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MUHAMMAD IMRAN

BT201 Ecology, Biodiversity & Evolution-II

MSC ZOOLOGY

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

Muhammad Imran

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.

Ecological Genomics:

The field of ecological genomics seeks to understand the genetic mechanisms underlying responses of organisms to their natural environments.

Ecological genomics seeks to understand genomic responses to environmental variation and in turn how genomic variation shapes the responses of organisms to their environment.

Genome annotation:

Genome annotation is the process of identifying functional elements along the sequence of a genome, thus giving meaning to it. It is necessary because the sequencing of DNA produces sequences of unknown function. OR

Genome annotation consists of describing the function of the product of a predicted gene (through an in silico approach). This can be achieved using bioinformatics software with specific features, including **(1) signal sensors** (e.g., for TATA box, start and stop codon, or poly-A signal detection), **(2) content sensors** (e.g., for G+C content, codon usage, or dicodon frequency detection), and **(3) similarity detection** (e.g., between proteins from closely related organisms, mRNA from the same organism, or reference genomes).

Genome evolution is the process by which a genome changes in structure over time, through mutation, horizontal gene transfer, and sexual reproduction. The study of genome evolution involves multiple fields including structural analysis of the genome, genomic parasites, gene and ancient genome duplications, polyploidy, and comparative genomics.

Computational biology, a branch of biology involving the application of computers and computer science to the understanding and modeling of the structures and processes of life.

Computational molecular biology brings together computational, statistical, experimental, and technological methods in order to further scientific discovery and develop new analytical tools for molecular biology.

Challenges to Bioinformatics:

Bioinformatics is the field that focuses on information, data, and knowledge in the context of biological and biomedical research.

The key challenges to bioinformatics essentially all relate to the current flood of raw data, aggregate information, and evolving knowledge arising from the study of the genome and its manifestation.

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.

Approaches for Identifying Genes

- Two research approaches are commonly used to identify the specific genes involved. These are the candidate gene approach and the genomic screening approach.
- I. Candidate gene approach
- II. Genomic screening approach

Candidate Gene Approach

- Genes are selected based on their known or predicted biological function and on their hypothesized relation to the disease or trait
- The problem with the candidate gene approach is that it relies on assumptions about the molecular mechanisms underlying the development of a trait
- The candidate gene approach can be very time consuming

- Chromosomal abnormalities, such as deletions, inversions, or translocations, in individuals exhibiting a trait, as well as animal models mimicking the trait, are especially important for a candidate gene approach
- They provide clues to the genetic basis of the trait

Genomic Screen Approach

- A genomic screen is a systematic survey in which polymorphic DNA markers, evenly spaced along all the chromosomes, are used to determine if a marker is inherited along with the trait, indicating genetic linkage.
- Genomic screening does not require prior biological understanding of the pathophysiology of a disease. It requires large sets of data from families containing multiple members who are affected with the trait, and it tends to be the more expensive of the two approaches

Positional Cloning

- Positional cloning is the process of identifying a disease gene based on its location on a chromosome.
- Genetic screening is the initial step of positional cloning. The usual steps are:
 - I. linkage (locates a chromosome area)
 - II. fine mapping (narrows down the initial genomic area to a smaller region)
 - III. candidate gene analysis (looks for mutations in genes lying in that small area).
 - IV. Before the Human Genome Project was completed, such a physical representation was constructed by using a "contig," a group of overlapping DNA fragments that together cover the linked region.
 - V. The contig is a scaffold or platform on which to place genes and other sequences in the correct position.
 - VI. Positional cloning is a laborious process if the region is large and if the genes and polymorphisms making up the contig are not known.
 - VII. The gene identified through positional cloning was the cystic fibrosis transmembrane conductance regulator gene. The gene, identified in 1989, regulates chloride ion transport across the plasma membrane and consists of twenty-seven exons spread over a 230-kilobase-pair region on chromosome seven.

Gene Discovery:

Gene discovery is the process of identifying genes that contribute to the development of a trait or phenotype. Researchers often try to discover the genes that are involved in specific diseases. They also try to find the genes that contribute to many other traits.

Gene discovery begins with clearly defining a trait of interest and determining if that trait has a genetic and/or environmental basis. This is done using several approaches, such as sibling recurrence risk ratio, familial aggregation, and twin and adoption studies. The sibling recurrence risk ratio is the frequency of a disease among the relatives of an affected person, divided by the frequency of the disease in the general population. The greater the ratio, the stronger the genetic component of the disease.

A trait also is suspected of having a strong genetic component when familial aggregation, which is the clustering of patients in a single family, occurs. Familial aggregation can sometimes be misleading, however. Since families often share the same environment, it is difficult to know whether environmental or genetic factors are the cause of clustering.

In twin studies, concordance rates play a critical role. Concordance is the percentage of second twins that exhibit a trait when the trait occurs in the first twin. Twins generally also share environments, so concordance rates are often compared between monozygotic twins, who are genetically identical, and dizygotic or "fraternal" twins, who share on average 50 percent of their genetic material. The greater the difference in concordance

rates between monozygotic and fraternal twins, the stronger the genetic contribution to the trait. The combination of evidence from all these approaches indicates whether a particular phenotype is likely to have a genetic basis.

Approaches for Identifying Genes

Once genetic influence has been established, two research approaches are commonly used to identify the specific genes involved. These are the candidate gene approach and the genomic screening approach.

Candidate Gene Approach.

In the candidate gene approach, genes are selected based on their known or predicted biological function and on their hypothesized relation to the disease or trait. These genes are subject to mutation analysis to determine whether they are really involved. The problem with the candidate gene approach is that it relies on assumptions about the molecular mechanisms underlying the development of a trait. However, diseases are usually studied because little is known about their causes, so initial ideas about these "molecular mechanisms" often prove to be wrong.

In addition, the candidate gene approach can be very time consuming, and it has been successful only infrequently. Chromosomal abnormalities, such as deletions, inversions, or translocations, in individuals exhibiting a trait, as well as animal models mimicking the trait, are especially important for a candidate gene approach, since they provide clues to the genetic basis of the trait.

Genomic Screen Approach.

A genomic screen is a systematic survey in which polymorphic DNA markers, evenly spaced along all the chromosomes, are used to determine if a marker is inherited along with the trait, indicating genetic linkage. This is performed taking the DNA from each individual in the study and identifying the type of marker each has on his chromosomes. These data are then analyzed using statistical programs to see if the marker and the trait that is being studied travel together through families significantly more often than would be expected just by chance. If a DNA marker is found to be linked with a trait, it suggests that the marker and the gene responsible for the trait are rarely separated by crossing over and are therefore near each other on a region of a chromosome. Further fine mapping of this region with more closely spaced markers can narrow the region where the gene of interest lies.

Genomic screening does not require prior biological understanding of the pathophysiology of a disease. It requires large sets of data from families containing multiple members who are affected with the trait, and it tends to be the more expensive of the two approaches.

Genomic screening usually leads to the identification of one or several loci, or relatively large areas in the genome, that are linked with a trait but that contain many different genes. The genes in such regions need to be prioritized.

Genes are considered to be good candidates when their putative functions fit with the known or predicted pathway of the disease. If any known gene in the linkage region appears to be a good candidate gene, it is subjected to mutation analysis to determine if there is a potentially disease-causing mutation that segregates only with the affected individuals.

Both the gene candidate and the genetic screen approach require collecting data from a large number of families. Recruiting and medically evaluating affected and unaffected individuals for participation in a genetic study, and collecting their DNA samples, is a long and complicated phase of gene discovery.

Positional Cloning

Once one or more loci have been identified through a genomic screen as possibly containing a gene of interest, additional techniques are needed to locate the exact gene responsible. Positional cloning is the process of identifying a disease gene based on its location on a chromosome. Genetic screening is the initial step of positional cloning. The usual steps are: (1) linkage (locates a chromosome area); (2) fine mapping (narrows down the initial genomic area to a smaller region); (3) candidate gene analysis (looks for mutations in genes lying in that small area). By using positional cloning, researchers can identify or "clone" a gene knowing only its location on a chromosome, as determined through linkage analysis. Once the location is identified, a physical representation of the genes and DNA in the linked region is constructed.

Before the Human Genome Project was completed, such a physical representation was constructed by using a "contig," a group of overlapping DNA fragments that together cover the linked region. The contig is a scaffold or platform on which to place genes and other sequences in the correct position. The geneticist continues to collect families looking for new recombinations that reduce the piece of DNA that all the affected family members share but that has not been inherited by any of the unaffected individuals.

Positional cloning is a laborious process if the region is large and if the genes and polymorphisms making up the contig are not known. This portion of the process has been greatly helped by the Human Genome Project, as it provides the contig all filled out and correctly mapped.

In most cases, the smallest inherited piece of DNA is still quite large molecularly, and can contain many genes. Only one gene causes the disease, though, so each gene must be tested for mutations that segregate with the trait. This can be very time consuming as well. If no mutations are found, the process is repeated with the next gene in the smallest shared region of DNA.

The third gene identified through positional cloning was the cystic fibrosis transmembrane conductance regulator gene. The gene, identified in 1989, regulates chloride ion transport across the plasma membrane and consists of twenty-seven exons spread over a 230-kilobase-pair region on chromosome seven. This gene was difficult to clone because of the lack of chromosome abnormalities that would have helped locate it. No human genome sequence was available at that time. Numerous technical problems also arose in constructing a physical map of the linkage region, creating the need to screen numerous libraries to obtain a full-length clone of the gene. More than 550 mutations were identified by late 2001.

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

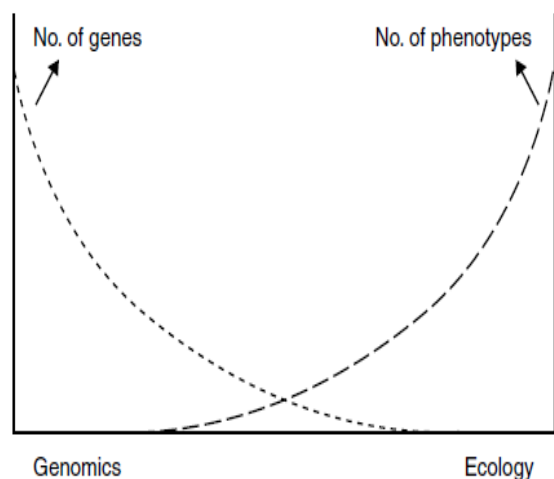
- It emphasizes the role of genetic turbulence (gene duplication, genetic sweeps, exon shuffling, transposition, etc.)
- illustrates that there is ample scope for ‘innovation from within genetic turbulence

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.

Ecological genomics

The natural environments of organisms present a multitude of biotic and abiotic challenges that require both short-term ecological and long-term evolutionary responses.

Recent technical advances in high-throughput sequencing, genotyping and genome-wide expression profiling, coupled with bioinformatics approaches for handling such data, hold great promise for dissecting these responses with unprecedented resolution.

The application of new techniques and resources will not be enough; a deeper understanding of these responses will necessarily require a multidisciplinary approach, combining organismal analyses with molecular genetics and genomics, laboratory experiments with field studies and all within an ecologically relevant framework.

Such an integration of fields faces many challenges but nonetheless is underway and will revolutionize our understanding of a broad range of biological phenomena.

Ecological and laboratory-based genetic/genomic investigations traditionally have occupied different areas of the biological sciences. With a few notable exceptions, research programs are generally positioned in one domain or the other, but do not regularly cross the boundary that separates these disciplines by utilizing the tools and approaches of both.

Ecological genomic studies seek to integrate these disciplines through the use of genomic approaches in an ecological context. For example, how can genomics be used to link population and community responses through organisms at the level of genes and gene expression? We can see this emerging interdisciplinary field that combines ecological and genomic approaches (that is, ecological genomics).

By 'genomic approaches', we refer to any genome-enabled approach, whether aimed at discovering the ecological functions of single or multiple genes. We define ecological genomics as an integrative field of study that seeks to understand the genetic mechanisms underlying responses of organisms to their natural environment. These responses include modifications of biochemical, physiological, morphological or behavioral traits of adaptive significance.

Now that we are in the age of genomics, we witness an enormous growth of our knowledge on the very mechanisms about which Darwin was ignorant. Some authors have therefore applied Darwin's analogy of the tangled bank to the genome. Dover (1999) made a distinction between the 'external tangled bank' (the ecology) and the 'internal tangled bank' (the genome), attributing to them complementary functions in the evolutionary process. The concept of the internal tangled bank emphasizes the role of

genetic turbulence (gene duplication, genetic sweeps, exon shuffling, transposition, etc.) in the genome and it illustrates that there is ample scope for 'innovation from within'.

The genomics revolution is not only due to advances in molecular biology. Three major technological developments that took place in the 1990s also made it possible: microtechnology, computing, and communication.

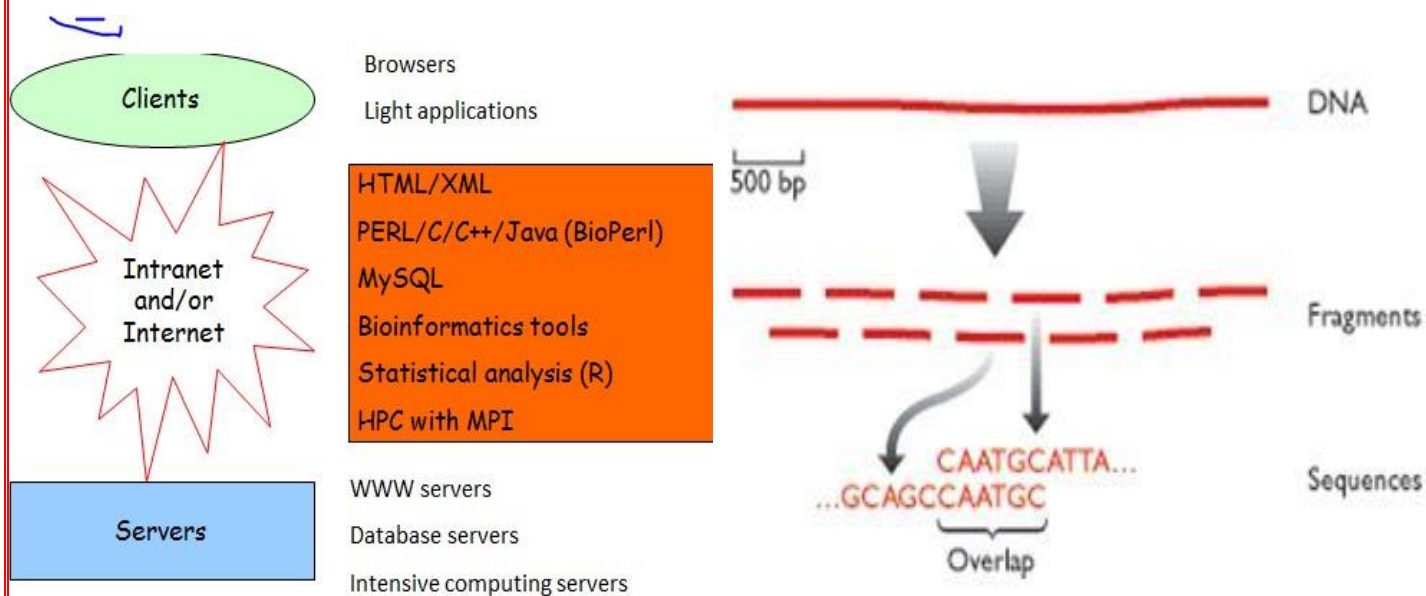
Microtechnology: The possibility of working with molecules on the scale of a few micrometres, given by advances in laser technology, has been very important for one of genomics' most conspicuous achievements, the development of the gene chip.

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.

Communication technology: 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.

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?

```
CGGTTGAAAGCGGTAGCGTCCATGCGTATTACTCTTGAGCGGTGCAACCTTCTGAAATCGCT
GAACCACGTCCACCGGGTCGTCGAGCGTCGCAACACGATCCCGATCCTGTCCAACGTTCTGC
.....ACTGAATTTTCTCA
GTTACGACATTTTGCCTTGTTTTTGCGCCAAATGGGATCAACAGTACGTAACAATTTTTTGAC
AATGACCAATACATCCGAGGGGAATCATGGCACTCAACCTGAAGCAACGGCTT
```

1. Transcriptional control sites
2. Non-coding RNAs
3. mRNAs

Evidence-based prediction

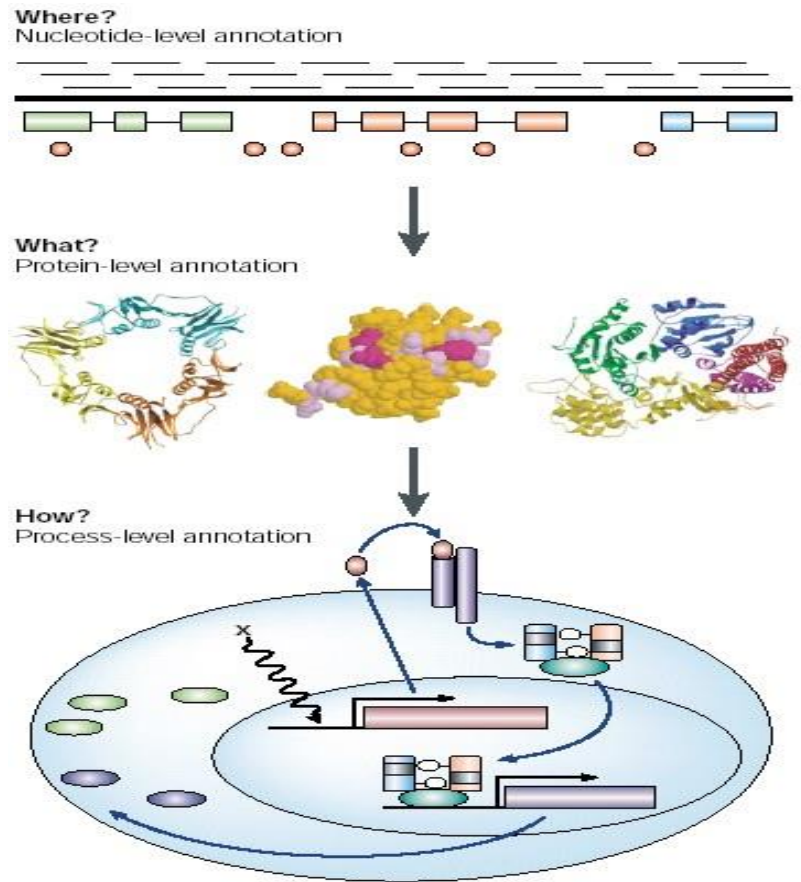
- Cis-alignment
- Trans-alignment
- *Ab initio* / *de novo* prediction

Three Layers of Genome Annotation.

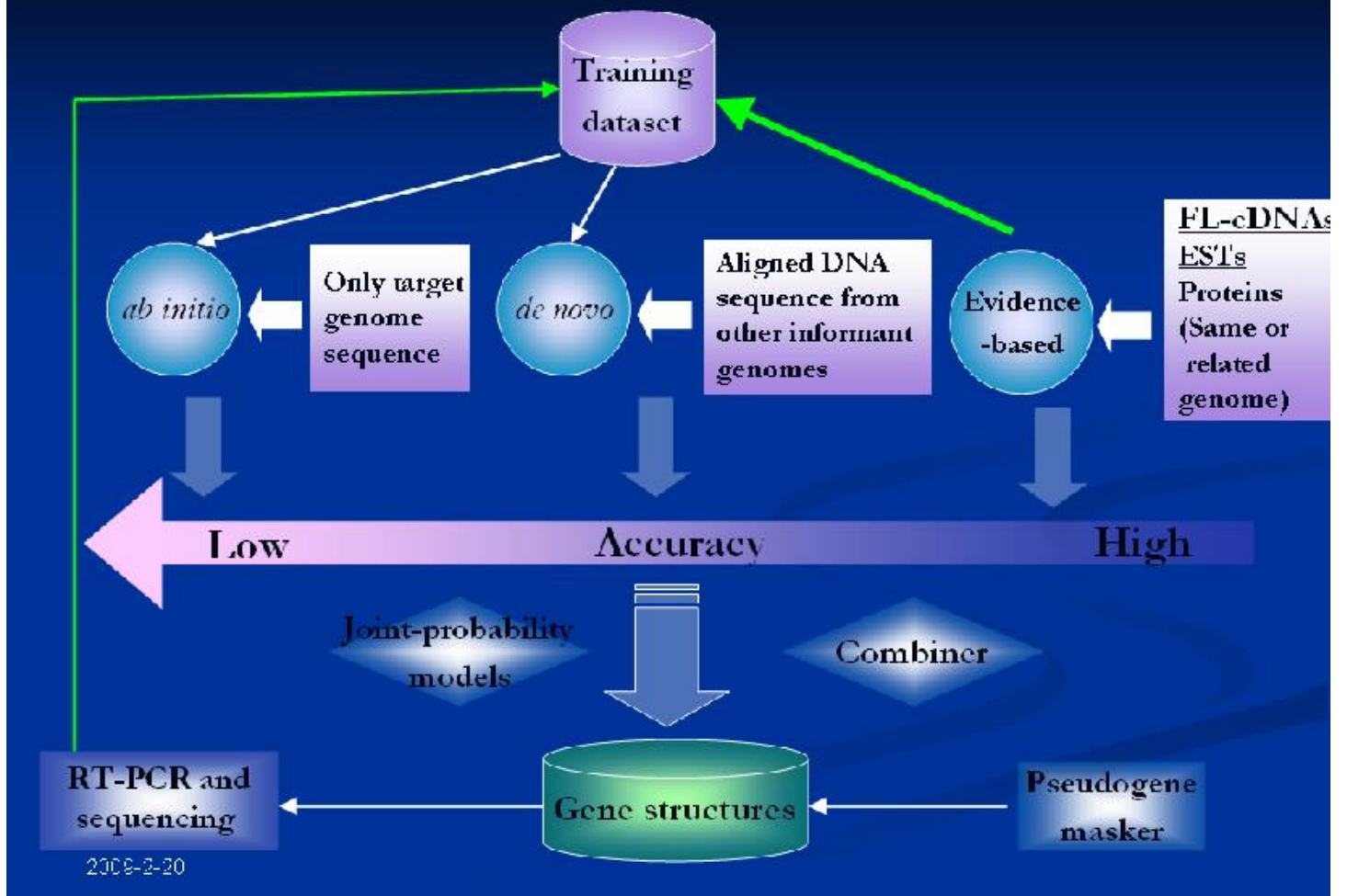
From Stein, L. 2001. Nature Reviews genetics 2:493-503

Some models

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



Genome annotation flowchart



What is XML?

XML is a markup language which is designed to store data. It's popularly used for transfer of data. It is case sensitive. XML offers you to define markup elements and generate customized markup language. The basic unit in the XML is known as an element. Extension of XML file is .xml.

What is HTML?

HTML is the markup language which helps you to create and design web content. It has a variety of tag and attributes for defining the layout and structure of the web document. It is designed to display data in a formatted manner. A HTML document has the extension .htm or .html.

You can edit HTML code in any basic code editor, even notepad. The edited code can be executed in any browser. Browsers render the tags used and present the content you want to display with or without applied formatting.

KEY DIFFERENCE

- XML is abbreviation for eXtensible Markup Language whereas HTML stands for Hypertext Markup Language.
- XML mainly focuses on transfer of data while HTML is focused on presentation of the data.
- XML is content driven whereas HTML is format driven.
- XML is Case sensitive while HTML is Case insensitive.
- XML provides namespaces support while HTML doesn't provide namespaces support.
- XML is strict for closing tag while HTML is not strict.
- XML tags are extensible whereas HTML has limited tags.
- XML tags are not predefined whereas HTML has predefined tags.

Parameter	XML	HTML
Type of language	XML is a framework for specifying markup languages.	HTML is predefined markup language.
Language type	Case sensitive	Case insensitive
Structural details	It is provided	It is not provided.
Purpose	Transfer of data	Presentation of the data
Coding Errors	No coding errors are allowed.	Small errors are ignored.
Whitespace	You can use whitespaces in your code.	You can't use white spaces in your code.
Nesting	Should be done appropriately.	Does not have any effect on the code.
Driven by	XML is content driven	HTML is format driven
End of tags	The closing tag is essential in a well-formed XML document.	The closing tag is not always required. <HTML> tag needs an equivalent </HTML> tag but tag does not require </br> tag
Quotes	Quotes required around XML attribute values.	Quotes are not required for the values of attributes.
Object support	Objects have to be expressed by conventions. Mostly using attributes and elements.	Offers native object support
Null support	Need to use xsi:nil on elements in an XML instance document and also need to import the corresponding namespace.	Natively recognizes the null value.

Namespaces	XML provides support for namespaces. It helps you to remove the risk of name collisions when combining with other documents.	Does not support the concept of namespaces. Naming collisions can be avoided either using a prefix in an object member name or by nesting objects.
Formatting decisions	Require more significant effort to map application types to XML elements and attributes.	Provides direct mapping for application data.
Size	Documents are mostly lengthy in size, especially when an element-centric approach used in formatting.	The syntax is very brief and yields formatted text.
Parsing in Javascript	Requires an XML DOM implementation and application code to map text back into JavaScript objects.	No extra application code required to parse text. For this purpose, you can use the eval function of JavaScript.
Learning curve	Very hard as you need to learn technologies like XPath, XML Schema, DOM, etc.	HTML is a simple technology stack that is familiar to developers.

BioPerl

Perl is an interpreted programming language that resembles both a real programming language and a shell.

A Language for easily manipulating text, files, and processes

Provides more concise and readable way to do jobs formerly accomplished using C or shells.

Perl stands for Practical Extraction and Report Language.

Easy to use

Basic syntax is C-like

Type-"friendly" (no need for explicit casting)

Lazy memory management

A small amount of code goes a long way

Fast

Perl has numerous built-in optimization features which makes it run faster than other scripting language.

Portability

One script version runs everywhere (unmodified).

Efficiency

For programs that perform the same task (C and Perl), even a skilled C programmer would have to work harder to write code that:

Runs as fast as Perl code

Is represented by fewer lines of code

Correctness

Perl fully parses and pre-"compiles" script before execution.

Efficiently eliminates the potential for runtime SYNTAX errors.

Free to use

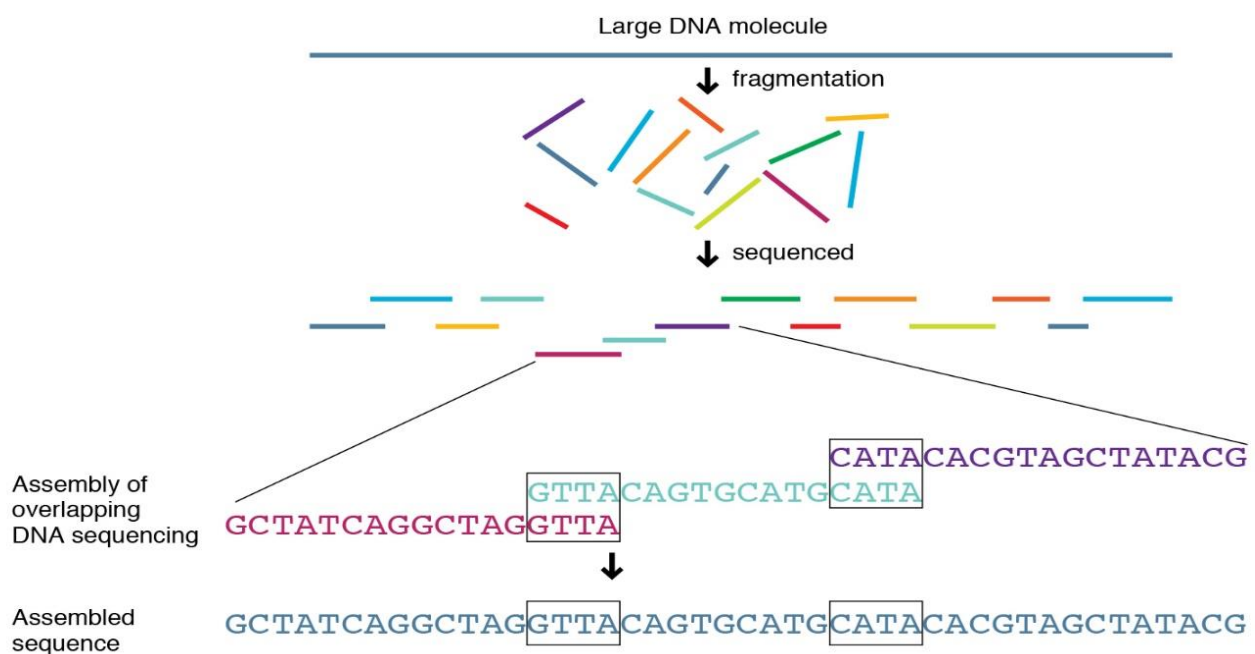
MySQL:

MySQL is an open-source relational database management system (RDBMS). Its name is a combination of "My", the name of co-founder Michael Widenius's daughter, and "SQL", the abbreviation for Structured Query Language. A relational database organizes data into one or more data tables in which data types may be related to each other; these relations help structure the data. SQL is a language programmers use to create, modify and extract data from the relational database, as well as control user access to the database. In addition to relational databases and SQL, an RDBMS like MySQL works with an operating system to implement a relational database in a computer's storage system, manages users, allows for network access and facilitates testing database integrity and creation of backups.

MySQL is free and open-source software under the terms of the GNU General Public License, and is also available under a variety of proprietary licenses. MySQL was owned and sponsored by the Swedish company MySQL AB, which was bought by Sun Microsystems (now Oracle Corporation).

Shotgun sequencing:

Shotgun sequencing is a laboratory technique for determining the DNA sequence of an organism's genome. The method involves breaking the genome into a collection of small DNA fragments that are sequenced individually. A computer program looks for overlaps in the DNA sequences and uses them to place the individual fragments in their correct order to reconstitute the genome.



The most efficient way to sequence a large piece of DNA involves a process known as shotgun sequencing. For this, the starting DNA is broken up randomly into many smaller pieces, sort of in a shotgun fashion, with each of those pieces then sequenced individually. The resulting sequence reads generated from the different pieces are then analyzed by a computer program, looking for stretches of sequence from different reads that are identical with one another. When identical regions are identified, they are overlapped with one another, allowing the two sequence reads to be stitched together. This computer process is repeated over and over and over again, eventually yielding the complete sequence of the starting piece of DNA. The initial random fragmenting and reading of the DNA gave this approach the name "shotgun sequencing".

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)**

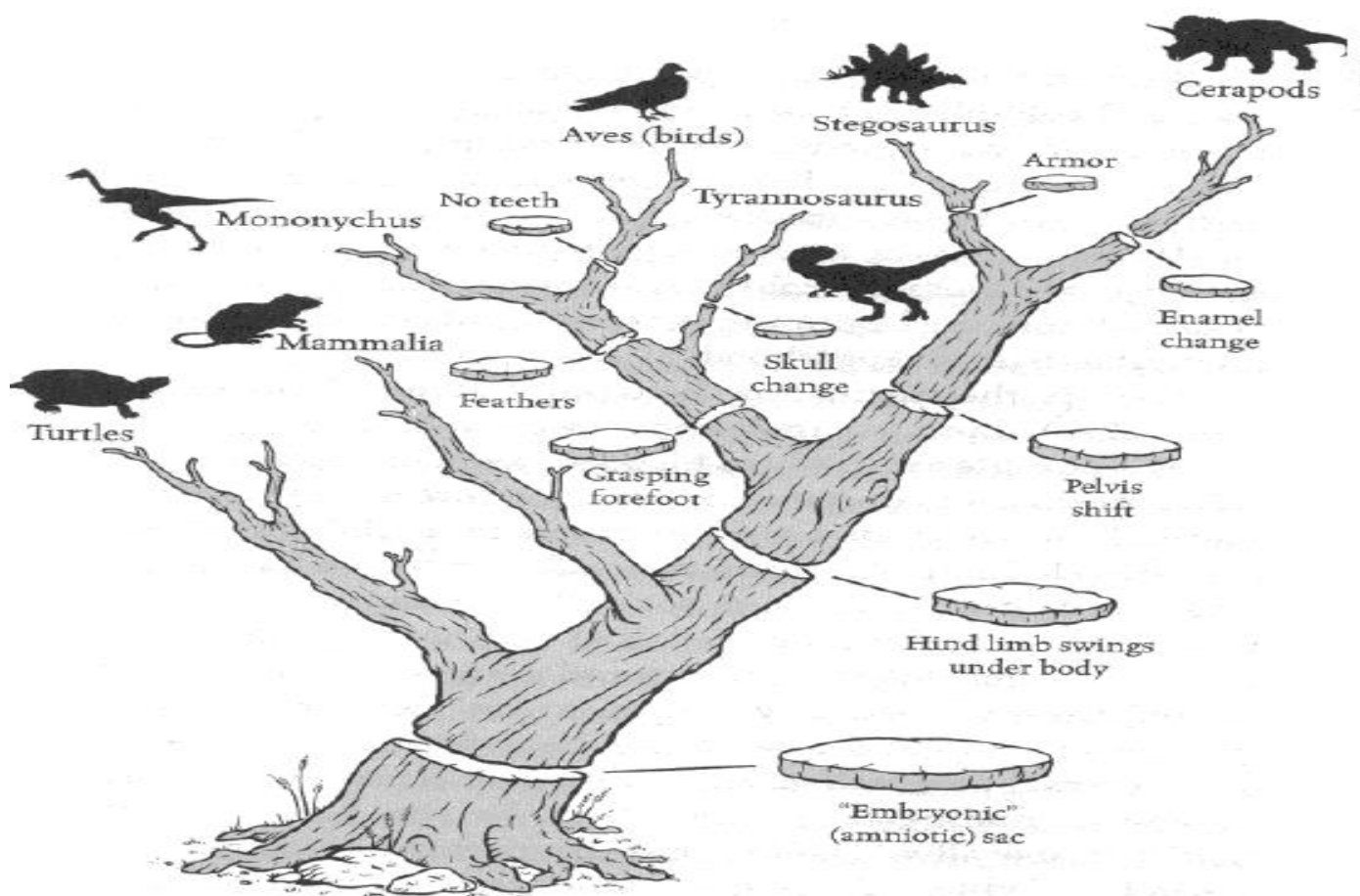
Species/Gene Trees

@ Species tree (how are my species related?)

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

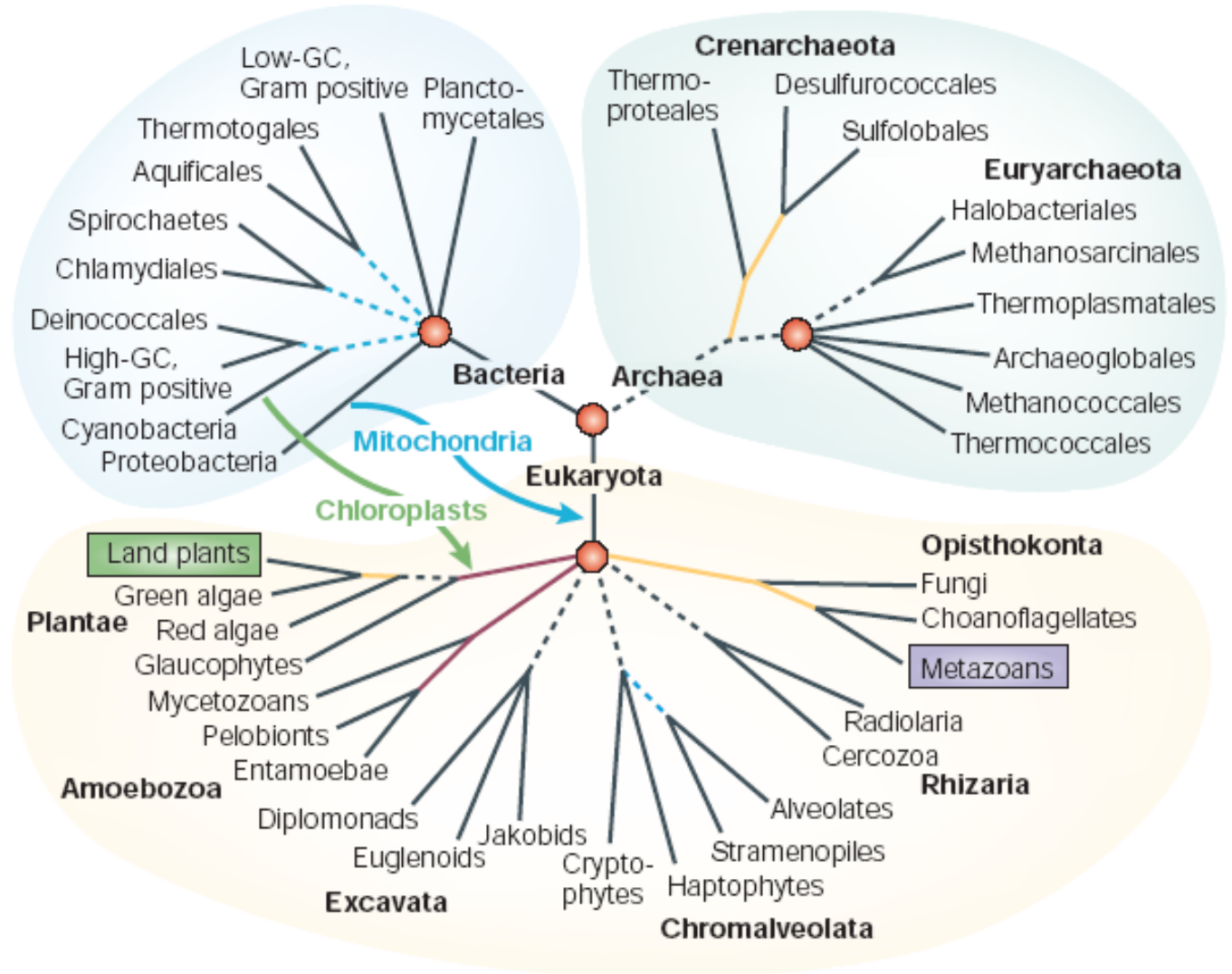
@ Gene tree (how are my genes related?)

- 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).



Phylogenomics and the tree of life

Cladistics:

Cladistics is an approach to biological classification in which organisms are categorized in groups ("clades") based on the most recent common ancestor. Hypothesized relationships are typically based on shared derived characteristics (synapomorphies) that can be traced to the most recent common ancestor and are not present in more distant groups and ancestors. A key feature of a clade is that a common ancestor and all its descendants are part of the clade. Importantly, all descendants stay in their overarching ancestral clade.

For example, if within a strict cladistic framework the terms animals, bilateria/worms, fishes/vertebrata, or monkeys/anthropoidea were used, these terms would include humans. Many of these terms are normally used paraphyletically, outside of cladistics, e.g. as a 'grade'. Radiation results in the generation of new subclades by bifurcation, but in practice sexual hybridization may blur very closely related groupings.

Cladistics is now the most commonly used method to classify organisms.

Phylogenetics:

In biology, phylogenetics is a part of systematics that addresses the inference of the evolutionary history and relationships among or within groups of organisms (e.g. species, or more inclusive taxa). These relationships are hypothesized by phylogenetic inference methods that evaluate observed heritable traits, such as DNA sequences or morphology, often under a specified model of evolution of

these traits. The result of such an analysis is a phylogeny (also known as a phylogenetic tree) a diagrammatic hypothesis of relationships that reflects the evolutionary history of a group of organisms.

The tips of a phylogenetic tree can be living taxa or fossils, and represent the 'end', or the present, in an evolutionary lineage.

A phylogenetic diagram can be rooted or unrooted.

A **rooted tree** diagram indicates the hypothetical common ancestor, or ancestral lineage, of the tree. An **unrooted tree** diagram (a network) makes no assumption about the ancestral line, and does not show the origin or "root" of the taxa in question or the direction of inferred evolutionary transformations. In addition to their proper use for inferring phylogenetic patterns among taxa, phylogenetic analyses are often employed to represent relationships among gene copies or individual organisms. Such uses have become central to understanding biodiversity, evolution, ecology, and genomes.

A **phylogenetic tree or evolutionary tree** is a branching diagram or "tree" showing the evolutionary relationships among various biological species or other entities-their phylogeny based upon similarities and differences in their physical or genetic characteristics. All life on Earth is part of a single phylogenetic tree, indicating common ancestry.

In a rooted phylogenetic tree, each node with descendants represents the inferred most recent common ancestor of those descendants, and the edge lengths in some trees may be interpreted as time estimates. Each node is called a taxonomic unit. Internal nodes are generally called hypothetical taxonomic units, as they cannot be directly observed. Trees are useful in fields of biology such as bioinformatics, systematics, and phylogenetics.

Unrooted trees illustrate only the relatedness of the leaf nodes and do not require the ancestral root to be known or inferred.

Dendrogram:

A dendrogram is a general name for a tree, whether phylogenetic or not, and hence also for the diagrammatic representation of a phylogenetic tree.

Cladogram:

A cladogram only represents a branching pattern; i.e., its branch lengths do not represent time or relative amount of character change, and its internal nodes do not represent ancestors.

Phylogram:

A phylogram is a phylogenetic tree that has branch lengths proportional to the amount of character change.

Chronogram:

A chronogram is a phylogenetic tree that explicitly represents time through its branch lengths.

Phylogenetic trees composed with a nontrivial number of input sequences are constructed using computational phylogenetics methods. Distance-matrix methods such as neighbor-joining or UPGMA,

which calculate genetic distance from multiple sequence alignments, are simplest to implement, but do not invoke an evolutionary model.

Many sequence alignment methods such as ClustalW also create trees by using the simpler algorithms (i.e. those based on distance) of tree construction. Maximum parsimony is another simple method of estimating phylogenetic trees, but implies an implicit model of evolution (i.e. parsimony). More advanced methods use the optimality criterion of maximum likelihood, often within a Bayesian framework, and apply an explicit model of evolution to phylogenetic tree estimation.[10] Identifying the optimal tree using many of these techniques is NP-hard, so heuristic search and optimization methods are used in combination with tree-scoring functions to identify a reasonably good tree that fits the data.

Tree-building methods can be assessed on the basis of several criteria:

- Efficiency (how long does it take to compute the answer, how much memory does it need?)
- Power (does it make good use of the data, or is information being wasted?)
- Consistency (will it converge on the same answer repeatedly, if each time given different data for the same model problem?)
- Robustness (does it cope well with violations of the assumptions of the underlying model?)
- Falsifiability (does it alert us when it is not good to use, i.e. when assumptions are violated?)
- Tree-building techniques have also gained the attention of mathematicians. Trees can also be built using T-theory.

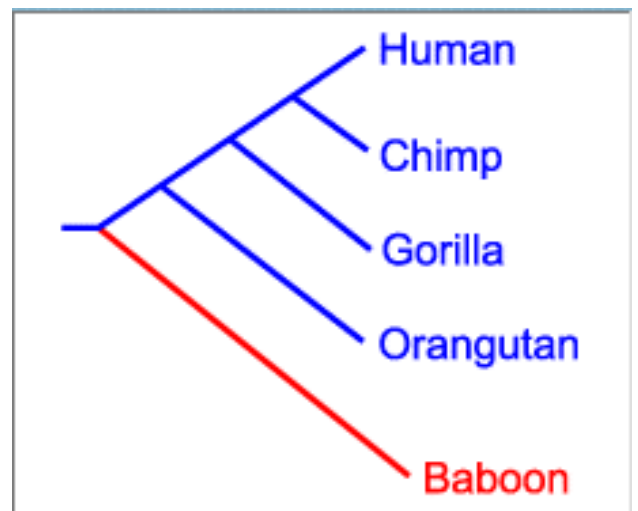
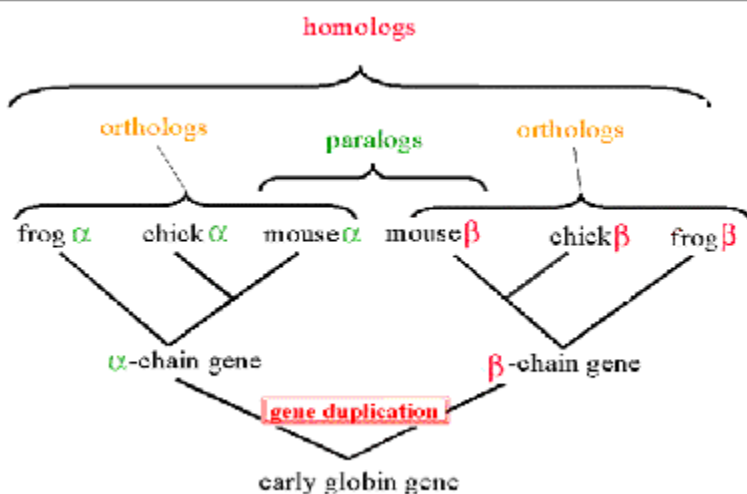
Species Tree:

- Species" trees recover the genealogy of taxa, individuals of a population, etc.
- Internal nodes represent speciation or other taxonomic events.
- Species trees should contain sequences from only orthologous genes.

Gene Tree:

Gene" trees represent the evolutionary history of the genes included in the study.

Gene trees can provide evidence for gene duplication events, as well as speciation events.



Sequences from different homologs can be included in a gene tree; the subsequent analyses should cluster orthologs, thus demonstrating the evolutionary history of the orthologs.

Species tree

Gene tree

6 Yeast, fly, worm, and weed Part 1

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	

A striking feature of genomics is its focus on a limited number of model species with fully sequenced genomes and large research networks organized around them. The genomes of these model species have been sequenced completely and the information is shared on the Internet, allowing scientists to take maximal advantage of progress made by others.

This explains the extreme speed with which the field is developing. Ecology does not have a strong tradition in standardized experimentation with one species. Thus the genomics approach is all the more striking to an ecologist, who is often more fascinated by the diversity of life than by a single organism, and engaged in a very wide variety of topics, systems, and approaches. In this section we examine the arguments for introducing model species in ecological genomics.

The best-known completely sequenced genomes, in addition to those of mouse and human, are those of the yeast *Saccharomyces cerevisiae*, the 'fly' *Drosophila melanogaster*, the 'worm' *Caenorhabditis elegans* and the 'weed' *Arabidopsis thaliana*.

Investigations into the genomes of these model organisms are supported by extensive databases on the Internet that provide a wealth of information about genome maps, genomic sequences, annotated genes, allelic variants, cDNAs, and expressed sequence tags (ESTs), as well as news, upcoming events, and publications. These are the four model genomes and their relationships with evolutionary related species will be discussed in more detail. The genomics of the mouse and human are not discussed at length in this lesson because the model status of these two species has mainly a medical relevance.

The first genome to be sequenced completely was that of *Haemophilus influenzae* (Fleischmann et al. 1995). This bacterium is associated with influenza outbreaks, but is not the cause of the disease, which

is a virus. Although several years earlier the 'genome' of bacteriophage FX174 had been sequenced (Sanger 1977a), 1995 is considered by many as the true beginning of genomics as a science, not in the least because the H. influenza project demonstrated the usefulness of a new strategy of sequencing and assembly (wholegenome shotgun sequencing). With 1.8Mbp the genome of H. influenzae was about 10 times larger than that of any virus sequenced before, but still two to four orders of magnitude smaller than the genome of most eukaryotes.

Genome sequences of many other prokaryotes soon followed, including that of *Methanococcus jannaschii* an archaeon living at a depth of 2600m near a hydrothermal vent on the floor of the Pacific Ocean (Bult et al. 1996). The genome of this extremophile was interesting because of the many genes that were completely unknown before. In 1989, a large network of scientists embarked on a project for sequencing the yeast genome, which was completed in 1996 and was the first eukaryotic genome to be elucidated (Goffeau et al. 1996). Thus, by 1996, the first genomic comparisons were possible between the three domains of life: Bacteria, Archaea, and Eucarya.

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 (Fig.). 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 (Table). Bacteria dominate the list, as the small size of their genomes makes these organisms well-suited for whole-genome sequencing. By June 2005, no fewer than 730 prokaryotic organisms and 496 eukaryotes were the subject of ongoing genome sequencing projects.

The list of species with completed genome sequences does not represent a random choice from the Earth's biodiversity. From an ecologist's point of view, the absence of reptiles, amphibians, molluscs, and annelids is striking, as also is the scarcity of birds and arthropods other than the insects.

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<i>Total</i>	279	

7 Yeast, fly, worm, and weed Part 2

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 3

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 (Pühler 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 (rolling 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.

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 analysing the genomes of these (Pühler 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 (Roiling et al. 2004).

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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 (see Chapter 3), 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. cerevisiae*.

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. Jackson et al. (2002) have formulated arguments for the selection of ecological model species, and we present them in slightly adapted form.

9 Yeast, fly, worm, and weed Part 4

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

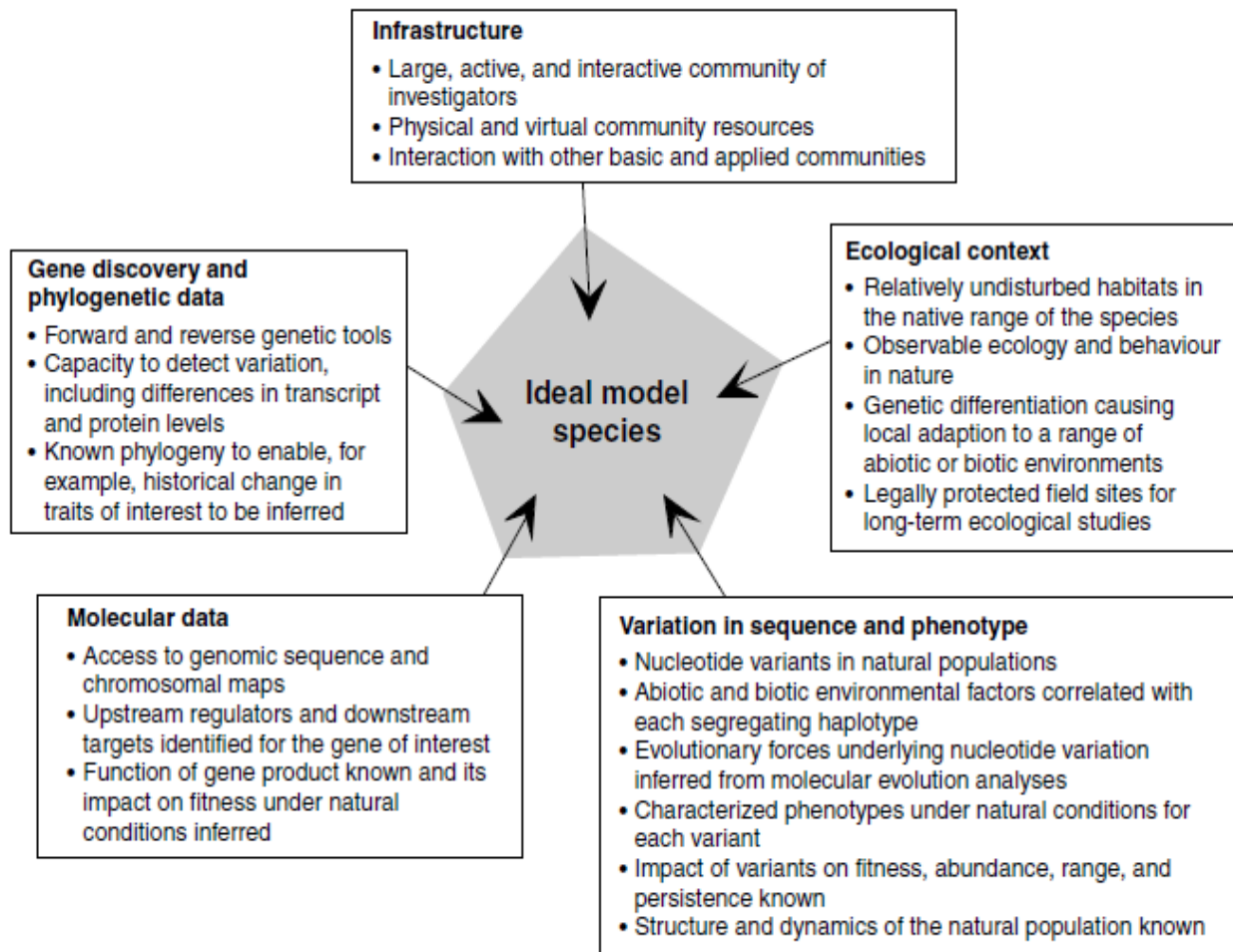
Ecological interactions.

- 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.
- Other investigators are less hesitant about the prospects of microarrays in ecology. Gibson (2002) emphasized that today it is feasible to establish a 5000-clone microarray resource within 12 months of a commencing project and that neither the estimated expense nor the availability of technology need to be a major obstacle for progress. We share this optimism. Given the fact that the number of almost completely sequenced organisms is increasing month by month, we can expect that the genome of several species of great interest to ecologists may be completed

within a few years. In addition, we expect that almost all ecologically relevant species will have basic genomics databases—for example, an annotated EST library—sufficient to answer a considerable number of ecological questions.

10 -Omics speak Part 1

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.

- Classical molecular phylogenetics (see Graur and Li 2000) is based on variation of homologous DNA sequences across species. However, the same structural DNA can be regulated in different ways in different species.
- We illustrate this argument with an example from Enard et al . (2002), who did one of the first studies in comparative transcriptomics .
- Enard et al . (2002) analysed the expression of 18 000 genes in liver, blood leucocytes, and brain tissue of humans, chimpanzee (Pan troglodytes), and rhesus monkey (Macaca mulatta).
- There are more reasons why a functional analysis of the genome can provide a different picture than an inventory of genes. Obviously, all cells of an organism have the same genome, but not the same transcriptome. Even when looking at cells of the same type, the transcriptome depends on environmental conditions, physiological state, developmental state, etc. So the transcriptome allows a glimpse of the living cell much more than the genome itself. The argument also holds when making comparisons across species. Classical molecular phylogenetics (see Graur and Li 2000) is based on variation of homologous DNA sequences across species. However, the same structural DNA can be regulated in different ways in different species. We illustrate this argument with an example from Enard et al. (2002), who did one of the first studies in what may be called comparative transcriptomics.
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- Enard et al. (2002) analysed the expression of 18 000 genes in liver, blood leucocytes, and brain tissue of humans, chimpanzee (Pan troglodytes), and rhesus monkey (Macaca mulatta). The expression patterns in human blood and liver turned out to be more similar to chimpanzees than to rhesus monkeys, which is in accordance with the phylogenetic distances between the three primate species; however, the expression profiles in the brain were more similar between chimpanzee and rhesus monkey than between either of the two monkey species and human (Fig.). So, although chimpanzees share 98.7% of their DNA with humans, the human species expresses that DNA in a different manner, especially in the brain. Gene expression in the brain has undergone accelerated evolution compared to gene expression elsewhere in the body, and evolution has resulted in a divergence of humans from chimpanzees, mostly due to regulatory change rather than structural reorganization of the DNA.
-
- Figure-Distance trees showing the similarity of gene expression profiles in brain, blood leucocytes, and liver of human, chimpanzee, and rhesus monkey. Numbers refer to the ratio between the rate of evolution in the human and the chimpanzee lineages, taking the rhesus monkey as an outgroup. Reprinted with permission from Enard et al . (2002). Copyright 2002 AAAS

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,
Toxicogenomics	analysis of genetic polymorphisms that determine a person's disposition to drug action 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 Ecology as a science

Ecology as a science

Ecology is the scientific study of the relationships between organisms and their environment. These relationships are complex, varied and hierarchical. The word 'ecology' was first used by German biologist Ernst Haeckel in 1869. The word is derived from the Greek words, oikos (meaning 'house' or 'dwelling place') and logos (meaning the study of).

Haeckel defined ecology as 'the study of the natural environment including the relations of organisms to one another and to their surroundings'. Ecology describes the relationships between living organisms and their environments, the interaction of organisms with each other and the pattern and cause of the abundance and distribution of organisms in nature. The environment includes everything (biotic as well as abiotic) that surrounds an organism. Thus, it is the science that attempts to answer questions about how the nature works.

According to one of the most widely accepted definition, 'Ecology is the scientific study of the distribution and abundance of organisms and the interactions that determine distribution and abundance.' Ecology is an interdisciplinary science Ecology, as a unifying science, is integrating the knowledge of life on our planet. It has changed from a basic science to applied science. It has become an essential science in learning how life survive and grow.

Several questions such as why do animals live in groups, what determines the distribution of a species, how does organism interact with biotic and abiotic components, behavioural aspects of animals often drive us to look into this subject. Ecology is not just biology but an interdisciplinary science that deals with the totality of living organisms and their relationship with the environment. Different kinds of physical, chemical and biological processes occurring within ecological systems involve complex interactions among different components of the system. To study these interactions, ecologists must involve other sciences like physiology, biochemistry, genetics, geology, hydrology and meteorology. Ecology has turned into more experimental rather than philosophical subject. With increasing scientific informations, this science also involves complex mathematical modeling and algorithms – a true interdisciplinary sciences

Ecotype and Ecads

Many populations show a series of phenotypic variations as a result of environmental variations. These phenotypic variations usually remain even if the organisms are put in a different environment, and are inherited by their offspring, indicating that the characters are genetically rather than environmentally determined. A Swedish ecologist Turesson (1925) studied a plant species which showed some genetically fixed phenotypic variations between populations of the *Campanula rotundifolia*. He found that mountain populations were shorter and flowered earlier than the lowland forms. This suited their growth in short mountain turf and their adaptation for rapid flowering and seed production in the shorter growing season in high altitude mountain habitats. Turesson called these phenotypically different forms ecotypes. An ecotype describes a genetically different population (subspecies) within a species which is adapted to specific environmental conditions. In ecotypes, adaptations become irreversible or genetically fixed. The different ecotypes of a particular species may differ in their edaphic, biotic or microclimatic requirements. Thus, ecotypes are genetically adapted local population. However, they are able to reproduce with other ecotypes of the same species and produce fertile offspring.

Ecotypes can be classified and grouped together. A unit of classification which contains one or more ecotypes of a species is termed ecospecies. The term ecospecies has been proposed by Turesson. It is a unit of classification which contains one or more ecotypes, which although interfertile but do not cross or at least do not produce viable offsprings if crossed with ecotypes of other ecospecies. A species with a continuous distribution cannot be divided at any one point into two ecotypes. For this pattern of distribution, the term ecocline has been applied. Ecocline represents the continuous variation or gradual change in plant phenotype, and associated genotype along an environmental gradient. An ecad (also known as ecophene) is a plant species is a population of individuals which although belong to the same genetic stock, but differ markedly in phenotypes such as size, shape and number of leaves, etc. These variations are environmentally induced, and thus are temporary or reversible, i.e. one type of ecad may change into another with a change in its habitat. So, if different ecads are transplanted in the same habitat, all would become similar in appearance. Thus, ecads show phenotypic plasticity i.e. environmentally induced phenotypic variation. The phenotypic plasticity is the capacity of a single genotype to exhibit variable phenotypes in different environments. It is considered one of the major means by which plants can cope with environmental factor variability

15 Ecosystem Ecology

Ecosystem Ecology

An ecosystem (or ecological system) is a functional unit comprising all the organisms in a particular place interacting with one another and with their physical environment and interconnected by an ongoing flow of energy and a cycling of materials. The concept of an ecosystem was first formally proposed by the English botanist Arthur Tansley in 1935.

The term biogeocoenosis (proposed in the 1940s by the Soviet ecologist V. N. Sukachev) frequently used in Russian literature is roughly equivalent to the ecosystem. Its literal meaning is 'life and earth functioning together'. A key advance in the adoption of the ecosystem concept occurred after the appearance of a popular textbook by Eugene Odum. Odum's textbook was organized around the ecosystem concept. After Odum's textbook, a famous article in *Science* by Francis Evans (1956) mentioned the ecosystem as 'the basic unit in ecology'.

In the broadest sense, an ecosystem is the interacting system made up of all the living and non-living objects in a physically defined space. According to this simple definition, the size, location and timescale

at which ecosystems are defined can therefore precisely match the question that the scientist is trying to answer. An ecosystem could be of any size depending on the communities to be studied and its boundaries can be either real or arbitrary. An ecosystem may be as small as a single tree or as large as the entire Earth and can be studied for time periods as long as millions of years. An ecosystem can be visualized as a functional unit of nature. It has all components: biological and physical, necessary for survival. Accordingly, it is the basic unit around which theories and experiments of ecology are organized.

All ecosystems are open systems in the sense that energy and matter are exchanged with their surroundings. It might be theoretically possible to define particular examples of ecosystems that are closed systems, not exchanging matters with their surroundings, but nearly all ecosystems do exchanges of energy and matters with their surroundings. Ecosystems change through time. These changes may be gradual and subtle (losses of minerals from a weathering soil) or fast and dramatic (a fire sweeping through a forest). Both external forces (changes in climate or nutrient inputs) and internal dynamics (accumulation or depletion of materials in a soil or a lake) are important in driving temporal changes in ecosystems. In some cases, changes are directional and predictable (e.g. soil weathering, the filling of a lake basin), while in other cases changes may be specific and difficult to predict (e.g. the arrival of an invasive species).

Ecosystems ecology deals with the flow of energy and cycling of nutrients among organisms within a community and between organisms and the environment.

A thermodynamic system (or simply 'system') is a definite macroscopic region or space in the universe, in which one or more thermodynamic processes take place. Everything external to a thermodynamic system is called surroundings. System and surroundings are separated by a definite border called boundary.

Levels of organization

To study how organisms interact with each other and with their physical environments, several hierarchical levels of the organization have been recognized. Ecological patterns and processes vary as a function of the level of organization at which they operate.

Ecologists have identified four fundamental levels of the organization to study the interactions between organisms and their environment. These levels of organization include individual organism, population, community and ecosystem. Therefore, ecology ranges in scale from the study of an individual organism through the study of populations to the study of communities and ecosystems.

The most basic level of the ecological organization starts with the individual (a single plant, insect or bird). At the level of the organism, ecology deals with how individual organisms are affected by (and how they affect) their environment. Organismal ecology gives focus on the individual organisms' behaviour, physiology, morphology, etc. in response to the environment.

The next level of organization is the population. The term population has many uses and meanings in other fields of study. In ecology, a population is a group of individuals of the same species that occupy a given area. The population ecology deals with population growth and how and why a population changes over time

Populations of different species in an area do not function independently of each other. They interact with each other. Hence, the next, more complex level of organization of the interacting population of different species form is the community. Ecological communities are made up of interacting populations of different species within some defined geographical area. Community ecology deals with the composition and organization of ecological communities and community development. Communities occur on a wide variety of scales from small pond communities to huge tropical rainforests. At the largest scales, these communities are known as 'biomes'. A biome is a distinct ecological community of plants and animals living together in a particular climate (for example, tropical rainforests, coniferous forests, savannas). It is characterized by distinctive vegetation distributed over a wide geographical area and defined largely by regional climatic conditions

An ecosystem (or ecological system) is the interacting system made up of all the living and non-living components in a physically defined space. Because an ecosystem is a system, it has boundaries. All systems that encompass interacting biotic and abiotic components may be considered as an ecosystem. Ecosystems are complex, open, hierarchically organized, self-organizing and self-regulated systems. Ecosystems ecology deals with the flow of energy and cycling of nutrients among organisms within a community and between organisms and the environment. The highest level of organization for the ecological study is the biosphere. It is an ultimate ecosystem. It includes all ecosystems present on the Earth. In a strict sense, the biosphere represents all the living organisms of the Earth. But in ecology, the biosphere (also known as the ecosphere) is a functional concept which emphasizes the interrelationship between all living organisms and their environment on a planetary scale.

Although many ecologists have recognized 'ecosystem' as the fourth level of organization for an understanding of ecological phenomena. Some ecologists are considering the use of 'ecosystem' as the fourth level of organization is inappropriate because it does not include any new biological organization. Some have argued that the term 'landscape' would be a suitable term for a level of organization defined as an ecological system containing more than one community type.

Autecology is the study of the interaction between organisms and their environments at the level of an individual, a population or an entire species.

Synecology is the study of an ecological community. It is also called community ecology. It is the synecology which describes the ecological community as a whole, especially the links between organisms.

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 numbers¹¹start superscript, 1, end superscript. 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?

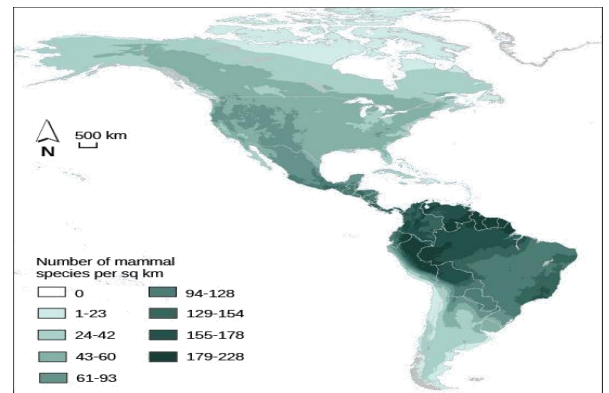
Two important measures ecologists use to describe the composition of a community are species richness and species diversity

- 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. (for instance, with 90 percent of the trees belonging to a single species). 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.

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.

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.

The intertidal sea star *Pisaster ochraceus*, which is found in the northwestern United States, is perhaps the most famous example of a keystone species.

In a classic experiment of community ecology, the sea stars were experimentally removed from the intertidal zone where they lived. As a result, populations of their prey (mussels) increased, altering the species composition of the community and sharply reducing species diversity.

When the sea stars were present, about 25 species of barnacles and algae were found in the lower part of the intertidal zone, but when they were missing, the mussel population expanded downward and almost entirely replaced these other species.

This type of sharp reduction in diversity or collapse of community structure commonly occurs when a keystone species is removed. In this case, the loss of diversity happened because the mussels crowded out other species, which could normally persist because the sea stars kept the mussels in check.

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 examples 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. 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
- Hetrotroths
- 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:

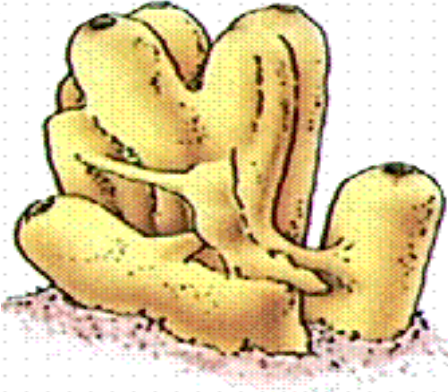
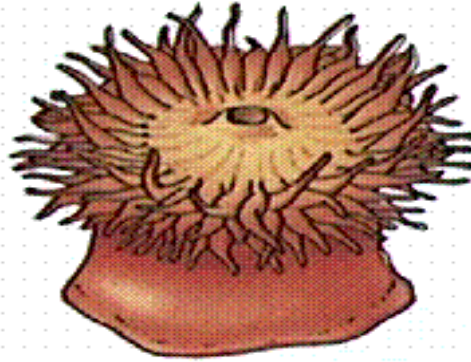
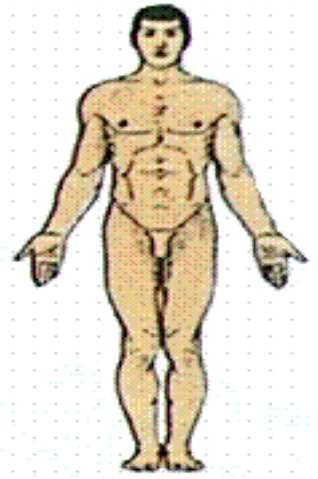
- Makes up only 5% of all animal species
- They have a backbone or vertebral column
- Examples: Humans, Fish, Reptiles, Amphibians & Birds

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

Asymmetrical**Radial****Bilateral****Introduction to the Animal Kingdom**

Animal evolution began in the ocean over 600 million years ago with tiny creatures that probably do not resemble any living organism today. Since then, animals have evolved into a highly-diverse kingdom. Although over one million extant (currently living) species of animals have been identified, scientists are continually discovering more species as they explore ecosystems around the world. The number of extant species is estimated to be between 3 and 30 million.

But what is an animal? While we can easily identify dogs, birds, fish, spiders, and worms as animals, other organisms, such as corals and sponges, are not as easy to classify. Animals vary in complexity, from sea sponges to crickets to chimpanzees, and scientists are faced with the difficult task of classifying them within a unified system. They must identify traits that are common to all animals as well as traits that can be used to distinguish among related groups of animals. The animal classification system characterizes animals based on their anatomy, morphology, evolutionary history, features of embryological development, and genetic makeup. This classification scheme is constantly developing as new information about species arises. Understanding and classifying the great variety of living species help us better understand how to conserve the diversity of life on earth.

Even though members of the animal kingdom are incredibly diverse, most animals share certain features that distinguish them from organisms in other kingdoms. All animals are eukaryotic, multicellular organisms, and almost all animals have a complex tissue structure with differentiated and specialized tissues. Most animals are motile, at least during certain life stages. All animals require a source of food and are, therefore, heterotrophic: ingesting other living or dead organisms. This feature distinguishes them from autotrophic organisms, such as most plants, which synthesize their own nutrients through photosynthesis. As heterotrophs, animals may be carnivores, herbivores, omnivores, or parasites. Most animals reproduce sexually with the offspring passing through a series of developmental stages that establish a fixed body plan. The body plan refers to the morphology of an animal, determined by developmental cues.

Animal Characterization Based on Body Symmetry

At a very basic level of classification, true animals can be largely divided into three groups based on the type of symmetry of their body plan: radially symmetrical, bilaterally symmetrical, and asymmetrical. Only a few animal groups display radial symmetry, while asymmetry is a unique feature of phyla Porifera (sponges). All types of symmetry are well suited to meet the unique demands of a particular animal's lifestyle.

Radial Symmetry:

Radial symmetry is the arrangement of body parts around a central axis, like rays on a sun or pieces in a pie. Radially symmetrical animals have top and bottom surfaces, but no left and right sides, or front and back. The two halves of a radially symmetrical animal may be described as the side with a mouth ("oral side") and the side without a mouth ("aboral side"). This form of symmetry marks the body plans

of animals in the phyla Ctenophora (comb jellies) and Cnidaria (corals, sea anemones, and other jellies) . Radial symmetry enables these sea creatures, which may be sedentary or only capable of slow movement or floating, to experience the environment equally from all directions.

Bilateral Symmetry

Bilateral symmetry involves the division of the animal through a sagittal plane, resulting in two mirror-image, right and left halves, such as those of a butterfly, crab, or human body . Animals with bilateral symmetry have a "head" and "tail" (anterior vs. posterior), front and back (dorsal vs. ventral), and right and left sides. All true animals, except those with radial symmetry, are bilaterally symmetrical. The evolution of bilateral symmetry and, therefore, the formation of anterior and posterior (head and tail) ends promoted a phenomenon called cephalization, which refers to the collection of an organized nervous system at the animal's anterior end. In contrast to radial symmetry, which is best suited for stationary or limited-motion lifestyles, bilateral symmetry allows for streamlined and directional motion. In evolutionary terms, this simple form of symmetry promoted active mobility and increased sophistication of resource-seeking and predator-prey relationships.

Animals in the phylum Echinodermata (such as sea stars, sand dollars, and sea urchins) display radial symmetry as adults, but their larval stages exhibit bilateral symmetry . This is termed secondary radial symmetry. They are believed to have evolved from bilaterally symmetrical animals; thus, they are classified as bilaterally symmetrical.

Asymmetry

Only members of the phylum Porifera (sponges) have no body plan symmetry. There are some fish species, such as flounder, that lack symmetry as adults. However, the larval fish are bilaterally symmetrical.

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

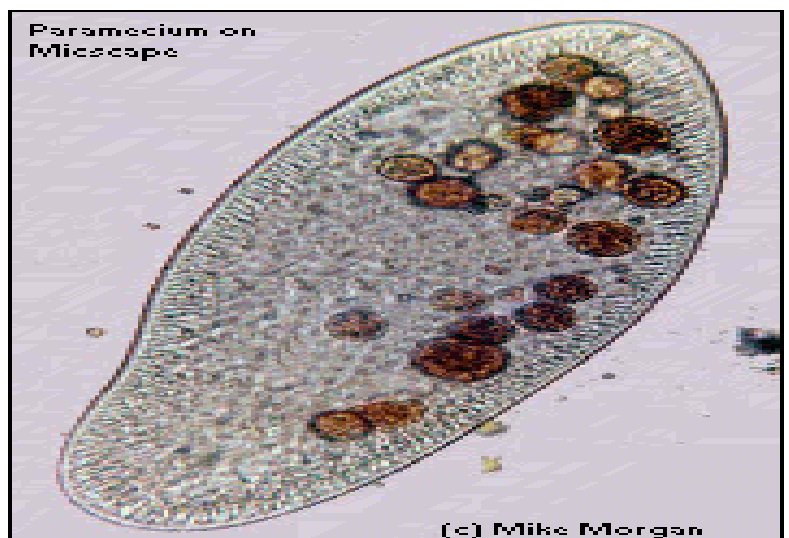
Grouped by movement

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

Protozoan Characteristics

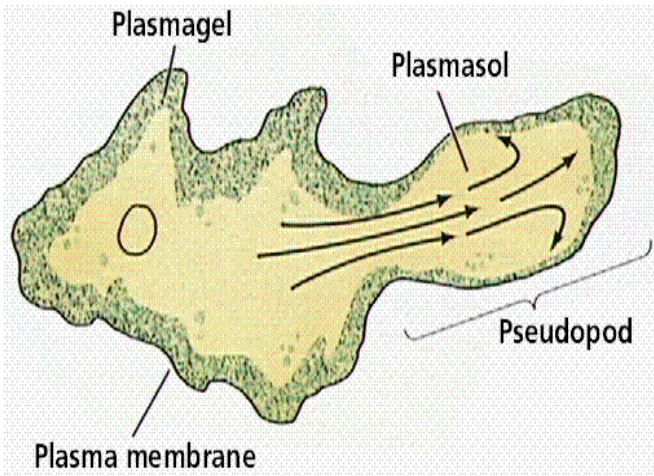
- ✓ No cell wall
- ✓ Free-living or parasitic
- ✓ Consumers
- ✓ Habitat – aquatic (ponds,lakes, oceans)
- ✓ Examples: amoeba, paramecium, dinoflagellates

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

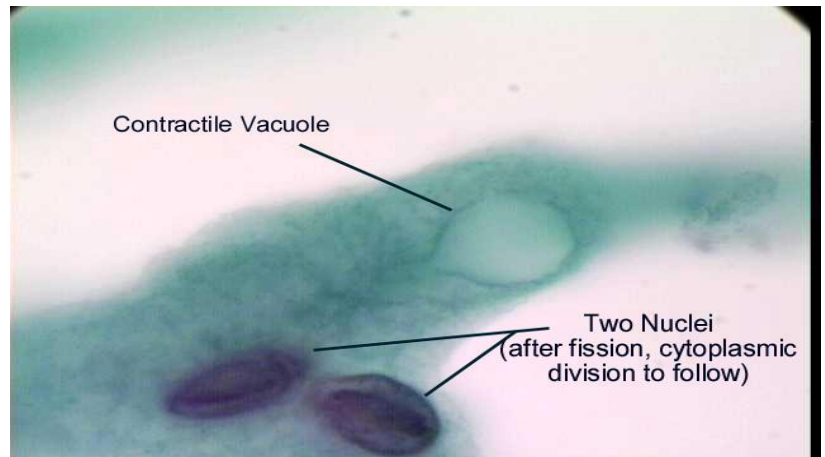
Dysentery (an illness)

- 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
- Exmaples:

2. Trypanosoma - causes African Sleeping Sickness

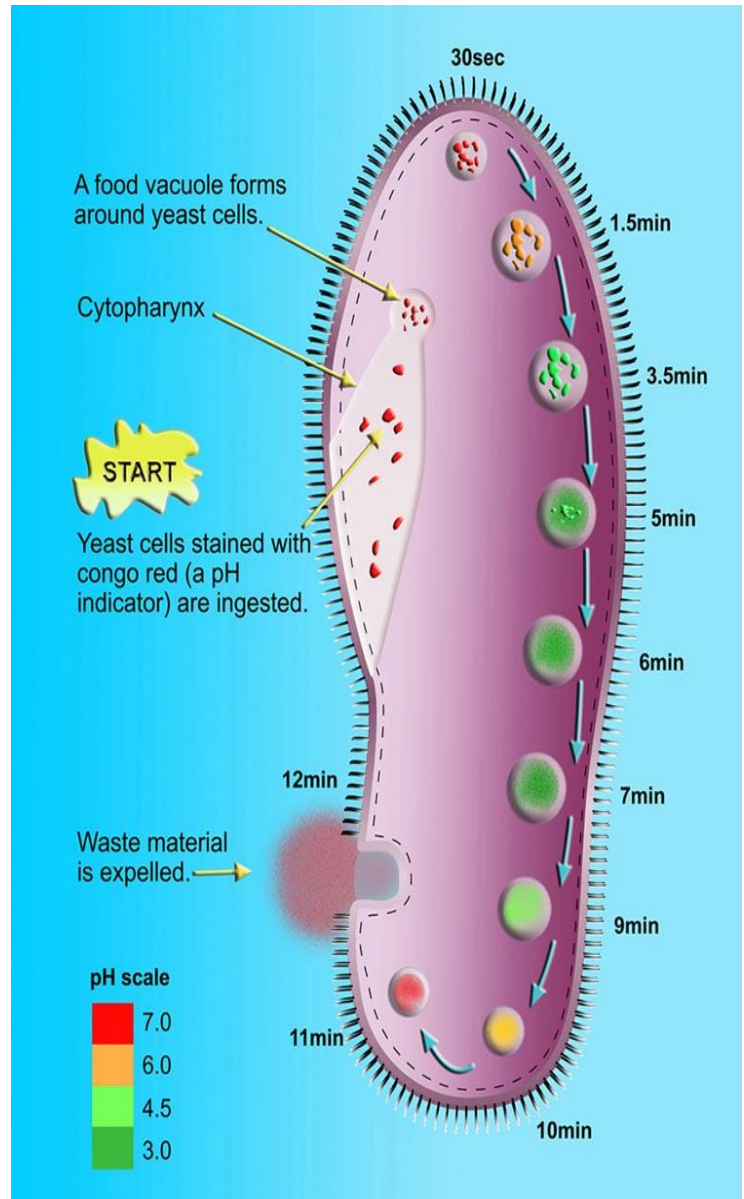
- spread by tsetse fly

4. Example 4: Protozoan - sporozoans

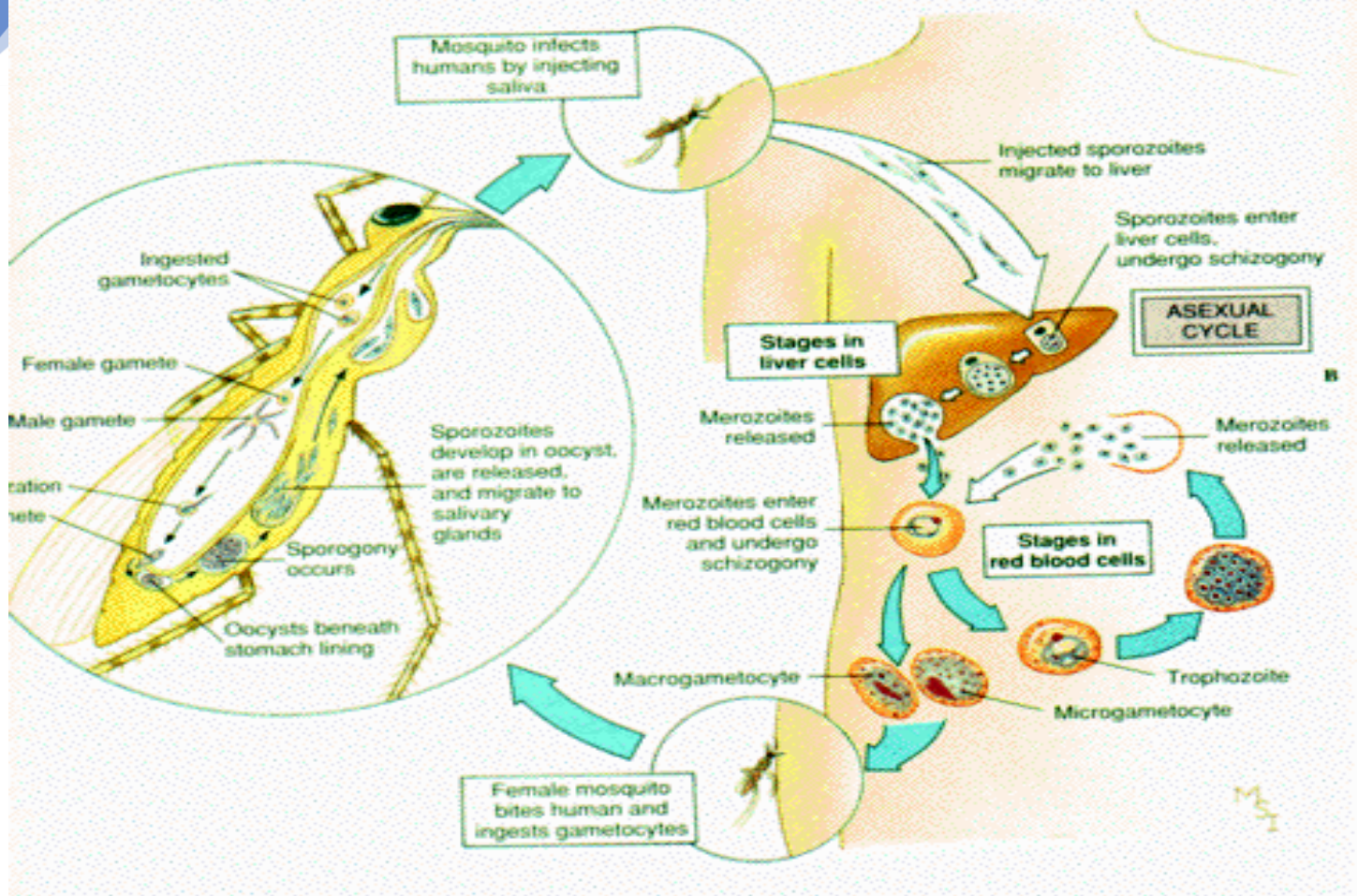
- Locomotion - parasitic
- reproduction
 - spores

Plasmodium - Causes [Malaria](#)

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



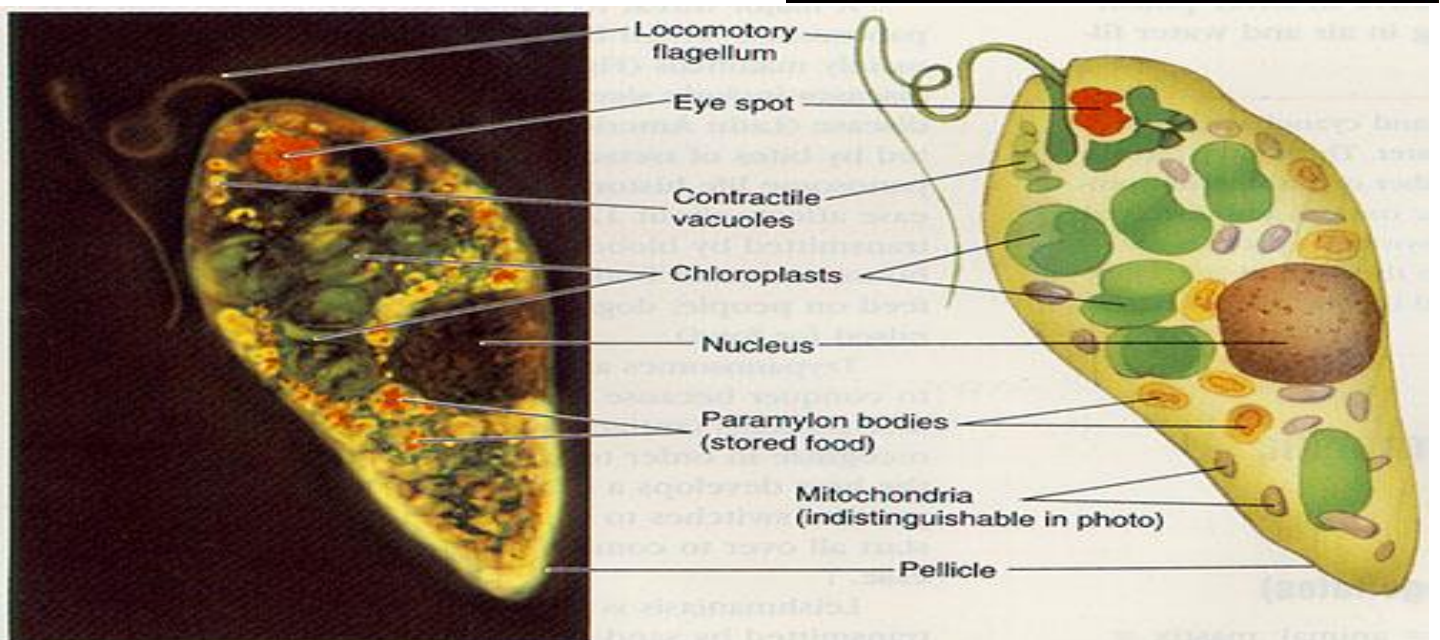
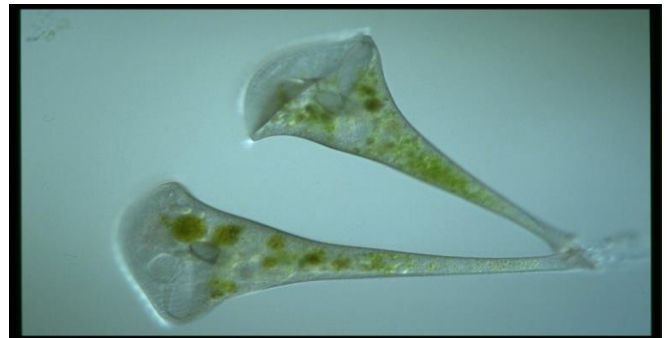
III The Diversity of Animal Life

**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, spirogyra

1. Diatoms

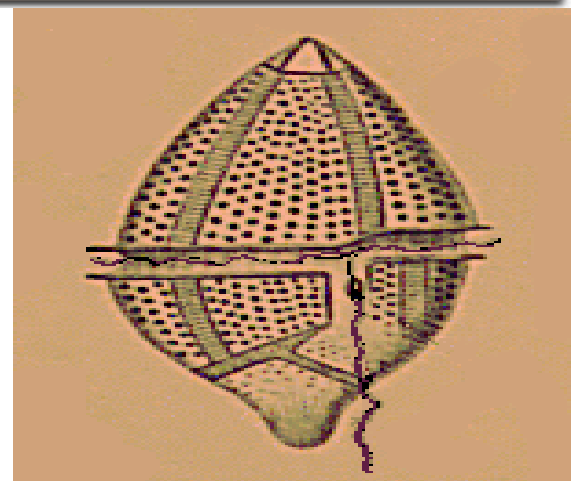
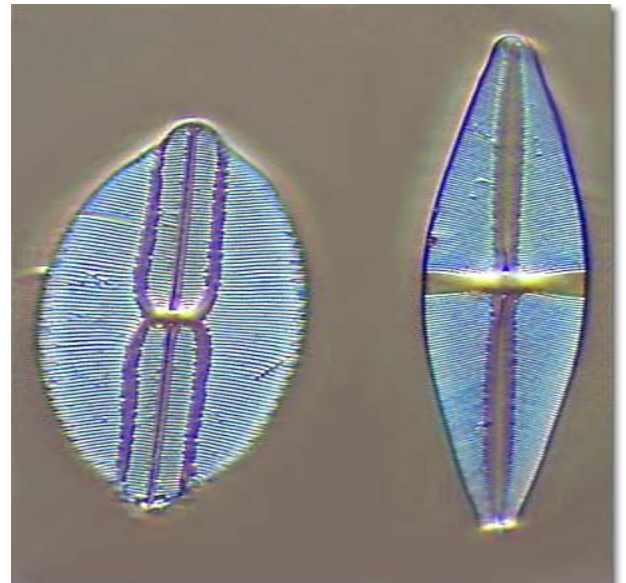
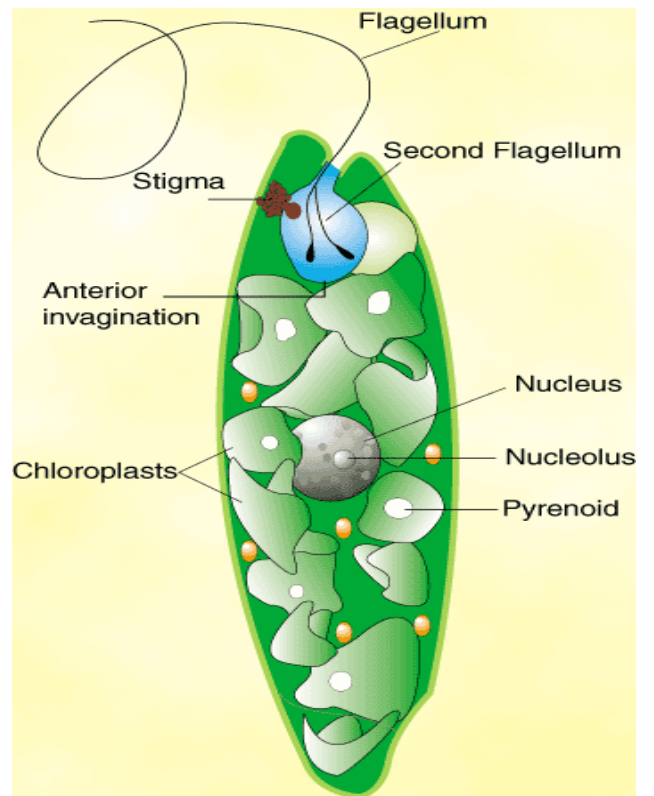
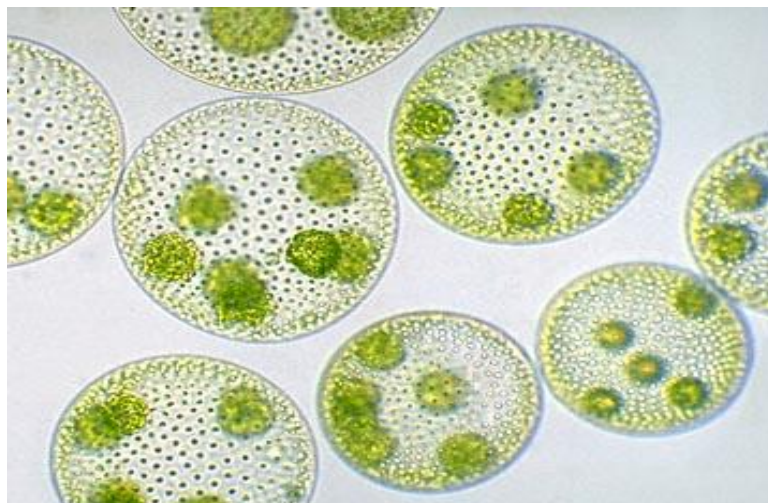
- - float in water
- - photosynthesis
- - unicellular
- - silica shells
- Commercial value: Insulating materials, Abrasives , Ceramics, Filtering

2. Dinoflagellates

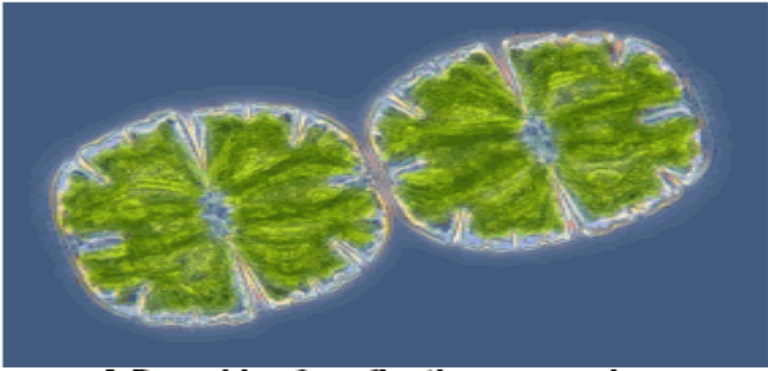
- - move by two flagella
- - autotrophs
- - green glow and red tides

3. Green Algae (Lab 37)

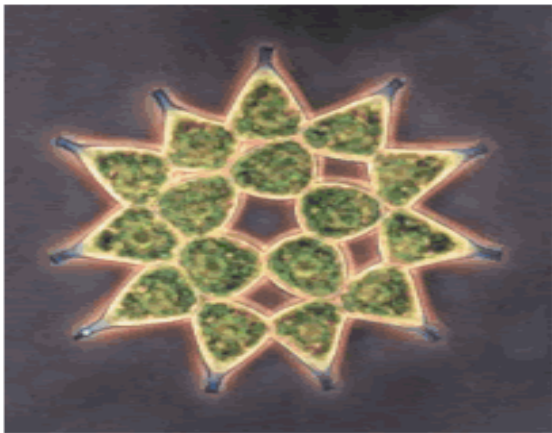
- Most freshwater
- Food Source – called Plankton
- Some are:
 - Free-living
 - Colony
 - filament



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.

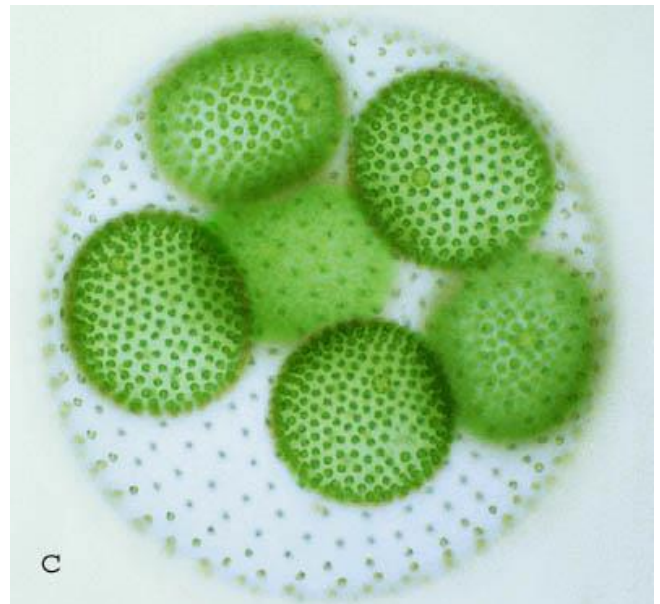
Fungus Protists

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

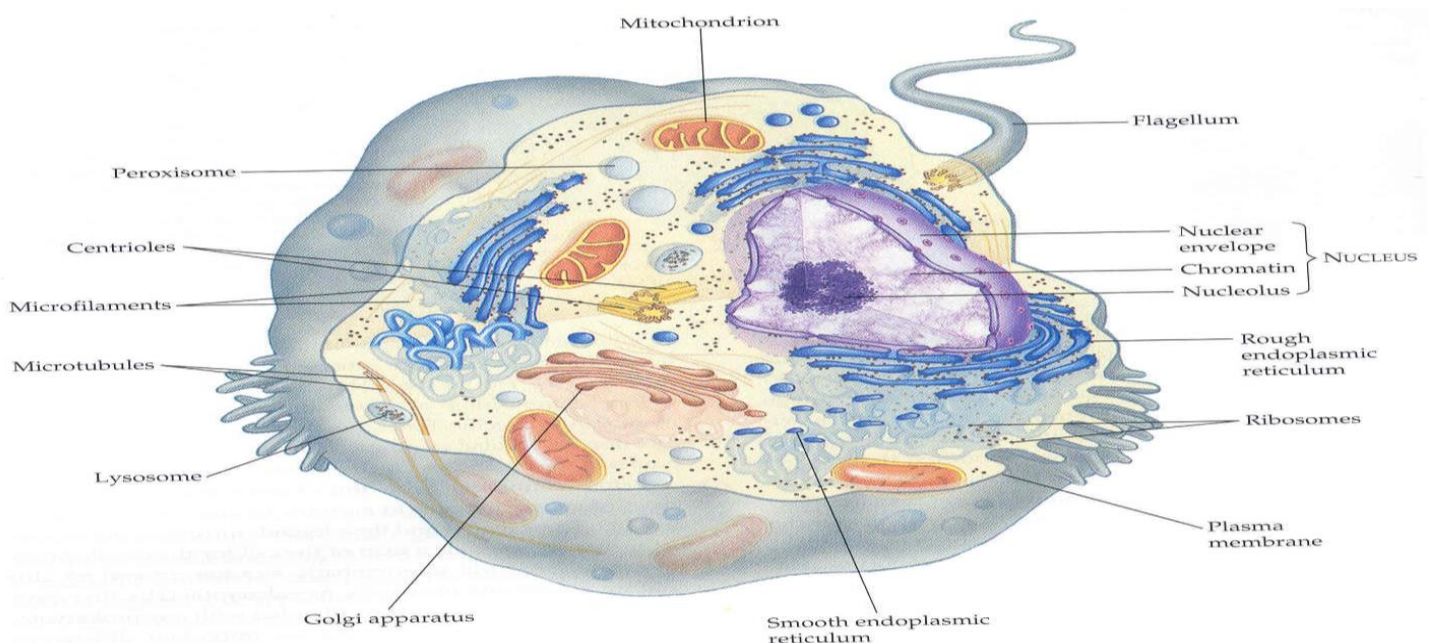
Ciliates

Amoeboid Protozoans

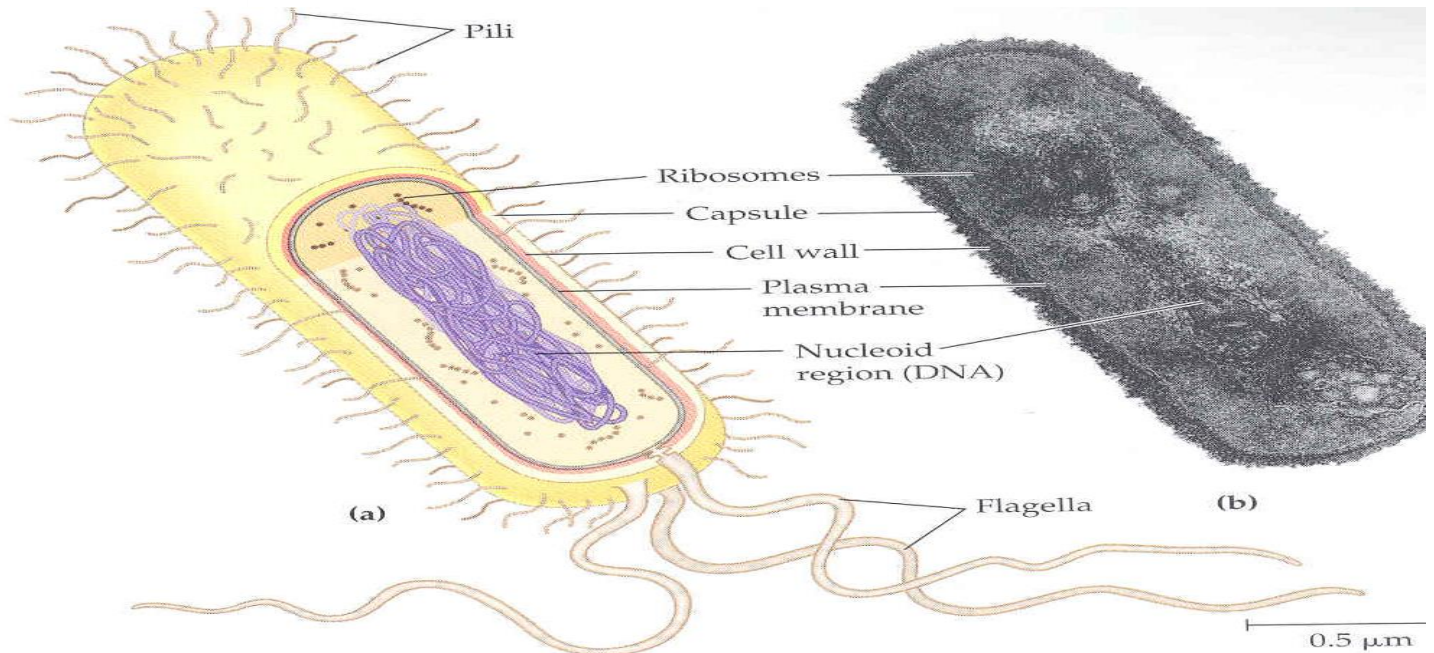
Flagellated Protozoans

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



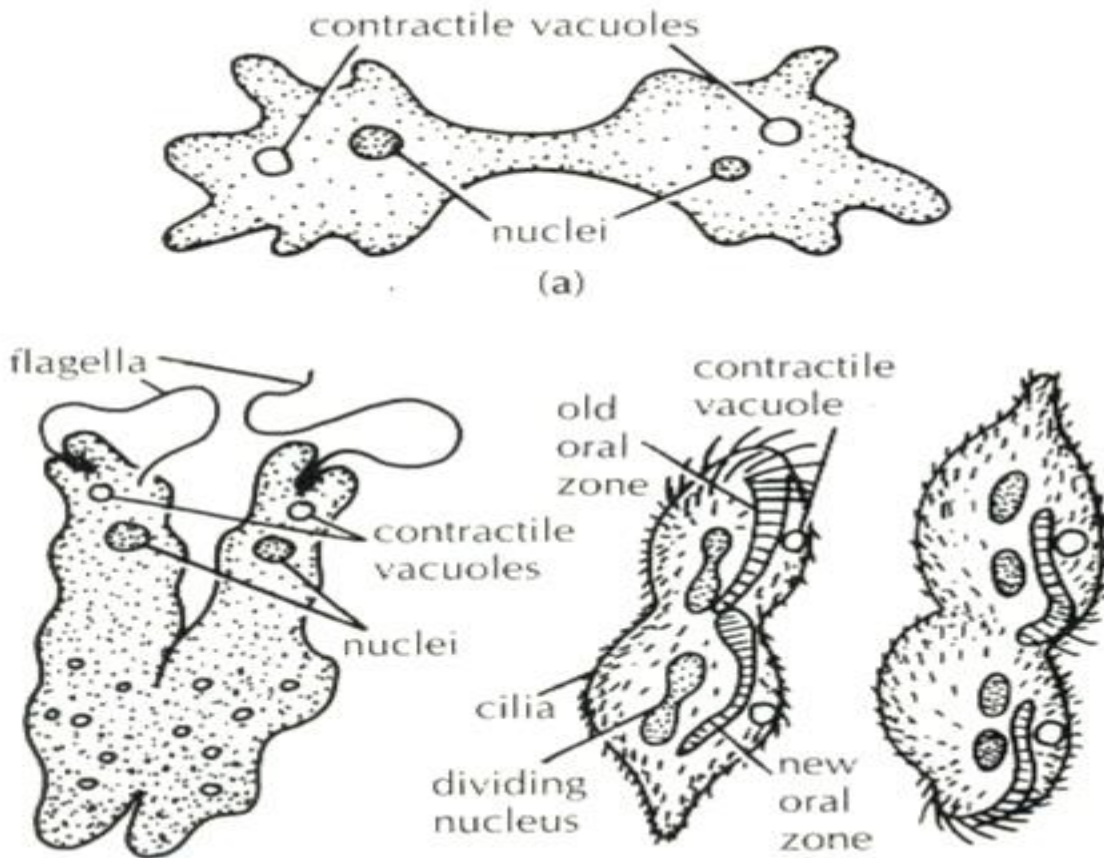
Adaptability

- 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

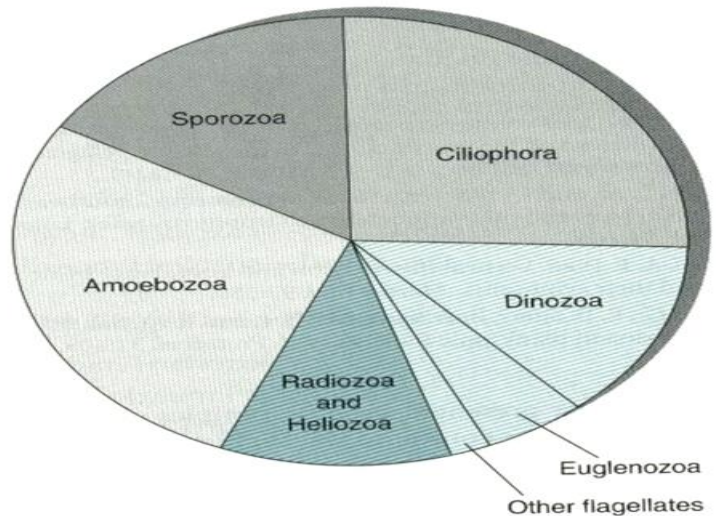
Phylum Radiozoa

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 (CaCO₃)

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

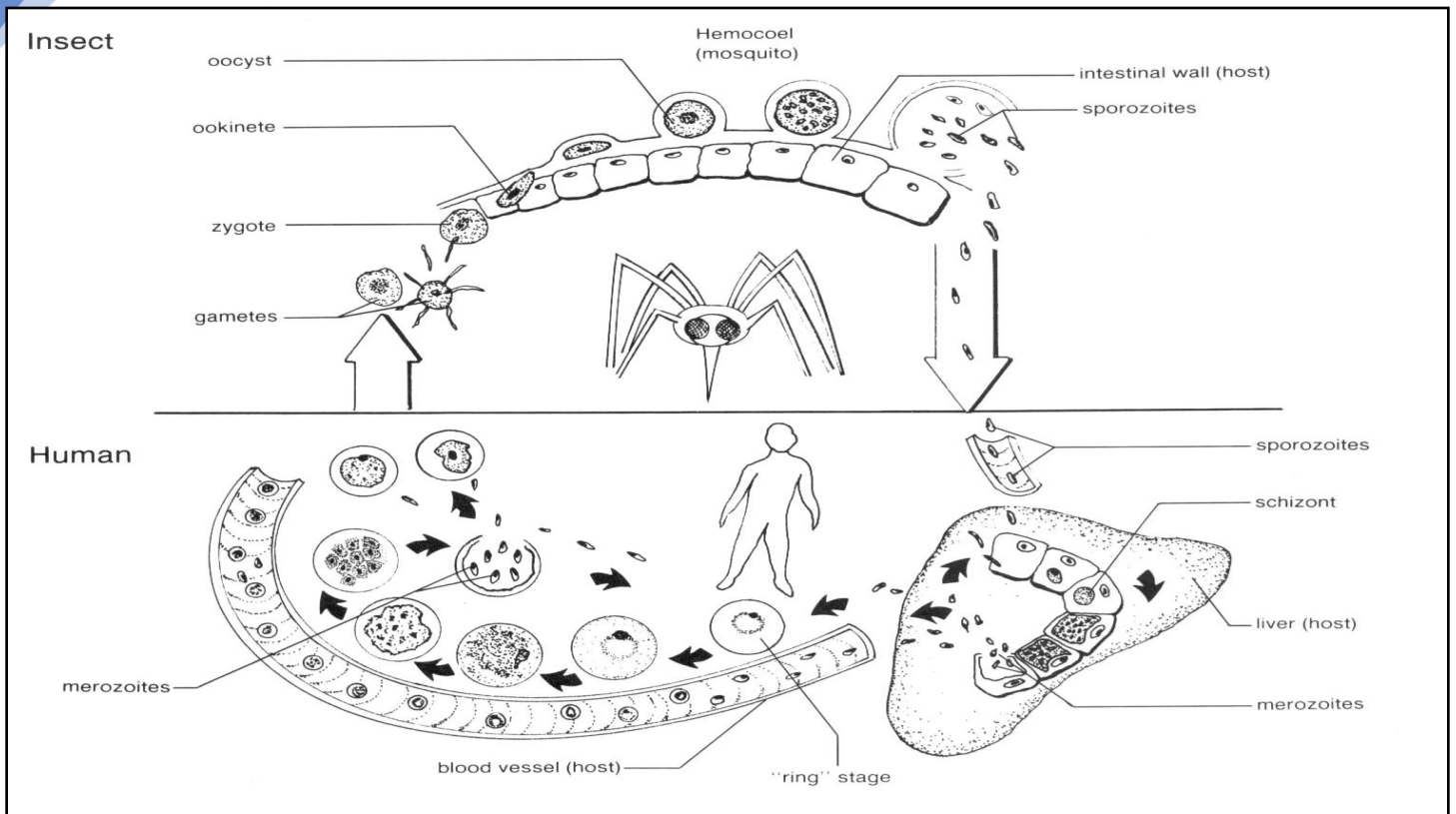
Most individuals are sessile and have a single flagellum that beats to obtain food and nutrients

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*)



Protozoa: Introduction

Protozoa

Protozoa are one-celled animals found worldwide in most habitats. Most species are free living, but all higher animals are infected with one or more species of protozoa. Infections range from asymptomatic to life threatening, depending on the species and strain of the parasite and the resistance of the host.

Structure

Protozoa are microscopic unicellular eukaryotes that have a relatively complex internal structure and carry out complex metabolic activities. Some protozoa have structures for propulsion or other types of movement.

Classification

On the basis of light and electron microscopic morphology, the protozoa are currently classified into six phyla. Most species causing human disease are members of the phyla Sacromastigophora and Apicomplexa.

Life Cycle Stages

The stages of parasitic protozoa that actively feed and multiply are frequently called trophozoites; in some protozoa, other terms are used for these stages. Cysts are stages with a protective membrane or thickened wall. Protozoan cysts that must survive outside the host usually have more resistant walls than cysts that form in tissues.

Reproduction

Binary fission, the most common form of reproduction, is asexual; multiple asexual division occurs in some forms. Both sexual and asexual reproduction occur in the Apicomplexa.

Nutrition

All parasitic protozoa require preformed organic substances—that is, nutrition is holozoic as in higher animals.

Introduction

The Protozoa are considered to be a subkingdom of the kingdom Protista, although in the classical system they were placed in the kingdom Animalia. More than 50,000 species have been described, most of which are free-living organisms; protozoa are found in almost every possible habitat. The fossil record in the form of shells in sedimentary rocks shows that protozoa were present in the Precambrian era. Anton van Leeuwenhoek was the first person to see protozoa, using microscopes he constructed with simple lenses. Between 1674 and 1716, he described, in addition to free-living protozoa, several parasitic species from animals, and *Giardia lamblia* from his own stools. Virtually all humans have protozoa living in or on their body at some time, and many persons are infected with one or more species throughout their life. Some species are considered commensals, i.e., normally not harmful, whereas others are pathogens and usually produce disease. Protozoan diseases range from very mild to life-threatening. Individuals whose defenses are able to control but not eliminate a parasitic infection become carriers and constitute a source of infection for others. In geographic areas of high prevalence, well-tolerated infections are often not treated to eradicate the parasite because eradication would lower the individual's immunity to the parasite and result in a high likelihood of reinfection.

Many protozoan infections that are inapparent or mild in normal individuals can be life-threatening in immunosuppressed patients, particularly patients with acquired immune deficiency syndrome (AIDS). Evidence suggests that many healthy persons harbor low numbers of *Pneumocystis carinii* in their lungs. However, this parasite produces a frequently fatal pneumonia in immunosuppressed patients such as those with AIDS. *Toxoplasma gondii*, a very common protozoan parasite, usually causes a rather mild initial illness followed by a long-lasting latent infection. AIDS patients, however, can develop fatal toxoplasmic encephalitis. *Cryptosporidium* was described in the 19th century, but widespread human infection has only recently been recognized. *Cryptosporidium* is another protozoan that can produce serious complications in patients with AIDS. Microsporidiosis in humans was reported in only a few instances prior to the appearance of AIDS. It has now become a more common infection in AIDS patients. As more thorough studies of patients with AIDS are made, it is likely that other rare or unusual protozoan infections will be diagnosed.

Acanthamoeba species are free-living amoebae that inhabit soil and water. Cyst stages can be airborne. Serious eye-threatening corneal ulcers due to *Acanthamoeba* species are being reported in individuals who use contact lenses. The parasites presumably are transmitted in contaminated lens-cleaning solution. Amoebae of the genus *Naegleria*, which inhabit bodies of fresh water, are responsible for almost all cases of the usually fatal disease primary amoebic meningoencephalitis. The amoebae are thought to enter the body from water that is splashed onto the upper nasal tract during swimming or diving. Human infections of this type were predicted before they were recognized and reported, based on laboratory studies of *Acanthamoeba* infections in cell cultures and in animals.

The lack of effective vaccines, the paucity of reliable drugs, and other problems, including difficulties of vector control, prompted the World Health Organization to target six diseases for increased research and training. Three of these were protozoan infections—malaria, trypanosomiasis, and leishmaniasis. Although new information on these diseases has been gained, most of the problems with control persist.

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

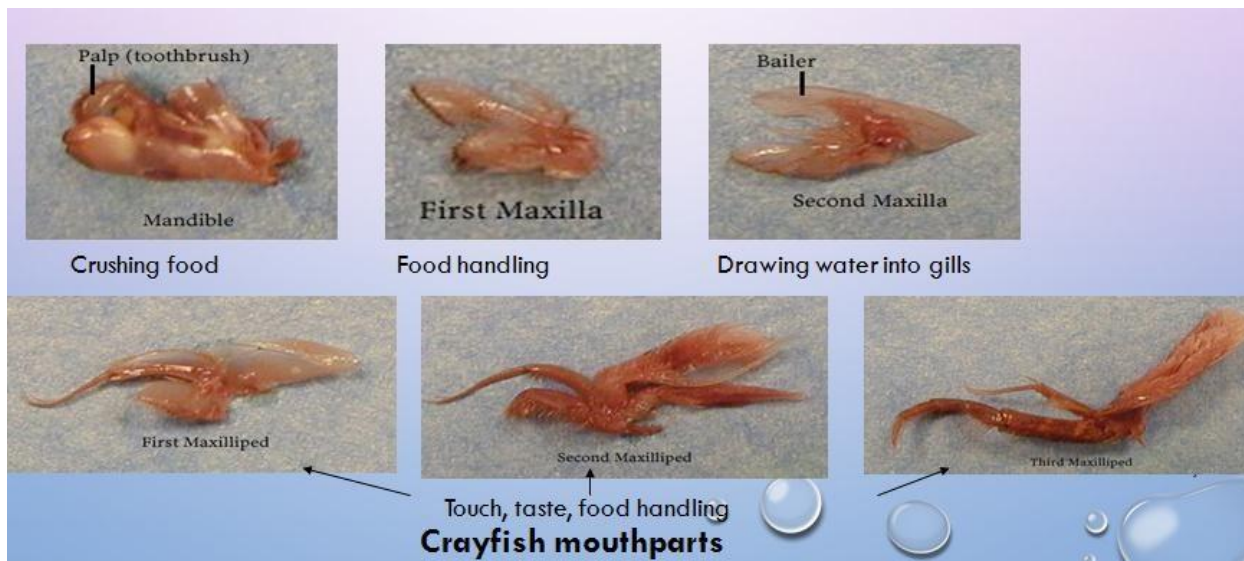
Soft and permeable or hard, impermeable

- 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

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 CaCO₃ 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

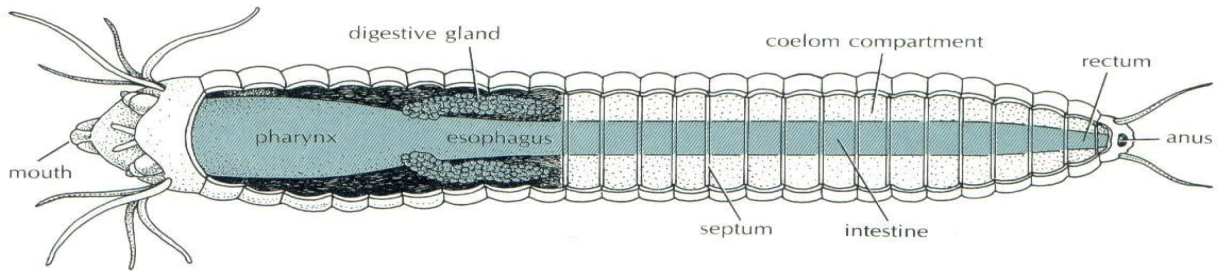
Locomotion

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.

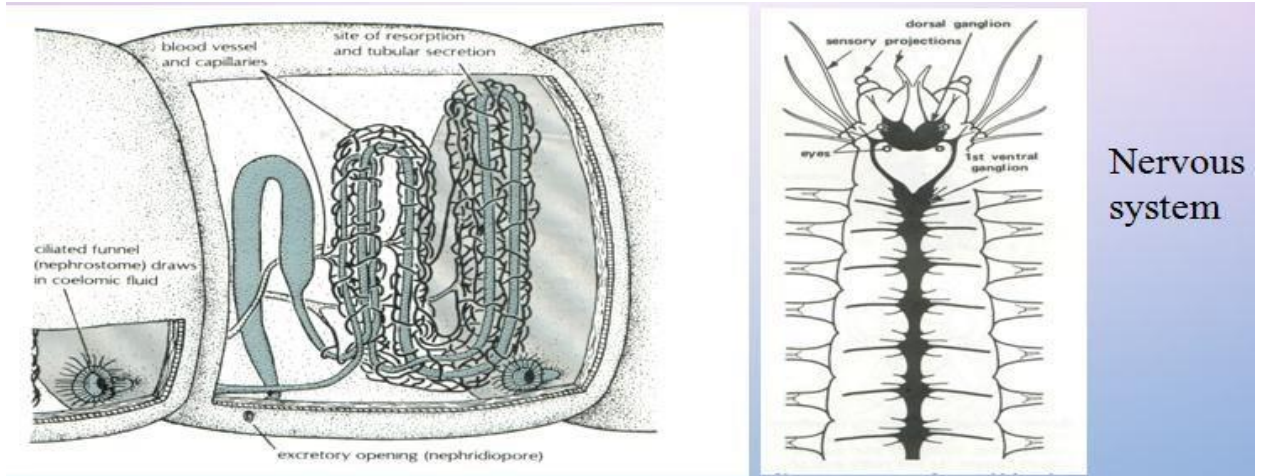
Digestive System



Circulatory System

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

Excretory & Nervous System



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 worlds 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 Stelleroidea
- 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 "Cuverian tubules". Sticky and toxic tentacles which are shot out the anus. Also eviscerates to avoid predation. Internal organs regenerate after a period of time

Phylum Echinodermata

Echinodermata are so named owing to their spiny skin (from the Greek "echinos" meaning "spiny" and "dermos" meaning "skin"). This phylum is a collection of about 7,000 described living species. Echinodermata are exclusively marine organisms. Sea stars, sea cucumbers, sea urchins, sand dollars, and brittle stars are all examples of echinoderms. To date, no freshwater or terrestrial echinoderms are known.

Sea stars

Star stars are among the most familiar of marine invertebrates. They are members of the phylum Echinodermata.

Morphology and Anatomy

Adult echinoderms exhibit pentaradial symmetry and have a calcareous endoskeleton made of ossicles, although the early larval stages of all echinoderms have bilateral symmetry. The endoskeleton is developed by epidermal cells and may possess pigment cells that give vivid colors to these animals, as well as cells laden with toxins. Echinoderms possess a simple digestive system which varies according to the animal's diet. Starfish are mostly carnivorous and have a mouth, oesophagus, two-part pyloric stomach with a pyloric duct leading to the intestine and rectum, with the anus located in the center of the aboral body surface. In many species, the large cardiac stomach can be everted and digest food outside the body. Gonads are present in each arm. In echinoderms such as sea stars, every arm bears two rows of tube feet on the oral side which help in attachment to the substratum. These animals possess a true coelom that is modified into a unique circulatory system called a water vascular system. The more notably distinct trait, which most echinoderms have, is their remarkable powers of regeneration of tissue, organs, limbs, and, in some cases, complete regeneration from a single limb.

Sea cucumbers

Sea cucumbers are a member of the phylum Echinodermata which are found on the sea floor worldwide. As with all echinoderms, sea cucumbers have an endoskeleton just below the skin, calcified structures that are usually reduced to isolated microscopic ossicles joined by connective tissue.

Water Vascular System

Echinoderms possess a unique ambulacral or water vascular system, consisting of a central ring canal and radial canals that extend along each arm. Water circulates through these structures and facilitates gaseous exchange as well as nutrition, predation, and locomotion. The water vascular system also projects from holes in the skeleton in the form of tube feet. These tube feet can expand or contract based on the volume of water (hydrostatic pressure) present in the system of that arm

The water vascular system of the sea star

1. Pyloric stomach 2. Intestine 3. Rectal gland 4. Stone canal 5. Madreporite 6. Pyloric duct 7. Pyloric cecum 8. Cardiac stomach 9. Gonad 10. Ambulacral plates 11. Ampullae

The madreporite is a light-colored, calcareous opening used to filter water into the water vascular system of echinoderms. Acting as a pressure-equalizing valve, it is visible as a small red or yellow button-like structure (similar to a small wart) on the aboral surface of the central disk of a sea star. Close up, it is visibly structured, resembling a "madrepore" colony. From this, it derives its name. Water enters the madreporite on the aboral side of the echinoderm. From there, it passes into the stone canal, which moves water into the ring canal. The ring canal connects the radial canals (there are five in a pentaradial animal), and the radial canals move water into the ampullae, which have tube feet through which the water moves. By moving water through the unique water vascular system, the echinoderm can move and force open mollusk shells during feeding.

Other Body Systems

The nervous system in these animals is a relatively simple structure with a nerve ring at the center and five radial nerves extending outward along the arms. Structures analogous to a brain or derived from fusion of ganglia are not present in these animals.

Podocytes, cells specialized for ultrafiltration of bodily fluids, are present near the center of echinoderms. These podocytes are connected by an internal system of canals to the madreporite.

Echinoderms are sexually dimorphic and release their eggs and sperm cells into water; fertilization is external. In some species, the larvae divide asexually and multiply before they reach sexual maturity. Echinoderms may also reproduce asexually, as well as regenerate body parts lost in trauma.

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.

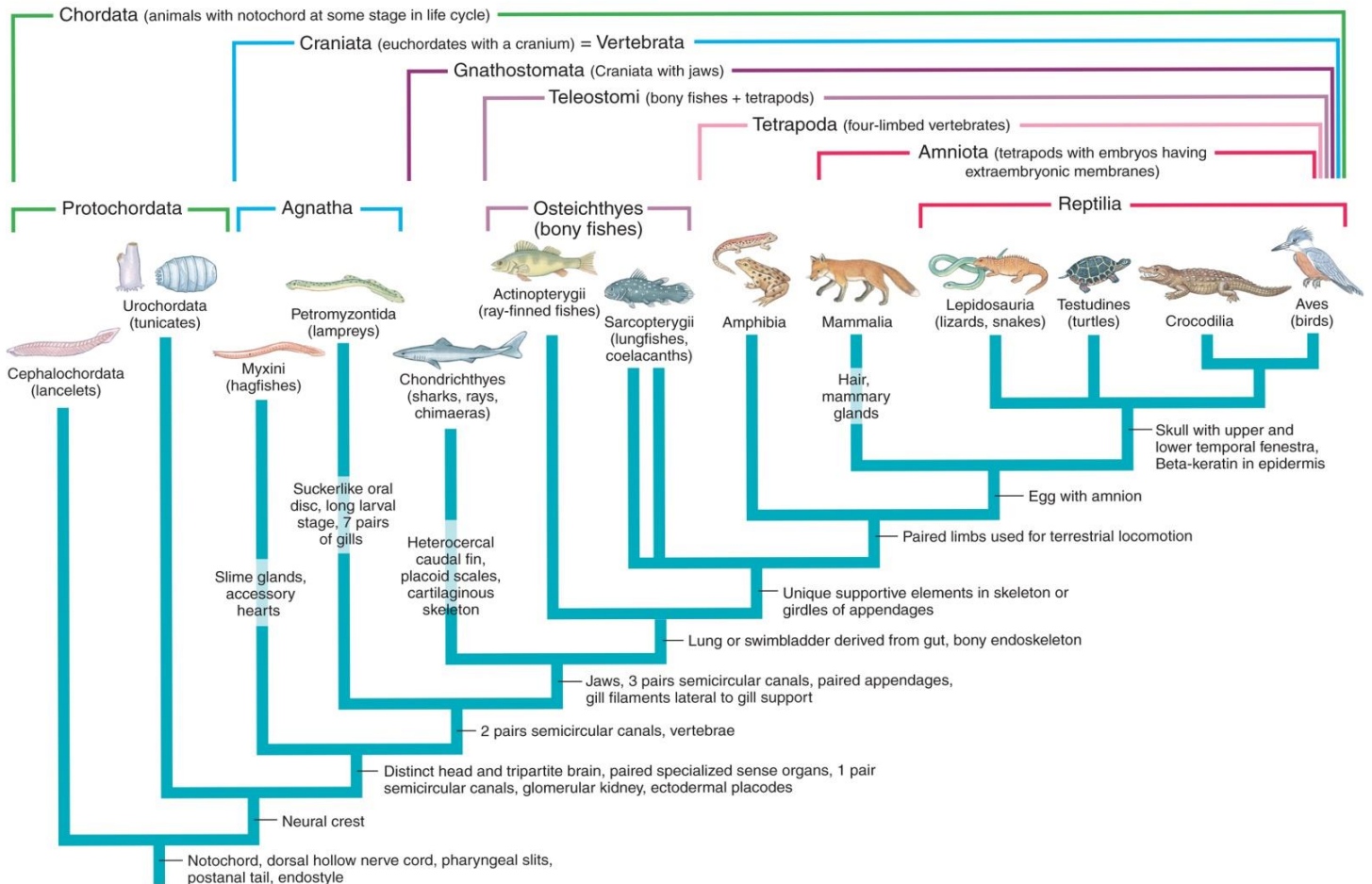
4. Endostyle or Thyroid Gland

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.

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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 boney 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 high yielding, 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**
- **Amog 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
- There 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

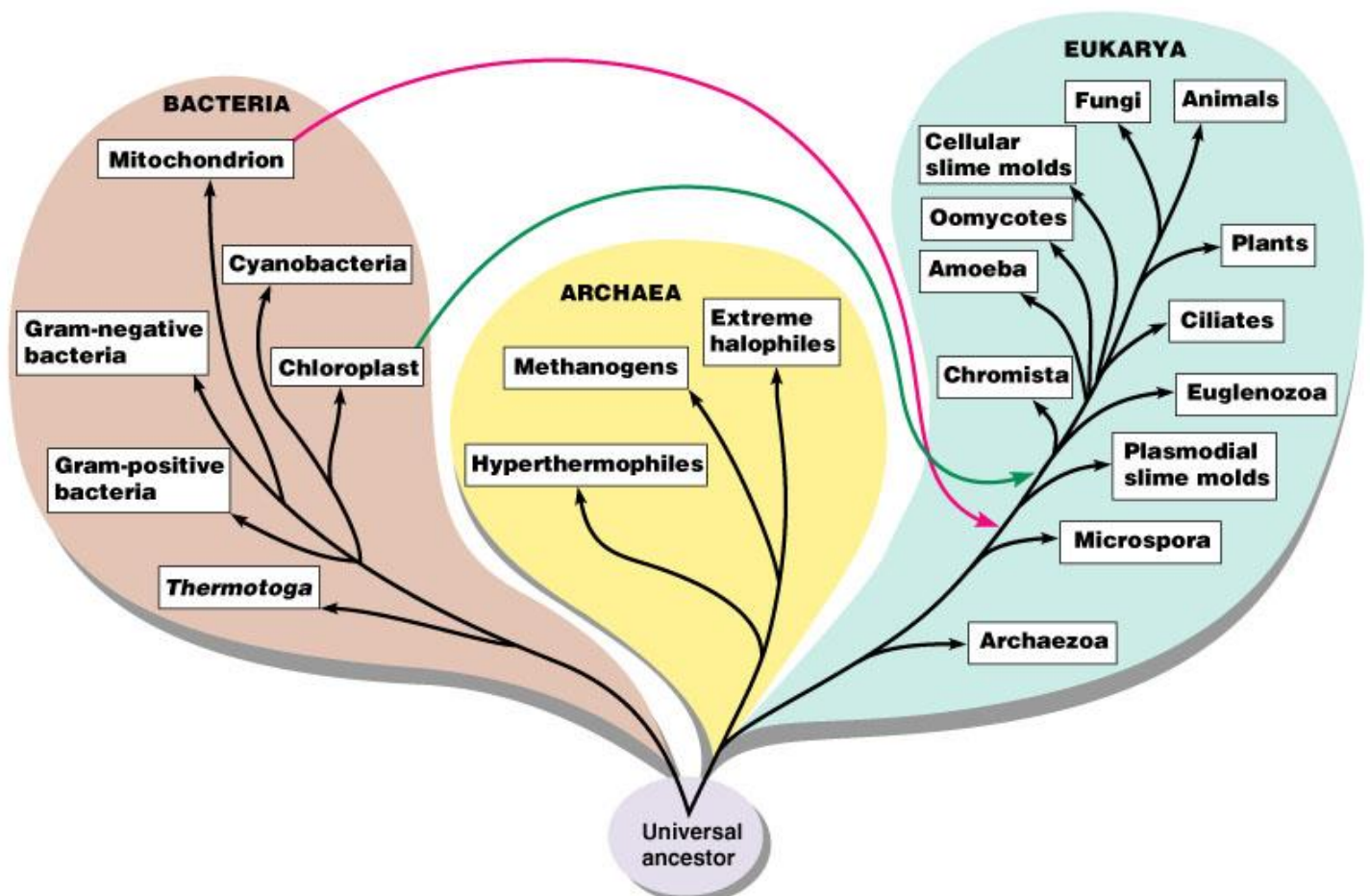
- Appendix 1: Total ban on exploitation
- Appendix 2: Limited exploitation subject to quotas
- Appendix 3: Species requiring protection in certain states only
- Species are reassessed every 2 years

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

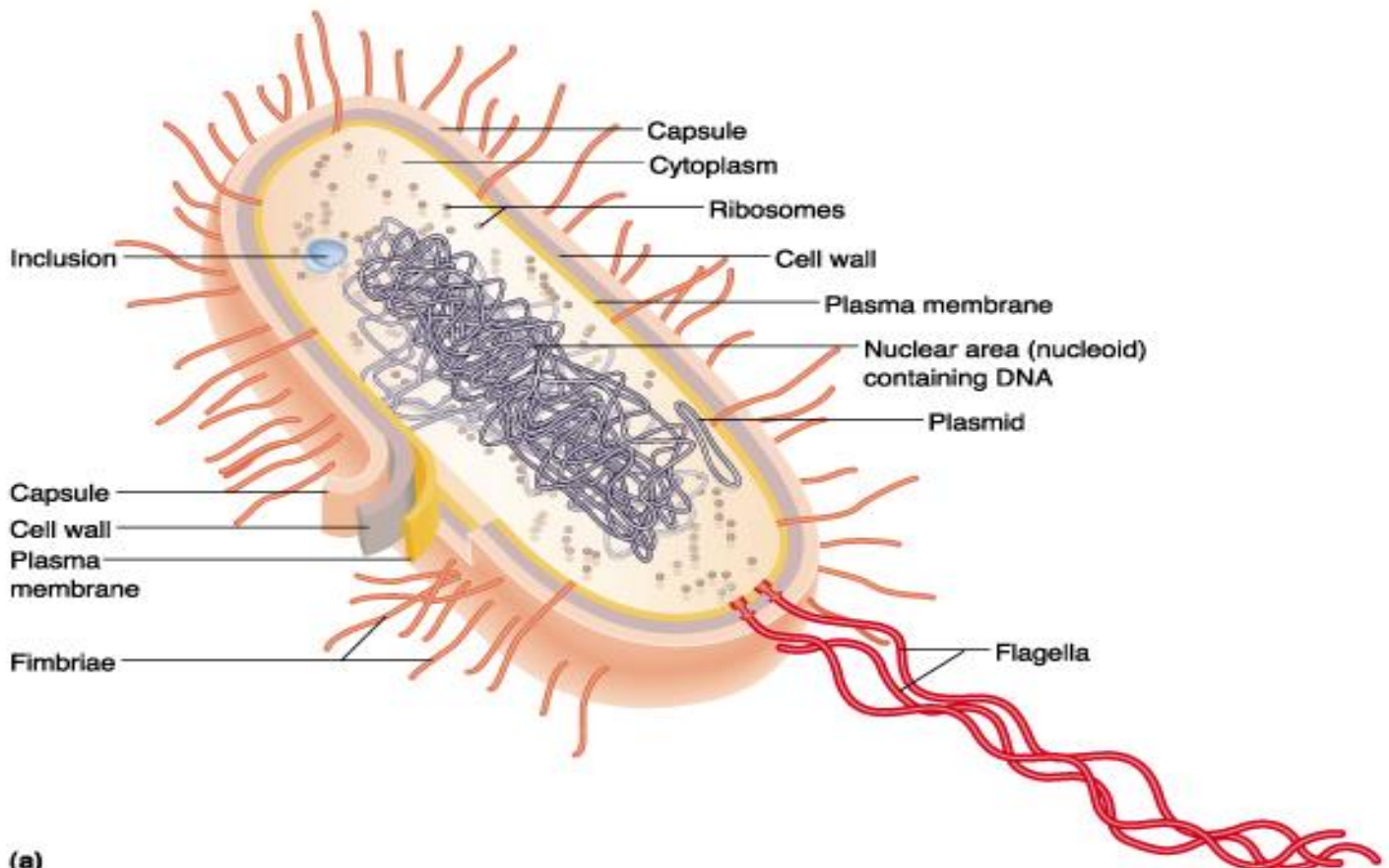
- Set up in 1961 as a non-governmental organisation
- Raises funds for conservation
- Lobbies parliaments for conservation
- Runs education programmes
- Provides advice to government conservation agencies
 - Raises awareness on conservation issues

38 Physiology of Microbial life

Phylogenetic Tree of Life (3 Domains)



Prokaryote "Anatomy" Overview

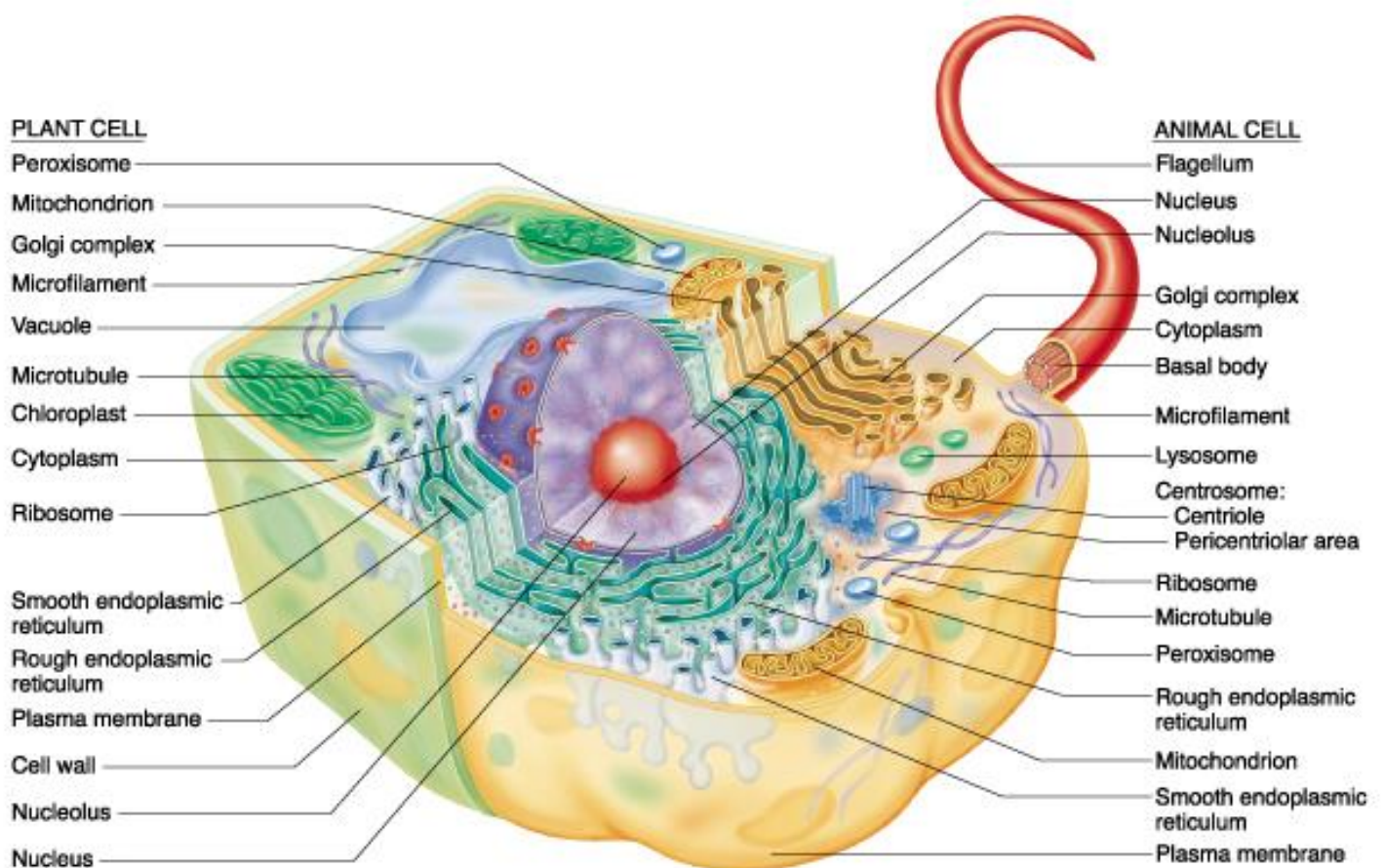


(a)

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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

CO₂ sole or principal biosynthetic carbon source (*pp. 207–8*)^a

Heterotrophs

Reduced, preformed, organic molecules from other organisms (*chapters 9 and 10*)

Energy Sources

Phototrophs

Light (*pp. 195–201*)

Chemotrophs

Oxidation of organic or inorganic compounds (*chapter 9*)

Electron Sources

Lithotrophs

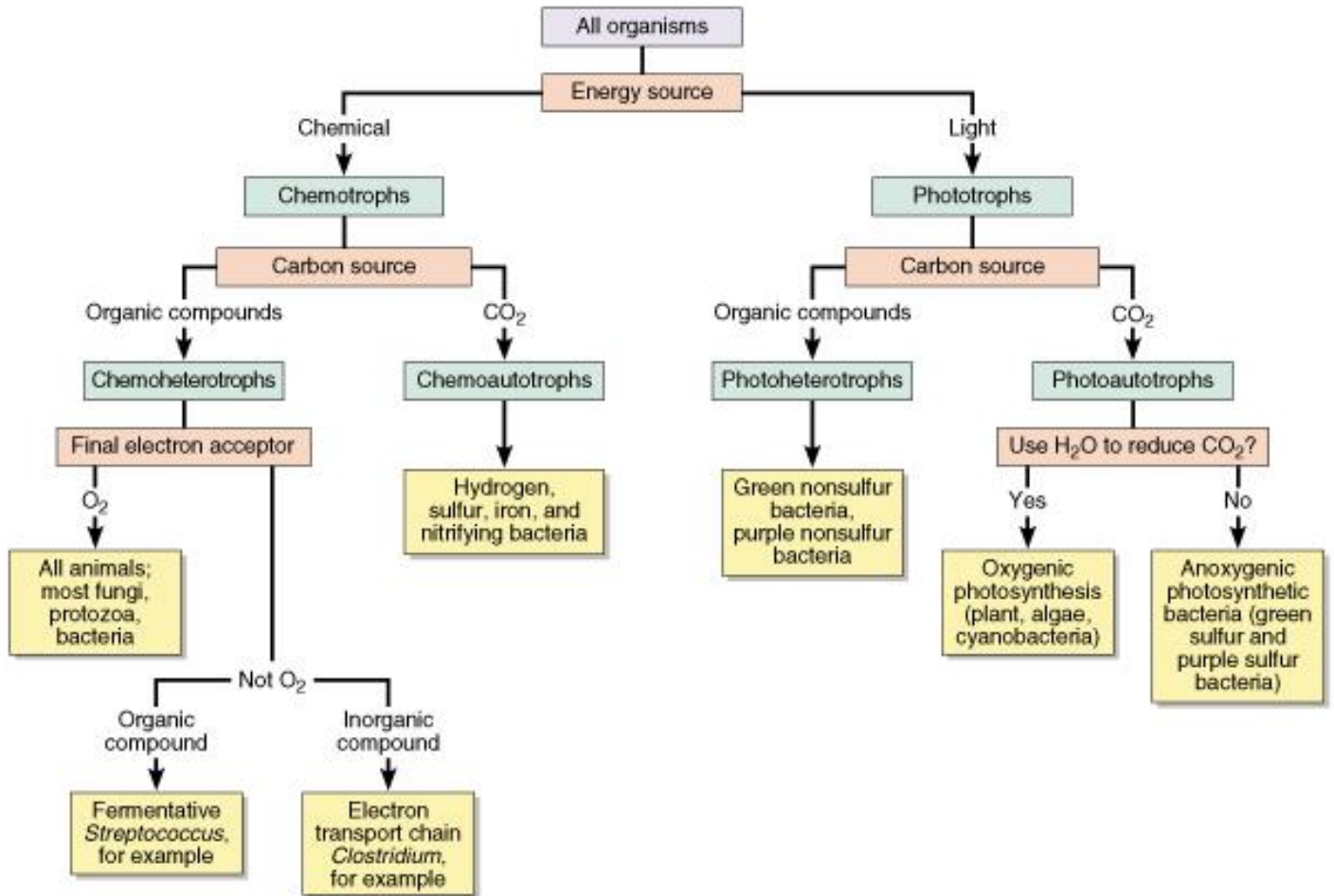
Reduced inorganic molecules (*pp. 193–94*)

Organotrophs

Organic molecules (*chapter 9*)

^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"

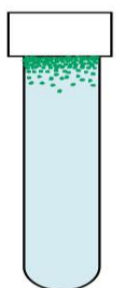
Martinus Beijerinck (ca. 1890)

- 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

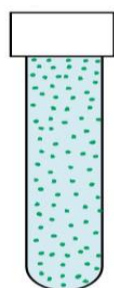
Oxygen Requirement Types



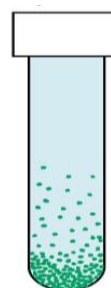
Obligate aerobe



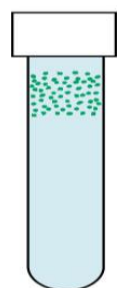
Facultative anaerobe



Aerotolerant anaerobe

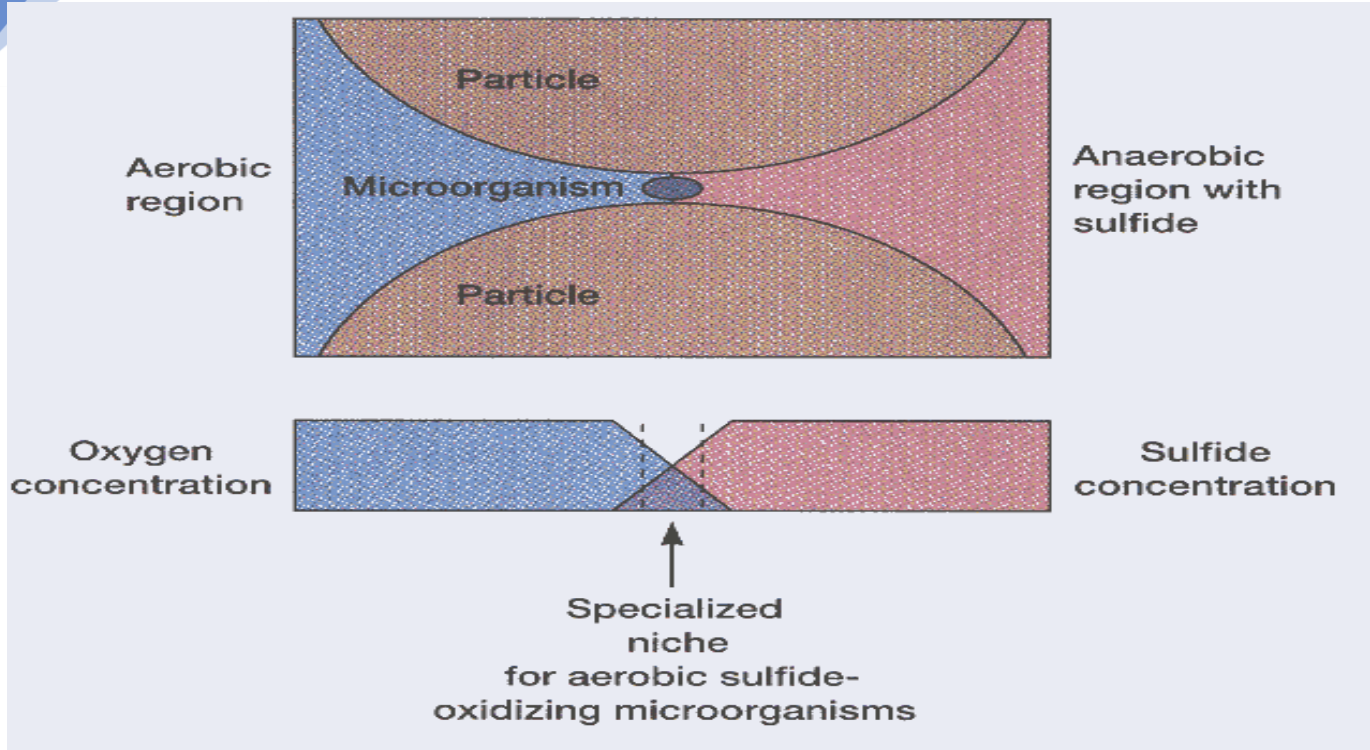


Strict anaerobe



Microaerophile

“Microbial Lasagna”



Microbial interactions control populations, too

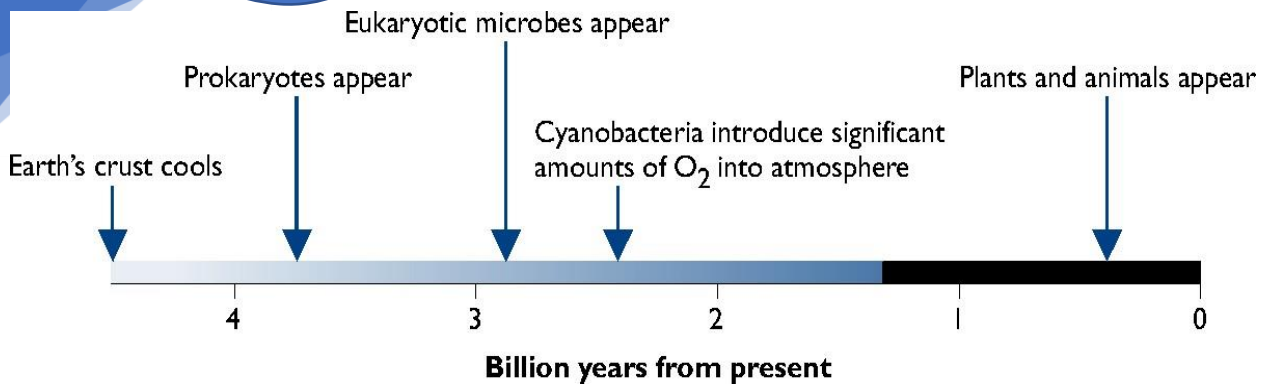
- **Positive interactions:**
 - Commensalism
 - Proto cooperation
 - Mutualism
- **Negative Interactions:**
 - Amensalism:
 - Competition:
 - Intraspecific
 - Interspecific
 - Predation (e.g. *Bdellovibrio*)
 - Parasitism

Predation and Disease (Parasitism) Control Populations Too!

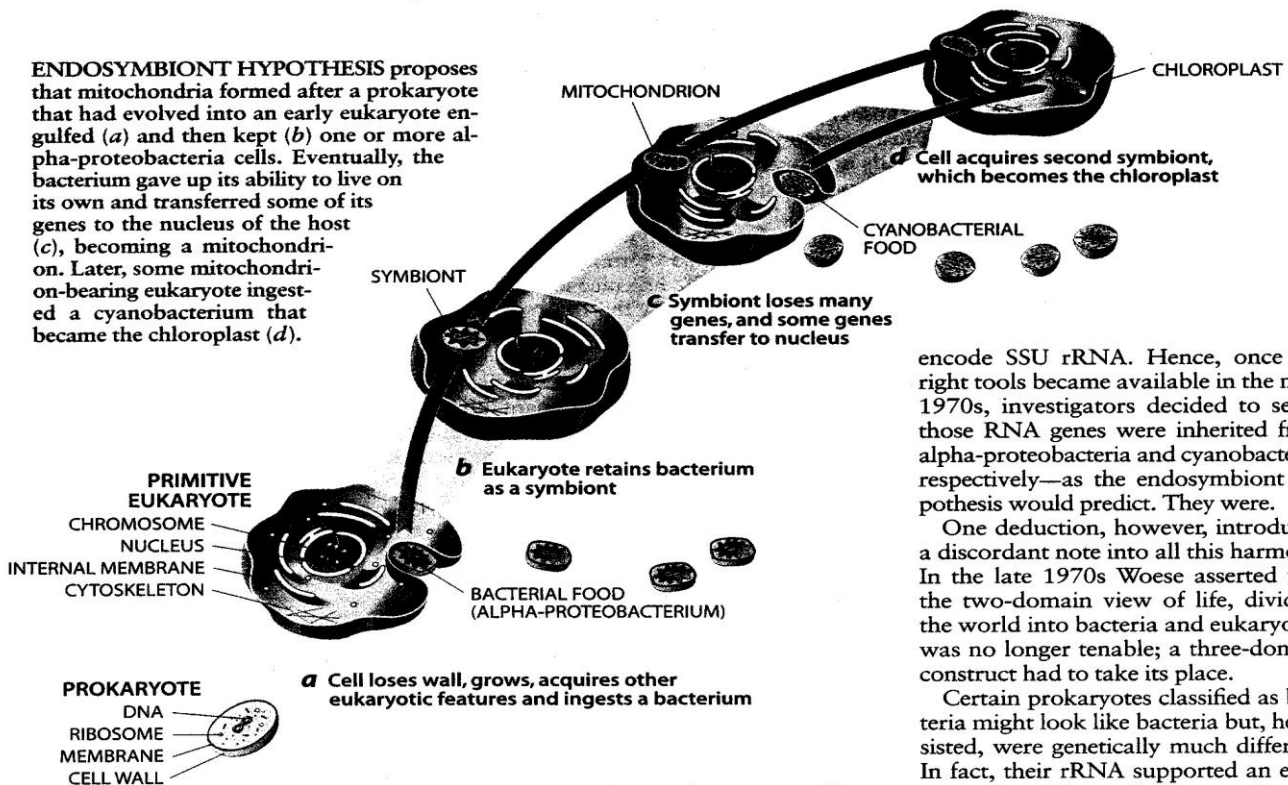
- Protozoa and other “grazers”
 - May be selective.
- Viral Lysis
 - Highly selective.

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.

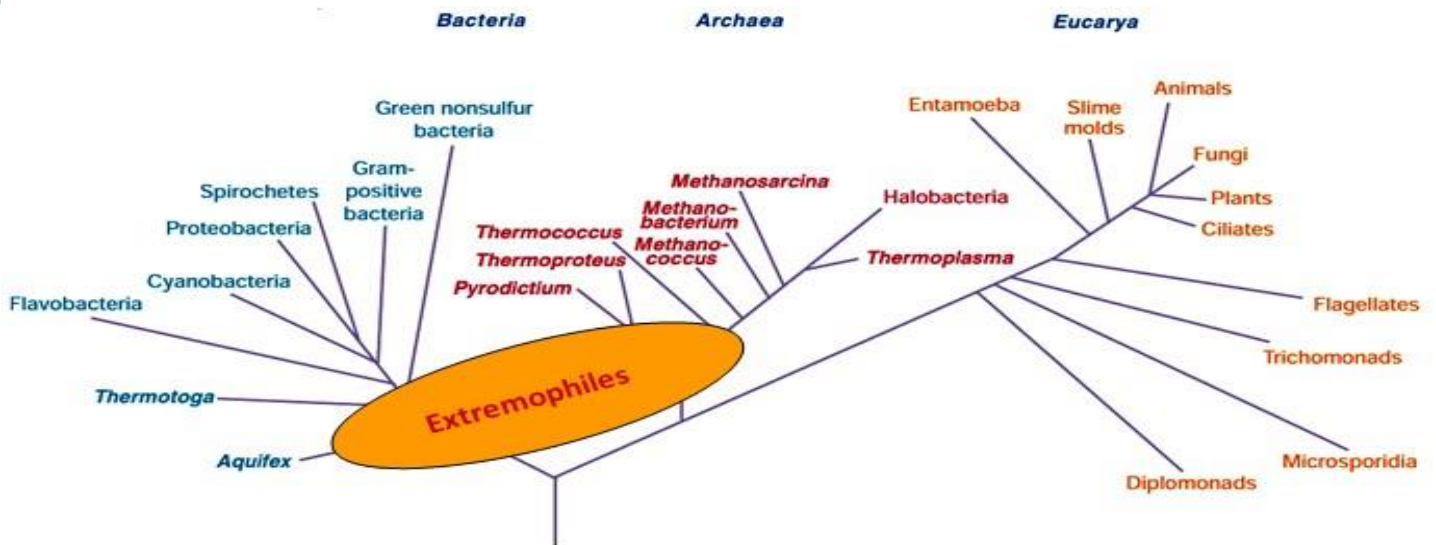
Acquisition of photosynthesis and Calvin Cycle from cyanobacterium.

• 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.)

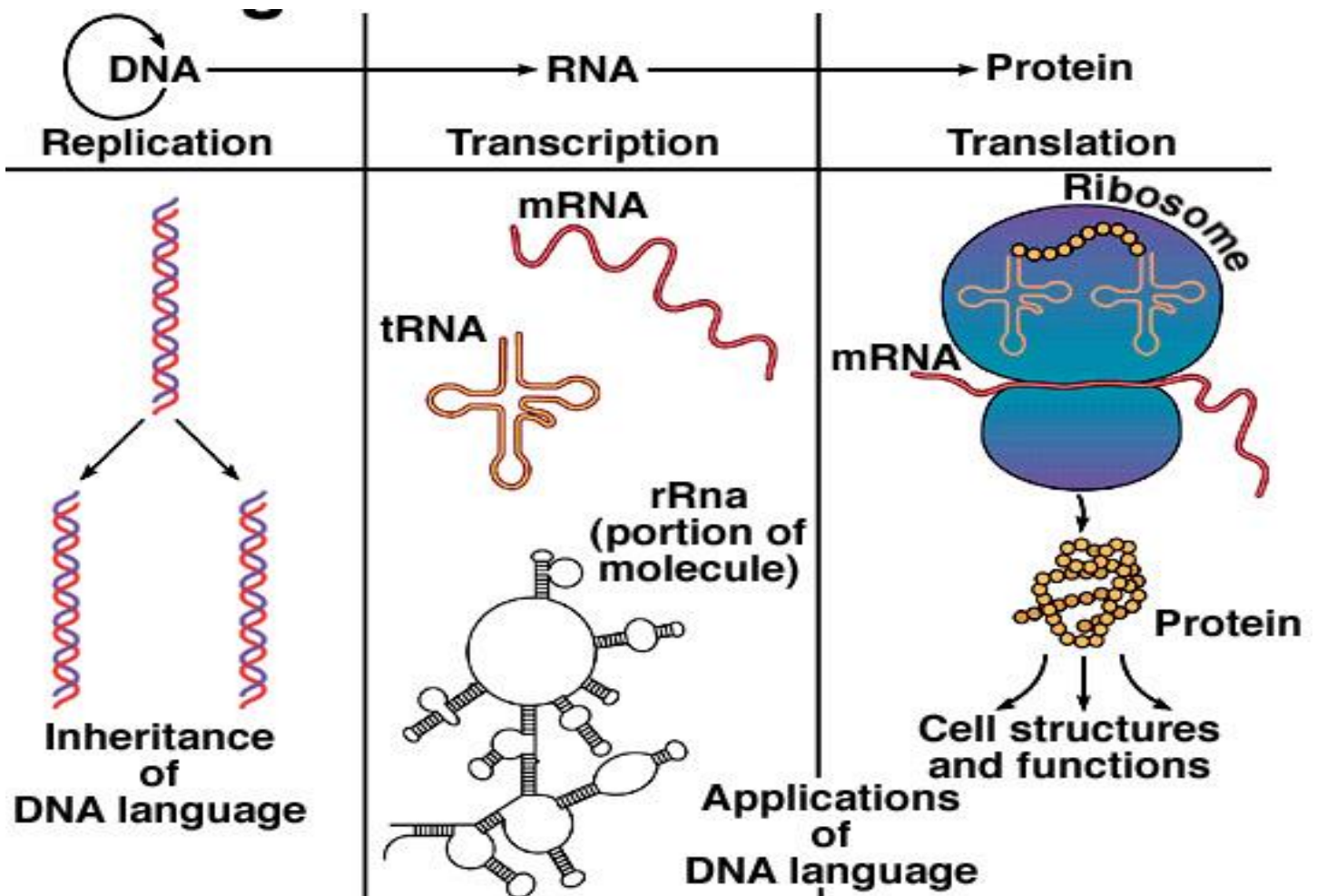
Phylogenetic Tree of Life:



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

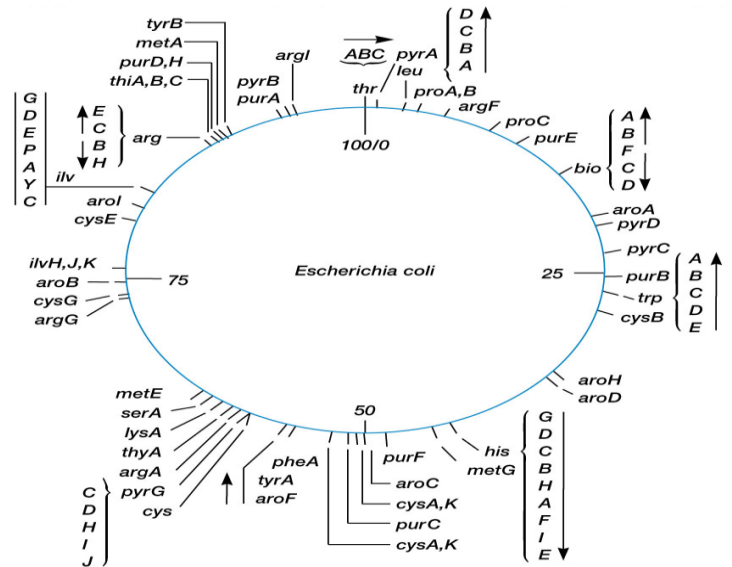
- Only structural genes versus splash map
- Mostly single chromosome
- Size: 1-5 Mbp
- Many complete sequences ([TIGR](#))!

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)

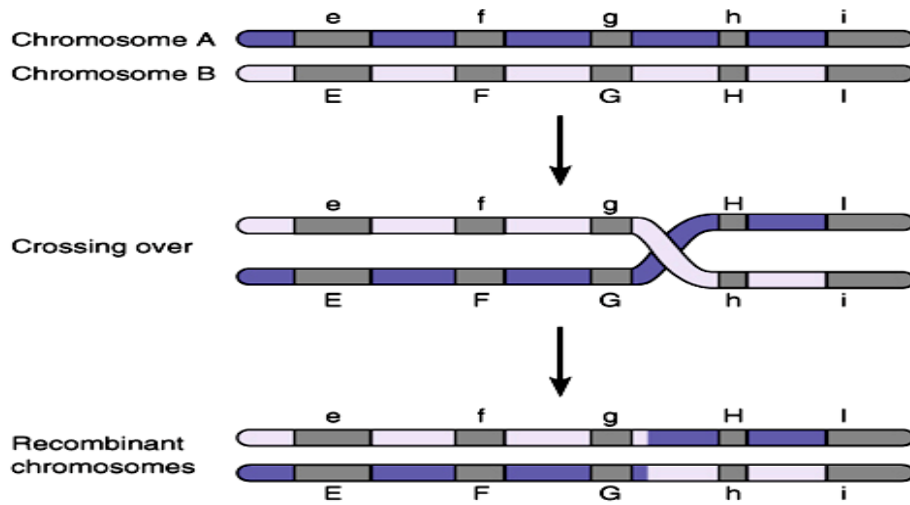
- Point Mutations (Base Substitutions) $ACTG \rightarrow ATTG$
- Frameshifts (Insertions or Deletions)
see the cat eat the rat \rightarrow *see thc ate att her at*

– Mechanisms of microlesion mutation types

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

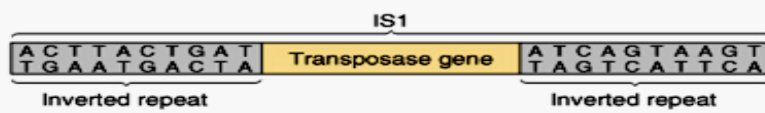
Genetic Recombination

- 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.

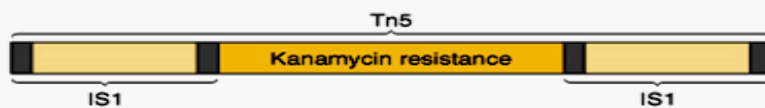


Transposable Elements: "Jumping Genes"

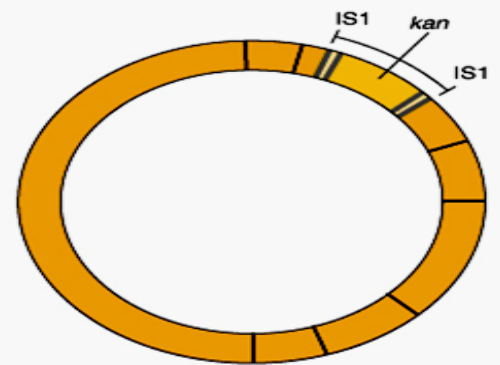
- Transposable elements (insertion sequences and transposons) can transfer copies of themselves to other DNA molecules (chromosome, plasmid, or viral DNA).
- Antibiotic resistance genes rapidly spread within and between bacterial populations by transposons carried on F factors called R plasmids.



(a) Insertion sequence "IS1"



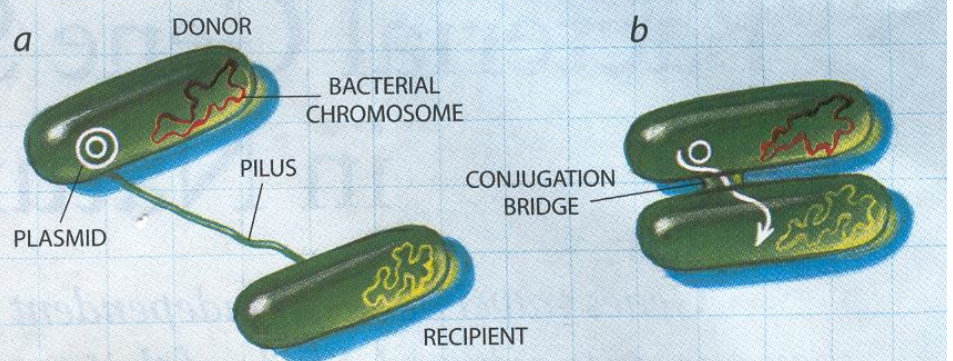
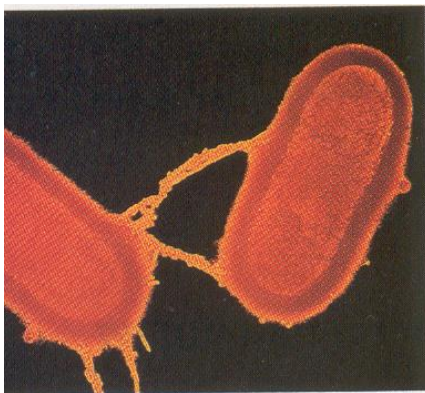
(b) Complex transposon "Tn5"

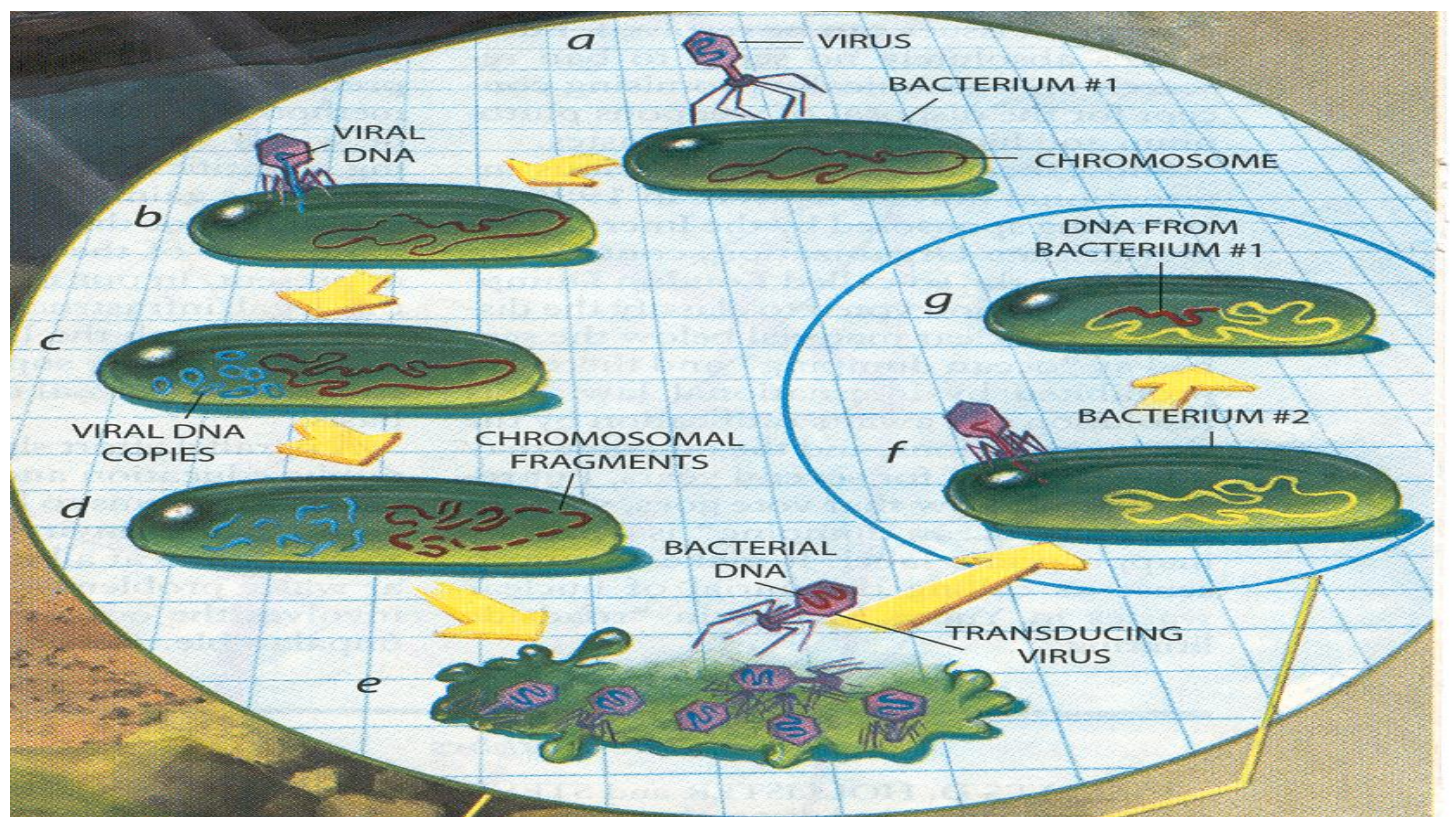
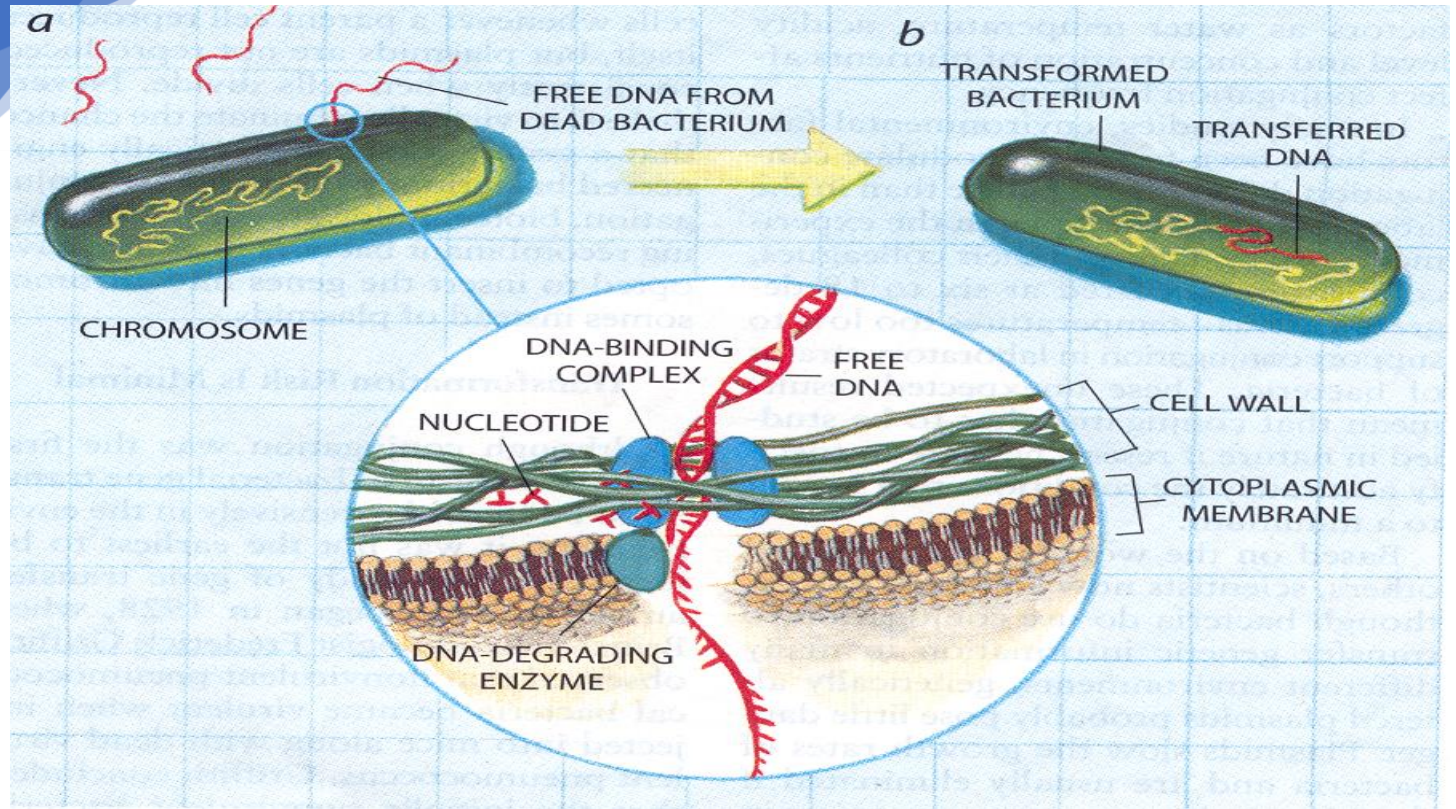


(c) R plasmid

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

- □ Additional 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

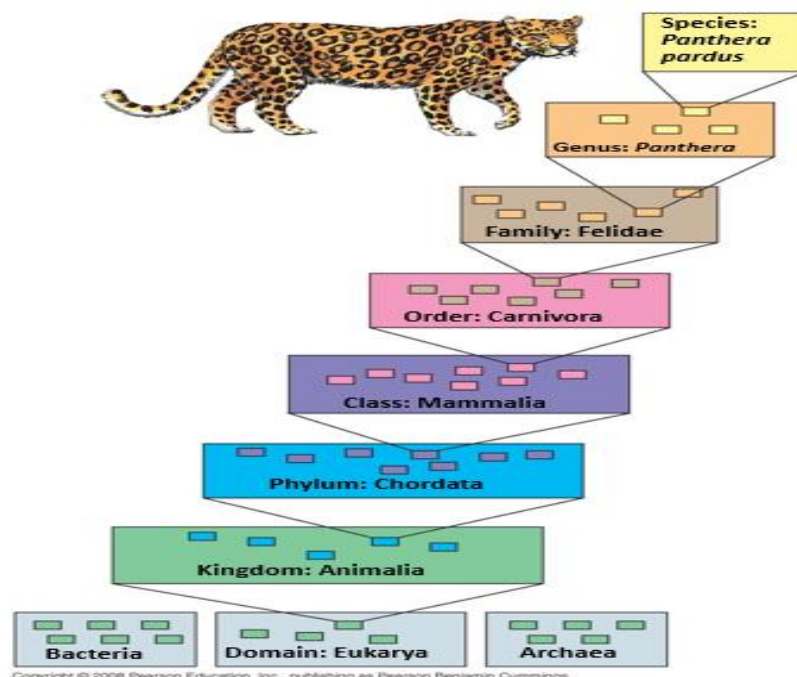
Taxonomy is the ordered division and naming of organisms

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

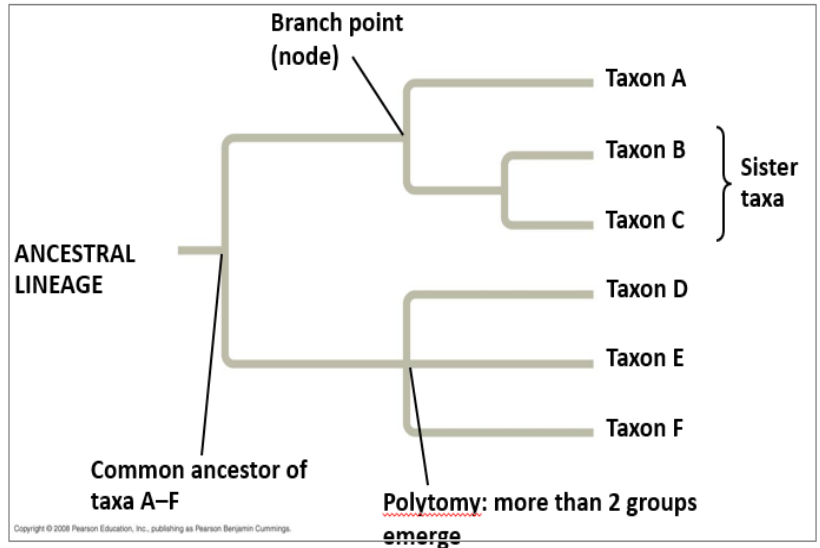
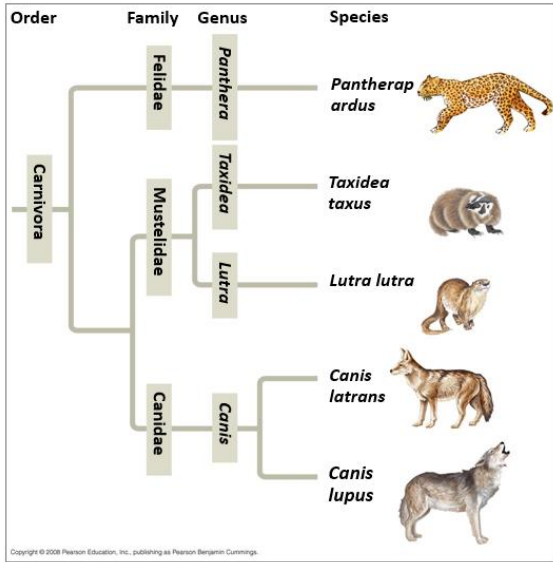
Hierarchical Classification

- 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 Japa

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

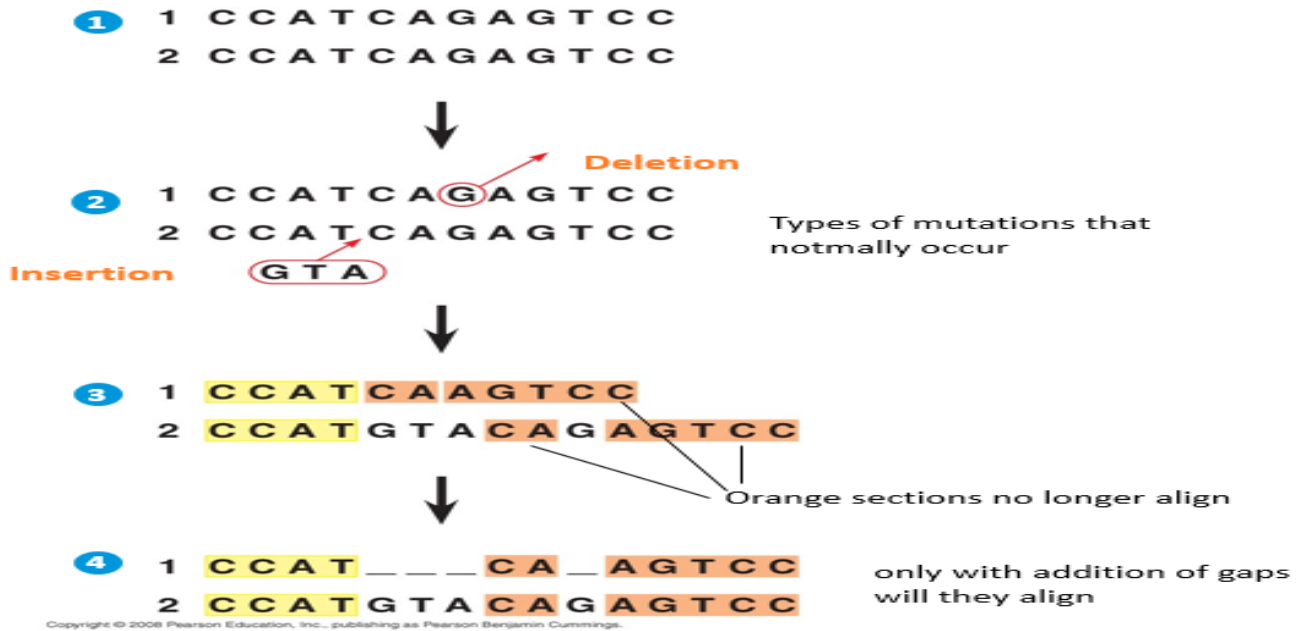
Sorting Homology from Analogy

- 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 austrian mole and NorthAmerican mole lokks alike but but evolved independantly 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

```

A C G G A T A G T C C A C T A G G C A C T A
T C A C C G A C A G G T C T T T G A C T A G

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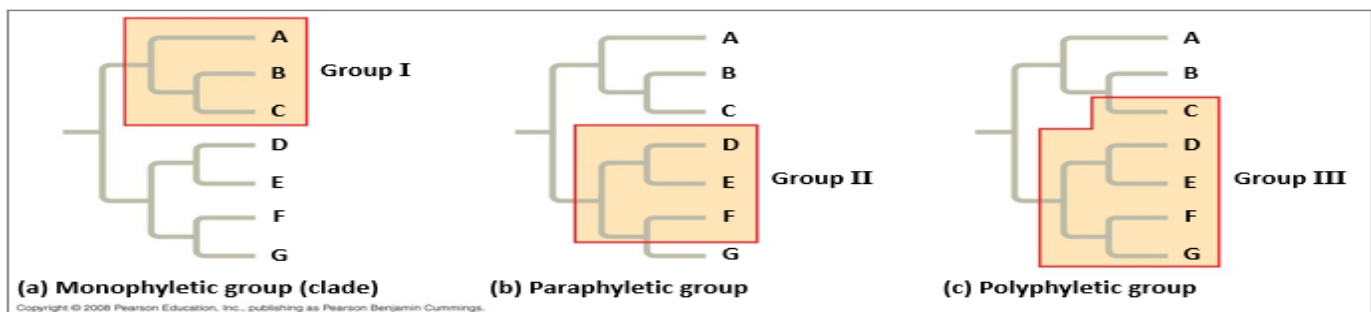
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- **Molecular systematics** uses DNA and other molecular data to determine evolutionary relationships

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



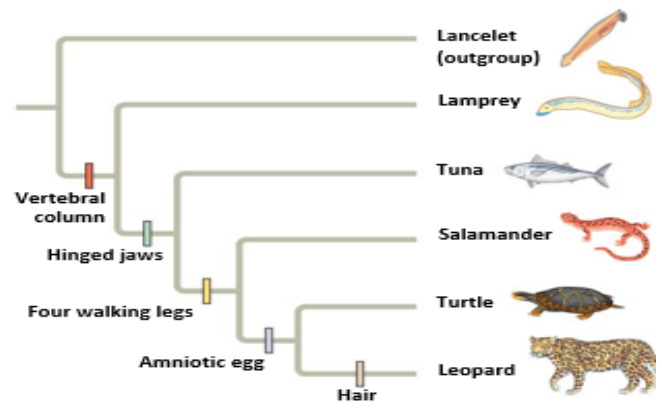
Shared Ancestral and Shared Derived Characters

- 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
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

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(b) Phylogenetic tree

Phylogenetic Trees with Proportional Branch Lengths

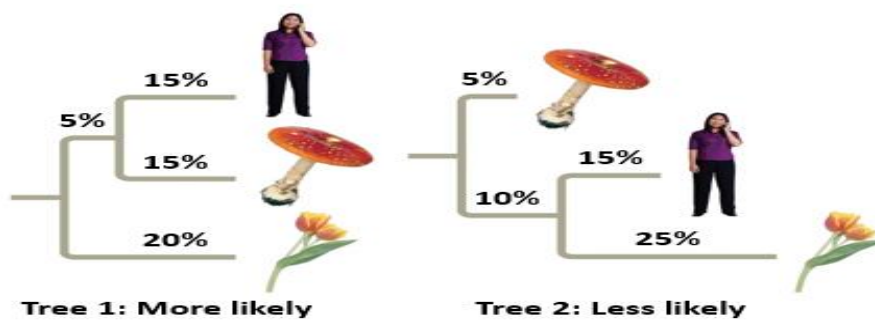
- In some trees, the length of a branch can reflect the number of genetic changes that have taken place in a particular DNA sequence in that lineage
- In other trees, branch length can represent chronological time, and branching points can be determined from the fossil record

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

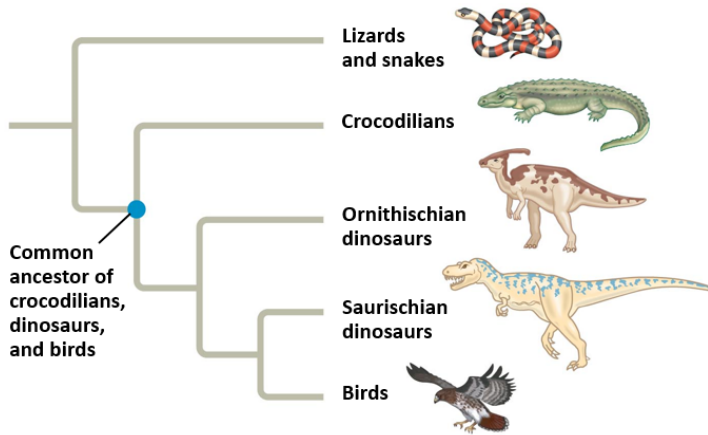


(b) Comparison of possible trees

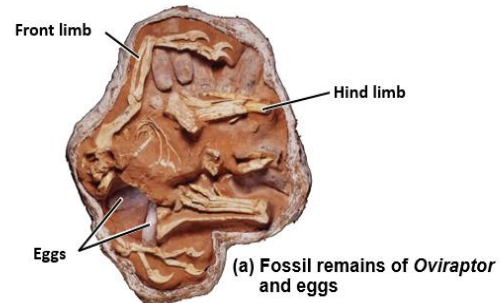
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43 Phylogenetic Trees as Hypotheses

- 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 descendants
- This has been applied to infer features of dinosaurs from their descendants: birds and crocodiles



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(b) Artist's reconstruction of the dinosaur's posture

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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

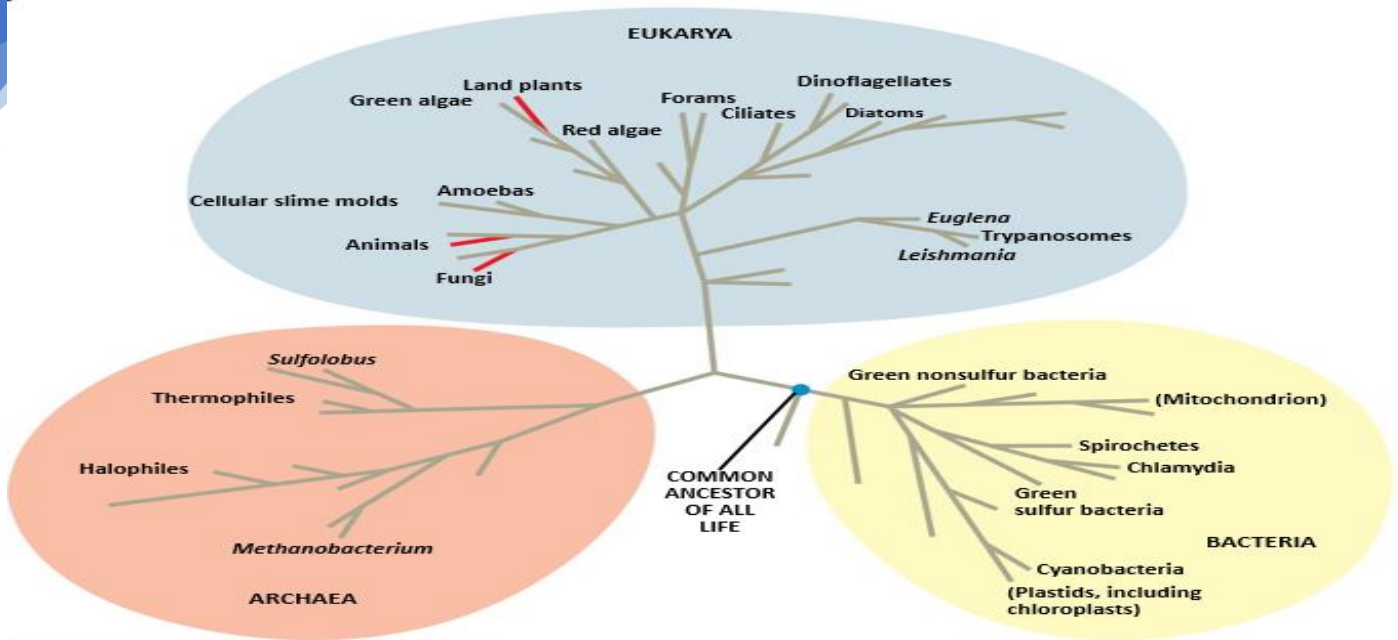
- Orthologous genes are widespread and extend across many widely varied species
- Gene number and the complexity of an organism are not strongly linked
- Genes in complex organisms appear to be very versatile and each gene can perform many functions

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



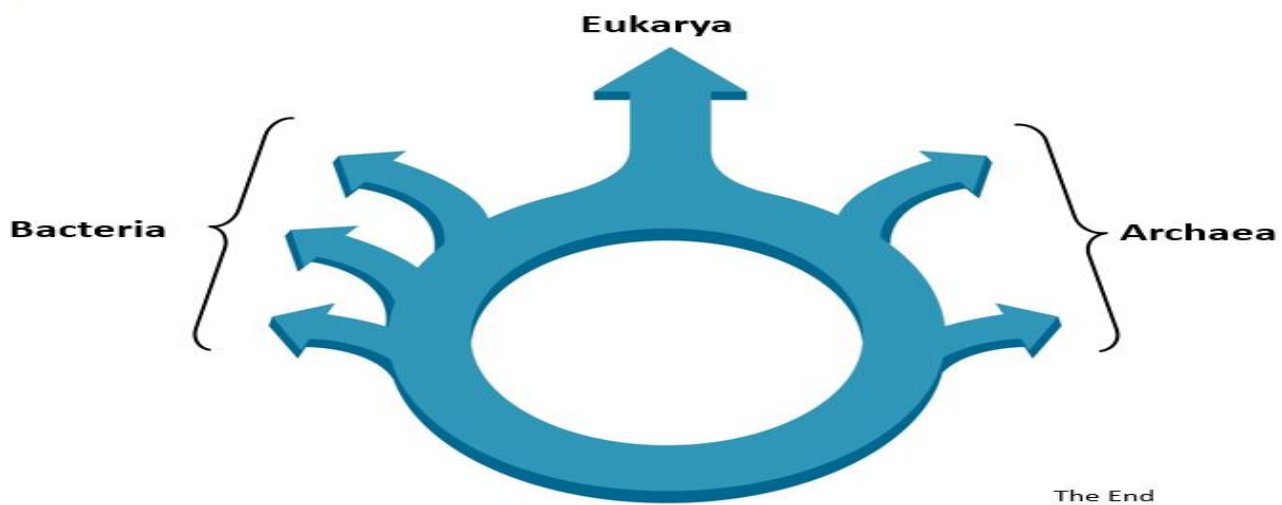
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A Simple Tree of All Life

- 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



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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.

Species richness on habitat islands

- Species richness on habitat islands, such as mountain islands in the American Southwest, increases with area and decreases with isolation.
- Lakes can also be considered as habitat islands. They are aquatic environments isolated from other aquatic environments by land. Fish species richness generally increases with lake area.

Species richness and island isolation

Species richness is usually negatively correlated with island isolation. However, because organisms differ substantially in dispersal rates, an island that is very isolated for one group of organisms may be completely accessible to another group.

Models of Species richness on islands

Species richness on islands can be modelled as a dynamic balance between immigration and extinction of species. The equilibrium model of island biogeography proposes that the difference between rates of immigration and extinction determines the species richness on islands.

The equilibrium model of island biogeography

The equilibrium model of island biogeography assumes that rates of species immigration to islands are mainly determined by distance from sources of immigrants. The model assumes that rates of extinction on islands are determined mainly by island size.

Species richness and latitude

Species richness generally increases from middle and high latitudes to the equator. Most groups of organisms are more species-rich in the tropics.

Many factors may contribute to higher tropical species richness, including

- time since perturbation,
- productivity,
- environmental heterogeneity,
- favorableness,
- niche breadths and interspecific interactions, and
- differences in speciation and extinction rates. Several lines of evidence support the hypothesis that differences in surface area play a primary role in determining latitudinal gradients in species richness.

Structure of biotas and ecosystems

Long-term historical and regional processes significantly influence the structure of biotas and ecosystems. Much geographic variation in species richness can be explained by historical and regional processes.

Exceptional situations

Some exceptional situations that seem to have resulted from unique historical and regional processes include the exceptional species richness of the Cape floristic region of South Africa, the high species richness of temperate trees in east Asia, and the low bird diversity in beech forests of South America.

A word of advise

The ecologist interested in understanding large-scale patterns of species richness must consider processes occurring over similarly large scales and over long periods of time.

Global positioning systems

- Global positioning systems, remote sensing, and geographic information systems are important tools for effective geographic ecology.
- A global positioning system determines locations on the earth's surface, including latitude, longitude, and altitude, using satellites as reference points.

Remote sensing satellites

- Remote sensing satellites are generally fitted with electro-optical sensors that scan several bands of the electromagnetic spectrum.

- These sensors convert electromagnetic radiation into electrical signals that are in turn converted to digital values by a computer. These digital values can be used to construct an image.

Geographic information systems

Geographic information systems are computer-based systems that store, analyze, and display geographic information. Global positioning systems, remote sensing, and geographic information systems are increasingly valuable parts of the ecologist's tool kit.

Future avenues

Ecologists are using these new tools to study large-scale, dynamic ecological phenomena such as interannual variation in regional terrestrial primary production, dynamics of marine primary production, and potential population responses to climate change.

45 Evidence for evolution

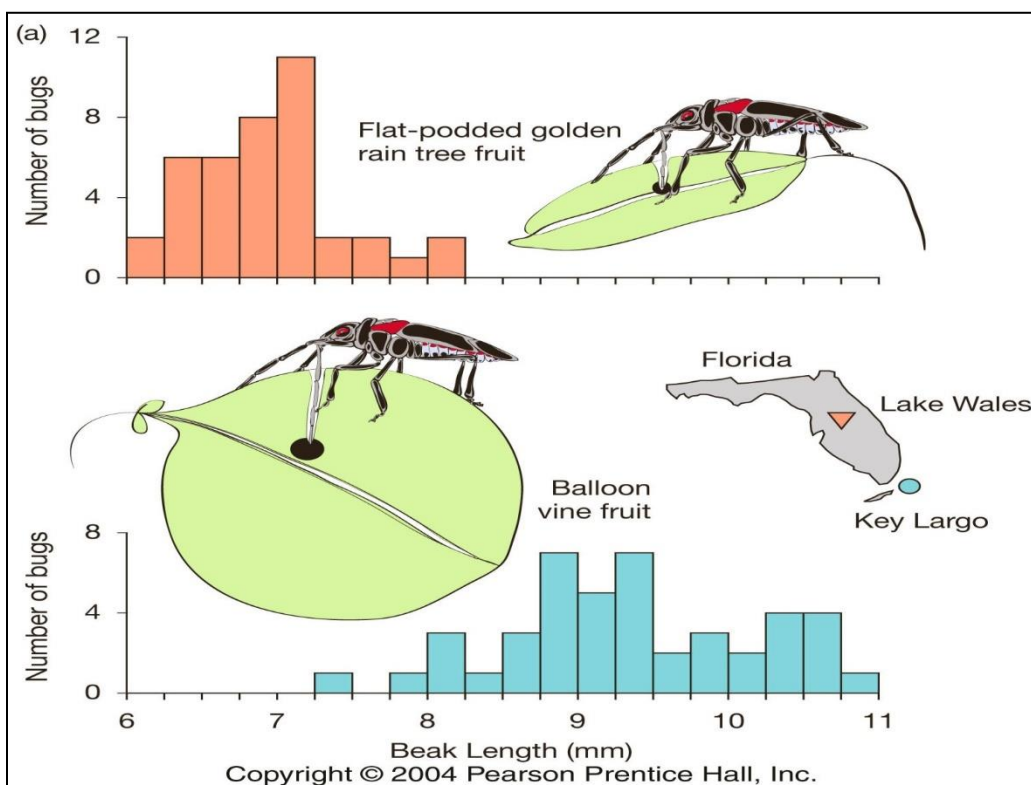
Darwin's Theory of Evolution by Natural Selection

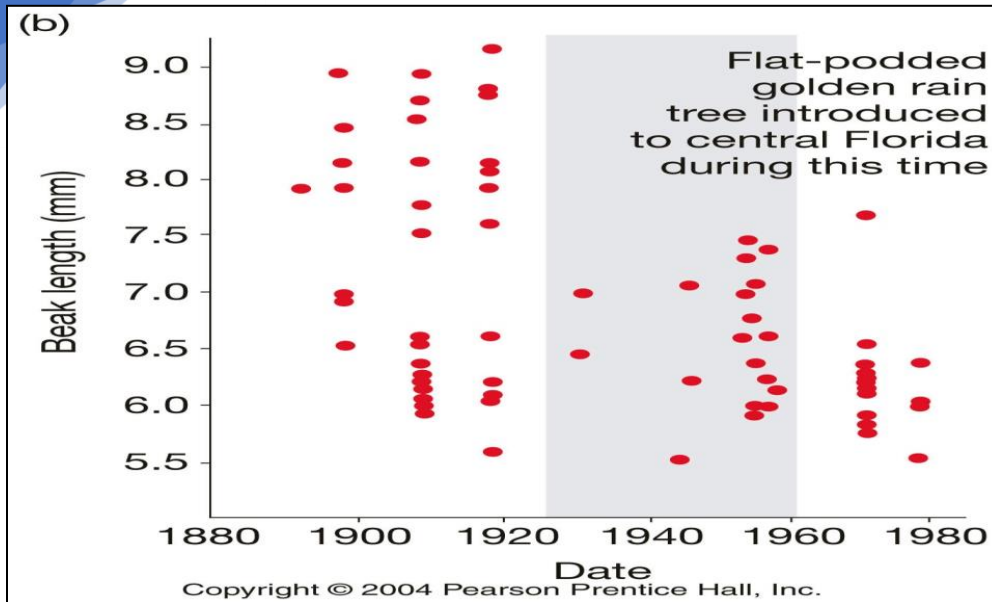
- Species have changed through time and are related by descent from a common ancestor
- The primary mechanism of Evolutionary Change is Natural Selection

Evidence that Species have Changed Through Time?

- **Hypothesis:** Species have changed through time
- **Prediction:** we should be able to find signs of evolutionary history
 - direct observation
 - fossil record
 - vestigial structures

Direct observation of Evolution





Fossil Record

The fossil record is the history of life recorded by remains from the past. Most fossils are at least 10,000 years old.

1. Body Fossil
2. Trace Fossil

What is found?

- Fossils exist and fossil forms are unlike species living today

1. Fossil Sequence?

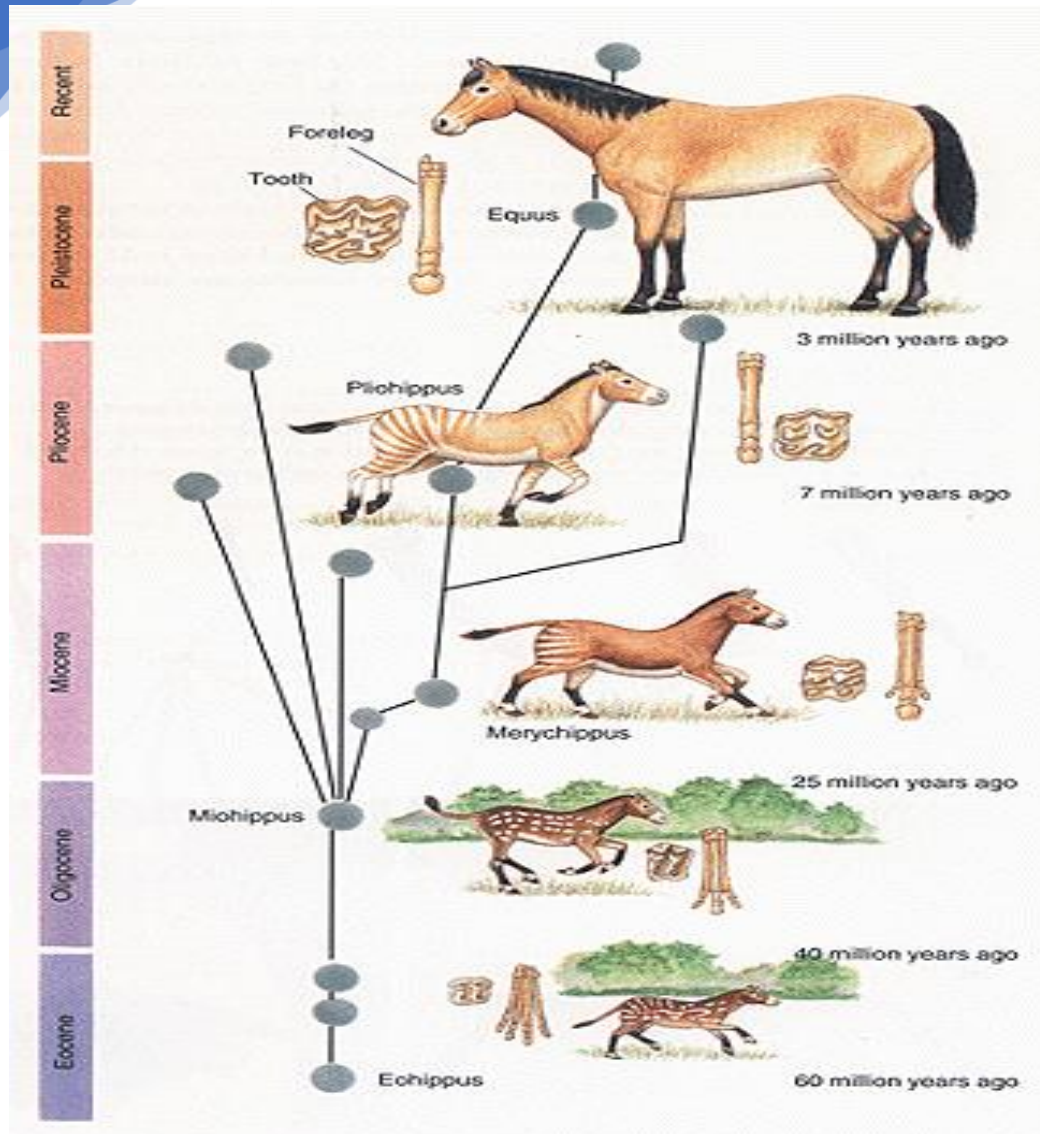
When fossils are arranged according to their age, they show successive evolutionary change

2. Fossil Intermediates?

Transitional fossils have been found between: Amphibians & reptiles, reptiles & birds, reptiles & mammals, apes and humans

The Evolution of Horses

A particularly well-documented case of evolution within a group



The fossil Record is Incomplete

At the time of Darwin, the fossil record was VERY scanty. A great deal of progress has been made since, but it is far from finished.

The fossil record is relatively incomplete for several reasons:

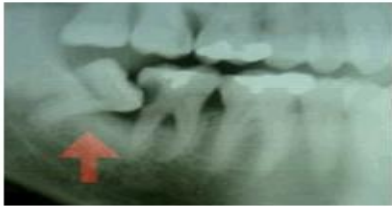
1. Soft tissues are rarely preserved
2. Movement of the earth's crust has obliterated and/or covered many fossils
3. Fossilization takes place only in certain types of habitats and favorable environments
4. Paleontologists have not dug up every place on earth

Even if there were no fossil record, the evidence from living organisms would be more than sufficient to demonstrate the historical reality of evolution

Vestigial Structures

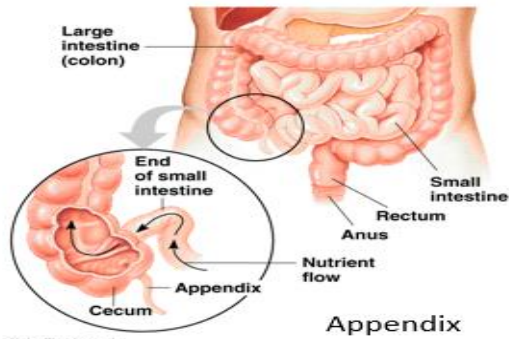
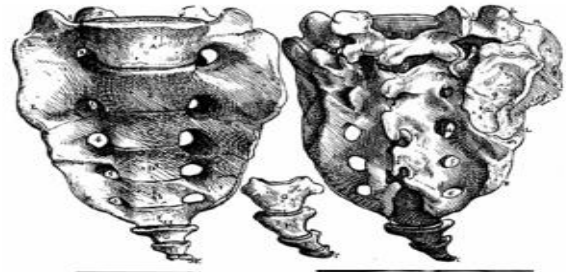
- Features that have no apparent function
- Typically have an important function in related spp.
- Ex: Hindlimb joints in whales and snakes
- In humans Wisdom teeth, Tail bone, Appendix are vestigial structures.

Vestigial Structures in Humans



Wisdom Teeth

Tailbone



Appendix

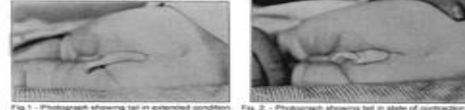


Fig. 1 - Photograph showing tail in extended condition. Fig. 2 - Photograph showing tail in state of contraction.



Evidence for the Relatedness of Life Forms?

- Hypothesis: all living organisms have descended from a common ancestor
- Prediction: we should also be able to see evidence of relatedness of species
 - Homology
 - Geographic distribution

Homology:

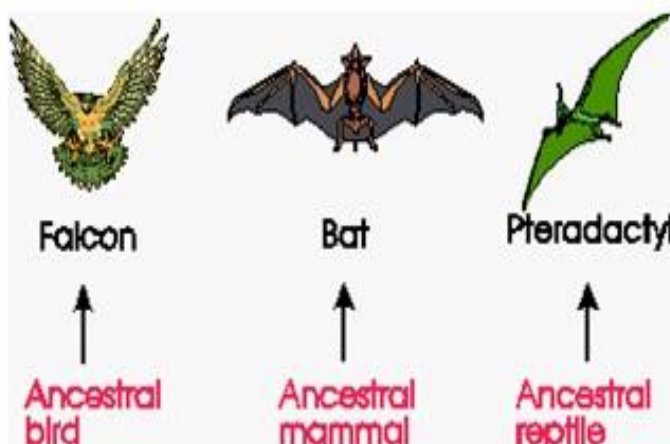
- Homology: a similarity between species that is the result from the inheritance of traits from a common ancestor
- The features of every creature reflect history as well as adaptation

3 types of homologies

- structural
- developmental
- genetic

Homology vs. Analogy:

Natural selection appears to have favored similar adaptations in unrelated organisms in similar environments--> these structures are **analogous**

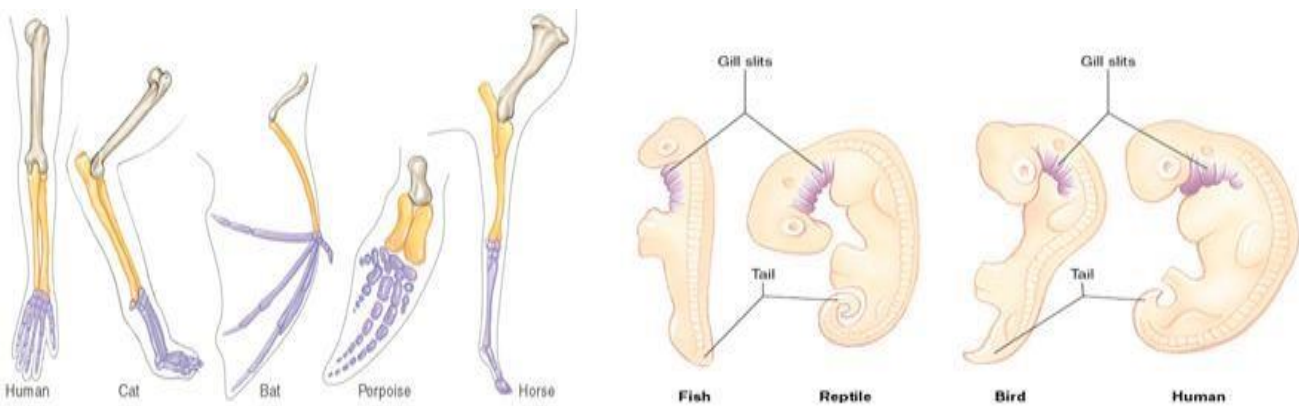


Whereas homologous structures share structural similarity, but not function, analogous structures share function but not structural similarity since they evolved independently

Convergent Evolution

Niche	Placental Mammals	Australian Marsupials
Burrower	Mole	Marsupial mole
Anteater	Anteater	Numbat (anteater)
Mouse	Mouse	Marsupial mouse
Climber	Lemur	Spotted cuscus
Glider	Flying squirrel	Flying phalanger
Cat	Bobcat	Tasmanian "tiger cat"
Wolf	Wolf	Tasmanian wolf

Homologous structures: bones of the forelimb:



The underlying design of each structure is similar despite their functional differences

Homologous structures in adults develop from homologous groups of cells in embryos --> they share developmental pathways

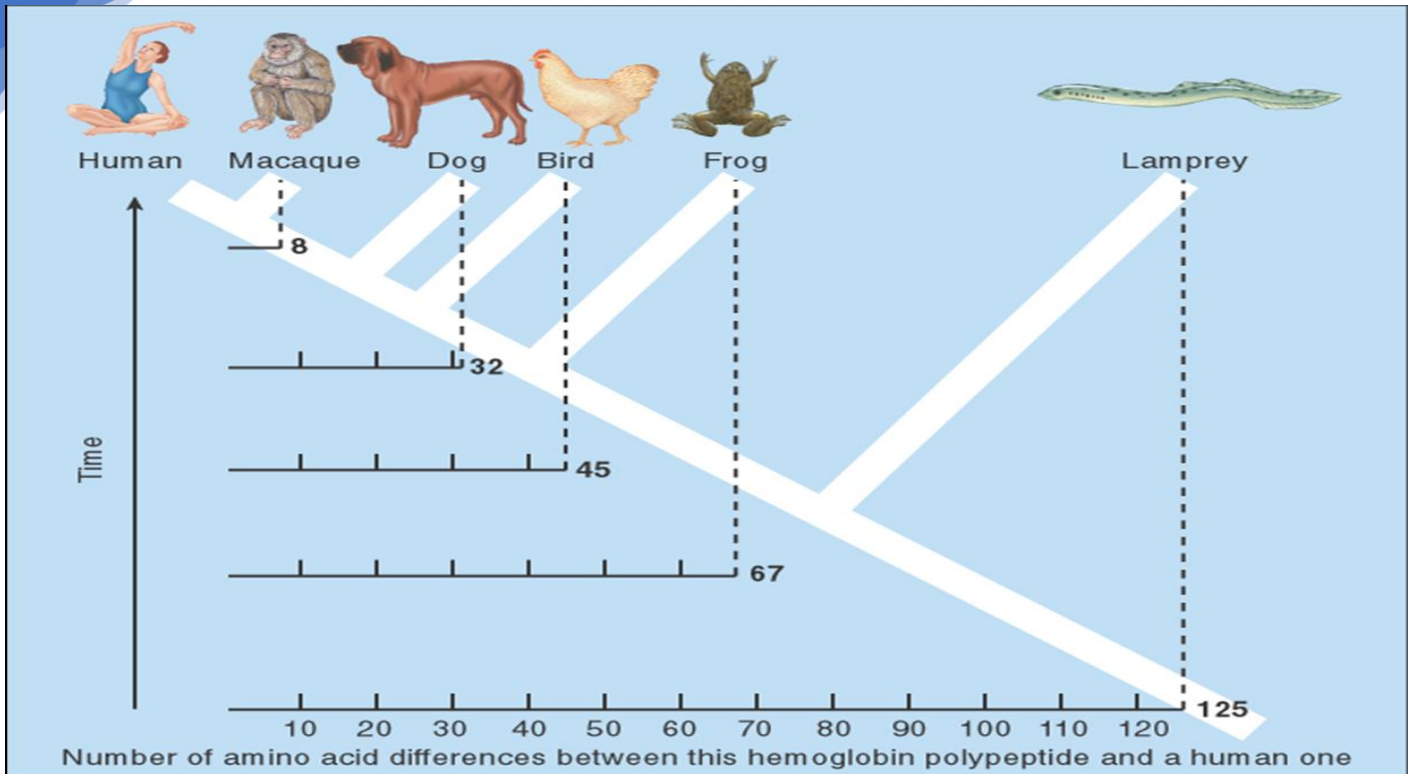
Convergent Evolution:

Convergent evolution is the process by which unrelated or distantly related organisms evolvesimilar body forms, coloration, organs, and adaptations. Natural selection can result in**evolutionary convergence** under several different circumstances.

Genetic Homologies

All living organisms share the same genetic code. Chromosome and gene similarities between species match evolutionary similarities. This is true for both coding regions and "junk DNA"

Molecules reflect evolutionary divergence



Geographic Distributions

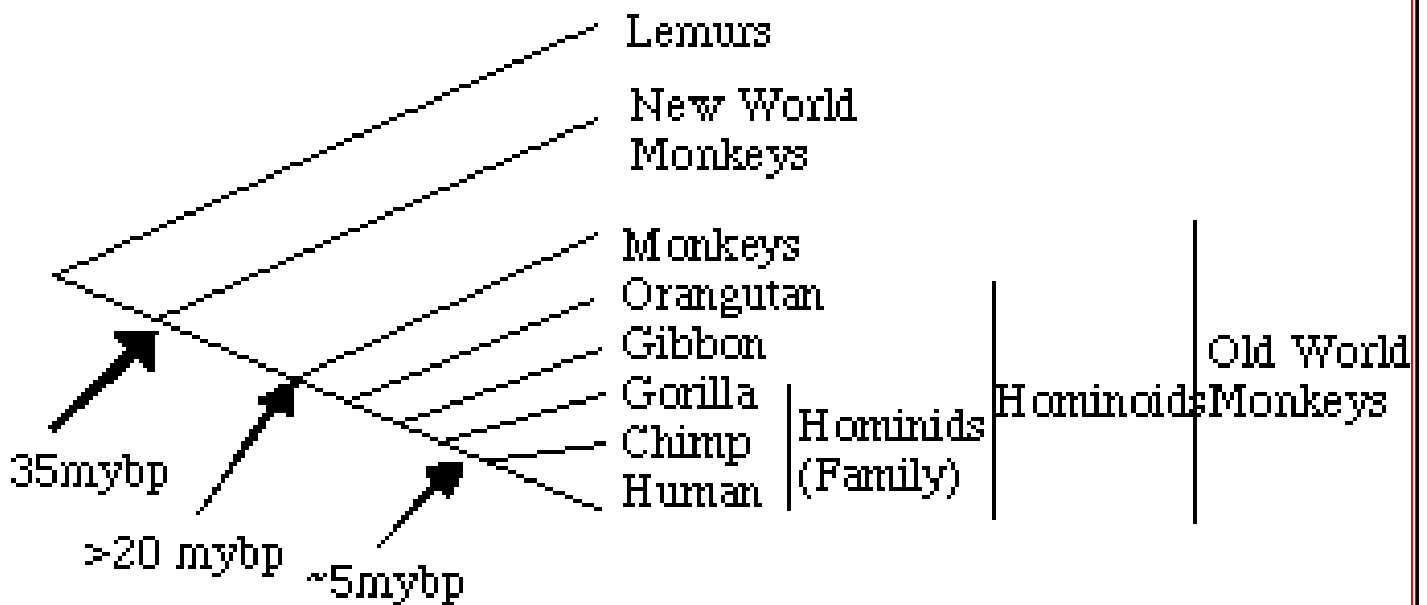
- Species that are extremely similar to one another tend to be clustered geographically (Ex.: Darwin's finches).
- Living species are more similar to fossil species in the same area than they are to living species in other areas

The law of succession

- General correspondence between fossil and living forms in same geographical area
- Darwin used this observation to predict that fossils of ancient humans should be found in Africa

46 Human Evolution

- Humans are too complex to be "understood" by any one field. Thus we will look at a few major steps in evolution and some of the things affecting human evolution.
- Humans are members of the order Primates which consists of about 180 species (there are 17 different orders of mammals which diverged 80-65 million years ago). Primates are a relatively old order of mammals. Most of the synapomorphies of this order are associated with an arboreal way of life: flexible digits, forward facing eyes, vision as a primary sense.
- These traits may have played a role in the evolution of brain size in the lineage leading to humans. Humans are a member of the family Hominidae which is believed to have diverged about 5 million years before the present (mybp) from the other members of the Old world monkeys. At least 20 mybp the Hominoids split off from the other old world monkeys. The dates are rough and get changed now and then.



Relationship of humans to African apes

Relationship of humans to African apes (chimps, gorillas) and orangutan DNA hybridization indicates that apes are our closest relatives. Human/chimp/gorilla relationships not proven but chimps are most likely our closest relatives. The molecular clock says ~ 5 million years ago the human-chimp line split.

While Chimp and gorilla have knuckle walking, the humans possess many traits associated with bipedality: vertebral column, shape of pelvis, angle of femur, foramen magnum at base of skull. Bipedality seems to be a major "innovation" which allowed humans to enter a new "adaptive zone". The first human (*Australopithecus afarensis*) seems to have an angle between the femur and tibia (Upper and lower leg) that is intermediate to that of humans and gorillas.

The evolution of modern humans from our hominid ancestor is commonly considered as having involved four major steps:

- evolving terrestriality,
- bipedalism,
- a large brain (encephalization)
- civilization.

There are (and have been) several competing hypotheses that have acknowledged these four steps, but put them in a different sequence during human evolution.

Origin of *Homo sapiens*: *Australopithecus afarensis* = first bipedal hominid, found in east Africa about 3.0-3.2 MYBP. Later forms became more slender (= "gracile"). *Homo habilis* and *H. erectus* (~1.5mybp) came later. The evolution of bipedalism may have freed the hands for us in other functions: carrying, tool use. The trends in the evolution of tool use (more types, more specific tasks, different types of materials, more efficient use of materials) seems to follow (lead??) the evolution of increase cranial capacity. These both seem to increase noticeably about 2 mybp.

Bipedalism and Brain development

- One theme that involves each of the different sequences of evolution is that there was some feedback that led to the increase in cranial capacity, e.g., becoming bipedal creates selection pressure for a more elaborate brain to control motor function and to process incoming sensory information. This in turn would allow for more successful bipedalism, etc.
- The same argument could be leveled about culture leading to an increase in brain size, and vice versa, so the sequence cannot be resolved just on the logic of feedback loops alone.

Human Origins

- Origin of "modern humans": Two alternative scenarios for origins:
 - humans originated in more than one site ("Multiregional" model). Evidence supporting this are modern *Homo sapiens* samples found in Asia and Africa

- a single origin ("Noah's Ark" model: one origin and dispersal out from site of origin). Homo sapiens are believed to have originated ~100,000 - 200,000 years ago.
- Paleontological evidence suggests a single origin in Africa. Molecular data shows low genetic diversity worldwide with the highest diversity in Africa, also suggesting an African origin. Recent re-analyses shown that the cladograms of mtDNA cannot support an African origin on statistical grounds.

Humans, out of Africa

The spread of Homo out of Africa is presumed to have taken place about 1.5 MYBP by Homo erectus. This species seems to be on a trajectory of brain size and body size that looks anagenetic, whereas one lineage that lead to Australopithecus robustus seems to be on another line. In a broad sweep of time, the notion of the chimp leading to the Australopithecine, to Homo, to the Neanderthal to the modern American family standing in their driveway is a myth. There were lineages that diverged in a branching cladogram, some of which did not make it to the present. Evidence for this is provided by more than one distinct morphological type of early humans present at the same time (see below). As time gets closer to modern humans, however (Homo erectus on up), a phyletic gradualist anagenesis is more easy to accept.

Brain and human evolution

- Once a big brain is achieved and this provides the intellect for an organism to anticipate its environment, the notion that an organism evolves in response to changes of the environment becomes too simplistic..
 - Humans evolved the power to alter their environment so as to protect themselves from its abiotic pressures. This means that they are altering their own selective pressures and a dialectic emerges between the organism and the environment such that these cannot be separated. Other organisms do this (beaver dams, deciduous trees), but in humans this cycle is accelerating

47 Proterozoic Eon

The Length of the Proterozoic

The Proterozoic Eon alone, at 1.955 billion years long, accounts for 42.5% of all geologic time.

Phanerozoic

Yet the Phanerozoic, consisting of

- Paleozoic,
- Mesozoic,
- Cenozoic eras,

lasted a comparatively brief 545 million years.

Gunflint Microfossils

Even in well-known Early Proterozoic fossils assemblages, only fossils of bacteria are recognized. Photomicrograph of spheroidal and filamentous microfossils from the Gunflint Chert of Ontario Canada

Prokaryote and Eukaryotes

An organism made up of prokaryotic cells is called a prokaryote, whereas those composed of eukaryotic cells are eukaryotes is the basis for the most profound distinction between all living things

Lack of Organic Diversity

Prokaryotic cells reproduce asexually. Most variation in sexually reproducing populations comes from the shuffling of genes, and their alleles, from generation to generation. Mutations introduce new variation into a population, but their effects are limited in prokaryotes

Sexual Reproduction Increased the Pace of Evolution

Prior to the appearance of cells capable of sexual reproduction, evolution was a comparatively slow process, thus accounting for the low organic diversity. This situation did not persist. Sexually reproducing cells probably evolved by Early Proterozoic time, and the tempo of evolution increased

Eukaryotic Cells Evolve

The appearance of eukaryotic cells marks a milestone in evolution comparable to the development of complex metabolic mechanisms such as photosynthesis during the Archean. How do they differ from their predecessors, the prokaryotic cells? All prokaryotes are single-celled, but most eukaryotes are multicelled.

Eukaryotes

Most eukaryotes reproduce sexually, in marked contrast to prokaryotes, and nearly all are aerobic, that is, they depend on free oxygen to carry out their metabolic processes. Accordingly, they could not have evolved before at least some free oxygen was present in the atmosphere

Prokaryotic Cell

Prokaryotic Cell are smaller and not nearly as complex as eukaryotic cells

Eukaryotic Cell

Eukaryotic cells have a cell nucleus containing such as mitochondria and plastids, as well as chloroplasts in plant cells

Eukaryotic Fossil Cells

The Negaunee Iron Formation in Michigan 2.1 billion years old . Fossils are oldest known eukaryotic cells Bitter Springs Formation of Australia –1 billion yrs old, fossils of single-celled eukaryotes, evidence of meiosis and mitosis, processes carried out only by eukaryotic cells

Evidence for Eukaryotes

Prokaryotic cells are mostly rather simple spherical or platelike structures. Eukaryotic cells are large much more complex have a well-defined, membrane-bounded cell nucleus, which is lacking in prokaryotes have several internal structures called organelles such as plastids and mitochondria their organizational complexity is much greater than it is for prokaryotes

Acritarc

These common Late Proterozoic microfossils are probably from eukaryotic organisms. Acritarchs are very likely the cysts of algae

Late Proterozoic Microfossil

Numerous microfossils of organisms with vase-shaped skeletons have been found in Late Proterozoic rocks, in the Grand Canyon. These too have tentatively been identified as cysts of some kind of algae

48 evolutionary biodiversity in Proterozoic Eon

Evolutionary Biodiversity in Proterozoic Eon

Endosymbiosis and the Origin of Eukaryotic Cells

Formed from several prokaryotic cells . In a symbiotic relationship Symbiosis involving a prolonged association of two or more dissimilar organisms, is quite common today. In many cases both symbionts benefit from the association as occurs in lichens, once thought to be plants but actually symbiotic fungi and algae

Evidence for Endosymbiosis

Supporting evidence for endosymbiosis comes from studies of living eukaryotic cells containing internal structures called organelles, such as mitochondria and plastids which contain their own genetic material. In addition, prokaryotic cells synthesize proteins as a single system, whereas eukaryotic cells are a combination of protein-synthesizing systems.

Organelles Capable of Protein Synthesis

That is, some of the organelles within eukaryotic cells are capable of protein synthesis. These organelles with their own genetic material and protein-synthesizing capabilities are thought to have been free-living bacteria that entered into a symbiotic relationship, eventually giving rise to eukaryotic cells

Multicelled Organisms

Obviously multicelled organisms are made up of many cells, perhaps billions as opposed to a single cell as in prokaryotes. In addition, multicelled organisms have cells specialized to perform specific functions such as respiration, food gathering and reproduction

Dawn of Multicelled Organisms

We know from the fossil record that multicelled organisms were present during the Proterozoic but we do not know exactly when they appeared. What seem to be some kind of multicelled algae appear in the 2.1 billion-year-old fossils from the Negaunee Iron Formation in Michigan as carbonaceous filaments from 1.8 billion-year-old rocks in China as somewhat younger carbonaceous impressions of filaments and spherical forms.

Multicelled Algae?

Carbonaceous impressions in Proterozoic rocks, Montana. These may be impressions of multicelled algae

The Multicelled Advantage?

Is there any particular advantage to being multicelled? For something on the order of 1.5 billion years all organisms were single-celled and life seems to have thrived. In fact, single-celled organisms are quite good at what they do but what they do is very limited. Single celled organisms can not grow very large, because as size increases proportionately less of a cell is exposed to the external environment in relation to its volume and the proportion of surface area decreases. Transferring materials from the exterior to the interior becomes less efficient. Multicelled organisms live longer, since cells can be replaced and more offspring can be produced. Cells have increased functional efficiency when they are specialized into organs with specific capabilities.

Other Proterozoic Animal Fossils

- Although scarce, a few animal fossils older than those of the Ediacaran fauna are known.
- A jellyfish-like impression is present in rocks 2000 m below the Ediacara Hills Pound Quartzite.
- Burrows in many areas presumably made by worms, occur in rocks at least 700 million years old.
- Wormlike and algae fossils come from 700 to 900 million-year-old rocks in China but the identity and age of these "fossils" has been questioned

Soft Bodies

All known Proterozoic animals were soft-bodied, but there is some evidence that the earliest stages in the origin of skeletons was underway. Even some Ediacaran animals may have had a chitinous carapace and others appear to have had areas of calcium carbonate. The odd creature known as *Kimberella* from the latest Proterozoic of Russia had a tough outer covering similar to that of some present-day marine invertebrates.

Latest Proterozoic *Kimberella*

Kimberella, an animal from latest Proterozoic rocks in Russia. Exactly what *Kimberella* was remains uncertain. Some think it was a sluglike creature whereas others think it was more like a mollusk

Durable Skeletons

Latest Proterozoic fossils of minute scraps of shell-like material and small tooth like denticles and spicules, presumably from sponges indicate that several animals with skeletons or at least partial skeletons existed. More durable skeletons of silica, calcium carbonate, and chitin (a complex organic substance) did not appear in abundance until the beginning of the Phanerozoic Eon 545 million years ago --- Cambrian age

49 Evolution of definition of Ecology

Evolution of Definitions of Ecology

- **Ecology** = from the Greek root OIKOS, "at home", and OLOGY, "the study of" Haeckle (1870):
- "By ecology we mean the body of knowledge concerning the economy of Nature - the investigation of the total relations of the animal to its inorganic and organic environment."
- Burdon-Sanderson (1890s): Elevated Ecology to one of the three natural divisions of Biology: Physiology - Morphology - Ecology
- Elton (1927): "Scientific natural history"
- Andrewartha (1961): "The scientific study of the distribution and abundance of organisms" □
- Odum (1963): "The structure and function of Nature"

Our Definition

- "Ecology is the scientific study of the processes regulating the distribution and abundance of organisms and the interactions among them, and the study of how these organisms in turn mediate the transport and transformation of energy and matter in the biosphere (i.e., the study of the design of ecosystem structure and function).
- Beyond Fundamental Ecology Applied Ecology: Using ecological principles to maintain conditions necessary for the continuation of present day life on earth.

Industrial Ecology

The design of the industrial infrastructure such that it consists of a series of interlocking "technological ecosystems" interfacing with global natural ecosystems. Industrial ecology takes the pattern and processes

of natural ecosystems as a design for sustainability. It represents a shift in paradigm from conquering nature to becoming nature.

Ecological Engineering

Unlike industrial ecology, the focus of Ecological Engineering is on the manipulation of natural ecosystems by humans for our purposes, using small amounts of supplemental energy to control systems in which the main energy drives are still coming from non-human sources. It is the design of new ecosystems for human purposes, using the self-organizing principles of natural ecosystems.

Ecological Economics

Integrating ecology and economics in such a way that economic and environmental policies are reinforcing rather than mutually destructive.

Urban ecology

For ecologists, urban ecology is the study of ecology in urban areas, specifically the relationships, interactions, types and numbers of species found in urban habitats. Also, the design of sustainable cities, urban design programs that incorporate political, infrastructure and economic considerations.

Conservation Biology

The application of diverse fields and disciplines to the conservation of biological diversity. Restoration Biology: Application of ecosystem ecology to the restoration of deteriorated landscapes in an attempt to bring it back to its original state as much as possible. Example, prairie grass.

Landscape Ecology

"Landscape ecology is concerned with spatial patterns in the landscape and how they develop, with an emphasis on the role of disturbance, including human impacts" (Smith and Smith). It is a relatively new branch of ecology, that employs Global Information Systems. The goal is to predict the responses of different organisms to changes in landscape, to ultimately facilitate ecosystem management

Organizing principles

All these disciplines require an understanding of the "organizing principles" of ecosystems, i.e., their ecology. This involves the detailed study of the structure and function of ecosystems in their undisturbed state, and using their designs to: determine the resilience of ecosystem functions to human activities. design ecosystems which function in the service of human beings with minimal fossil energy input (ideally none) and minimal waste. design the industrial infrastructure. integrate the value of "goods and services" of natural ecosystems into the global economic system.

What is "Sustainability"?

There are many definitions of this one, depending on your perspective. Here's ours: Sustainability is a property of a human society in which ecosystems (including humans) are managed such that the conditions supporting present day life on Earth can continue.

50 Levels of studying ecology

Biosphere: The earth's ecosystem interacting with the physical environment as a whole to maintain a steady state system intermediate in the flow of energy between the high energy input of the sun and the thermal sink of space (merges with atmosphere, lithosphere, hydrosphere...).

Biome: Large scale areas of similar vegetation and climatic characteristics.

Ecosystem: Set of organisms and abiotic components connected by the exchange of matter and energy (forest, lake, coastal ocean). Or, "the smallest units that can sustain life in isolation from all but atmospheric surroundings."

Community: Interacting populations which significantly affect each other's distributions and abundance (intertidal, hot spring, wetland).

Population: Group of interacting and interbreeding organisms

- Cell/Organism
- Organelle
- Molecule
- Atom

Oxidation/reduction reactions

The energy that drives all life processes is organized around oxidation/reduction reactions. Ultimately on Earth today, oxygenic photosynthesis, and energy from the sun, fuels the entire biosphere. Oxygenic photosynthesis produces (by the splitting of water as a reducing agent) one of the most powerful oxidants known – oxygen. The biosphere on the contemporary Earth runs largely on the carbon produced by CO₂ fixation by oxygenic photosynthesis, and on the free energy difference between O₂ and organic carbon, which heterotrophs use to fuel their metabolism.

Autotrophs

The autotrophs synthesize glucose using solar or chemical energy, which is broken down through respiration (either their own or that of the organisms that eat them) to provide the energy necessary for “biological work”. Redox reactions are central to all of these energy transformations, and the resulting flows of electrons manifest themselves, collectively, in the form of global biogeochemical cycles.

Role of bacteria

The activities of bacteria keep these cycles moving. For example, the chemosynthetic bacteria oxidize many essential elements in the process of getting the energy required to reduce CO₂. Certain anaerobic

bacteria in turn reduce these compounds in the process of anaerobic respiration □ i.e., they use them as an electron acceptor in the absence of oxygen. This keeps the element cycles cycling maintaining balanced amounts of oxidants and reductants necessary for diverse metabolic processes. This keeps the system from “running down” energetically. Stay tuned for section on Biogeochemical Cycles.

Keystone predator

Starfish prey on mussels, barnacles, limpets, and chitons

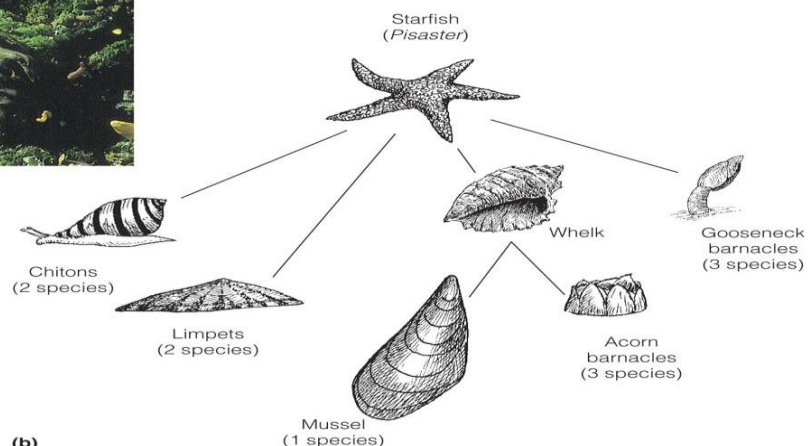
Remove starfish, what would happen?

Species diversity increase or decrease?

Why?



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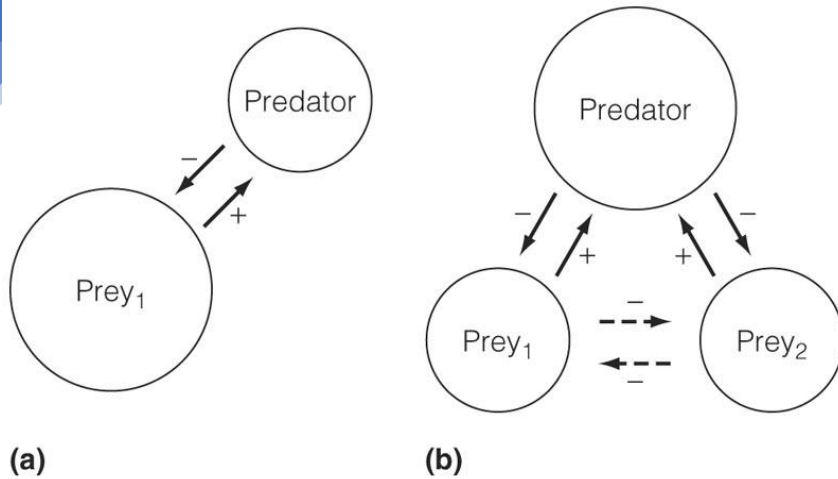


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Apparent competition

Combined populations of two prey species support a larger predator population neither can support alone. As a result, two prey populations reduced, gives outward appearance of interspecific competition.



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Apparent competition

- In the absence of predator, the population of each prey is regulated by purely intraspecific density-dependent mechanisms
- Neither prey species compete, directly or indirectly, with each other
- Predator abundance depends on the total abundance of prey
- Under these conditions, the combined population abundance of two prey species will support a higher predator density.

75-Energy and Nutrient Relations

Three main sources of energy

- Organisms use one of three main sources of energy:
 - light,
 - inorganic molecules, or
 - organic molecules.
- Photosynthetic plants and algae CO_2 as a source of carbon and light, of wavelengths between 400 and 700 nm, as a source of energy
- Light within this band, which is called photosynthetically active radiation, or PAR, accounts for about 45% of the total energy content of the solar spectrum at sea level.

PAR quantification

- PAR can be quantified as photosynthetic photon flux density, generally reported as μmol per square meter per second
- Among plants, there are three major alternative photosynthetic pathways, C_3 , C_4 , and CAM. C_4 and CAM plants are more efficient in their use of water than are C_3 plants.

Heterotrophs

- Heterotrophs use organic molecules both as a source of carbon and as a source of energy.
- Herbivores, carnivores, and detritivores face fundamentally different trophic problems.
- Herbivores feed on plant tissues. which often contain a great deal of carbon but little nitrogen.
- Herbivores must also overcome the physical and chemical defences of plants

76-Energy and Nutrient Relations

Detritivores

- Detritivores feed on dead plant material, which is even lower in nitrogen than living plant tissues
- Carnivores consume prey that are nutritionally rich but very well defended.
- Chemosynthetic autotrophs, which consist of a highly diverse group of chemosynthetic bacteria, use inorganic molecules as a source of energy
- Bacteria are the most tropically diverse organisms in the biosphere.

Rate of uptake of energy

- The rate at which organisms can take in energy is limited, either by external or internal constraints.
- The relationship between photon flux density and plant photosynthetic rate is called photosynthetic response.
- Herbs and short-lived perennial shrubs from sunny habitats have high maximum photosynthetic rates that level on at high light intensities.
- The lowest maximum rates of photosynthesis occur among plants from shady environments
- The relationship between food density and animal feeding rate is called the functional response.
- The shape of the functional response is generally one of three types.
- The forms of photosynthetic response curves and type 2 animal functional responses are remarkably similar

77-Rate of uptake of energy

Optimal foraging theory

- Optimal foraging theory attempts to model how organisms feed as an optimizing process.
- Evolutionary ecologists predict that if organisms have limited access to energy, natural selection is likely to favour individuals that are more effective at acquiring energy and nutrients.
- Many animals select food in a way that appears to maximize the rate at which they capture energy
- Plants appear to allocate energy to roots versus shoots in a way that increases their rate of intake of the resources that limit their growth.
- Plants in environments with abundant nutrients but little light tend to invest more energy in the growth of stems and leaves and less in roots.
- In environments rich in light but poor in nutrients, plants tend to invest more energy in the growth of roots.

Trophic diversity of bacteria

- The trophic diversity of bacteria, which is critical to the health of the biosphere, can also be used as a tool to address some of our most challenging waste disposal problems
- Bacteria can be used to eliminate the huge quantities of sewage produced by human populations, clean up soils and aquifers polluted by petroleum products such as benzene,
- And eliminate the pollution caused by some kinds of mine waste.

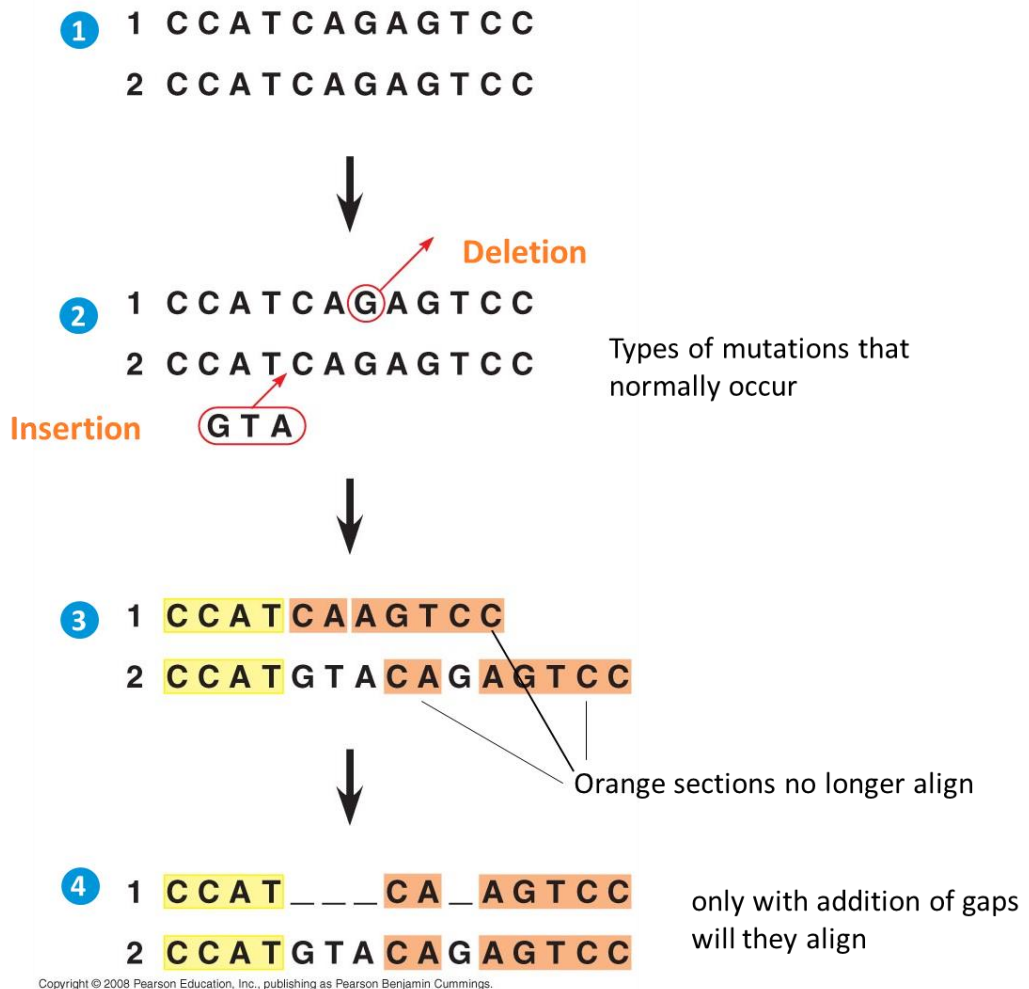
Role of bacteria

- The success of these projects requires that ecologists understand the energy and nutrient relations of bacteria.
- Bacteria will likely continue to play a great role as we address some of our most disturbing environmental problems.

78-Evaluating Molecular Homologies

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

Fig. 26-8



- It is also important to distinguish homology from analogy in molecular similarities
- Mathematical tools help to identify molecular homoplasies, or coincidences

A C G G A T A G T C C A C T A G G C A C T A
T C A C C G A C A G G T C T T T G A C T A G

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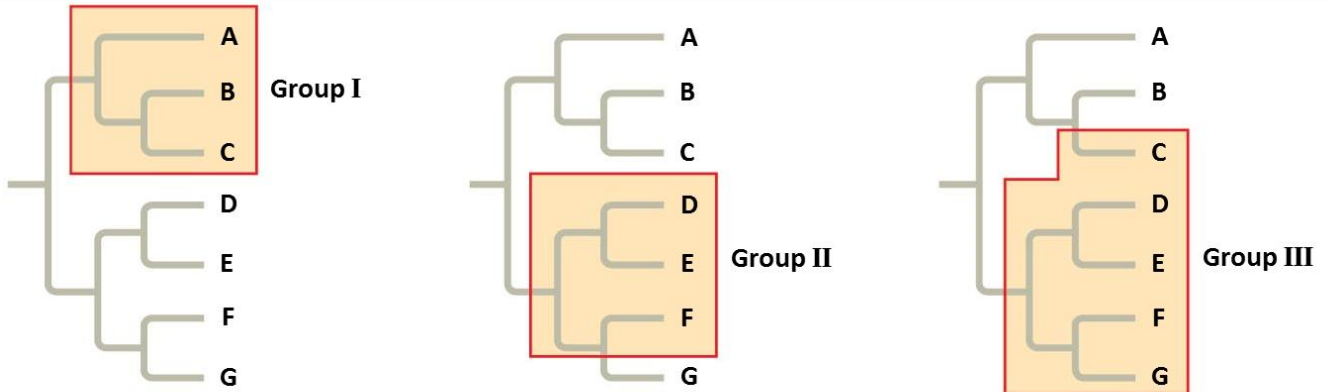
- Molecular systematics uses DNA and other molecular data to determine evolutionary relationships

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



(a) Monophyletic group (clade)

(b) Paraphyletic group

(c) Polyphyletic group

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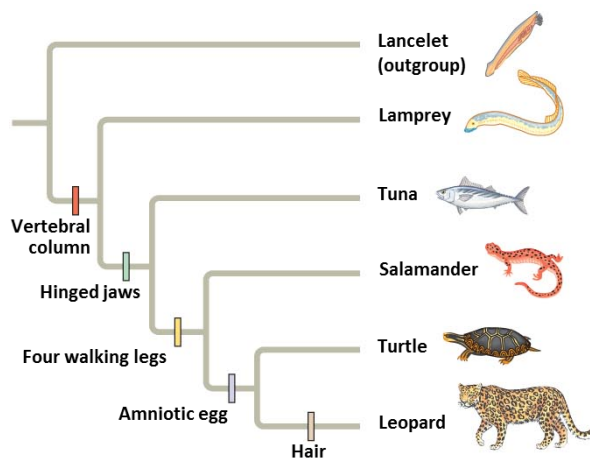
79-Shared Ancestral and Shared Derived Characters

- 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

CHARACTERS	TAXA					
	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard
Vertebral column (backbone)	0	1	1	1	1	1
Hinged jaws	0	0	1	1	1	1
Four walking legs	0	0	0	1	1	1
Amniotic (shelled) egg	0	0	0	0	1	1
Hair	0	0	0	0	0	1

(a) Character table

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(b) Phylogenetic tree

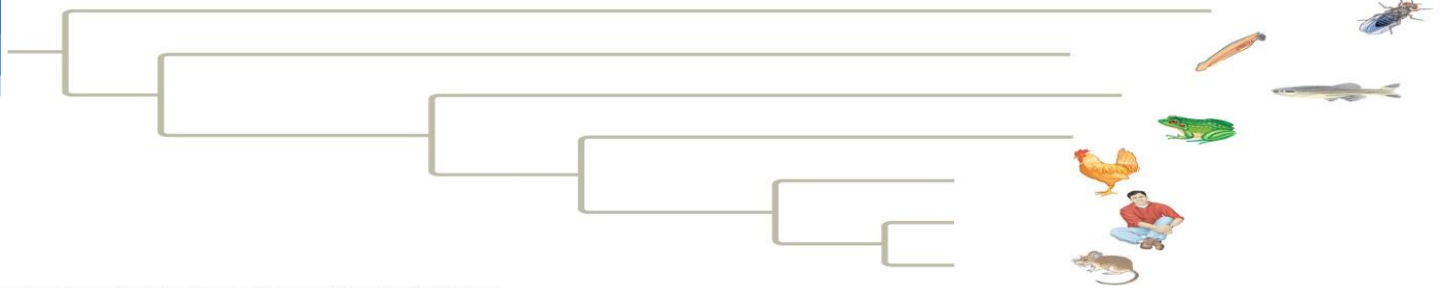
- An out-group is a species or group of species that is closely related to the in-group, the various species being studied
- Systematists compare each in-group species with the out-group to differentiate between shared derived and shared ancestral characteristics

80-Shared Ancestral and Shared Derived Characters

- Homologies shared by the out-group and in-group are ancestral characters that predate the divergence of both groups from a common ancestor

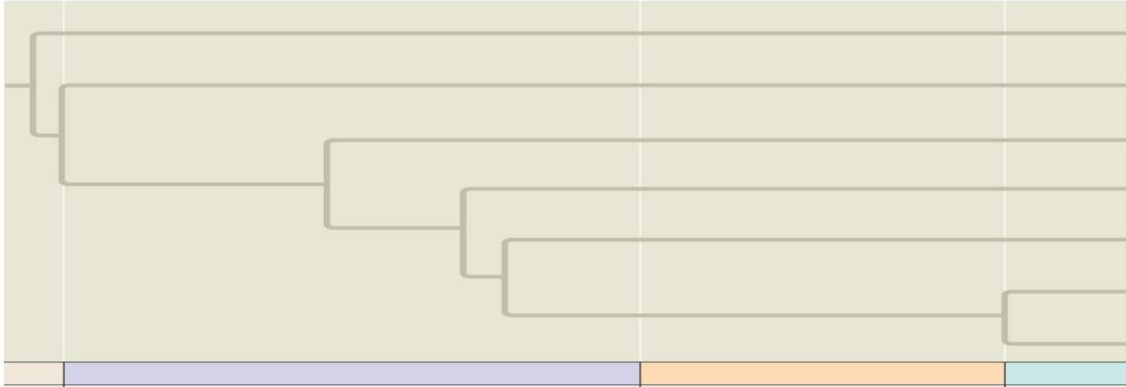
Phylogenetic Trees with Proportional Branch Lengths

- 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



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- In other trees, branch length can represent chronological time, and branching points can be determined from the fossil record



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- 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 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

81-Evolution of Definitions of Ecology

- Ecology = from the Greek root OIKOS, "at home", and OLOGY, "the study of" Haeckle (1870):
- "By ecology we mean the body of knowledge concerning the economy of Nature - the investigation of the total relations of the animal to its inorganic and organic environment."
- Burdon-Sanderson (1890s): Elevated Ecology to one of the three natural divisions of Biology: Physiology - Morphology - Ecology
- Elton (1927): "Scientific natural history"
- Andrewartha (1961): "The scientific study of the distribution and abundance of organisms"
- Odum (1963): "The structure and function of Nature"

Our Definition

- "Ecology is the scientific study of the processes regulating the distribution and abundance of organisms and the interactions among them, and the study of how these organisms in turn mediate the transport and transformation of energy and matter in the biosphere (i.e., the study of the design of ecosystem structure and function).
- Beyond Fundamental Ecology Applied Ecology:

- Using ecological principles to maintain conditions necessary for the continuation of present day life on earth.

Industrial Ecology

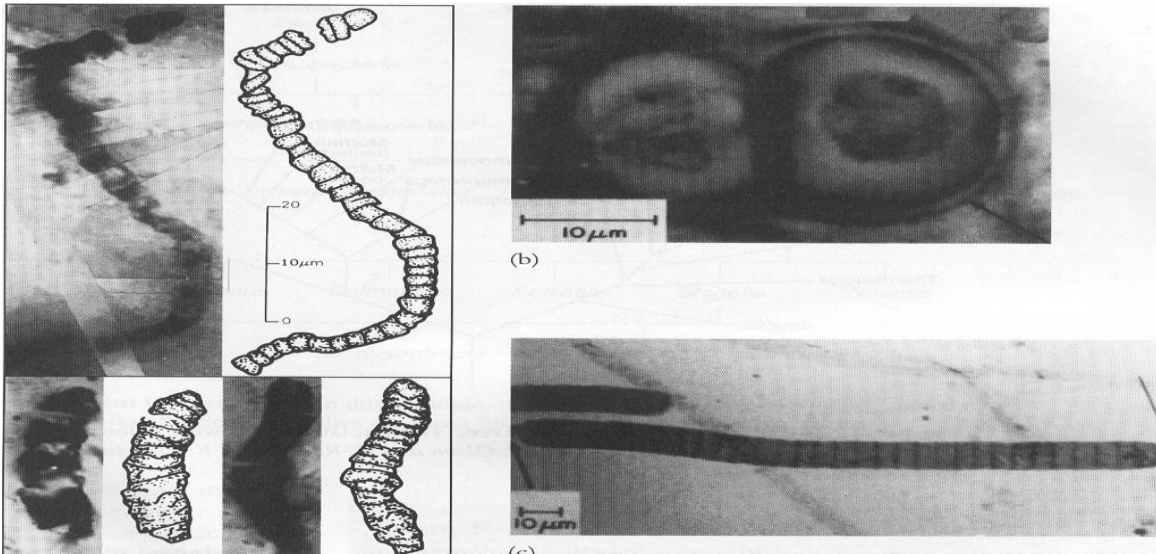
- The design of the industrial infrastructure such that it consists of a series of interlocking "technological ecosystems" interfacing with global natural ecosystems.
- Industrial ecology takes the pattern and processes of natural ecosystems as a design for sustainability. It represents a shift in model from conquering nature to becoming nature.

Ecological Engineering

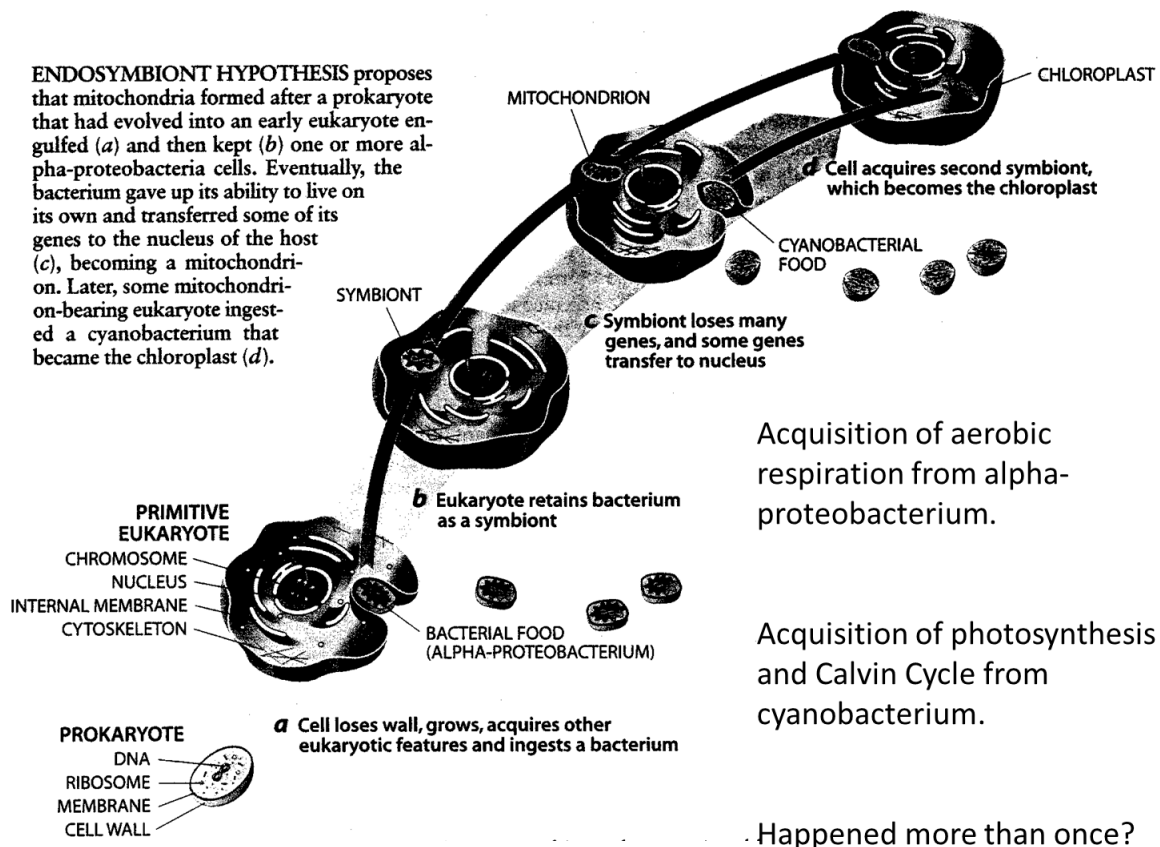
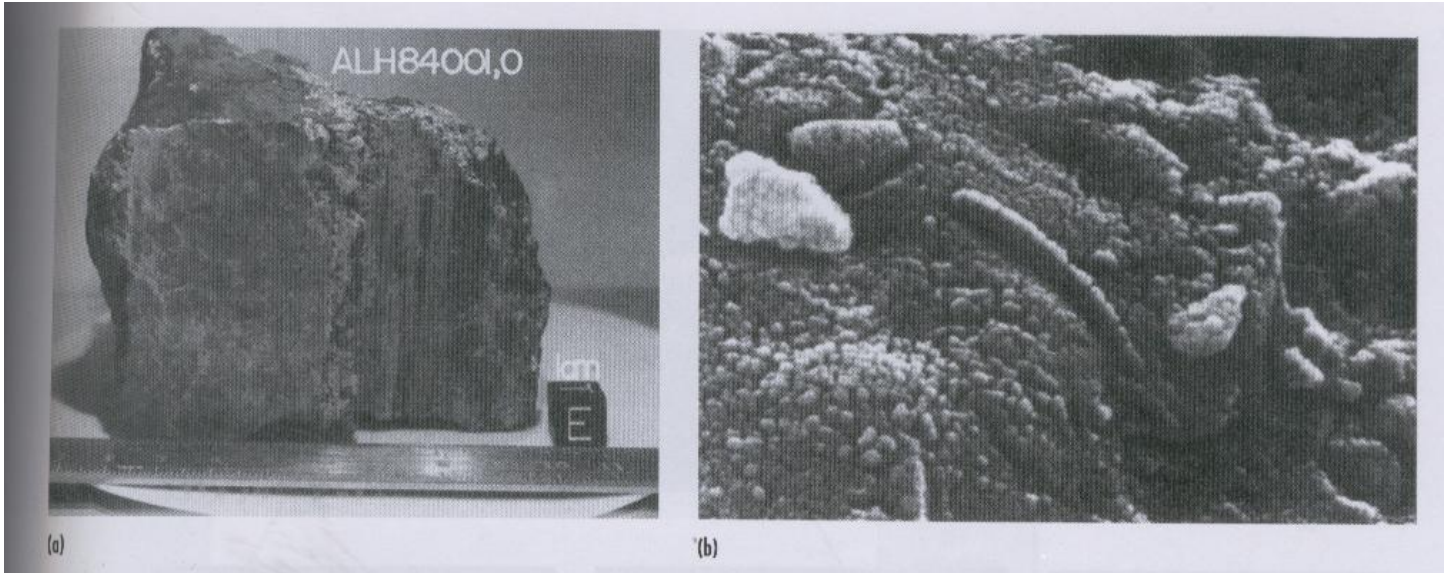
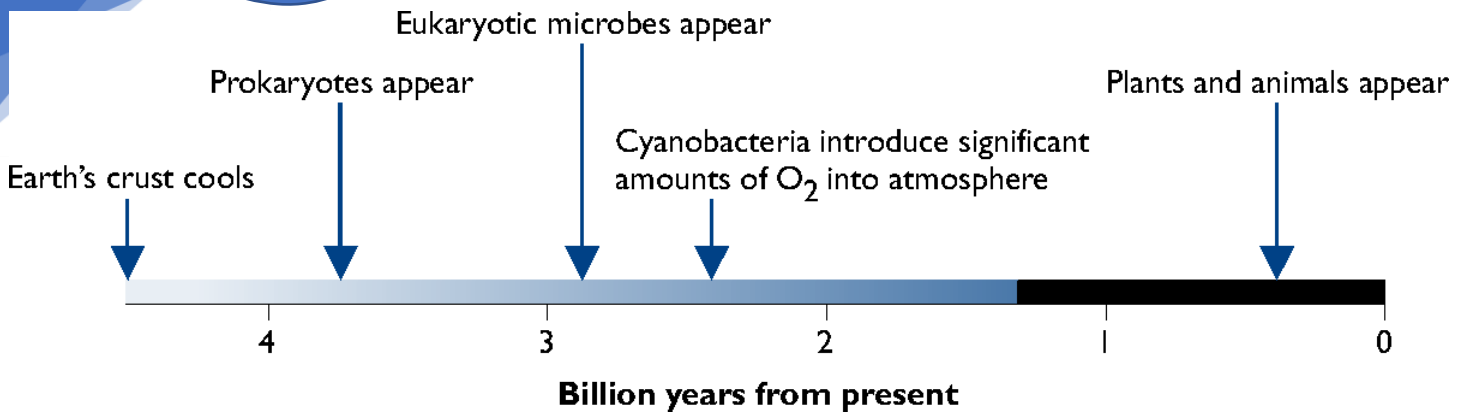
- Unlike industrial ecology, the focus of Ecological Engineering is on the manipulation of natural ecosystems by humans for our purposes, using small amounts of supplemental energy to control systems in which the main energy drives are still coming from non-human sources.
- It is the design of new ecosystems for human purposes, using the self-organizing principles of natural ecosystems.

82-Ecological Economics

Over 3.5 billion years of "microbes"



Micro-fossils of "cyanobacteria" and contemporary stromatolites.

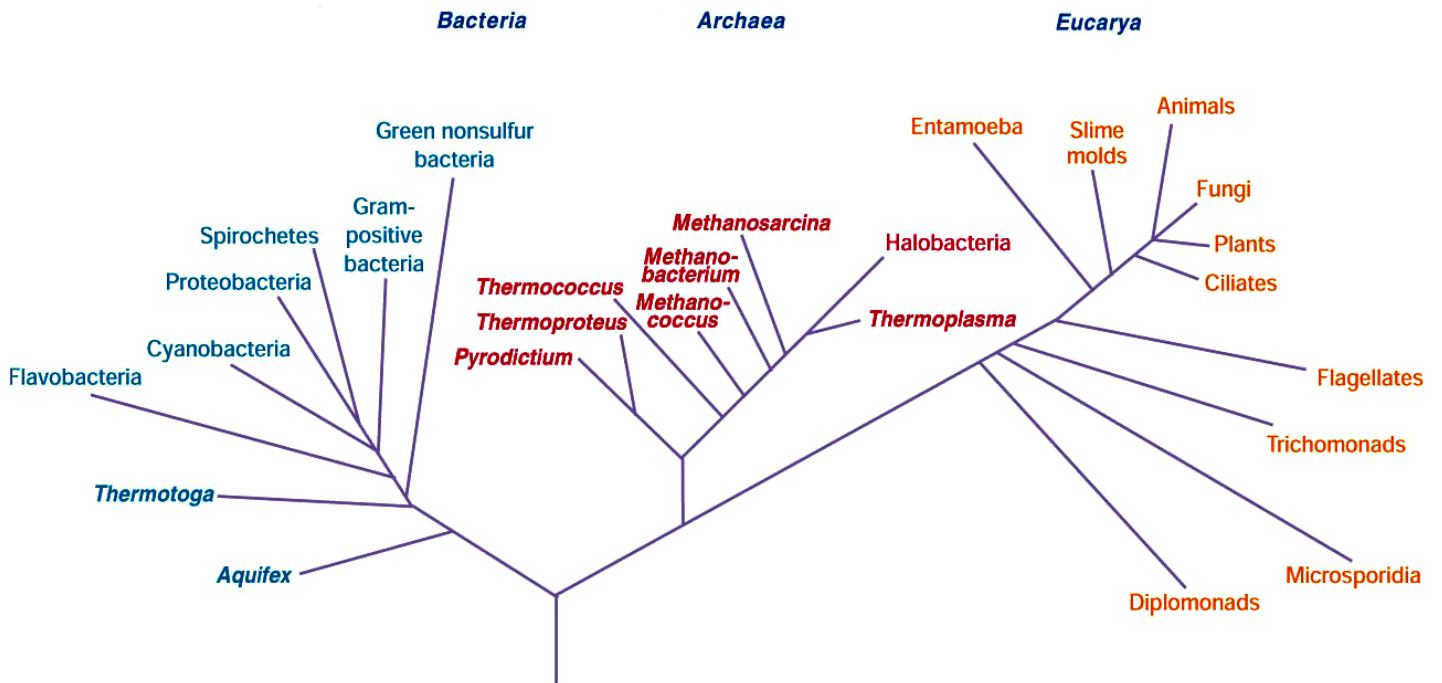


Major challenges for endosymbiotic theory

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.)

83-Evolution of Microbes

84-Phylogenetic Tree of Life



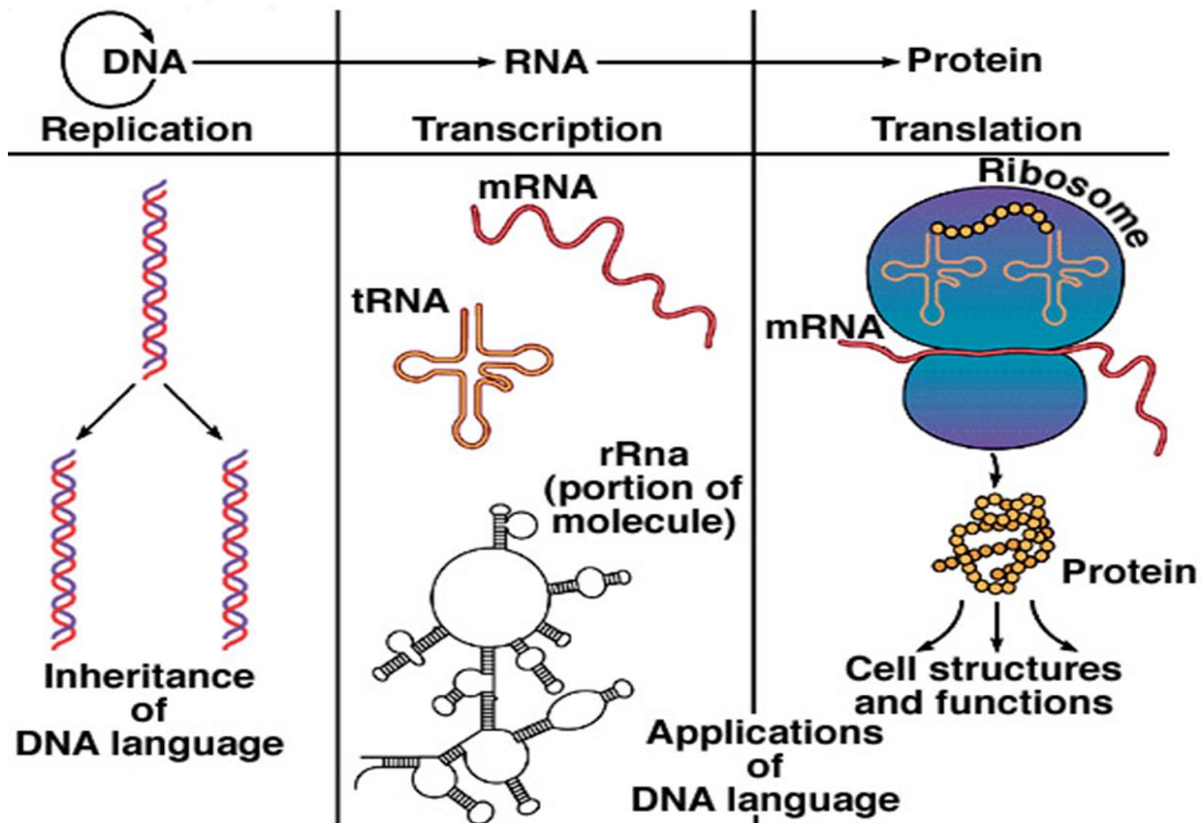
Rooted Tree based on 16SrRNA and 18SrRNA sequence data.

All extant life has evolved; evidence lost by extinction.

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

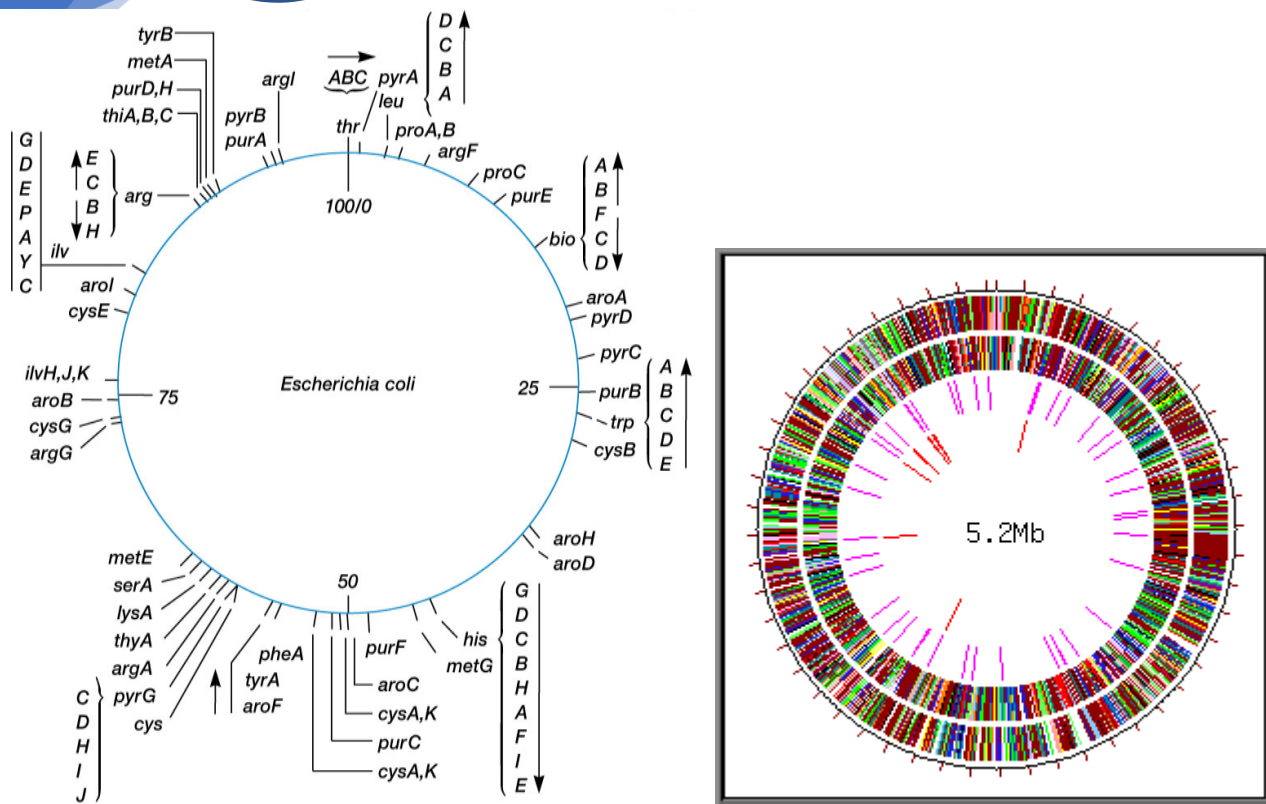
Genotype

Phenotype



Bacterial Genomes

- 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) $ACTG \rightarrow AITG$
 - Frameshifts (Insertions or Deletions)

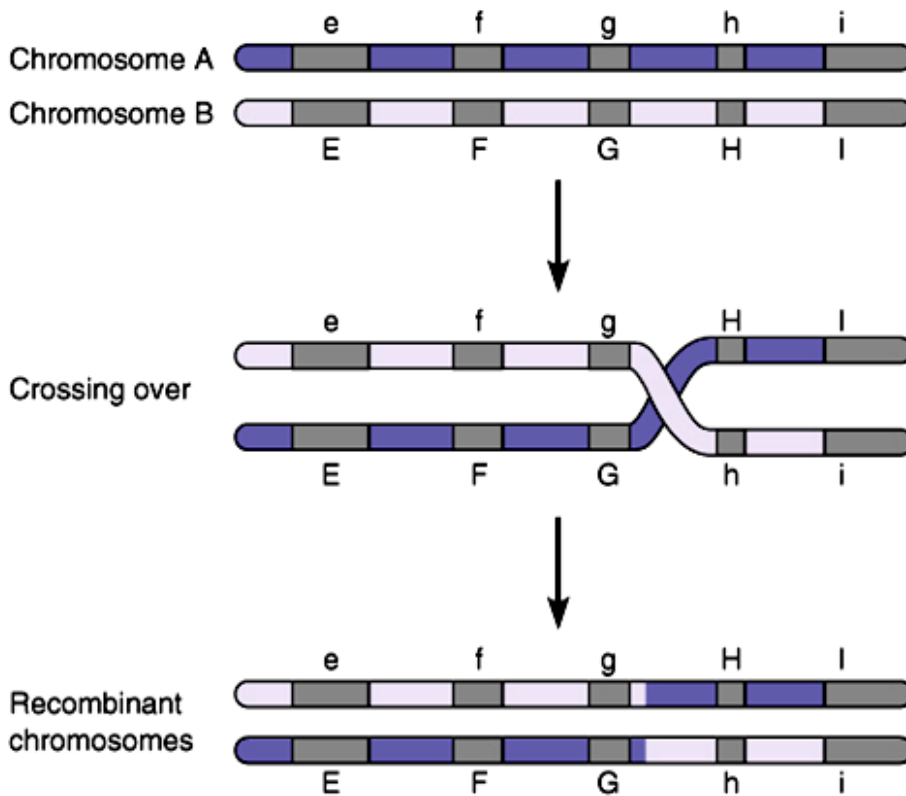
see the cat eat the rat \rightarrow see thc ate att her at

- Mechanisms of microlesion mutation types
 - Spontaneous (1 per million; most corrected; 1 per billion remain)
 - Chemical mutagens
 - Radiation as mutagens

85-Genetic Recombination

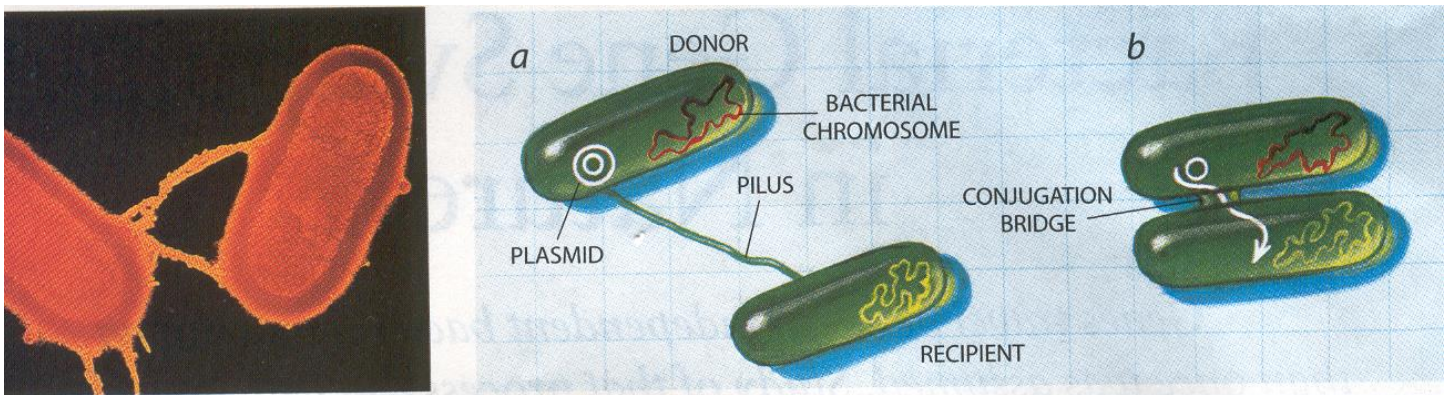
Genetic Recombination:

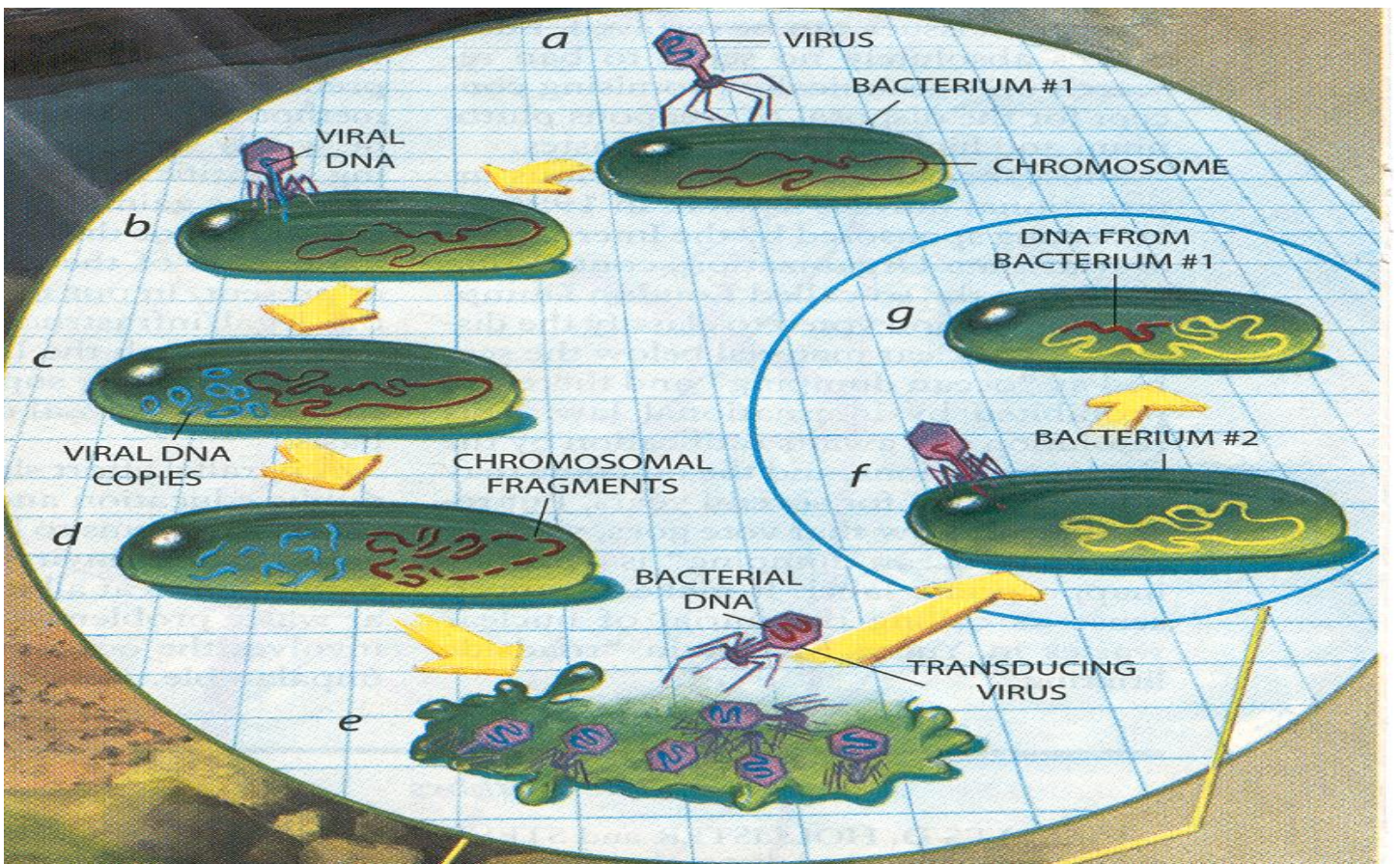
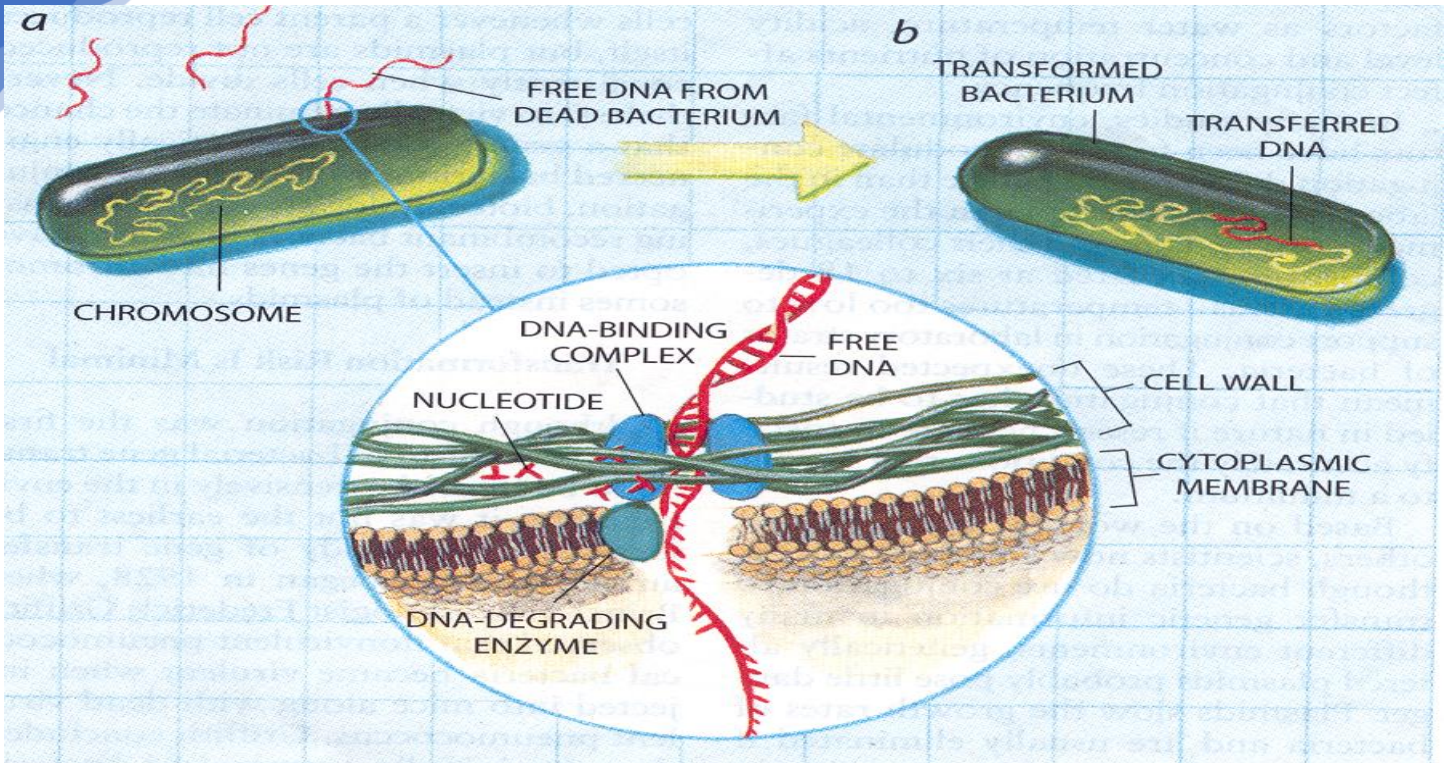
- Two DNA molecules may recombine segments of their molecule in a process called crossing over.
- This is a relatively common event between chromosome copies in eukaryotes during meiosis. (Note the example here.)
- Prokaryote chromosomes, viral DNA, and smaller fragments of “foreign” DNA may recombine, 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.







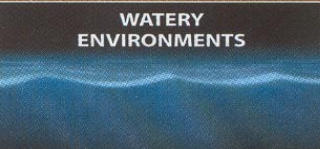
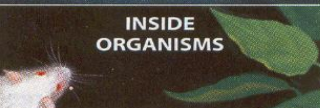
Horizontal Gene Transfer(= lateral gene exchange)

- Conjugation
- Transformation
- Transduction





Where in Nature?

	 <p>TRANSDUCTION</p>	 <p>CONJUGATION</p>	 <p>TRANSFORMATION</p>
 <p>TERRESTRIAL ENVIRONMENTS</p>	Soil, plant surfaces	Soil, plant surfaces	Soil
 <p>WATERY ENVIRONMENTS</p>	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
 <p>INSIDE ORGANISMS</p>	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.

86-Evolutionary Biodiversity in Proterozoic Eon

Endosymbiosis and the Origin of Eukaryotic Cells

- Formed from several prokaryotic cells
 - In a symbiotic relationship
 - Symbiosis,
 - involving a prolonged association of two or more dissimilar organisms,
 - is quite common today
- In many cases both symbionts benefit from the association
 - as occurs in lichens,
 - once thought to be plants
 - but actually symbiotic fungi and algae

Evidence for Endosymbiosis

- Supporting evidence for endosymbiosis
 - comes from studies of living eukaryotic cells
 - containing internal structures called organelles,
 - such as mitochondria and plastids,
 - which contain their own genetic material
- In addition, prokaryotic cells
 - synthesize proteins as a single system,
- whereas eukaryotic cells
 - are a combination of protein-synthesizing systems

Organelles Capable of Protein Synthesis

- That is, some of the organelles
 - within eukaryotic cells are capable of protein synthesis
- These organelles
 - with their own genetic material

- and protein-synthesizing capabilities
- are thought to have been free-living bacteria
 - that entered into a symbiotic relationship,
 - eventually giving rise to eukaryotic cells

Multi-celled Organisms

- Obviously multi-celled organisms
 - are made up of many cells,
 - perhaps billions,
 - as opposed to a single cell as in prokaryotes
- In addition, multi-celled organisms
 - have cells specialized to perform specific functions
 - such as respiration,
 - food gathering,
 - and reproduction

87-Dawn of Multicelled Organisms

- We know from the fossil record
 - that multi-celled organisms were present during the Proterozoic,
 - but we do not know exactly when they appeared
- What seem to be some kind of multi-celled algae appear
 - in the 2.1-billion-year-old fossils
 - from the Negaunee Iron Formation in Michigan
 - as carbonaceous filaments
 - from 1.8 billion-year-old rocks in China
 - as somewhat younger carbonaceous impressions of filaments and spherical forms

Multi-celled Algae?

- Carbonaceous impressions
 - in Proterozoic rocks, Montana
- These may be impressions of multi-celled algae

The Multi-celled Advantage?

- Is there any particular advantage to being multi-celled?
- For something on the order of 1.5 billion years
 - all organisms were single-celled
 - and life seems to have thrived
- In fact, single-celled organisms
 - are quite good at what they do

- but what they do is very limited
- single celled organisms
 - can not grow very large, because as size increases proportionately less of a cell is exposed to the external environment in relation to its volume
 - and the proportion of surface area decreases
- Transferring materials from the exterior to the interior becomes less efficient
- Multi-celled organisms live longer,
 - since cells can be replaced and more offspring can be produced
- Cells have increased functional efficiency
 - when they are specialized into organs with specific capabilities

88-Other Proterozoic Animal Fossils

- A jellyfish-like impression is present in rocks 200 m below the Ediacara Hills
- Wormlike and algae fossils come from 700 to 900 million-year-old rocks in China but the identity and age of these "fossils" has been questioned

Wormlike Fossils from China

- Wormlike fossils from Late Proterozoic rocks in China

Soft Bodies

- All known Proterozoic animals were soft-bodied, but there is some evidence that the earliest stages in the origin of skeletons was underway
- Even some Ediacaran animals may have had a chitinous carapace and others appear to have had areas of calcium carbonate
- The odd creature known as *Kimberella* from the latest Proterozoic of Russia had a tough outer covering similar to that of some present-day marine invertebrates

Latest Proterozoic *Kimberella*

- *Kimberella*, an animal from latest Proterozoic rocks in Russia
 - Exactly what *Kimberella* was remains uncertain
 - Some think it was a sluglike creature
 - whereas others think it was more like a mollusk

Durable Skeletons

- Latest Proterozoic fossils
 - of minute scraps of shell-like material and small tooth like denticles and spicules, presumably from sponges indicate that several animals with skeletons or at least partial skeletons existed
- More durable skeletons of
 - silica, calcium carbonate, and chitin (a complex organic substance) did not appear in abundance until the beginning of the Phanerozoic Eon 545 million years ago = Cambrian age

89-Exploitation

Predation, Herbivory, Parasites and Disease

- The diversity of interactions between herbivores and plants, between predators and prey, and between parasites, pathogens, and hosts can be grouped under the heading of exploitation-- interactions between species that enhance the fitness of one individual at the expense of another.
- Exploitation weaves populations into a web of relationships that defy easy generalization.
- The number of exploitative interactions between species far exceeds the number of species in the biosphere, and the nature of exploitation goes far beyond the typical consumption of one organism by another.
- For instance, many parasites and pathogens manipulate host behaviour to enhance their own fitness at the expense of the host.
- Spiny-headed worms alter the behaviour of a variety of crustacean hosts in a way that increases the probability that the one host species will be eaten by another.
- A pathogenic fungus manipulates the growth program of its host plant in a way to produce "pseudoflowers," structures aimed at promoting the reproduction of the pathogen.
- In the process the pathogen usually kills the host plant and always renders it sterile.
- Predation by one flour beetle species on another can be used as a potent means of interference competition except in the presence of a protozoan parasite, which seems to give a competitive advantage to less predaceous species.

Examples

- Predators, parasites, and pathogens influence the distribution, abundance, and structure of prey and host populations.
- Herbivorous stream insects have been shown to control the density of their algal and bacterial food.
- The herbivorous moth larva *Cactoblastis cactorum* combined with pathogenic microbes reduced the coverage of prickly pear cactus in Australia from millions of hectares to a few thousand.
- A parasitic infestation reduced the red fox population in Sweden by 70%, which in turn led to increases in the abundance of several prey species eaten by foxes.
- This parasitic disease revealed the influence of a predator on its prey populations.

90-Ecological Relationships Ecological Relationships of Predator-prey, parasite-host, and pathogen-host

Relationships

- Predator-prey, parasite-host, and pathogen-host relationships are dynamic.
- Populations of a wide variety of predators and prey show highly dynamic fluctuations in abundance ranging from days to decades.
- A particularly well-studied example of predator-prey cycles is that of snowshoe hares and their predators, which have been shown to result from the combined effects of the snowshoe hares on the quantity and quality of their food and of the predators on the snowshoe hare population.

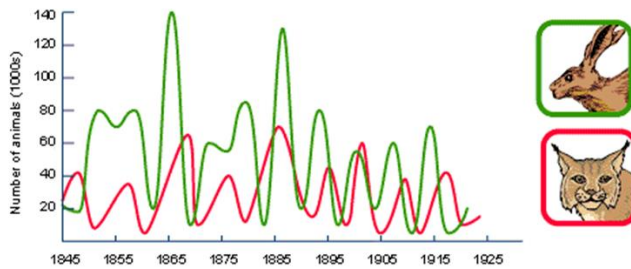
1. Predator Prey Relationships

Learning Objectives

- Be able to describe the relationship between predators and their prey.



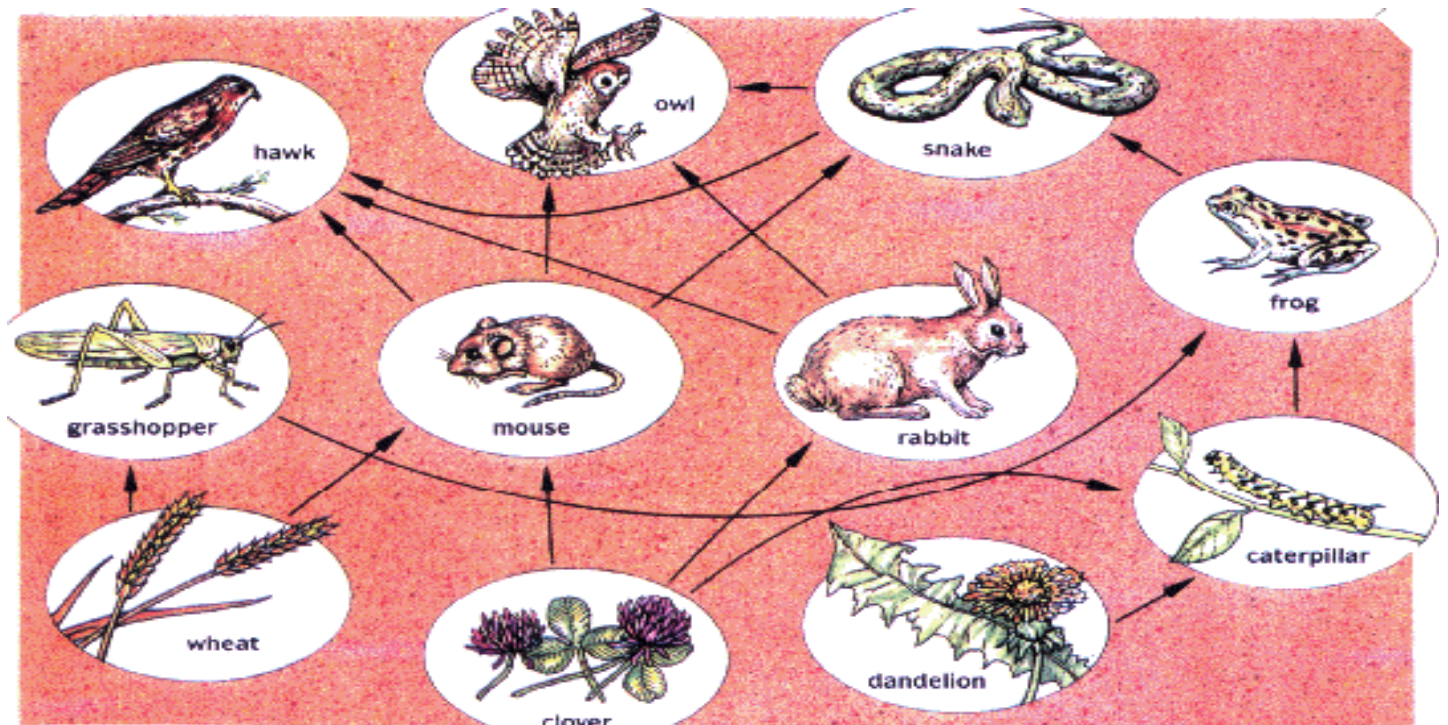
- Be able to explain the shape of a predator – prey graph.



2. Food web - Interdependence

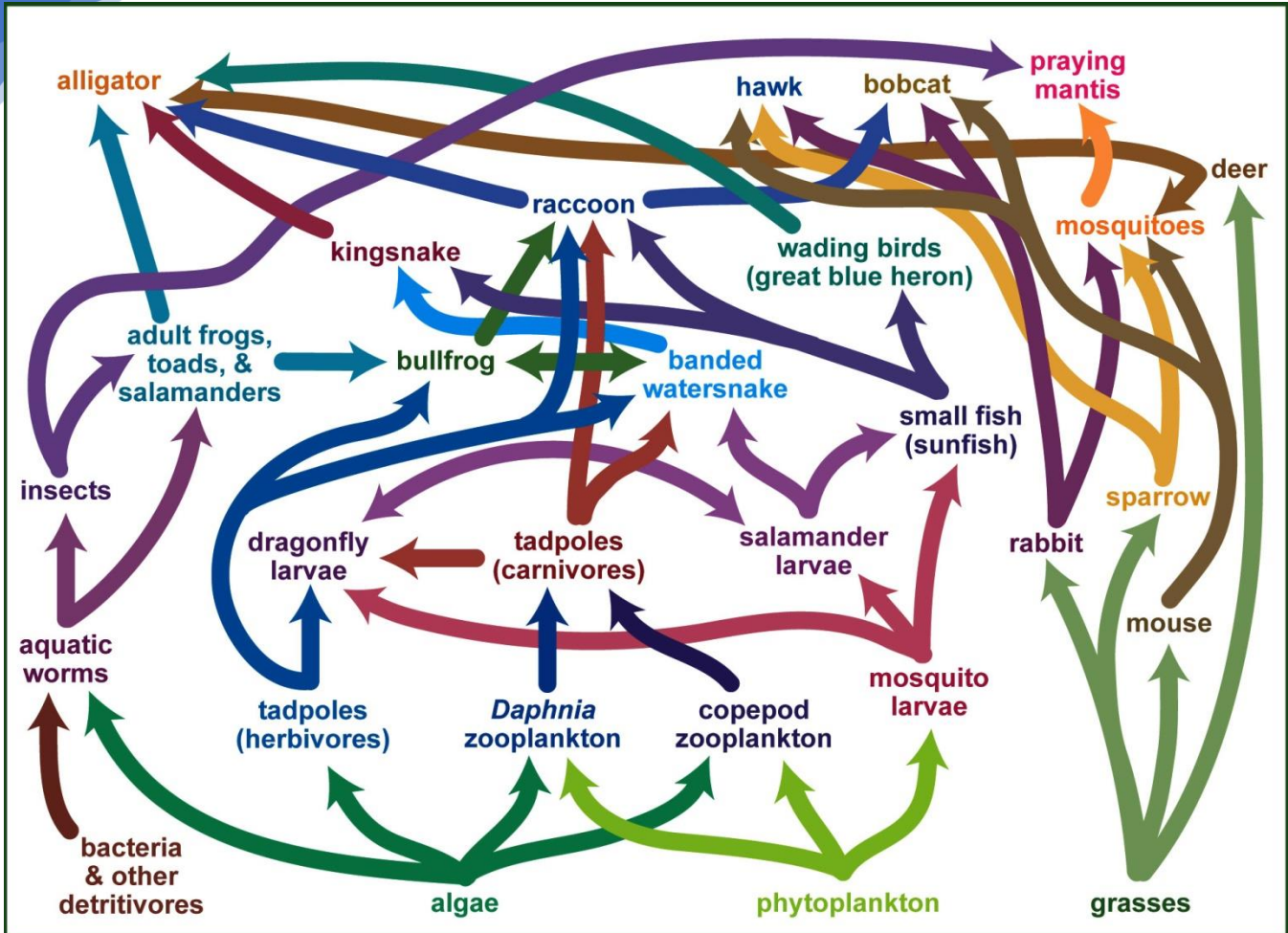
Starter

If the mouse is considered a pest and baited, find as many effects on the food web as you can, in 3 minutes.



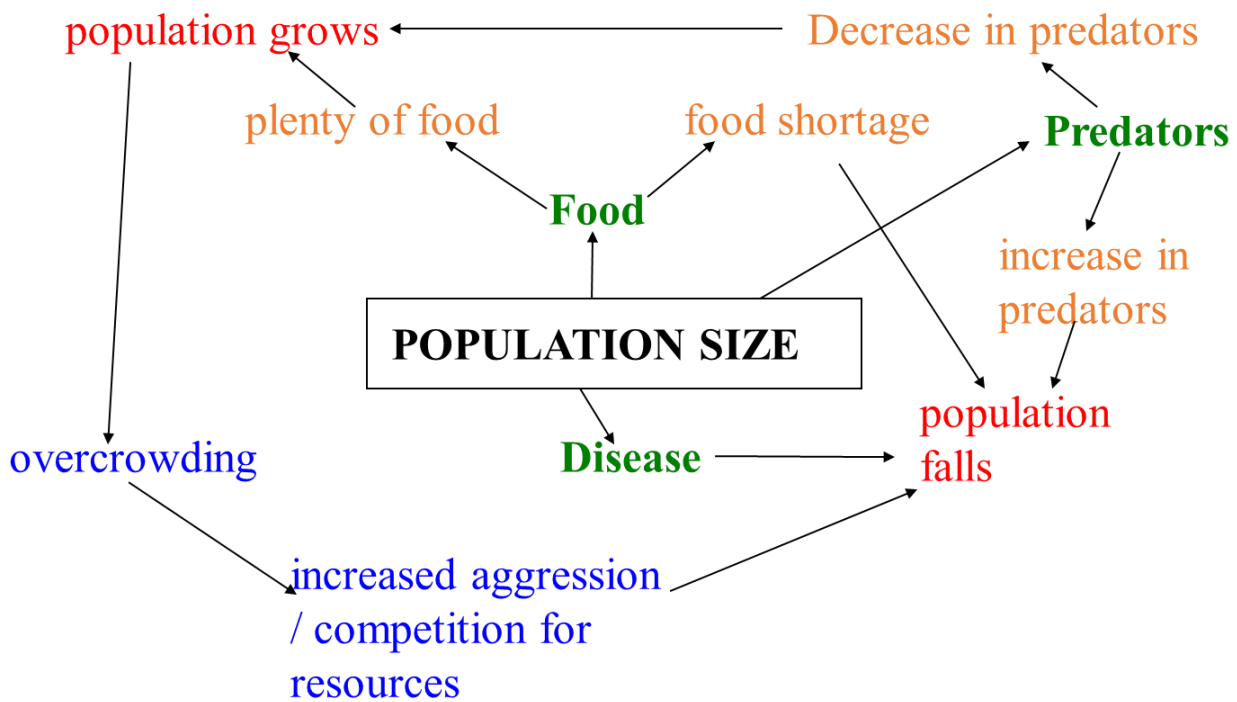
3. Food web – Interdependence

... and that was a simplified food web. Imagine the interactions in a less simplified web. Do you think the bobcat would be affected if the mosquito larvae were destroyed as a malaria risk?



4. Population Size

To do: Draw a concept map of what effects the size of a population.



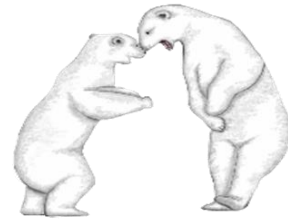
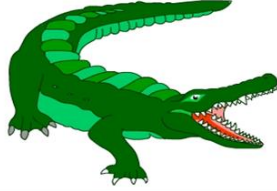
91-Predator-prey interactions

5. Animals that eat other animals

- Populations of animals are often limited by the amount of food.
- What are animals that eat other animals called?



predators



- What are the animals that predators eat called?



prey



To do: Define the words Predator and Prey and give an example of each.

Predator-prey interactions

- Mathematical models of predator-prey interactions by Lotka and Volterra suggest that exploitative interactions themselves can produce population cycles without any influences from outside forces such as weather.
- Predator-prey cycles have also been observed in a few laboratory populations under restricted circumstances.
- To persist in the face of exploitation, hosts and prey need refuges.
- The refuges that promote the persistence of hosts and prey include secure places to which the exploiter has limited access.
- However, living in large groups can be considered as a kind of refuge since it reduces the probability that an individual host or prey will be attacked.
- It appears that predator satiation is a defensive tactic used by a wide variety of organisms from rain forest trees to temperate insects.
- Growing to large size can also represent a kind of refuge when the prey species is faced by size-selective predators,
- Size is used as a refuge by prey species ranging from stream insects and intertidal invertebrates to rhinoceros.

Population control

- Predators and parasites have been used to control populations of insects that attack crops or to control invasive weeds.
- Recent research in Kenya has shown that a crayfish, *Procambarus clarkii*, controls the snails that act as intermediate hosts for *Schistosoma*, a highly pathogenic human parasite.

- Preliminary results indicate that crayfish successfully control host snails in the artificial impoundments used for livestock watering and domestic water, important sources of infection by *Schistosoma*.

92-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

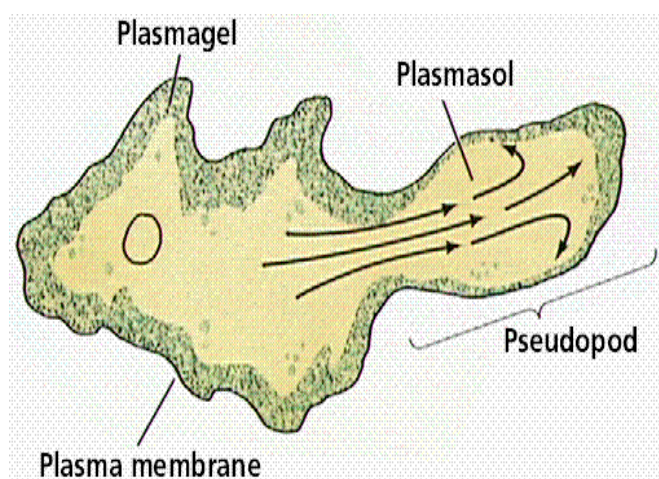
Protozoan Characteristics

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

Example 1: Protozoans – amoebas

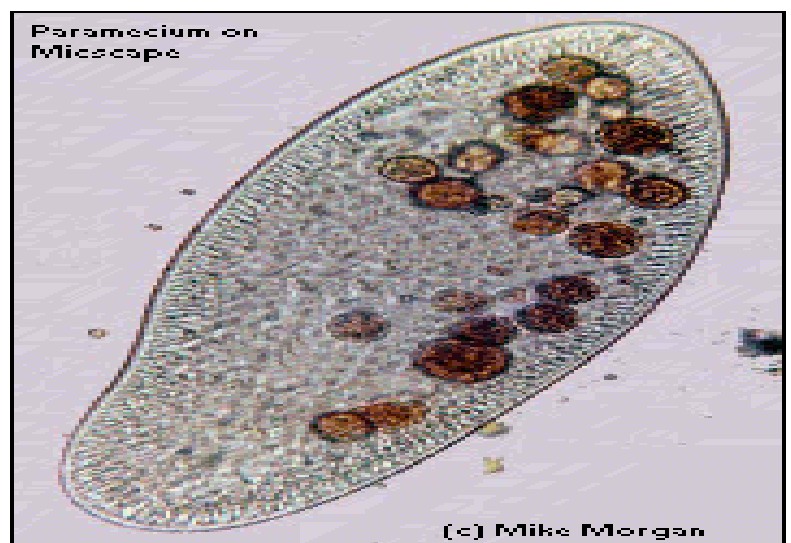
- Amoebas
 - shapeless, aquatic

Pseudopods in Amoebas



How Amoebas Eat ?

- feeding structures-



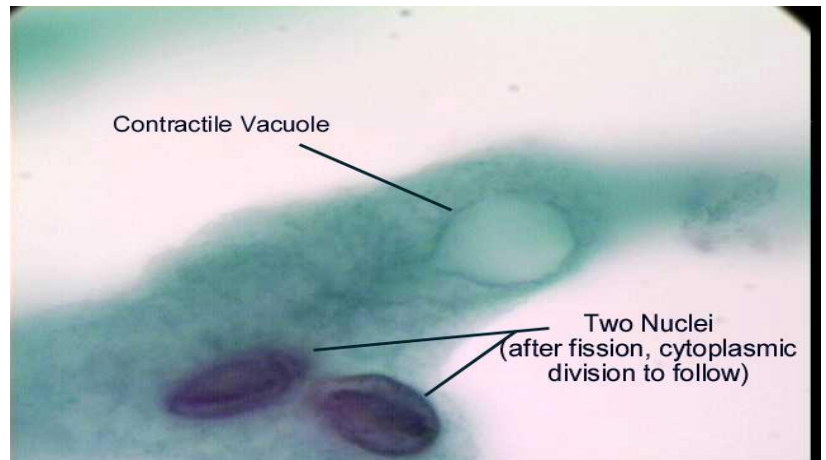
- food vacuole
- digestive enzymes
- diffusion

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



93-Groups of protists

Dysentery (an illness)

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

2. Example 2: Protozoans: Ciliates

- Locomotion - Cilia

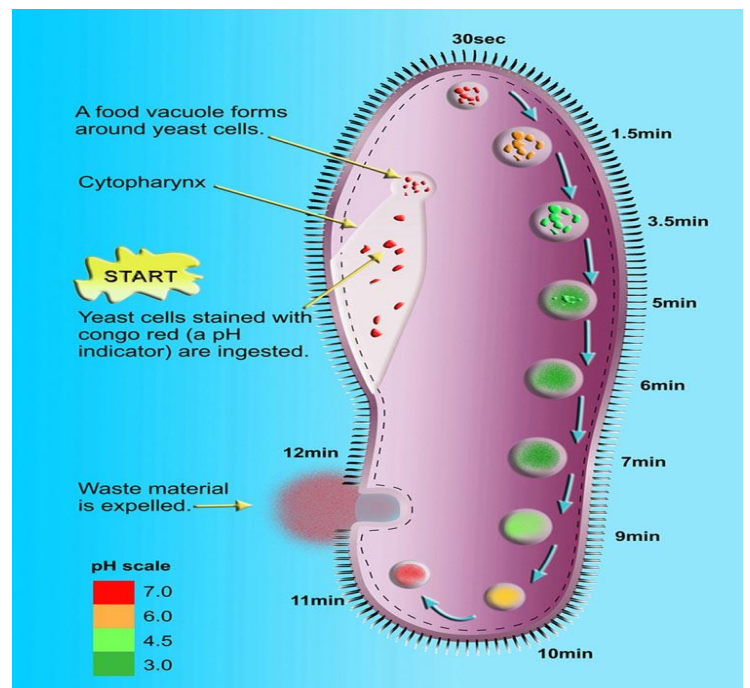
1. Paramecium - fresh water ciliate

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
- Exmaples:

2. Trypanosoma - causes African Sleeping Sickness

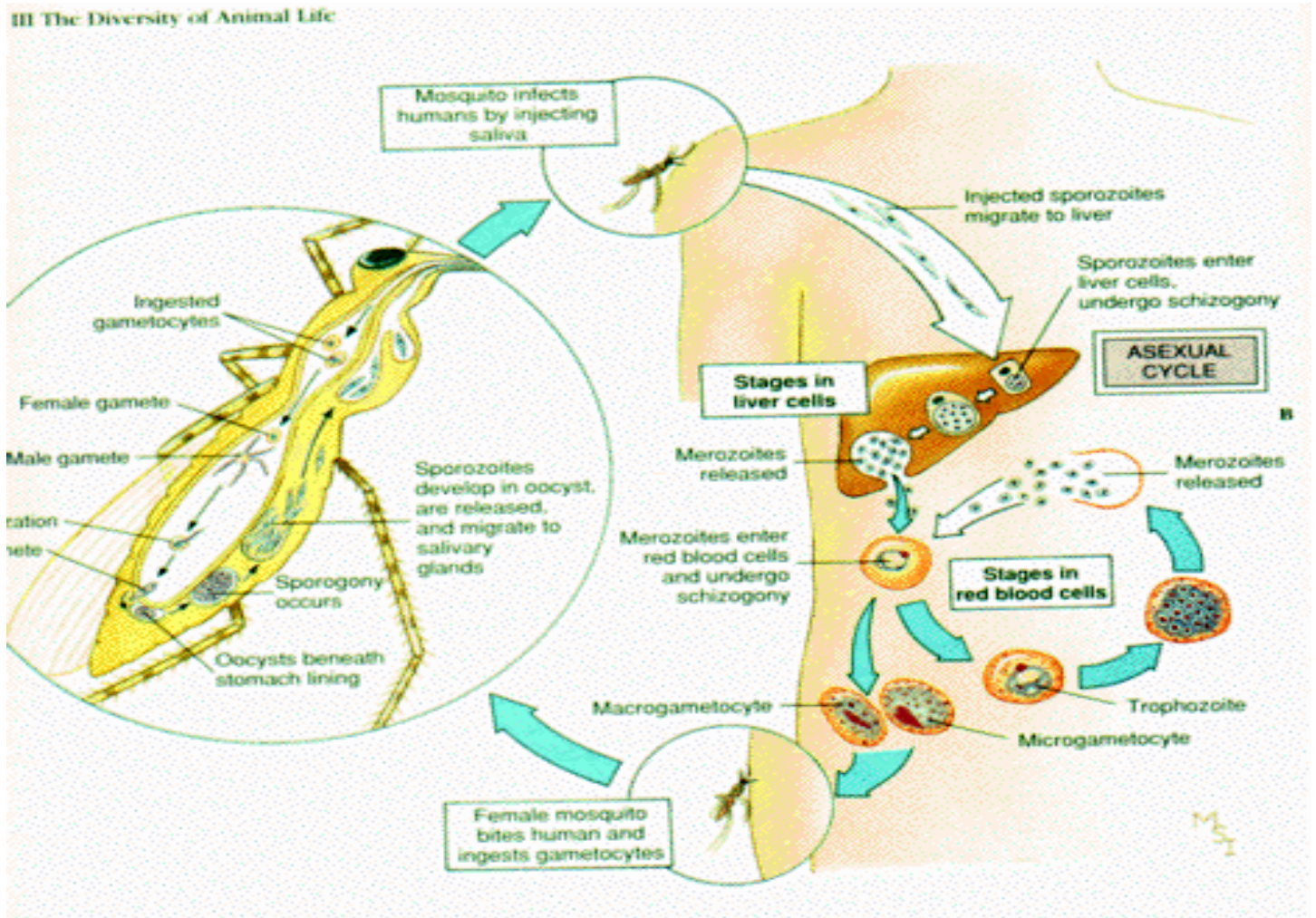
- spread by tsetse fly

4. Example 4: Protozoan - sporozoans

- Locomotion - parasitic
- reproduction
 - spores

Plasmodium - Causes [Malaria](#)

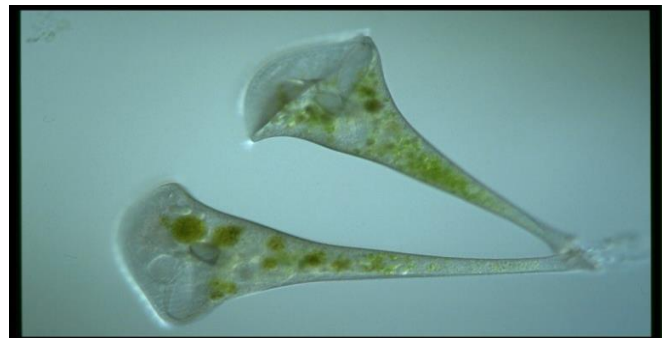
- Spread by mosquito
- Quinine – drug used to treat malaria



Vorticella

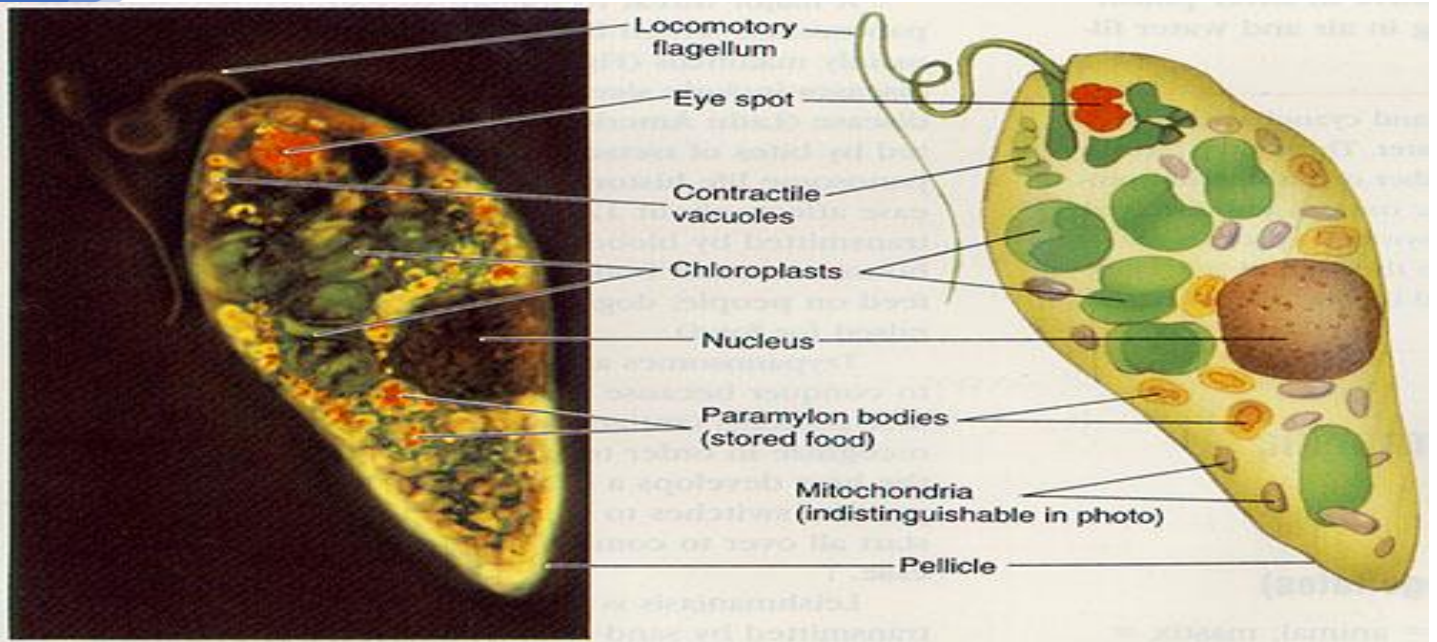
- Attaches to and spins its cilia to create a vortex (water movement)

Stentor



94-Groups of protists

- Both plant-like and animal-like



Euglenoids

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

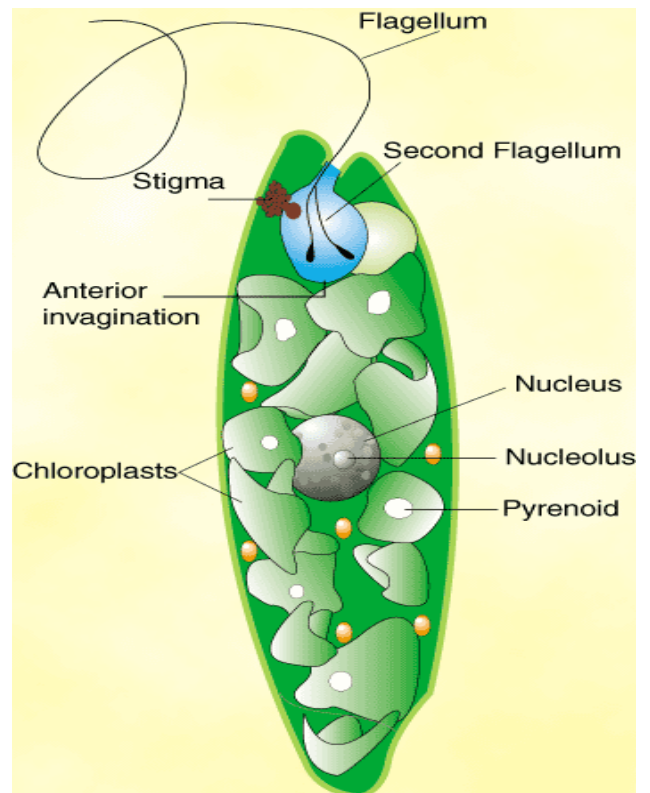
Algae

Plant like protists

B. Algae - plant-like

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

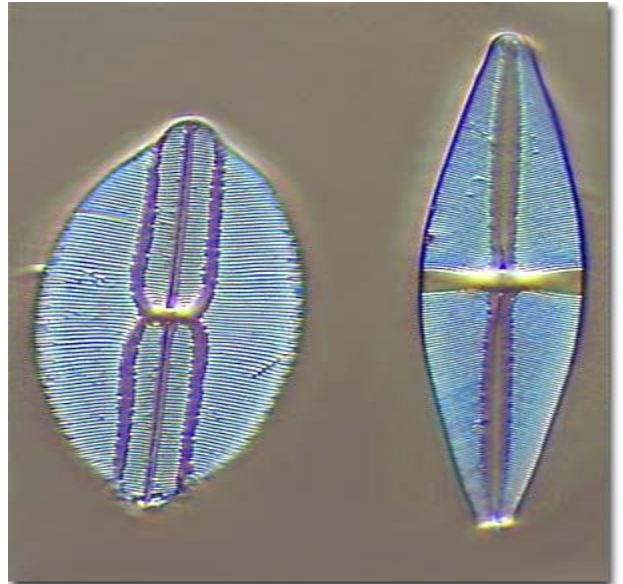
1. Diatoms



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

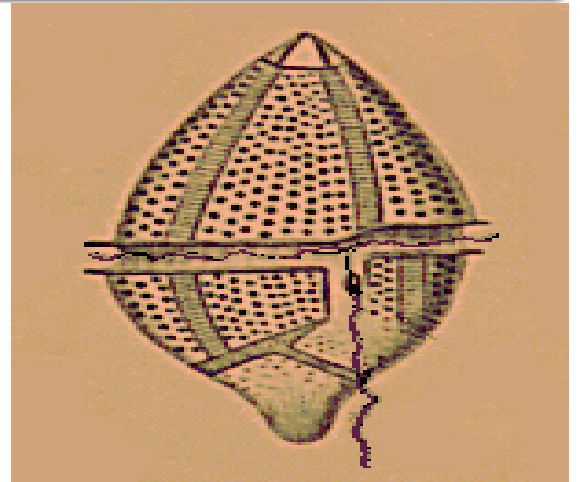
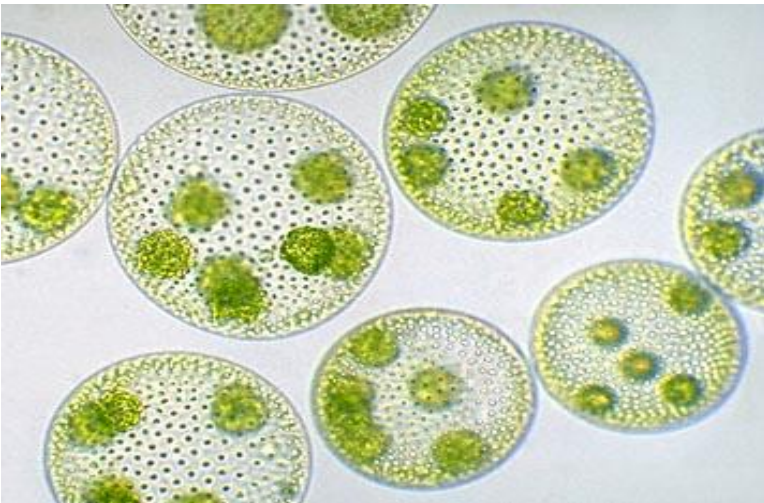
2. Dinoflagellates

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

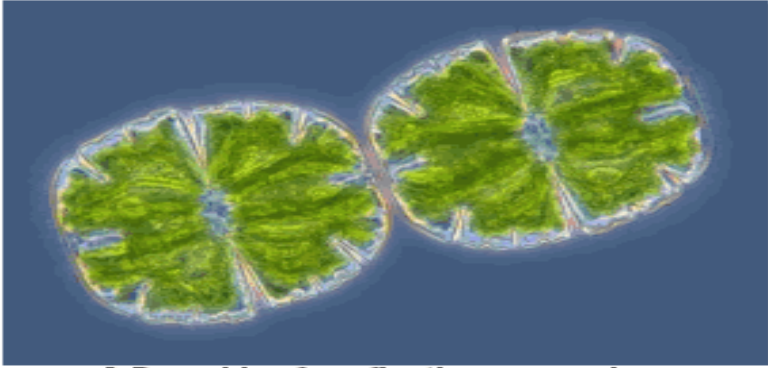


3. Green Algae (Lab 37)

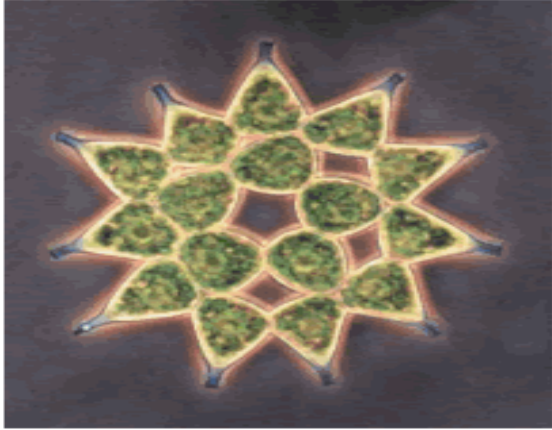
- Most freshwater
- Food Source – called Plankton
- Some are:
 - Free-living
 - Colony
 - filament



Free-Floating –



A Desmid: a free-floating green alga



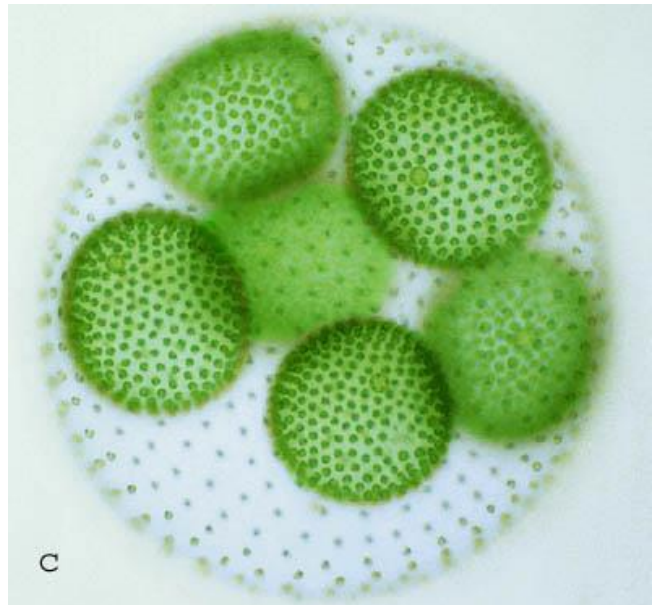
Green alga -*Pediastrum*

- Filament type – exist as a thread

Colony –

Label and Draw

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



95-Features of protists

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

96-Food Webs

- A food web summarizes the feeding relations in a community.
- The earliest work on food webs concentrated on simplified communities in areas such as the Arctic islands.
- However, researchers such as Charles Elton (1927) soon found that even these so-called simple communities included very complex feeding relations.
- The level of food web complexity increased substantially, however, as researchers began to study complex communities.
- Studies of the food webs of tropical freshwater fish communities revealed highly complex networks of trophic interaction that persisted even in the face of various simplifications.
- A focus on strong interactions can simplify food web structure and identify those interactions responsible for most of the energy flow in communities.

97-Food web and structure of communities

- Manipulative studies of predaceous species have identified many keystone species, including starfish and snails in the marine intertidal zone and fish in rivers.
- On land, birds exert substantial influences on communities of their arthropod prey.

Jane Lubchenko (1978)

- Jane Lubchenko (1978) demonstrated that the influence of consumers on community structure depends upon their feeding preferences, their local population density, and the relative competitive abilities of prey species.
- Keystone species are those that, despite low biomass, exert strong effects on the structure of the communities they inhabit.

Exotic predators and the structure of food webs

- Exotic predators can collapse and simplify the structure of food webs.
- Introduced fishes have devastated the native fishes of Lake Atitlan and Gatun Lake in Central America.

Examples

- The influence of the Nile perch on the fish community of Lake Victoria is tangled with massive changes in the lake's ecosystem.
- Introduction of the Nile perch is rapidly reducing the species-rich fish fauna of Lake Victoria to a community dominated by a handful of species.

Humans

- Humans have acted as keystone species in communities. People have long manipulated food webs both as a consequence of their own feeding activities and by introducing or deleting species from existing food webs.
- In addition, many of these manipulations have been focused on keystone species.
- Hunters in tropical rain forests have been responsible for removing keystone animal species from large areas of the rain forests of Central and South America. Chinese farmers have used ants as keystone predators to control pests in citrus orchards for over 1,700 years.

98-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. In some sources, foundation species are viewed as a subcategory of keystone species.

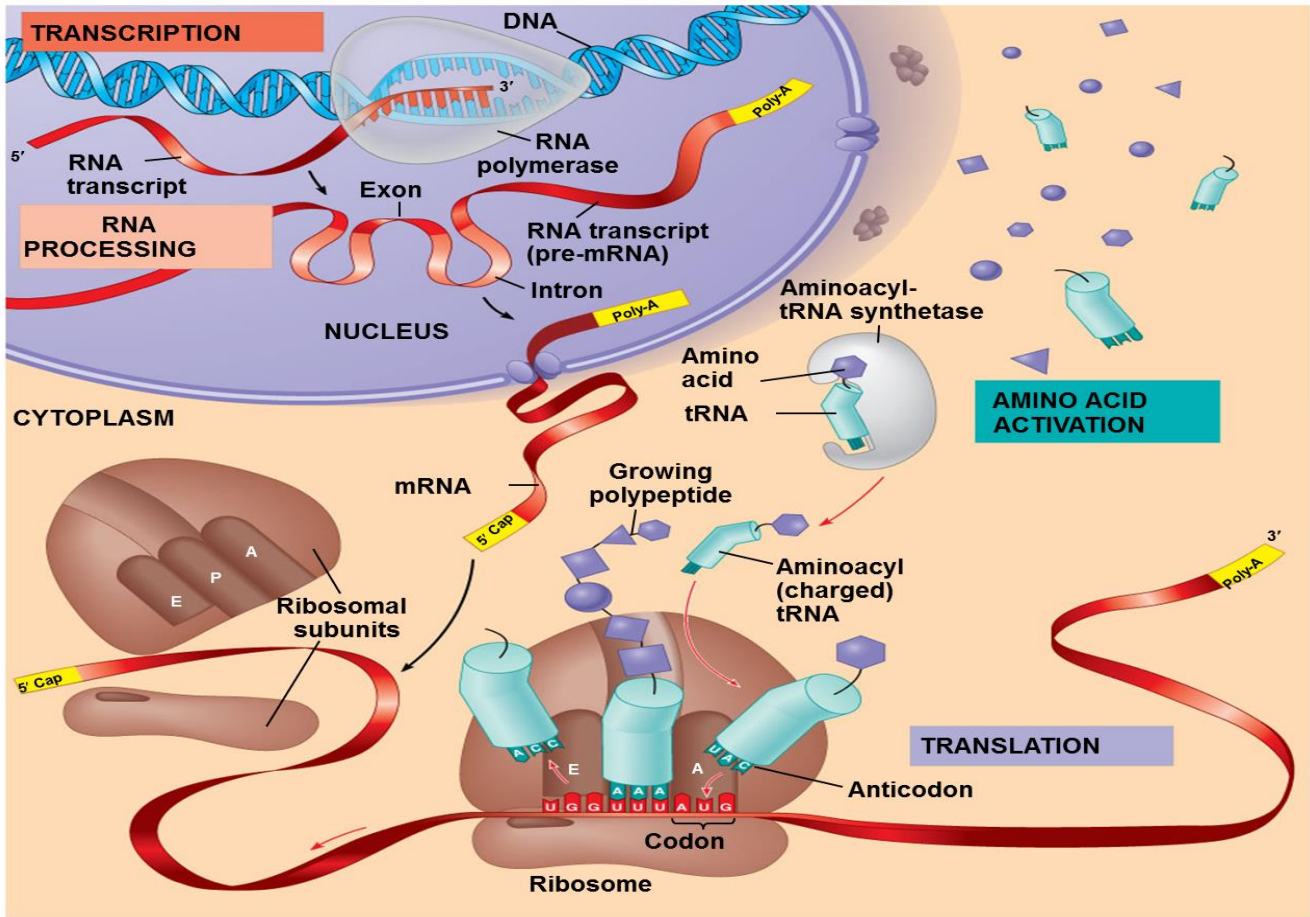
99-From gene product to gene

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.

- 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.

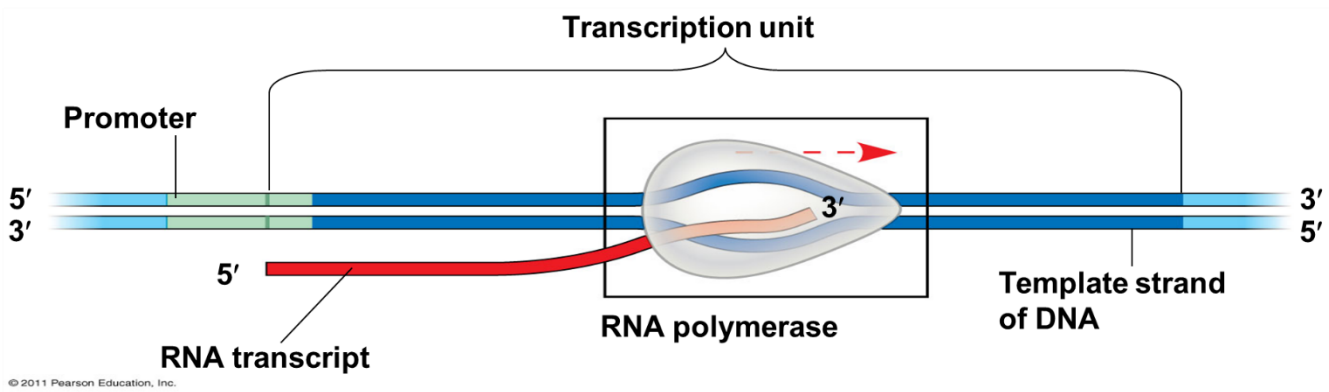
What Is a Gene?

- The idea of the gene has evolved through the history of genetics
- We have considered a gene as
 - A discrete unit of inheritance
 - A region of specific nucleotide sequence in a chromosome
 - A DNA sequence that codes for a specific polypeptide chain
 - In summary, a gene can be defined as a region of DNA that can be expressed to produce a final functional product, either a polypeptide or an RNA molecule



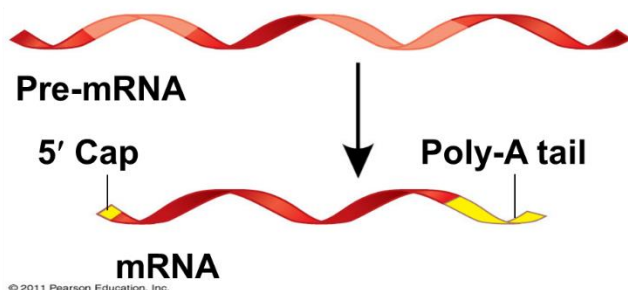
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Figure 17.UN02

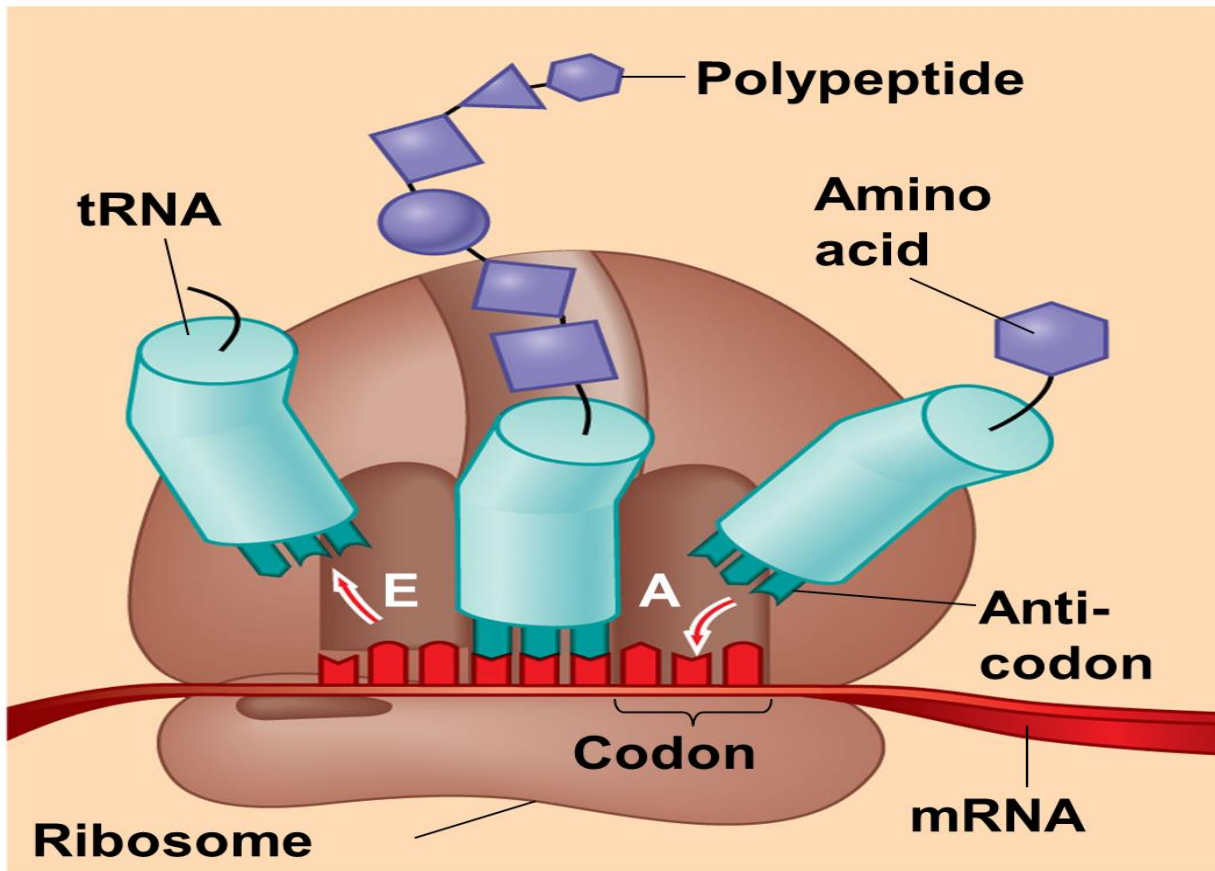


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Figure 17.UN03



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Colinearity of Gene and Protein

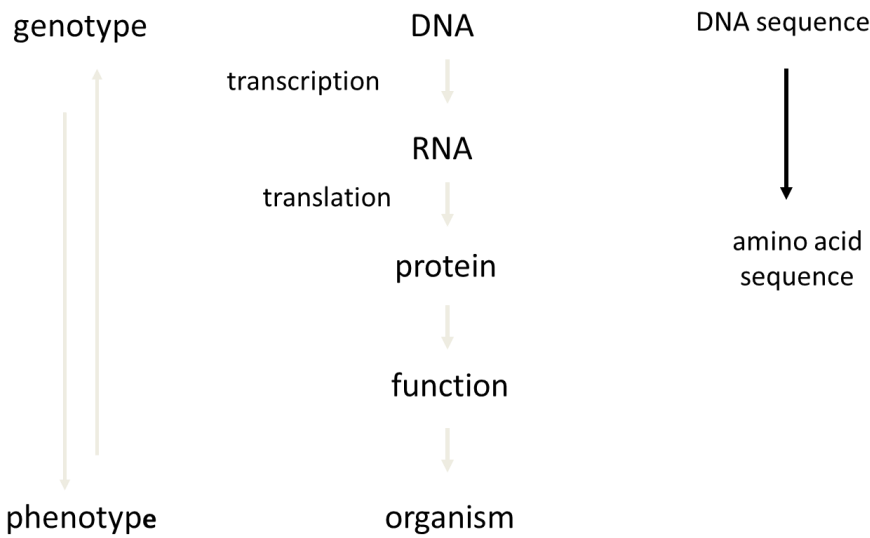


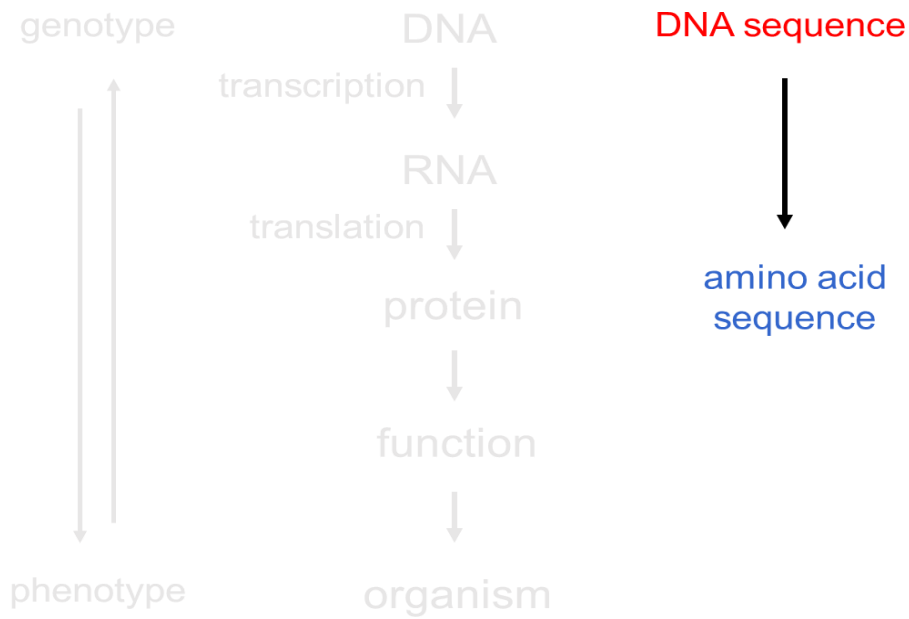
Figure 17.UN05

Type of RNA	Functions
Messenger RNA (mRNA)	
Transfer RNA (tRNA)	
Primary transcript	Plays catalytic (ribozyme) roles and structural roles in ribosomes
Small nuclear RNA (snRNA)	

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100-Colinearity of Gene and Protein

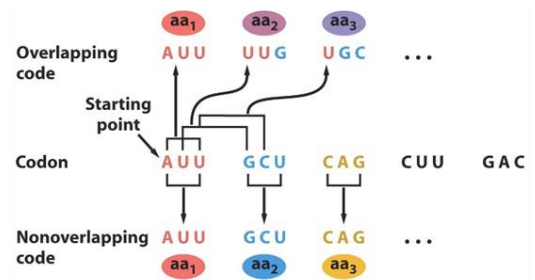
Colinearity of Gene and Protein



Genetic Code

		Second letter					
		U	C	A	G		
First letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } UAA Stop UAG Stop	UGU } Cys UGC } UGA Stop UGG Trp	U C A G	
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G	
	A	AUU } AUC } Ile AUA } AUG Met	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G	
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }	U C A G	

Genetic Code is nonoverlapping.



A codon (three bases or triplet) encodes an amino acid.

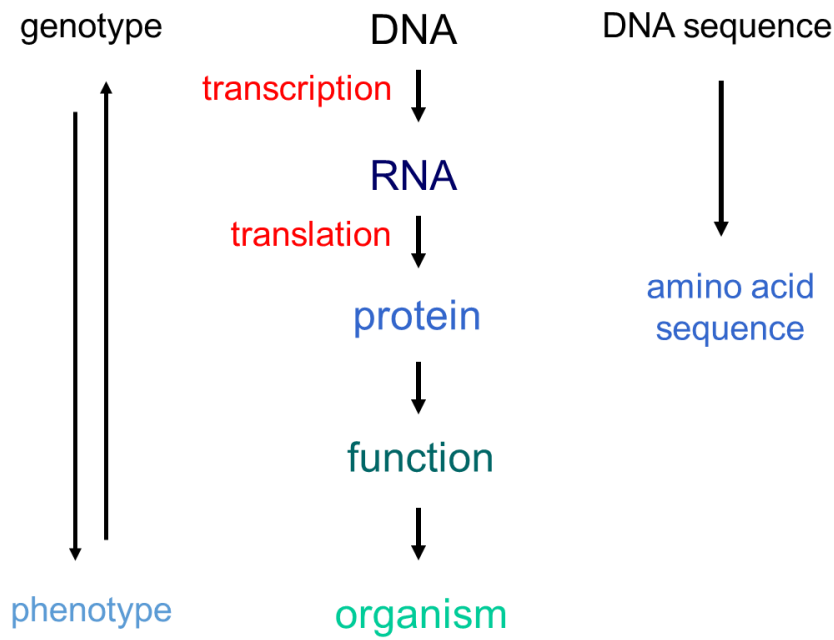
Genetic Code is read continuously from a fixed starting point.

There is a start codon (AUG).

There are three stop (termination) codons. They are often called nonsense codons.

Genetic Code is degenerate. Some amino acids are encoded by more than one codon.

Molecular Basis for Relationship between Genotype and Phenotype



Eukaryotic RNA

Three RNA Polymerases

RNA Polymerase

Synthesis of

I

rRNA (except 5S rRNA)

II

mRNA*, some snRNA

III

tRNA, some snRNA, 5S rRNA

* eukaryotic RNA is monocistronic
prokaryotic RNA can be polycistronic