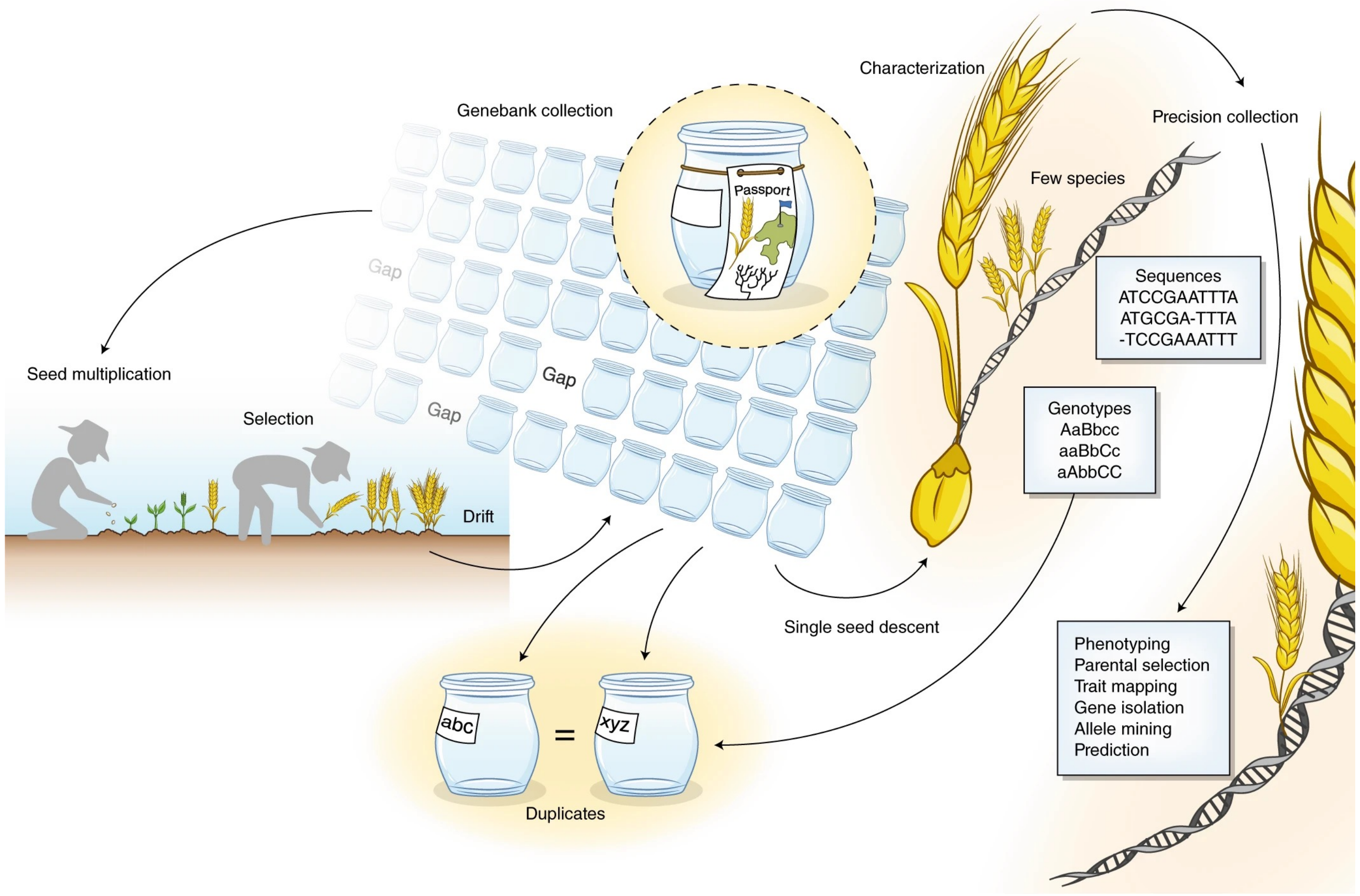
Quantitative genetics course

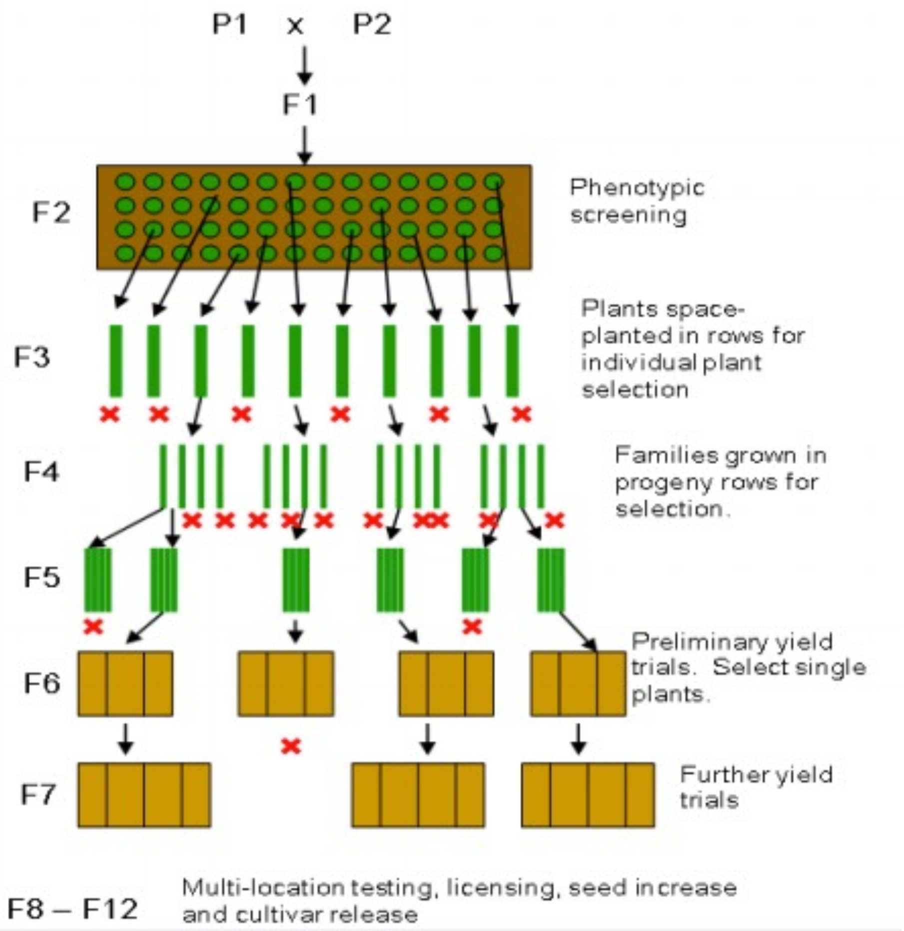
Where are we and where are we want to go?

- Conventional breeding
- Marker Assisted Selection
- Genomic Selection



Mascher et al 2019

Conventional Plant Breeding



Phenotypic screening

Plants space-planted in rows for individual plant selection

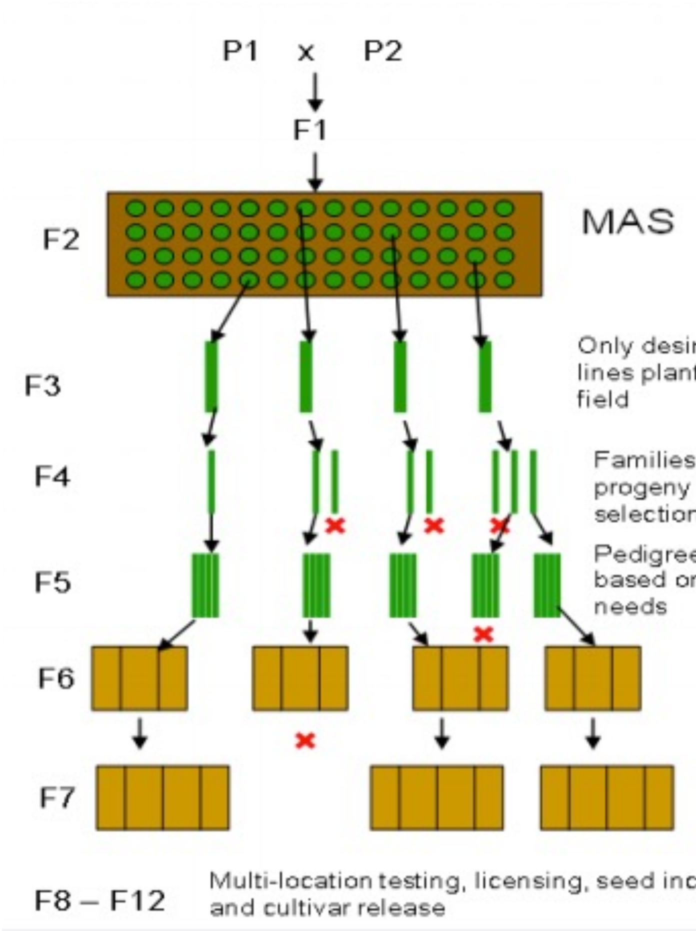
Families grown in progeny rows for selection.

Preliminary yield trials. Select single plants.

Further yield trials

Multi-location testing, licensing, seed increase and cultivar release

Marker Assisted Selection



Only desirable F3 lines planted in field

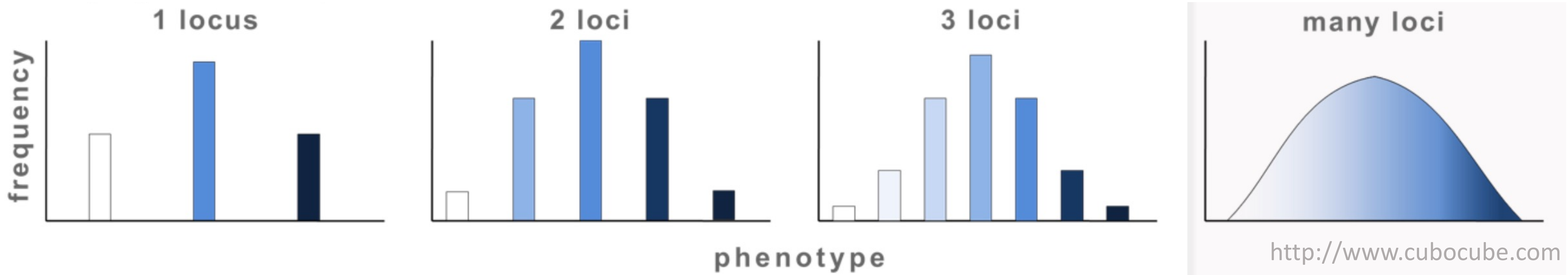
Families grown in progeny rows for selection.

Pedigree selection based on local needs

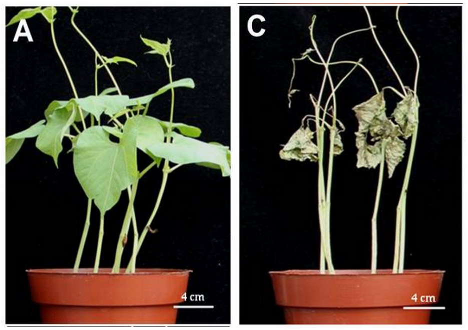
Multi-location testing, licensing, seed increase and cultivar release

Lema 2018

What happens in quantitative traits?

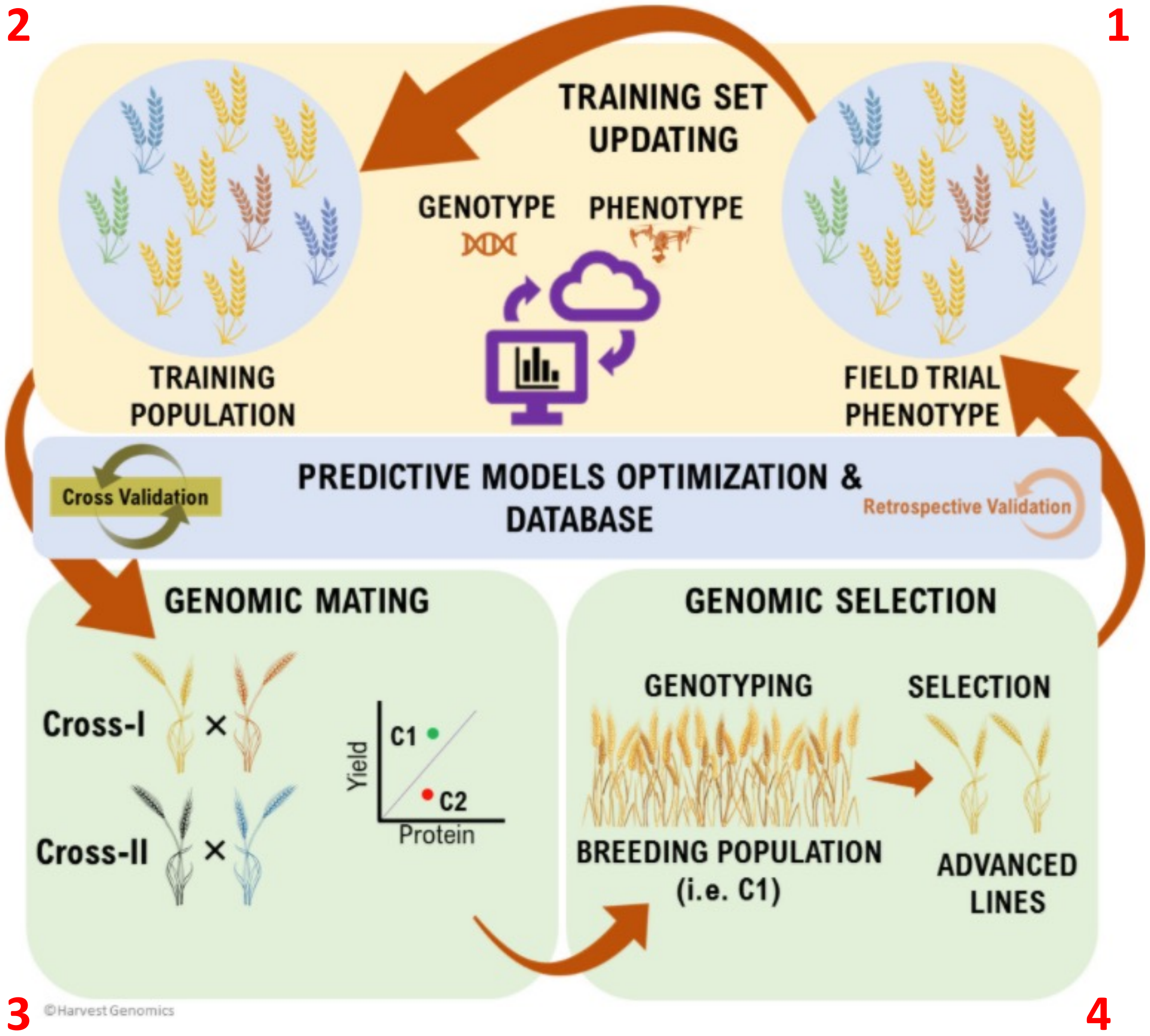


http://www.cubocube.com

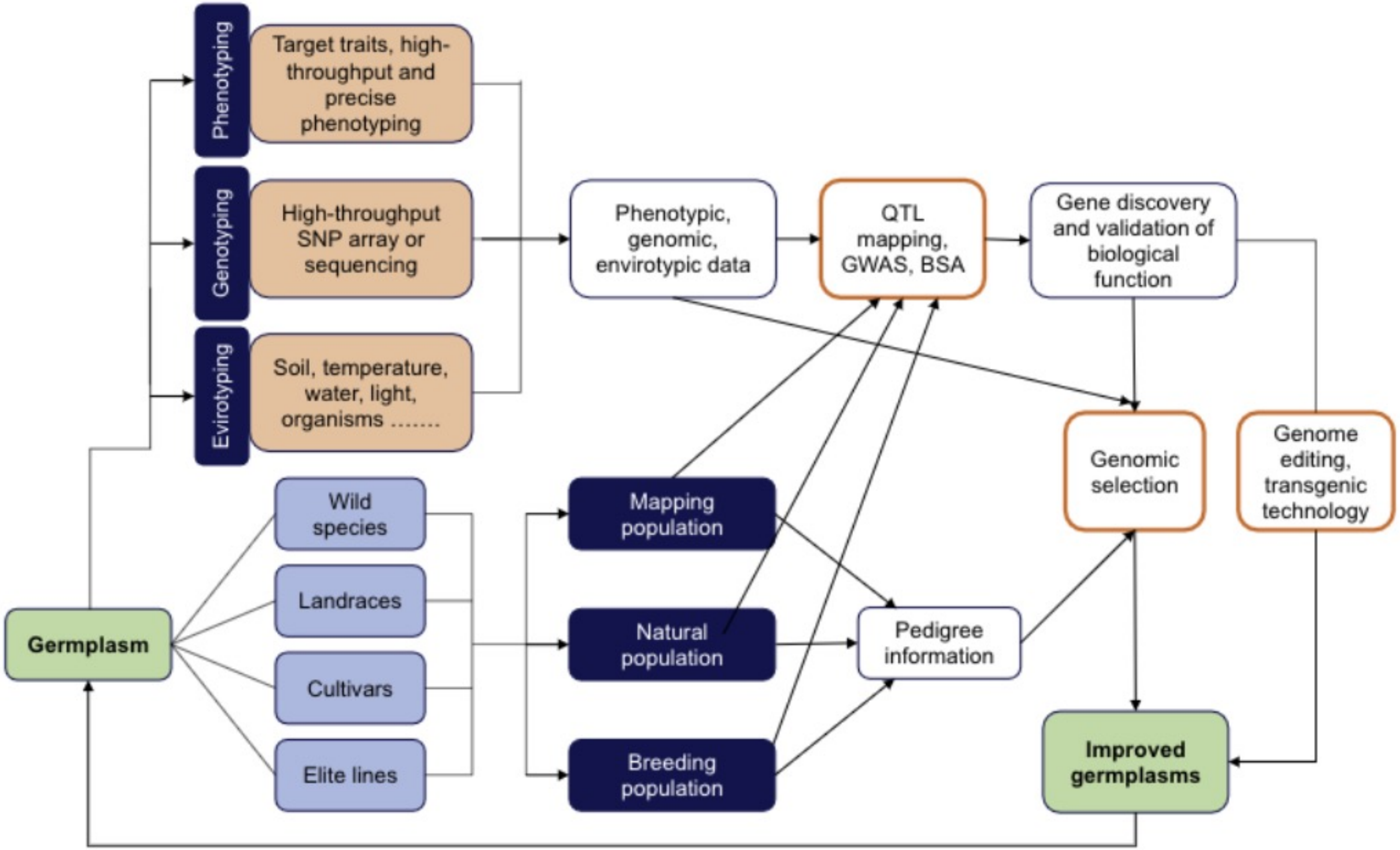


Chen *et al* 2017

Genomic Selection



Mascher et al 2019



Phenotyping

Target traits, high-throughput and precise phenotyping

Genotyping

High-throughput SNP array or sequencing

Evirotyping

Soil, temperature, water, light, organisms ....

Phenotypic, genomic, envirotypic data

QTL mapping, GWAS, BSA

Gene discovery and validation of biological function

Genomic selection

Genome editing, transgenic technology

Germplasm

Wild species

Landraces

Cultivars

Elite lines

Mapping population

Natural population

Breeding population

Pedigree information

Improved germplasms

Xu et al 2020

The molecular basis of genetics:

- Genome
- Chromosomes
- Genes (alternative splicing)
- Mitosis and meiosis
- Crossing over
- DNA sequencing
- Genotyping by sequencing (GBS)

greenhousegrower.com

The molecular basis of genetics:

- Genome
- Chromosomes
- Genes (alternative splicing)
- Mitosis and meiosis
- Crossing over
- DNA sequencing
- Genotyping by sequencing (GBS)

greenhousegrower.com

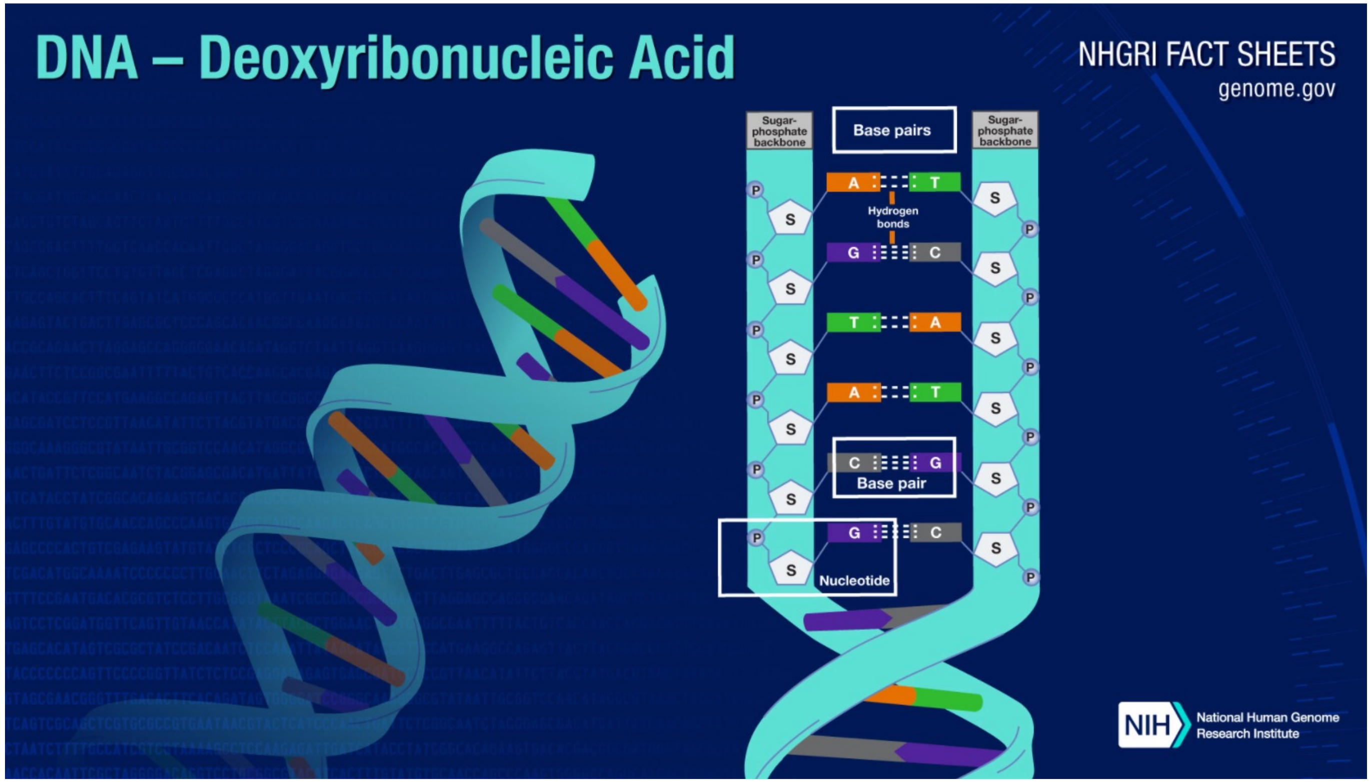
Genome

A genome is all genetic material of an organism. It consists of DNA.

Deoxyribonucleic acid (DNA) is a molecule that contains the genetic instructions for the development, functioning, growth and reproduction of nearly all living organisms.

DNA is made of four chemical units, called nucleotide bases (adenine (A), thymine (T), guanine (G), and cytosine (C)).

A - T
C - G



Genome

***Phaseolus vulgaris* genome**

~540 Millions bases!

Image Credit: fotohunter / Shutterstock

Genome

Phaseolus vulgaris genome

~540 Millions bases!

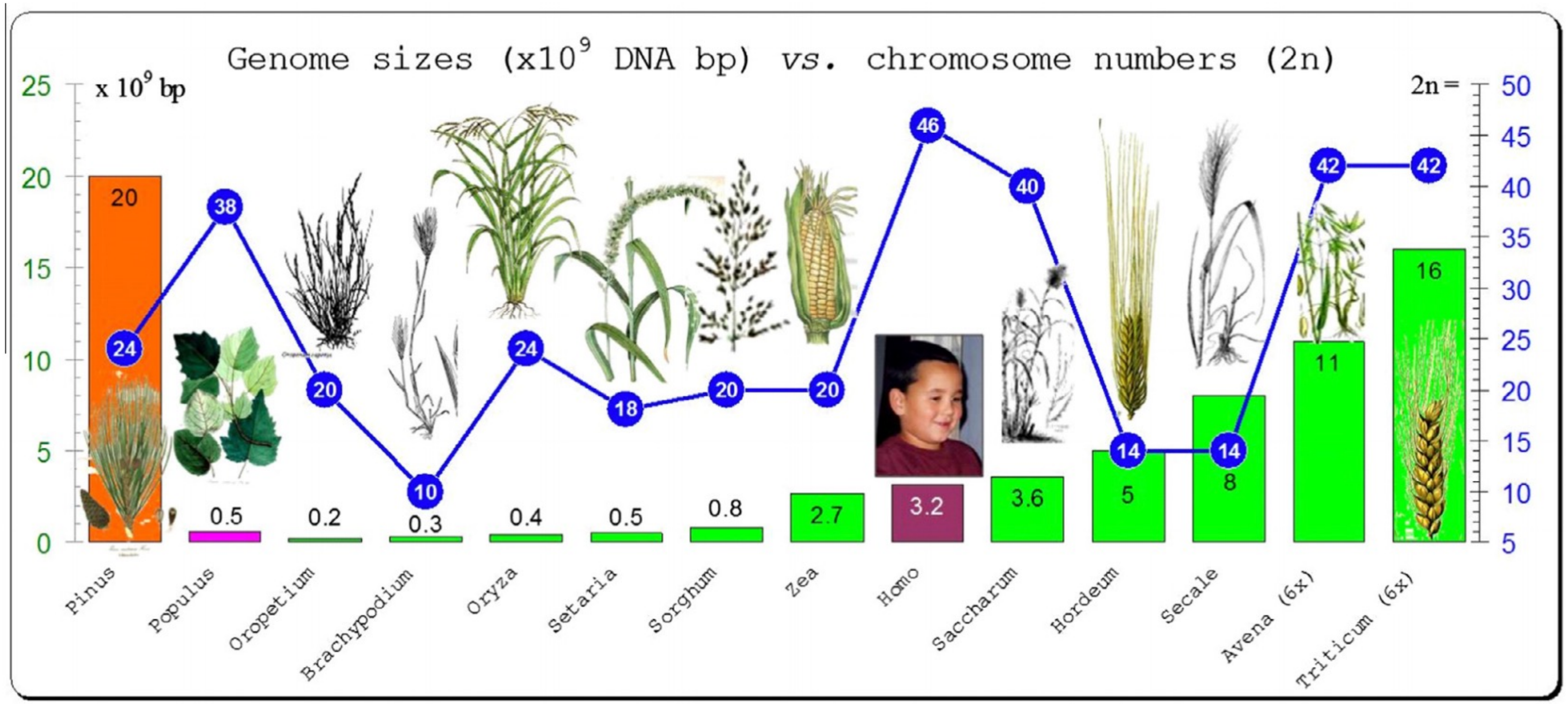


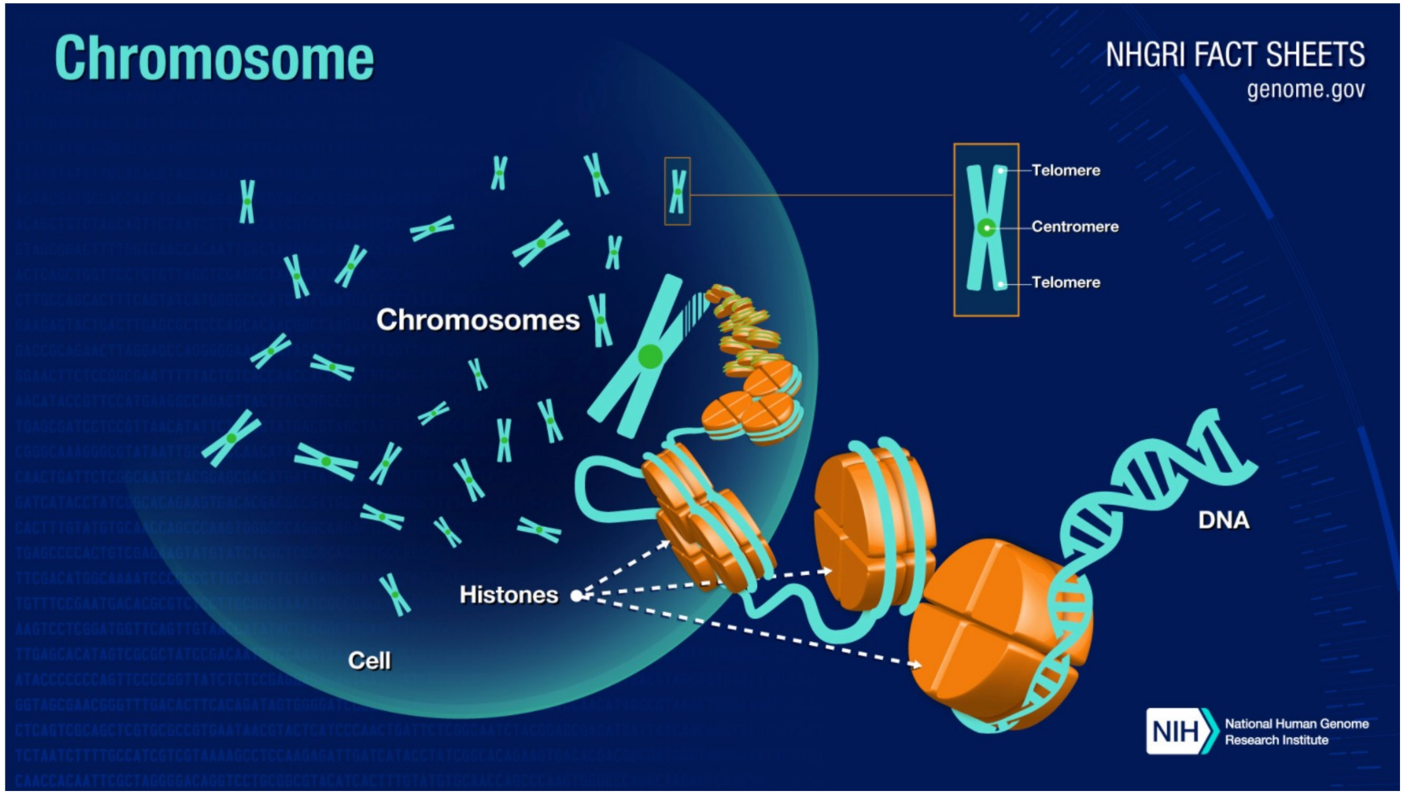
Figure 1 Sizes of plant genomes. Sizes (bp) vs. chromosome numbers ($2n$) of plant genomes from different taxa and compared to human genome size (3.2×10^9 bp).

Ali *et al* 2014

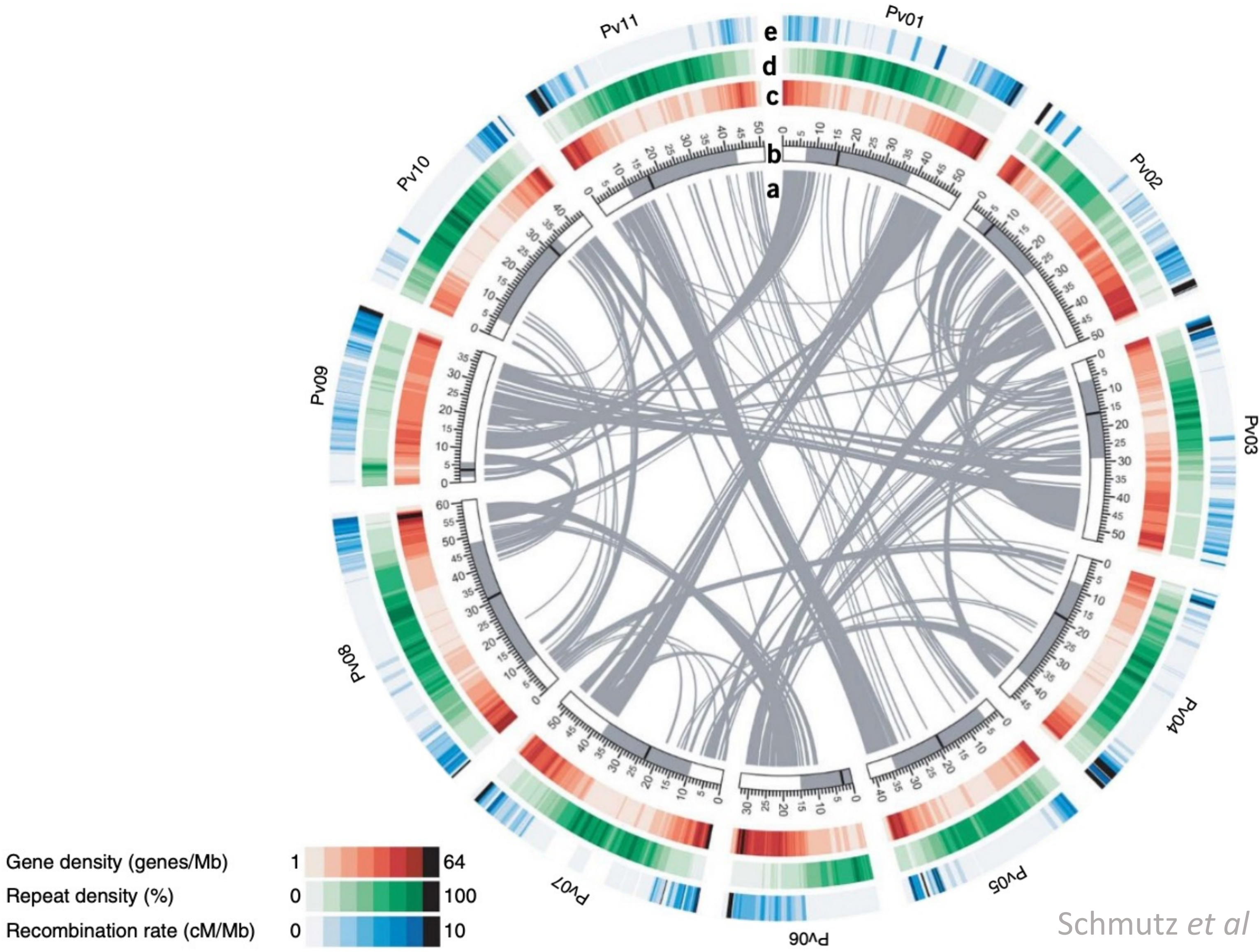
Chromosomes

Chromosomes contained part of the genetic material (DNA).

Chromosomes keeps DNA wrapped around proteins called histones which bind to and condense the DNA molecule to maintain its integrity.



Chromosomes

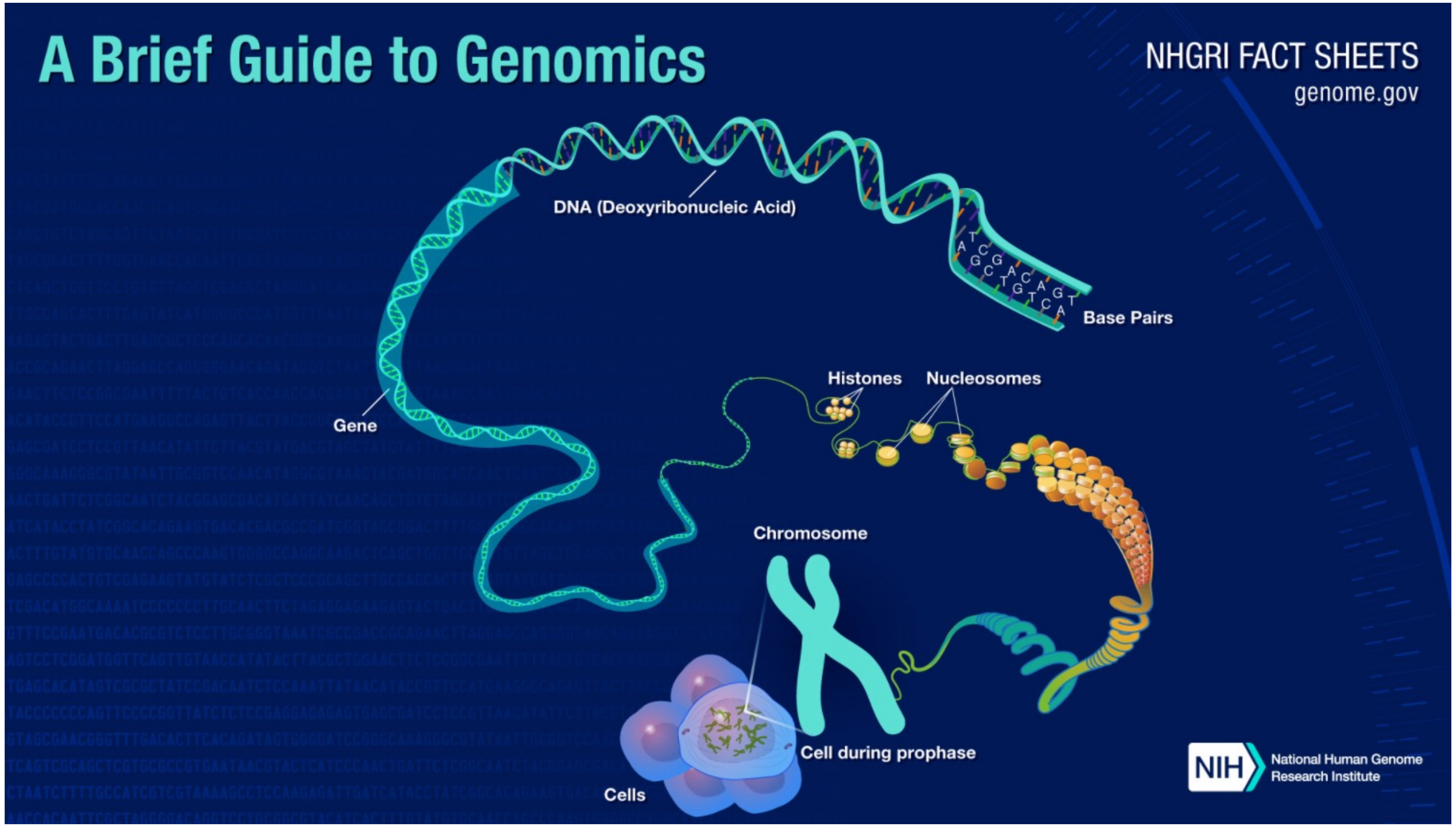


Schmutz *et al* 2014

(a) Gray lines connect duplicated genes.
(b) Centromeric and pericentromeric regions in black and gray.
(c) Gene density in sliding windows of 1 Mb.
(d) Repeat density in sliding windows of 1 Mb (e) Recombination rate

Genes

The gene is the basic physical unit of inheritance and contain the information needed to specify traits.

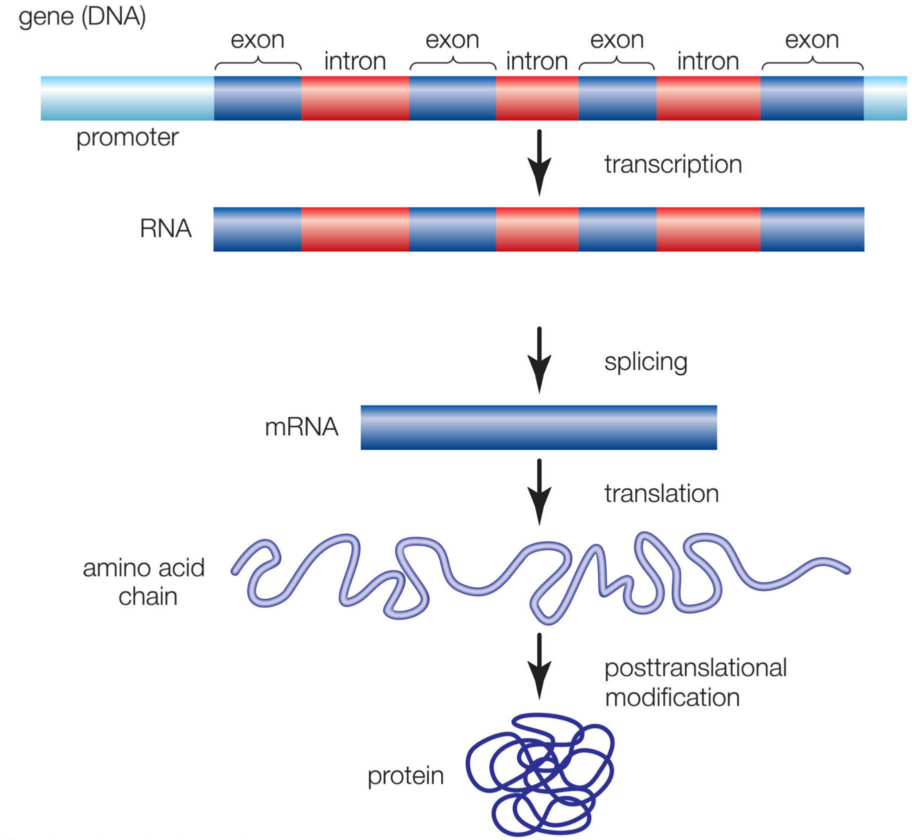


Genes

Promoter: sequence of DNA needed to turn a gene on or off.

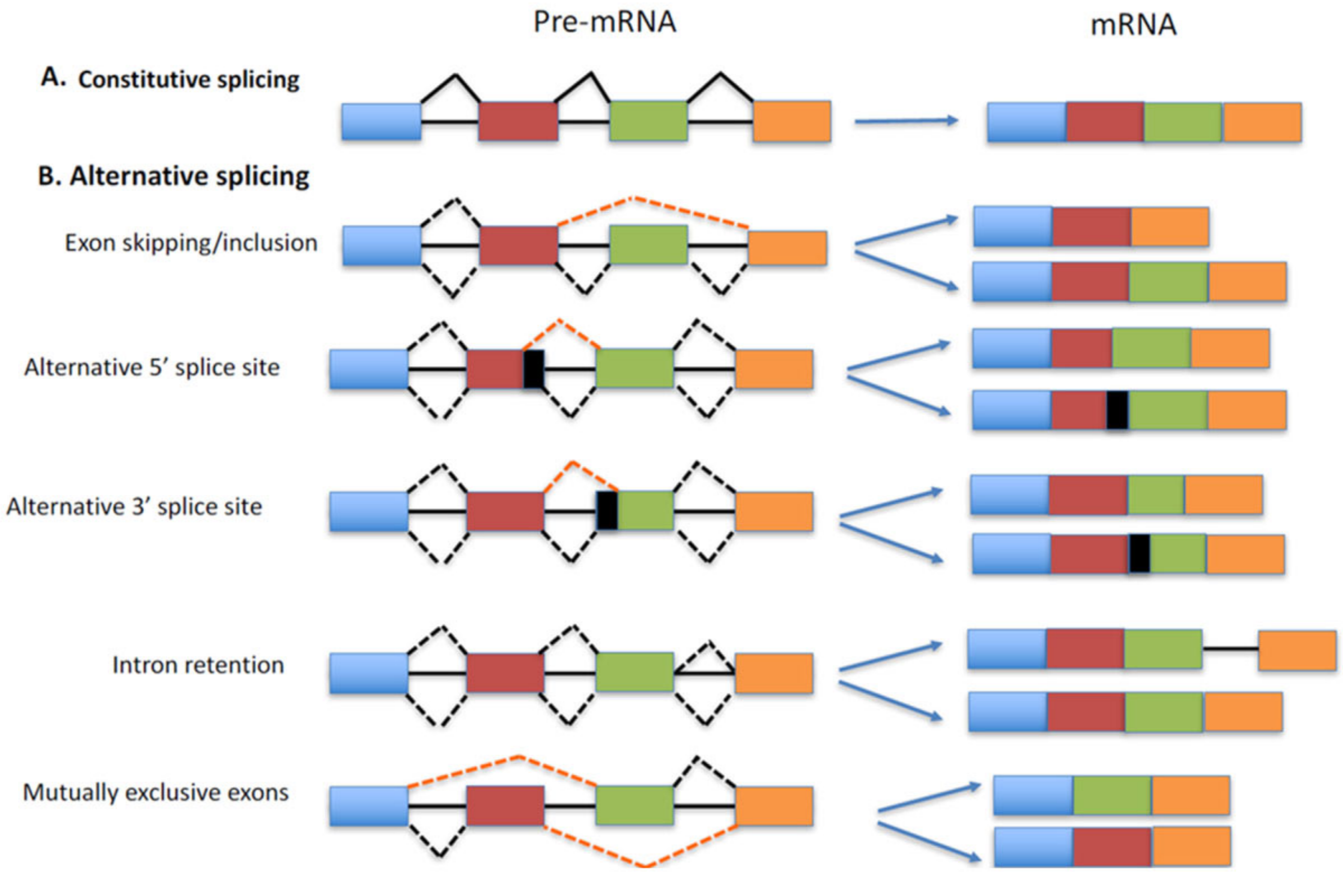
Exons: parts of the gene sequence that are expressed in the protein.

Introns: parts of the gene sequence that are not expressed in the protein.



© 2013 Encyclopædia Britannica, Inc.

Genes



Sen 2018

Genes

Phaseolus vulgaris

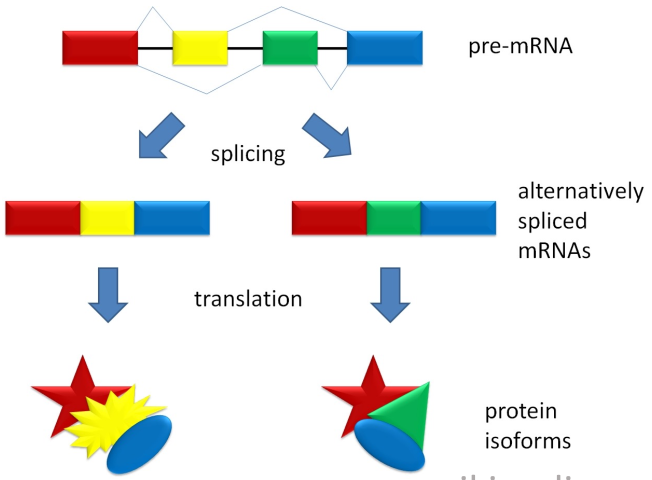
Loci

27,433 total loci containing 36,995 protein-coding transcripts

Alternative Transcripts

36,995 – 27,433 = 9,562 total alternatively spliced transcripts

Schmutz *et al* 2014



pre-mRNA

splicing

alternatively
spliced
mRNAs

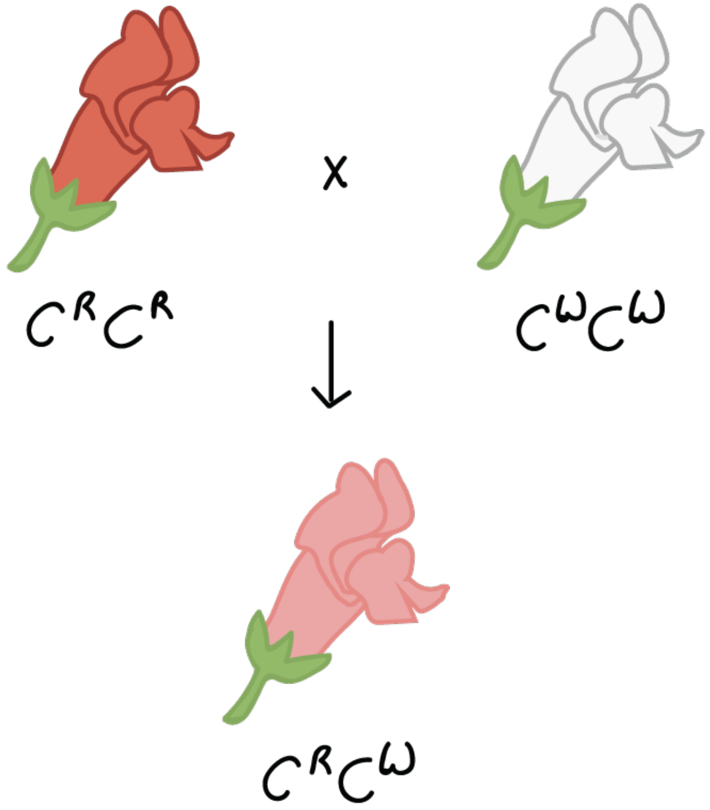
translation

protein
isoforms

wikipedia.org

Alleles

- An allele is one of two or more versions of a gene.
- If the two alleles are the same, the individual is homozygous for that gene.
- If the alleles are different, the individual is heterozygous.
- The use of the allele also refers to variation among non-coding DNA sequences.



https://www.khanacademy.org/

The molecular basis of genetics:

- Genome
- Chromosomes
- Genes (alternative splicing)
- Mitosis and meiosis
- Crossing over
- DNA sequencing
- Genotyping by sequencing (GBS)

greenhousegrower.com

Mitosis

The mitosis occurs in the somatic cells, and it is meant for the multiplication of cells.

- Development and growth
- Cell replacement
- Regeneration
- Asexual reproduction

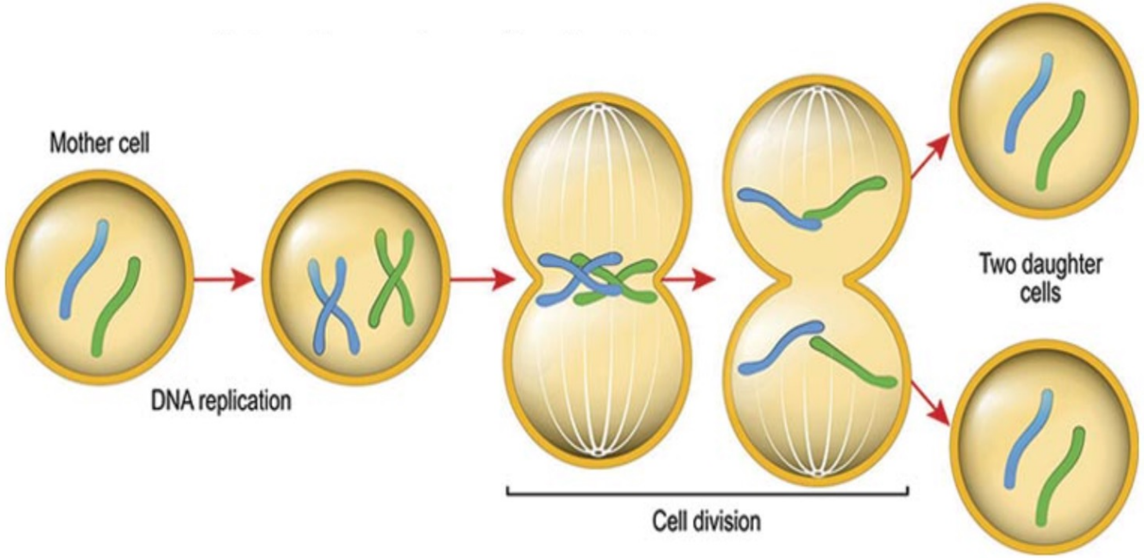


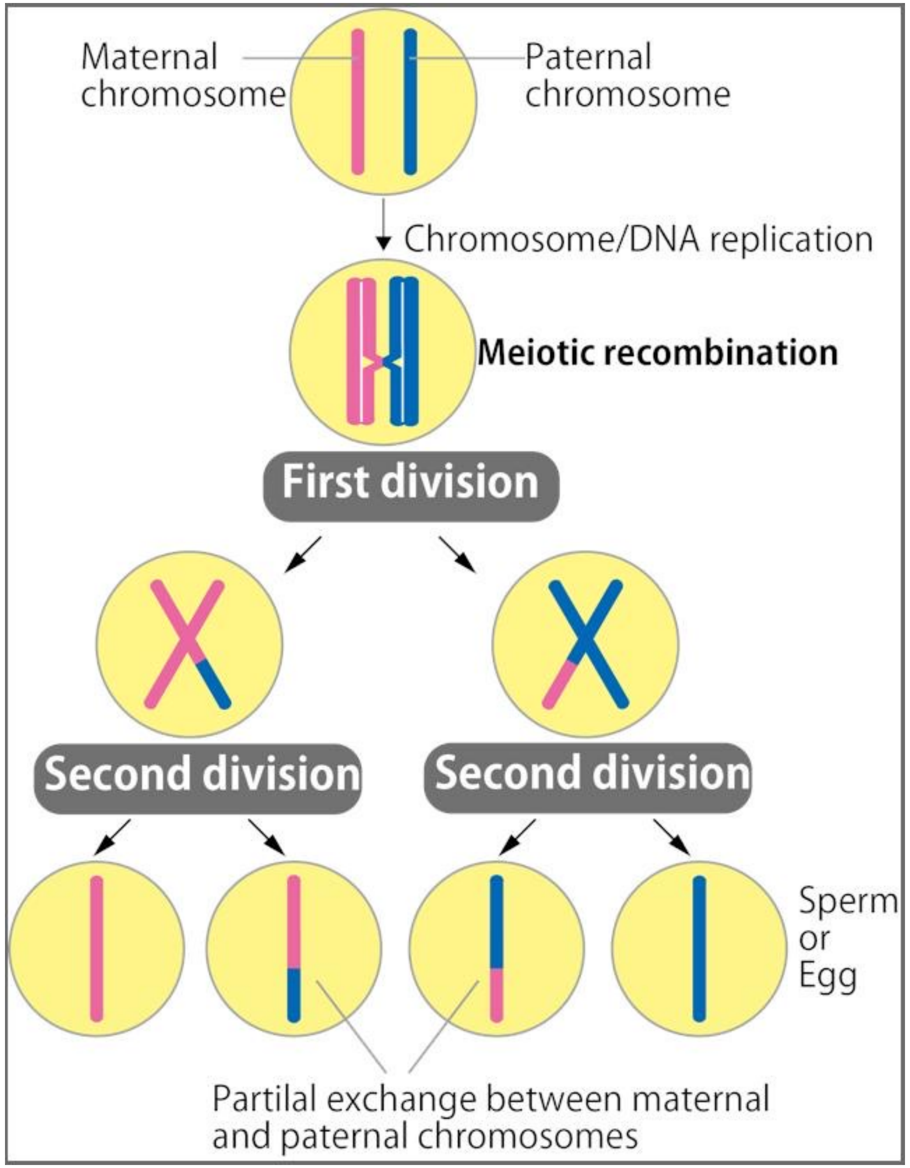
Image Source: Biology Wise.

Meiosis

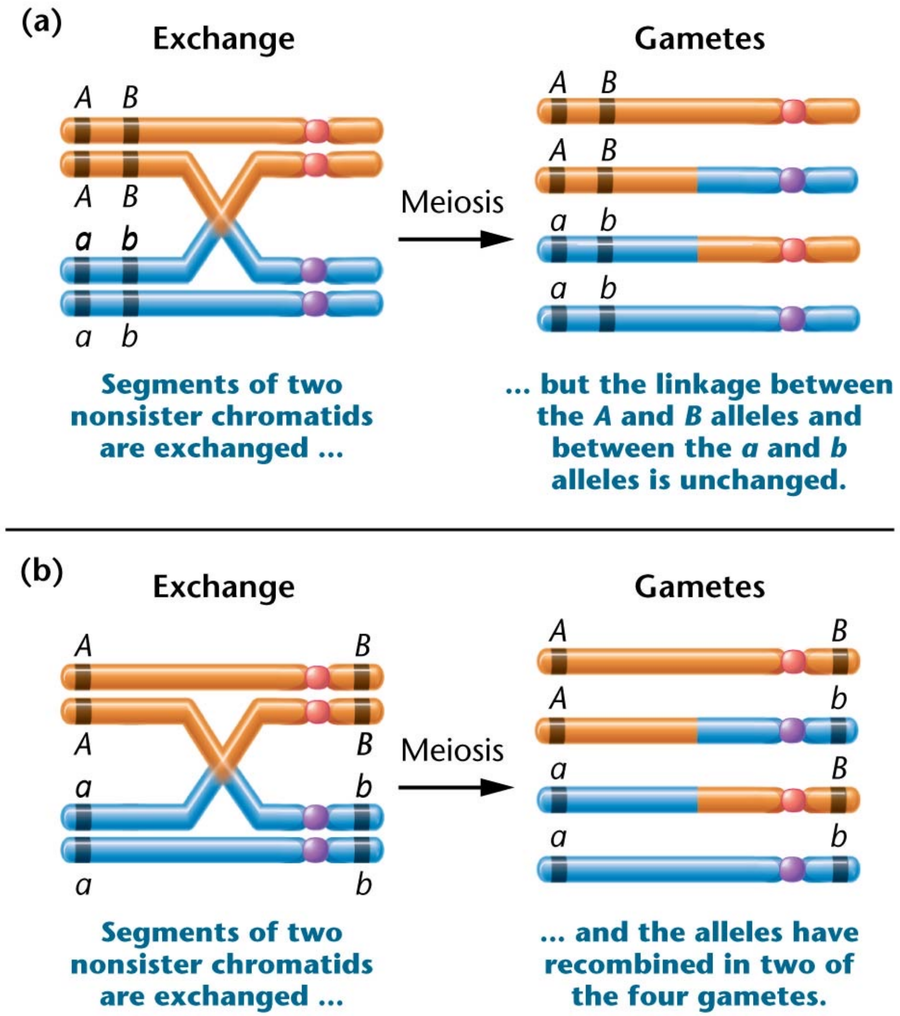
During meiosis, diploid cells undergo DNA replication, followed by two rounds of cell division in germ cells, producing four haploid sex cells.

Meiosis maintains genetic continuity from generation to generation and gives rise to genetic variation in gametes through:

- Crossing over of homologous chromosomes.
- Unique combinations of maternal/paternal chromosomes.



Crossing Over



Segments of two nonsister chromatids are exchanged ...

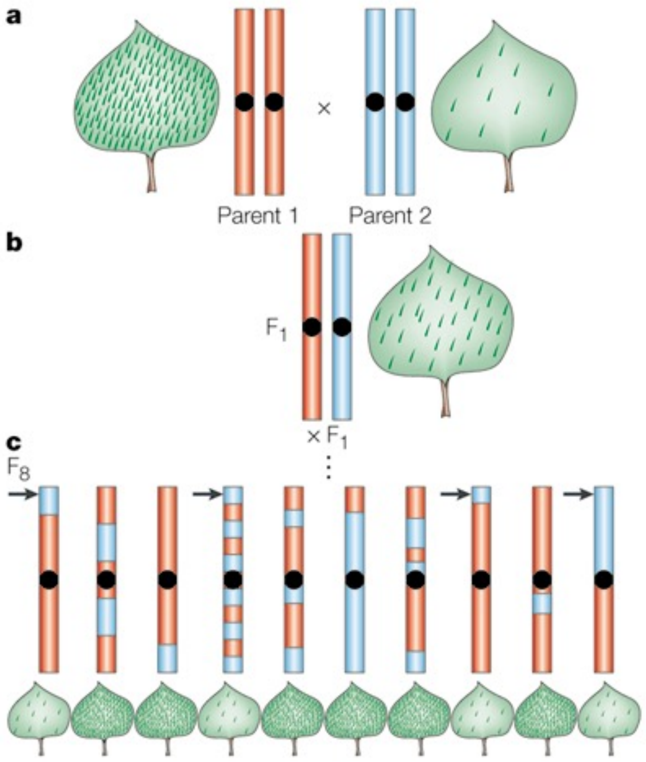
... but the linkage between the *A* and *B* alleles and between the *a* and *b* alleles is unchanged.

Segments of two nonsister chromatids are exchanged ...

... and the alleles have recombined in two of the four gametes.

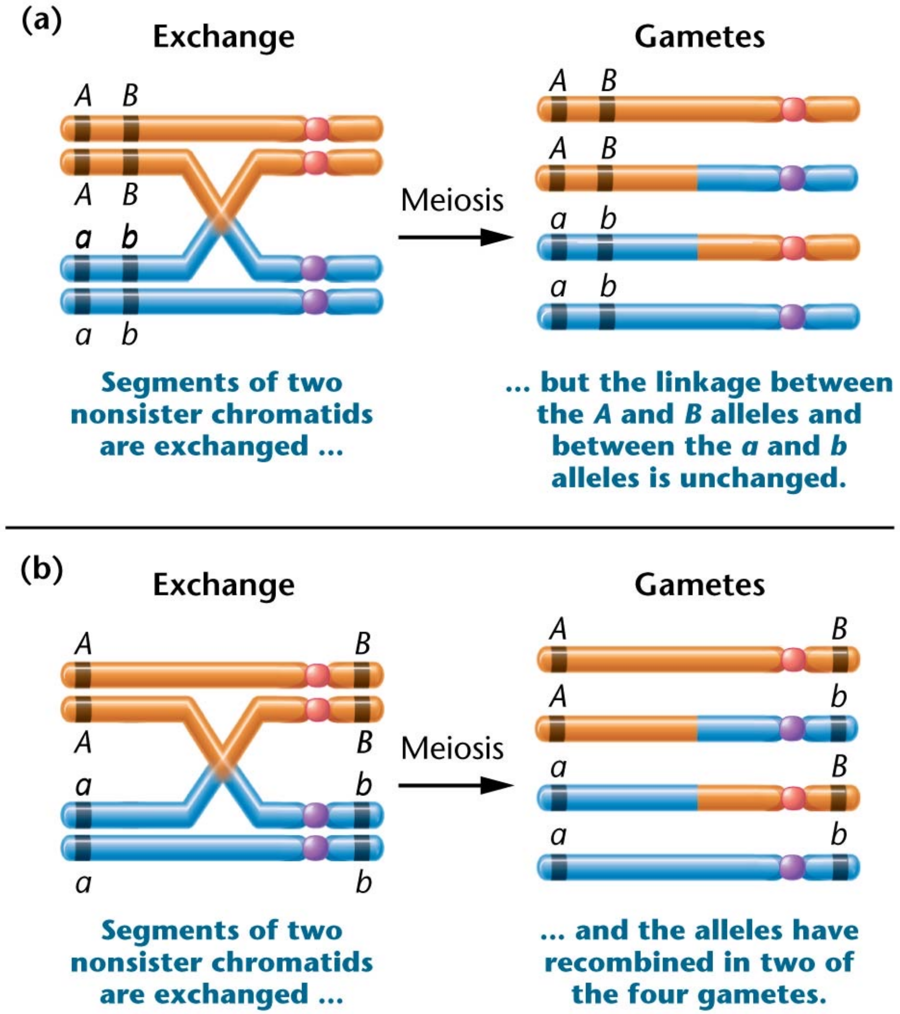
https://quizlet.com/

Crossing Over



Nature Reviews | Genetics

Mauricio 2001

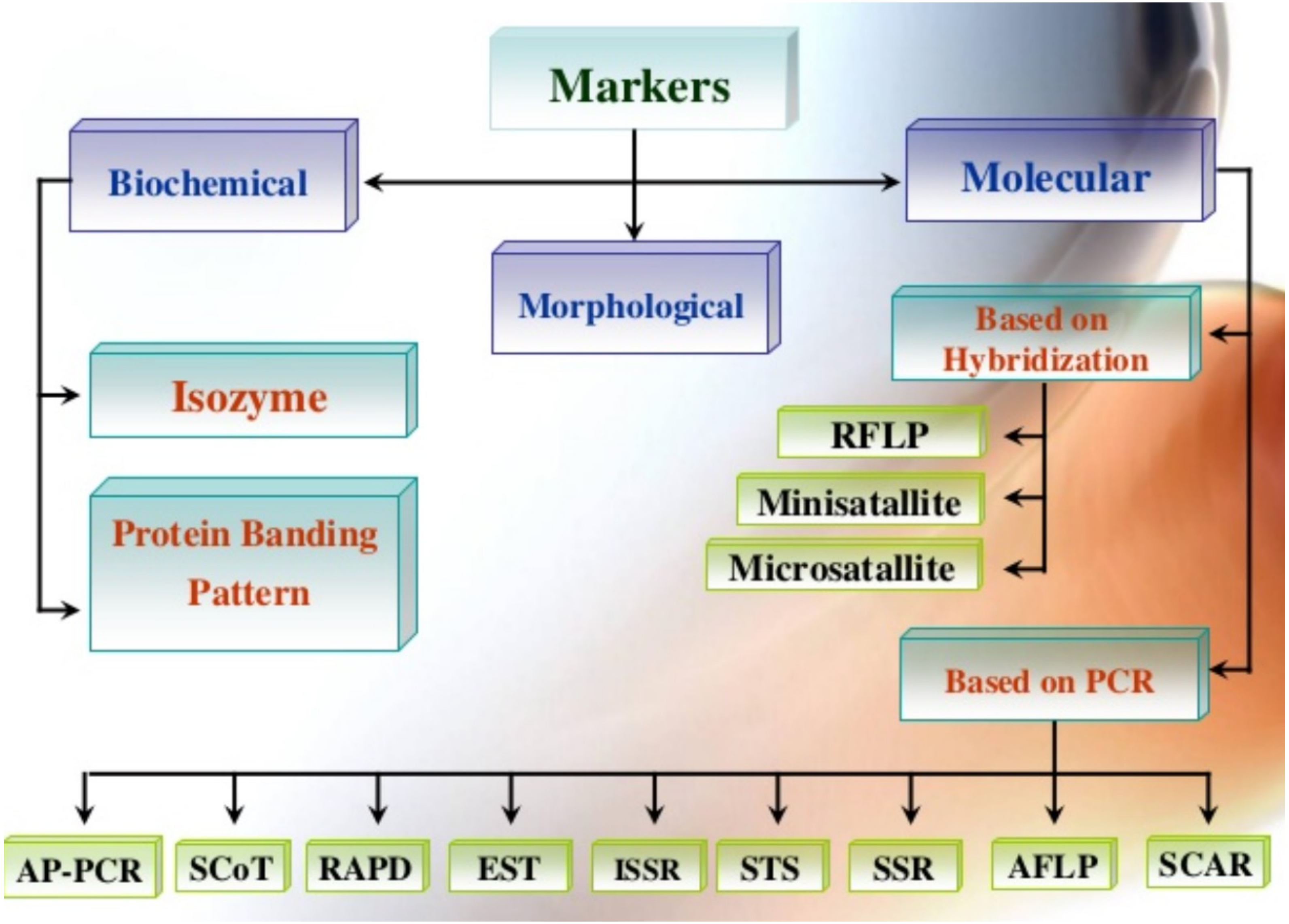


https://quizlet.com/

The molecular basis of genetics:

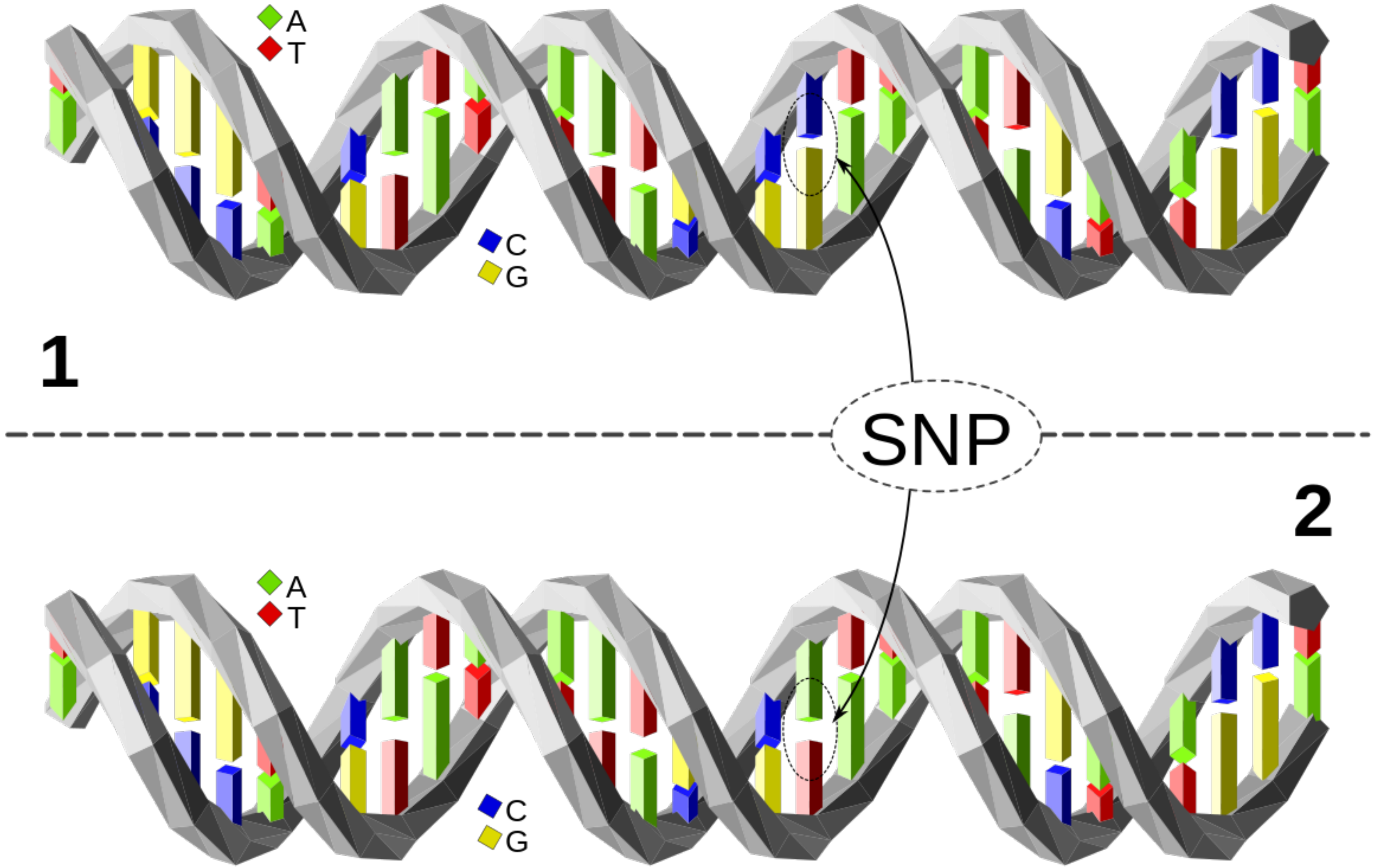
- Genome
- Chromosomes
- Genes (alternative splicing)
- Mitosis and meiosis
- Crossing over
- DNA sequencing
- Genotyping by sequencing (GBS)

greenhousegrower.com



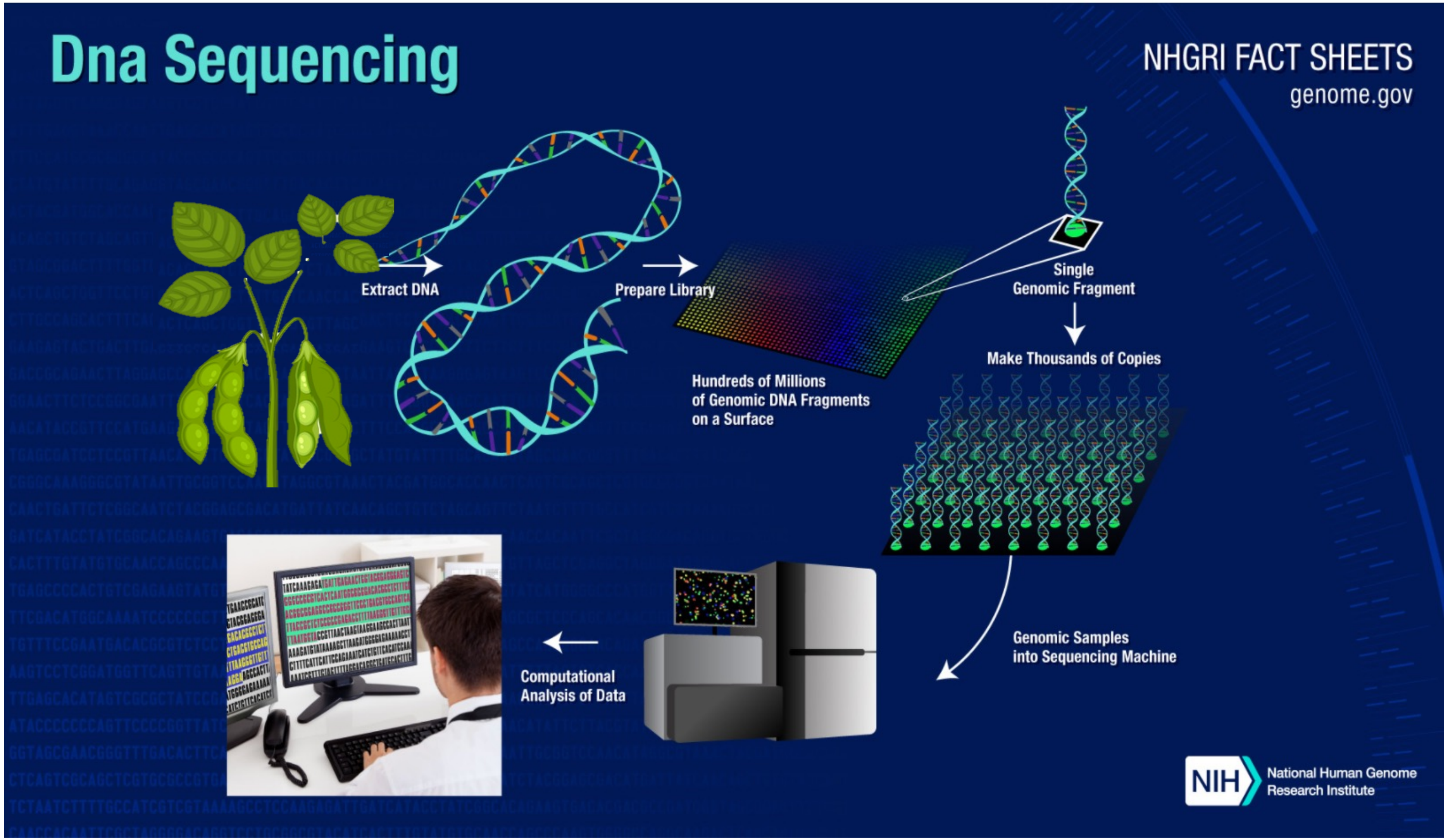
- Markers
  - Biochemical
    - Isozyme
    - Protein Banding Pattern
  - Morphological
  - Molecular
    - Based on Hybridization
      - RFLP
      - Minisatallite
      - Microsatallite
    - Based on PCR
      - AP-PCR
      - SCoT
      - RAPD
      - EST
      - ISSR
      - STS
      - SSR
      - AFLP
      - SCAR

http://www.fao.org

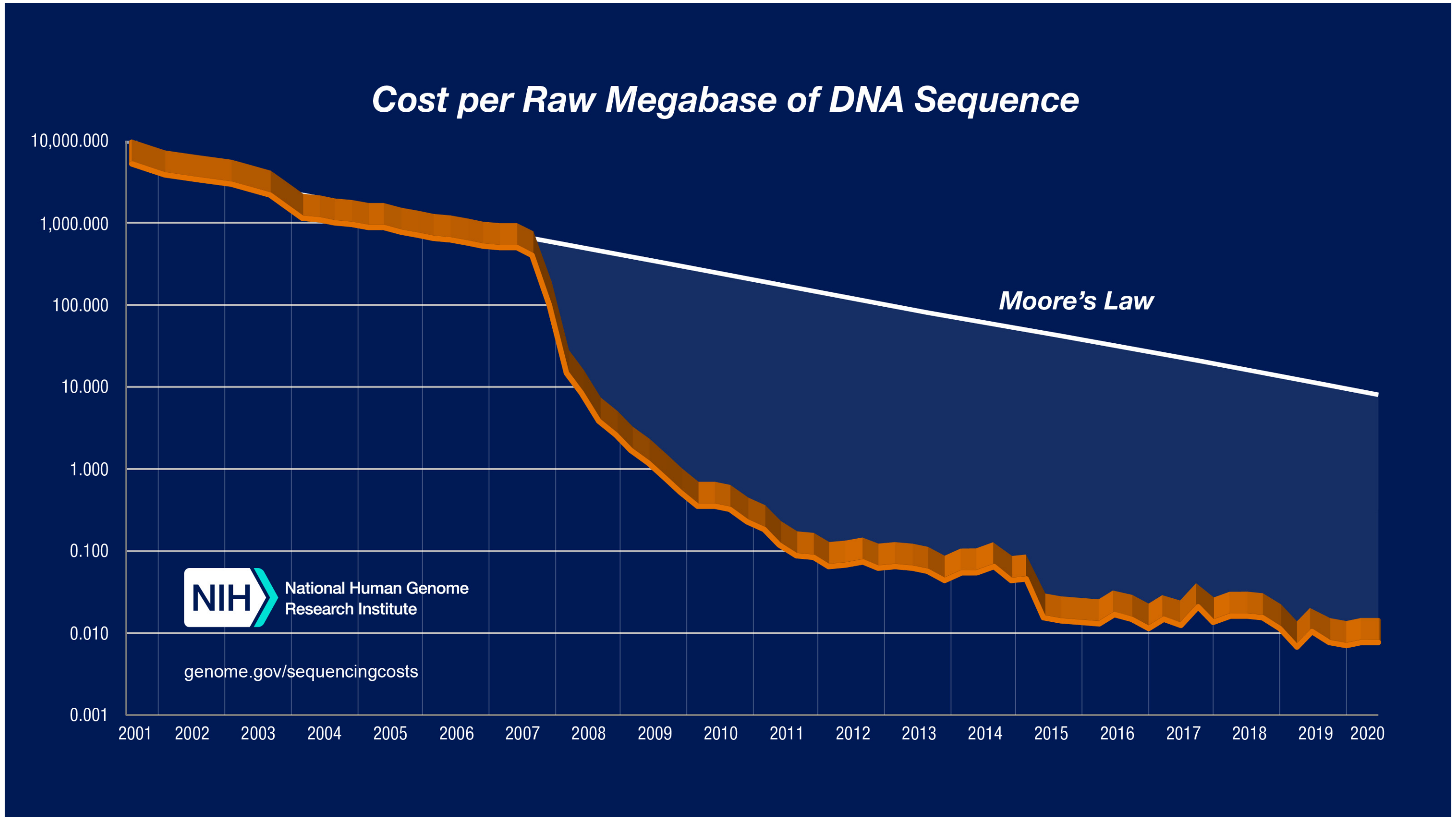


https://en.wikipedia.org/

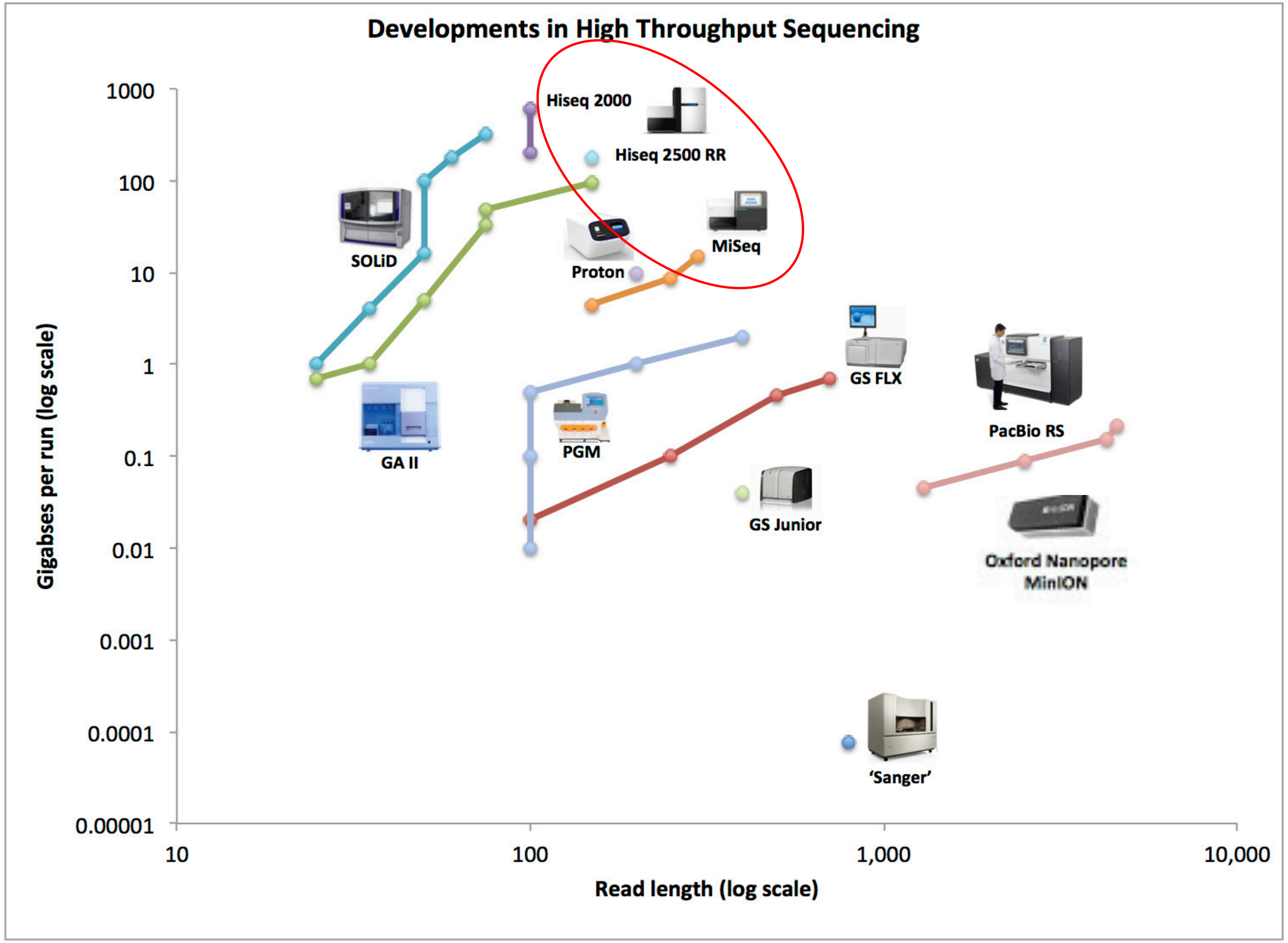
DNA Sequencing



DNA Sequencing



DNA Sequencing

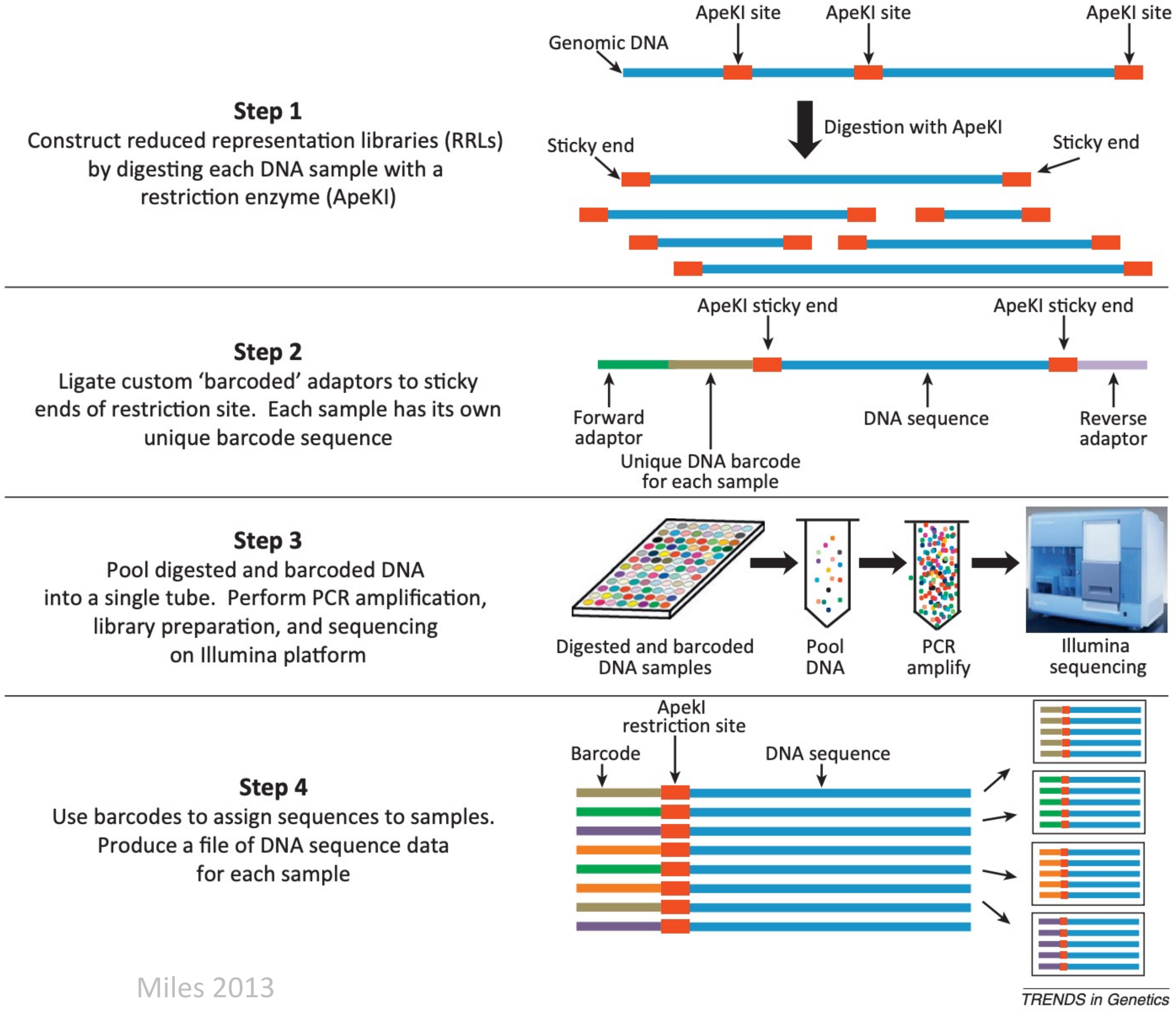


flxlexblog.wordpress.com

Genotyping-by-Sequencing (GBS)

This approach is simple, quick, specific, highly reproducible, and may reach important regions of the genome

Elshire *et al.* 2011



Step 1
Construct reduced representation libraries (RRLs) by digesting each DNA sample with a restriction enzyme (ApeKI)

Step 2
Ligate custom 'barcoded' adaptors to sticky ends of restriction site. Each sample has its own unique barcode sequence

Step 3
Pool digested and barcoded DNA into a single tube. Perform PCR amplification, library preparation, and sequencing on Illumina platform

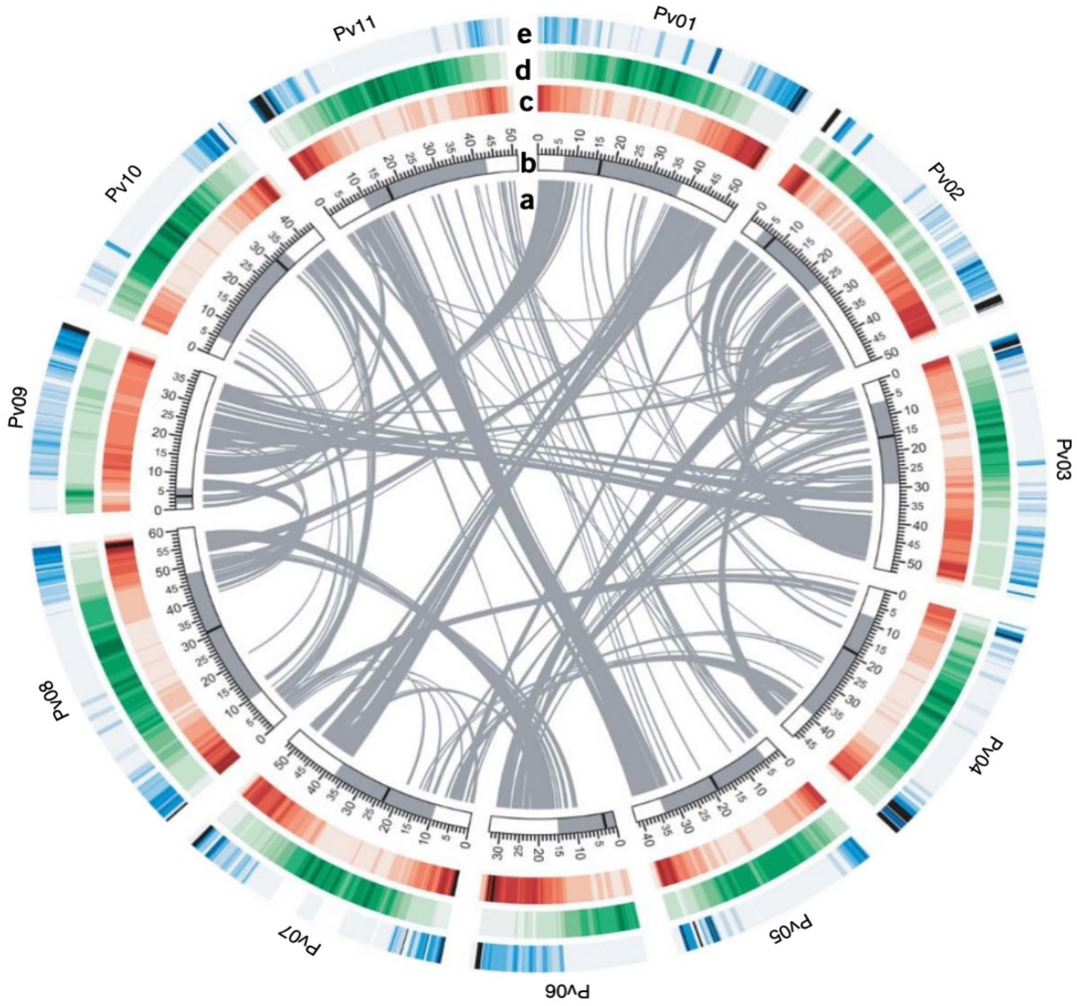
Step 4
Use barcodes to assign sequences to samples. Produce a file of DNA sequence data for each sample

TRENDS in Genetics

Miles 2013

Review

- Big picture of GS
- Genome
- Meiosis
- DNA sequencing
- GBS

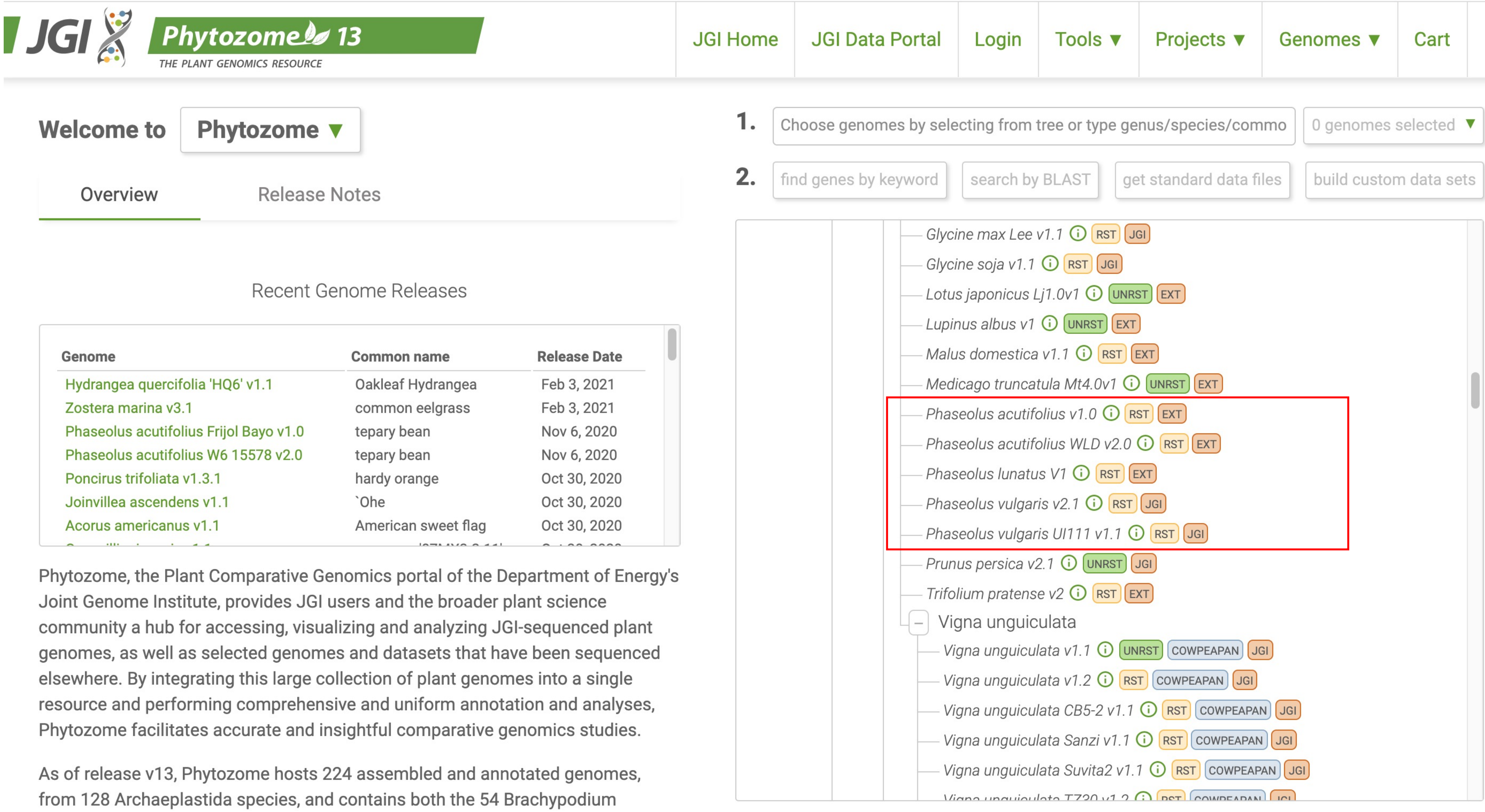


Genome
~537.2 Mb

Loci
27,433 total loci containing 36,995 protein-coding transcripts

Alternative Transcripts
9,562 total alternatively spliced transcripts

As of release v13, Phytozome hosts 224 assembled and annotated genomes!



Recent Genome Releases

Genome	Common name	Release Date
Hydrangea quercifolia 'HQ6' v1.1	Oakleaf Hydrangea	Feb 3, 2021
Zostera marina v3.1	common eelgrass	Feb 3, 2021
Phaseolus acutifolius Frijol Bayo v1.0	tepary bean	Nov 6, 2020
Phaseolus acutifolius W6 15578 v2.0	tepary bean	Nov 6, 2020
Poncirus trifoliata v1.3.1	hardy orange	Oct 30, 2020
Joinvillea ascendens v1.1	`Ohe	Oct 30, 2020
Acorus americanus v1.1	American sweet flag	Oct 30, 2020

Phytozome, the Plant Comparative Genomics portal of the Department of Energy's Joint Genome Institute, provides JGI users and the broader plant science community a hub for accessing, visualizing and analyzing JGI-sequenced plant genomes, as well as selected genomes and datasets that have been sequenced elsewhere. By integrating this large collection of plant genomes into a single resource and performing comprehensive and uniform annotation and analyses, Phytozome facilitates accurate and insightful comparative genomics studies.

As of release v13, Phytozome hosts 224 assembled and annotated genomes, from 128 Archaeplastida species, and contains both the 54 Brachypodium

- *Glycine max Lee v1.1* ⓘ RST JGI
- *Glycine soja v1.1* ⓘ RST JGI
- *Lotus japonicus Lj1.0v1* ⓘ UNRST EXT
- *Lupinus albus v1* ⓘ UNRST EXT
- *Malus domestica v1.1* ⓘ RST EXT
- *Medicago truncatula Mt4.0v1* ⓘ UNRST EXT
- *Phaseolus acutifolius v1.0* ⓘ RST EXT
- *Phaseolus acutifolius WLD v2.0* ⓘ RST EXT
- *Phaseolus lunatus V1* ⓘ RST EXT
- *Phaseolus vulgaris v2.1* ⓘ RST JGI
- *Phaseolus vulgaris UI111 v1.1* ⓘ RST JGI
- *Prunus persica v2.1* ⓘ UNRST JGI
- *Trifolium pratense v2* ⓘ RST EXT
- Vigna unguiculata
  - *Vigna unguiculata v1.1* ⓘ UNRST COWPEAPAN JGI
  - *Vigna unguiculata v1.2* ⓘ RST COWPEAPAN JGI
  - *Vigna unguiculata CB5-2 v1.1* ⓘ RST COWPEAPAN JGI
  - *Vigna unguiculata Sanzi v1.1* ⓘ RST COWPEAPAN JGI
  - *Vigna unguiculata Suvita2 v1.1* ⓘ RST COWPEAPAN JGI

https://phytozome-next.jgi.doe.gov/