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BT201 Ecology, Biodiversity & Evolution-II

MSC ZOOLOGY

**BT201 Ecology, Biodiversity &
Evolution-II (1 to 100)full mid and
final merged ppt handouts**

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MSC ZOOLOGY 4TH SEMESTER

1 Ecological Genomics Introduction, Bioinformatics

Biology and Informational Science

- ❑ The HGP changed how we view & practice biology.
- ❑ Biology is an informational science.
 - ✓ Digital genome
 - ✓ Environmental signals
- ❑ Biology has become a cross-disciplinary science.

Bioinformatics and intersecting discipline

- Mathematical sciences
- Computer science
- Life sciences

Developing the high throughput technologies and computational/mathematical tools required for this new biology

Why? Where? What? How?

Why: Ideas for what to produce these huge datasets? Biological background needed.

Where: Raw data need to store, IT platforms required.

What: Patterns in datasets that can be analyzed using computers. Various data models and their respective algorithms are needed.

How: Different resources need to be integrated.

What is Bioinformatics?

The field of biology specializing in developing *hardware* and *software* to store and analyze the huge amounts of data being generated by life scientists. (NIH). More than 20 different definitions can be found from Google!

Computational Biology?

Computational Molecular Biology?

Data integration

Various molecular biology databases

Bioinformatics applications

Data analysis

Key Challenge of Bioinformatics

The world of biology is very different from what it was even ten years ago. To bridge the considerable gap between technical data production and its use by scientists for biological discovery.

2 Gene discovery

(Genome analysis)

Gene Discovery

In a fully sequenced genome, genes are found by scanning the sequence using gene-predicting computer programmes and assigning putative functions by searching for similarities in already existing databases. For many organisms under investigation in ecological genomics, no genomic database is available and genes must be identified in other ways. There are some so-called pregenomic molecular approaches that may be used to identify ecologically important genes in incompletely characterized genomes.

From gene product to gene

In some cases the primary structure of a gene product (a protein) may be the starting point of gene discovery. This holds especially for proteins that can be isolated relatively easily by some marker or bioassay, or proteins that are highly induced by some experimental treatment. As an example we discuss the isolation of the metallothionein (mt) gene in a species of springtail, *orchesella sancta* (hens Bergen et al. 1999). Attempts to pick up the gene by polymerase chain reaction (PCR) using primers from the then-known *drosophila* mt sequence remained unsuccessful.

3 Genomics Revolution Invading Ecology

- the suffix -ome :the collectivity of units (Lederberg and McCray 2001),
- example in coelome, the system of body cavities,
- biome, the entire community of plants and animals in a climatic region.
- In aiming to investigate many genes at the same time genomics differs from ecology, which although investigating many phenotypes, usually deals with only a few genes at a time.

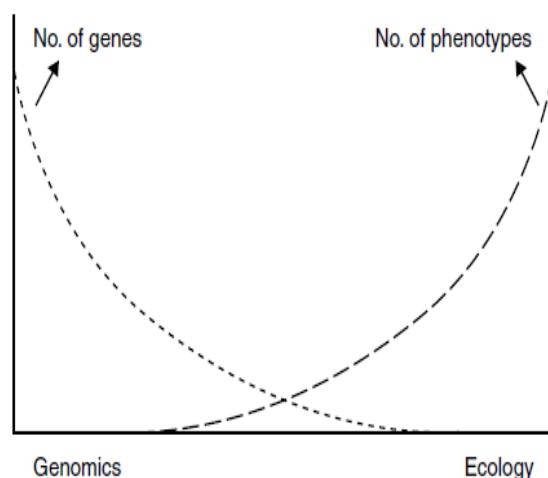
The playing field of ecological genomics

In between genomics, with its focus on the single genome of a model organism, studying all the genes that it contains, and ecology, studying a few genes in many species.

The interactions between the genes within the genome and the dynamic character of the genome

sketched by Dover (1999) as an internal tangled bank.

- idea of Darwin (1859)
- Dover (1999 :
 - ‘external tangled bank’ (the ecology)
 - the ‘internal tangled bank’ (the genome)



The internal tangled bank

- It emphasizes the role of genetic turbulence (gene duplication, genetic sweeps, exon shuffling, transposition, etc.)
- illustrates that there is ample scope for ‘innovation from within genetic turbulence

The genomics revolution

Three major technological developments of 1990s

- microtechnology
- computing
- communication.

Microecology. The possibility of working with molecules on the scale of a few micrometers, given by advances in laser technology, has been very important for one of genomics’ most conspicuous achievements, the development of the gene chip.

Three major technological developments

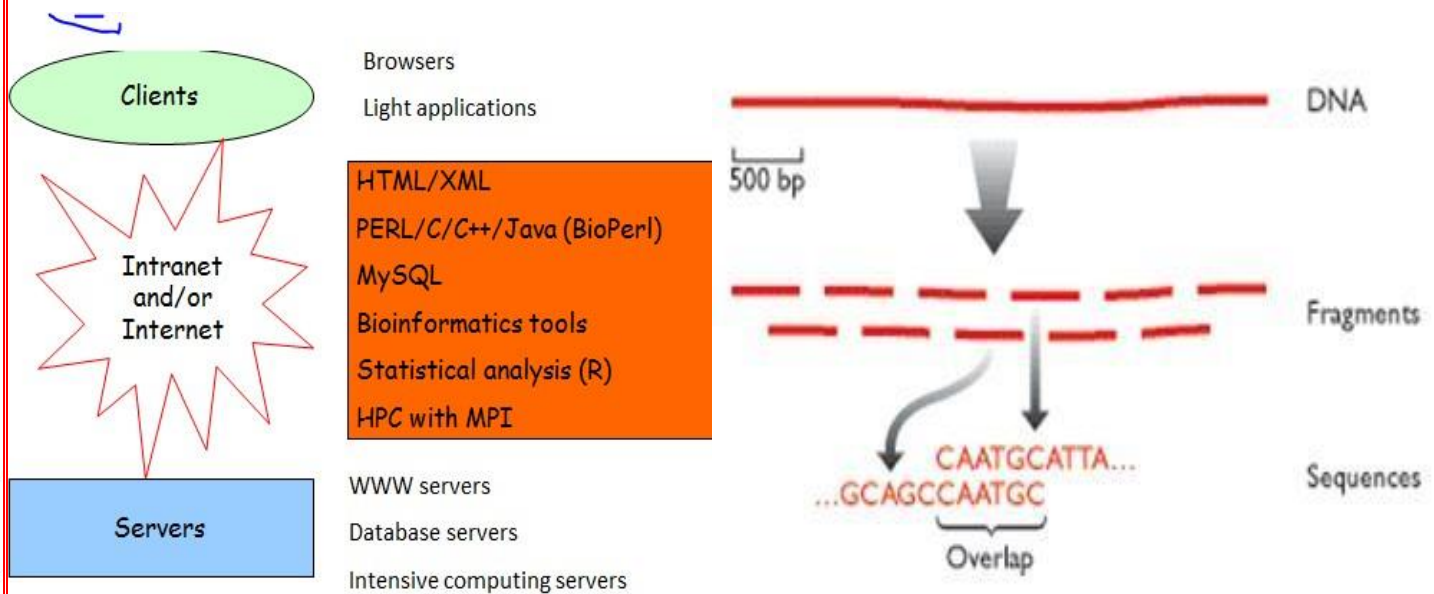
Computing technology

To assemble a genome from a series of sequences requires tremendous computational power. Extensive calculations are also necessary for the analysis of expression matrices and protein databases. Without the advent of high-speed computers and data-storage systems of vast capacity all this would have been impossible. Consulting genome databases all over the world has become such normal practice that the scientific progress of any genomics laboratory has become completely dependent on communication with the

rest of the World Wide Web. The Internet has become an indispensable part of genomics. The essence of genomics is that it is the study of the genome and its products as a unitary whole.

4 Schematic platform for Bioinformatics

Sequence assembly by the shotgun approach



- Master sequence ← short sequences, simply by examining the sequences for overlaps.
- No need any prior knowledge of the genome.

What is Gene?

CGGTTGAAAGCGGTAGCGTCCATGCGTATTACTCTTGAGCGGTGGAACCTTCTGAAATCGCT
 GAACCACGTCCACCGGGTCGTCGAGCGTCGCAACACGATCCCGATCCTGTCCAACGTTCTGC
ACTGAATTTTCTCA
 GTTACGACATTTTGCCTTGTTTTTGCGCCAAATGGGATCAACAGTACGTAACAATTTTGTGAC
 AATGACCAATACATCCGAGGGGAATCATGGCACTCAACCTGAAGCAACGGCTT

1. Transcriptional control sites

2. Non-coding RNAs

3. mRNAs

Evidence-based prediction

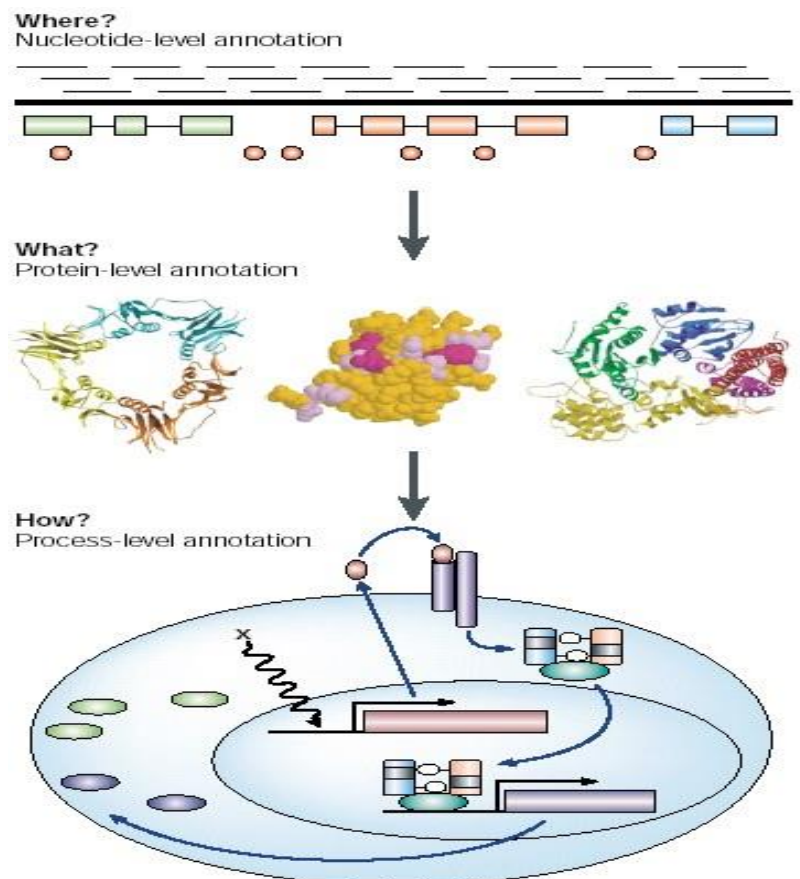
- Cis-alignment
- Trans-alignment
- *Ab initio* / *de novo* prediction

Three Layers of Genome Annotation.

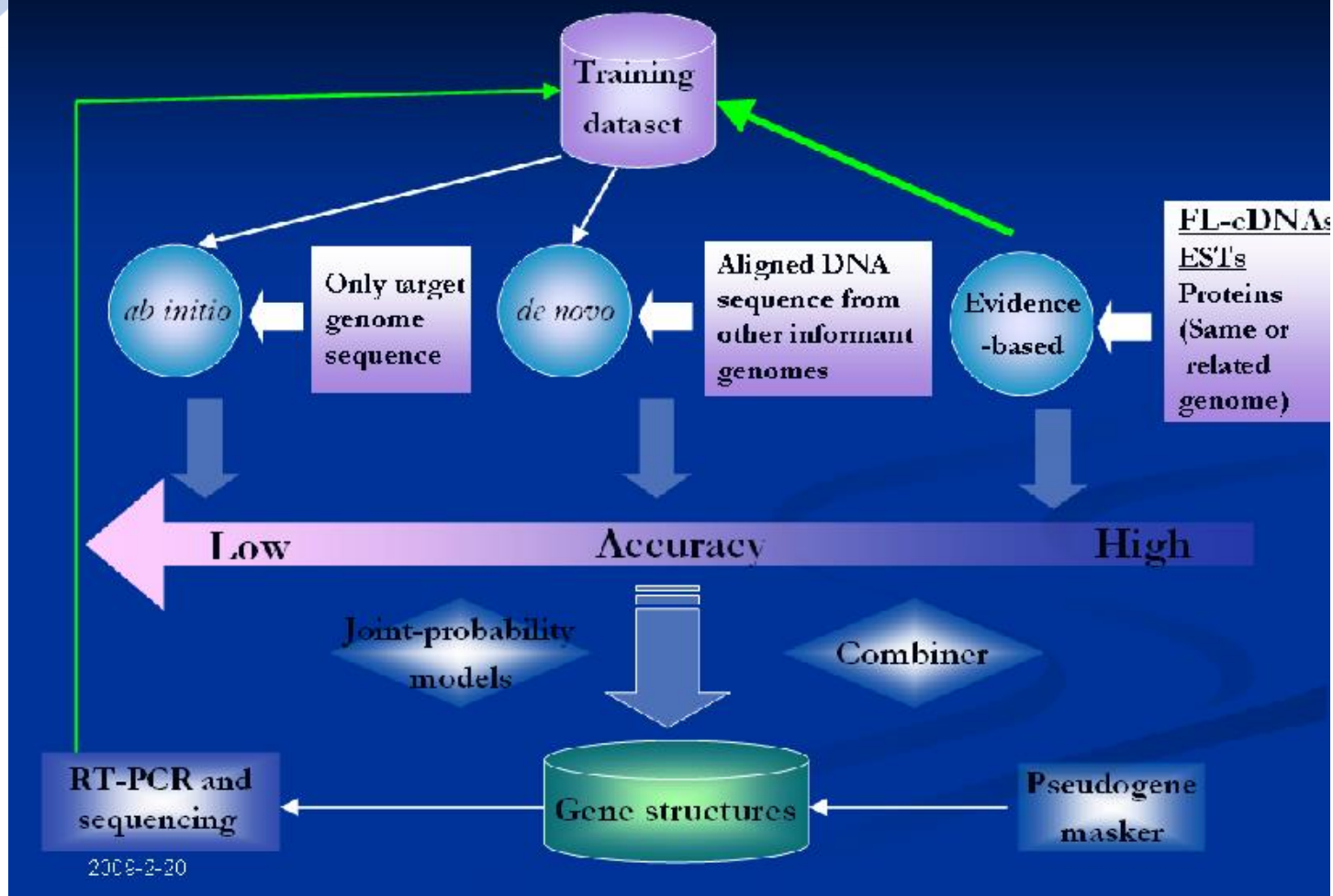
From Stein, L. 2001. Nature Reviews genetics 2:493-503

Some models

- Dynamic programming
- Hidden Markov Models (HMMs)
- Conditional random field (CRF)
- Support vector machines (SVMs)



Genome annotation flowchart



5 Phylogenetics

Evolutionary theory states that groups of similar organisms are descended from a common ancestor. Phylogenetic systematics (cladistics) is a method of taxonomic classification based on their evolutionary history. It was developed by Willi Hennig, a German entomologist, in 1950.

Major reasons to use phylogenetics

1. **Understand the lineage of different species:** Organizing principle to sort species into a taxonomy
2. **Understand how various functions evolved:** Understand forces and constraints on evolution
3. **Perform multiple sequence alignment**
4. **Predict gene function (phylogenetic footprint)**

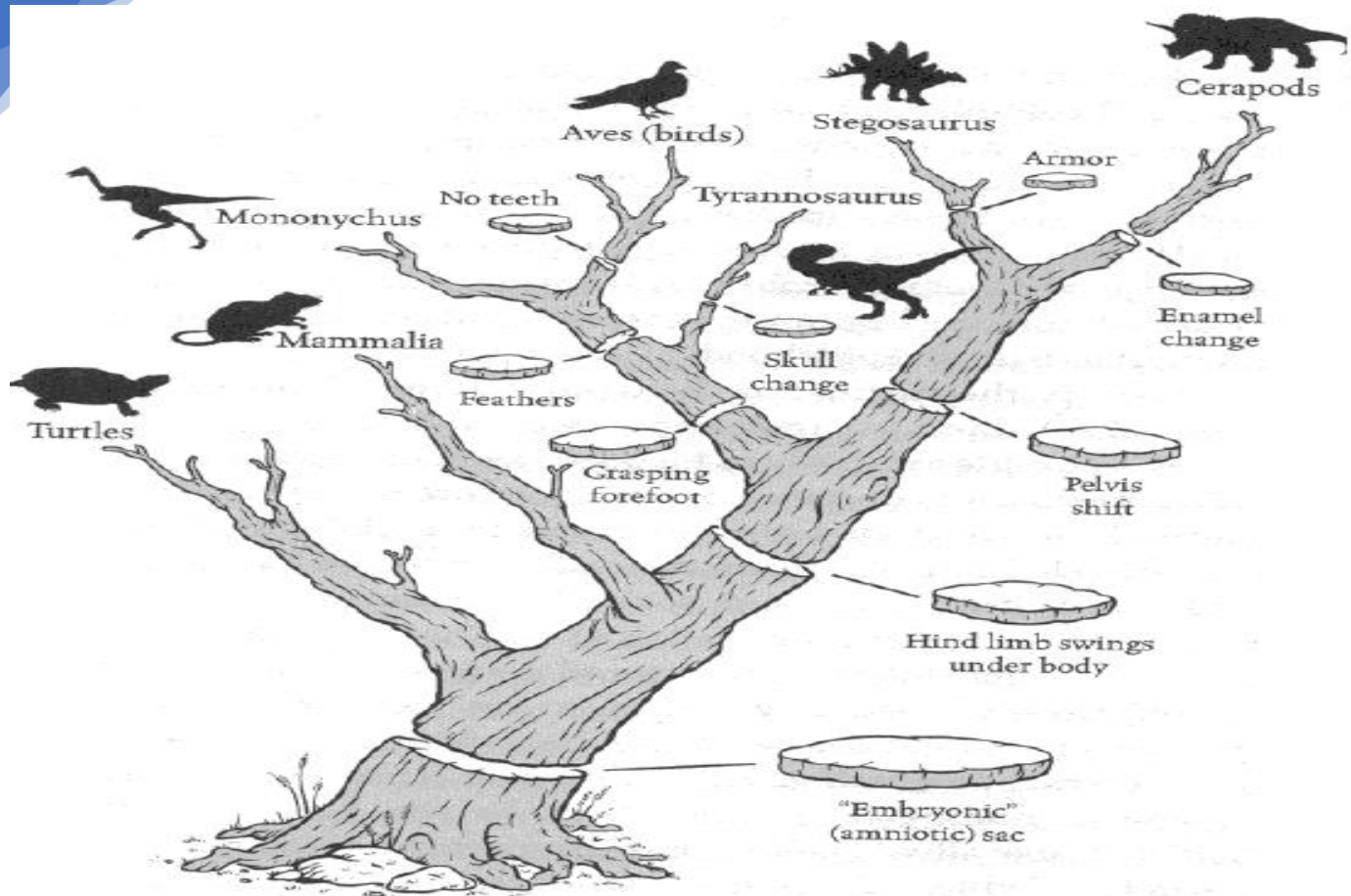
Species/Gene Trees

@ Species tree (how are my species related?)

- contains only one representative from each species
- when did speciation take place?
- all nodes indicate speciation events

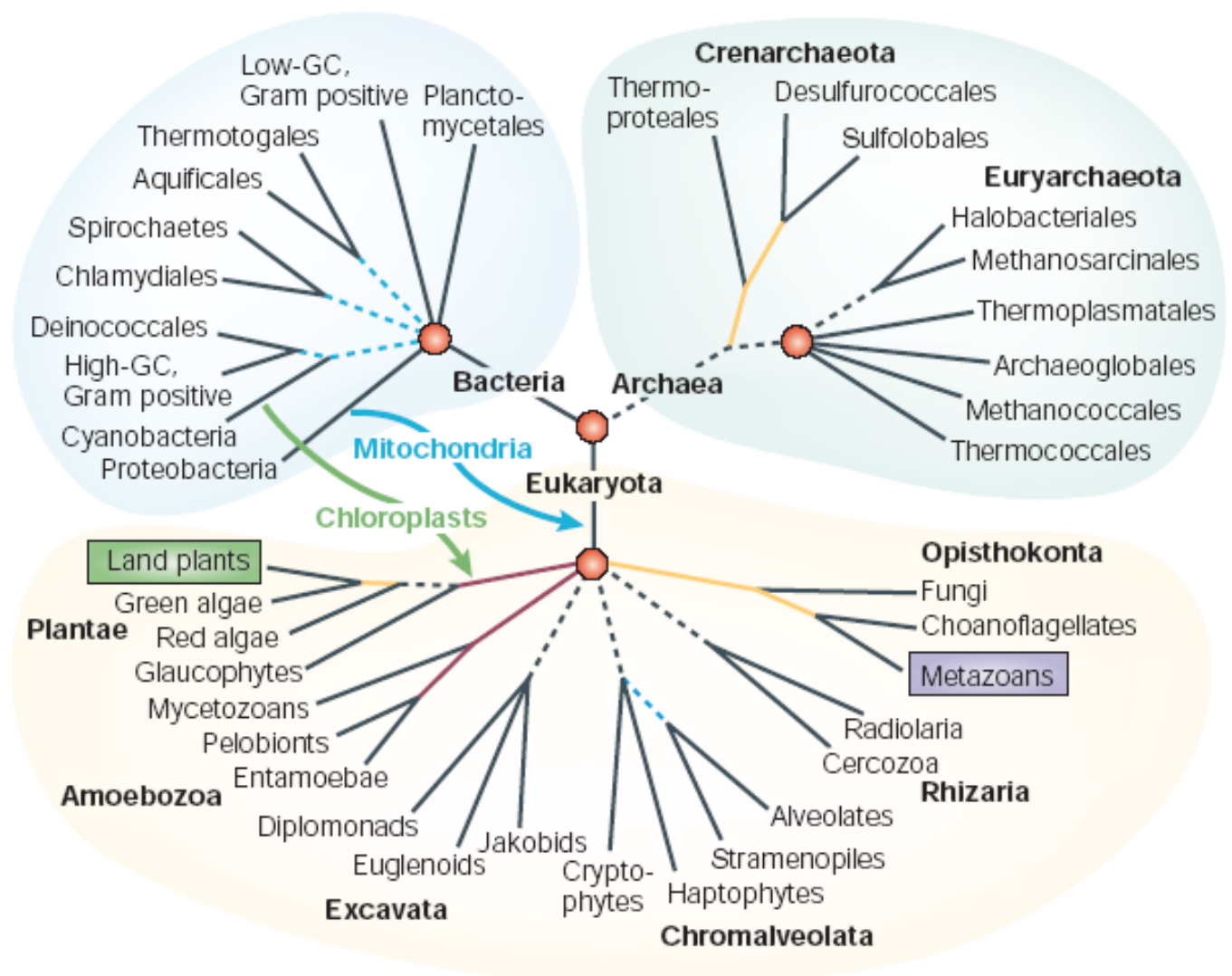
@ Gene tree (how are my genes related?)

- often contains a number of genes from a single species.
- nodes relate either to speciation or gene duplication events.



Phylogenomics: Genome trees

Explore genome evolution based on large data sets of DNA or protein sequences. Using entire genomes to infer a species tree (Eisen and Fraser 2003). Based on maximum genetic information and average out the anomalies. Has become the standard for reconstructing reliable phylogenies (Ciccarelli et al, 2006; Daubin et al. 2002).



6 Yeast, fly, worm, and weed Part 2

The international Human Genome Project

- The international human genome project initiated by the US national institutes of health and the US department of energy, was launched in 1990 with completion due in 2005. However, in the meantime a private enterprise, Celera genomics, embarked on a project with the same aim but a different approach and actually overtook the human genome project. The competition was settled with the historic press conference on 26 June 2000, when US president Bill Clinton, J. Craig venter of Celera genomics, and Francis Collins of the national institutes of health jointly announced that a working draft of the human genome had been completed.
- Many commentators have qualified this announcement as more a matter of public communication than scientific achievement.
- At that time the accepted criterion for completion of a genome sequence, namely that only a few gaps or gaps of known size remained to be sequenced and that the error rate was below 1 in 10 000 bp, had not been met by far. The euchromatin part of the genome was not completed until mid-2004, although that milestone was again considered by some to be only the end of the beginning (stein 2004). Nevertheless, the human genome project can be regarded as one of the most successful scientific endeavours in history and the assembly of the 3.12 billion bp of DNA, requiring some 500 million trillion sequence comparisons, was the most extensive computation that had ever been undertaken in biology.
- The number of organisms whose genome has been sequenced completely and published is now approaching 300
- Bacteria dominate the list, as the small size of their genomes makes these organisms well-suited for whole-genome sequen-cing.
- By june 2005, no fewer than 730 prokaryotic organisms and 496 eukaryotes were the subject of ongoing genome sequencing projects.

List of complete and published genomes (not including viruses) by June 2005

Taxonomic group	No. of genomes	Remarks on species
Bacteria total	211	Many common laboratory models and pathogens
Archaea total	21	Several methanogens and extremophiles
Eukarya*		
Myxomycota	1	Dictyostelium discoideum (slime mould)
Entamoeba	1	Entamoeba histolytica (amoeba causing dysentery)
Apicomplexa	6	Four Plasmodium and two Microsporidium species

Taxonomic group	No. of genomes	Remarks on species
Kinetoplastida	2	Trypanosoma brucei, Leishmania tropica (parasites)
Cryptomonadina	1	Guillardia theta (flagellated unicellular alga)
Bacillariophyta	1	Thalassiosira pseudonana (marine diatom)
Rhodophyta	1	Cyanidioschyzon merolae (small unicellular red alga)
Plants	4	Chlamydomonas reinhardtii (green alga), Populus trichocarpa (black cottonwood), Arabidopsis thaliana (thale cress),
		Oryza sativa var. japonica, var. indica (rice)

Taxonomic group	No. of genomes	Remarks on species
Fungi	14	Including <i>Saccharomyces cerevisiae</i> (baker's yeast)
Animals		
Nematoda	2	<i>Caenorhabditis elegans</i> (free-living roundworm), <i>Caenorhabditis briggsae</i>
Insecta	4	<i>Bombyx mori</i> (silk worm), <i>Drosophila melanogaster</i> (fruit fly),
		<i>Anopheles gambiae</i> (mosquito, malaria vector), <i>Apis mellifera</i> (honey bee)
Tunicata	1	<i>Ciona intestinalis</i> (sea squirt)

Taxonomic group	No. of genomes	Remarks on species
Pisces	3	<i>Takifugu rubripes</i> (puffer or fugu fish), <i>Tetraodon nigroviridis</i> (puffer fish),
		<i>Danio rerio</i> (zebrafish)
Aves	1	<i>Gallus gallus</i> (red jungle fowl)
Mammalia	5	<i>Rattus norvegicus</i> (brown rat), <i>Mus musculus</i> (house mouse),
		<i>Canis familiaris</i> (domestic dog), <i>Pan troglodytes</i> (chimpanzee),
		<i>Homo sapiens</i> (human)
Animals: total	16	
Eukarya: total	47	
Total	279	

7 Yeast, fly, worm, and weed Part 3

Previously established reputation

Yeast, *C. Elegans*, *drosophila*, mouse, and rat.

species had already proven their usefulness as models before the genomics revolution and were adopted by genomicists because so much was known about their genetics and biochemistry, and, perhaps just as important, because a large research community was interested, could support the work, and use the results

Genome size

- One of the first questions that is asked when a species is considered for whole-genome sequencing is,
 - what is the size of its genome?
- A relatively small genome was a major advantage for a sequencing project.
- The genome size of living organisms ranges across nine orders of magnitude, from 103 bp (0.001 mbp) in RNA viruses to nearly 10¹² bp (1 000 000 mbp) in some protists, ferns, and amphibians.
- The puffer fish, *takifugu rubripes*, was indeed chosen because of its relatively small genome (one-eighth of the human genome).

Possibility for genetic manipulation

- The possibility of genetic manipulation was an important reason why *Arabidopsis*, *Drosophila*, and mouse became such popular genomic models. The ultimate answer about the function of a gene comes from studies in which the genome segment is
 - ✓ knocked out,
 - ✓ downregulated, or
 - ✓ overexpressed
- against a genetic background that is the same as that of the wild type.
- the introduction of constructs in the genome that can report activity of certain genes by means of signal molecules is very important. This can only be done if the species is accessible using recombinant- DNA techniques.

Medical or agricultural significance

- Many bacteria and parasitic protists were chosen because of their pathogenicity to humans
- Other bacteria and fungi were taken as genomic models because of their potential to cause plant diseases (phytopathogenicity).
- The sequencing of rice was motivated by the huge importance of this species as a staple food for the world population (adam 2000).
- Some agriculturally important species have great relevance for ecological questions; for example, the bacterium *sinorhizobium meliloti*, a symbiont of leguminous plants, is known for its nitrogen-fixing capacities, but it also makes an excellent model system for the analysis of ecological interactions in nutrient cycling, together with its host *medicago truncatula*.

Possibility for genetic manipulation

- Foreign DNA can be introduced using transposons; for example, modified p-elements that can 'jump' into the DNA of *drosophila*, or bacteria such as *agrobacterium tumefaciens* that can transfer a piece of DNA to a host plant. DNA can also be introduced by physical means, especially in cell cultures, using electroporation, microinjection, or bombardment with gold particles. Another popular approach is post-transcriptional gene silencing using RNA interference (RNAi), also called inhibitory RNA expression.
- The question can be asked, should the possibility for genetic manipulation be an argument for selecting model species in ecological genomics? We think that it should, knowing that the capacity to generate mutants and transgenes of ecologically relevant species is crucial for confirming the function of genes. Ecologists should also use the natural variation in ecologically relevant traits to guide their explorations of the genome (koornneef 2004, tonsor et al. 2005). A basic resource for genome investigation can be obtained by using natural varieties of the study species, and developing genetically defined culture stocks

8 Yeast, fly, worm, and weed Part 4

Biotechnological significance.

- Many bacteria and fungi are important as producers of valuable products,
 - **for example**
 - ✓ antibiotics,
 - ✓ medicines,
 - ✓ vitamins,
 - ✓ soy sauce,
 - ✓ cheese,
 - ✓ yoghurt,
 - ✓ and other foods made from milk.
- There is considerable interest in analyzing the genomes of these (pu"bler and selbitschka 2003).
- Other bacteria are valuable genomic models because of their capacity to degrade environmental pollutants;
 - **For example,**
 - the marine bacterium ***Alcanivorax borkumensis*** is a genomic model because it produces surfactants and is associated with the biodegradation of hydrocarbons in oil spills (ro"ling et al. 2004).

Evolutionary position

- Whole-genome analysis of organisms at crucial or disputed positions in the tree of life can be expected to contribute significantly to our knowledge of evolution.
- The sea squirt, **ci. Intestinalis**, was chosen as a model because it belongs to a group, the Urochordata, with properties similar to the ancestors of vertebrates.
- The study of this species should provide valuable information about the early evolution of the phylum to which we belong ourselves.
- Many other organisms, although not on the list for a genome project to date, have a strong case for being declared as model species for evolutionary arguments. These include the velvet worm, *Peripatus*, traditionally seen as a missing link between the arthropods and annelids, but now classified as a separate phylum in the panarthropoda lineage (nielsen 1995), and the springtail, *folsomia candida*, formerly regarded as a primitive insect, but now suggested to have developed the hexapod bodyplan before the insects separated from the crustaceans (nardi et al. 2003).

Comparative purposes

- Over the last few years, genomicists have realized that assigning functions to genes and recognizing promoter sequences in a model genome can greatly benefit from comparison with a set of carefully chosen reference organisms at defined phylogenetic distances.
- Comparative genomics is developing an increasing array of bioinformatics techniques, such as
 - ✓ synteny analysis,
 - ✓ phylogenetic footprinting,
 - ✓ and phylogenetic shadowing
- by which it is possible to understand aspects of a model genome from other genomes.
- One of the main reasons for sequencing the chimpanzee's Genome was to illuminate the human genome, and a variety of fungi were sequenced to illuminate the genome of **S. Cerevisae**.

Ecological significance

- It will be clear that ecological arguments have only played a minor role in the selection of species for whole-genome sequencing, but we expect them to become more important in the future.

9 Yeast, fly, worm, and weed Part 5

Biodiversity

- The new range of models should embrace diverse phylogenetic lineages, varying in their physiology and life-history strategy.
- For example, the model plants *arabidopsis* and rice both employ the C3 photosynthetic pathway. To complement our genomic knowledge of primary production, new models should be chosen among plants utilizing C4 photosynthesis or crassulacean acid metabolism (CAM). Considering the diversity of life histories, species differing in their mode of reproduction and dispersal capacity should be chosen; for example, hermaphroditism versus gonochorism, parthenogenesis versus bisexual reproduction, etc

Ecological interactions.

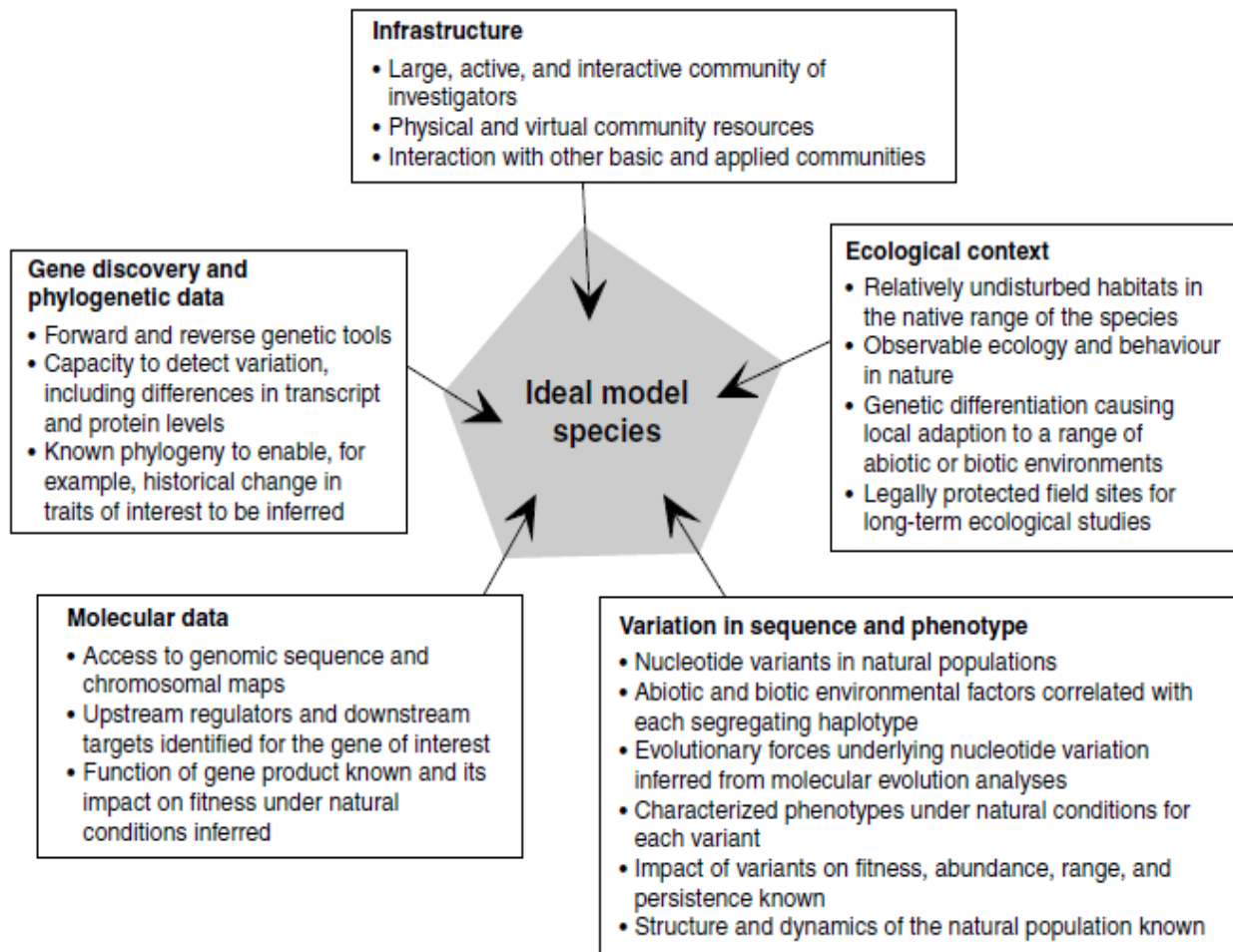
- Species that take part in critical ecological interactions (mutualisms, antagonisms) are obvious candidates for genomic analysis.
- One may think of mycorrhizae, nitrogen-fixing symbionts, pollinators, natural enemies of pests, parasites, etc.
- The most obvious strategy for analysing such interactions would be to sequence the genomes of the players involved and to try and understand interactions between them from mutualisms or antagonisms in gene expression.

Suitability for field studies.

- The wealth of knowledge from experienced field ecologists should play a role in deciding about new 'ecogenomic' models.
- Not all species lend themselves to studies of behaviour, foraging strategy, habitat choice, population size, age structure, dispersal, or migration in the field, simply because they are too rare, not easily

spotted, difficult to sample quantitatively, impossible to mark and recapture, not easy to distinguish from related species, or inaccessible to invasive techniques

Figure 1.5 Criteria in evolutionary and ecological functional genomics for a model species, according to Feder and Mitchell-Olds (2003). At present few species satisfy all criteria. Reproduced by permission of Nature Publishing Group.



DNA microarrays

- With their associated massive generation of data on expression profiles, are one of the most tangible features of modern genomics and are often seen as holding the greatest promise for solving problems in ecology.
- However, not all ecologists are convinced that microarray-based transcription profiling is the best way to advance the genomics revolution into ecology.
- Commercial microarrays are available only for genomic model species, whereas the interest of ecologists is with species that are important in the environment and amenable to ecological studies; these two interests do not necessarily coincide.
- Ecologists have two options.
 - One is to develop their own micro-arrays, starting with spotted cDNAs of unknown sequence, doing a lot of tedious sequencing work, and gradually finding out more about the genome of their study species.
 - Another option is to apply transcriptome samples of non-models to micro-arrays of model species.
- For example, arabidopsis may function as a model for other species of the brassicaceae, and drosophila as a model for other higher insects. Obviously, how useful such an approach is will depend on how far the sequences of model and non-model diverge. This will not be the same for all parts of the genome and therefore there is some doubt on the validity of cross-species hybridization, although there will certainly be situations where it works well.

Because of the immediately attractive upswing created by the genomics revolution, and the large financial resources made available in many industrialized countries, adjacent fields of science have adopted similar terms, leading to a great proliferation of designations such as

- ✓ transcriptomics,
- ✓ proteomics,
- ✓ and metabolomics,
- Such that some biologists have complained that what was molecular biology before is now named after one of the 'omics' but in fact is still molecular biology.
- Zhou et al. (2004) proposed a classification of genomics according to
 - three main categories:
 - approach (structural or functional),
 - scientific discipline (evolutionary genomics, ecological genomics, etc.),
 - And object of study (plant genomics, microbial genomics, etc.).

The list includes

- obvious terms such as
 - pharmacogenomics and
 - cardiogenomics, and
- **awkward ones**
 - such as saccharomics (the study of all the carbohydrates in the cell) and
 - vaccinomics (the use of bioinformatics and genomics for vaccine development).
 - The three most common extensions of genomics are transcriptomics, proteomics, and metabolomics.

11 -Omics speak Part 2

Transcriptomics

- Transcriptomics is the study of all the transcripts that are present at any time in the cell.
- In principle the transcriptome includes messenger RNAs (mRNAs) in addition to ribosomal RNAs (rRNAs), transfer RNAs (tRNAs), and small nuclear RNAs (snRNAs), but transcriptomics is usually limited to mrna, the template for translation into protein.
- The main activity in transcriptomics is to obtain a profile of global gene expression in relation to some condition of interest.
 - Which genes are turned 'on' and 'off' during certain phases of the cell cycle?
 - Which genes are upregulated by certain physiological conditions?
 - Which genes change their expression in response to adaptation to the environment?
 - The study of transcriptomes is part of functional genomics, because it does not look at the DNA as such, but at its functions.
- In general, it is expected that there are more transcripts than there are protein encoding genes in the genome, even when considering only those genes that are actually transcribed.

This is due to the mechanism of alternative splicing:

- the generation of different mRNAs from the same premRNAs during the removal of introns.
- RNA editing (posttranscriptional insertion or deletion of nucleotides, or conversion of one base for another) is another reason for incongruence between the genome and the transcriptome.

12 -Omics speak Part 3

Proteomics

- Proteomics is the study of all the proteins in the cell.

- Mass spectrometry may also be used to determine the amino acid sequence of a protein.
- For this application, the protein is cleaved with a protease, for example trypsin, which generates a collection of fragments characteristic of the protein.
- These fragments may be compared to an in silico (computer-simulated) digestion derived from the genome and the known cleavage sites of the protease.
- The proteome provides a different picture of a cell's activities to the transcriptome.
- Several authors have indeed wondered about the lack of correlation between mrna and protein abundances.
- One of the reasons for this is the existence of control mechanisms at the ribosomes, where mrna is translated to peptides. Translational control allows the cell to select only certain mRNAs for translation and block others.
- The selection is often dependent on environmental conditions, so this mechanism allows for physiological adaptation on the level of the proteome, even though the transcriptome remains the same.
- Another issue is posttranslational modification or protein processing, processes that can greatly affect the function of a protein, for example by acetylation or ubiquitination of the n-terminal residue, hydroxylation of prolines, or cleavage of the molecule into smaller units.
- The proteome and the genome are linked by many feedback mechanisms, because some proteins are transcription factors necessary for gene activation, others are enzymes involved in transcription or translation, and still others are structural components of chromosomes. So, in a molecular biology context, the living cell can only be understood fully by considering genome, transcriptome, and proteome together.

13 -Omics speak Part 4

Metabolomics

- Metabolomics is the study of all low molecular weight cellular constituents.
- Usually only metabolites belonging to a limited category are included, for example all soluble carbohydrates, or all metabolites that can be measured by a certain analytical technique such as pyrolysis gas chromatography or infrared spectrometry.
- No single method can measure the thousands of different chemical compounds that may be present at any time in a cell, because of the greatly diverging chemical properties (hydrophilic versus hydrophobic compounds, acids versus bases, reactive versus inert compounds, etc.).
- The metabolome requires a diversity of analytical approaches to obtain a complete picture.

List of some of the more common omics

Term	Object of study
Pathogenomics	Genomes of human pathogens: analysis of genes involved in disease generation
Pharmacogenomics	Genomic responses to drugs, analysis of expression profiles that indicate similarity of action across compounds,
	analysis of genetic polymorphisms that determine a person's disposition to drug action
Toxicogenomics	Mode of action of toxic compounds, development of expression profiles that indicate similarity of toxic
	action across compounds
Ecotoxicogenomics	Genomic responses of organisms exposed to environmental pollution
Ionomics	All mineral nutrients and trace elements in an organism, for example using inductively coupled plasma
	mass spectrometry (ICPMS)

14 Gene discovery Part 1

- In a fully sequenced genome, genes are found by scanning the sequence using gene-predicting computer programmes and assigning putative functions by searching for similarities in already existing databases

- For many organisms under investigation in ecological genomics, no genomic database is available and genes must be identified in other ways.
- There are some so-called pre-genomic molecular approaches that may be used to identify ecologically important genes in incompletely characterized genomes.

From gene product to gene

- In some cases the primary structure of a gene product (a protein) may be the starting point of gene discovery.
- This holds especially for proteins that can be isolated relatively easily by some marker or bioassay, or proteins that are highly induced by some experimental treatment.
- As an example we discuss the isolation of the metallothionein (mt) gene in a species of springtail, *Orchesella cincta* (Hensbergen et al. 1999).
- Attempts to pick up the gene by polymerase chain reaction (PCR) using primers from the then-known *Drosophila* mt sequence were unsuccessful, which was

15 Gene discovery Part 2

In some cases the primary structure of a gene product (a protein) may be the starting point of gene discovery. This holds especially for proteins that can be isolated relatively easily by some marker or bioassay, or proteins that are highly induced by some experimental treatment.

- Working backwards from protein structure to gene characterization is very laborious and may only be applicable in cases where ecological functions can be associated a priori with a suspected protein
- The laborious Edman degradation technique has now been replaced mostly by sequencing using mass spectrometry, in which masses are estimated for peptides generated from proteolytic digests of the protein, while the fragment pattern obtained is compared with entries in a database that include sizes predicted from the genomic sequence. Working backwards from protein structure to gene characterization, and in some ecological applications this may be the only way to begin genomic explorations.

16 Structure and function in communities

- The relationship between ecosystem processes and species richness in communities, Lawton (1994: 'what do species do in ecosystems?') ecological genomics opens new avenues to explore this question.
- Scientific evidence concerning genome diversity in the environment and the function of genomes in nutrient cycles. Because microorganisms are in a key position at many crucial links of nutrient cycles, most of this chapter will deal with the ecological genomics of microorganisms.
- Different ecological communities can be pretty different in terms of the types and numbers of species they contain. For instance, some arctic communities include just a few species, while some tropical rainforest communities have huge numbers of species packed into each cubic meter.
- One way to describe this difference is to say that the communities have different structures. **Community structure** is essentially the composition of a community, including the number of species in that community and their relative numbers¹¹. It can also be interpreted more broadly, to include all of the patterns of interaction between these different species.

17 How do we measure community structure?

How do we measure community structure?

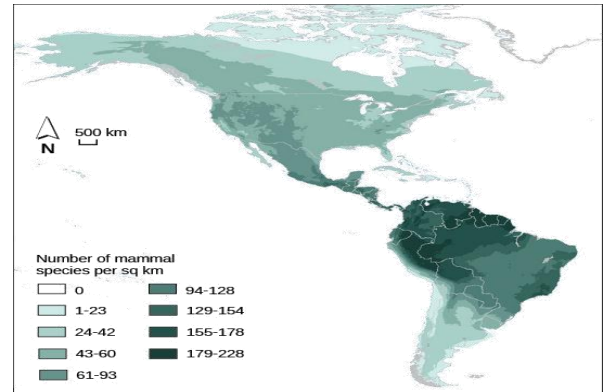
Two important measures ecologists use to describe the composition of a community are species richness and species diversity

- Species richness
- Species diversity

Species richness

Species richness is the number of different species in a particular community.

If we found 30 species in one community, and 300 species in another, the second community would have much higher species richness than the first. Communities with the highest species richness tend to be found in areas near the equator, which have lots of solar energy (supporting high primary productivity), warm temperatures, large amounts of rainfall, and little seasonal change. Communities with the lowest species richness lie near the poles, which get less solar energy and are colder, drier, and less amenable to life. This pattern is illustrated below for mammalian species richness (species richness calculated only for mammal species, not for all species). Many other factors in addition to latitude can also affect a community's species-richness.



Map shows the spatial distribution of mammal species richness in North and South America. The highest number of mammal species, 179-228 per square kilometer, occurs in the Amazon region of South America. Species richness is generally highest in tropical latitudes, and then decreases to the north and south, with zero species in the Arctic regions.

Species diversity

Species diversity is a measure of community complexity.

It is a function of both the number of different species in the community (species richness) and their relative abundances (species evenness). Larger numbers of species and more even abundances of species lead to higher species diversity. **For example:** A forest community with 20 different kinds of trees would have greater species diversity than a forest community with only 5 kinds of trees (assuming that the tree species were even in abundance in both cases).

A forest community with 20 different kinds of trees in even abundances would have greater species diversity than a forest community with the same number of species in very uneven abundances. In general, ecologists think that more diverse ecological communities are more stable (that is, more able to recover after a disturbance) than less diverse communities. However, the diversity-stability relationship isn't a universal rule, and there are some cases where other factors (besides species diversity) are more important in determining community and ecosystem stability superscript.

18 What factors shape community structure

The structure of a community is the result of many interacting factors, both abiotic (non-living) and biotic (living organism-related).

Here are some important factors that influence community structure:

- The climate patterns of the community's location.
- The geography of the community's location.
- The heterogeneity (patchiness) of the environment
- The frequency of disturbances, or disruptive events.
- Interactions between organisms.

A community's structure can also be shaped by the chance events that happened during its history. For instance, suppose that a single seed blows into the dirt of a particular area. If it happens to take root, the species may establish itself and, after some period of time, become dominant (excluding similar species). If the seed fails to sprout, another similar species may instead be the lucky one to establish itself and become dominant.

The climate patterns of the community's location:

Global climate patterns (variation in temperature, solar energy input, etc. With distance from the equator) can affect community structure. So can more local climate patterns, such effects created by mountain ranges, bodies of water, and even streams and valleys. The predictability or variability of climate can also affect community structure – for instance, some species may be unable to survive in a region with sporadic droughts or sporadic drops below freezing.

The geography of the community's location:

Geographical features of the area in which the community is found can affect community structure. For instance, island communities that are further away from a mainland tend to have smaller numbers of species

than those that are closer to the mainland. This reflects that the chance event of a species arriving from the mainland is less likely when the island is more distant.

The heterogeneity (patchiness) of the environment:

If there is more variation, or heterogeneity, in a community's environment, this may allow for greater species richness because there are more distinct habitats to be occupied. **For example**, imagine a community occupying a field, and another occupying a field that is dotted with piles of rock. The second community may have greater species richness because species that can live in the rocks (but not in the open field) will be present, in addition to those species that can live in the field.

The frequency of disturbances, or disruptive events.

The frequency of disruptive events (including storms, wildfires, and landslides) can affect the structure of a community. The **intermediate disturbance hypothesis** suggests that communities with a medium (intermediate) level of disturbance may have greater species diversity than communities with very frequent or very rare disturbances.

Interactions between organisms:

All of the interspecies interactions that can occur between organisms (competition, predation, and various forms of symbiosis) have the potential to shape a community. For instance, two species that compete intensively with one another may be unable to coexist in the same community, or a prey species may be unable to persist in a community that contains a highly effective predator.

19 Foundation and keystone species

Some species have unusually strong impacts on community structure, preserving the balance of the community or even making its existence possible. These "special" species include foundation and keystone species.

Foundation species

A foundation species plays a unique, essential role in creating and defining a community. Often, foundation species act by modifying the environment so that it can support the other organisms that form the community.

Kelp (brown algae) is a foundation species that forms the basis of the kelp forests off the coast of California. Kelps create environments that allow the survival of other organisms that make up the kelp forest community. The corals of a coral reef are another foundation species. The exoskeletons of living and dead coral make up most of the reef structure, which protects other species from waves and ocean currents. Beavers, which modify their environment by building dams, can also be seen as a foundation species.

Keystone species

A keystone species is a species that has a disproportionately large effect on community structure relative to its biomass or abundance. Keystone species differ from foundation species in two main ways: they are more likely to belong to higher trophic levels (to be top predators), and they act in more diverse ways than foundation species, which tend to modify their environment.

Different sources use different definitions for keystone and foundation species. If your class requires you to know these definitions, make sure to consult your book or teacher for the definition you should use. In some sources, foundation species are viewed as a subcategory of keystone species.

20 Invasive Species

- Invasive species are species that have been introduced into areas outside their native range and can cause—or have caused—harm in their new area
- Invasive species may outcompete native species for resources or habitat, altering community structure and potentially leading to extinctions.
- Asian carp illustrate the potential impact of invasive species. Introduced into the United States by humans, these fish species have colonized waterways and may threaten native fish populations, and fisheries, in the Great Lakes.

Kudzu, an Example of invasive species

Kudzu is one dramatic example of what can happen when a species gets introduced into a new ecosystem where it has abundant resources and few predators. The kudzu plant was introduced to the United States

from asia in the late 1800s as an ornamental plant, and it was planted widely in the south in the early 1900s to reduce soil erosion. What the people who planted this vine did not know was that it would rapidly take over the landscape, growing as much as a foot a day and enshrouding ground, shrubs, trees, and even houses and old cars in a suffocating girdle of vines. Invasive species like kudzu are example of how ecological changes, including those caused by humans, can alter communities and ecosystems. In this article, we'll look in more detail at what an invasive species is and how invasive species can disrupt ecosystems—often reducing the numbers of native species and altering the overall structure of the community.

What is an invasive species?

An *invasive species* is a species that has been introduced to an area outside of its native range and has the potential to cause harm—or has already caused harm—in its new location, many invasive species are found in the united states, and a few examples are shown in the pictures below. Whether you're enjoying a forest hike, taking a summer boat trip, or just walking down a city street, chances are that you've encountered an invasive species.

Case study: Asian carp

Let's take a look at what's arguably the kudzu of the aquatic world: the asian carp. Since they were introduced to the united states in the 1970s, asian carp have rocketed in numbers thanks to their vast appetite and speedy reproduction, now forming up to 95% of the biomass in some mississippi and illinois rivers. Not only that, these fish have led to an international lawsuit about waterway access between the united states and canada! This is a dramatic example of what can happen when an invasive species gets a foothold in a new place.

Where did this story begin? Asian carp—which are not a single species, but a group of related species—were introduced to the united states in the 1970s they were imported largely by fisheries and sewage treatment plants, which used the carp's filter feeding abilities to rid ponds of excess plankton. However, some fish escaped. By the 1980s, these fish had colonized waterways of the mississippi river basin, including the illinois and missouri rivers. Because they are big eaters and fast reproducers, asian carp can often outcompete native fish species with whom they share habitats and food sources. Black carp eat mussels and snails, limiting their availability for native fish and damaging shellfish populations. Another asian carp species, the silver carp, eats plankton, a key food for many native fish species in their larval and juvenile stages.²² Although asian carp can be eaten, the fish are bony and are generally not a desired food in most parts of the united states. The great lakes and their prized salmon and lake trout fisheries are also threatened by the asian carp. These invasive fish have already colonized rivers and canals that lead into lake michigan, including the major supply waterway linking the great lakes to the mississippi river.

To keep the carp from leaving this canal, electric barriers have been used to discourage migration. However, the threat is serious enough that several states and canada have sued to have the chicago channel permanently cut off from lake michigan. We don't yet know whether the asian carp will prove to be mostly a nuisance—like invasive species such as the zebra mussel— or whether it will ultimately destroy the largest freshwater fishery in the world. The story of the asian carp shows how population and community ecology, fisheries management, and politics can intersect and how ecology can have very real importance for the human food supply and the US economy.

21 Introduction to the Animal kingdom

Animals are

- Multicellular
- Eukaryotic
- Hetrotrophs
- Organisms with cells without cell walls

All animals carry out the following functions:

- Feeding: animals “eat” or “ingest” their food
- Respiration: taking in oxygen and giving off carbon dioxide
- Circulation: to move materials around inside of body
- Excretion: system to eliminate bodily wastes
- Response: after sensing changes in environment, animals respond to change
- Movement: Although some do not move, most animals are motile (able to move)

- Reproduction: carrying on genetic code in offspring

Invertebrates:

- Makes up 95% of Animal species
- Don't have a backbone or vertebral column
- Examples: Worms, Insects, Crabs, Starfish & Jellyfish

Vertebrates:

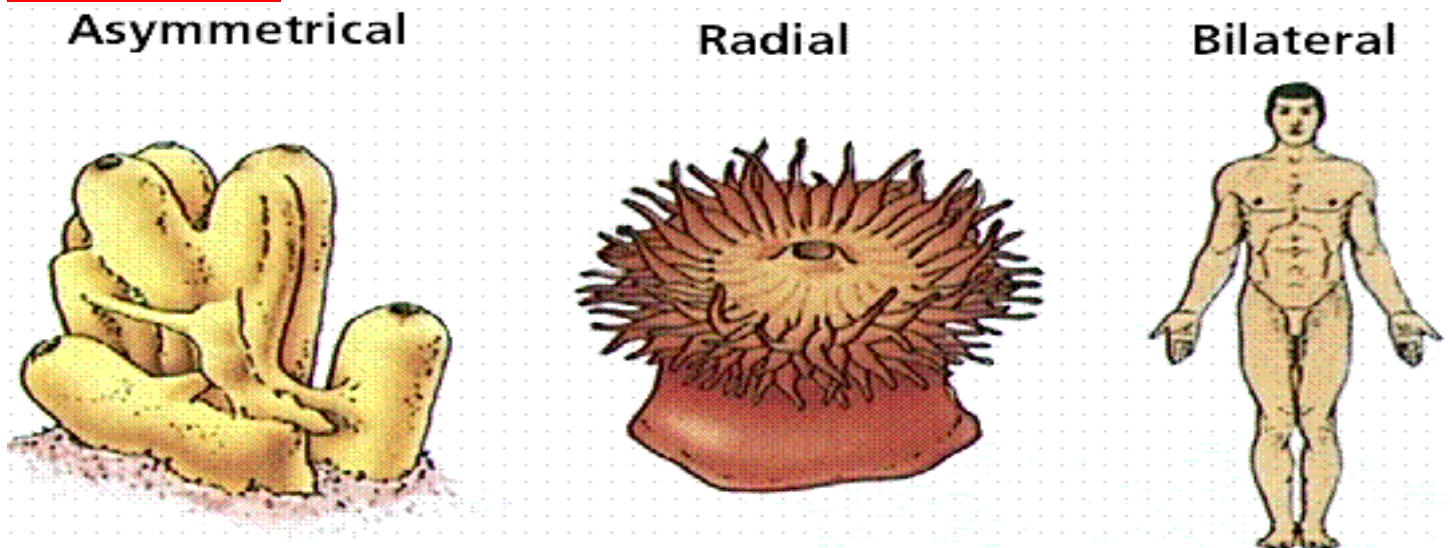
- Makes up only 5% of all animal species
- They have a backbone or vertebral column
- Examples: Humans, Fish, Reptiles, Amphibians & Birds

Body Symmetry

Categorizes animals based on 3 basic body plans:

- **Asymmetrical**: lacking an organized body plan; **only in the sponges.
- **Radial Symmetry**: body plan of an organism that can be divided into two equal halves when **any line** is drawn through its center (examples: starfish, jellyfish, and sea anemones).
- **Bilateral Symmetry**: body plan of organism that can be divided into two equal halves by only **one line** drawn through its center (examples: crabs, insects, fish and humans)

Symmetry Review



22 Features of protists

Characteristics of Protists

- ✓ Eukaryotes
- ✓ unicellular

3 Main groups of protists;

- ✓ Protozoans
- ✓ algae
- ✓ fungus-like

1. Protozoans

Animal like protists

Protozoans - Animal like

Grouped by movement

- ✓ pseudopods

- ✓ cilia
- ✓ flagella
- ✓ parasites - no movement

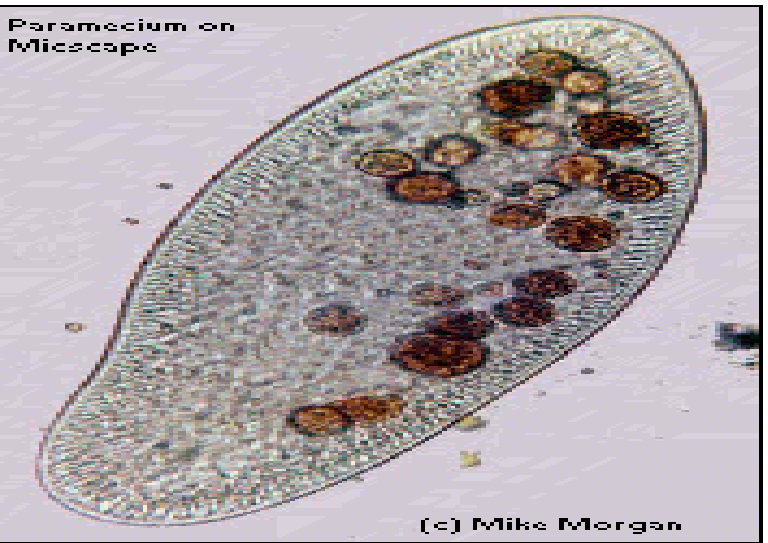
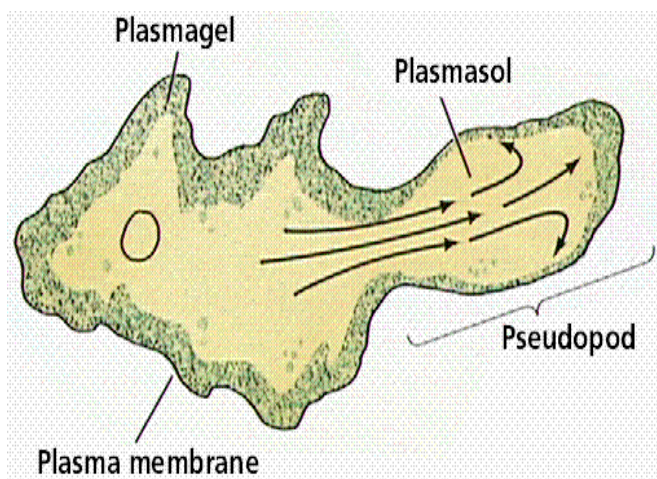
Protozoan Characteristics

- ✓ No cell wall
- ✓ Free-living or parasitic
- ✓ Consumers
- ✓ Habitat – aquatic (ponds, lakes, oceans)
- ✓ Examples: amoeba, paramecium, dinoflagellates

Example 1: Protozoans – amoebas

- Amoebas
 - shapeless, aquatic

Pseudopods in Amoebas



How Amoebas Eat ?

- feeding structures-
 - food vacuole
 - digestive enzymes
 - diffusion

Getting Rid of Waste

- Contracting vacuole – collect excess water from inside the cell and gets rid of it.

Reproduction of Amoeba

- asexual reproduction
 - Binary fission

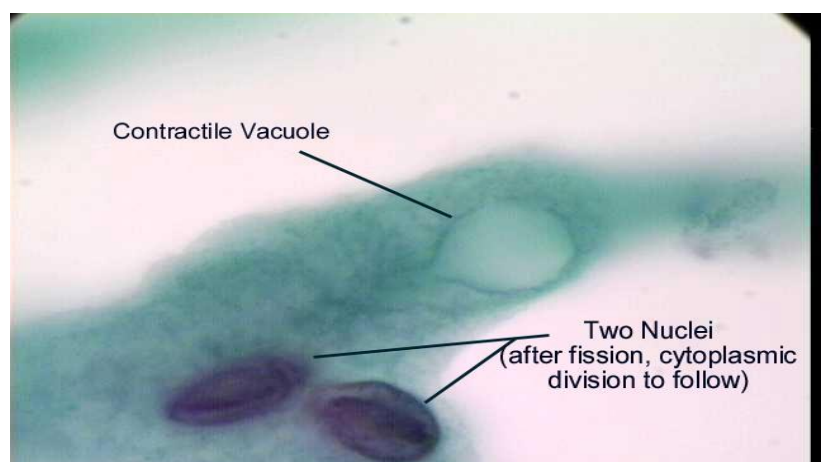
Dysentery (an illness)

- Inflammation of the large intestine
- Diarrhea and vomiting
- Caused by an amoeba

2. Example 2: Protozoans: Ciliates

- Locomotion - Cilia

1. Paramecium - fresh water ciliate



How do Paramecium eat?

- Feed on bacteria
 - Food enters oral groove,
 - moves to the food vacuole,
 - anal pore

Paramecium Reproduction

- **Asexual**- create identical organisms
- **Conjugation** - sexual reproduction
 - *exchange of genetic information*
 - *Not identical - adds diversity*



3. Example 3: Protozoans - Flagellates

- Locomotion - use flagella
- Examples:

2. Trypanosoma - causes African Sleeping Sickness

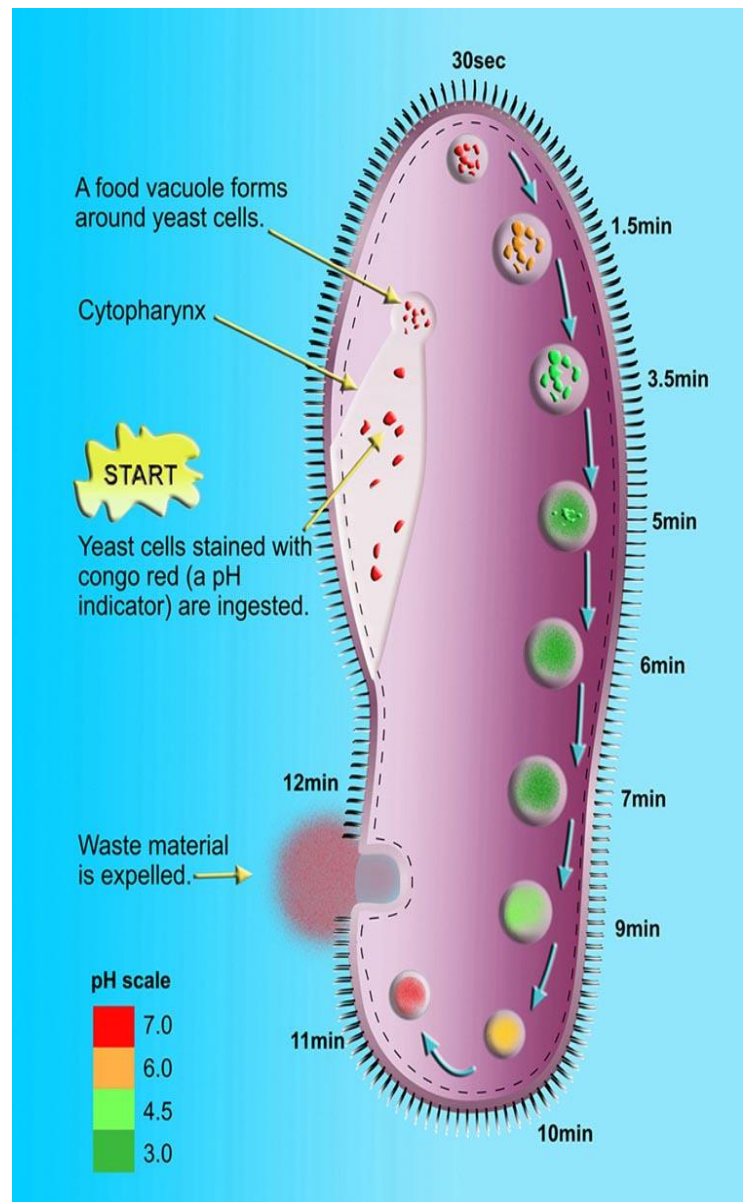
- spread by tsetse fly

4. Example 4: Protozoan - sporozoans

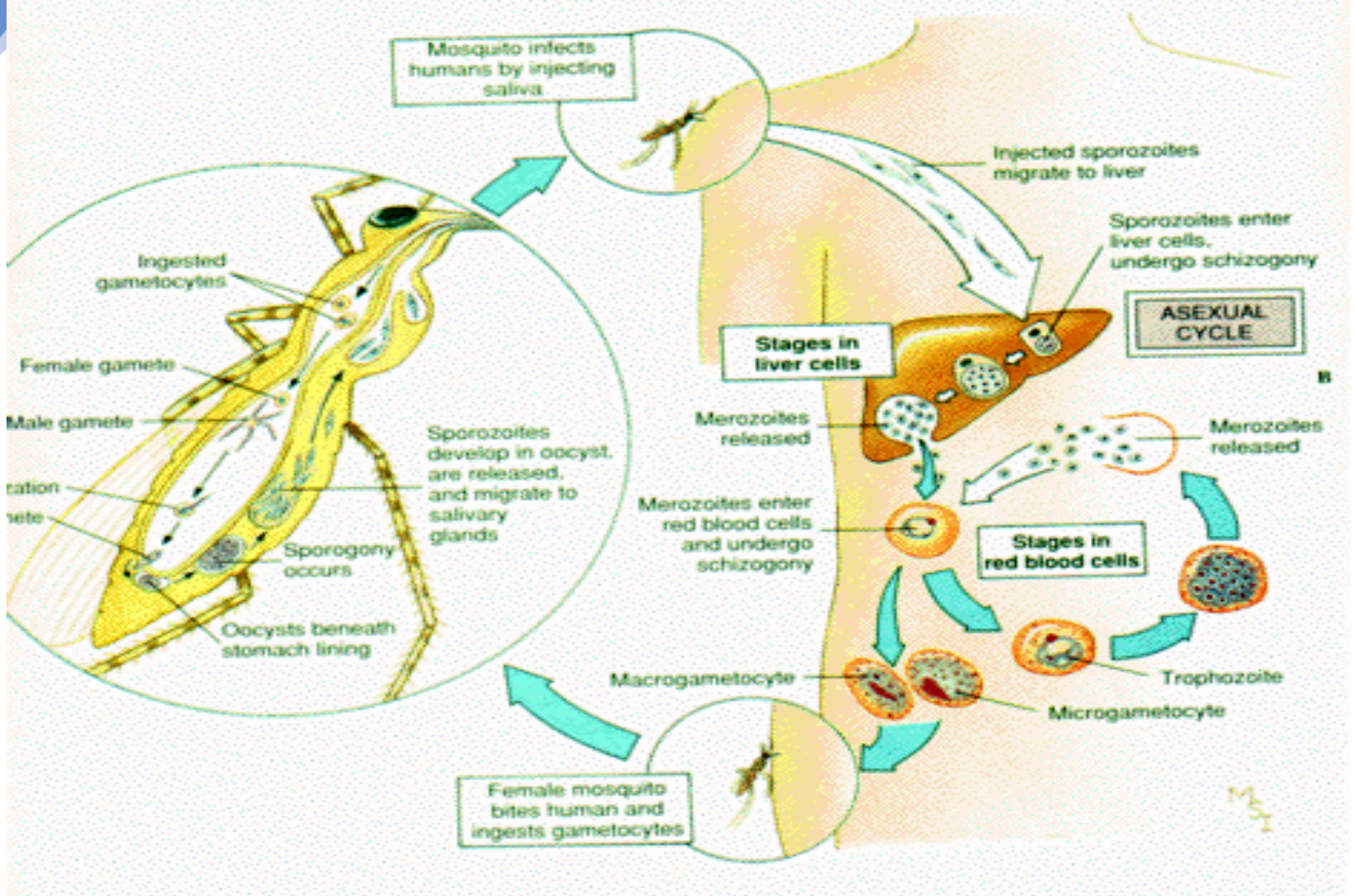
- Locomotion - parasitic
- reproduction
 - spores

Plasmodium - Causes [Malaria](#)

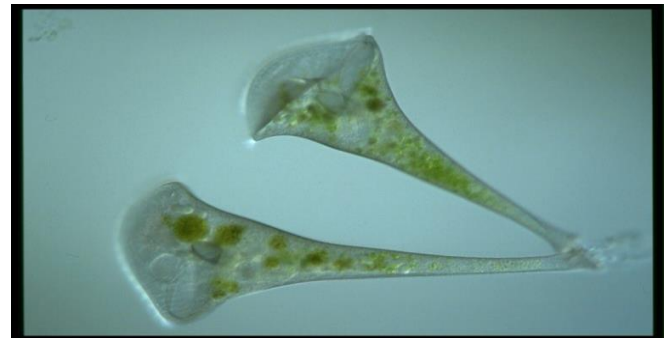
- Spread by mosquito
- Quinine – drug used to treat malaria



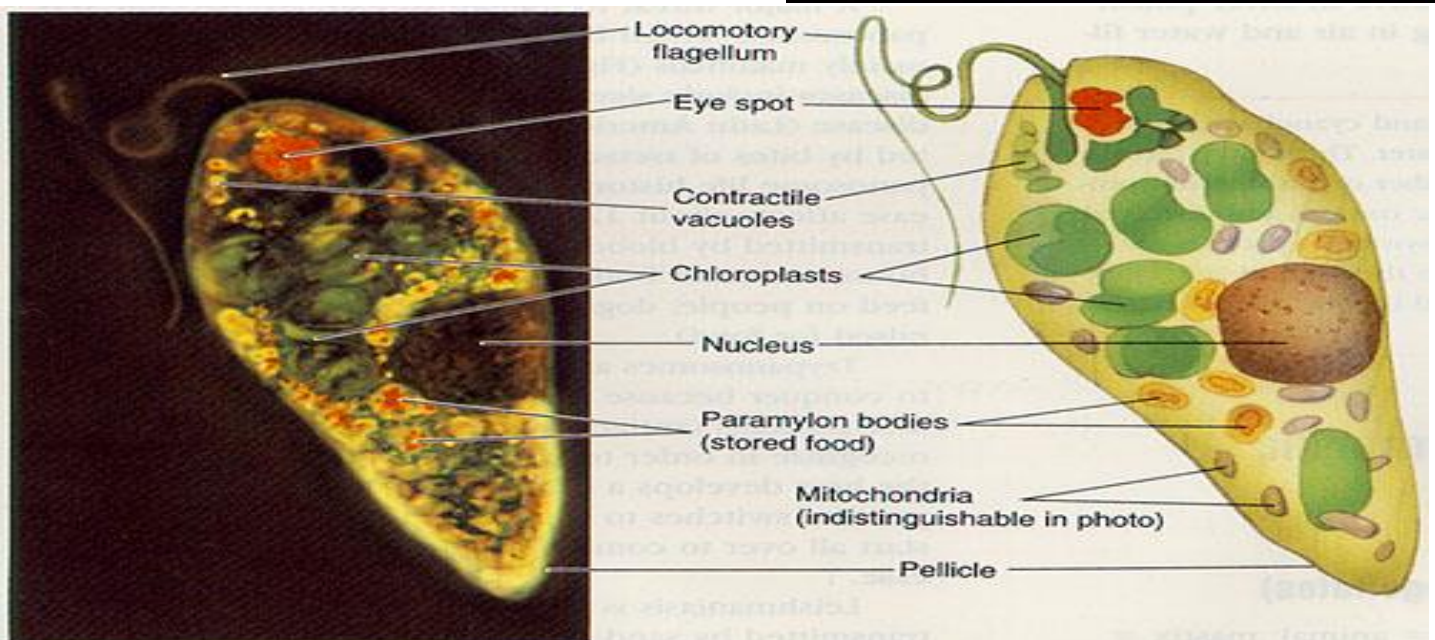
III The Diversity of Animal Life

**Vorticella**

- Attaches to and spins its cilia to create a vortex (water movement)

Stentor**2. Euglena – 2nd group in protists**

- Both plant-like and animal-like

**Euglenoids**

- - contain chlorophyll
- - move by flagella
- - Euglena (unique)-
 - eyespot,

- chloroplast,
- flagellum

Algae

Plant like protists

B. Algae - plant-like

- Photosynthetic
- Multi-cellular and unicellular
- Classified by pigments (Types of Algae)
 - red
 - brown
 - Green+
- Examples; Volvox, diatoms, spiroyra

1. Diatoms

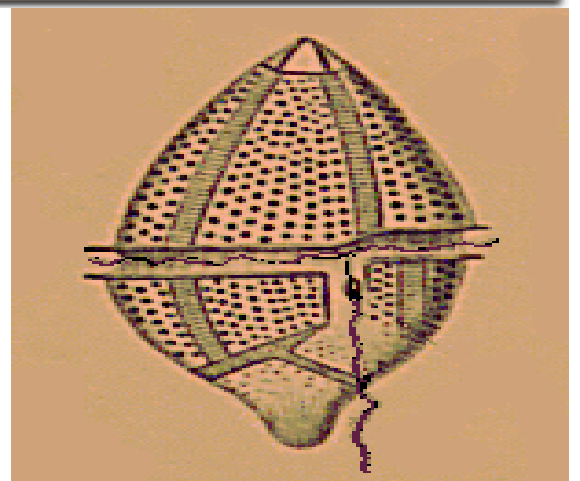
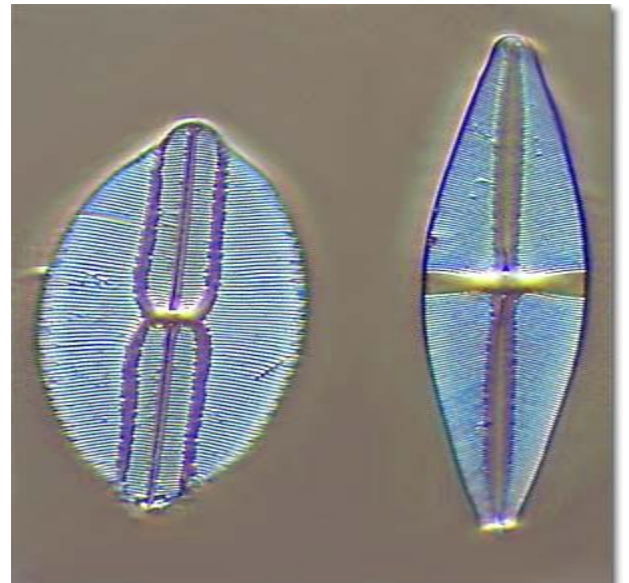
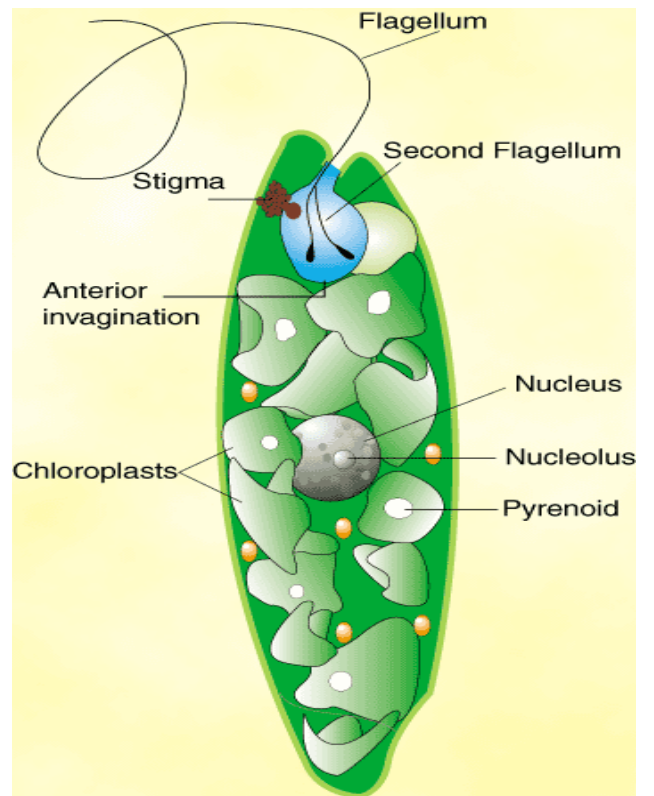
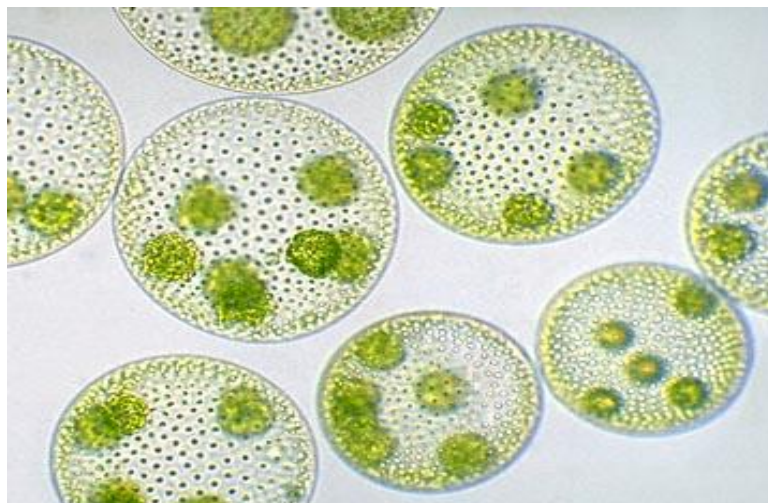
- - float in water
- - photosynthesis
- - unicellular
- - silica shells
- Commercial value: Insulating materials, Abrasives , Ceramics, Filtering

2. Dinoflagellates

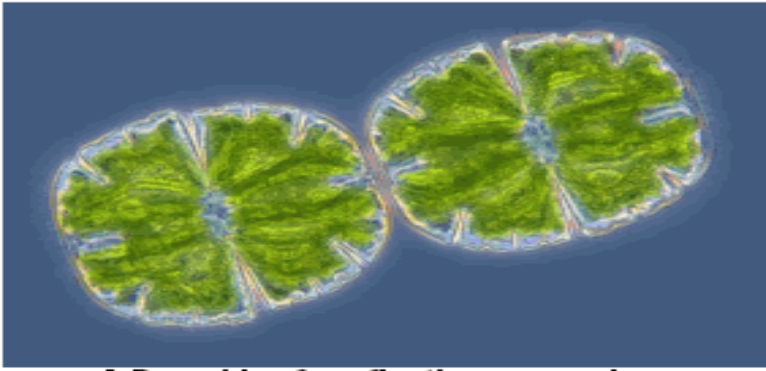
- - move by two flagella
- - autotrophs
- - green glow and red tides

3. Green Algae (Lab 37)

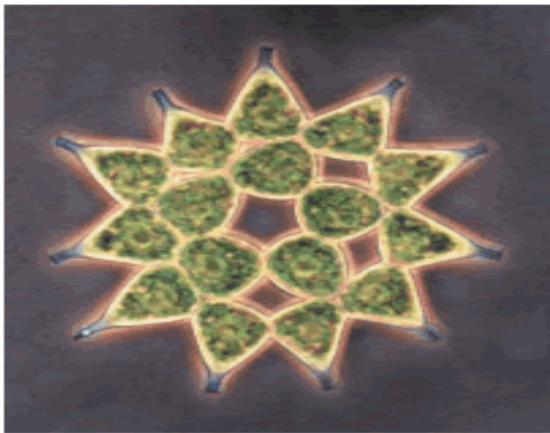
- Most freshwater
- Food Source – called Plankton
- Some are:
 - Free-living
 - Colony
 - filament



Free-Floating –



A Desmid: a free-floating green alga



Green alga -*Pediatrum*

- Filament type – exist as a thread

Colony –

Label and Draw

- ✓ Ulothrix
- ✓ Zygnema
- ✓ Spirogyra
- ✓ Hydrodictyon
- ✓ Peridinium
- ✓ chlamydomonas

Red and Brown Algae

- ✓ All multicellular
- ✓ Marine
- ✓ Kelp – a form of brown algae
- ✓ Red algae – used in food.

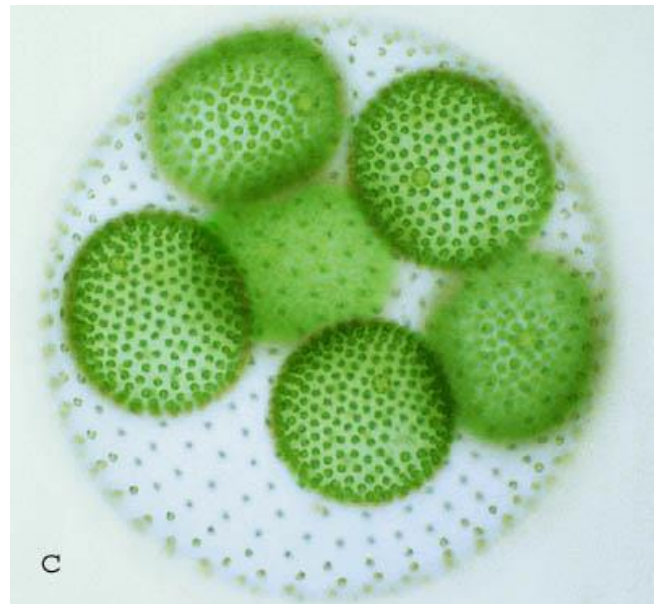
Fungus Protists

Slime Molds

- - plasmodium- visible slime mass
- - moves
- - no cell membrane
- - many nuclei
- - grow on damp organic matter - decompose
- - form a stalk, release spores
- - Reproduce - asexual reproduction, making spores

Fungus Like Protists

- Classified by how they reproduce



- slime molds
- mold and mildew - disease causing

Mildew and Water Molds

- - fuzzy growths
- - found on bathroom tiles
- - live off of dead material
- - potato famine- 2 million people died in Ireland
- - caused immigration to the United States

Origins and Importance of Protists

- Green algae

Importance of :

- green algae - oxygen source
- food source -
 - plankton
 - zooplankton
 - phytoplankton

23 Protozoa

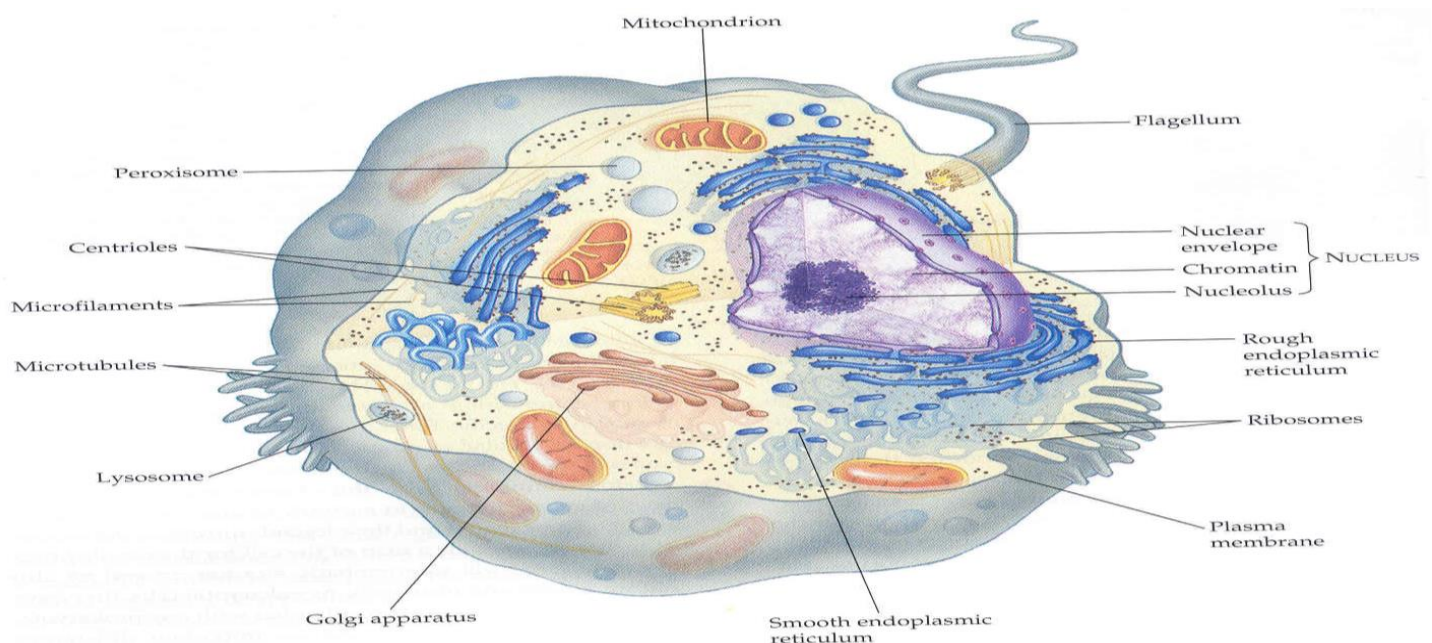
Ciliates

Amoeboid Protozoans

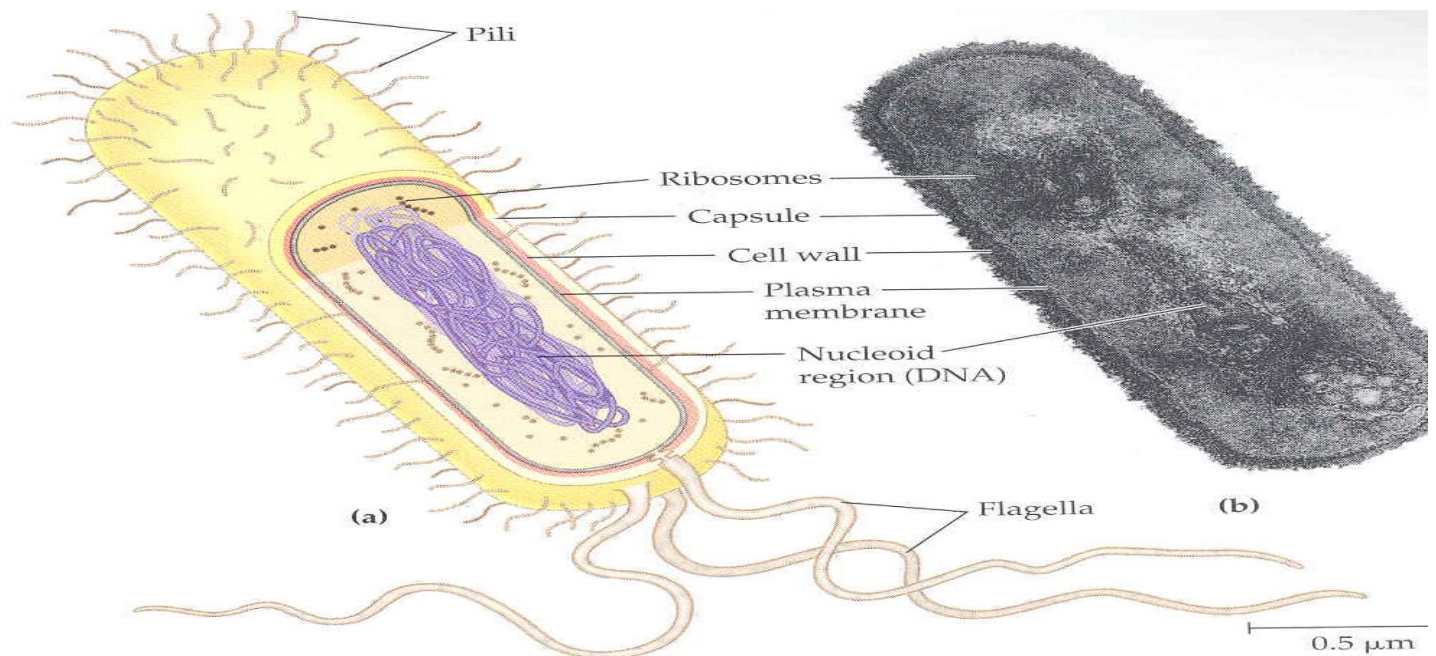
Flagellated Protozoans

Kingdom Protozoa

- Defining Characteristics
 - All are unicellular **eukaryotes**
 - What is a **prokaryote**?
 - Many species are both **heterotrophic** and **autotrophic** simultaneously or at different stages of the lifecycle
- Eukaryote Cell



Prokaryote Cell



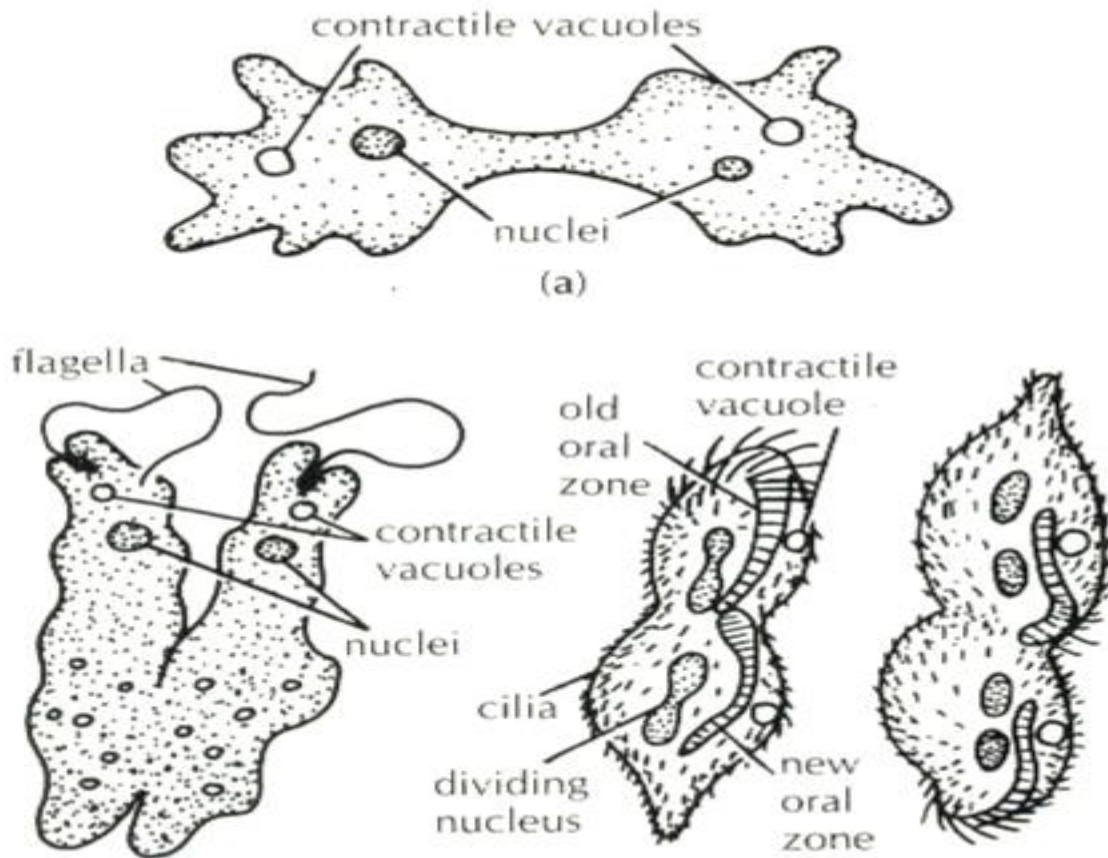
Adaptability

- Protozoans are ecologically important primary producers, consumers and as vital links in the food chain
- Humans are greatly effected by parasitic protozoans either directly or indirectly
 - Effects range from irritating - fatal
 - Malaria (*Plasmodium spp.*) worldwide epidemic

Reproduction

- Asexual reproduction
 - Replication of chromosomes and the splitting of the parent into two or more parts
 - Binary fission
 - Multiple fission
 - Budding
- Protozoans are problematic in their associations as colonial forms

Asexual Reproduction



Classification

Kingdom Protozoa

Phylum Ciliophora (Ciliates)

The Sarcodinids (Amoeboid Protozoans)

Phylum Foraminifera

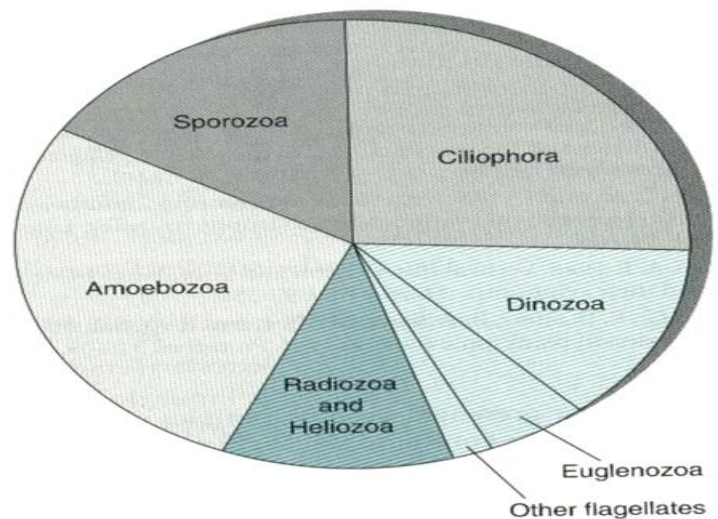
Phylum Radiozoa

The Flagellated Protozoans

Phytoflagellated protozoans

Zooflagellated protozoans

Taxonomic Detail



1. Phylum Ciliophora

Body externally ciliated in at least some lifecycle stages. Have the highest degree of subcellular specialization and are considered advanced protozoans. E.g paramecium, verticilla

Cilia

Hair-like structures by which the organism moves, collects food and senses their surroundings . Fastest of all the protozoans

Ciliate Biology

- Oral groove
- Cytostome
- Cytoproct
- Contractile vacuole

Ciliate Lifestyles

- 65% of all ciliate species are free-living and mobile

- Some ciliates form colonial aggregations and have sessile habits
- Other ciliates have symbiotic relationships in invertebrates and vertebrates

2. The Sarcodinids (Amoeboid Protozoans)

Contains 4 phyla: Foraminifera, Radiozoa, Amoebozoa, and Heliozoa. Most reproduce asexually through binary fission. Characterized by pseudopodia. Food is usually captured by phagocytosis. Body types range from free flowing to rigid with skeletal supports

A. Phylum Foraminifera

Individuals secrete multi-chambered tests, generally made of calcium carbonate (CaCO_3)

Foraminiferans

Extremely abundant, most are benthic and marine. Feed on diatoms and algae, very slow movers. Organisms are extremely common and form ooze

- White cliffs of Dover are foraminiferan tests
- Extremely abundant, most are benthic and marine
- Feed on diatoms and algae, very slow movers
- Organisms are extremely common and form ooze □ White cliffs of Dover are foraminiferan tests

B. Phylum Radiozoa

Radiolarians

Have shells made of silicon dioxide that can be very intricate. Feed on diatoms and other phytoplankton. Benthic individuals move by use of pseudopodia. Can occur in large concentrations that form ooze as well.

3. The Flagellated Protozoans

Characterized by the possession of a definite body shape and the possession of one or more flagella. Most species are free-living and mobile. E.g Noctiluca

1. Phytoflagellated Protozoans

Have chlorophyll and obtain energy directly from the sunlight. Some are strictly autotrophic or heterotrophic. Some are a combination of both.

E.g *Euglena*, dinoflagellates, chlamadomonas, ceratium

Dinoflagellates

Know for bioluminescence and highly **toxic red tides**: Dense aggregations produce saxitoxin killing fish and crustaceans

Also contaminates shellfish causing diarrheic shellfish poisoning. Some benthic dinoflagellates produce a neurotoxin that accumulates in tropical fish called Ciguatera

2. Zooflagellated Protozoans

1. Free-living forms

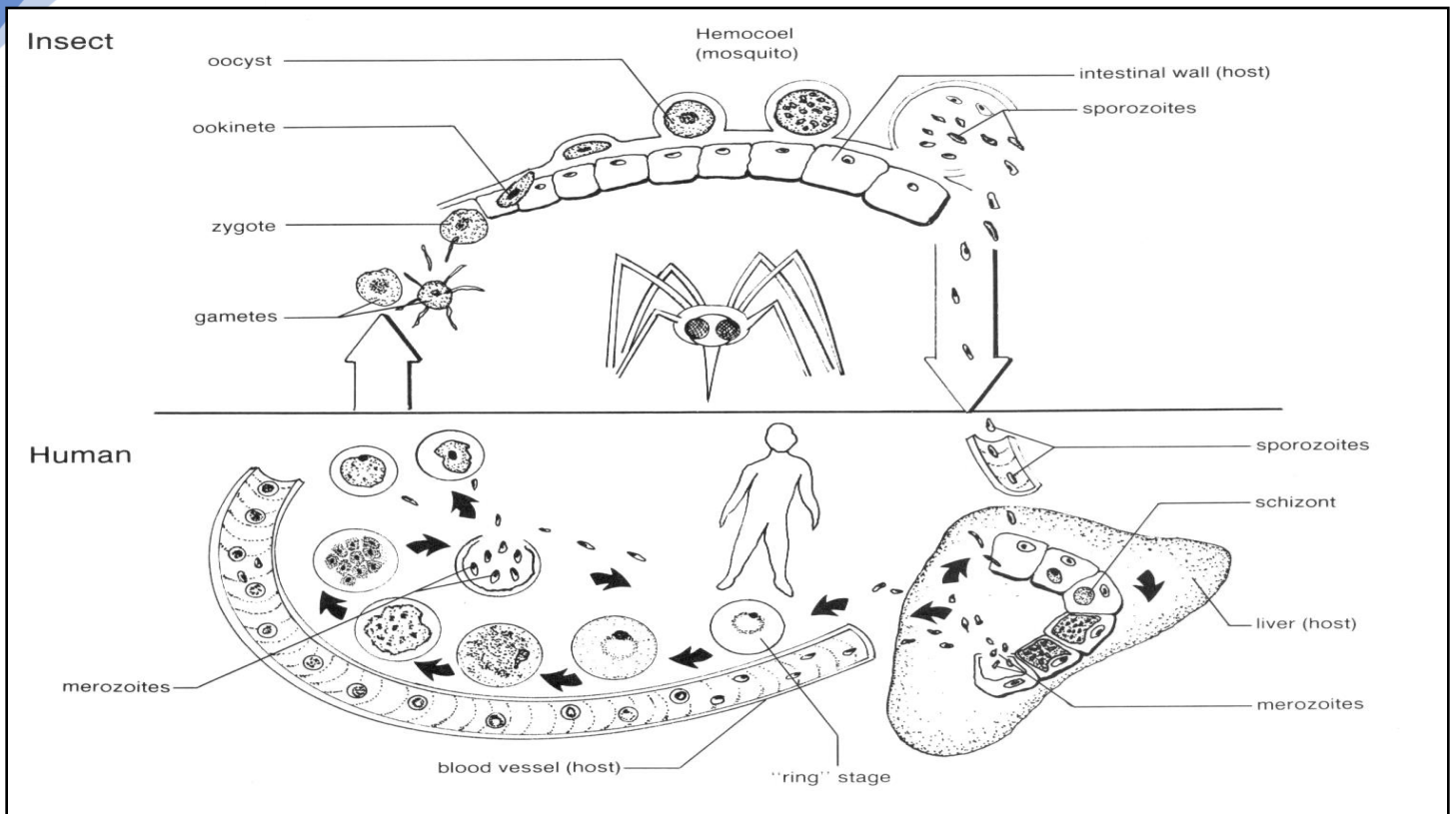
Most individuals are sessile and have a single flagellum that beats to obtain food and nutrients

2. **Parasitic forms**

25% of zooflagellate spp. are parasitic in humans, invertebrates, and other vertebrates. Usually have complex lifecycles with intermediate hosts. Malaria is caused by the genus *Plasmodium* technically a member of the phylum Sporozoa.

Chanoflagellates are example of Zooflagellated prptozoans.

Malaria (*Plasmodium*)



24 Phylum Arthropoda

- ✓ jointed foot"
- ✓ Largest phylum
- ✓ 900,000 species
- ✓ 75% of all known species

Insects, spiders, crustaceans, millipedes, scorpions, ticks, etc

Most successful phylum ecologically diverse. Present in all regions of the earth. Adapted to air, land, freshwater, marine, other organisms

Reasons for success

- Versatile exoskeleton
- Efficient locomotion
- Air piped directly to cells (terrestrial)
- Highly developed sensory organs
- Complex behavior
- Metamorphosis

Exoskeleton

External: not enveloped by living tissue

Protection

Secreted by underlying epidermis

- Waterproof barrier
- Chitin +/- calcium, lipoproteins

Modifications

- Can be site for muscle attachment
- Energy stores- flying
- Sensory receptors
- Gas exchange
- Bristles

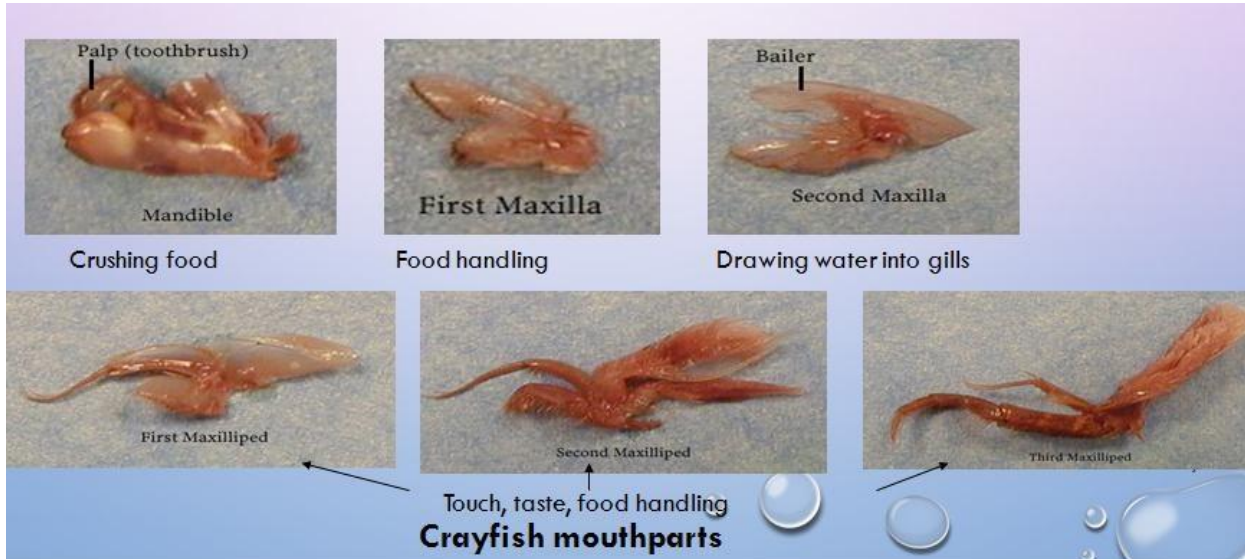
Soft and permeable or hard, impermeable

- Between segments of body/appendages= thin + flexible
- Must be shed (ecdysis= molting) to allow growth
- Relatively heavy: Limits size

1. Efficient locomotion

Tagmatization, more specialized than annelids

- Regions= tagma/tagmata
- Jointed appendages



2. Air piped directly to cells

- More efficient than most other invertebrates
- Most have efficient tracheal system of air tubes; some breathe by gills
- Limits size

3. Highly developed sense organs

- Sight, touch, smell, hearing, balance, chemical reception

4. Complex behavior patterns

- Complex, organized activities
- May be innate (unlearned) or learned

5. Limited intraspecific competition

- Many arthropods undergo metamorphosis
 1. meta= between/after; morphē= form; osis= state of
- Different stages (ie. larva, adult) have different nutrition/habitats → no competition

Other Characteristics of Arthropods

- Bilateral, triploblastic, schizocoelous
 - No septa

Arthropod Groups

1. Subphylum Trilobita

- extinct trilobites

2. Subphylum Chelicerata

- horseshoe crabs, spiders, ticks, mites, and some extinct groups

3. Subphylum Myriapoda

- centipedes, millipedes

4. Subphylum Crustacea

- crabs, lobsters, shrimps, barnacles

5. Subphylum Hexapoda

- Insects

Subphylum Trilobita

- tri= three; lobos= lobes
- Divided into 3 longitudinal regions
- Extinct
- Oval, flattened

Subphylum Chelicerata

- Horseshoe crabs, spiders, ticks, mites, scorpions

Cephalothorax (prosoma)

- Fused head and thoracic region

Abdomen (opisthosoma)

- contains digestive, reproductive, excretory, and respiratory organs

Appendages attached to cephalothorax

- Pair of chelicerae (clawlike feeding appendages)
- Pair of pedipalps (usually sensing or feeding)
- four pairs of legs (5 in horseshoe crabs)
 - No antennae

- Most suck liquid food from prey

Class Arachnida

- Spiders, ticks, scorpions
- Most are predaceous
- Most are harmless/beneficial to humans
- Some spiders (ie. black widow, brown recluse spider) give painful, dangerous bites
- Scorpion sting can be painful, dangerous
- Some ticks and mites spread disease, cause irritation
- Lyme disease caused by tick

More on spiders: _Order Araneae Spiders

- cephalothorax and abdomen shows no external segmentation
- tagma are joined by a narrow pedicel
- All predaceous
- Mostly insects
- Chelicerae have fangs

• Prey capture among the spiders

- ✓ Some species are cursorial predators
- ✓ stalk and ambush their prey
- ✓ they usually have well-developed eyes
- ✓ Some are web-building spiders
- ✓ Eyes not as well developed
- ✓ sensory hairs for detecting vibrations
- ✓ Many spiders (and mites) producing silk
- ✓ trapping Used for prey, building nests, forming egg cases
- ✓ silk glands that open to the exterior part of the abdomen through spinnerets
- ✓ Many species have evolved poison glands associated with the chelicerae
- ✓ Spider venom is used to subdue prey
- ✓ Venom liquifies tissues with a digestive fluid
- ✓ Spider sucks up soupy prey

• Spiders: Class Araneae

- Spider love: Spiders, like most arthropods, are dioecious: Mating habits
- Pheromones- chemicals that elicit behavioral change: Rituals- males pluck female's web (pattern is species-specific)
- Male builds small web, deposits sperm: Collects sperm in cavities of pedipalps
- Pedipalps have ejaculatory duct + embolus: inserts pedipalps into female genital opening Eggs laid in silk case Carried, attach to web, bury.
- Wolf spider parental care- after the eggs hatch, the young ride on mom for several days.
- Young spiders disperse by silk lines (ballooning)

• Brown recluse

- Violin-shaped stripe on back
- Necrotoxin: Hemolytic

- *Loxosceles reclusa*

Necrosis of tissue

The Crustaceans

Phylum Arthropoda Subphylum Crustacea

- crusta= shell
- Lobster, crayfish, shrimp, crab, water flea, barnacles
- Aquatic (mostly marine), a few terrestrial forms
- Major ecological and economical importance
- Biramous appendages (at least primitively), 2 main branches
- Only arthropods with 2 pairs of antennae
- Great specialization of appendages: Mouthparts chewing, grinding, handling
- appendages strengthened for walking or protection (chelipeds, pincer-like claws)
- Respiration: gills (usually)
- Compound eye is typical of phylum

What's the difference between a crayfish and a lobster

Same Order, but different families, Lobsters are bigger, Lobsters are marine; crayfish live in freshwater creeks, ditches, or lakes

Barnacles:

living and nonliving substrates, most species secrete CaCO_3 shell, Head reduced, rudimentary abdomen

Krill: Component of plankton, Major food for whales.

25 Phylum Annelida

Class Polychaeta • Class Clitellata

Phylum Annelida Annelid Characteristics

Defining Characteristics

- ✓ One or more pairs of chitinous setae
- ✓ The phylum includes polychaetes, earthworms, leeches, and vestimentiferans
- ✓ True segmented worms
- ✓ Metameric segmentation

Body Structure

The body is a tube within a tube. The coelom is important to annelids for: The epidermis is what secretes the tough cuticle

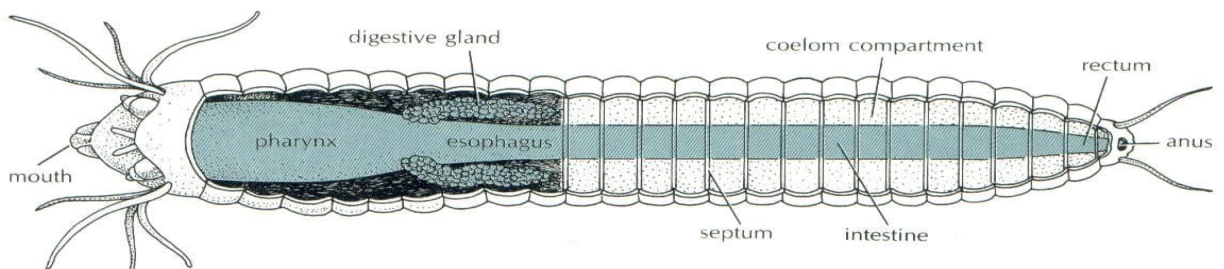
Locomotion

On each side of the animal is a parapod (parapodia) consisting of fleshy lobes, which are supported by chitinous rods. Each parapod have setae, which can be sharp (protection), and aid in locomotion

Feeding

Annelids range from carnivores, herbivores, scavengers, deposit feeders, and filter feeders. With very few defenses, many remain in a burrow or secreted tube. Carnivores can capture prey with strong jaws and quickly drag it back to its burrow. Can use a muscular pharynx = eversible proboscis.

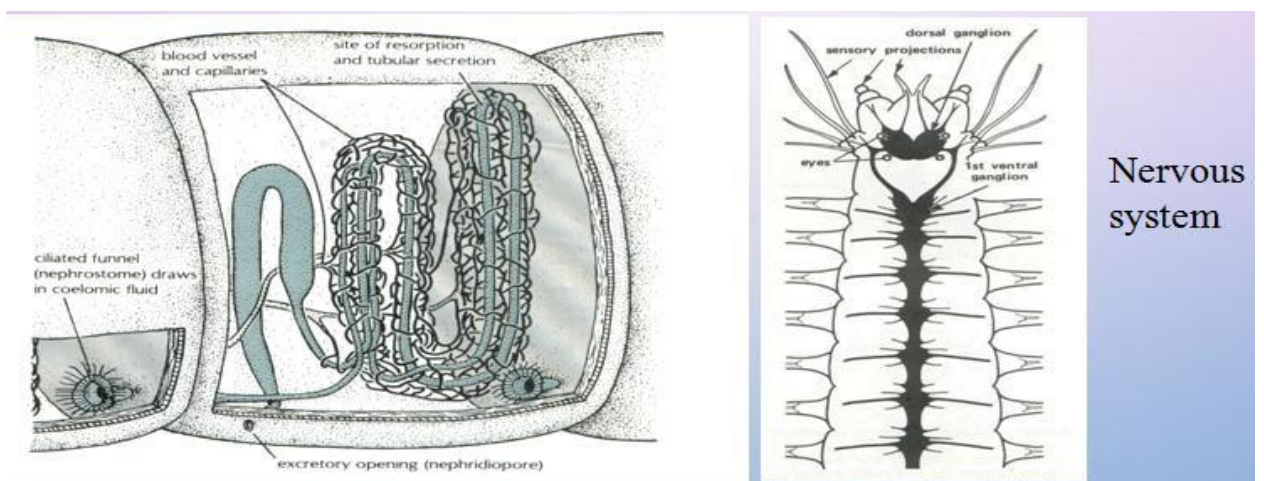
Digestive System



Circulatory System

Blood flows entirely in closed vessels. Some spp. have hearts. Blood contains hemoglobin, which increases oxygen carrying ability.

Excretory & Nervous System



Nervous system

REPRODUCTION

Sexes are usually separate with gonads occurring in each segment. Some species have gonad specific segments. Breeding is usually seasonal (spring or fall). As gametes mature they fill the coelom and are released by the nephridia. Fertilization can be internal or external. Trochophore larvae develop, which are remarkably similar to the Molluscs

Taxonomic Summary

- **Phylum Annelida Class Polychaeta**
 - Family Siboglinidae
 - Class Clitellata**
 - Subclass Oligochaeta. Subclass Hirudinea

1. Class Polychaeta

Some tube species lack parapodia but it is believed to have been lost. Parapodia differ from species to species and play an important role in identification

Reproduction

Dioecious with gametes released into the coelom. Many species reproduce *en masse* at the surface at night. Moonlight and artificial light attract spawning masses

Epitokes

These are given the task of reproduction. Some individuals bud epitokes from the body and remain in the habitat. Some species lack a free-swimming or plankton stage, and are produced in protective gelatinous egg masses

Family Siboglinidae

Gut tissue forms an organ (trophosome) that becomes filled with chemosynthetic bacteria. Segmentation confined to small rear portion of animal (the opisthosoma). Small intriguing class of tube dwelling worms found throughout the world's oceans

Trophosome

The major organs (gonads and trophosome) are found in the coelom. The trophosome of all species contains closely packed bacteria and play a crucial role in nutrition. The last segment is the opisthosoma, which has many segments and septa like polychaetes

Chemosynthetic Bacteria

The most interesting aspect of pogonophora is the lack of a digestive system. Bacteria in the trophosome fix the chemicals leaving the vents. The bacteria can occur at concentrations of 10 billion per gram of trophosome tissue

2. Class Clitellata

1. Subclass Oligochaeta

- Pronounced cylindrical glandular region of the body = clitellum
 - Second largest class in the phylum Annelida
 - Most spp. are earthworms, very few are marine

Polychaetes and Oligochaetes

Oligochaetes differ from polychaetes in several ways: No parapods, fewer setae (if at all), Hermaphroditic with sex cells produced in a separate section. No larval stages

2. Subclass Hirudinea

- Posterior sucker
- Predominately freshwater, but do occur in all seas and moist soil

- • Leeches do not burrow or crawl, lack parapods and setae

LEECH ANATOMY

Leeches do not burrow or crawl, lack parapods and setae. Anterior sucker is small and contains the mouth. Anterior sucker creates a wound with saw like jaws. Leeches drink other animals' blood, usually vertebrates. Can be carnivores, or scavengers; leeches are not set in their feeding habits

Blood Sucker

The salivary glands excrete hirudin which prevents the blood from coagulating. May also secrete an anesthetic and substance to dilate small blood vessels. Blood is broken down by symbiotic bacteria that is then used by the leeches. Leeches were commonly used in the 19th century for bloodletting . Recent medical uses are to relieve pressure after vascular tissue is damaged. Snake bites or the reattachment of a finger or ear.

Leech Reproduction

- Leeches are simultaneous hermaphrodites that lack a free-living larvae stage
- Fertilization is internal through copulation
 - Development occurs in a cocoon similar to the Oligochaetes

26 Echinodermata

A complex series of fluid filled canals with numerous flexible feeding and locomotory appendages. 5 pointed radial symmetry in adult

Echinoderms Skeleton

Have an internal skeleton of calcium carbonate. Ossicles vary in size and structure and are manufactured by specialized cells

Water vascular system

A separate coelom is used with interconnecting fluid filled tubes and canals. A ring canal circles the mouth and gives off 5 radial canals. The radial canal is exposed and runs along the ambulacral groove

Tubefeet

The ampullae is a small ball that sits above the tube foot. Contraction and expansion of the ampulla accomplishes movement

Mutable connective tissue

Another unique Echinodermata characteristic is the presence of mutable connective tissue

Taxonomic Summary

- Phylum Echinodermata
- Class Crinoidea
- Class Concentricycloidea
- Class Stellerioidea
- Subclass Asteroidea
- Subclass Ophiuroidea
- Class Echinoidea
- Class Holothuroidea

Sea Stars

The oral surface of each arm has a single ambulacral groove. Have a large coelom where all the main organs occur

Reproduction

Can reproduce asexually by disk division. Sexual Reproduction: Dioecious with sperm or eggs produced in 2 or more gonads in each arm. Larval stage = bipinnaria

Regeneration

Many species autotomize, leaving predators with a nutritious souvenir while they escape. Most spp. can regenerate from fragments that include the disk

Ingestion and Digestion

Feed on alga material, encrusting bryozoans or scavenge. Food is chopped by 5 sharp pointed teeth. The digestive system is long to deal with vegetable matter. The anus is located aborally

Reproduction: Most conspicuous organs are those responsible for reproduction. At spawning the entire coelom will fill with sperm or eggs. **Pluteus** larva is formed

Ossicles

Although somewhat soft they do have an internal skeleton. The skeletal elements (ossicles) are microscopic with complex shapes. May compose up to 80% of the dry body weight

Defense

Many spp. have powerful toxins in the body wall "Cuvierian tubules". Sticky and toxic tentacles which are shot out the anus. Also eviscerates to avoid predation. Internal organs regenerate after a period of time

27 chordates,

A chordate is an animal belonging to the phylum chordata; they possess a notochord, a hollow dorsal nerve cord, pharyngeal slits, an endostyle, and a post-anal tail, for at least some period of their life cycle.

Chordates are deuterostomes, as during the embryo development stage the anus forms before the mouth.

They are also bilaterally symmetric coelomates. In the case of vertebrate chordates, the notochord is usually replaced by a vertebral column during development, and they may have body plans organized via

segmentation. By the end of the cambrian period, 540 million years ago, an astonishing variety of animals inhabited earth's oceans. One of these types of animals gave rise to vertebrates, one of the most successful groups of animals. Chordates are **bilaterian** animals that belong to the **clade** of animals known as **deuterostomia**. Two groups of invertebrate deuterostomes, the urochordates and cephalochordates are more closely related to vertebrates than to invertebrates.

Phylum Chordata

Chordates have:

- Bilateral symmetry
- A coelom
- Deuterostome development: Radial, indeterminate cleavage, Enterocoelous coelom development
- Metamerism
- Cephalization.

Five distinctive characteristics define the chordates:

- Notochord
- Dorsal tubular nerve cord
- Pharyngeal pouches (gill slits)
- Endostyle
- Postanal tail

All are found at least at some embryonic stage in all chordates, although they may later be lost.

1. Notochord

The notochord is a flexible, rod-like structure derived from mesoderm. The first part of the endoskeleton to appear in an embryo. Place for muscle attachment. In vertebrates, the notochord is replaced by the vertebrae. Remains of the notochord may persist between the vertebrae.

2. Dorsal Tubular Nerve Cord

In chordates, the nerve cord is dorsal to the alimentary canal and is a tube. The anterior end becomes enlarged to form the brain. The hollow cord is produced by the infolding of ectodermal cells that are in contact with the mesoderm in the embryo. Protected by the vertebral column in vertebrates.

3. Pharyngeal Pouches and Slits

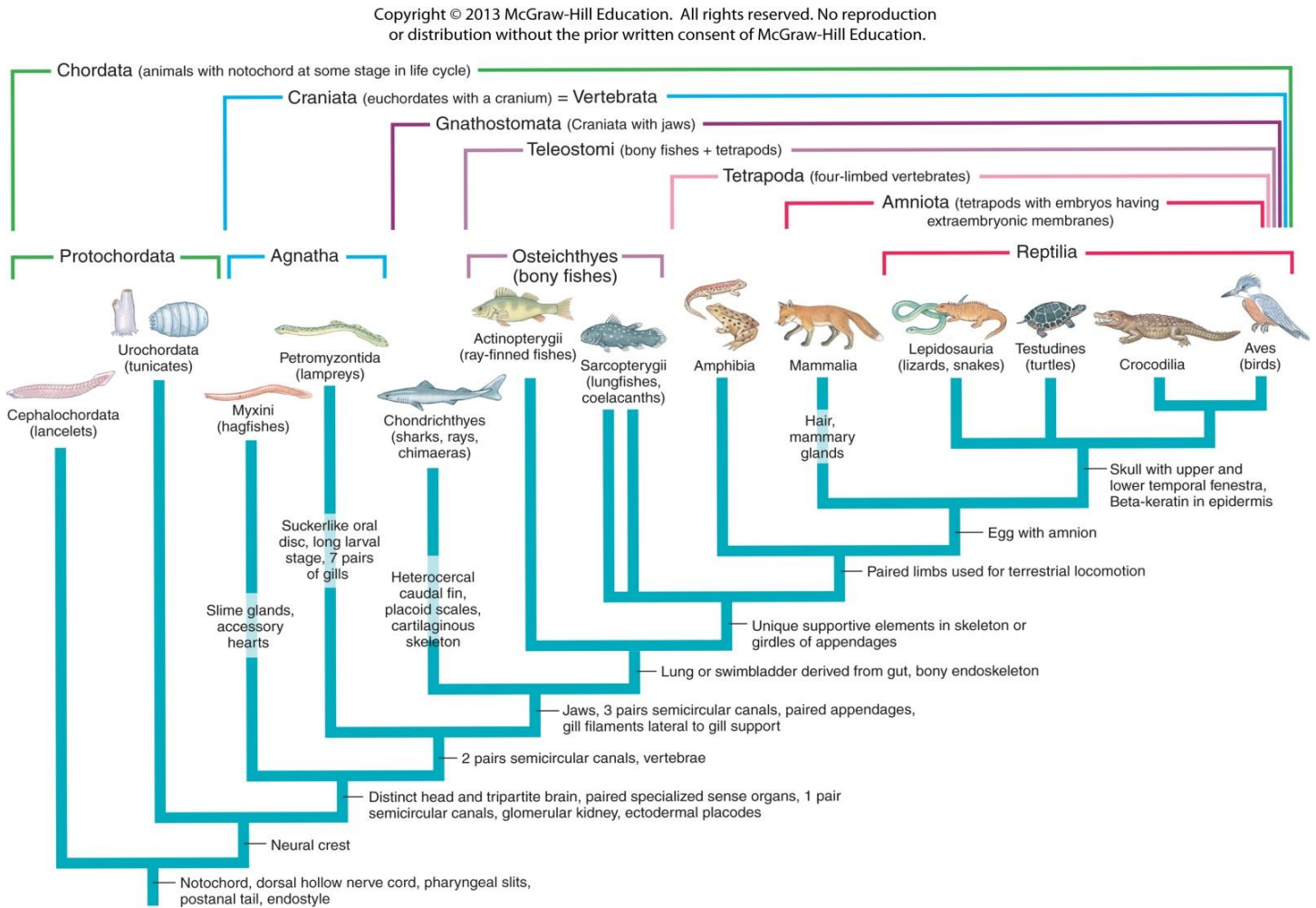
Pharyngeal slits are openings that lead from the pharyngeal cavity to the outside. They are formed when pharyngeal grooves and pharyngeal pouches meet to form an opening. In tetrapods, the pharyngeal pouches give rise to the Eustachian tube, middle ear cavity, tonsils, and parathyroid glands. The perforated pharynx evolved as a **filter feeding apparatus**. Later, they were modified into **internal gills** used for respiration.

4. Endostyle or Thyroid Gland

The endostyle in the pharyngeal floor secretes mucus that traps food particles. Found in protochordates and lamprey larvae. Secretes iodinated proteins. Homologous to the iodinated-hormone-secreting thyroid gland in adult lampreys and other vertebrates.

5. Postanal Tail

The postanal tail, along with somatic musculature and the stiffening notochord, provides motility in larval tunicates and amphioxus. Evolved for propulsion in water. Reduced to the coccyx (tail bone) in humans.



28 reptiles and birds.

- Vertebrate
- Feathers
- Wings (but not all fly)
- Scale-covered legs
- Homoeothermic (keeps their body temperature at one temperature)
- Endothermic (warm blooded)

Designed for flying

- Ornithologist – zoologists that study birds

The following characteristics equip birds for flying:

- Compact, lightweight, and very strong skeleton
- Lightweight beaks and skulls.
- A nearly rigid backbone that gives a solid support for the strenuous muscle activity required for flying
- Hollow spaces in the skeleton that provide room for air sacs, which contribute to the efficiency of the respiratory system and make the bird lighter.
- Bipedal (“two-footed”) anatomy, which leaves the wings free for flying.
- A prominent ridge, or keel, on the breastbone to allow for the attachment of flight muscles by strong tendons.
- Three bones in the shoulder to support each wing.
- An efficient circulatory system, including a four-chambered heart.
- Powerful muscles to power the wings during flight.
- Three toes pointing forward and one toe pointing backward.
- Leg has a special design that allows the bird to stay on their perch even if they are sleeping.

Perching Birds

Leg has a special design that allows the bird to stay on their perch even if they are sleeping.

- Thrushes
- Robins
- Bluebird
- Goldfinch
- House sparrow
- Humming bird
- Woodpecker

Birds of Prey

Especially acute eyesight they have sharp, powerful talons (grasping and killing their prey)

- Hooked beak
- Vultures
- California condor
- Sea eagle
- Bald eagle
- Golden eagle
- Hawks
- Osprey
- Falcons
- Owls

Swimming and Wading Birds

Many have water repellent feathers they have webbed or lobed feet for swimming. Some birds have very long legs designed for wading

- Ducks
- Geese
- Storks
- Herons
- Flamingos
- Cranes
- Egrets

Game Birds

Have been hunted for food and sport. Large flight muscles (breast meat) allow them to burst into flight

- Quail
- Pheasant
- Partridge
- Grouse
- Doves
- Turkey

Tropical Birds and Flightless Birds

1. Tropical Birds

Live in the world's tropical forests, brightly colored and many have large unusual beaks

- Parakeets
- Toucans
- Macaw

2. Flightless birds

Have wings or wing-like structures. Usually equipped with powerful legs for running

- Ostrich
- Emu
- Kiwi
- Penguins

Extinct birds:

Some became extinct because of the pressures put on their habitat. Some have been extinct for thousands of years

- Dodo
- Moa
- Great auk
- Passenger pigeon
- Archaeopteryx
- Diatryma

Class Reptilia

Reptiles are tetrapod (four-limbed vertebrate) animals in the class reptilia, comprising today's turtles, crocodilians, snakes, amphisbaenians, lizards, tuatara, and their extinct relatives. The study of these traditional reptile orders, historically combined with that of modern amphibians, is called herpetology.

- Order chelonia
- Order crocodilia
- Order squamata
- Order rhynchocephalia

Order Chelonia

Turtles and tortoises

Shell consists of fused bony plates: Carapace (dorsal, top) and Plastron (ventral, lower).

Earliest fossils dated to 200 m.Y.A. 250 species worldwide, Variety of habitats, Most species ribs and spine fused to inner surface of carapace, Pelvic and pectoral girdles lie within the ribs, Sharp beak instead of teeth, Shell and limbs reflect habitat

Order Crocodilia

This includes Crocodiles, alligators, caimans, and gavial. Most closely related to dinosaurs. Heavy bodied, mostly aquatic. Carnivorous

Order Squamata

Lizards and snakes

- Upper jaw is loosely joined to the skull.
- Jacobson's organ

Lizards

Only 2 species venomous

- Gila monster
- Bearded lizard
- Autotomy
- Snakes

Backbone of 100 – 400 vertebrates

- Pair of ribs attached to each vertebra

Seize and swallow prey

Constrictors

Venom

- Fangs back of mouth
- Elapid, inject poison through fixed fangs in front
- Vipers, inject venom using large mobile fangs

Order Rhynchocephalia

Ancient order inhabit few small islands of new Zealand. 24 inches in length. Spiny crest that runs down the animal's back. Tolerate cool temp, burrow during day and hunt at night.

29 Plant biodiversity

Gymnosperm- naked seeds,

Angiosperms- flowering plants

Plant biodiversity, vital to ecosystems, food crops, and medicine production, is threatened by habitat destruction and species extinction. Plant biodiversity is invaluable because it balances ecosystems, protects watersheds, mitigates erosion, moderates climate, and provides shelter for animals. Threats to plant biodiversity include the increasing human population, pollution, deforestation, and species extinction. Plant extinction is progressing at an alarming rate; this, in turn, affects other species, which also become extinct because they depend on the delicate ecological balance. Efforts to preserve plant biodiversity currently include heirloom seed collections and barcoding DNA analysis.

Biodiversity of Plants

Heirloom seed

Seeds which are not of agricultural importance yet hold traditional importance; these seeds are kept in seed banks and are still maintained by some gardeners and farmers

Barcoding

A taxonomic method that uses a short genetic marker in an organism's DNA to identify it as belonging to a particular species

Biodiversity

The diversity (number and variety of species) of plant and animal life within a region

Threats to Plant Biodiversity

1. Plants play a key role in ecosystems. They are a source of food and medicinal compounds while also providing raw materials for many industries. Rapid deforestation and industrialization, however, threaten plant biodiversity. In turn, this threatens the ecosystem.
2. Biodiversity of plants ensures a resource for new food crops and medicines. Plant life balances ecosystems, protects watersheds, mitigates erosion, moderates climate, and provides shelter for many animal species.
3. The explosion of the human population, especially in tropical countries where birth rates are highest and economic development is in full swing, is leading to human encroachment into forested areas. To feed the larger population, humans need to obtain arable land which leads to massive clearing of trees. The need

for more energy to power larger cities and economic growth results in the construction of dams, the consequent flooding of ecosystems, and increased emissions of pollutants. Other threats to tropical forests come from poachers who log trees for their precious wood. Ebony and Brazilian rosewood, both on the endangered list, are examples of tree species driven almost to extinction by indiscriminate logging.

4. The number of plant species becoming extinct is increasing at an alarming rate. Because ecosystems are in a delicate balance and because seed plants maintain close symbiotic relationships with animals, whether predators or pollinators, the disappearance of a single plant can lead to the extinction of connected animal species. A real and pressing issue is that many plant species have not yet been cataloged; their place in the ecosystem is unknown. These unknown species are threatened by logging, habitat destruction, and loss of pollinators.

They may become extinct before we have the chance to begin to understand the possible impacts resulting from their disappearance. Efforts to preserve biodiversity take several lines of action, from preserving heirloom seeds to barcoding species. Heirloom seeds come from plants that were traditionally grown in human populations, as opposed to the seeds used for large-scale agricultural production. Barcoding is a technique in which one or more short gene sequences, taken from a well-characterized portion of the genome, are used to identify a species through DNA analysis.

30 History of Biodiversity

Biodiversity is the result of 3.5 billion years of evolution. The origin of life has not been definitely established by science, however some evidence suggests that life may already have been well-established only a few hundred million years after the formation of the earth. Until approximately 600 million years ago, all life consisted of

- Archaea
- Bacteria
- Protozoans and similar single-celled organisms

Historical Milestones of Biodiversity

- The history of biodiversity during the phanerozoic (the last 540 million years), starts with rapid growth during the cambrian explosion—a period during which nearly every phylum of multicellular organisms first appeared. Over the next 400 million years or so, invertebrate diversity showed little overall trend and vertebrate diversity shows an overall exponential trend.
- This dramatic rise in diversity was marked by periodic, massive losses of diversity classified as mass extinction events. A significant loss occurred when rainforests collapsed in the carboniferous.
- The worst was the permian-triassic extinction event, 251 million years ago.
- Vertebrates took 30 million years to recover from this event.
- The fossil record suggests that the last few million years featured the greatest biodiversity in history.
- However, not all scientists support this view, since there is uncertainty as to how strongly the fossil record is biased by the greater availability and preservation of recent geologic sections
- Some scientists believe that corrected for sampling artefacts, modern biodiversity may not be much different from biodiversity 300 million years ago., Whereas others consider the fossil record reasonably reflective of the diversification of life.
 - Estimates of the present global macroscopic species diversity vary from 2 million to 100 million, with a best estimate of somewhere near 9 million, the vast majority arthropods. Diversity appears to increase continually in the absence of natural selection.

31 Importance of Biodiversity

Biodiversity has a number of functions on the Earth.

These are as follows:

- Maintaining balance of the ecosystem:
- Recycling and storage of nutrients,
- combating pollution, and stabilizing climate, protecting water resources,
- forming and protecting soil and maintaining Eco-balance.
- Intrinsic value
- A philosophical concept of the value of something independent of its value to anyone or anything

Provision of biological resources

- Provision of medicines and pharmaceuticals, food for the human population and animals, ornamental plants, wood products, breeding stock and diversity of species, ecosystems and genes.
- Quinine is a drug used for the treatment of malaria which is obtained from the Cinchona genus of plants.

Social benefits:

Recreation and tourism, cultural value and education and research. The role of biodiversity in the following areas will help make clear the importance of biodiversity in human life:

Biodiversity and food:

80% of human food supply comes from 20 kinds of plants. But humans use 40,000 species for food, clothing and shelter. Biodiversity provides for variety of foods for the planet.

Biodiversity and human health

The shortage of drinking water is expected to create a major global crisis. Biodiversity also plays an important role in drug discovery and medicinal resources. Medicines from nature account for usage by 80% of the world's population.

Biodiversity and industry

Biological sources provide many industrial materials. These include fiber, oil, dyes, rubber, water, timber, paper and food.

Biodiversity and culture

- Biodiversity enhances recreational activities like bird watching, fishing, trekking etc. It inspires musicians and artists.

32 Modern plant breeding

Modern facilities in molecular biology are now used in plant breeding.

Modern plant breeding may use techniques of molecular biology to select, or in the case of genetic modification, to insert, desirable traits into plants. Application of biotechnology or molecular biology is also known as molecular breeding.

Steps of plant breeding

The following are the major activities of plant breeding:

- Collection of variation
- Selection
- Evaluation
- Release
- Multiplication
- Distribution of the new variety
- Selling to people
- Marker assisted selection

Genetic modification

Transgenic plants

Genetic modification of plants is achieved by adding a specific gene or genes to a plant, or by knocking down a gene with RNAi, to produce a desirable phenotype. The plants resulting from adding a gene are often referred to as transgenic plants. If for genetic modification genes of the species or of a crossable plant are used under control of their native promoter, then they are called cisgenic plants. Sometimes genetic modification can produce a plant with the desired trait or traits faster than classical breeding because the majority of the plant's genome is not altered.

Traits improved by Transgenic techniques and breeding

- Water use efficiency
- Nutrient use efficiency (particularly nitrogen and phosphorus)
- Weed competitiveness
- Tolerance of mechanical weed control
- Pest/disease resistance
- Early maturity (as a mechanism for avoidance of particular stresses)
- Abiotic stress tolerance (i.e. drought, salinity, etc...)
- Addressing global food security through plant breeding
- Increased yield without expansion
- Breeding for increased nutritional value
 - Breeding for tolerance

33 Reasons for Loss of biodiversity

The earth's biodiversity is in grave danger In the present era, human beings are the most dangerous cause of destruction of the earth's biodiversity. In 2006, the terms threatened, endangered or rare were used to describe the status of many species. The "evil quartet" identified by Jared Diamond is overkill, habitat destruction, secondary extinctions and introduced species. Factors identified by Edward Wilson are described by the acronym- HIPPO standing for habitat destruction, climate change, invasive species, pollution, human overpopulation and overharvesting

Habitat destruction is a major cause for biodiversity

Habitat loss is caused by deforestation, overpopulation, pollution and global warming. Species which are physically large and those living in forests or oceans are more affected by habitat reduction. Some expert's estimate that around 30% of all species on earth will be extinct by 2050. According to the International Union for Conservation of Nature (IUCN), globally about one third of all known species are threatened with extinction. Even it is estimated that 25% of all mammals will be extinct within 20 years.

The whole system's balance is threatened

Fresh water ecosystems are nowadays the most threatened ecosystems. Invasive species refer to those that would normally remain constrained from an ecosystem because of the presence of natural barriers. Since these barriers are no longer existing, invasive species invade the ecosystem, destroying native species. Human activities have been the major cause for encouraging invasive species.

Effects on species

Species can also be threatened by genetic pollution- uncontrolled hybridization and gene swamping. For instance, abundant species can interbreed with rare species thus causing swamping of the gene pool. Over exploitation is caused by activities such as over fishing, over hunting, excessive logging and illegal trade of wildlife. Over 25% of global fisheries are being overfished at unsustainable levels.

Global warming

Global warming is also becoming a major cause for loss of biodiversity. For example if the present rate of global warming continues, coral reefs which are biodiversity hotspots will disappear in 20-40 years. 10% of all species might become extinct by 2015, if global warming continues.

Point to ponder

biodiversity which is crucial for the wellbeing of life on earth, is coming under the threat of many factors related to human activities. There is an urgent need to take action to protect the magnificent biodiversity of our planet. We must create economic policies in order to maintain the Earth's biodiversity and take appropriate measures to protect habitats and species

34 Plant conservation

Consequences of deforestation

The consequences of deforestation are

- Increase in the temperature and pollution level on the earth.
- Increase in the level of carbon dioxide in the atmosphere leading to global warming.

- Lowering of ground water level.
- Disturbs the balance in nature.
- Decrease in rainfall leading to draught.
- Soil erosion and decrease in soil fertility leading to desertification.
- Decrease in the water holding capacity of soil leading to floods

Conservation of forest and wildlife

- Forest and wildlife can be conserved by setting up areas like Biosphere reserves Wildlife sanctuaries, National parks, etc.

Biosphere reserves: - are large areas of protected land for conservation of biodiversity and the traditional life of the tribals living there.

National parks: - are areas reserved for wildlife where they can freely use the habitats and natural resources.

Wildlife sanctuaries: - are areas where animals are protected from any disturbance to them or their habitat.

• **Biosphere Reserve**

Biosphere reserves are large areas of protected land for conservation of biodiversity and the traditional life of the tribes living there.

Biodiversity is the variety of plants, animals and microorganisms found in the area.

• **Flora and fauna**

- **Flora** are the plants found in a particular area.
- **Fauna** are the animals found in a particular area.

Endemic species are those species of plants and animals found only in a particular area and not found anywhere else.

• **National parks**

National parks are areas reserved for wildlife where they can freely use the habitats and natural resources. Eg Ayubia National Park is the first Reserve Forest in Pakistan.

Reforestation

Reforestation is the restocking of destroyed forests by planting new trees. We should plant at least as many trees as we cut. We have already caused a lot of damage to our forests. If we have to regain our green wealth, reforestation is the only option.

35 Plant breeding and Improvement

- Plant breeding is the art and science of changing the traits of plants in order to produce desired characteristics. Plant breeding can be accomplished through many different techniques ranging from simply selecting plants with desirable characteristics for propagation, to methods that make use of knowledge of genetics and chromosomes, to more complex molecular techniques.
- Plant breeding has been practiced for thousands of years, since near the beginning of human civilization. It is practiced worldwide by individuals such as gardeners and farmers, or by professional plant breeders employed by organizations such as government institutions, universities, crop-specific industry associations or research centres.
- International development nation agencies believe that breeding new crops is important for ensuring food security by developing new varieties that are higheryielding, disease resistant, drought-resistant or regionally adapted to different environments and growing conditions

History of plant breeding

- Plant breeding started with sedentary agriculture and particularly the domestication of the first agricultural plants, a practice which is estimated to date back 9,000 to 11,000 years. Initially early farmers simply selected food plants with particular desirable characteristics, and employed these as progenitors for subsequent generations, resulting in an accumulation of valuable traits over time. Modern bread wheat is a mixture of recombined genes from three different wild species.

- Gregor Mendel's experiments with plant hybridization led to his establishing laws of inheritance. Once this work became well known, it formed the basis of the new science of genetics, which stimulated research by many plant scientists dedicated to improving crop production through plant breeding
- Modern plant breeding is applied genetics, but its scientific basis is broader, covering molecular biology, cytology, systematics, physiology, pathology, entomology, chemistry, and statistics (biometrics). It has also developed its own technology.

Classical plant breeding

- One major technique of plant breeding is selection, the process of selectively propagating plants with desirable characteristics and eliminating or "culling" those with less desirable characteristics.
- Deliberate interbreeding (crossing) of closely or distantly related individuals to produce new crop varieties or lines with desirable properties. Plants are crossbred to introduce traits/genes from one variety or line into a new genetic background. For example, a mildew-resistant pea may be crossed with a high-yielding but susceptible pea, the goal of the cross being to introduce mildew resistance without losing the high-yield characteristics
- Classical breeding relies largely on homologous recombination between chromosomes to generate genetic diversity. The classical plant breeder may also make use of a number of in vitro techniques such as protoplast fusion, embryo rescue or mutagenesis (see below) to generate diversity and produce hybrid plants that would not exist in nature.

Traits that breeders have tried to incorporate into crop plants include:

- Improved quality, such as increased nutrition, improved flavor, or greater beauty
- Increased yield of the crop
- Increased tolerance of environmental pressures (salinity, extreme temperature, drought)
- Resistance to viruses, fungi and bacteria
- Increased tolerance to insect pests
- Increased tolerance of herbicides
- Longer storage period for the harvested crop

36 Genetic Diversity in Ecosystem Management

What is genetic diversity?

- Genetic diversity is the variation at the level of
 - individual genes,
 - In a population,

Genetic diversity, means that the population contains most of the possible alleles for each particular gene locus. Provides a mechanism for populations to adapt to their changing environment. The more variation, the better the chance that at least some of the individuals will have an allelic variant that is suited for the new environment, and will produce offspring with the variant that will in turn reproduce and continue the population into subsequent generations.

Why study genetics in Ecosystem Management

- Loss of genetic diversity can imply lack of evolution and premature extinction.
- Fitness decreases with reduced genetic variation.
- Populations of endangered species are small and tend to lose genetic diversity.
- When genetic variation disappears the basis for life on earth becomes impoverished

Some useful definitions

- Locus: physical location of a gene.
- Allele: one of the genes at a particular locus.
- Homozygous: two of the same alleles at a given locus.
- Heterozygous: two different alleles at a given locus.

- Fitness: contribution of an individual's genotype to the next generation

Levels of genetic diversity

- Within individuals,
- Among individuals within the same population, Among populations
- Among Population

Within individuals,

Every diploid organism has duplicated genetic information (from its mother and father, It is the same type of information (locus) but the specific forms may differ (alleles)

Among individuals within a population,

Different individuals carry different genetic information, The sum of the variation of an interbreeding population is called **Gene pool**

Among populations,

- Different gene pools among populations.

Isolation is an important factor responsible for among population genetic diversity (natural or man made barriers).

Can lead to

- local adaptation,
- Natural local adaptation: Example of mistletoe species in Argentina and Chile,
- Ultimate effect of among population variability: Speciation

Heterozygosity

- In an individual organism, is the state of possessing different alleles at a given locus in regard to a given character,
- At the population level: "The fraction of individuals in a population that are heterozygous for a specific locus",
 - Often positively correlated with fitness,
 - Often positively correlated with population size (declines in small populations),
- When an organism is referred to as a heterozygote, or being heterozygous for a specific gene, it means that the organism carries two different versions of that gene on the two corresponding chromosomes.
- Heterozygosity refers to both the state of being a heterozygote, but more commonly in population genetics to the fraction of individuals in a population that are heterozygous for that locus.

Loss of genetic diversity

Two ways of losing it

Loss of genetic diversity in small populations,

- Changes in the natural distribution of genetic diversity among populations (artificial isolation and mixing)
- Population size critical factor,
- Census population size (N_c) vs. Effective population size (N_e), Usually N_e is much smaller than N_c (10 to 30%)

Four factors responsible for genetic diversity loss in small populations :

- Genetic drift,
- Founder effect,
- Demographic bottleneck,
- Inbreeding

– Genetic drift

- " Random change in gene frequency within a population" (Meffe et al.),

- Not necessarily adaptive, Stronger in small populations

– **Founder effect,**

"The establishment of a new population by a few original founders which carry only a small fraction of the total genetic variation of the parental population." (Ernst Mayr), Alleles may be lost, Differentiation from the parental population, Example: Irish Potato Famine

– **Demographic bottleneck,**

Population suffers reduction in size and then recovers, Random losses of genetic diversity, Usually associated with catastrophic events or diseases, Genetic variation doesn't rebound from a decrease as quickly as population size.

– **Inbreeding**

Inbreeding is breeding between close relatives. Leads to a reduction in genetic diversity (inbreeding depression: reduced health and fitness). The primary problem with inbreeding is that two closely related individuals are likely to have very similar genomes, and if one individual has a gene for a given negative trait, then the other is likely to have it as well., Inbreeding increases homozygosity (therefore decreases heterozygosity)

The other way to loss genetic diversity

- Changes in the natural distribution of genetic diversity among populations
- Related with the geographical distribution of the species and therefore with landscape management issues
- Artificial isolation
- Avoids genetic flux among populations due to barriers such as highways, dams, etc
- Artificial mixing Enhances genetic flux among populations where that flux was not possible due to natural barriers (examples: bridges, tunnels)

Allelic richness

- Allelic richness Is the number of alleles in a sample (population),
- Rare alleles are important during extreme environmental events,
- Loss of allelic richness is perhaps more serious than loss of quantitative variation because alleles are lost forever while quantitative variation can be recovered,
- Rare alleles are more important than their frequency in the population
- Example: Peppered moth and pollution in Manchester, Small sized populations are more prone to lose allelic richness

Usefulness of Ecosystem Management and Genetics in Conservation

Ecosystem Management and Genetics in Conservation Useful in

- Endangered small populations,
- Captive breeding,
- Translocation of individuals,
- Determining dispersal patterns,
- Recognize limitations and scale of application, I

It's easy to lose the sight of the larger picture and try to apply a genetics approach when it is not appropriate to do so.

Conclusion

Ecosystem Management and Genetics in Conservation is Very powerful tool usually useful to solve specific problems. Rarely useful if it is not combined with other type of approaches

37 in situ and ex situ conservation

- **In situ**

Conservation of species in their natural habitat E.g. natural parks, nature reserves

- **Ex situ:**

Conserving species in isolation of their natural habitat E.g. zoos, botanical gardens, seed banks

- **In situ conservation**

Setting up wild life reserves is not just a matter of building a fence around an area and letting it grow “wild”

Nature reserves and national parks

- First the area that is suitable for the creation of a reserve has to be identified and delimited. □ This requires surveys to collect data on key species. Property may have to be expropriated.
- A legal framework may need to be set up to control human activities in the area and in its immediate surroundings
- Policing the area may also be necessary o If part of the area has been degraded due to bad land use it may need restoring o Alien species that have penetrated the area may need excluding or eliminating o Constant management will be needed to maintain the habitat of the species being conserved o This may mean arresting natural succession

The advantages of in situ conservation

- The species will have all the resources that it is adapted too
- The species will continue to evolve in their environment
- The species have more space
- Bigger breeding populations can be kept
- It is cheaper to keep an organism in its natural habitat

However there are problems

- It is difficult to control illegal exploitation (e.g. poaching)
- The environment may need restoring and alien species are difficult to control

Ex situ conservation Captive breeding

- The Hawaiian goose was practically extinct in the wild
- 12 birds were taken into captivity
- A population of 9000 was released back into the wild
- The experiment failed because the original cause rats had not been eliminated.
- The rats eat the eggs and the nestlings of the geese

Pere David's deer success or failure?

- Pere David's deer was a native species of China
- In 1865 18 were taken into zoological collections
- Meanwhile it became extinct in the wild
- By 1981 there were 994 individuals scattered through zoological collections

Ex situ conservation

- Captive breeding of endangered species is a last resort
- These species have already reached the point where their populations would not recover in the wild
- It works well for species that are easily bred in captivity but more specialised animals are difficult to keep (aye aye)
- Isolated in captivity they do not evolve with their environment

Zoos: The land of the living dead?

- They have a very small gene pool in which to mix their genes
- Inbreeding is a serious problem

- Zoos and parks try to solve this by exchanging specimens or by artificial insemination where it is possible
- In vitro fertilisation and fostering by a closely related species has even been tried (Indian Guar – large species of cattle - cloned)
- Even if it is possible to restore a population in captivity the natural habitat may have disappeared in the wild
- Species that rely on this much help are often considered to be “the living dead”

Botanical gardens

- Botanical gardens show the same problems as captive breeding of animals
- Originally the role of botanical gardens was economic, pharmaceutical and aesthetic
- Their range of species collected was limited
- The distribution of botanical gardens reflects the distribution of colonial powers
- Most are found in Europe and North America
- But plant diversity is greatest in the tropics
- Botanical gardens show the same problems as captive breeding of animals

Seed banks

- Seeds can be maintained for decades or even centuries if the conditions are controlled • <5% humidity and –20°C
- Not all species are suited to this treatment
- Seeds need to be regularly germinated to renew stock or the seeds will eventually lose their viability
- Seed banks are at risk from power failure, natural disasters and war
- Duplicate stocks can be maintained
- Seeds kept in seed banks do not evolve with changes in the environment

International agencies

CITES (The Convention in International Trade in Endangered Species). Set up in 1988 to control and encourage the sustainable exploitation of species. The CITES conferences determine the status of a species and whether or not its exploitation requires regulation. Species are placed into different appendices depending on their status.

CITES Appendices

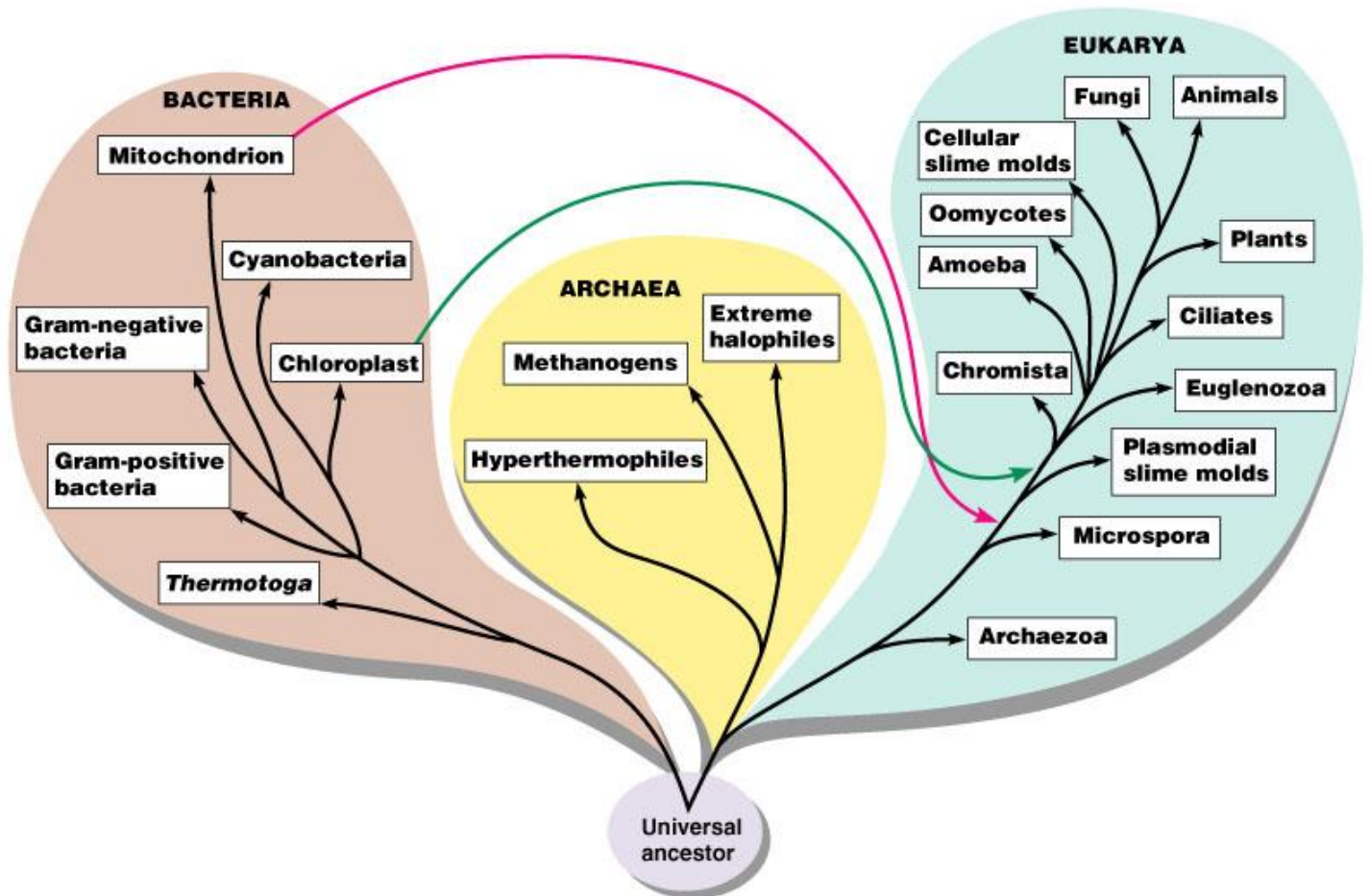
- Appendix 1: Total ban on exploitation
- Appendix 2: Limited exploitation subject to quotas
- Appendix 3: Species requiring protection in certain states only
- Species are reassessed every 2 years

WWF (World Wide Fund for Nature formerly World Wildlife Fund)

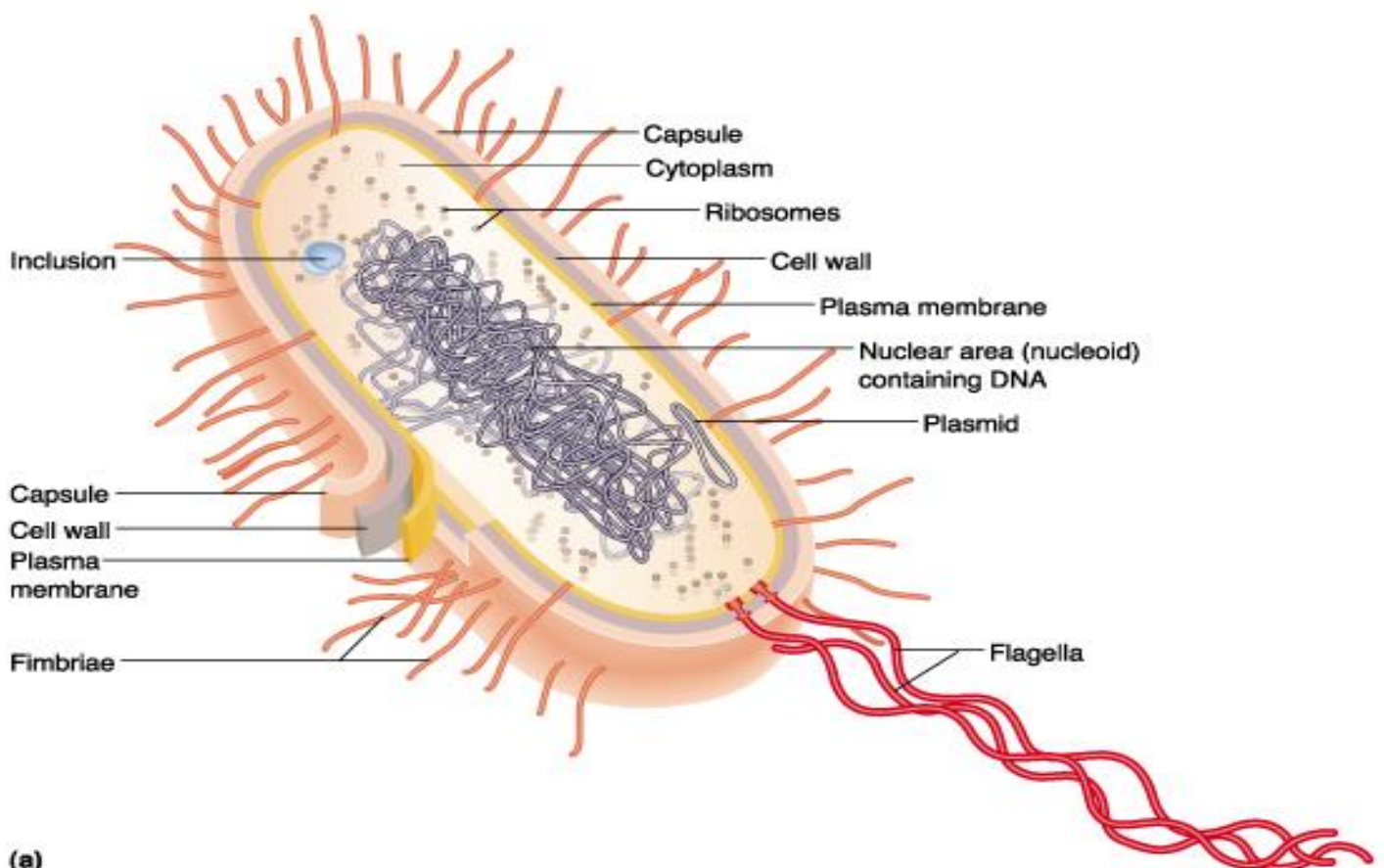
- Set up in 1961 as a non-governmental organisation
- Raises funds for conservation
- Lobbies parliaments for conservation
- Runs education programmes
- Provides advice to government conservation agencies
 - Raises awareness on conservation issues

38 Physiology of Microbial life

Phylogenetic Tree of Life (3 Domains)



Prokaryote “Anatomy” Overview

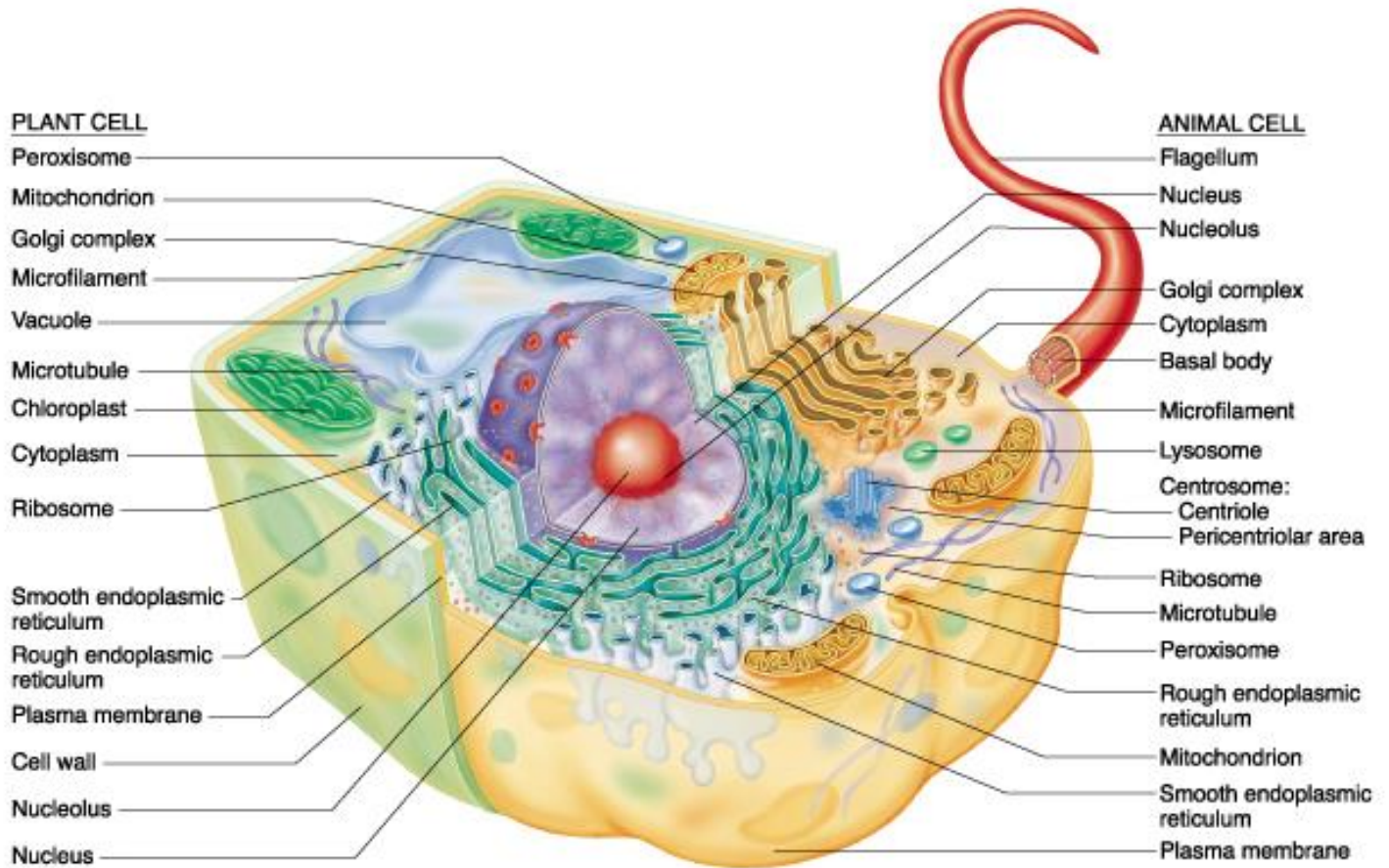


(a)

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Cell envelope: Collectively all the structures outside from the plasma membrane.

Eukaryote Cell “Anatomy”



(a) Highly schematic diagram of a composite eukaryotic cell, half plant and half animal
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Peroxisome: Oxidizes amino acids, fatty acids and alcohol; self replicating.

Vacuole: membrane bound; liquid filled; storage of reserves and/or wastes.

Cell Wall: cellulose and lignin in plants; chitin in fungi; no peptidoglycan

TABLE 10.1 | Some Characteristics of Archaea, Bacteria, and Eukarya

	Archaea	Bacteria	Eukarya
	 <i>Methanosarcina</i>	 <i>E. coli</i>	 <i>Amoeba</i>
Cell Type	Prokaryotic	Prokaryotic	Eukaryotic
Cell Wall	Varies in composition; contains no peptidoglycan	Contains peptidoglycan	Varies in composition; contains carbohydrates
Membrane Lipids	Composed of branched carbon chains attached to glycerol by ether linkage	Composed of straight carbon chains attached to glycerol by ester linkage	Composed of straight carbon chains attached to glycerol by ester linkage
First Amino Acid in Protein Synthesis	Methionine	Formylmethionine	Methionine
Antibiotic Sensitivity	No	Yes	No
rRNA Loop*	Lacking	Present	Lacking
Common Arm of tRNA†	Lacking	Present	Present

*Binds to ribosomal protein; found in all bacteria.
†A sequence of bases in tRNA found in all eukaryotes and bacteria: guanine-thymine-pseudouridine-cytosine-guanine.

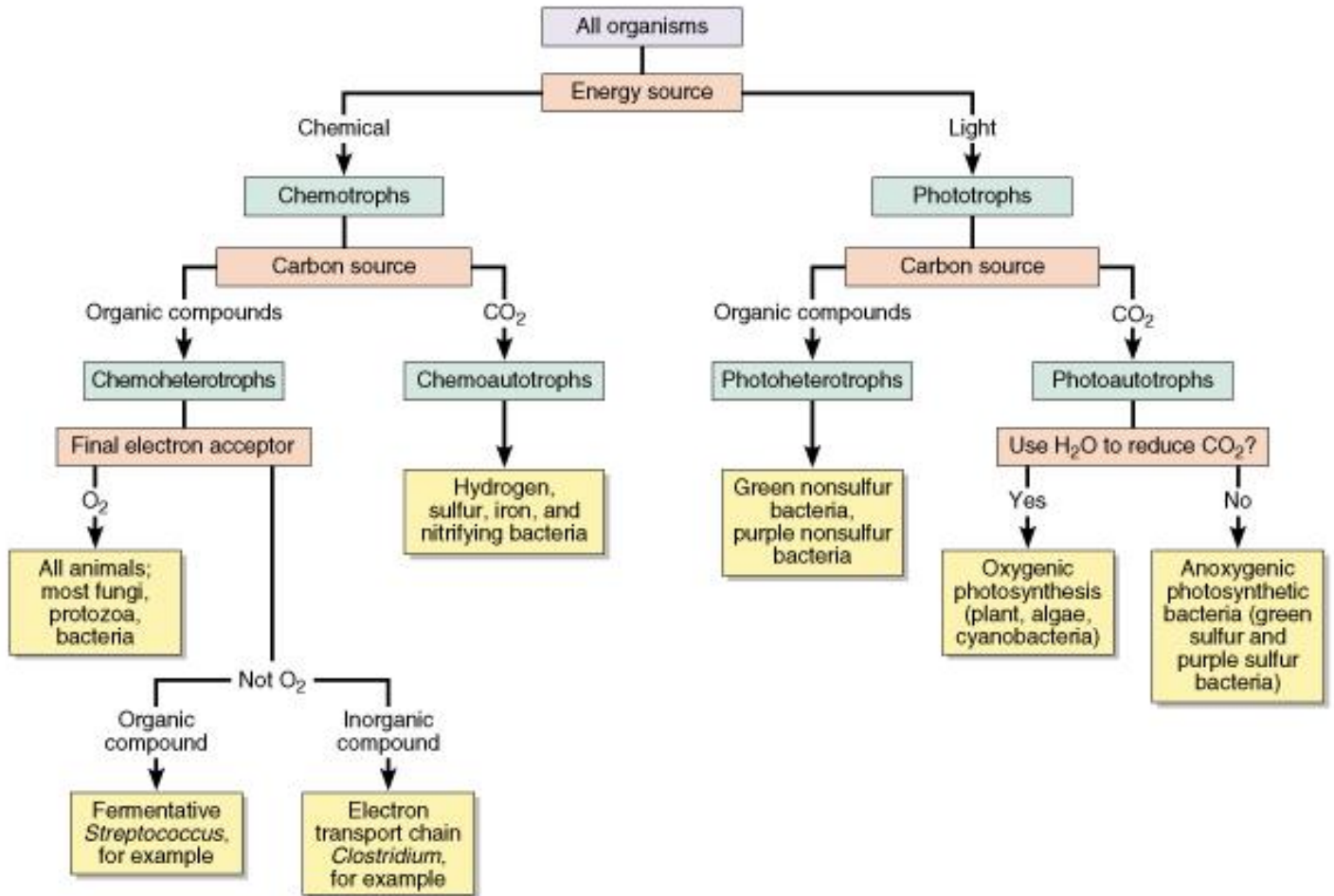
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Table 5.1 Sources of Carbon, Energy, and Electrons

Carbon Sources	
Autotrophs	CO ₂ sole or principal biosynthetic carbon source (<i>pp.</i> 207–8) ^a
Heterotrophs	Reduced, preformed, organic molecules from other organisms (<i>chapters 9 and 10</i>)
Energy Sources	
Phototrophs	Light (<i>pp.</i> 195–201)
Chemotrophs	Oxidation of organic or inorganic compounds (<i>chapter 9</i>)
Electron Sources	
Lithotrophs	Reduced inorganic molecules (<i>pp.</i> 193–94)
Organotrophs	Organic molecules (<i>chapter 9</i>)

^aFor each category, the location of material describing the participating metabolic pathways is given within the parentheses.

Nutritional Types



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What Lives Where and Why?

"Everything is everywhere, the environment selects"

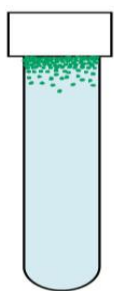
Martinus Beijerinck (ca. 1890)

- Tolerance to All Environmental Factors (Shelford's Law of Tolerance)
- Growth Limiting Resource (Liebig's Law of the Minimum)

Environmental Factors

- Nutrients (org/inorg; macro/micro/trace)
- Temperature
- Solute Concentration and Water Activity
- pH (acidity versus alkalinity)
- Oxygen Concentration
- Barometric Pressure
- Electromagnetic Radiation

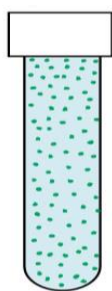
Oxygen Requirement Types



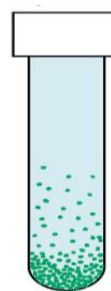
Obligate aerobe



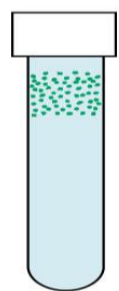
Facultative anaerobe



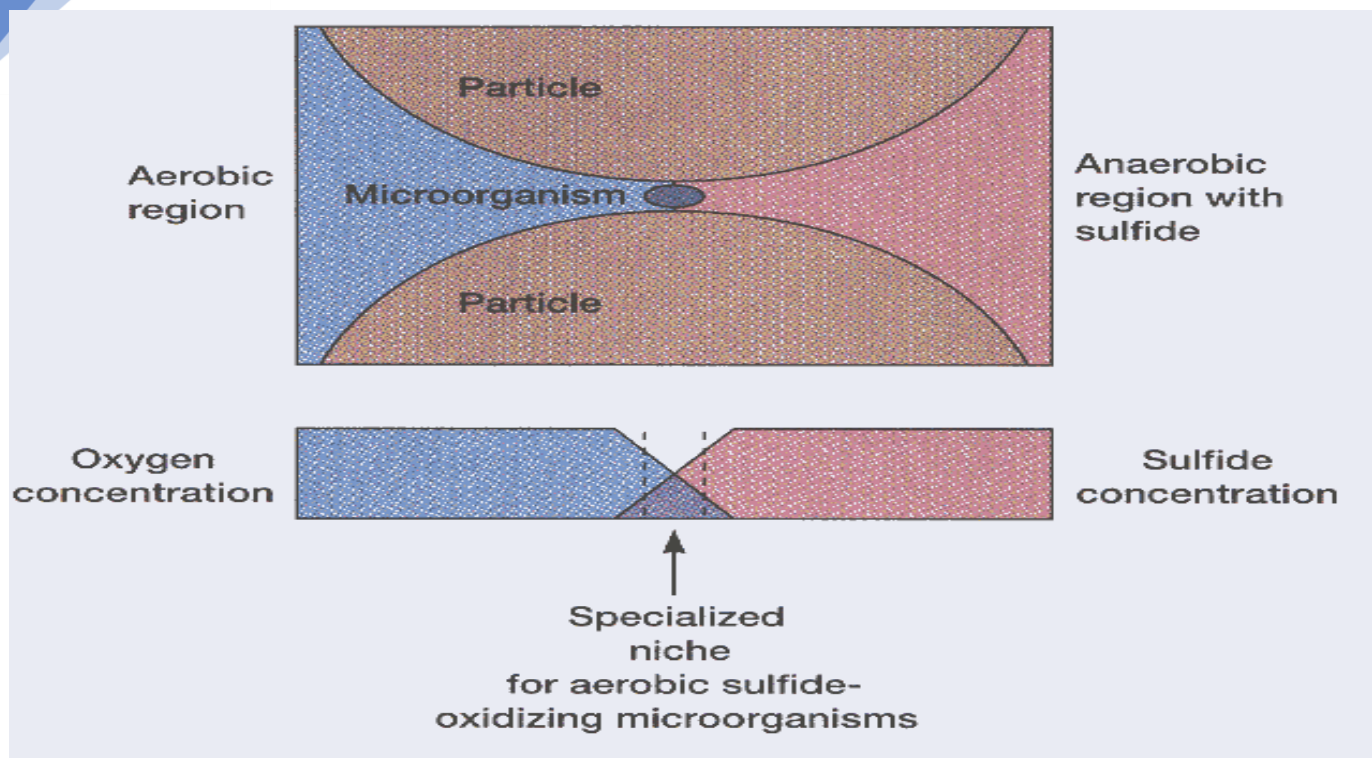
Aerotolerant anaerobe



Strict anaerobe



Microaerophile



Microbial interactions control populations, too

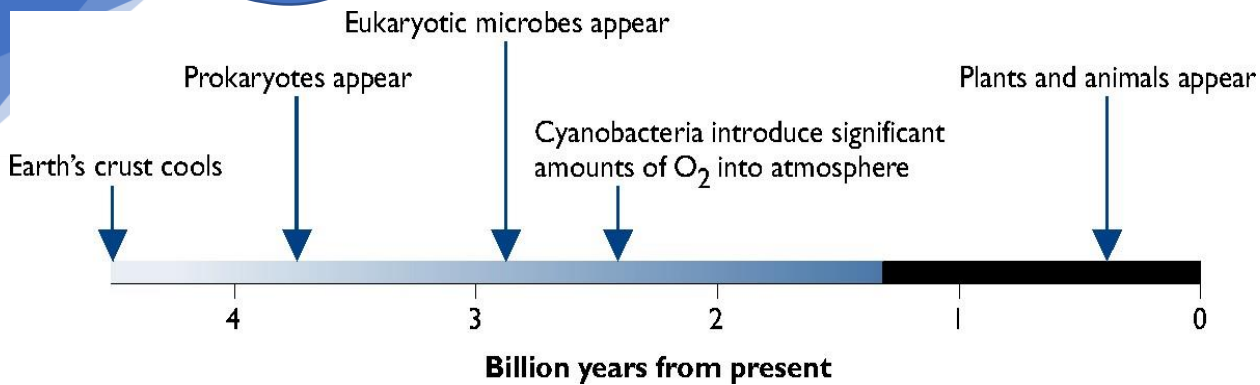
- **Positive interactions:**
 - Commensalism
 - Protocooperation
 - Mutualism
- **Negative Interactions:**
 - Amensalism:
 - Competition:
 - Intraspecific
 - Interspecific
 - Predation (e.g. *Bdellovibrio*)
 - Parasitism

Predation and Disease (Parasitism) Control Populations Too!

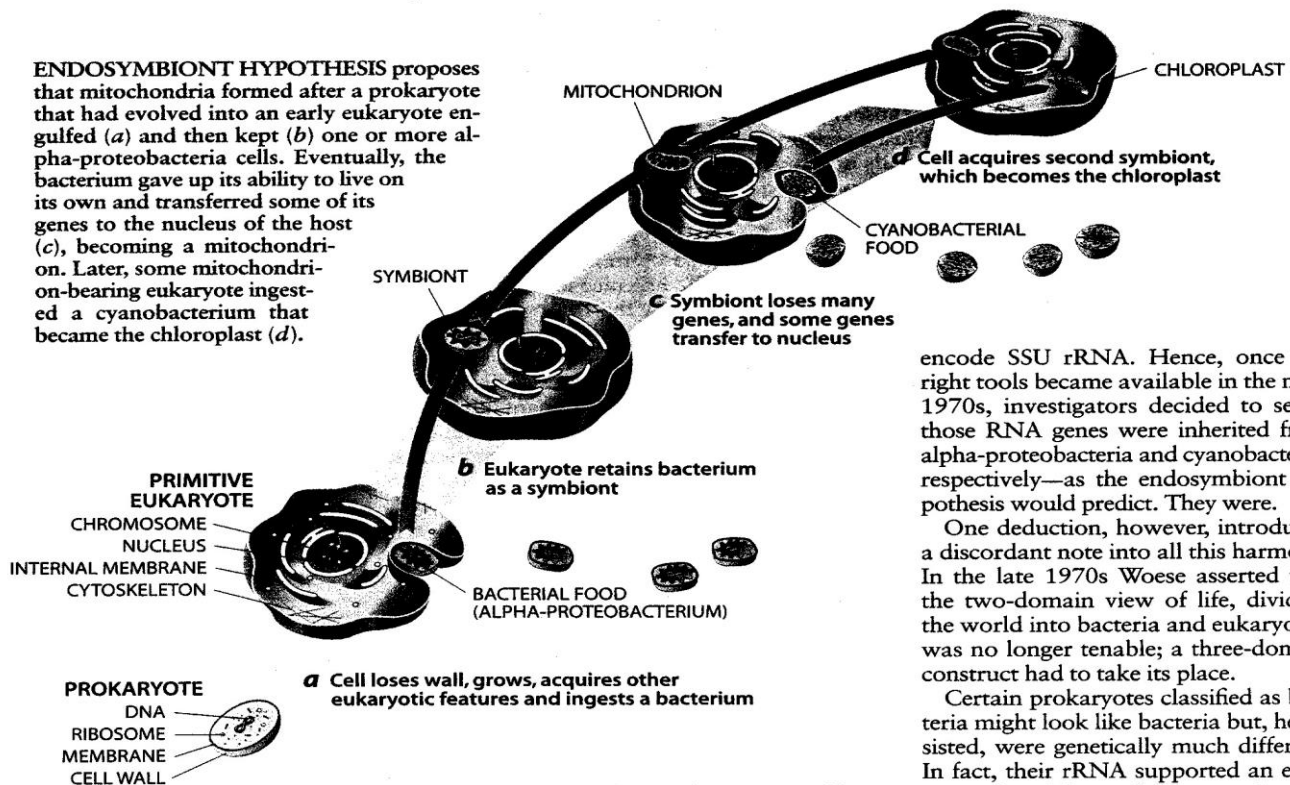
- Protozoa and other “grazers”
 - May be selective.
- Viral Lysis
 - Highly selective.

39 Evolution of Microbial Life

Over 3.5 billion years of “microbes”
 Micro-fossils of “cyanobacteria” and contemporary stromatolites.



ENDOSYMBIONT HYPOTHESIS proposes that mitochondria formed after a prokaryote engulfed (a) and then kept (b) one or more alpha-proteobacteria cells. Eventually, the bacterium gave up its ability to live on its own and transferred some of its genes to the nucleus of the host (c), becoming a mitochondrion. Later, some mitochondrion-bearing eukaryote ingested a cyanobacterium that became the chloroplast (d).



encode SSU rRNA. Hence, once the right tools became available in the mid-1970s, investigators decided to see if those RNA genes were inherited from alpha-proteobacteria and cyanobacteria, respectively—as the endosymbiont hypothesis would predict. They were.

One deduction, however, introduced a discordant note into all this harmony. In the late 1970s Woese asserted that the two-domain view of life, dividing the world into bacteria and eukaryotes, was no longer tenable; a three-domain construct had to take its place.

Certain prokaryotes classified as bacteria might look like bacteria but, he insisted, were genetically much different. In fact, their rRNA supported an early

Acquisition of aerobic respiration from alpha-proteobacterium.

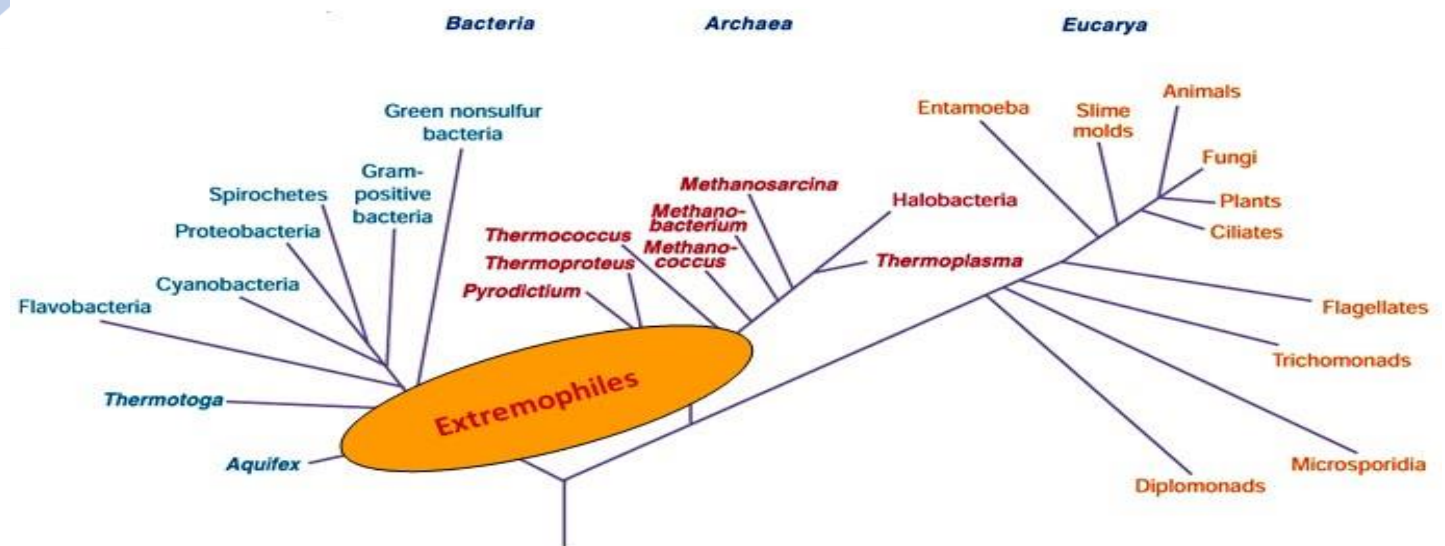
Acquisition of photosynthesis and Calvin Cycle from cyanobacterium.

• Happened more than once?

Major challenges for endosymbiotic theory

1. Most extant prokaryotes have rigid cell walls and don't do phagocytosis.
2. Hard to explain the nucleus (!) and flagella. (Eukaryotic flagella have a 9+2 arrangement of protein strands, vs. single strand for prokaryotic flagella.)

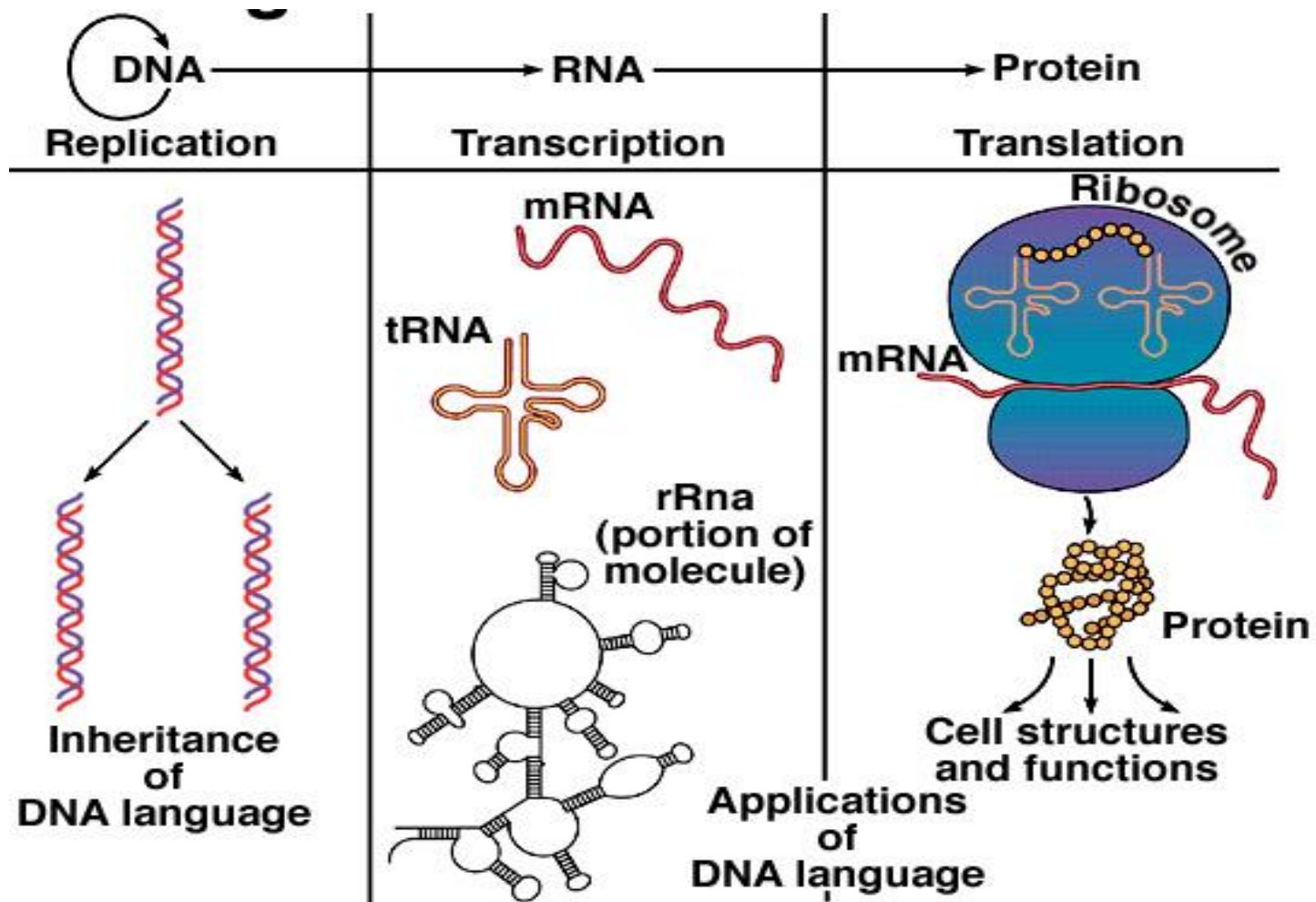
Phylogenetic Tree of Life:



Rooted Tree based on 16SrRNA and 18SrRNA sequence data.

All extant life has evolved; evidence lost by extinction.

How does evolution work? We need to consider the molecule processes!



Bacterial Genomes

Chromosomal Map

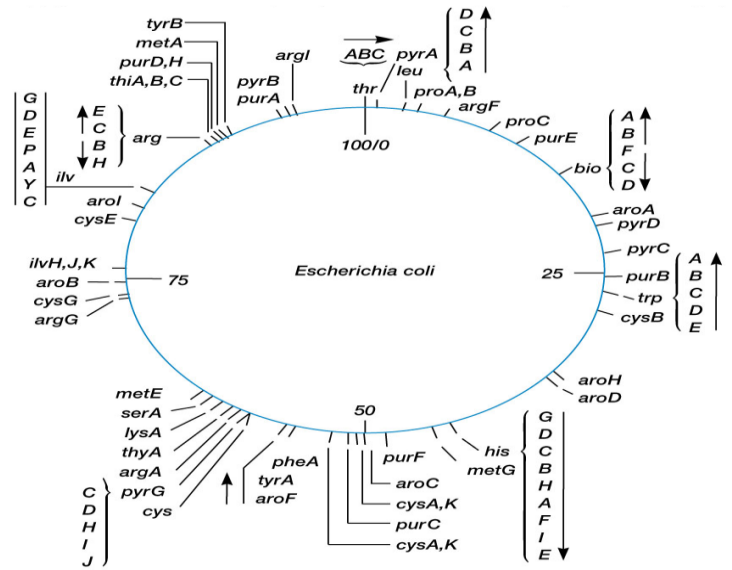
- Only structural genes versus splash map
- Mostly single chromosome
- Size: 1-5 Mbp
- Many complete sequences ([TIGR](https://www.tigr.org/))!

Plasmids:

- Size: 2-200 bp
- Conjugative or not
- Copy number varies
- Gene functions vary

Scope of Mutation:

- A mutation is any change in the proper nucleic acid sequence of a specific gene in a cell's genome. It may result from a single base pair mismatch during DNA replication.
- Mutation can create genetic diversity within a population; either beneficial, neutral, bad, or lethal.
- Mutation could result in a new phenotype that is advantageous to successful reproduction of the mutated individual; this depends on particular environmental conditions, called selective pressures.
- Such beneficial mutations stay within a population from generation to generation, and drive the evolution of that species.
- Bad or lethal mutations are often lost from a population over subsequent generations.



Mutation types:

– Macrolesions (large sequence sections)

- Deleted $a-b-c-d-e-f-g-h \rightarrow a-b-c-g-h$
- Inserted $a-b-c-d-e-f-g-h \rightarrow a-b-c-d-x-y-z-e-f-g-h$
- Inverted $a-b-c-d-e-f-g-h \rightarrow a-b-c-f-e-d-g-h$
- Duplicated $a-b-c-d-e-f-g-h \rightarrow a-b-c-d-e-f-d-e-f-g-h$

– Microlesions (1 or 2 bp alteration)

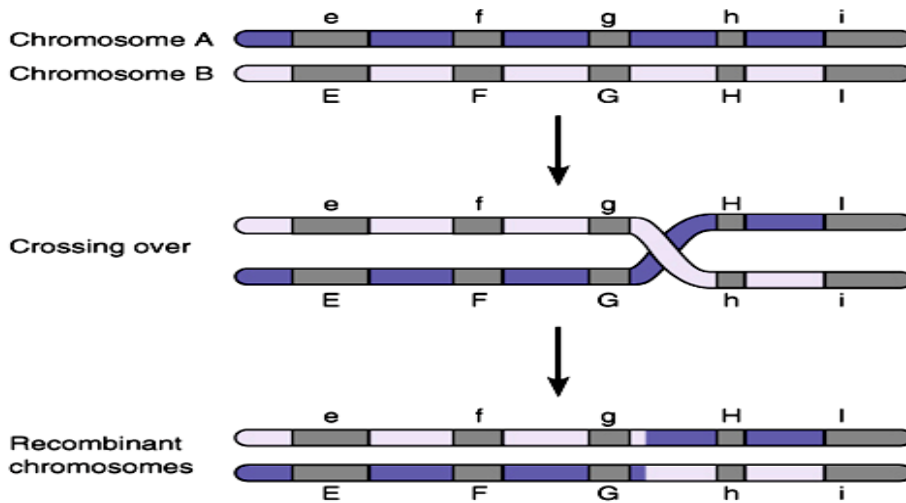
- Point Mutations (Base Substitutions) $ACTG \rightarrow ATTG$
- Frameshifts (Insertions or Deletions)
see the cat eat the rat $\rightarrow$ see thc ate att her at

– Mechanisms of microlesion mutation types

- Spontaneous (1 per million; most corrected; 1 per billion remain)
- Chemical mutagens
- Radiation as mutagens

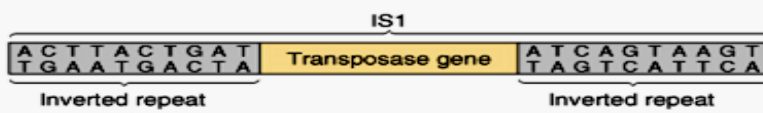
Genetic Recombination

- Two DNA molecules may recombine segments of their molecule in a process called crossing over.
- This is a relatively common event between chromosome copies in eukaryotes during meiosis. (Note the example here.)
- Prokaryote chromosomes, viral DNA, and smaller fragments of “foreign” DNA may recombine, adding new genes (or different alleles) to an individual cell.
- Bacteria can receive a foreign source of DNA for recombination through one of three different mechanisms of Genetic Exchange.

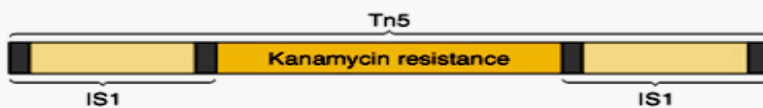


Transposable Elements: “Jumping Genes”

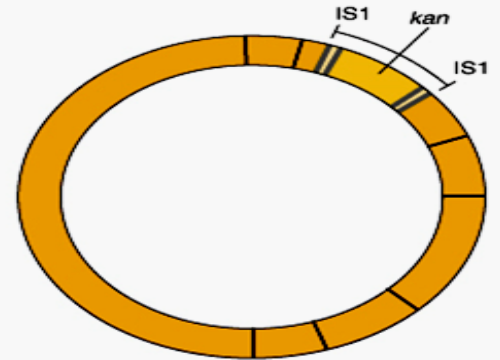
- Transposable elements (insertion sequences and transposons) can transfer copies of themselves to other DNA molecules (chromosome, plasmid, or viral DNA).
- Antibiotic resistance genes rapidly spread within and between bacterial populations by transposons carried on F factors called R plasmids.



(a) Insertion sequence “IS1”



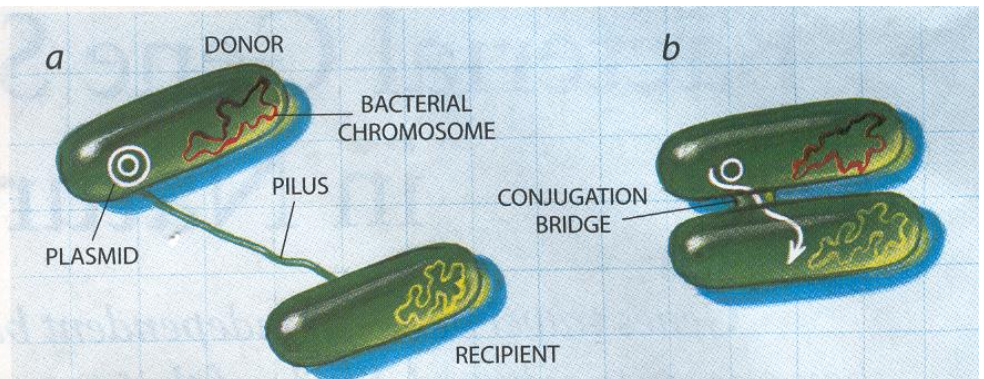
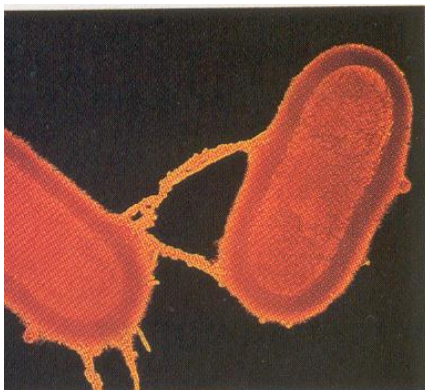
(b) Complex transposon “Tn5”

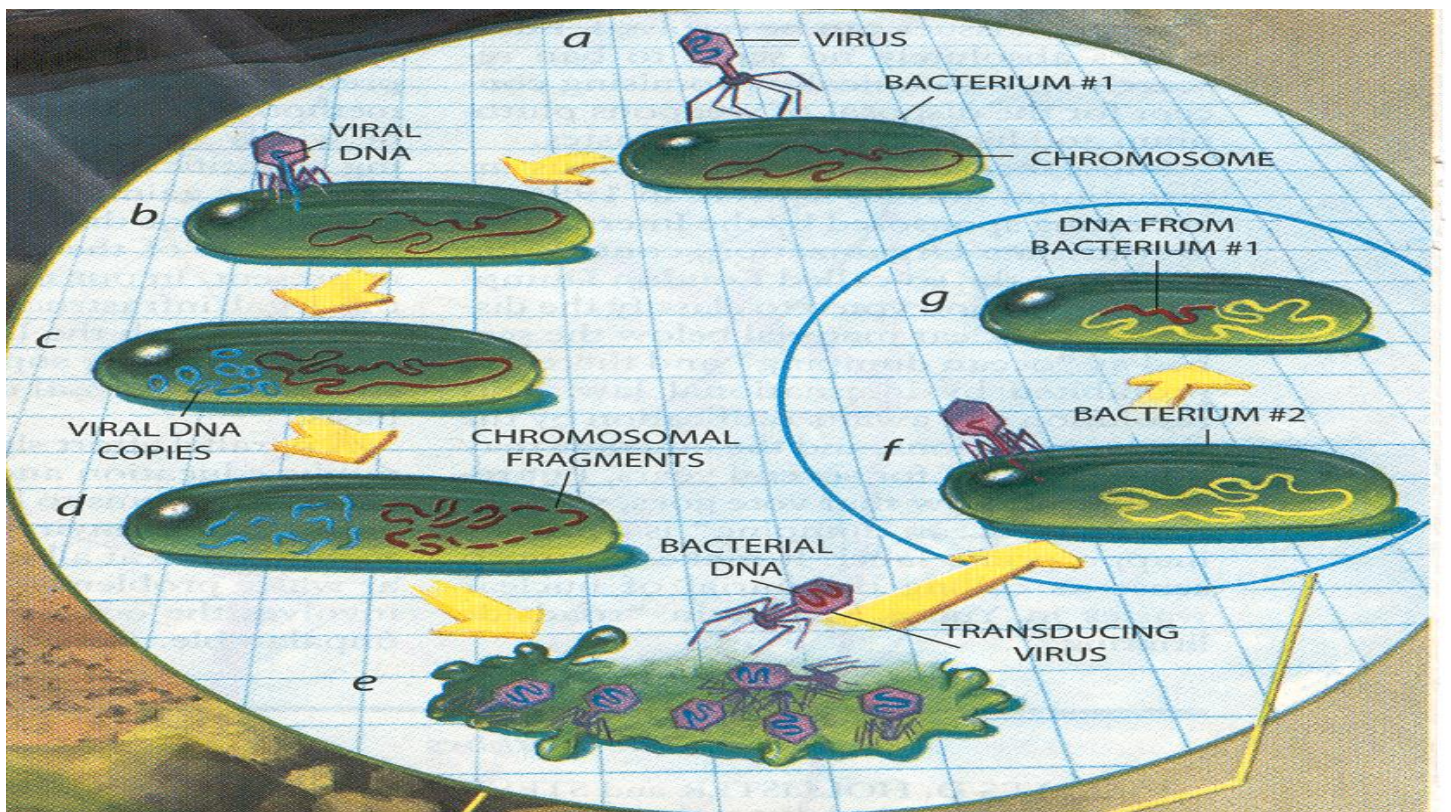
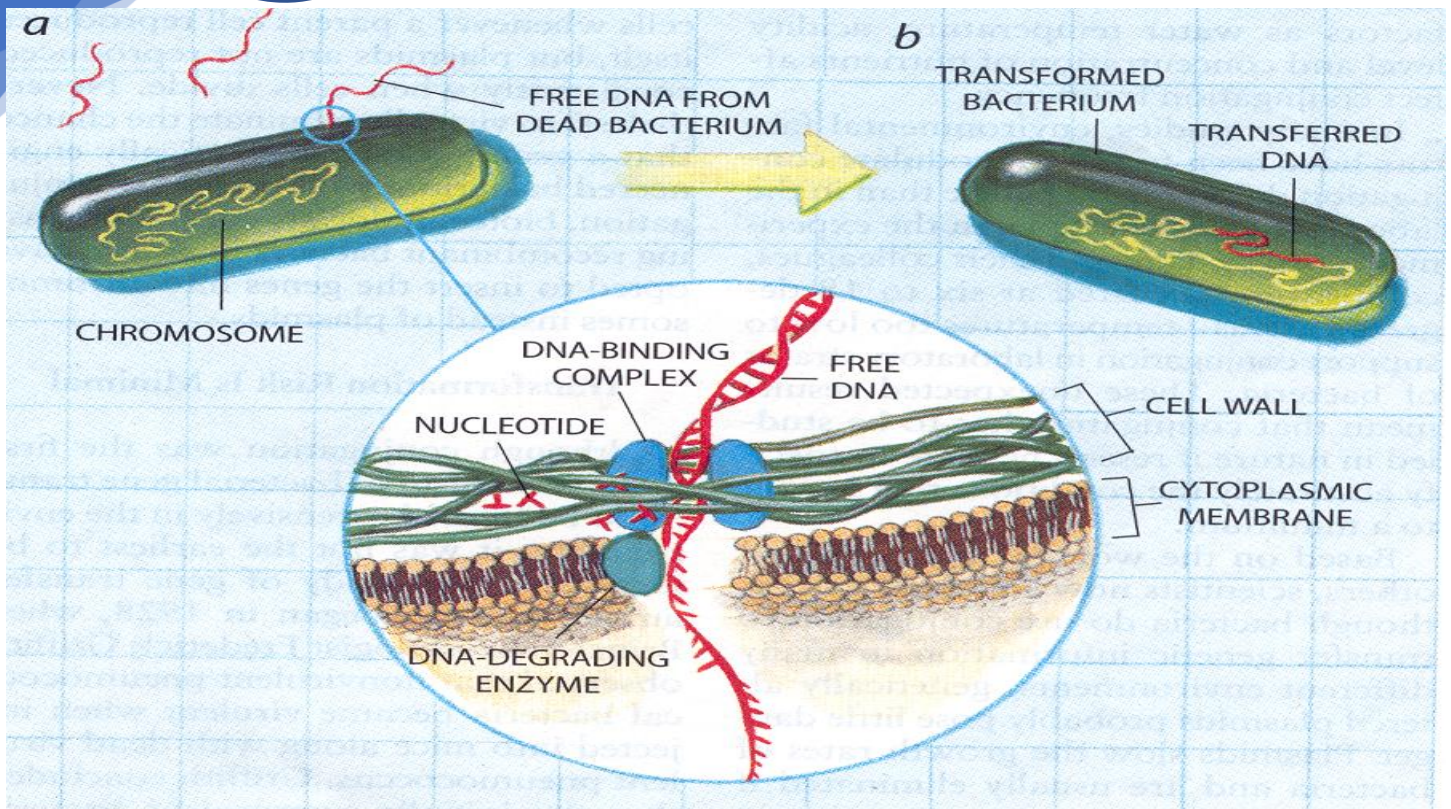


(c) R plasmid

Horizontal Gene Transfer (= lateral gene exchange)

- Conjugation
- Transformation
- Transduction





Where in Nature?

	 TRANSDUCTION	 CONJUGATION	 TRANSFORMATION
 TERRESTRIAL ENVIRONMENTS	Soil, plant surfaces	Soil, plant surfaces	Soil
 WATERY ENVIRONMENTS	Lakes, oceans, rivers, sewage in treatment facilities	Lakes, oceans, marine sediments, rivers, epilithon (slime layer) on river stones, sewage in treatment facilities	Marine sediments, rivers, epilithon on river stones
 INSIDE ORGANISMS	Shellfish, mice	Plants, insects, chickens, mice, humans	Plants, insects, mice

Summary of Prokaryote Evolution Mechanisms

- Mutation (micro or macro) changes genotype and possibly phenotype.
- Mobile genetic elements (insertions sequences and transposons) may rearrange genes between and within DNA molecules and this may cause mutations.
- Horizontal gene transfer (conjugation, transformation, transduction) may result in recombination of completely new genes.
- Selective pressures in the environment determine if a new phenotype becomes dominant in a population.
- Many changes in genotype are neutral or benign to phenotype and survival; these “cryptic” changes over time may result in genetic drift, i.e. a harmless variation of a gene randomly becomes dominant.

40 Origin of life

Life appeared after a period of chemical reactions □ According to physical and chemical laws.

Prebiotic Earth

- Conditions on the primitive Earth were not the same as those present today
- No spontaneous generation of life today (Pasteur)...
- because the necessary conditions no longer exist
- Abiogenesis

Oparin (1924): “Primeval soup” theory

Haldane (1929): “Hot, dilute soup” theory.

Conditions on early Earth

- Reducing atmosphere on the primitive Earth. No free oxygen (O2)
- Free hydrogen (H2) and saturated hydrides (CH4, NH3 and H2O)
- Energy for chemical reactions between these gases could come from electric discharge in storms or solar energy (no ozone layer)
- The Earth’s surface temperature probably hotter than today.

The formation of monomers

Miller and Urey recreate these conditions in vitro. The water is heated and the mixture circulates for many days.

Results

- After a week 15 amino acids in the mixture
- Other biologically important molecules had been formed including ethanoic acid, lactic acid and urea
- Later similar experiments were done using CO2 that produced nucleotides

- □ Additonal organic material may have been delivered by comets.

Conclusion

- These experiments cannot reproduce the exact conditions on the primitive Earth
- We shall never know exactly what happened
- BUT basic building blocks for the large macromolecules can be synthesised in vitro from inorganic compounds.

From monomers to polymers

- Amino acids □ polypeptides, could have occurred when dry or highly concentrated monomers are heated
- Condensation reactions take place forming:
peptide bonds between amino acids or phosphodiester bonds form between nucleotides.

Early catalysts

- As molecules adsorb to the clay mineral particles they become concentrated (stick to the surface particles)
- Clay particles (coacervates) may have been essential catalysts in the formation of polymers.

The first polynucleotides

- Polynucleotides show a tendency to copy themselves using complementary base pairing □ This was probably catalysed by the presence of clay particles and metal ions □ These single stranded polynucleotides would have been the equivalent of RNA.

The first hereditary information

- RNA was probably the first hereditary molecule having the ability to copy itself
- RNA shows enzymic (catalytic) properties – called ribozymes
- Polynucleotides are very good molecules at storing and transmitting information but they lack the versatility for all the chemical functions of a cell.

A great partnership

- Polypeptides can form complex 3-dimensional structures (proteins),
Polypeptides much better at complex cell functions
- A partnership must have formed between the polynucleotides and the polypeptides
- The polynucleotides directed the synthesis of the polypeptides
- Today it is clear that information only flows from polynucleotides to polypeptides. Translation had started.

The origin of DNA

- Hereditary information was probably stored in the form of DNA later
DNA is more stable than RNA
- The passage of information from RNA to DNA is possible in nature
- The reverse transcriptase enzyme of the retro viruses shows this.

The first membranes, the first cells

- If a piece of RNA codes for a particularly good protein then there is nothing to stop that protein being used by other RNA molecules
- If, however, the RNA is enclosed in a membrane then it can keep its protein to itself and it gains a selective advantage
- So membranes probably pushed evolution by natural selection forwards.

Membranes defined the first cell

- The phospholipids form lipid bilayers when they are surrounded by water
- All the components of a simple prokaryotic cell were now assembled
- They diversified in their metabolism
 - By 2 billion years ago free oxygen was appearing in the atmosphere due to the activity of photosynthetic bacteria.

41 Phylogeny and the Tree of Life

Investigating the Tree of Life

- **Phylogeny** is the evolutionary history of a species or group of related species
- The discipline of **systematics** classifies organisms and determines their evolutionary relationships
- Systematists use fossil, molecular, and genetic data to infer evolutionary relationships

Phylogenies show evolutionary relationships

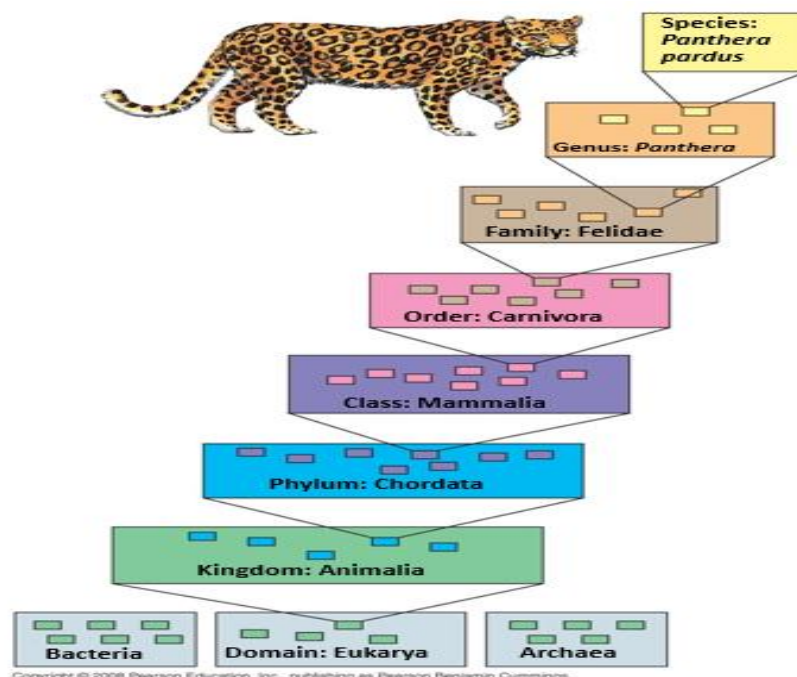
Taxonomy is the ordered division and naming of organisms

Binomial Nomenclature

In the 18th century, Carolus Linnaeus published a system of taxonomy based on resemblances. Two key features of his system remain useful today: two-part names for species and hierarchical classification. The two-part scientific name of a species is called a binomial. The first part of the name is the genus. The second part, called the specific epithet, is unique for each species within the genus. The first letter of the genus is capitalized, and the entire species name is italicized or underlined. Both parts together name the species

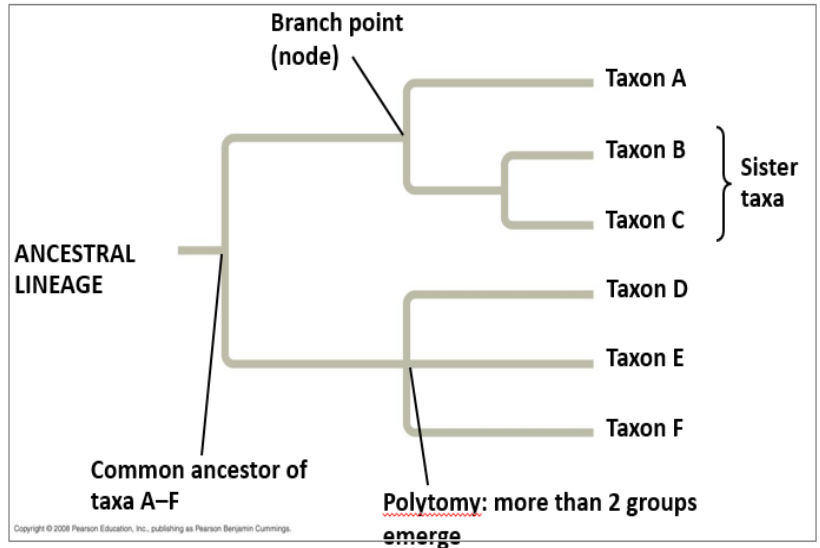
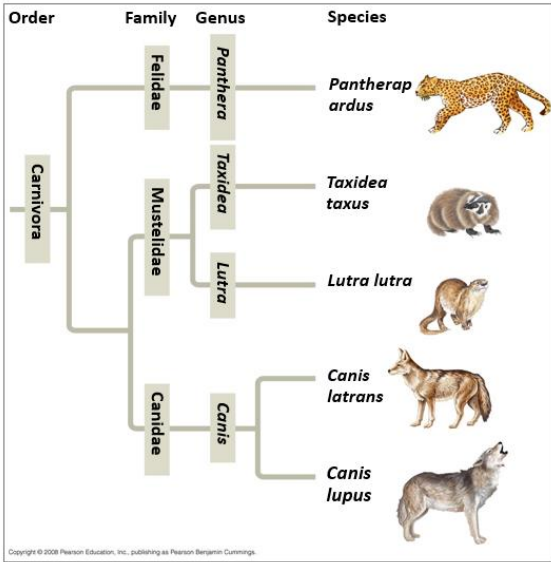
Hierarchical Classification

- Linnaeus introduced a system for grouping species in increasingly broad categories
- The taxonomic groups from broad to narrow are **domain, kingdom, phylum, class, order, family, genus, and species**
- A taxonomic unit at any level of hierarchy is called a **taxon**



Linking Classification and Phylogeny

- Systematists depict evolutionary relationships in branching **phylogenetic trees**
- Linnaean classification and phylogeny can differ from each other
- Systematists have proposed the PhyloCode, which recognizes only groups that include a common ancestor and all its descendents



Things to Learn from Phylogenetic Trees

- Phylogenetic trees do show patterns of descent
- Phylogenetic trees do not indicate when species evolved or how much genetic change occurred in a lineage
- It shouldn't be assumed that a taxon evolved from the taxon next to it
- Applications: whale meat sold illegally in Japan

Phylogenies are inferred from morphological and molecular data

- To infer phylogenies, systematists gather information about morphologies, genes, and biochemistry of living organisms
- Organisms with similar morphologies or DNA sequences are likely to be more closely related than organisms with different structures or sequences

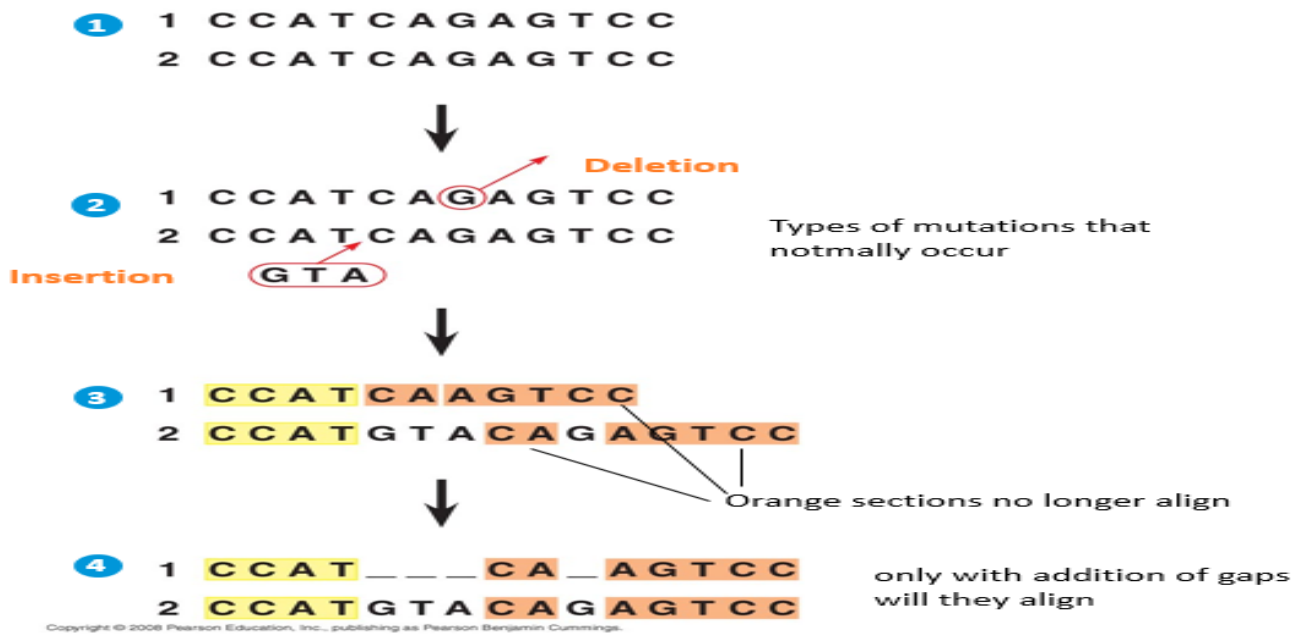
Sorting Homology from Analogy

- Homology is similarity due to shared ancestry like between a wolf and a coyote
- Analogy is similarity due to convergent evolution, similar conditions/adaptations
- E.g. Australian mole and North American mole look alike but evolved independently from each other
- Analogies are also known as **homoplasies** ("to mold the same way")
- Homology can be distinguished from analogy by comparing fossil evidence and the degree of complexity
 - The more complex two similar structures are, the more likely it is that they are homologous

42 Evaluating Molecular Homologies

Evaluating Molecular Homologies

- Systematists use computer programs and mathematical tools when analyzing comparable DNA segments from different organisms



It is also important to distinguish homology from analogy in molecular similarities

□ Mathematical tools help to identify molecular homoplasies, or coincidences

ACGGATAGTCCACTAGGCACTA
TCAACGACAGGTCTTTGACTAG

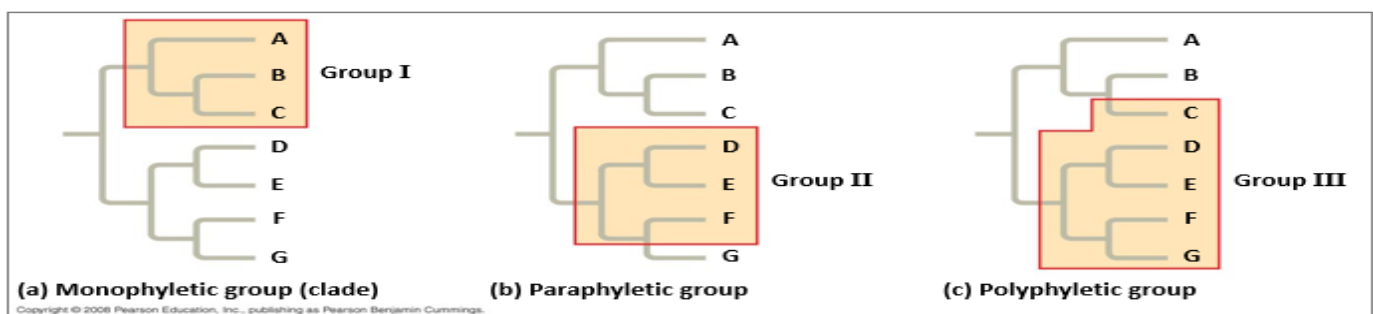
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- **Molecular systematics** uses DNA and other molecular data to determine evolutionary relationships

Shared characters are used to construct phylogenetic trees

- **Cladistics** groups organisms by common descent
- A **clade** is a group of species that includes an ancestral species and all its descendants
- A valid clade is **monophyletic**, signifying that it consists of the ancestor species and all its descendants
- A **paraphyletic** grouping consists of an ancestral species and some, but not all, of the descendants
- A **polyphyletic** grouping consists of various species that lack a common ancestor

Includes all descendants

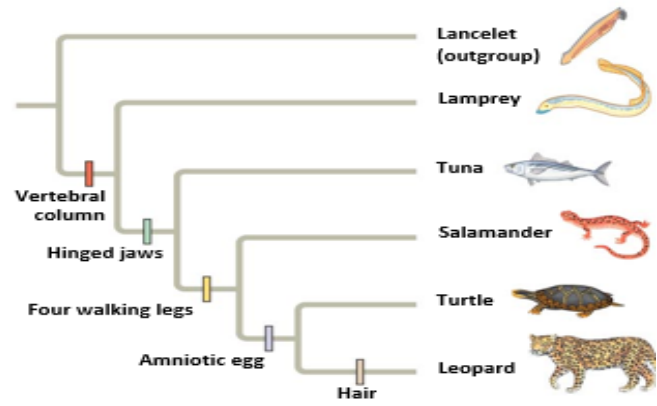


Shared Ancestral and Shared Derived Characters

- In comparison with its ancestor, an organism has both shared and different characteristics
- A shared ancestral character is a character that originated in an ancestor of the taxon
- A shared derived character is an evolutionary novelty unique to a particular clade
- A character can be both ancestral and derived, depending on the context, it is useful to know in which clade a shared derived character first appeared
- An outgroup is a species or group of species that is closely related to the ingroup, the various species being studied
- Systematists compare each ingroup species with the outgroup to differentiate between shared derived and shared ancestral characteristics
- Homologies shared by the outgroup and ingroup are ancestral characters that predate the divergence of both groups from a common ancestor

CHARACTERS	TAXA					
	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
	0	1	1	1	1	1
	0	0	1	1	1	1
	0	0	0	1	1	1
	0	0	0	0	1	1
	0	0	0	0	0	1

(a) Character table
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(b) Phylogenetic tree

Phylogenetic Trees with Proportional Branch Lengths

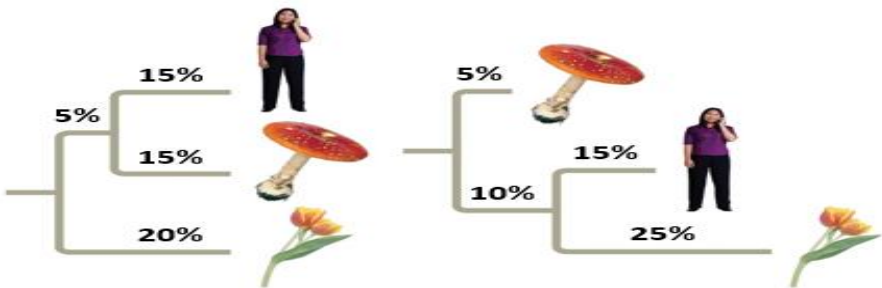
- In some trees, the length of a branch can reflect the number of genetic changes that have taken place in a particular DNA sequence in that lineage
- In other trees, branch length can represent chronological time, and branching points can be determined from the fossil record

Maximum Parsimony and Maximum Likelihood

- Systematists can never be sure of finding the best tree in a large data set
- They narrow possibilities by applying the principles of maximum parsimony and maximum likelihood
- **Maximum parsimony** assumes that the tree that requires the fewest evolutionary events (appearances of shared derived characters) is the most likely
- The principle of **maximum likelihood** states that, given certain rules about how DNA changes over time, a tree can be found that reflects the most likely sequence of evolutionary events

	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

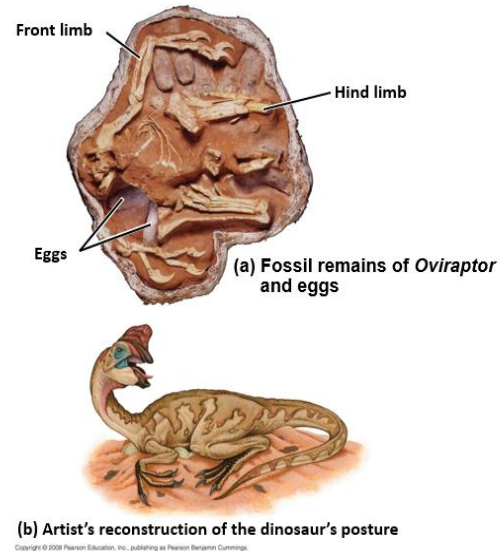
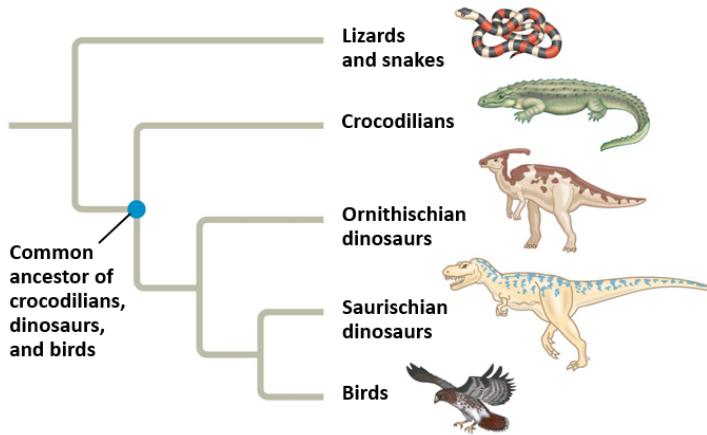
(a) Percentage differences between sequences



(b) Comparison of possible trees
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43 Phylogenetic Trees as Hypotheses

- The best hypotheses for phylogenetic trees fit the most data: morphological, molecular, and fossil
- **Phylogenetic bracketing** allows us to predict features of an ancestor from features of its descendents
- This has been applied to infer features of dinosaurs from their descendents: birds and crocodiles



An organism's evolutionary history is documented in its genome

- Comparing nucleic acids or other molecules to infer relatedness is a valuable tool for tracing organisms' evolutionary history
- DNA that codes for rRNA changes relatively slowly and is useful for investigating branching points hundreds of millions of years ago
- mtDNA evolves rapidly and can be used to explore recent evolutionary events

Gene Duplications and Gene Families

Gene duplication increases the number of genes in the genome, providing more opportunities for evolutionary changes. Like homologous genes, duplicated genes can be traced to a common ancestor.

Orthologous genes are found in a single copy in the genome and are homologous between species. They can diverge only after speciation occurs. **Paralogous genes** result from gene duplication, so are found in more than one copy in the genome. They can diverge within the clade that carries them and often evolve new functions

Genome Evolution

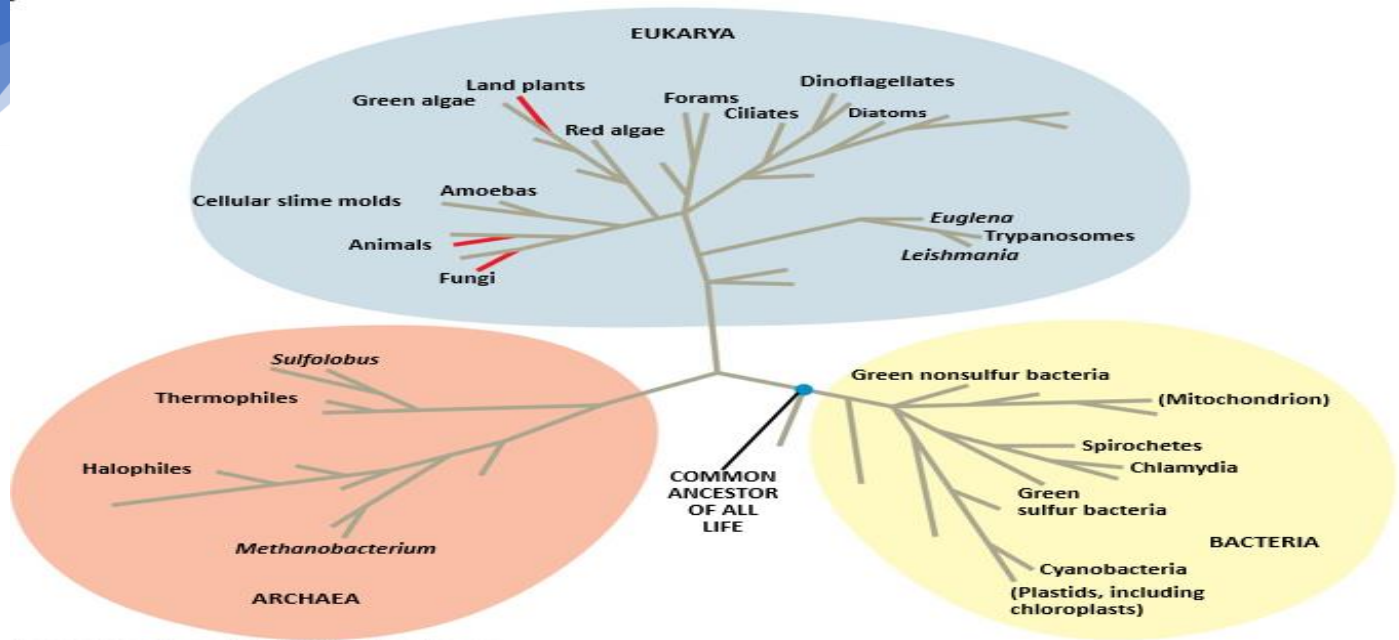
- Orthologous genes are widespread and extend across many widely varied species
- Gene number and the complexity of an organism are not strongly linked
- Genes in complex organisms appear to be very versatile and each gene can perform many functions

New information continues to revise our understanding of the tree of life

Recently, we have gained insight into the very deepest branches of the tree of life through molecular systematics

From Two Kingdoms to Three Domains

- Early taxonomists classified all species as either plants or animals
- Later, five kingdoms were recognized: Monera (prokaryotes), Protista, Plantae, Fungi, and Animalia
- More recently, the three-domain system has been adopted: Bacteria, Archaea, and Eukarya
- The three-domain system is supported by data from many sequenced genomes

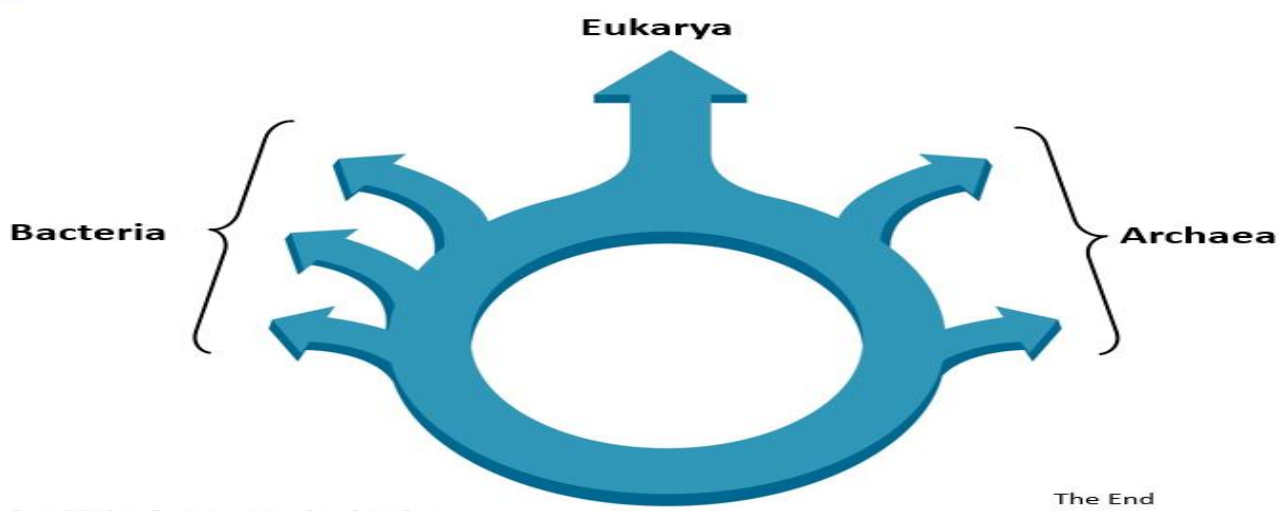


A Simple Tree of All Life

- The tree of life suggests that eukaryotes and archaea are more closely related to each other than to bacteria
- The tree of life is based largely on rRNA genes, as these have evolved slowly

Is the Tree of Life Really a Ring?

- Some researchers suggest that eukaryotes arose as an endosymbiosis between a bacterium and archaean
- If so, early evolutionary relationships might be better depicted by a ring of life instead of a tree of life



44 Natural Selection

Geographic ecology focuses on large-scale patterns of distribution and diversity of organisms, such as island biogeography, latitudinal patterns of species diversity, and the influences of large-scale regional and historical processes on biological diversity.

Isolation

On islands and habitat patches on continents, species richness increases with area and decreases with isolation.

- Larger oceanic islands support more species of most groups of organisms than small islands. Isolated oceanic islands generally contain fewer species than islands near mainland areas.
- Many habitats on continents are so isolated that they can be considered as islands.