PLNT2530
2025

Unit 5

Genomes: Organization and Comparisons

Genome

- the sum of all genes and intergenic DNA on all the chromosomes of a cell represents the cellular genome.

- Plants possess a plastid, a mitochondrial, and a nuclear genome while animals have only the latter two.

- Like other eukaryotes, plants have linear chromosomes, each containing hundreds or thousands of genes.

- Nuclear chromosomes consist primarily of non-coding, repetitive DNA. Genes coding for proteins make up only a small percentage of genomes of most higher plant species.

Organism	Chromosome number (n)	Genome size (bp)	Gene No.
Chlamydomonas reinhardtii (green alga)	17	1.11×10^8	17,742
Arabidopsis thaliana	5	1.19×10^8	27,549
Frageria vesca	7	2.80×10^8	25,050
Brassica rapa	10	2.84×10^8	41,174
Oryza sativa	12	4.66×10^8	58,000
Glycine max	20	1.10×10^9	46,430
Zea mays	10	2.80×10^9	63,000
Triticum aestivum	21	1.70×10^{10}	41,910

Genomes

Dependence and independence of cellular genome components

-separate transcription and translation machinery for each organelle

-nuclear genome possess overall control

Relative size (average)

	relative size*
plastid genome	1
mitochondrial genome	3
nuclear genome	30,000

**bp/haploid genome*

C-value paradox

1C value refers to the haploid genome size

bacteria < fungi < plants/animals

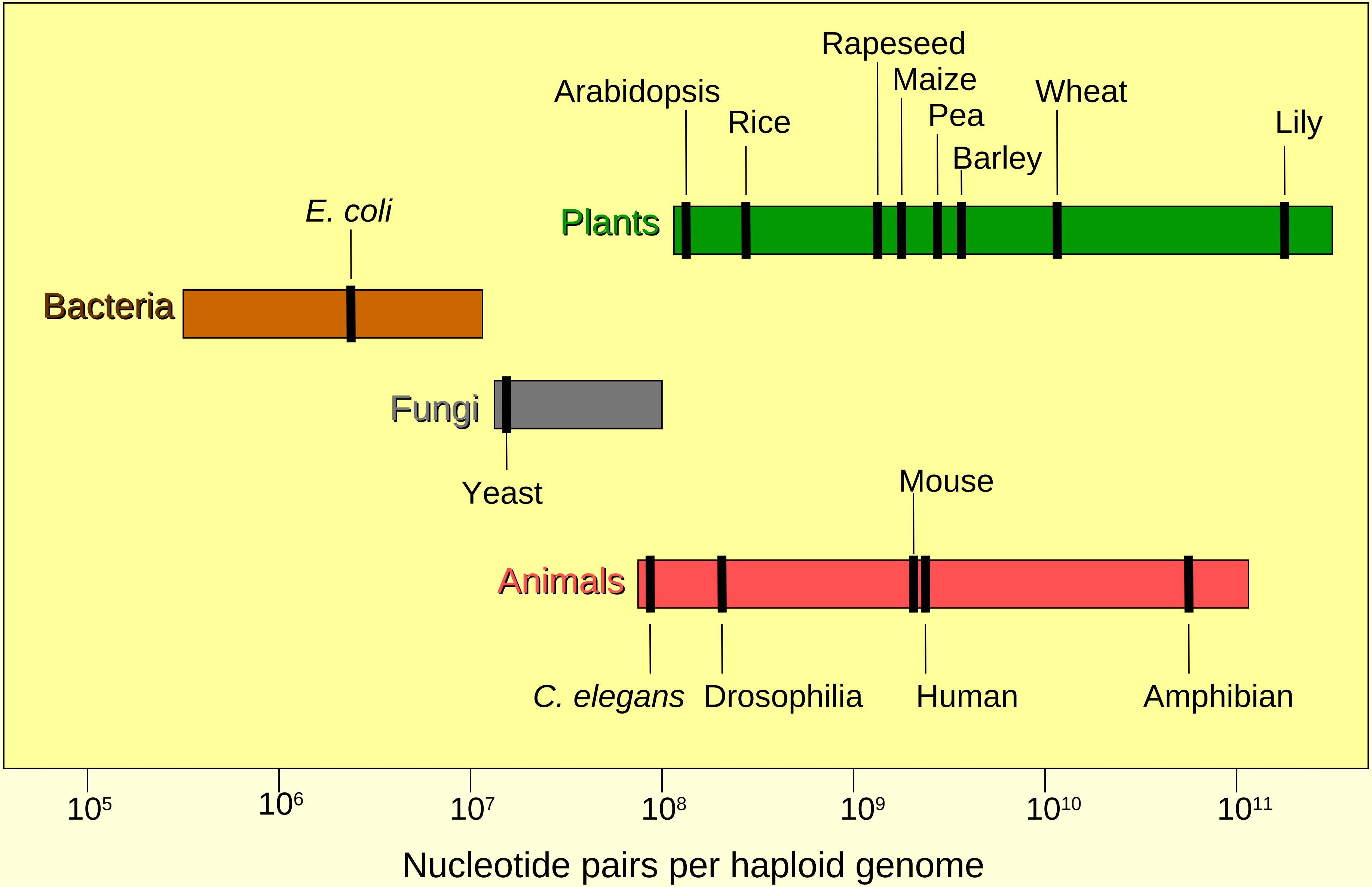
The paradox: Organism's complexity does not follow genome size completely.

But Arabidopsis is not 100 times less complex than wheat and 1000 times less than lily

	Genome size	Gene#
E. coli	~4 x 10^6 bp	~4,000 genes
Arabidopsis	1.20 x 10^8 bp	~25,400 genes

Gene # estimates for higher plants 24,000 - 60,000 genes

Genome size comparison among organisms



What portion of the genome is made up by genes?

Assume the average gene size = 3000 bp (promoter, coding region but not introns)

$$\frac{3000 \text{ bp x } 25{,}400 \text{ genes}}{1.20 \text{ x } 10^{8} \text{ bp}} \text{ X}100 = 61\% \quad \text{Arabidopsis}$$

$$\frac{4000 \text{ bp x } 35{,}000 \text{ genes}}{4.5 \text{ x } 10^{9} \text{ bp}} \text{ x } 100 = 3.1\% \quad \text{Pea}$$

pea genome size

What accounts for the extra DNA among different species?

1. Repetitive sequences (coding and non-coding)

2. Polyploidy

    -Autopolyploid (all chromosome sets are homologous)

        Eg. Sugar beet autotriploid (AAA)

    -Allopolyploid (subgenome sets of chromosomes arising from 2 or more species or genera)

        Eg. canola *Brassica napus* (n=19) allotetraploid (AACC)

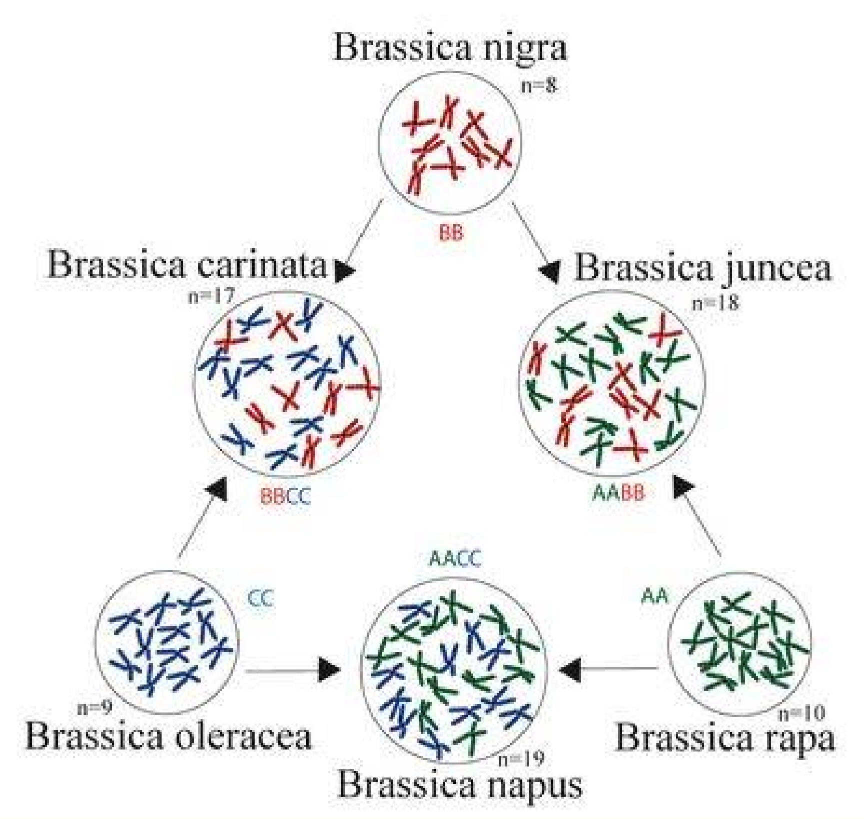
        B. oleracea (n=9) CC

        B. rapa (n=10) AA

    (wheat, oat, tobacco)

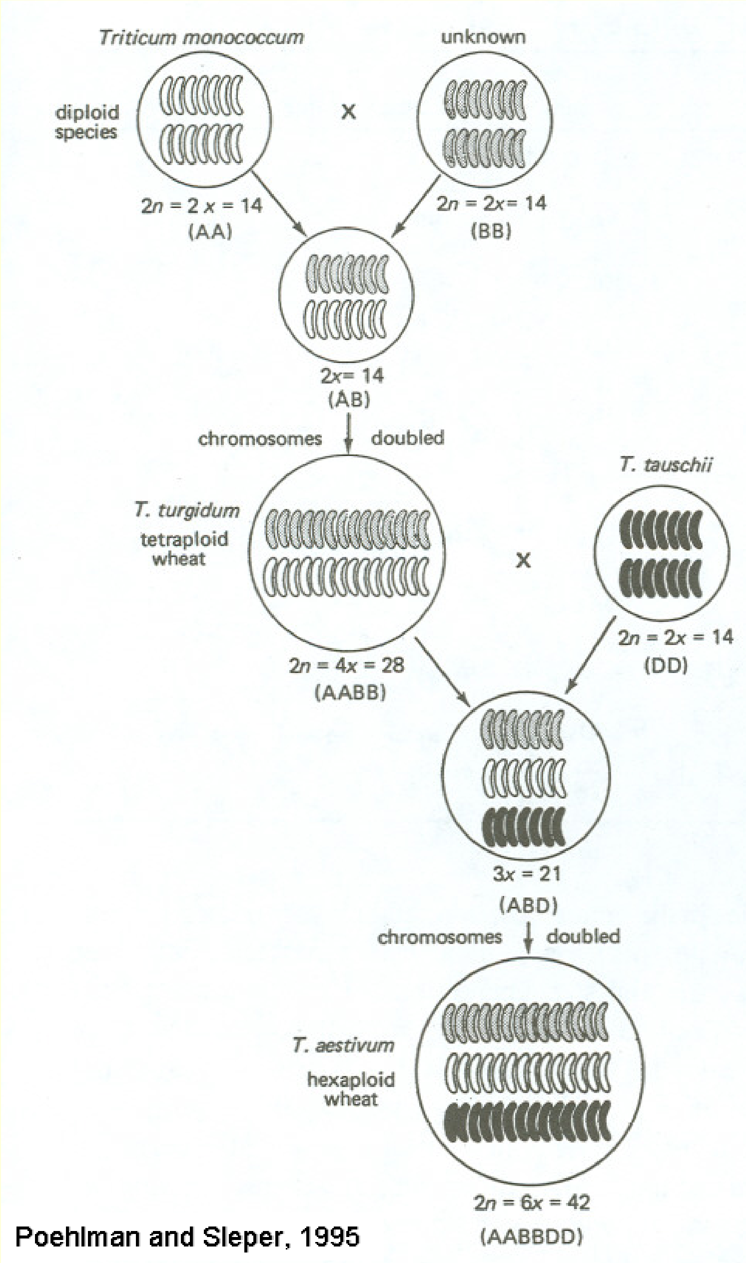
3. Different size and frequency of introns in genes

Canola/rapeseed



Overview of species relationships in the genus 'Brassica'.
Original work by Mike Jones, for Wikipedia.

Hexaploid wheat



Poehlman and Sleper, 1995

Major Classes of Genomic DNA

Genic and non-genic DNA

A. Genic DNA (<5% of total genome in large genomes)

1. "Single" copy genes
    - between 1 - 10 copies per haploid genome
    - represents the majority of genes

2. Duplicated and divergent genes
    - functional multi-gene families
    - may occur at a single or several loci on different chromosomes
    - in Arabidopsis (fully sequenced) [996 gene families] and [8,331 genes]

Specific examples: Calcium dependent protein kinase (1 family - 34 genes)
Cytochrome P450 (69 families with 256 genes)

wheat seed storage proteins (gliadens) (40-60)

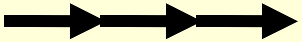
Major Classes of Genomic DNA

A. Genic DNA (cont'd)

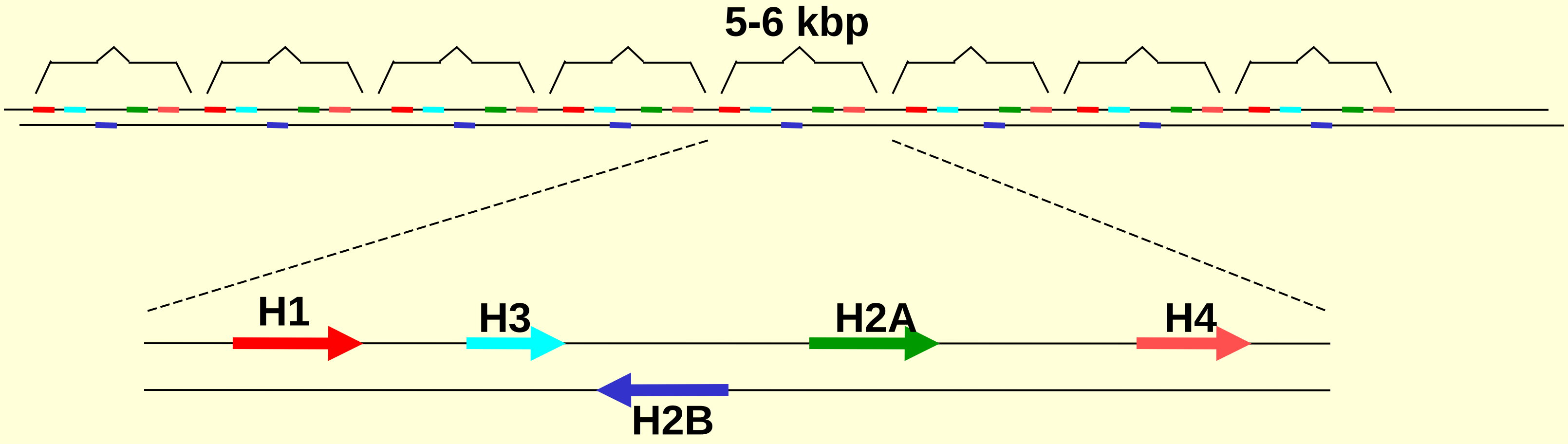
3. <u>Tandemly repeated genes</u> (non-divergent)
   a) Histones

5 histone genes are clustered in a 5-6 kb unit

Unit is tandemly repeated



Most multicellular organisms (50-500 tandem repeats/copies)

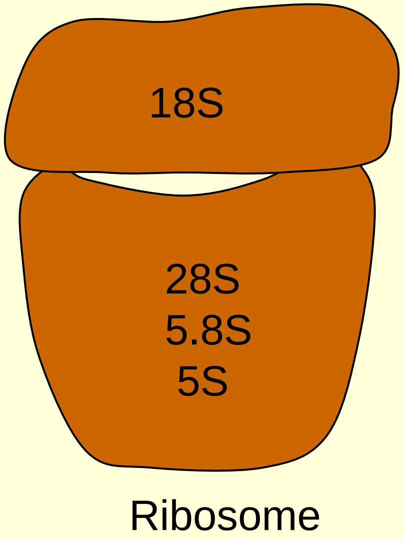


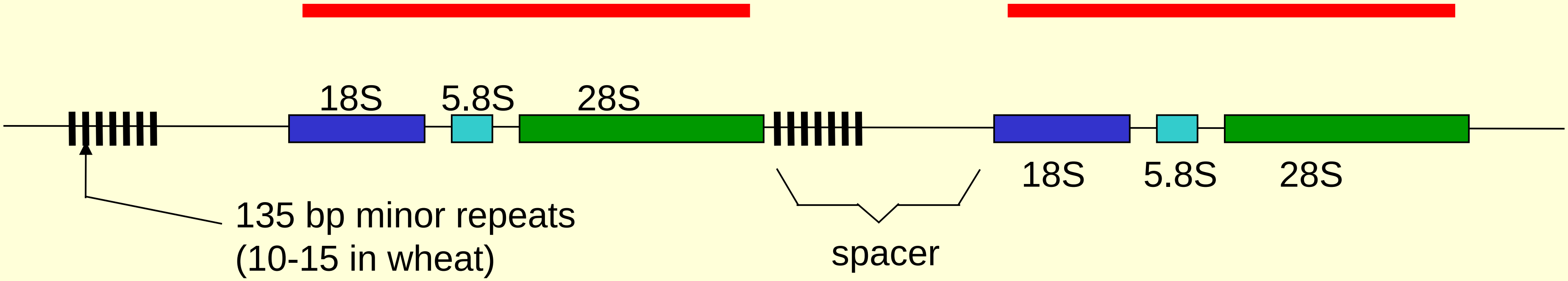
Tandemly Repeated DNA (cont'd)

b) Pre-rRNA genes

Repeat unit includes the 18S, 5.8S and 28S RNA coding regions plus a non-coding spacer region

Repeat unit 8-11 kb depending on species





b) Pre-rRNA genes (cont’d)

- Copies / haploid genome

– Arabidopsis	570 copies
– Most animals	100-200 copies
– Hexaploid wheat	1A 1000 copies
	1B 2600
	6B 6250

c) 5S-rRNA genes

100-2000 copies/haploid genome

2 size variants in wheat 410 bp and 500 bp
in flax 340 & 360 bp

Impact of repetitive genic elements

‘Single’ copy genes 30,000 genes x 3000 bp (avg)/gene = 9×10^7

Repetitive genes

Histones	500 copies x 6000 bp/repeat = 3×10^6
Wheat pre rRNA	9850 copies x 9000 bp/repeat = 8.8×10^7
5S RNA	1000 copies x 500 bp/repeat = 0.5×10^6

Major Classes of Genomic DNA

A. Non-genic sequence (>95% of genome)

1. Tandem repeats

simple sequence repeats ("satellite" sequences)

3-10 bp repeats repeated 10^4 - 10^6 times $[\mathrm{TTTAGGG}]_n$ (Arabidopsis) GAA (wheat) common at telomeres

centromere repeats are often multiple elements of short repeats

2. Dispersed repeats

Many families of repeats spread throughout the chromosomes

eg 150-300+ bases repeated 10^3 - 10^4 times throughout genome

eg Alu element (humans) (~300b)

Afa family of elements (wheat, barley, oat + related species (340 b)

Major Classes of Genomic DNA

Major source of dispersed repeats are transposable elements:

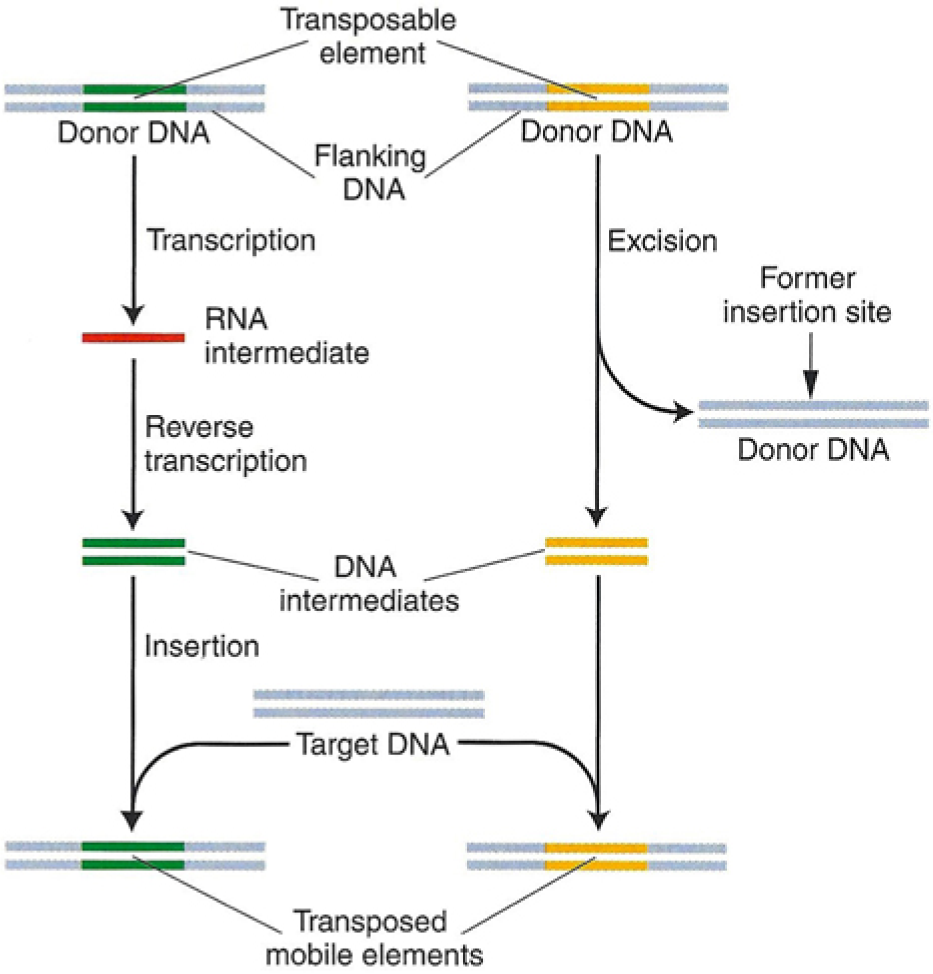
Transposable elements - sequences of DNA that can move around to different positions within the genome of a single cell (mobile genetic elements) (- Nobel Prize 1983 Barbara McClintock 1940s)

2 major classes

- **transposons** - replicate and move as DNA elements
- **retrotranposons** - (originally viral sequences) that replicate via an RNA intermediate method and are copied back into DNA by a reverse transcriptase

Two classes of mobile elements

Retro-transposons Transposons



from: http://sgugenetics.pbworks.com/w/page/78853139/Site%20background%20information

Retrotransposons

- Particularly abundant in plants
- Maize 49-78% of genome composed of retrotransposons
- Wheat (90% repetitive DNA, 68% transposable elements

Common elements (many are also found in plants, fungi and protists)

- LTR retrotransposons (with long terminal repeats 100bp - 5 kbp)
  - Ty1-copia retrotransposons
  - Ty3-gypsy retrotransposons
- Non-LTR retrotransposons (up to 250,000 copies in plant species)
  - LINEs long interspersed nuclear elements
  - SINEs short interspersed nuclear elements

- Human 42% of genome made up of <u>retrotransposons</u>
  - while DNA <u>transposons</u> account for about 2-3%

Maize genome
2×10^9 bp

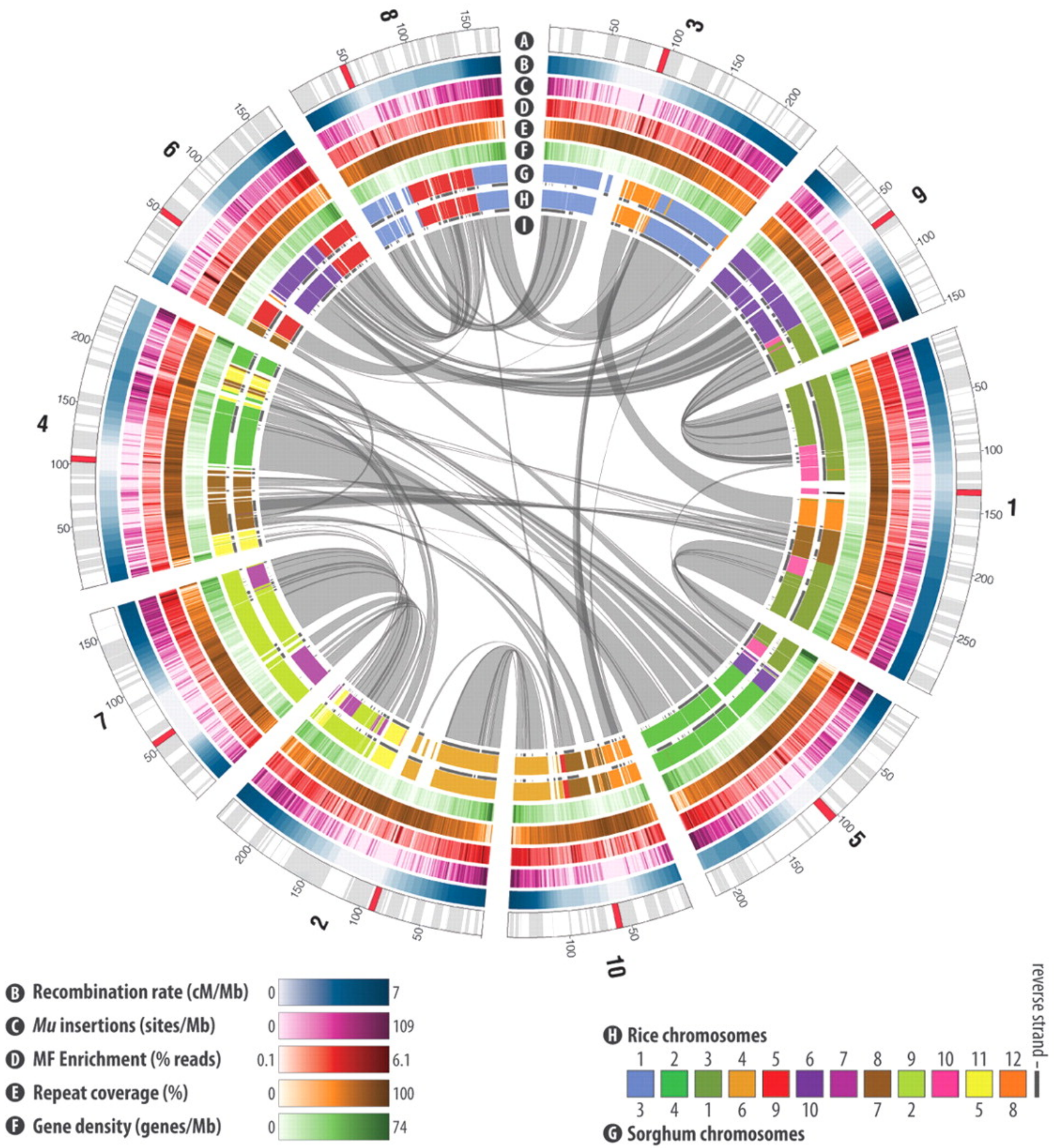
from Schnable PS et al. 2009

Science 326:1112-1115.

Main take home lesson from C,E and F:

Genes are islands in a sea of repetitive sequences.

E- repeats from previously characterized repeats, found by RepeatMasker or other programs.



Non-genic DNA is not necessarily non-functional

Functions of some repeat regions:

Scaffolding (Matrix) attachment regions (~10^4 in large genome)

Spindle fiber attachment sites (centromere)

Protection of chromosome termini (telomeres)

Origins of replication (in yeast ~250 bp long)

Estimate of the # of origins in the human genome:
~50,000 (Genome Res. 2013. 23: 1-11)

Plastid Genome

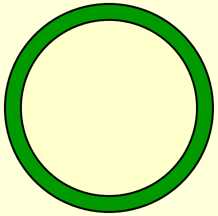
All plant cell contain plastids of some type - same genome (chloroplasts, amyloplast, chromoplast, elaioplast) all from etioplast

Replicate by division. When a cell divides plastid copies are shared

In angiosperms (all common crop plants) during fertilization both plastid and mitochondrial genomes come from the ovary never from pollen. Basis of maternal inheritance of certain traits.

Significant consideration in some genetic engineering as it is a way of preventing transgene gene transfer by pollen flow.

Plastid Genome



Similar in most plant species

120-270 kb per plastid genome   Circular dsDNA

Encodes 120-140 genes   -mostly involved in protein synthesis or photosynthesis

Majority of proteins in the chloroplast are nuclear-encoded

Typical leaf 10-20 chloroplasts

5-10 copies of the plastid genome/chloroplast

Thus 50-200 copies of the genome/leaf cell

–

Plastid Genome

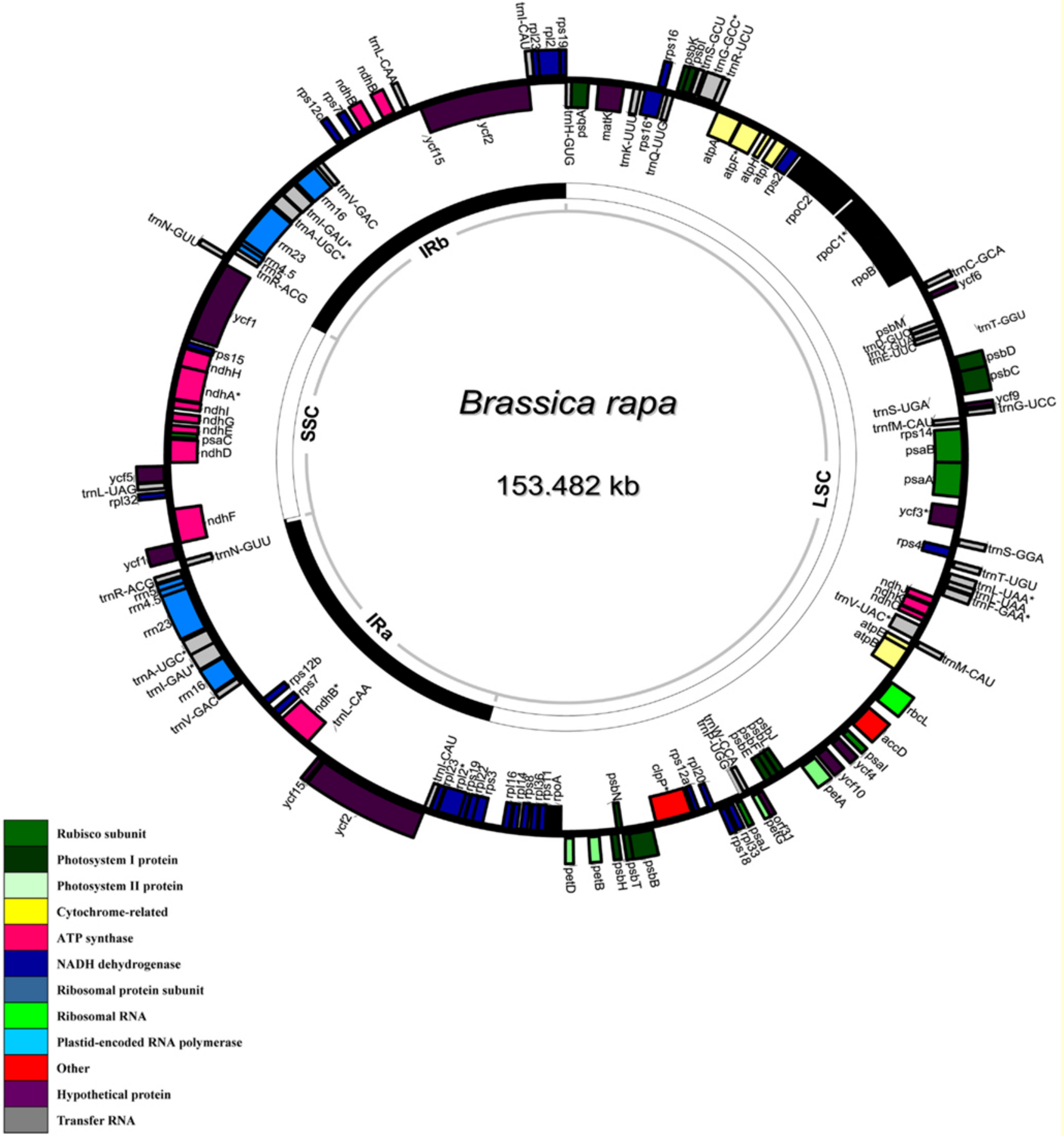
Genes transcribed on the forward strand are on the outer circle. Those transcribed
on the reverse strand are on the inner circle.

Regions found in plastid genomes of higher plants:

LSC - large single-copy region

SSC - small single-copy region

IRa, IRb - inverted repeats; duplicate copies of genes are seen in inverted orientation



Mitochondrial genome

Plant mitochondrial genome range 200-2500 kbp

Fewer genes than the chloroplast genome <100

Many mitochondria/per cell

Individual mitochondria divide and multiple organelles can re-fuse

Multiple copies of the genome/per mitochondrion

Genome exists as a series of subgenomic* circles of dsDNA molecules which can interchange parts of the circles by recombination (unlike mammalian and fungal mitochondria)

The majority of proteins in the mitochondria are nuclear-encoded

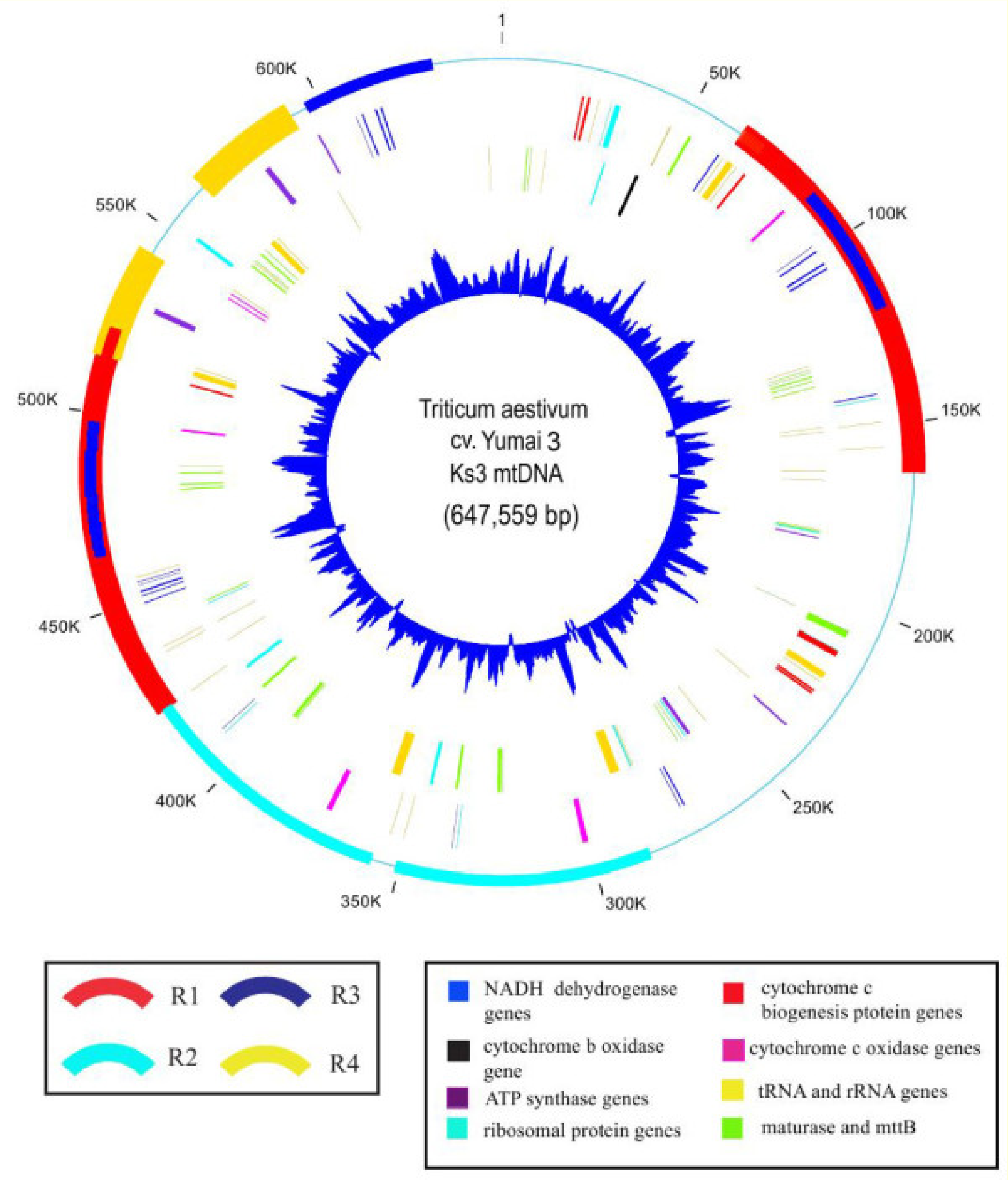
subgenomic* - portions of the full mitochondrial genome sometimes exist as separate circular molecules within the mitochondrion.

Mitochondrial genome

circle 1: Large repeats containing blocks of genes with related functions, R1 - R4.

circles 2 and 3: Transcribed regions on forward and reverse strands.

circle 4: GC content



from: http://bmcgenomics.biomedcentral.com/articles/10.1186/1471-2164-12-163