication with the environment. In the first stages of eukaryotic cell life, the membranes may have been interconnected and attached to the plasma membrane. Later on, as their functions diverged, the membranes may have become separate structures.

Chapter 9

Golgi Apparatus



Micrograph of Golgi apparatus, visible as a stack of semicircular black rings near the bottom. Numerous circular vesicles can be seen in proximity to the organelle

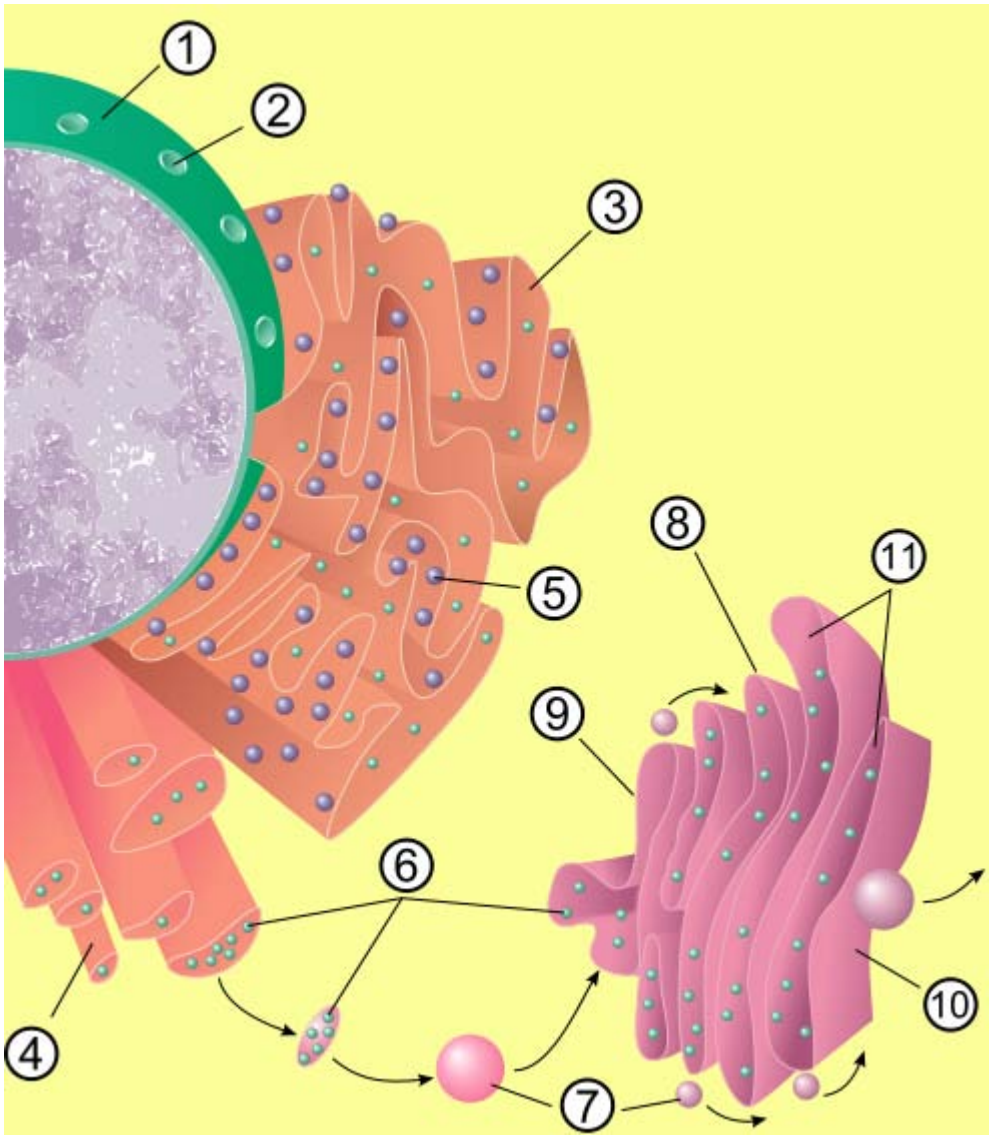


Diagram of secretory process from endoplasmic reticulum (orange) to Golgi apparatus (pink). 1. Nuclear membrane; 2. Nuclear pore; 3. Rough endoplasmic reticulum (RER); 4. Smooth endoplasmic reticulum (SER); 5. Ribosome attached to RER; 6. Macromolecules; 7. Transport vesicles; 8. Golgi apparatus; 9. *Cis* face of Golgi apparatus; 10. *Trans* face of Golgi apparatus; 11. Cisternae of lipids

The Golgi Apparatus (also **Golgi body** or the **Golgi complex**) is an organelle found in most eukaryotic cells. It was identified in 1897 by the Italian physician Camillo Golgi, after whom the Golgi apparatus is named.

It processes and packages macromolecules, such as proteins and lipids, after their synthesis and before they make their way to their destination; it is particularly important in the processing of proteins for secretion. The Golgi apparatus forms a part of the cellular endomembrane system.

Evolution

The Golgi apparatus appears to have existed even in the "ancestral eukaryote" from which all modern eukaryotes evolved, even though some no longer have it.

Discovery

Due to its fairly large size, the Golgi apparatus was one of the first organelles to be discovered and observed in detail. The apparatus was discovered in 1897 by Italian physician Camillo Golgi during an investigation of the nervous system. After first observing it under his microscope, he termed the structure the *internal reticular apparatus*. The structure was then renamed after Golgi not long after the announcement of his discovery in 1898. However, some doubted the discovery at first, arguing that the appearance of the structure was merely an optical illusion created by the observation technique used by Golgi. With the development of modern microscopes in the 20th century, the discovery was confirmed.

Structure

Found in both plant and animal cells, the Golgi is composed of stacks of membrane-bound structures known as cisternae (singular: *cisterna*). An individual stack is sometimes called a dictyosome (from Greek *dictyon*, net + *soma*, body), especially in plant cells. A mammalian cell typically contains 40 to 100 stacks. Between four and eight cisternae are usually present in a stack; however, in some protists as many as sixty have been observed. Each cisterna comprises a flat, membrane enclosed disc that includes special Golgi enzymes which modify or help to modify cargo proteins that travel through it.

The cisternae stack has four functional regions: the cis-Golgi network, medial-Golgi, endo-Golgi, and trans-Golgi network. Vesicles from the endoplasmic reticulum (via the vesicular-tubular clusters) fuse with the network and subsequently progress through the stack to the trans Golgi network, where they are packaged and sent to the required destination. Each region contains different enzymes which selectively modify the contents depending on where they reside. The cisternae also carry structural proteins important for their maintenance as flattened membranes which stack upon each other.

Function

Cells synthesize a large number of different macromolecules. The Golgi apparatus is integral in modifying, sorting, and packaging these macromolecules for cell secretion (exocytosis) or use within the cell. It primarily modifies proteins delivered from the rough endoplasmic reticulum but is also involved in the transport of lipids around the cell, and the creation of lysosomes. In this respect it can be thought of as similar to a post office; it packages and labels items which it then sends to different parts of the cell.

Enzymes within the cisternae are able to modify the proteins by addition of carbohydrates (glycosylation) and phosphates (phosphorylation). In order to do so, the Golgi imports substances such as nucleotide sugars from the cytosol. These modifications may also form a signal sequence which determines the final destination of the protein. For example, the Golgi apparatus adds a mannose-6-phosphate label to proteins destined for lysosomes.

The Golgi plays an important role in the synthesis of proteoglycans, which are molecules present in the extracellular matrix of animals. It is also a major site of carbohydrate synthesis. This includes the production of glycosaminoglycans (GAGs), long unbranched polysaccharides which the Golgi then attaches to a protein synthesised in the endoplasmic reticulum to form proteoglycans. Enzymes in the Golgi polymerize several of these GAGs via a xylose link onto the core protein. Another task of the Golgi involves the sulfation of certain molecules passing through its lumen via sulphotranferases that gain their sulphur molecule from a donor called PAPs. This process occurs on the GAGs of proteoglycans as well as on the core protein. The level of sulfation is very important to the proteoglycans' signalling abilities as well as giving the proteoglycan its overall negative charge.

The phosphorylation of molecules requires that ATP is imported into the lumen of the Golgi and then utilised by resident kinases such as casein kinase 1 and casein kinase 2. One molecule that is phosphorylated in the Golgi is Apolipoprotein, which forms a molecule known as VLDL that is a constitute of blood serum. It is thought that the phosphorylation of these molecules is important to help aid in their sorting for secretion into the blood serum.

The Golgi has a putative role in apoptosis, with several Bcl-2 family members localised there, as well as to the mitochondria. A newly characterized protein, GAAP (Golgi anti-apoptotic protein), almost exclusively resides in the Golgi and protects cells from apoptosis by an as-yet undefined mechanism.

Vesicular transport

The vesicles that leave the rough endoplasmic reticulum are transported to the *cis* face of the Golgi apparatus, where they fuse with the Golgi membrane and empty their contents into the lumen. Once inside the lumen, the molecules are modified, sorted and shipped towards their final destination. The Golgi apparatus tends to be larger and more numerous in cells that synthesise and secrete large amounts of substances, for example, the plasma B cells and the antibody-secreting cells of the immune system have prominent Golgi complexes.

Those proteins destined for areas of the cell other than either the endoplasmic reticulum or Golgi apparatus are moved towards the *trans* face, to a complex network of membranes and associated vesicles known as the *trans-Golgi network* (TGN). This area of the Golgi is the point at which proteins are sorted and shipped to their intended

destinations by their placement into one of at least three different types of vesicles, depending upon the molecular marker they carry:

Type	Description	Example
Exocytotic vesicles *(continuous)*	Vesicle contains proteins destined for extracellular release. After packaging the vesicles bud off and immediately move towards the plasma membrane, where they fuse and release the contents into the extracellular space in a process known as *constitutive secretion*.	Antibody release by activated plasma B cells
Secretory vesicles *(regulated)*	Vesicle contains proteins destined for extracellular release. After packaging, the vesicles bud off and are stored in the cell until a signal is given for their release. When the appropriate signal is received they move towards the membrane and fuse to release their contents. This process is known as *regulated secretion*.	Neurotransmitter release from neurons
Lysosomal vesicles	Vesicle contains proteins destined for the lysosome, an organelle of degradation containing many acid hydrolases, or to lysosome-like storage organelles. These proteins include both digestive enzymes and membrane proteins. The vesicle first fuses with the late endosome, and the contents are then transferred to the lysosome via unknown mechanisms.	Digestive proteases destined for the lysosome

Transport mechanism

The transport mechanism which proteins use to progress through the Golgi apparatus is not yet clear; however a number of hypotheses currently exist. Until recently, the vesicular transport mechanism was favoured but now more evidence is coming to light to support cisternal maturation. The two proposed models may actually work in conjunction with each other, rather than being mutually exclusive. This is sometimes referred to as the *combined* model.

- ***Cisternal maturation model***: the cisternae of the Golgi apparatus move by being built at the *cis* face and destroyed at the *trans* face. Vesicles from the endoplasmic reticulum fuse with each other to form a cisterna at the *cis* face, consequently this cisterna would appear to move through the Golgi stack when a new cisterna is formed at the *cis* face. This model is supported by the fact that structures larger than the transport vesicles, such as collagen rods, were observed microscopically to progress through the Golgi apparatus. This was initially a popular hypothesis, but lost favour in the 1980s. Recently it has made a comeback, as laboratories at the University of Chicago and the University of Tokyo have been able to use new technology to directly observe Golgi compartments maturing. Additional evidence comes from the fact that COPI vesicles move in the retrograde direction,

transporting Endoplasmic Reticulum proteins back to where they belong by recognizing a signal peptide.

- ***Vesicular transport model***: Vesicular transport views the Golgi as a very stable organelle, divided into compartments in the cis to trans direction. Membrane bound carriers transport material between the ER and the different compartments of the Golgi. Experimental evidence includes the abundance of small vesicles (known technically as shuttle vesicles) in proximity to the Golgi apparatus. To direct the vesicles, actin filaments connect packaging proteins to the membrane to ensure that they fuse with the correct compartment.

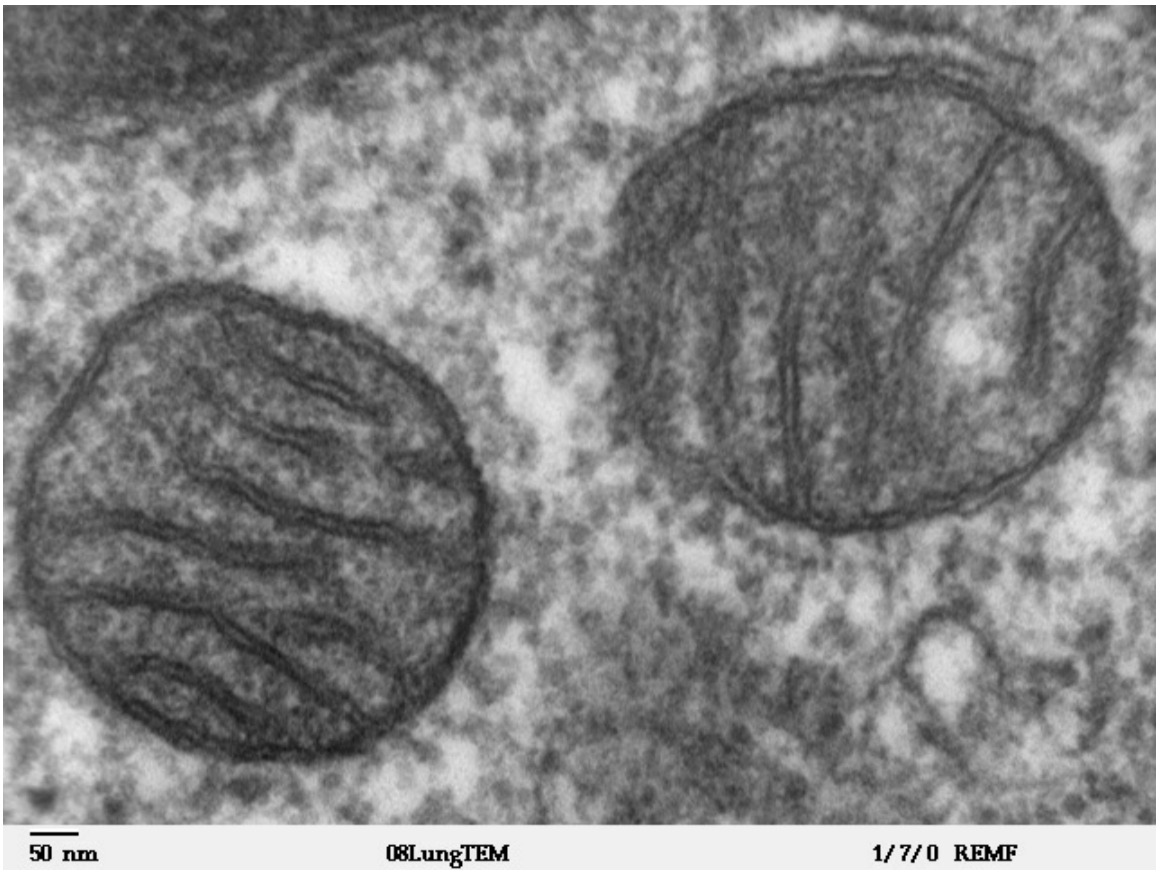
Golgi apparatus during mitosis

In animal cells, the Golgi apparatus will break up and disappear following the onset of mitosis, or cellular division. During the telophase of mitosis, the Golgi apparatus reappears; however, it is still uncertain how this occurs.

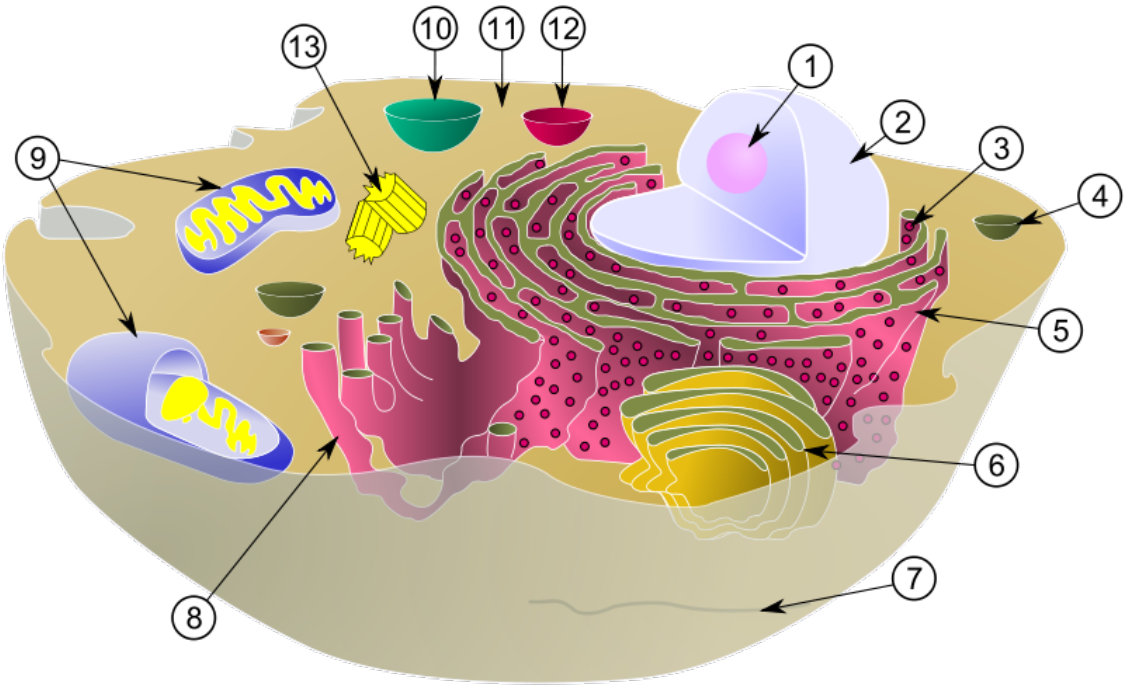
Intriguingly, the same is not true of plant or yeast Golgi stacks, which have been observed to remain intact throughout the cell cycle. The reason for this difference is not yet known, but it may, in part, be a consequence of golgin proteins.

Chapter 10

Mitochondrion



Two mitochondria from mammalian lung tissue displaying their matrix and membranes as shown by electron microscopy.



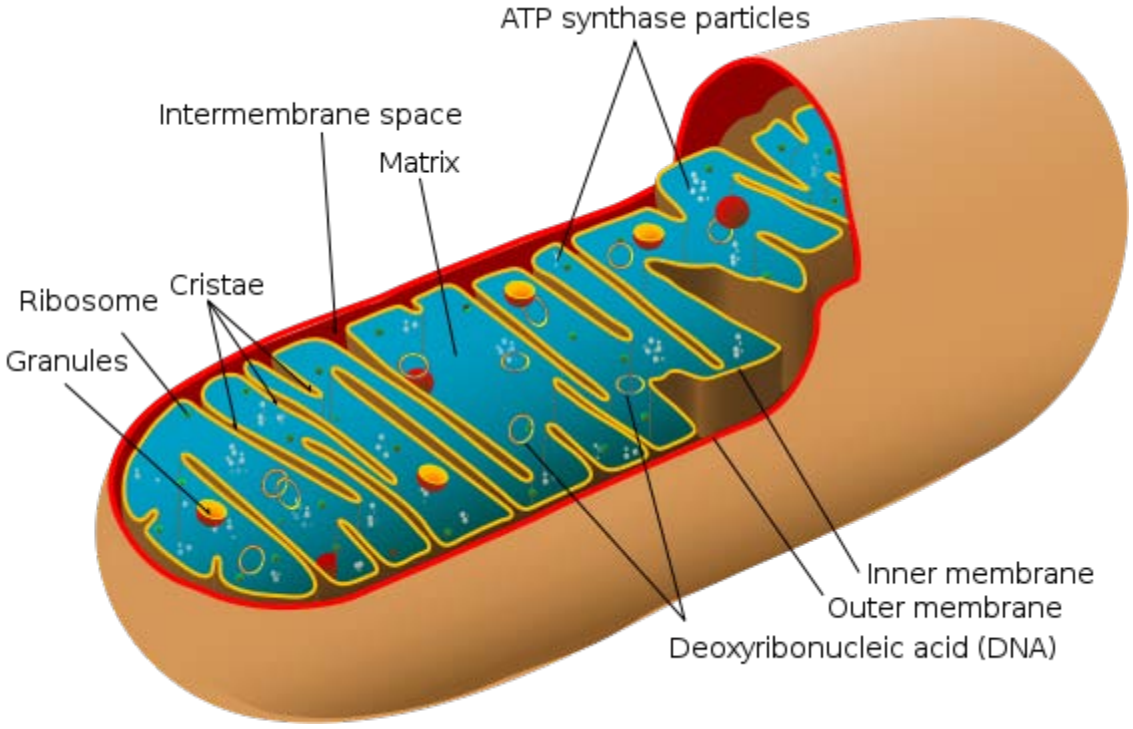
Schematic of typical animal cell, showing subcellular components. Organelles:
(1) nucleolus
(2) nuclear membrane
(3) Ribosomes
(4) Vesicle
(5) Rough endoplasmic reticulum (ER)
(6) Golgi body
(7) Cytoskeleton
(8) Smooth ER
(9) Mitochondria
(13) Centrioles within centrosome

In cell biology, a **mitochondrion** (plural **mitochondria**) is a membrane-enclosed organelle found in most eukaryotic cells. These organelles range from 0.5 to 10 micrometers (μm) in diameter. Mitochondria are sometimes described as "cellular power plants" because they generate most of the cell's supply of adenosine triphosphate (ATP), used as a source of chemical energy. In addition to supplying cellular energy, mitochondria are involved in a range of other processes, such as signaling, cellular differentiation, cell death, as well as the control of the cell cycle and cell growth. Mitochondria have been implicated in several human diseases, including mitochondrial disorders and cardiac dysfunction, and may play a role in the aging process. The word mitochondrion comes from the Greek *μίτος* or *mitos*, thread + *χονδρίον* or *chondrion*, granule.

Several characteristics make mitochondria unique. The number of mitochondria in a cell varies widely by organism and tissue type. Many cells have only a single mitochondrion, whereas others can contain several thousand mitochondria. The organelle is composed of

compartments that carry out specialized functions. These compartments or regions include the outer membrane, the intermembrane space, the inner membrane, and the cristae and matrix. Mitochondrial proteins vary depending on the tissue and the species. In humans, 615 distinct types of proteins have been identified from cardiac mitochondria, whereas in Murinae (rats), 940 proteins encoded by distinct genes have been reported. The mitochondrial proteome is thought to be dynamically regulated. Although most of a cell's DNA is contained in the cell nucleus, the mitochondrion has its own independent genome. Further, its DNA shows substantial similarity to bacterial genomes.

Structure



A mitochondrion contains outer and inner membranes composed of phospholipid bilayers and proteins. The two membranes, however, have different properties. Because of this double-membraned organization, there are five distinct compartments within the mitochondrion. There is the outer mitochondrial membrane, the intermembrane space (the space between the outer and inner membranes), the inner mitochondrial membrane, the cristae space (formed by infoldings of the inner membrane), and the matrix (space within the inner membrane).

Outer membrane

The outer mitochondrial membrane, which encloses the entire organelle, has a protein-to-phospholipid ratio similar to that of the eukaryotic plasma membrane (about 1:1 by weight). It contains large numbers of integral proteins called *porins*. These porins form channels that allow molecules 5000 Daltons or less in molecular weight to freely diffuse

from one side of the membrane to the other. Larger proteins can enter the mitochondrion if a signaling sequence at their N-terminus binds to a large multisubunit protein called translocase of the outer membrane, which then actively moves them across the membrane. Disruption of the outer membrane permits proteins in the intermembrane space to leak into the cytosol, leading to certain cell death. The mitochondrial outer membrane can associate with the endoplasmic reticulum (ER) membrane, in a structure called MAM (mitochondria-associated ER-membrane). This is important in ER-mitochondria calcium signaling and involved in the transfer of lipids between the ER and mitochondria.

Intermembrane space

The intermembrane space is the space between the outer membrane and the inner membrane. Because the outer membrane is freely permeable to small molecules, the concentrations of small molecules such as ions and sugars in the intermembrane space is the same as the cytosol. However, large proteins must have a specific signaling sequence to be transported across the outer membrane, so the protein composition of this space is different from the protein composition of the cytosol. One protein that is localized to the intermembrane space in this way is cytochrome c.

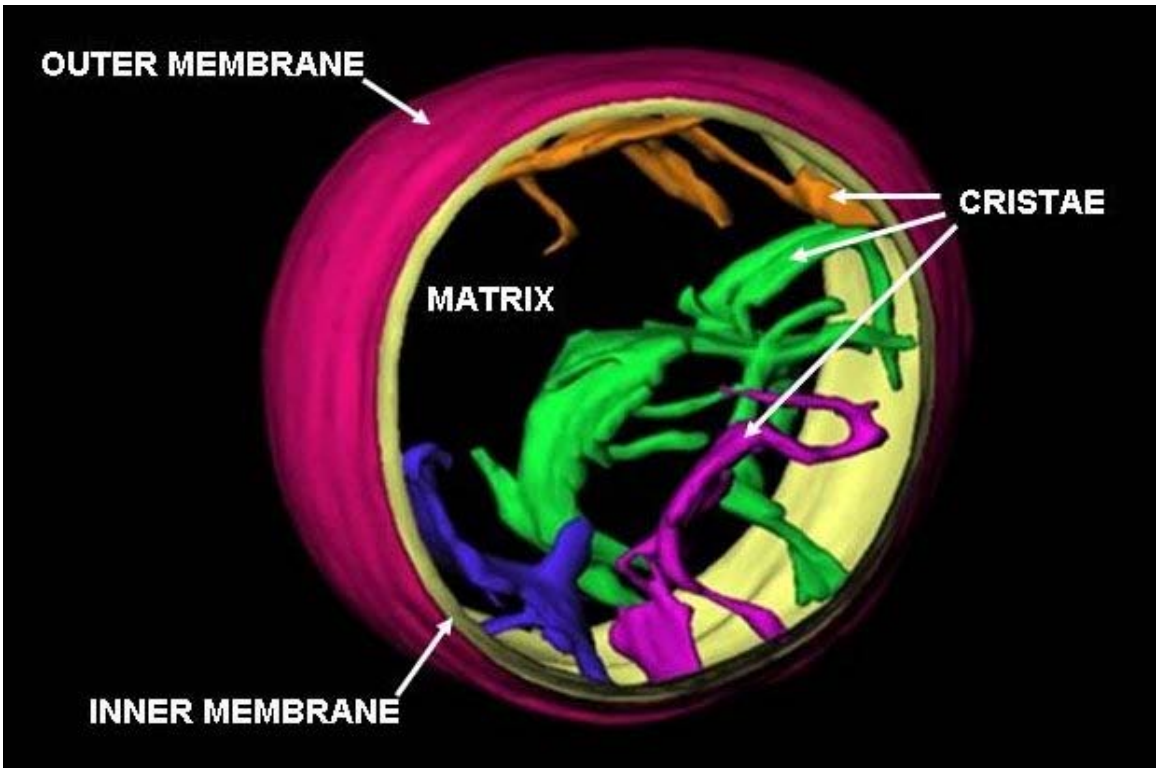
Inner membrane

The inner mitochondrial membrane contains proteins with five types of functions:

1. Those that perform the redox reactions of oxidative phosphorylation
2. ATP synthase, which generates ATP in the matrix
3. Specific transport proteins that regulate metabolite passage into and out of the matrix
4. Protein import machinery.
5. Mitochondria fusion and fission protein

It contains more than 151 different polypeptides, and has a very high protein-to-phospholipid ratio (more than 3:1 by weight, which is about 1 protein for 15 phospholipids). The inner membrane is home to around 1/5 of the total protein in a mitochondrion. In addition, the inner membrane is rich in an unusual phospholipid, cardiolipin. This phospholipid was originally discovered in cow hearts in 1942, and is usually characteristic of mitochondrial and bacterial plasma membranes. Cardiolipin contains four fatty acids rather than two and may help to make the inner membrane impermeable. Unlike the outer membrane, the inner membrane doesn't contain porins and is highly impermeable to all molecules. Almost all ions and molecules require special membrane transporters to enter or exit the matrix. Proteins are ferried into the matrix via the translocase of the inner membrane (TIM) complex or via Oxa1. In addition, there is a membrane potential across the inner membrane formed by the action of the enzymes of the electron transport chain.

Cristae



Cross-sectional image of cristae in rat liver mitochondrion to demonstrate the likely 3D structure and relationship to the inner membrane.

The inner mitochondrial membrane is compartmentalized into numerous cristae, which expand the surface area of the inner mitochondrial membrane, enhancing its ability to produce ATP. For typical liver mitochondria the area of the inner membrane is about five times greater than the outer membrane. This ratio is variable and mitochondria from cells that have a greater demand for ATP, such as muscle cells, contain even more cristae. These folds are studded with small round bodies known as F_1 particles or oxysomes. These are not simple random folds but rather invaginations of the inner membrane, which can affect overall chemiosmotic function.

One recent mathematical modeling study has suggested that the optical properties of the christae in filamentous mitochondria may affect the generation and propogation of light within the tissue.

Matrix

The matrix is the space enclosed by the inner membrane. It contains about 2/3 of the total protein in a mitochondrion. The matrix is important in the production of ATP with the aid of the ATP synthase contained in the inner membrane. The matrix contains a highly-concentrated mixture of hundreds of enzymes, special mitochondrial ribosomes, tRNA,

and several copies of the mitochondrial DNA genome. Of the enzymes, the major functions include oxidation of pyruvate and fatty acids, and the citric acid cycle.

Mitochondria have their own genetic material, and the machinery to manufacture their own RNAs and proteins (*see: protein biosynthesis*). A published human mitochondrial DNA sequence revealed 16,569 base pairs encoding 37 total genes: 22 tRNA, 2 rRNA, and 13 peptide genes. The 13 mitochondrial peptides in humans are integrated into the inner mitochondrial membrane, along with proteins encoded by genes that reside in the host cell's nucleus.

Organization and distribution

Mitochondria are found in nearly all eukaryotes. They vary in number and location according to cell type. A single mitochondrion is often found in unicellular organisms. Conversely, numerous mitochondria are found in human liver cells, with about 1000–2000 mitochondria per cell making up 1/5th of the cell volume. The mitochondria can be found nestled between myofibrils of muscle or wrapped around the sperm flagellum. Often they form a complex 3D branching network inside the cell with the cytoskeleton. The association with the cytoskeleton determines mitochondrial shape, which can affect the function as well. Recent evidence suggests vimentin, one of the components of the cytoskeleton, is critical to the association with the cytoskeleton.

Function

The most prominent roles of mitochondria are to produce ATP (i.e., phosphorylation of ADP) through respiration, and to regulate cellular metabolism. The central set of reactions involved in ATP production are collectively known as the citric acid cycle, or the Krebs Cycle. However, the mitochondrion has many other functions in addition to the production of ATP.

Energy conversion

A dominant role for the mitochondria is the production of ATP, as reflected by the large number of proteins in the inner membrane for this task. This is done by oxidizing the major products of glucose, pyruvate, and NADH, which are produced in the cytosol. This process of cellular respiration, also known as aerobic respiration, is dependent on the presence of oxygen. When oxygen is limited, the glycolytic products will be metabolized by anaerobic respiration, a process that is independent of the mitochondria. The production of ATP from glucose has an approximately 13-fold higher yield during aerobic respiration compared to anaerobic respiration. Recently it has been shown that plant mitochondria can produce a limited amount of ATP without oxygen by using the alternate substrate nitrite.

Pyruvate and the citric acid cycle

Each pyruvate molecule produced by glycolysis is actively transported across the inner mitochondrial membrane, and into the matrix where it is oxidized and combined with coenzyme A to form CO_2, acetyl-CoA, and NADH.

The acetyl-CoA is the primary substrate to enter the *citric acid cycle*, also known as the *tricarboxylic acid (TCA) cycle* or *Krebs cycle*. The enzymes of the citric acid cycle are located in the mitochondrial matrix, with the exception of succinate dehydrogenase, which is bound to the inner mitochondrial membrane as part of Complex II. The citric acid cycle oxidizes the acetyl-CoA to carbon dioxide, and, in the process, produces reduced cofactors (three molecules of NADH and one molecule of $FADH_2$) that are a source of electrons for the *electron transport chain*, and a molecule of GTP (that is readily converted to an ATP).

NADH and $FADH_2$: the electron transport chain

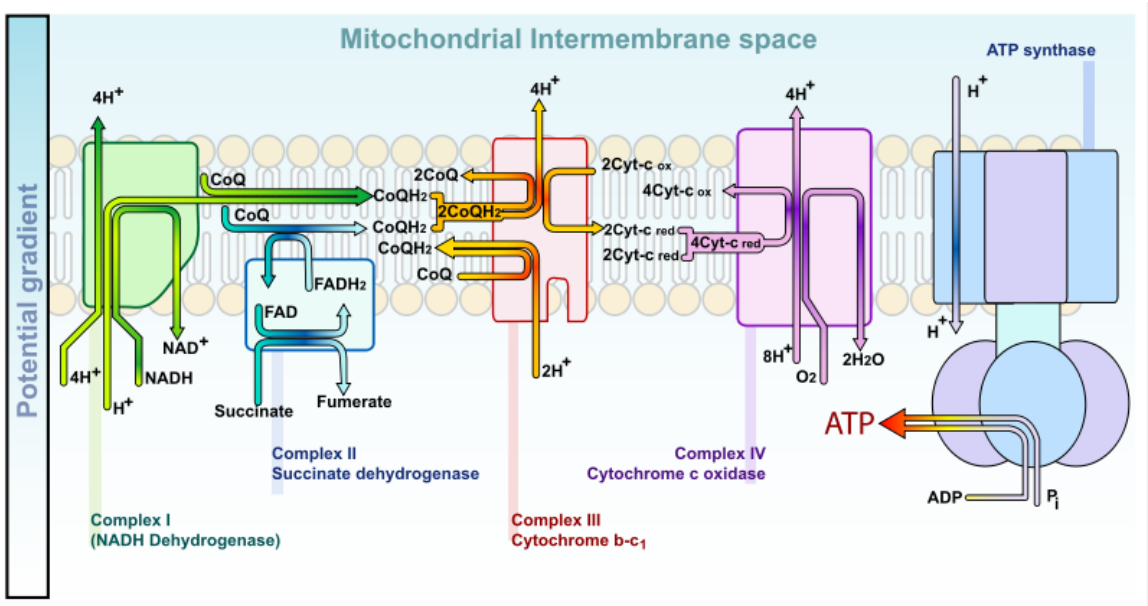


Diagram of the electron transport chain in the mitonchondrial intermembrane space

The redox energy from NADH and $FADH_2$ is transferred to oxygen (O_2) in several steps via the electron transport chain. These energy-rich molecules are produced within the matrix via the citric acid cycle but are also produced in the cytoplasm by glycolysis. Reducing equivalents from the cytoplasm can be imported via the malate-aspartate shuttle system of antiporter proteins or feed into the electron transport chain using a glycerol phosphate shuttle. Protein complexes in the inner membrane (NADH dehydrogenase, cytochrome c reductase, and cytochrome c oxidase) perform the transfer and the incremental release of energy is used to pump protons (H^+) into the intermembrane space. This process is efficient, but a small percentage of electrons may prematurely reduce oxygen, forming reactive oxygen species such as superoxide. This

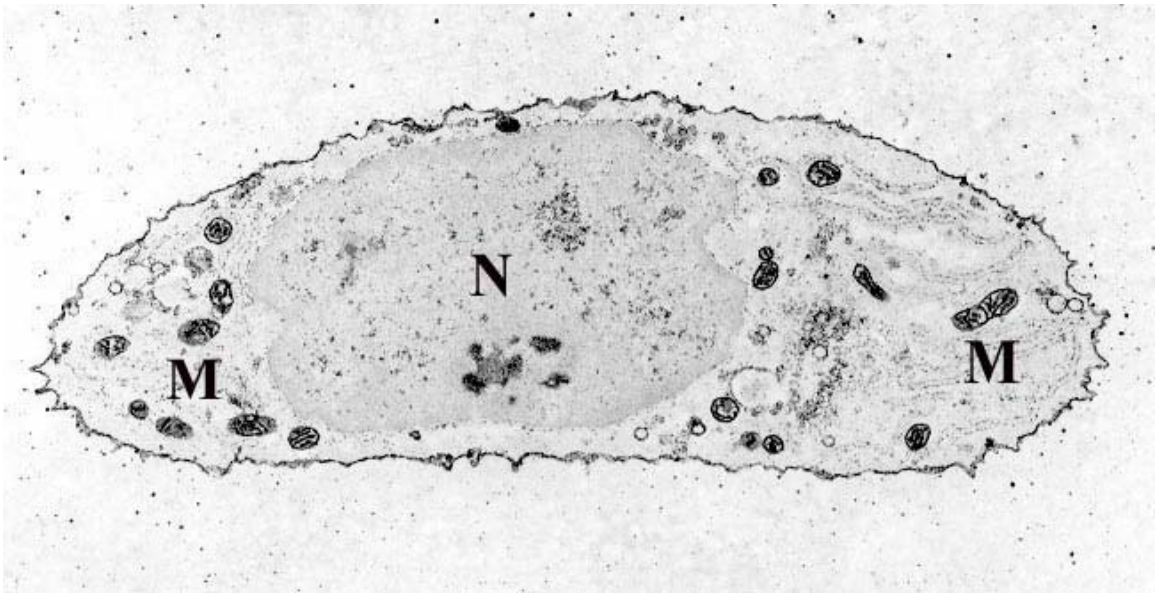
can cause oxidative stress in the mitochondria and may contribute to the decline in mitochondrial function associated with the aging process.

As the proton concentration increases in the intermembrane space, a strong electrochemical gradient is established across the inner membrane. The protons can return to the matrix through the ATP synthase complex, and their potential energy is used to synthesize ATP from ADP and inorganic phosphate (P_i). This process is called chemiosmosis, and was first described by Peter Mitchell who was awarded the 1978 Nobel Prize in Chemistry for his work. Later, part of the 1997 Nobel Prize in Chemistry was awarded to Paul D. Boyer and John E. Walker for their clarification of the working mechanism of ATP synthase.

Heat production

Under certain conditions, protons can re-enter the mitochondrial matrix without contributing to ATP synthesis. This process is known as *proton leak* or *mitochondrial uncoupling* and is due to the facilitated diffusion of protons into the matrix. The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat. The process is mediated by a proton channel called thermogenin, or UCP1. Thermogenin is a 33kDa protein first discovered in 1973. Thermogenin is primarily found in brown adipose tissue, or brown fat, and is responsible for non-shivering thermogenesis. Brown adipose tissue is found in mammals, and is at its highest levels in early life and in hibernating animals. In humans, brown adipose tissue is present at birth and decreases with age.

Storage of calcium ions



Mitochondria (M) within a chondrocyte stained for calcium as shown by electron microscopy.

The concentrations of free calcium in the cell can regulate an array of reactions and is important for signal transduction in the cell. Mitochondria can transiently store calcium, a contributing process for the cell's homeostasis of calcium. In fact, their ability to rapidly take in calcium for later release makes them very good "cytosolic buffers" for calcium. The endoplasmic reticulum (ER) is the most significant storage site of calcium, and there is a significant interplay between the mitochondrion and ER with regard to calcium. The calcium is taken up into the matrix by a calcium uniporter on the inner mitochondrial membrane. It is primarily driven by the mitochondrial membrane potential. Release of this calcium back into the cell's interior can occur via a sodium-calcium exchange protein or via "calcium-induced-calcium-release" pathways. This can initiate calcium spikes or calcium waves with large changes in the membrane potential. These can activate a series of second messenger system proteins that can coordinate processes such as neurotransmitter release in nerve cells and release of hormones in endocrine cells.

Additional functions

Mitochondria play a central role in many other metabolic tasks, such as:

- Regulation of the membrane potential
- Apoptosis-programmed cell death
- Calcium signaling (including calcium-evoked apoptosis)
- Cellular proliferation regulation
- Regulation of cellular metabolism
- Certain heme synthesis reactions
- Steroid synthesis.

Some mitochondrial functions are performed only in specific types of cells. For example, mitochondria in liver cells contain enzymes that allow them to detoxify ammonia, a waste product of protein metabolism. A mutation in the genes regulating any of these functions can result in mitochondrial diseases.

Origin

Mitochondria have many features in common with prokaryotes. As a result, they are believed to be originally derived from endosymbiotic prokaryotes.

A mitochondrion contains DNA, which is organized as several copies of a single, circular chromosome. This mitochondrial chromosome contains genes for redox proteins such as those of the respiratory chain. The CoRR hypothesis proposes that this **co**-location is required for **r**edox **r**egulation. The mitochondrial genome codes for some RNAs of ribosomes, and the twenty-two tRNAs necessary for the translation of messenger RNAs into protein. The circular structure is also found in prokaryotes, and the similarity is extended by the fact that mitochondrial DNA is organized with a variant genetic code similar to that of Proteobacteria. This suggests that their ancestor, the so-called proto-mitochondrion, was a member of the Proteobacteria. In particular, the proto-mitochondrion was probably closely related to the rickettsia. However, the exact

relationship of the ancestor of mitochondria to the alpha-proteobacteria and whether the mitochondria was formed at the same time or after the nucleus, remains controversial.

The ribosomes coded for by the mitochondrial DNA are similar to those from bacteria in size and structure. They closely resemble the bacterial 70S ribosome and not the 80S cytoplasmic ribosomes, which are coded for by nuclear DNA.

The endosymbiotic relationship of mitochondria with their host cells was popularized by Lynn Margulis. The endosymbiotic hypothesis suggests that mitochondria descended from bacteria that somehow survived endocytosis by another cell, and became incorporated into the cytoplasm. The ability of these bacteria to conduct respiration in host cells that had relied on glycolysis and fermentation would have provided a considerable evolutionary advantage. In a similar manner, host cells with symbiotic bacteria capable of photosynthesis would have had an advantage. The incorporation of symbiotes would have increased the number of environments in which the cells could survive. This symbiotic relationship probably developed 1.7-2 billion years ago.

A few groups of unicellular eukaryotes lack mitochondria: the microsporidians, metamonads, and archamoebae. These groups appear as the most primitive eukaryotes on phylogenetic trees constructed using rRNA information, which once suggested that they appeared before the origin of mitochondria. However, this is now known to be an artifact of long-branch attraction—they are derived groups and retain genes or organelles derived from mitochondria (e.g., mitosomes and hydrogenosomes).

Genome

The human mitochondrial genome is a circular DNA molecule of about 16 kilobases. It encodes 37 genes: 13 for subunits of respiratory complexes I, III, IV and V, 22 for mitochondrial tRNA (for the 20 standard amino acids, plus an extra gene for leucine and serine), and 2 for rRNA. One mitochondrion can contain two to ten copies of its DNA.

As in prokaryotes, there is a very high proportion of coding DNA and an absence of repeats. Mitochondrial genes are transcribed as multigenic transcripts, which are cleaved and polyadenylated to yield mature mRNAs. Not all proteins necessary for mitochondrial function are encoded by the mitochondrial genome; most are coded by genes in the cell nucleus and the corresponding proteins are imported into the mitochondrion. The exact number of genes encoded by the nucleus and the mitochondrial genome differs between species. In general, mitochondrial genomes are circular, although exceptions have been reported. In general, mitochondrial DNA lacks introns, as is the case in the human mitochondrial genome; however, introns have been observed in some eukaryotic mitochondrial DNA, such as that of yeast and protists, including *Dictyostelium discoideum*.

In animals the mitochondrial genome is typically a single circular chromosome that is approximately 16-kb long and has 37 genes. The genes while highly conserved may vary in location. Curiously this pattern is not found in the human body louse (*Pediculus*

humanus). Instead this mitochondrial genome is arranged in 18 minicircular chromosomes each of which is 3–4 kb long and has one to three genes. This pattern is also found in other sucking lice but not in chewing lice. Recombination has been shown to occur between the minichromosomes. The reason for this difference is not known.

While slight variations on the standard code had been predicted earlier, none was discovered until 1979, when researchers studying human mitochondrial genes determined that they used an alternative code. Many slight variants have been discovered since, including various alternative mitochondrial codes. Further, the AUA, AUC, and AUU codons are all allowable start codons.

Exceptions to the universal genetic code (UGC) in mitochondria

Organism	Codon	Standard	Novel
Mammalian	AGA, AGG	Arginine	Stop codon
	AUA	Isoleucine	Methionine
	UGA	Stop codon	Tryptophan
Invertebrates	AGA, AGG	Arginine	Serine
	AUA	Isoleucine	Methionine
	UGA	Stop codon	Tryptophan
Yeast	AUA	Isoleucine	Methionine
	UGA	Stop codon	Tryptophan
	CUA	Leucine	Threonine

Some of these differences should be regarded as pseudo-changes in the genetic code due to the phenomenon of RNA editing, which is common in mitochondria. In higher plants, it was thought that CGG encoded for tryptophan and not arginine; however, the codon in the processed RNA was discovered to be the UGG codon, consistent with the universal genetic code for tryptophan. Of note, the arthropod mitochondrial genetic code has undergone parallel evolution within a phylum, with some organisms uniquely translating AGG to lysine.

Mitochondrial genomes have far fewer genes than the bacteria from which they are thought to be descended. Although some have been lost altogether, many have been transferred to the nucleus, such as the respiratory complex II protein subunits. This is thought to be relatively common over evolutionary time. A few organisms, such as the *Cryptosporidium*, actually have mitochondria that lack any DNA, presumably because all their genes have been lost or transferred. In *Cryptosporidium*, the mitochondria have an altered ATP generation system that renders the parasite resistant to many classical mitochondrial inhibitors such as cyanide, azide, and atovaquone.

Replication and inheritance

Mitochondria divide by binary fission similar to bacterial cell division; unlike bacteria, however, mitochondria can also fuse with other mitochondria. The regulation of this division differs between eukaryotes. In many single-celled eukaryotes, their growth and division is linked to the cell cycle. For example, a single mitochondrion may divide synchronously with the nucleus. This division and segregation process must be tightly controlled so that each daughter cell receives at least one mitochondrion. In other eukaryotes (in mammals for example), mitochondria may replicate their DNA and divide mainly in response to the energy needs of the cell, rather than in phase with the cell cycle. When the energy needs of a cell are high, mitochondria grow and divide. When the energy use is low, mitochondria are destroyed or become inactive. In such examples, and in contrast to the situation in many single celled eukaryotes, mitochondria are apparently randomly distributed to the daughter cells during the division of the cytoplasm.

An individual's mitochondrial genes are not inherited by the same mechanism as nuclear genes. At fertilization of an egg cell by a sperm, the egg nucleus and sperm nucleus each contribute equally to the genetic makeup of the zygote nucleus. In contrast, the mitochondria, and therefore the mitochondrial DNA, usually comes from the egg only. The sperm's mitochondria enter the egg but do not contribute genetic information to the embryo. Instead, paternal mitochondria are marked with ubiquitin to select them for later destruction inside the embryo. The egg cell contains relatively few mitochondria, but it is these mitochondria that survive and divide to populate the cells of the adult organism. Mitochondria are, therefore, in most cases inherited down the female line, known as maternal inheritance. This mode is seen in most organisms including all animals. However, mitochondria in some species can sometimes be inherited paternally. This is the norm among certain coniferous plants, although not in pine trees and yew trees. It has been suggested that it occurs at a very low level in humans.

Uniparental inheritance leads to little opportunity for genetic recombination between different lineages of mitochondria, although a single mitochondrion can contain 2–10 copies of its DNA. For this reason, mitochondrial DNA usually is thought to reproduce by binary fission. What recombination does take place maintains genetic integrity rather than maintaining diversity. However, there are studies showing evidence of recombination in mitochondrial DNA. It is clear that the enzymes necessary for recombination are present in mammalian cells. Further, evidence suggests that animal mitochondria can undergo recombination. The data are a bit more controversial in humans, although indirect evidence of recombination exists. If recombination does not occur, the whole mitochondrial DNA sequence represents a single haplotype, which makes it useful for studying the evolutionary history of populations.

Population genetic studies

The near-absence of genetic recombination in mitochondrial DNA makes it a useful source of information for scientists involved in population genetics and evolutionary biology. Because all the mitochondrial DNA is inherited as a single unit, or haplotype,

the relationships between mitochondrial DNA from different individuals can be represented as a gene tree. Patterns in these gene trees can be used to infer the evolutionary history of populations. The classic example of this is in human evolutionary genetics, where the molecular clock can be used to provide a recent date for mitochondrial Eve. This is often interpreted as strong support for a recent modern human expansion out of Africa. Another human example is the sequencing of mitochondrial DNA from Neanderthal bones. The relatively large evolutionary distance between the mitochondrial DNA sequences of Neanderthals and living humans has been interpreted as evidence for lack of interbreeding between Neanderthals and anatomically-modern humans.

However, mitochondrial DNA reflects the history of only females in a population and so may not represent the history of the population as a whole. This can be partially overcome by the use of paternal genetic sequences, such as the non-recombining region of the Y-chromosome. In a broader sense, only studies that also include nuclear DNA can provide a comprehensive evolutionary history of a population.

Dysfunction and disease

Mitochondrial diseases

With their central place in cell metabolism, damage — and subsequent dysfunction — in mitochondria is an important factor in a wide range of human diseases. Mitochondrial disorders often present as neurological disorders, but can manifest as myopathy, diabetes, multiple endocrinopathy, or a variety of other systemic manifestations. Diseases caused by mutation in the mtDNA include Kearns-Sayre syndrome, MELAS syndrome and Leber's hereditary optic neuropathy. In the vast majority of cases, these diseases are transmitted by a female to her children, as the zygote derives its mitochondria and hence its mtDNA from the ovum. Diseases such as Kearns-Sayre syndrome, Pearson's syndrome, and progressive external ophthalmoplegia are thought to be due to large-scale mtDNA rearrangements, whereas other diseases such as MELAS syndrome, Leber's hereditary optic neuropathy, myoclonic epilepsy with ragged red fibers (MERRF), and others are due to point mutations in mtDNA.

In other diseases, defects in nuclear genes lead to dysfunction of mitochondrial proteins. This is the case in Friedreich's ataxia, hereditary spastic paraplegia, and Wilson's disease. These diseases are inherited in a dominance relationship, as applies to most other genetic diseases. A variety of disorders can be caused by nuclear mutations of oxidative phosphorylation enzymes, such as coenzyme Q10 deficiency and Barth syndrome. Environmental influences may interact with hereditary predispositions and cause mitochondrial disease. For example, there may be a link between pesticide exposure and the later onset of Parkinson's disease.

Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disorder, dementia, Alzheimer's disease, Parkinson's disease, epilepsy, stroke, cardiovascular disease, retinitis pigmentosa, and diabetes mellitus. A

common thread thought to link these seemingly-unrelated conditions is cellular damage causing oxidative stress. How exactly mitochondrial dysfunction fits into the etiology of these pathologies is yet to be elucidated.

Possible relationships to aging

Given the role of mitochondria as the cell's powerhouse, there may be some leakage of the high-energy electrons in the respiratory chain to form reactive oxygen species. This can result in significant oxidative stress in the mitochondria with high mutation rates of mitochondrial DNA. A vicious cycle is thought to occur, as oxidative stress leads to mitochondrial DNA mutations, which can lead to enzymatic abnormalities and further oxidative stress. A number of changes occur to mitochondria during the aging process. Tissues from elderly patients show a decrease in enzymatic activity of the proteins of the respiratory chain. Large deletions in the mitochondrial genome can lead to high levels of oxidative stress and neuronal death in Parkinson's disease. Hypothesized links between aging and oxidative stress are not new and were proposed over 50 years ago; however, there is much debate over whether mitochondrial changes are causes of aging or merely characteristics of aging. One notable study in mice demonstrated shortened lifespan but no increase in reactive oxygen species despite increasing mitochondrial DNA mutations, suggesting that mitochondrial DNA mutations can cause lifespan shortening by other mechanisms. As a result, the exact relationships between mitochondria, oxidative stress, and aging have not yet been settled.