

Comparative Eukaryotic genomics: Chloroplast, Mitochondrial and nuclear genome

- By Anandi Rebello

WHAT IS ORGANELLAR GENOME..?

- **ORGANELLE :**

Mitochondria , Chloroplast, Golgicomplex, Endoplasmic reticulum etc.,

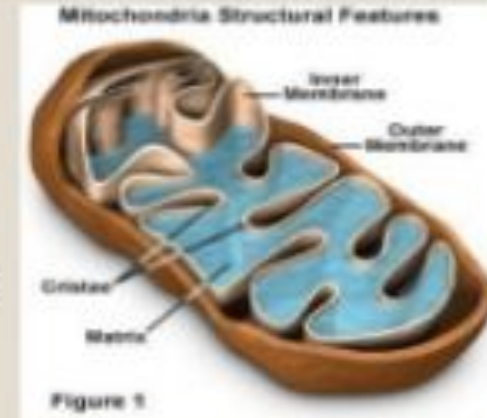
- The genome present in the Chloroplast and Mitochondria are called as Organellar Genome.

ORGANELLAR GENOMES / EXTRANUCLEAR GENOMES:

✓ **Mitochondria** (animals and plants)

✓ **Chloroplasts** (plants)

1. Mitochondria and chloroplasts occur outside the nucleus, in the cytoplasm of the cell.
2. Contain genomes (mtDNA/cpDNA) and genes, i.e., extrachromosomal genes, cytoplasmic genes, organelle genes, or extranuclear genes.
3. Inheritance is non-Mendelian (e.g., cytoplasm typically is inherited from the mother).



Organelle Genomes

- ❖ **Small but essential.**

 - Mitochondria (site of respiration).

 - Plastids (site of photosynthesis) .

- ❖ **Multiple organelles and organelle genomes per cell.**

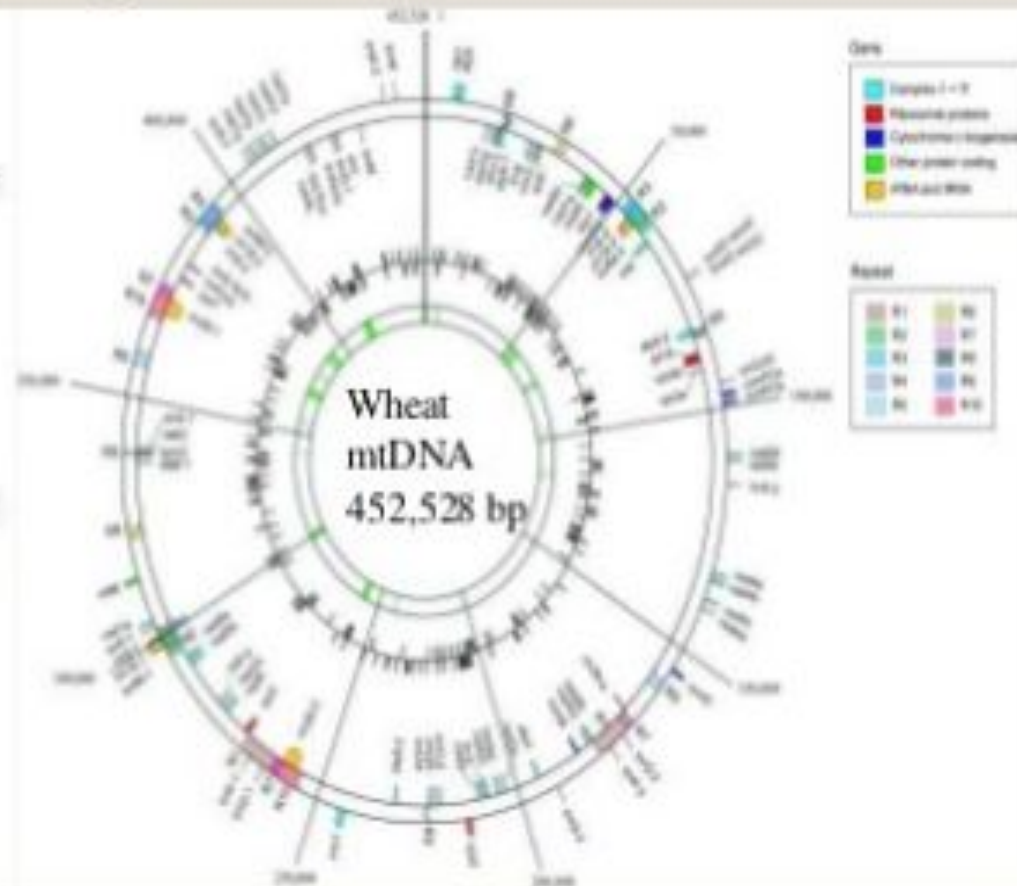
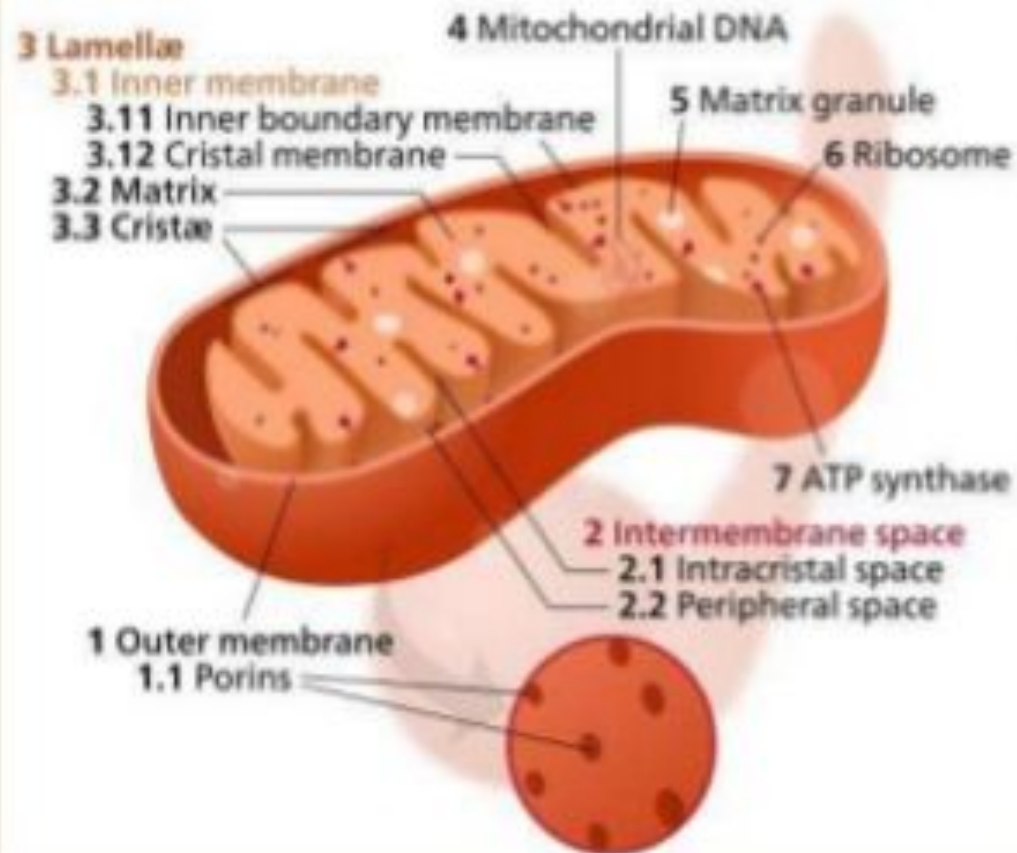
 - 20 – 20,000 genomes per cell, depending on cell type.

- ❖ **Organized in nucleoids.**

 - Nucleoprotein complexes containing multiple genome copies.

 - Not to be confused with nucleosomes.

Mitochondrial genome



CONTENTS OF THE **mtDNA** GENOME

❖ **mtDNA contains genes for:**

- tRNAs
- rRNAs
- cytochrome oxidase, NADH-dehydrogenase, & ATPase subunits.
- mtDNA genes occur on both strands.

• **Mitochondria's genetic information also occurs in the nuclear DNA:**

- DNA polymerase, replication factors
- RNA polymerase, transcription factors
- ribosomal proteins, translation factors, aa-tRNA synthetase
- Additional cytochrome oxidase, NADH, ATPase subunits.

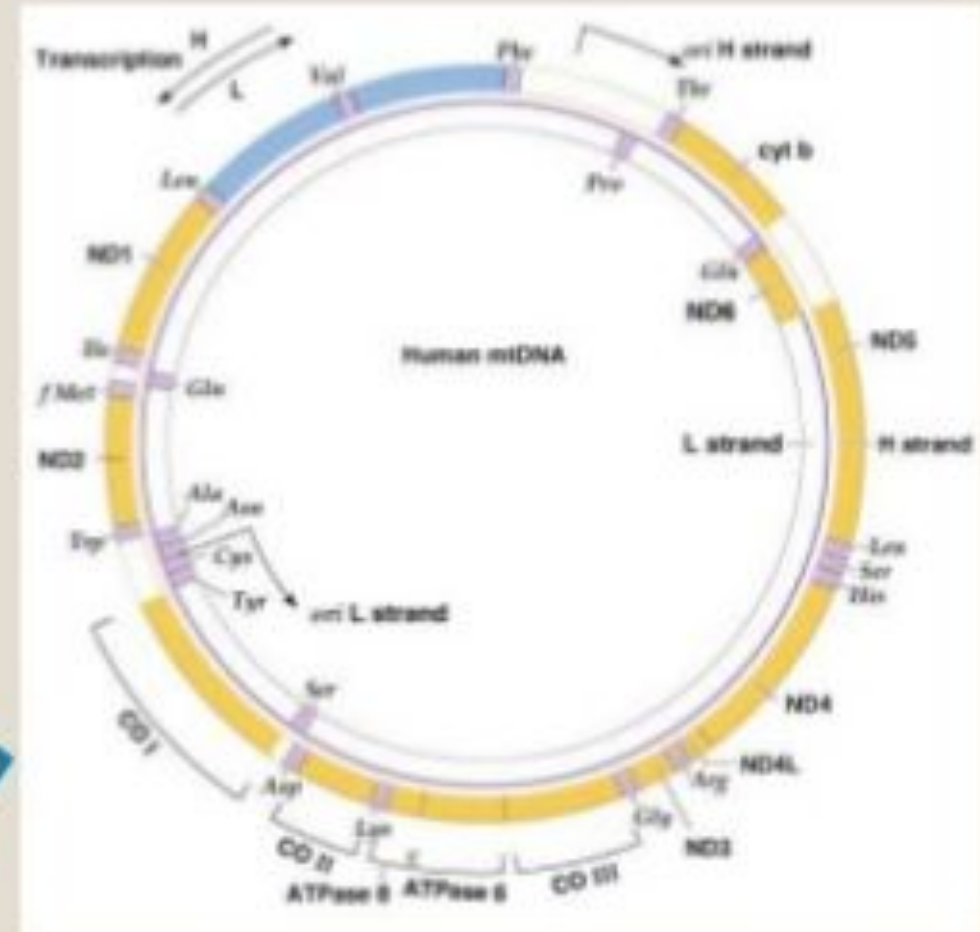
- Most required mitochondrial (and chloroplast) proteins are coded by nuclear genes in the nuclear genome.

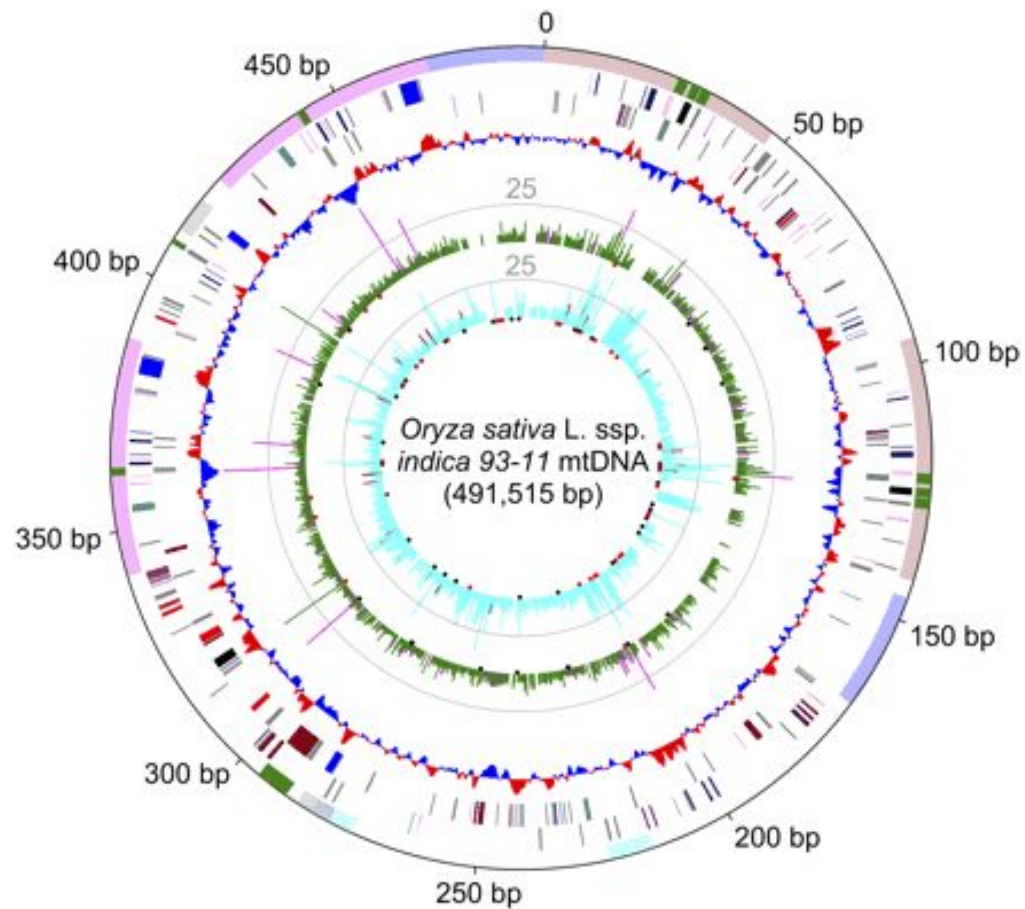
- Five mtDNA complexes with 13 mtDNA subunit genes are paired with 76 nuclear subunit genes to make the same proteins.

I – NADH; II - Succinate dehydrogenase; III - Cytochrome bc

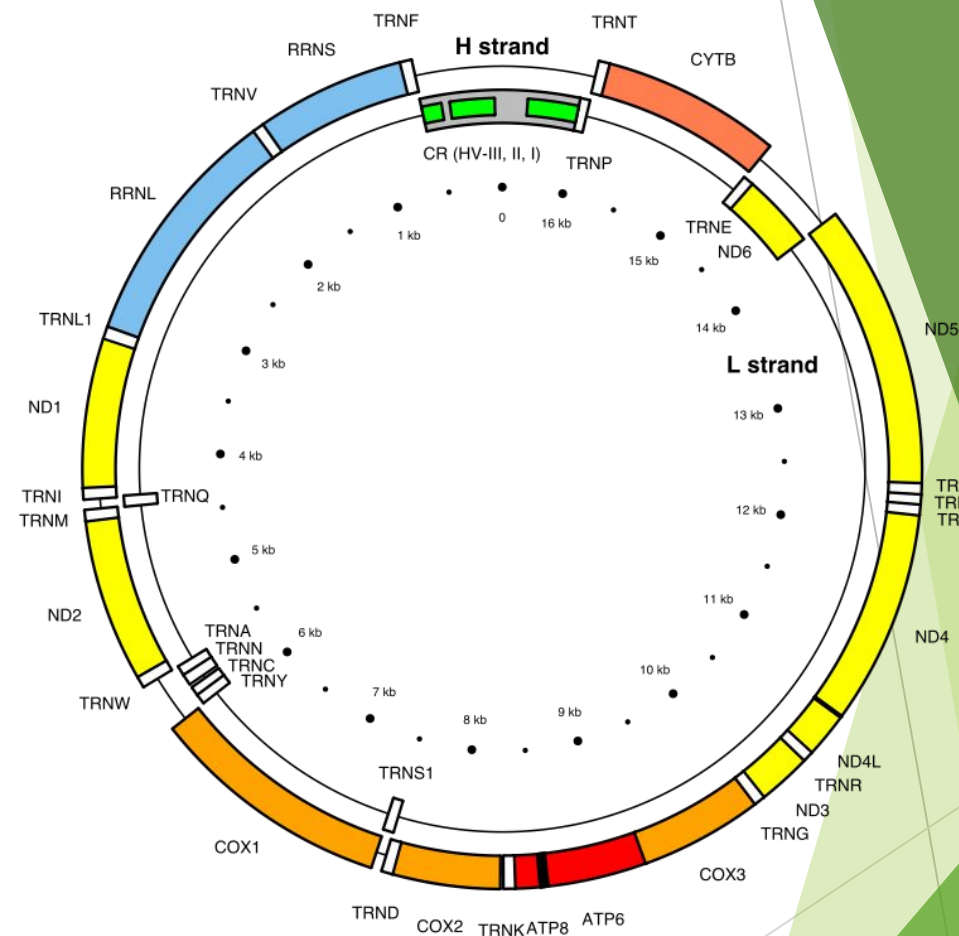
IV - Cytochrome c oxidase; V - ATP synthase

Physical map of the human mtDNA

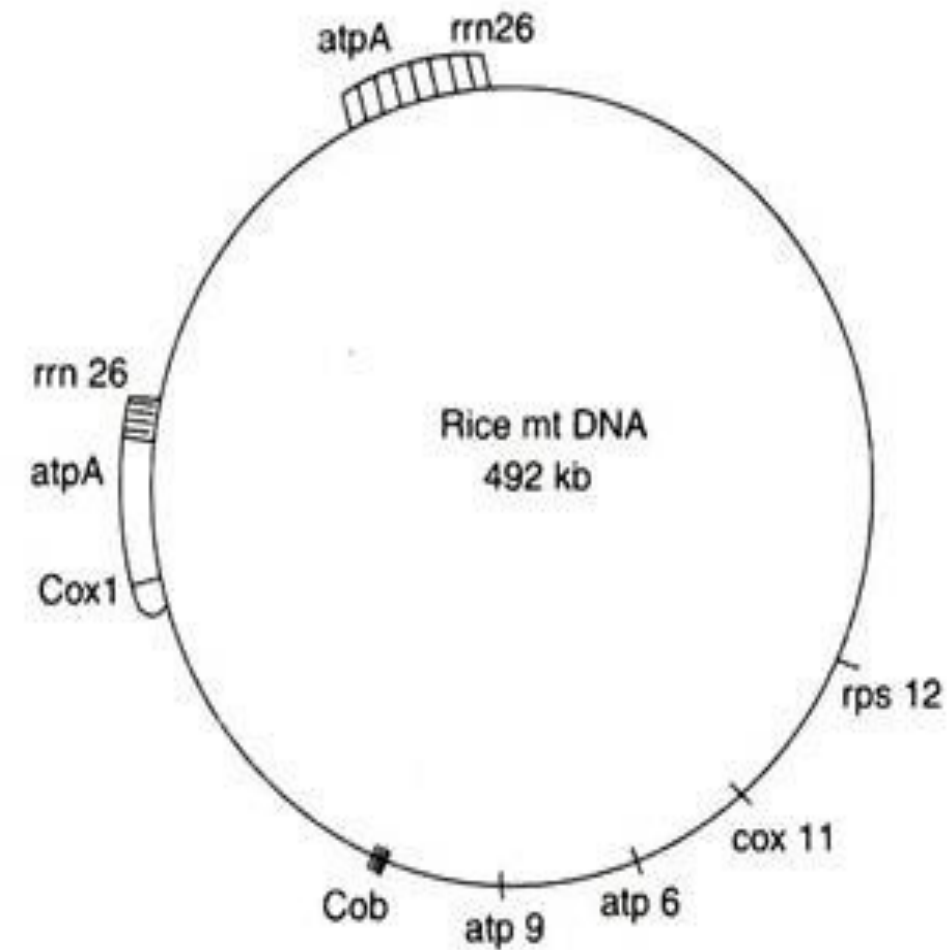




Rice mtDNA



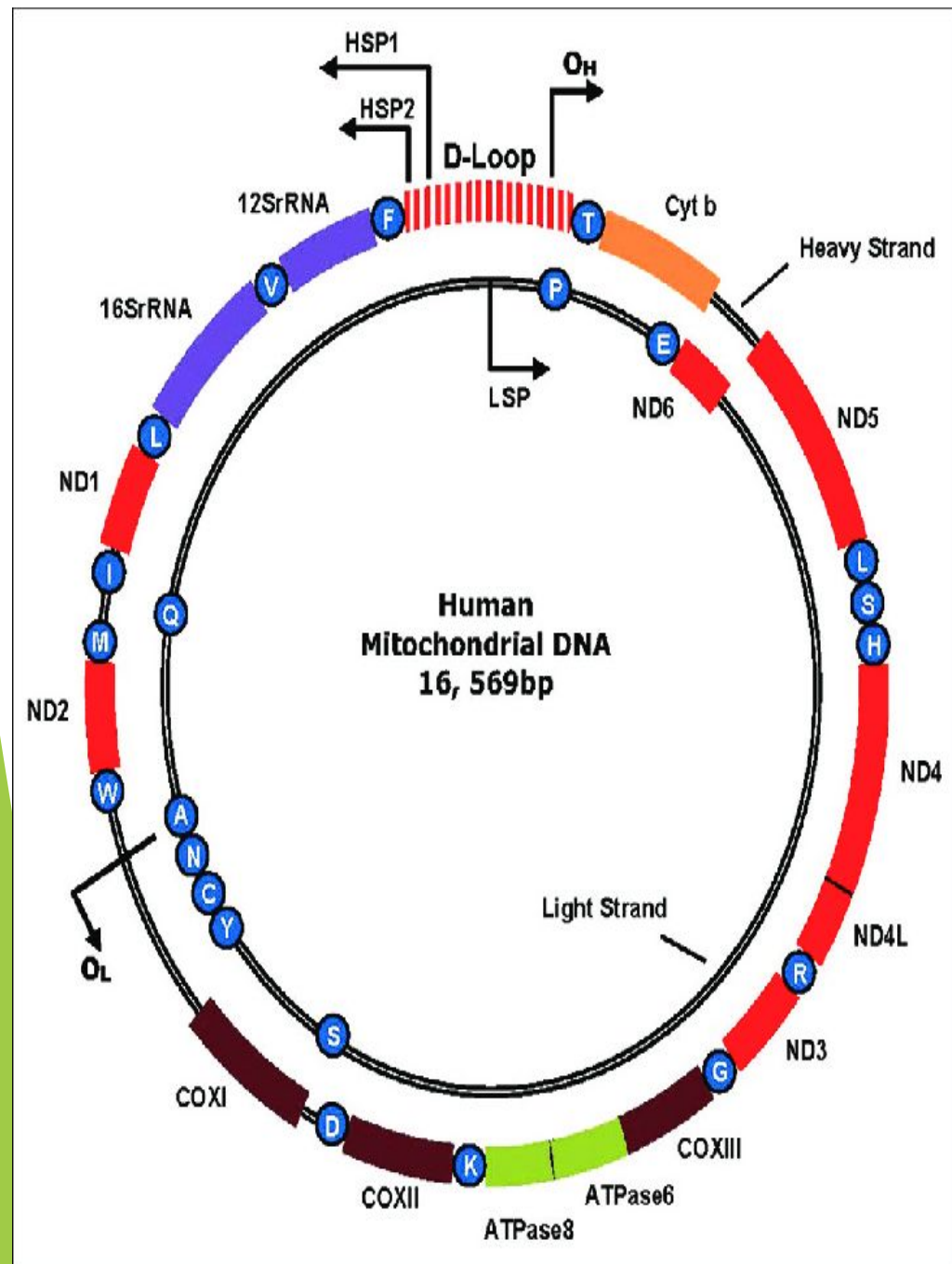
Human mtDNA



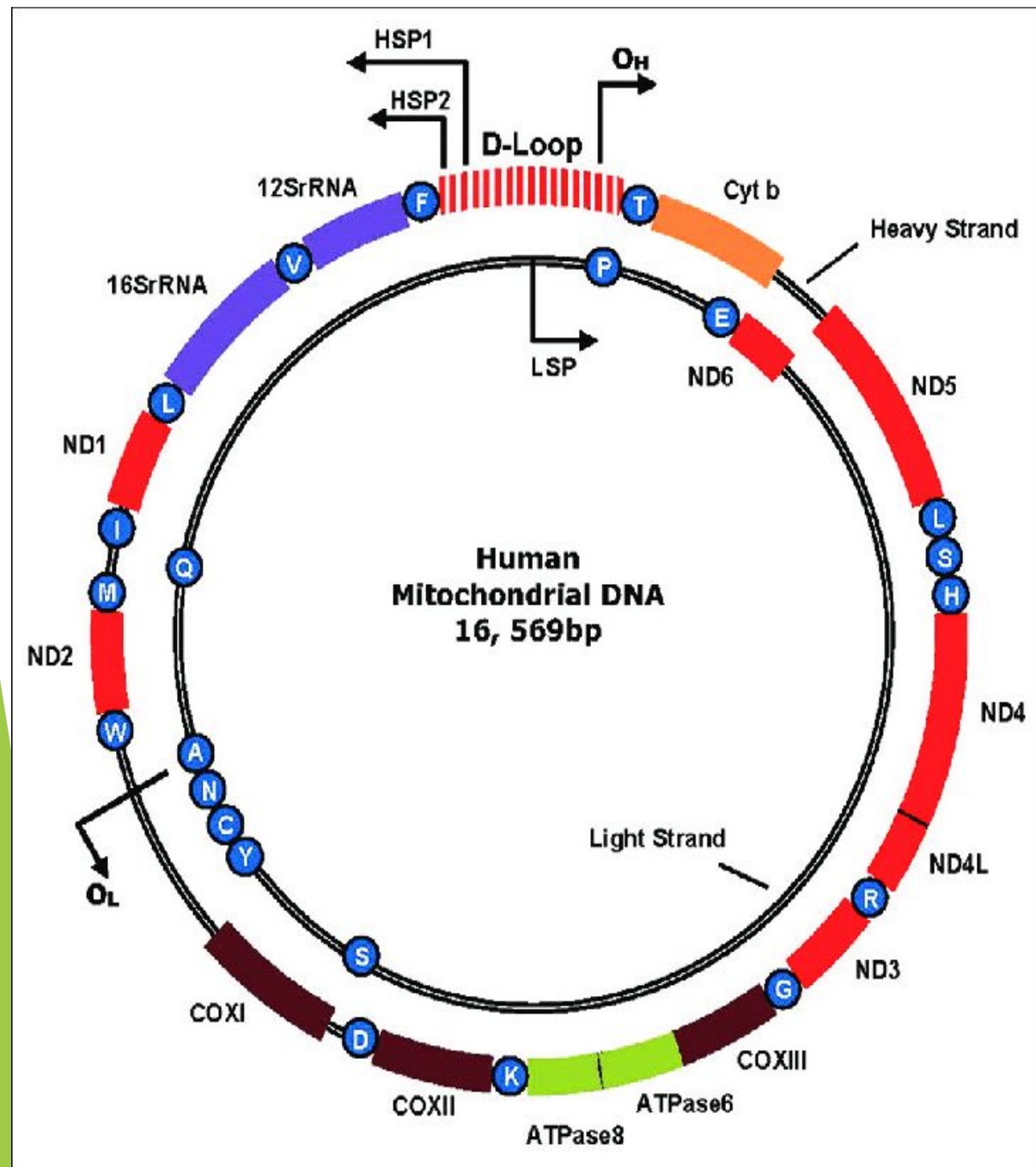
- Rice mitochondrial genome is made up of 492 kb nucleotides. The complexity of rice mitochondrial genome is due to the presence of chloroplast sequences. There are 16 chloroplast fragments in rice mtDNA ranging from 32 bp to about 6.8 kb in length. Thus, results show that about 6% (22 kb) of rice mtDNA is made up of chloroplast sequence.

The mitochondrial genome of rice contains rearranged cluster of chloroplast genes, namely, rpl2 and yrpl23-rcL-atpB-atp E-trnM- trnV.

One of the palindromic repeated sequences (PRS) located in the intron of rps3 in rice mtDNA, but not in maize mtDNA. Analysis of transferred sequences of ctDNA in mtDNA of rice was evidenced in that at least three repeated sequences about 60 bp in length are present in plant. It was also found that Rice mtDNA contained at least 10 copies of the small repeated sequence.



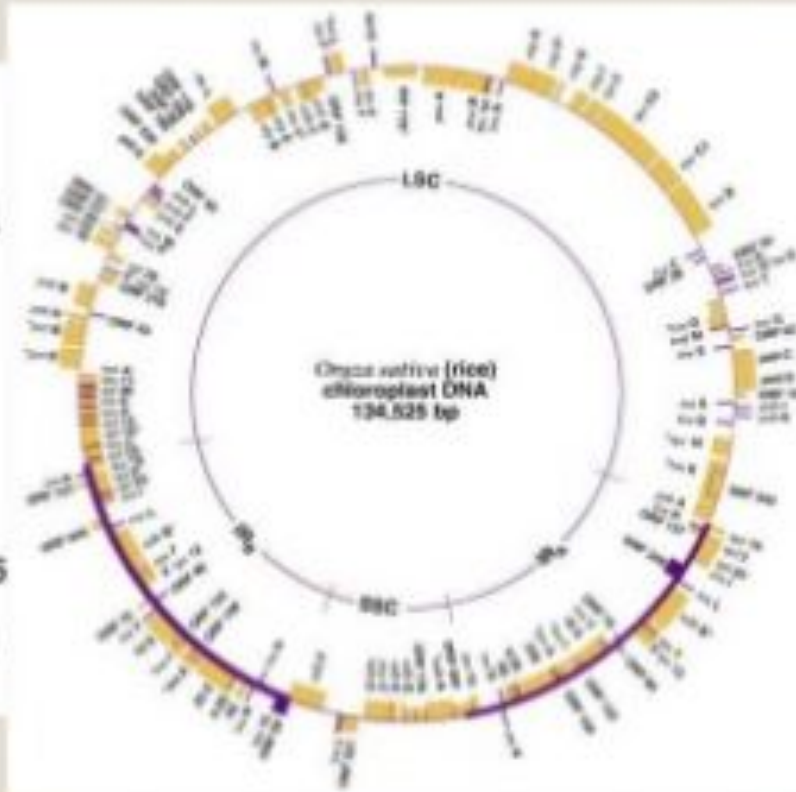
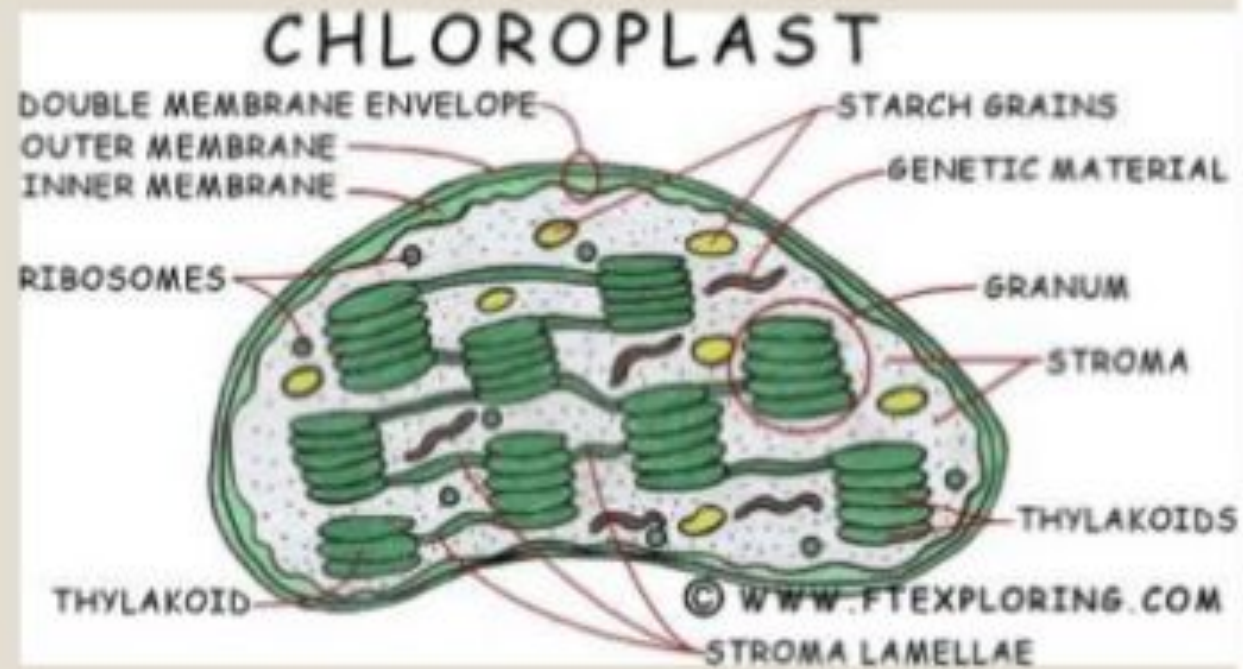
- ▶ Human mitochondrial DNA is a 16,569 base pair circle of double-stranded DNA that encodes 13 essential respiratory chain subunits.
- ▶ ND1-ND6 and ND4L encode seven complex I (NADH-ubiquinone oxidoreductase) subunits, CYT b encodes one subunit of complex III (ubiquinol: cytochrome c oxidoreductase), COX I-COX III encode the three major catalytic subunits of complex IV, and ATPase6 and ATPase8 encode two subunits of complex V (ATP synthase).
- ▶ There are the two ribosomal RNA (12S rRNA and 16S rRNA) genes and the 22 transfer RNA genes (blue spheres, depicted by single letter amino acid code abbreviation) required for mitochondrial protein synthesis. tRNAs are: F = Phenylalanine; V = Valine; L = Leucine; I = Isoleucine; Q = Glutamine; M = Methionine; W = Tryptophan; A = Alanine; N = Asparagine; C = Cysteine; Y = Tyrosine; S = Serine; D = Aspartic acid; K = Lysine; G = Glycine; R = Arginine; H = Histidine; E = Glutamic acid; T = Threonine; P = Proline.



The displacement loop or noncoding control region contains the promoters for transcription of the L (LSP) and H strands (HSP1 and HSP2) and the origin of replication of the H strand (OH).

The origin of light strand replication is shown as OL.

chloroplast genome

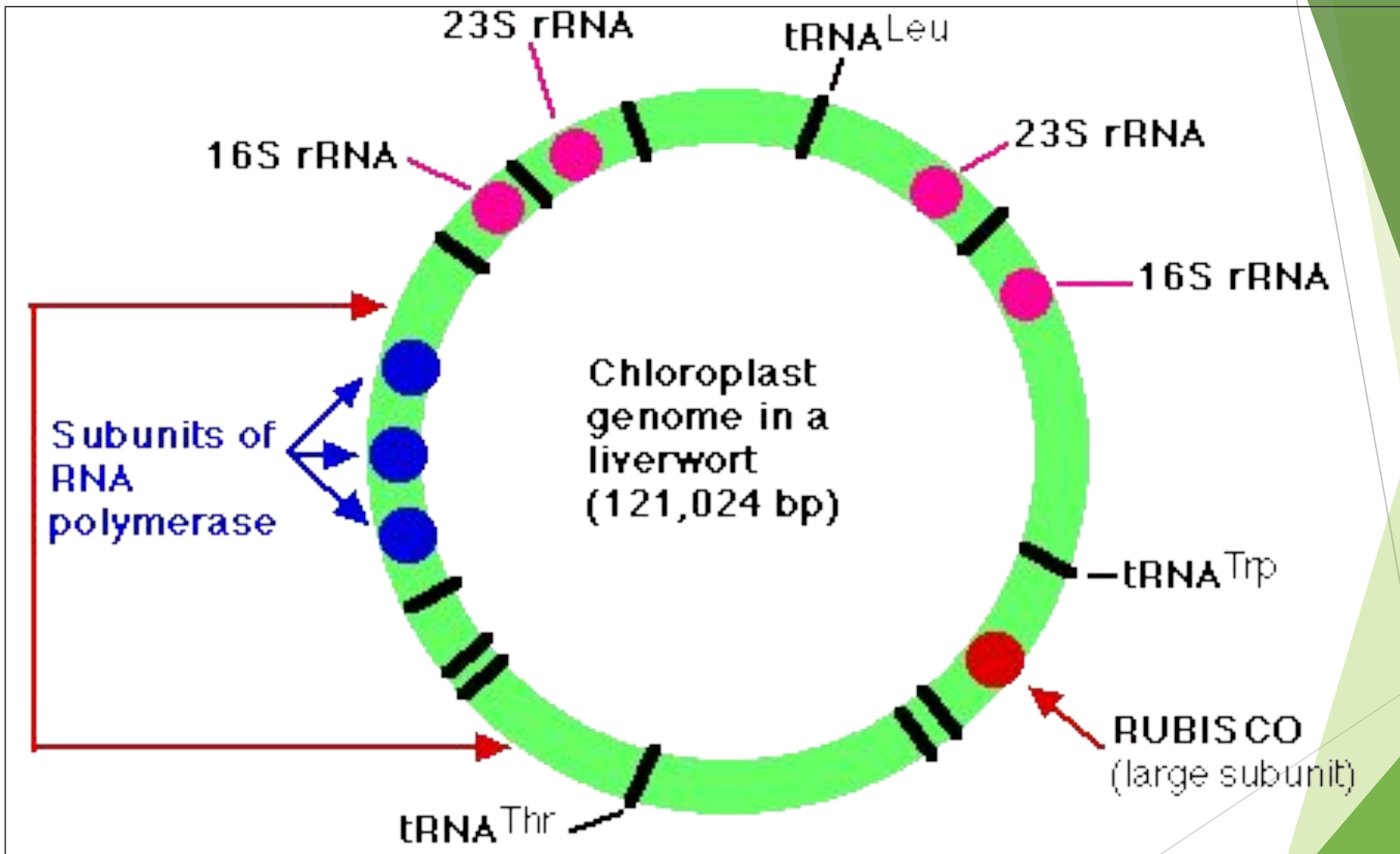


Chloroplast genomes (cpDNA)

- ❖ Chloroplast organelles are the site of photosynthesis and occur only in green plants and photosynthetic protists,
- ❖ Like mtDNA, chloroplast genome is:
 - Circular, double-stranded
 - Lacks structural proteins
 - %GC content differs
- ❖ Chloroplast genome is much larger than animal mtDNA, ~80-600 kb.
- ❖ Chloroplast genomes occur in multiple copies and carry lots of non-coding DNA.
- ❖ Complete chloroplast sequences have been determined for several organisms (tobacco 155,844 bp; rice 134,525 bp).

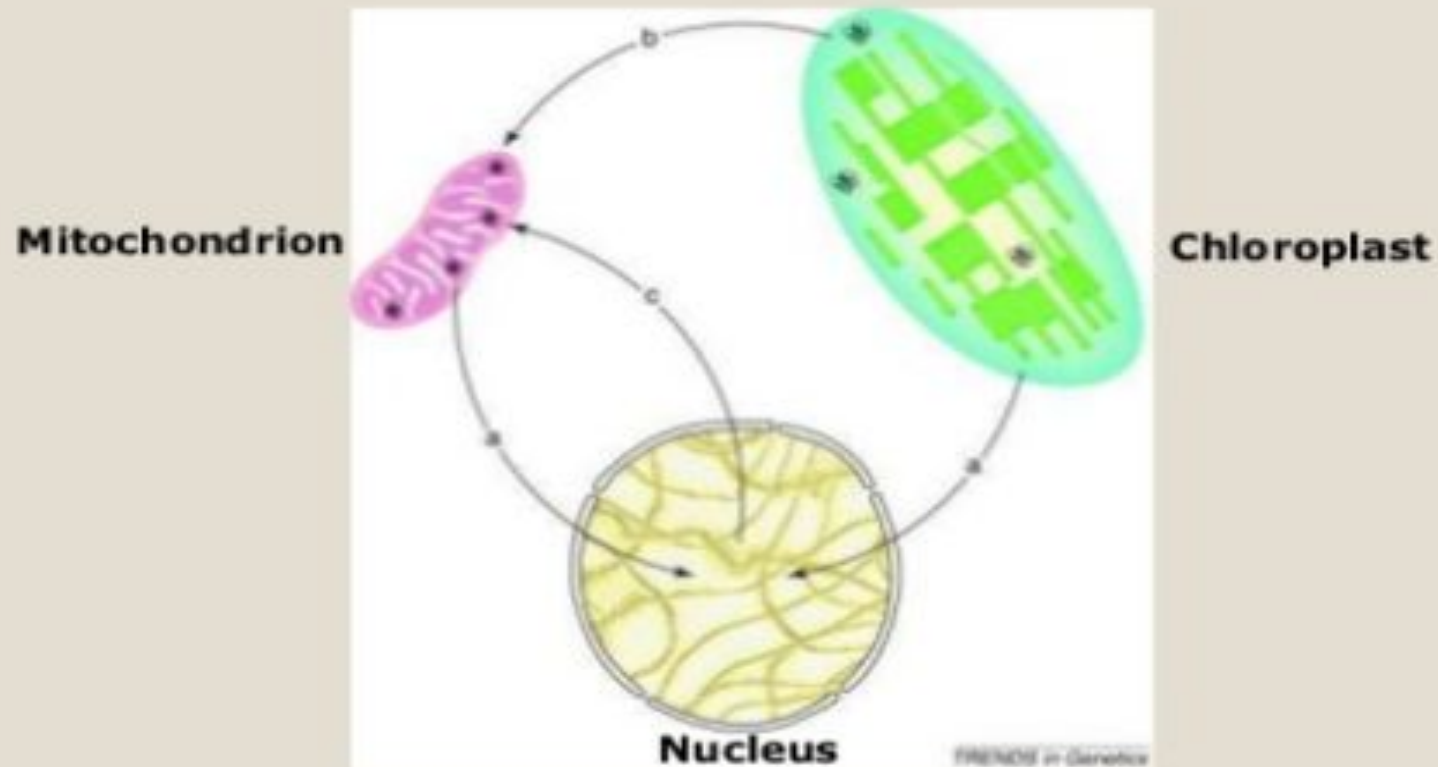
cpDNA organization

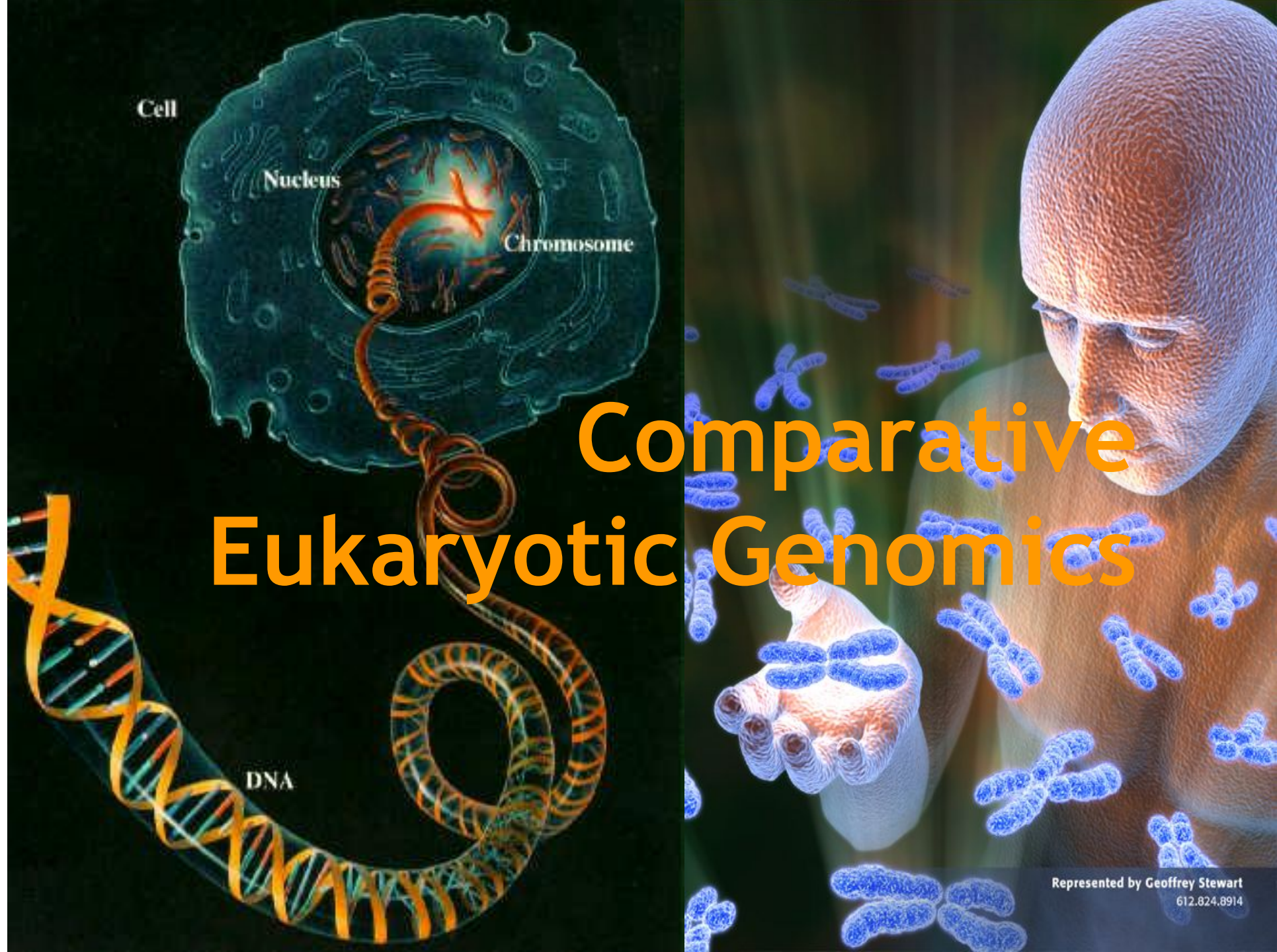
- ❖ Nuclear genome encodes some chloroplast components, and cpDNA codes the rest, including:
 - 2 copies of each chloroplast rRNA (16S, 23S, 4.5s, 5S)
 - tRNAs (30 in tobacco and rice, 32 in liverwort)
 - 100 highly conserved ORFs (~60 code for proteins required for transcription, translation, and photosynthesis).
- ❖ Genes are coded on both strands (like mtDNA).
- ❖ cpDNA translation- similar to prokaryotes:
 1. Initiation uses fMet-tRNA.
 2. Chloroplast specific IFs, EFs, and RFs.
 3. Universal genetic code.



Relation between mt,cl and nuclear DNA.

Copies of **mtDNA** and **chloroplast** genes can be transposed to the nuclear genome and vice versa.





Comparative Eukaryotic Genomics

Represented by Geoffrey Stewart
612.824.8914

COMPARING THE GENOMES OF DIFFERENT ORGANISMS

- ▶ **Why Compare?**
 - ▶ Need to better understand the individual genomes
 - ▶ To understand the functioning of individual genes
 - ▶ To derive a comparative study of basic functions
 - ▶ To better understand evolutionary processes

HUMAN GENOME

The Human Genome

- ▶ The human genome is by far **the most complex and largest genome**.
- ▶ Its size spans a length of about **6 feet of DNA, containing 30,000 to 40,000 genes**.



HUMAN GENOME PROJECT

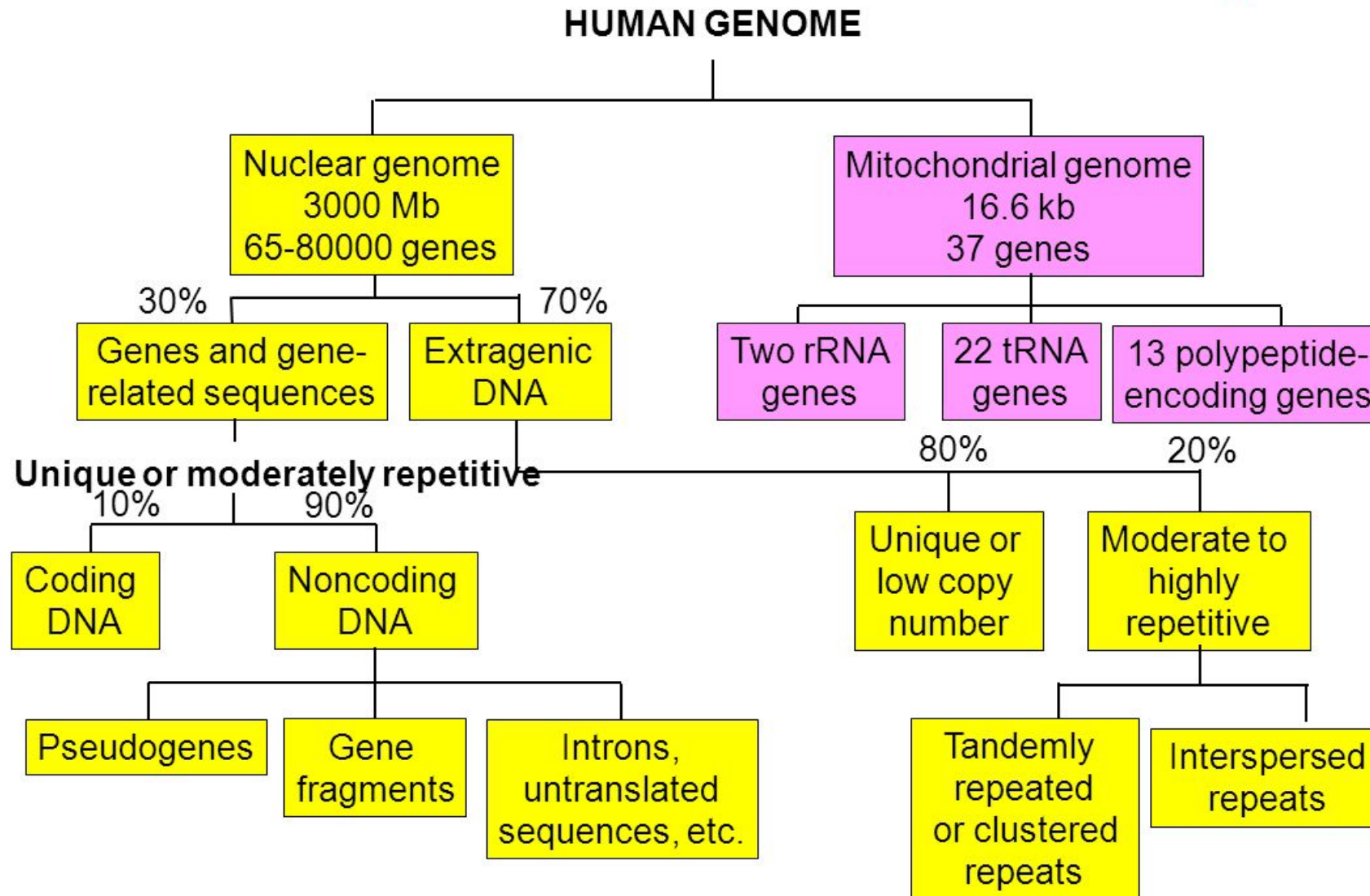
- ▶ Identify the approximate genes in human DNA.
- ▶ Determine the sequences of 3 billion chemical base pairs that make up human DNA.
- ▶ Store this information in databases.
- ▶ Improve tools for data analysis.



OVERVIEW OF HUMAN GENOME

- ▶ The human genome contains **3164.7 million nucleotide bases** (approx. 3 billion A,C,T and G).
- ▶ The average gene is made up of **3000 bases**, but sizes of genes vary greatly.

OVERVIEW OF HUMAN GENOME

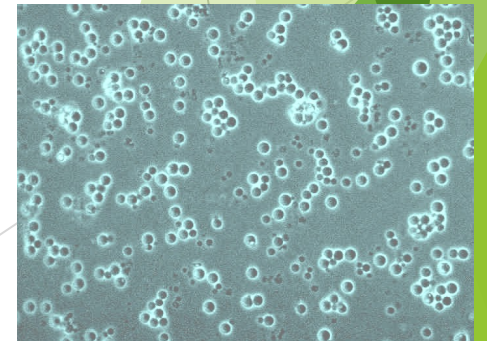


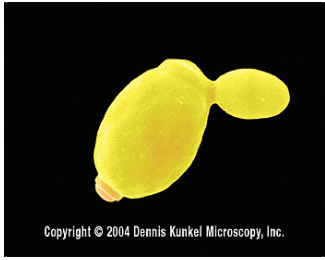


EUKARYOTIC GENOMES

Saccharomyces cerevisiae Genome

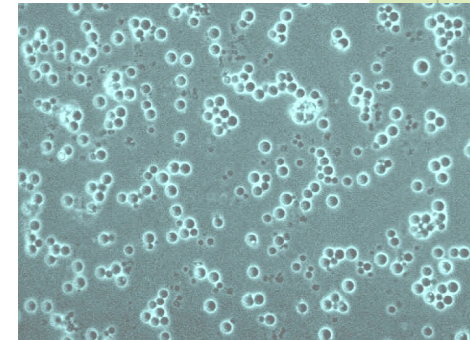
- ▶ One of the most important fungal organisms used in biotechnological processes.
- ▶ Considered as a **model eukaryotic organism**.
- ▶ The first eukaryotic organism to have its entire genome sequenced.





Saccharomyces cerevisiae Genome

- ▶ 16 chromosomes (2n)
- ▶ Approximate genome size - **15520 kb**
- ▶ **5885** potential protein-coding genes.





Drosophila melanogaster (Fruit Fly) Genome

- ▶ Has been the most important tool for genetics studies in the twentieth century.
- ▶ Second multicellular organism to have its genome sequenced.
- ▶ Genome is about **180 Mb** in size.
- ▶ 4 chromosomes ($2n$)
- ▶ **13601** predicted genes.





Drosophila melanogaster (Fruit Fly) Genome

- Interestingly, the *Drosophila* genome contains genes that are similar to 177 of 289 human genes that are responsible for diseases.





Oryza sativa L. (rice) Genome

- ▶ One of the most important food crops in the world.
- ▶ Scientists use rice as a **model plant in cereal genomics**.
- ▶ 24 chromosomes (2n).





Mus musculus (Laboratory Mouse) Genome

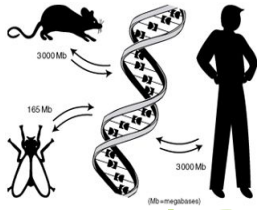
- ▶ The sequence of the mouse genome is important for understanding the contents of the human genome and it also serves as a key experimental tool for biomedical research.
- ▶ 20 chromosomes ($2n$)



Mus musculus (Laboratory Mouse) Genome

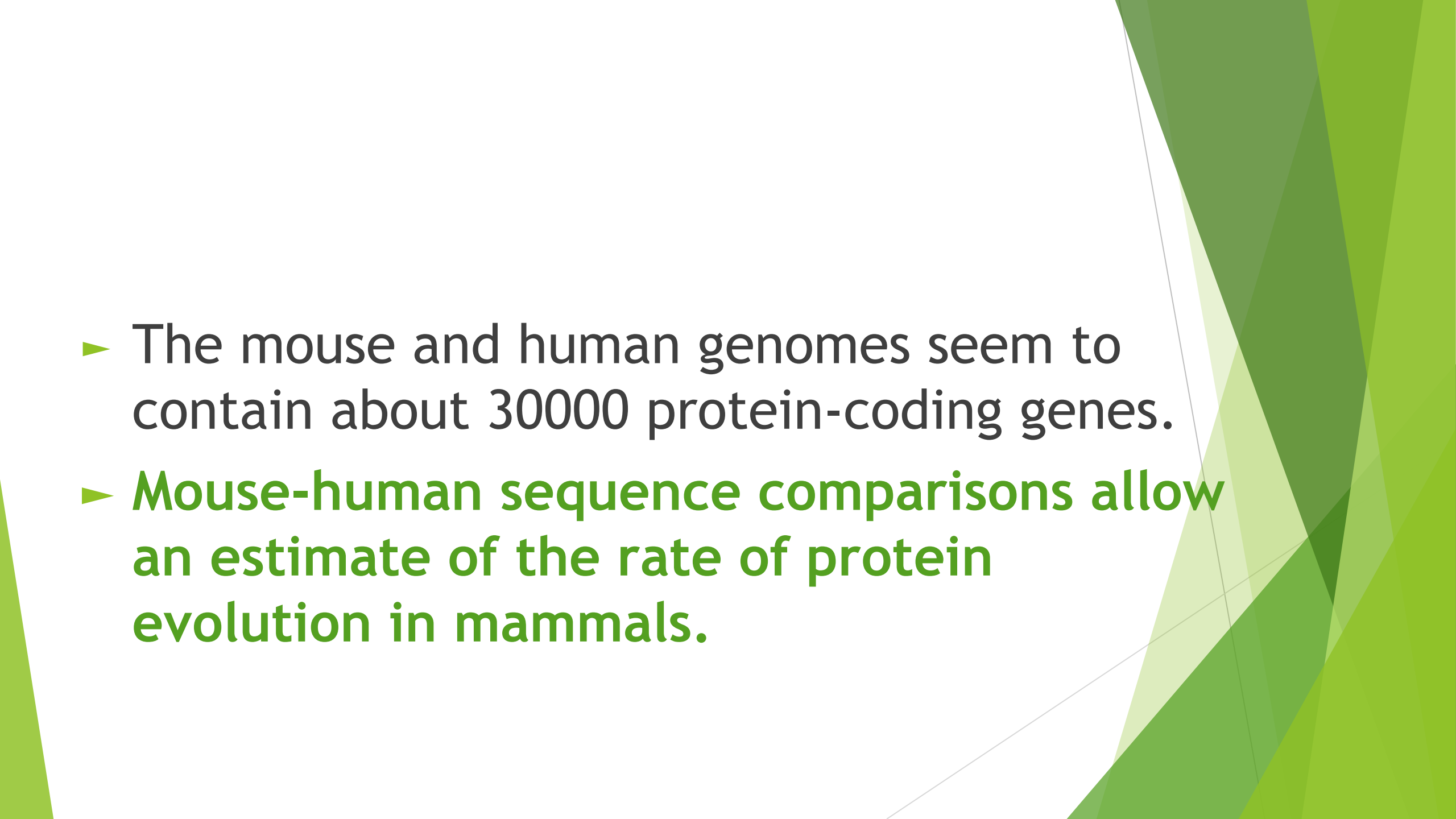
- ▶ The draft sequence was generated by assembling the sevenfold sequence coverage from female mice of the B6 strain.
- ▶ Genome size is 2.5 Gb.
- ▶ Seem to contain about 30000 protein-coding genes.





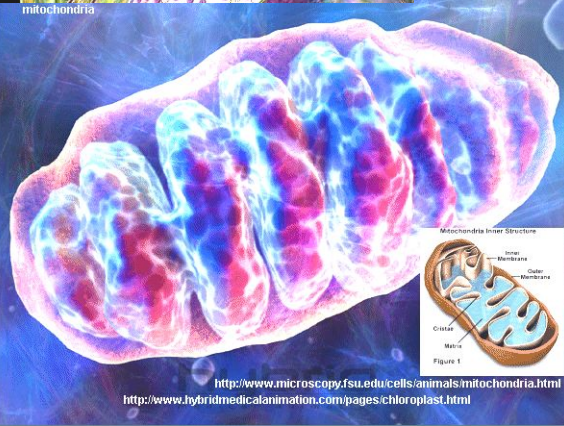
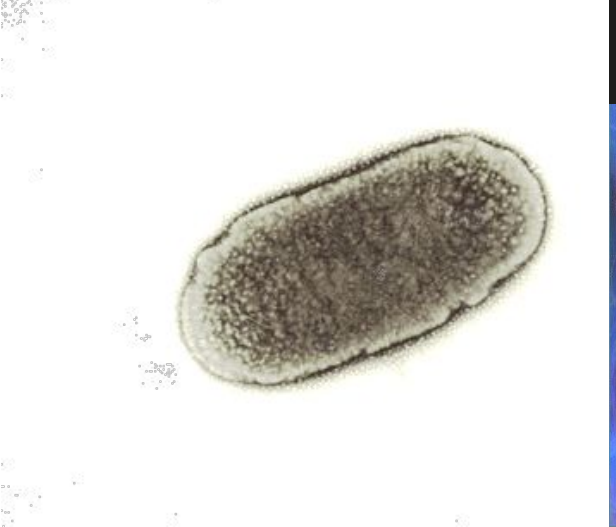
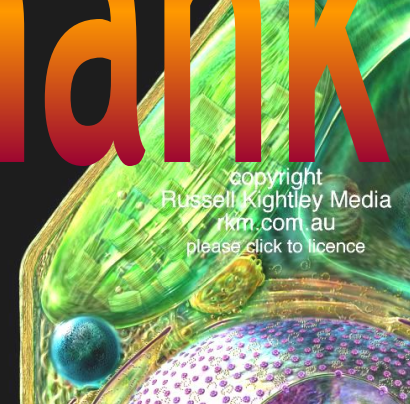
COMPARATIVE ANALYSIS OF THE HUMAN AND MOUSE GENOMES

- ▶ The mouse genome is 14% smaller than the human genome.
- ▶ At the nucleotide level, approximately 40% of the human genome can be aligned to the mouse genome.

- 
- The background of the slide features abstract, overlapping green geometric shapes, primarily triangles and polygons, in various shades of green, creating a modern and dynamic visual effect.
- ▶ The mouse and human genomes seem to contain about 30000 protein-coding genes.
 - ▶ **Mouse-human sequence comparisons allow an estimate of the rate of protein evolution in mammals.**

GENERAL GENOMIC COMPARISONS

Organism	Genome Size (Bases)	Estimated Genes
Human (<i>Homo sapiens</i>)	3 billion	30,000
Laboratory mouse (<i>M. musculus</i>)	2.6 billion	30,000
Thale cress (<i>A. thaliana</i>)	100 million	25,000
Roundworm (<i>C. elegans</i>)	97 million	19,000
Fruit fly (<i>D. melanogaster</i>)	137 million	13,000
Yeast (<i>S. cerevisiae</i>)	12.1 million	6,000
Bacterium (<i>E. coli</i>)	4.6 million	3,200
Human immunodeficiency virus (HIV)	9700	9



Thank You!

<http://www.microscopy.fsu.edu/cells/animals/mitochondria.html>
<http://www.hybridmedicalanimation.com/pages/chloroplast.html>