

Where plants rank

Based on **Arumuganathan and Earle, 1991**

- The following table is a partial listing. Non-plant values have been added to it.
- 1 pg = 965 million base pairs

Species	Common name	Family	DNA Mbp/1C	DNA pg/2C
<i>Escherichia coli</i>			4.6	0.04
<i>Genlisea tuberosa</i>	Corkscrew plant	Lentibulariaceae	61	0.13
<i>Drosophila melanogaster</i>	Fruit fly		130	0.24
<i>Arabidopsis thaliana</i>	Mouse-ear cress	Crucifereae	145	0.30
<i>Oryza sativa</i>	Rice	Gramineae	415	0.86
<i>Phaseolus vulgaris</i>	Bean	Leguminoseae	637	1.32
<i>Musca domestica</i>	House fly			1.78
<i>Glycine max</i>	Soybean	Leguminoseae	1115	2.31
<i>Zea mays</i>	Maize	Gramineae	2292	4.75
<i>Homo sapiens</i>	Human			6.00
<i>Pisum sativum</i>	Pea	Leguminoseae	3947	8.18
<i>Hordeum vulgare</i>	Barley	Gramineae	4873	10.10
<i>Gryllus domestica</i>	Crickett			12.00
<i>Bufo bufo</i>	Toad			12.00
<i>Allium cepa</i>	Onion	Amaryllidaceae	15,290	31.69
<i>Triticum aestivum</i>	Wheat	Gramineae	15,966	33.09
<i>Amphiuma means</i>	Congo eel			170.00
<i>Fritillaria platyptera</i> +++		Liliaceae	84,150	174.40
<i>Paris japonica</i>	Japanese canopy plant	Melanthiaceae	149,000	304.46

+++ True diploid ($2n = 2x = 24$) with largest genome

C-value paradox

Thomas, 1971

Angiosperm DNA C-values Database

Pellicer & Leitch, 2020

- Plant DNA C values can be found at <https://cvalues.science.kew.org/>
- 1 pg = 978 million base pairs (value from Delezel et al, 2003)

Plant DNA C-values Database

Release 7.1, April 2019. Leitch IJ, Johnston E, Pellicer J, Hidalgo O, Bennett MD

<https://cvalues.science.kew.org/>

All Plants



Angiosperm



Gymnosperm



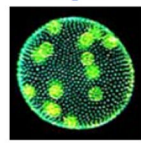
Pteridophyte



Bryophyte

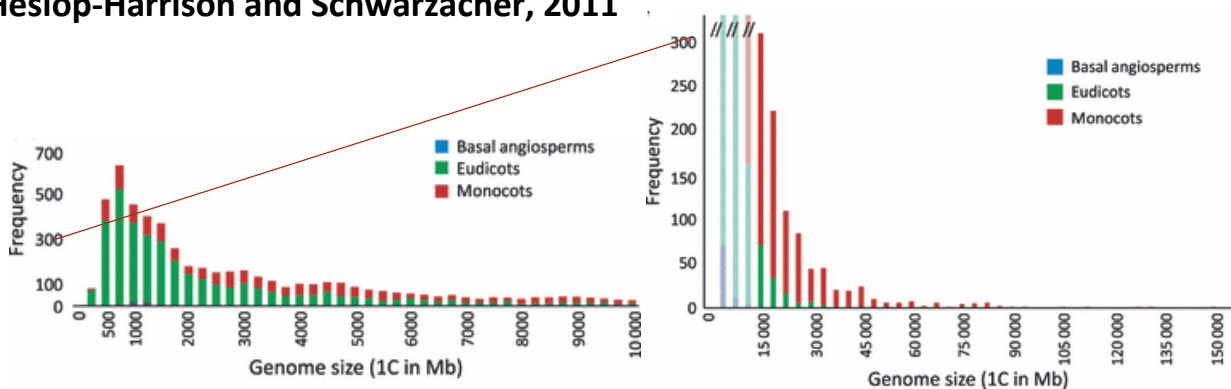


Algae



Range in angiosperm DNA content

Heslop-Harrison and Schwarzacher, 2011

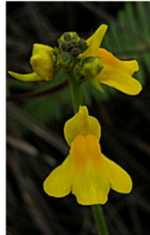


Smallest genome size

Heslop-Harrison and Schwarzacher, 2011
Fleischmann et al, 2014

Genlisea aurea

DNA Mbp/1C = 63
DNA pg/2C = 0.13



Genlisea tuberosa

DNA Mbp/1C = 61
DNA pg/2C = 0.126



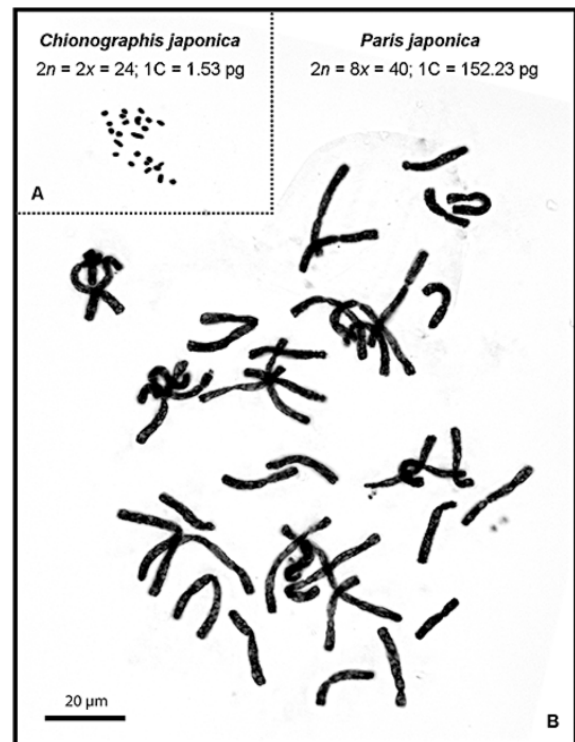
<http://cpphotofinder.com/genlisea-aurea-516.html>

Largest plant genome

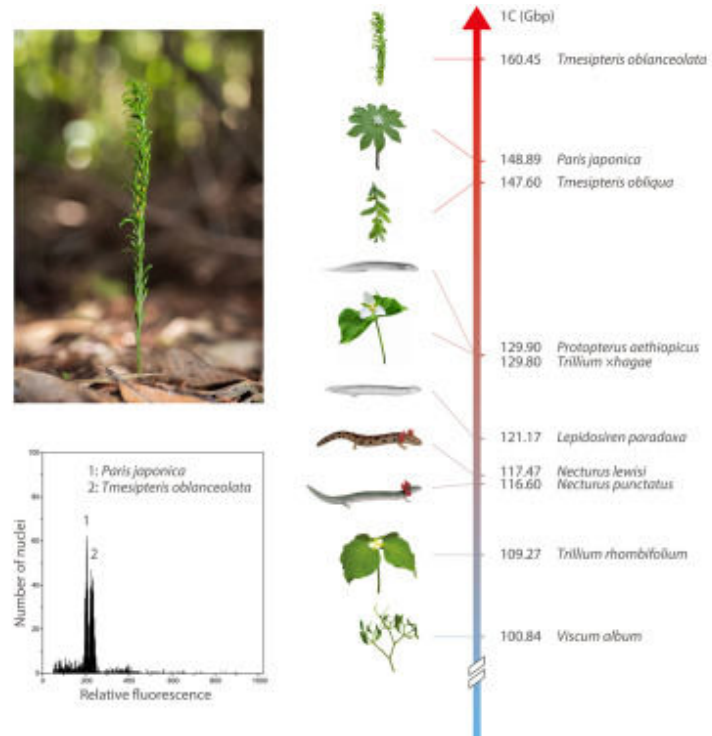
Pellicer et al., 2010



Paris japonica, $2n = 40$, Wikipedia

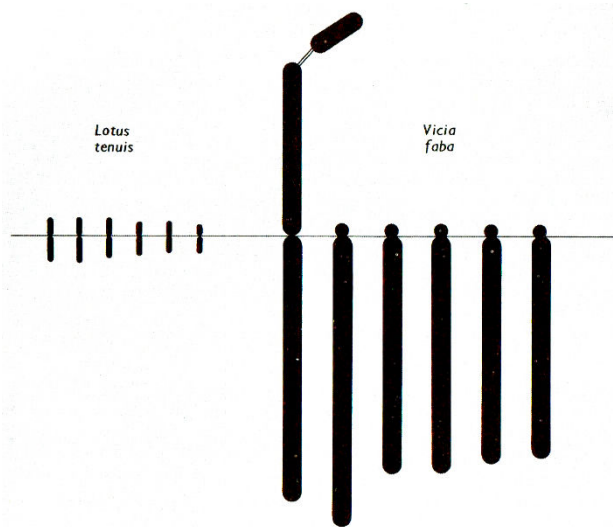


Fernández et al, 2024 (<https://doi.org/10.1016/j.isci.2024.109889>)



Changes in DNA amount & chromosome size

Review by Walbot & Cullis, 1985

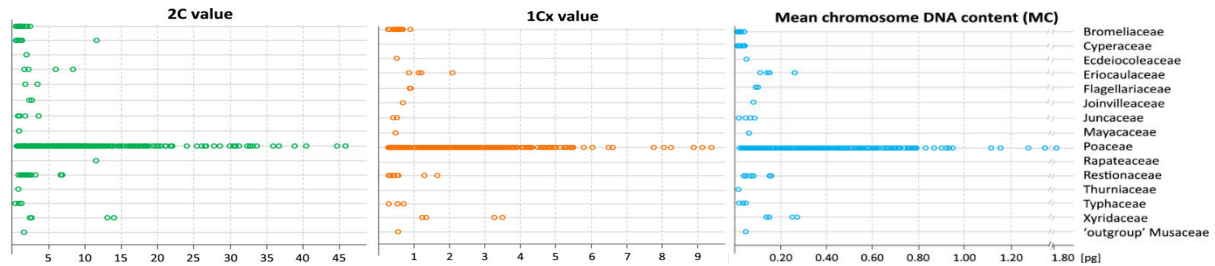


Variation in chromosome size in 2 leguminous species with the same chromosome number. **Stebbins 1971**

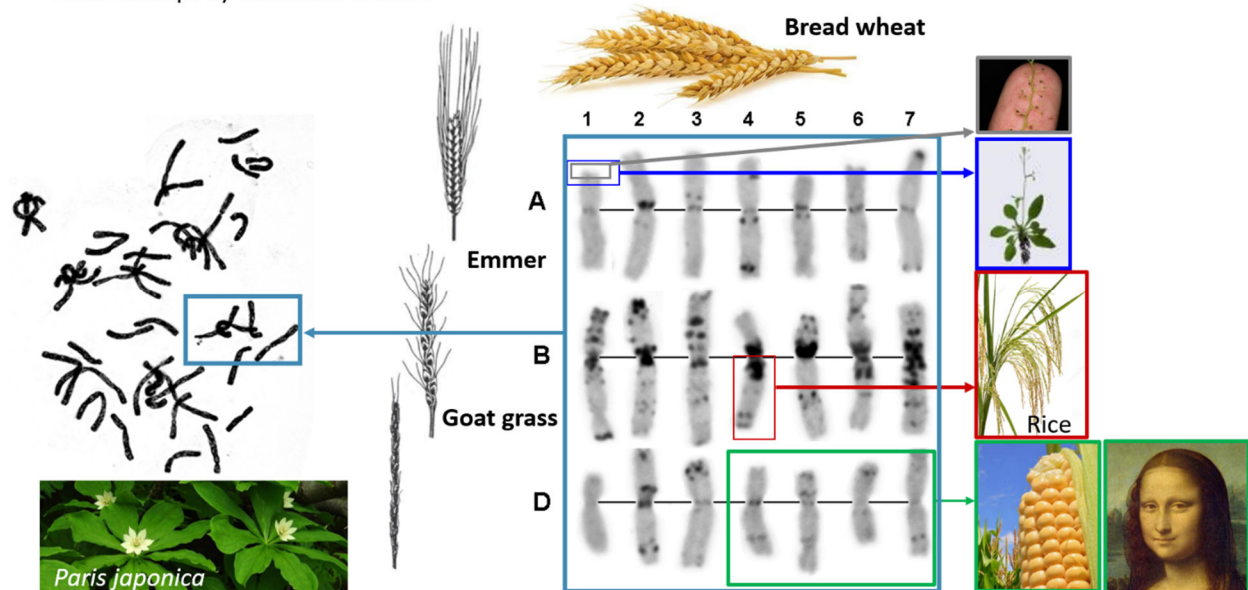
Family	Species	n	Chromosome length (μm)
Ranunculaceae	<i>Isopyrum fumarioides</i>	7	1.3
	<i>Anemone hepatica</i>	7	7.0
Oxalidaceae	<i>Oxalis cuneata</i>	6	1.5
	<i>Oxalis dispar</i>	6	15.1
Leguminosae	<i>Lotus tenuis</i>	6	1.8
	<i>Vicia faba</i>	6	14.8
Droseraceae	<i>Drosera rotundifolia</i>	10	0.8
	<i>Drosophyllum lusitanicum</i>	6	14.0
Compositae	<i>Agroseris heterophylla</i>	9	2.4
	<i>Chaetadelpha wheeleri</i>	9	6.4
Liliaceae	<i>Tofieldia nuda</i>	15	1.3
	<i>Lilium pardalinum</i>	12	20.0
Gramineae	<i>Chloris barbata</i>	10	1.5
	<i>Secale cereale</i>	7	7.2

Genome size variation in Poales vs WGDs

Winterfeld et al, 2025

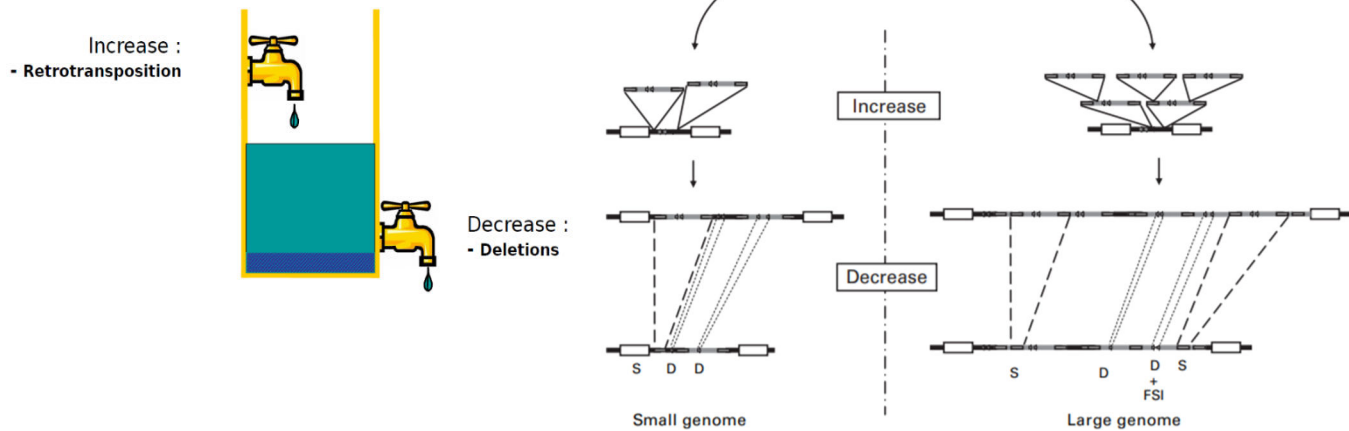


Slide concept by Catherine Feuillet



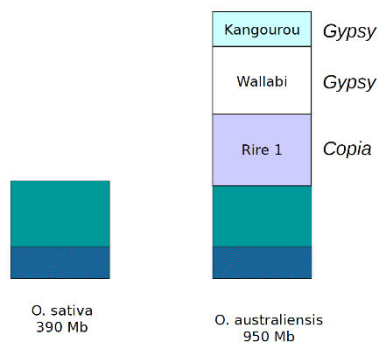
The increase/decrease model

Vitte and Panaud, 2005

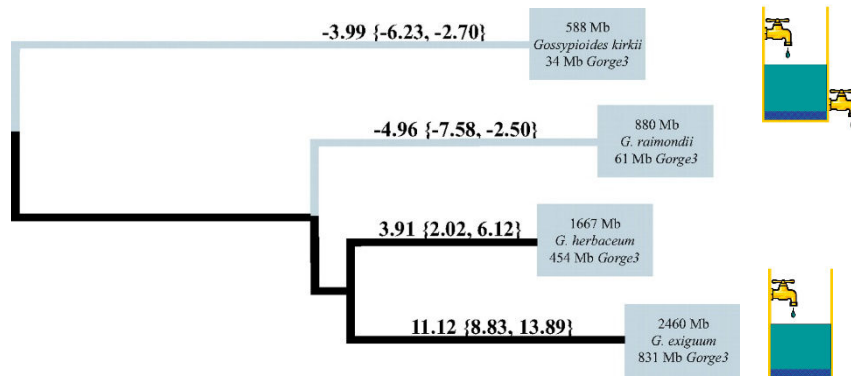


Piegu et al, 2006 (graphics by O Panaud)

- Doubling of rice EE genome size

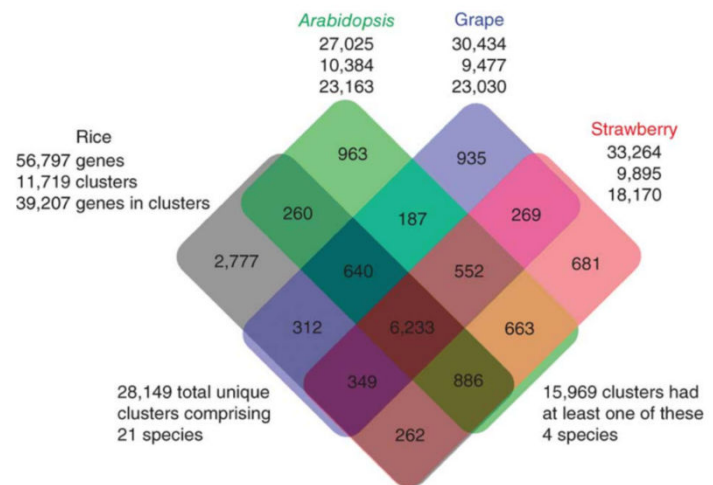
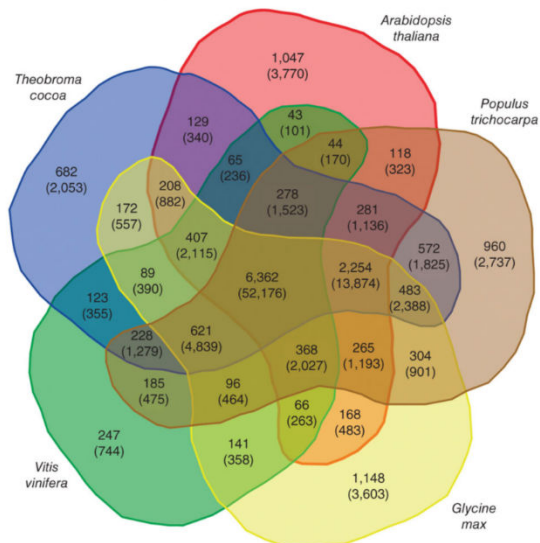


Hawkins et al., 2009



Number of genes to make an angiosperm?

Argout et al, 2011; Shulaev et al, 2011



Number of genes per monoploid genome

Goldberg, 1986



Edwards et al, 2017

Gibson and Sommerville, 1993



Arabidopsis sequence

Wang et al, 2022

Sequenced angiosperm genomes

- CoGepedia - https://genomeevolution.org/wiki/index.php/Sequenced_plant_genomes
- Wikipedia - https://en.wikipedia.org/wiki/List_of_sequenced_plant_genomes
 - Rosids
 - 18,397 marula tree – 73,013 for poplar
 - Asterids
 - 14,474 for milkweed – 52,232 for sunflower
 - Grasses
 - 25,225 for moso bamboo - 107,891 for wheat
 - Other monocots
 - 19,623 for duckweed – 52,342 for *Daemonorops jenkinsiana*

Besides protein-coding genes

Cacao - Argout et al, 2011

- 28,798 protein-coding genes
- 6 rRNA genes (many missing due to sequencing method!)
- 473 tRNA genes
- 83 miRNA genes
- 67,575 transposable elements (25.7% of assembly)



Strawberry - Shulaev et al, 2011

- 34,809 protein-coding genes
- TE's = 22% of genome
- 569 transfer RNAs (tRNAs)
- 177 ribosomal RNA (rRNA)
- 111 spliceosomal RNAs
- 168 small nucleolar RNAs
- 76 micro RNAs
- 24 other RNAs



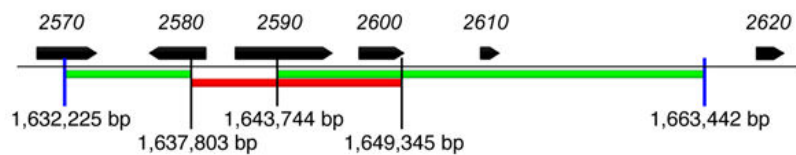
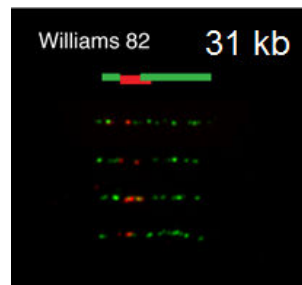
Bladderwort – Ibarra-Laclette et al, 2013

- 28,500 protein-coding genes – but genome is only 77 Mbp
 - Shorter promoters and introns; fewer introns
- Only 3% of DNA is repetitive
- Only 579 transposable elements
 - 375 are retroelements
 - 95 intact (and supposedly functional)
- All miRNA genes are there

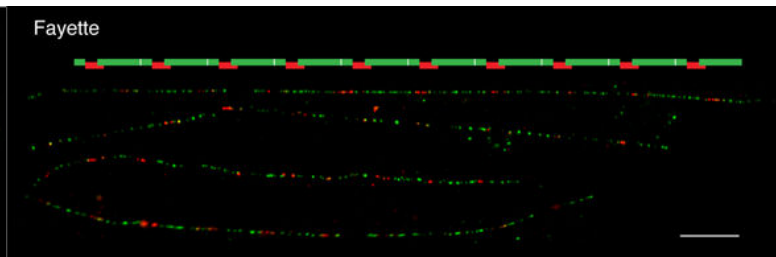
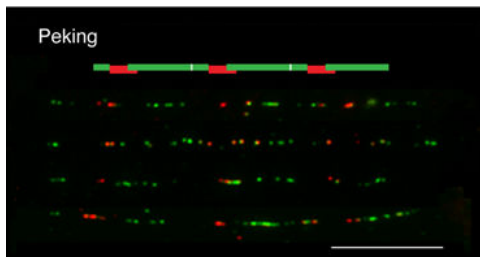


Copy Number Variation (CNV)

Eg, Cyst nematode resistance in soybean
Cook et al, 2012

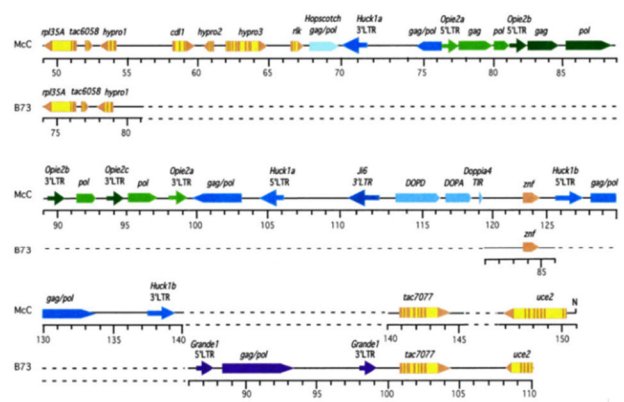
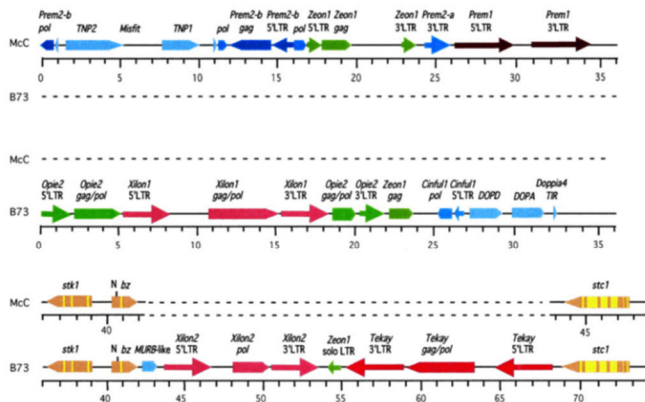


Presence



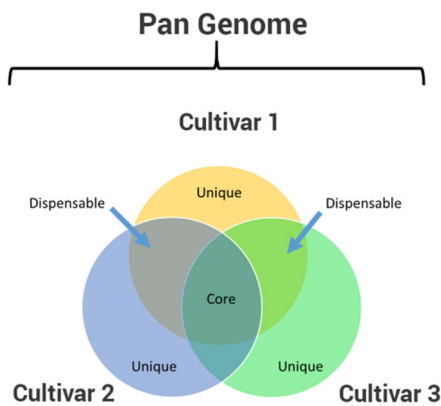
Absence Variation (PAV)

Fu & Dooner, 2002



The pangenome concept

Review by Della Coletta et al, 2021



- Pan genome
- Core genome
- Dispensable genome

<http://www.10wheatgenomes.com>

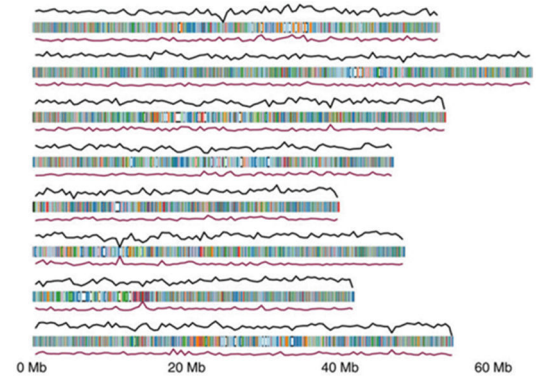
PAV in *Brassica oleracea*

Agnieska et al, 2016



N=10

- Broccoli
- Brussels sprout
- Cabbage1
- Cabbage2
- Cauliflower1
- Cauliflower2
- Kale
- Kohlrabi
- Macrocarpa



- 81.3% of genes always present (49,895) → Core genome
 - 18.7% are in variable numbers (11,484) → Dispensable, variable, or shell genome
 - 02.2% are present in only 1 line (1,322)
- } Pan Genome

PAV in *Glycine*

Li et al, 2010

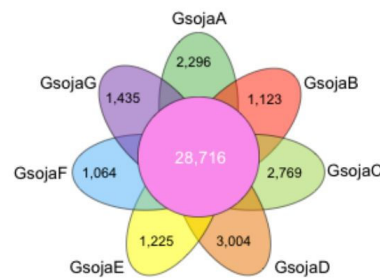


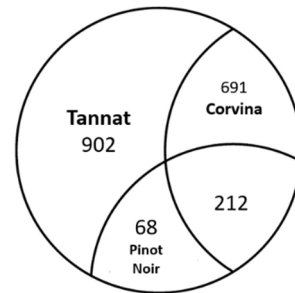
Figure 1. Gene families unique to each genotype

PAV in grapevine

Da Silva et al, 2013

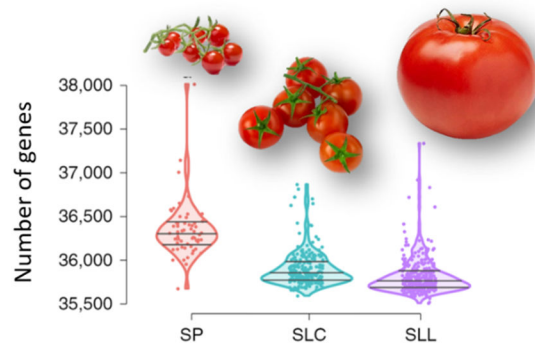
G. soja *G. max*

“Aromas and flavors of black berry custard tart, chocolate gelato, and praline with a fruity body and a long cranberry chutney and floral honey finish”



PAV in tomato

Gao et al, 2013



PAV in wheat

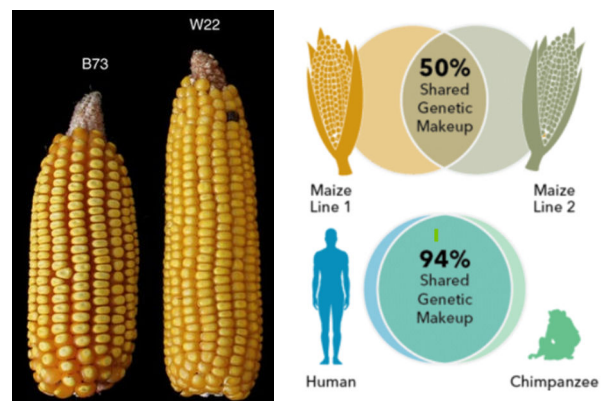
Montenegro et al, 2017

regulation of cellular metabolic process
 response to external stimulus
 cellular response to acid chemical
 regulation of meristem growth
 response to UV
 membrane organization
 immune system process
 protein phosphorylation
 innate immune response
 single-organism process
 signal transduction
 response to acid chemical
 ion transport
 response to stress
 response to organic substance
response to oxygen-containing compound
 cellular response to stimulus
 defense response to other organism
 defense response
 fucosylation
 cellular response to stress
 xenobiotic catabolic process
 butyrate metabolic process
 protein metabolic process
 immune response-regulating signaling pat...
 cellular component organization
 stomatal complex morphogenesis
 cellular response to organic substance
 cellular response to oxygen-containing c...
 defense response signaling pathway, rest...



PAV in maize

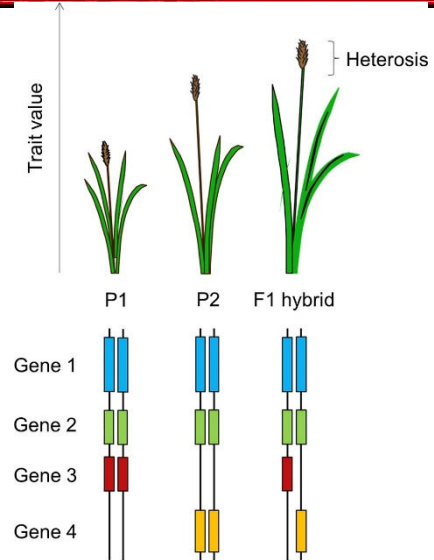
Springer et al, 2018



<https://www.pacb.com/blog/sequencing101pangenome>

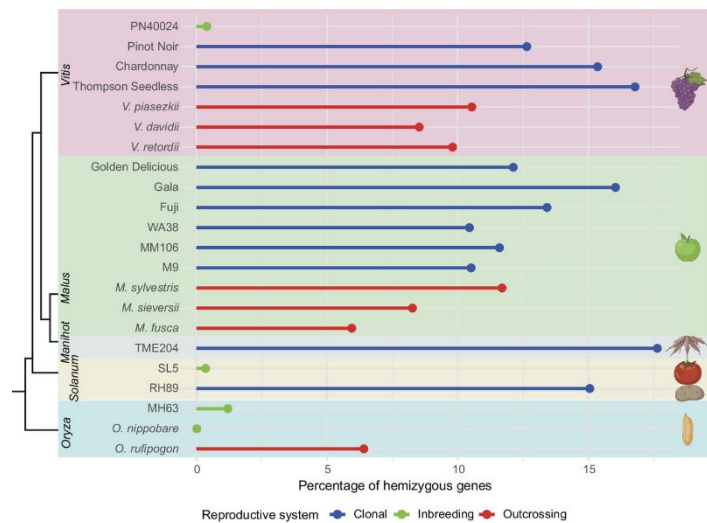
Pan genome hypothesis for heterosis

Tao et al, 2019



Hemizyosity

Peng et al, 2018



Trait accumulation in conventional plant breeding

IRRI 1980 Annual Report

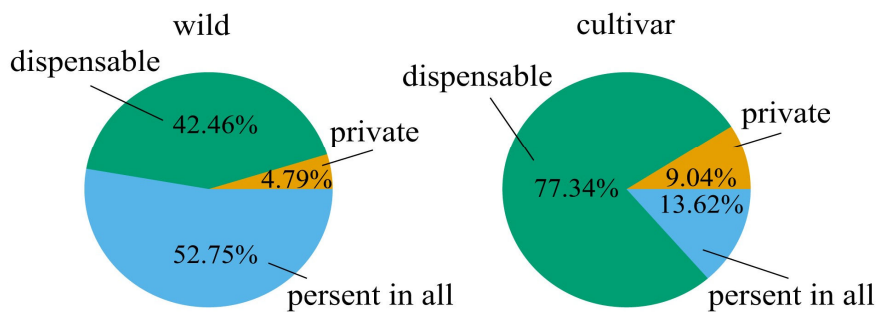
	IR8	IR42
Blast	MR	R
Bacterial Blight	S	MR
Grassy Stunt	S	R
Tungro	S	R
Ragged Stunt	S	R
Green Leafhopper	R	MR
Brown Planthopper	S	R
Stem Borer	MS	MR

1966/77

Susceptible; Resistant



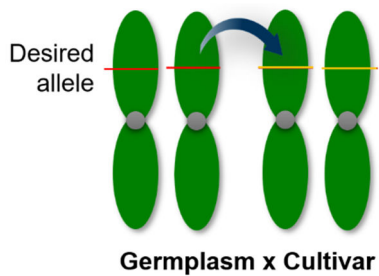
Long et al, 2024



Reevaluating the backcross

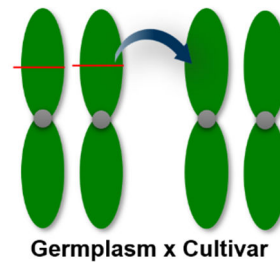
Traditional view

- Backcrossing replaces an existing allele with a desired allele



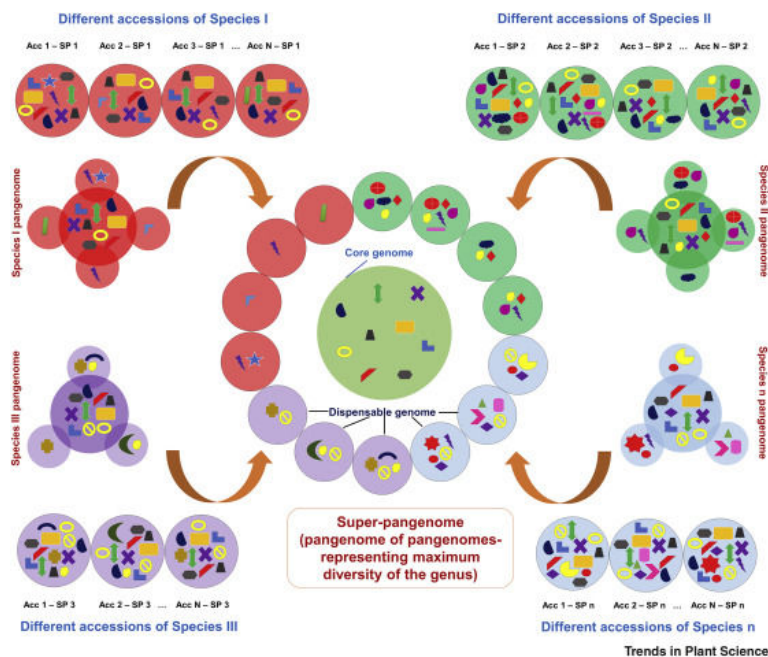
Emerging view

- Besides allele replacement, backcrossing can introduce a PAV gene
- Can also eliminate genes that were there



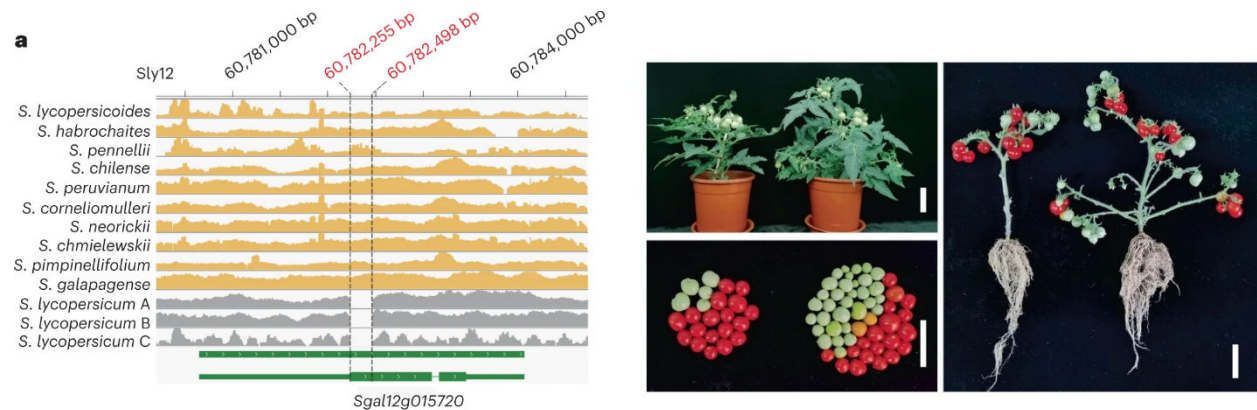
Super pan genome

Khan et al, 2020



Using a super pangenome

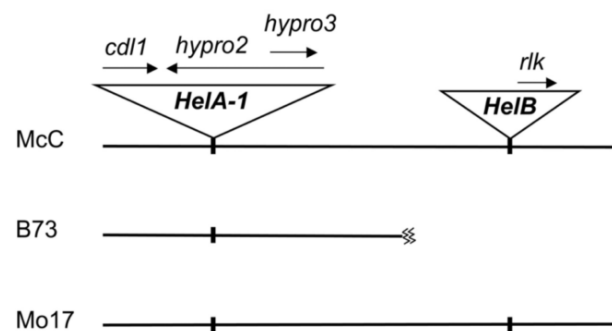
Li et al, 2023 (<https://www.nature.com/articles/s41588-023-01340-y>)



Origins of PAV

Helitrons

Lai et al., 2005



Fractionation/differential gene loss

Modified from Vision, 2005

Town et al, 2006; Eichten et al, 2011; Schnable et al, 2011

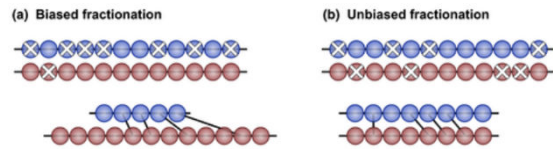
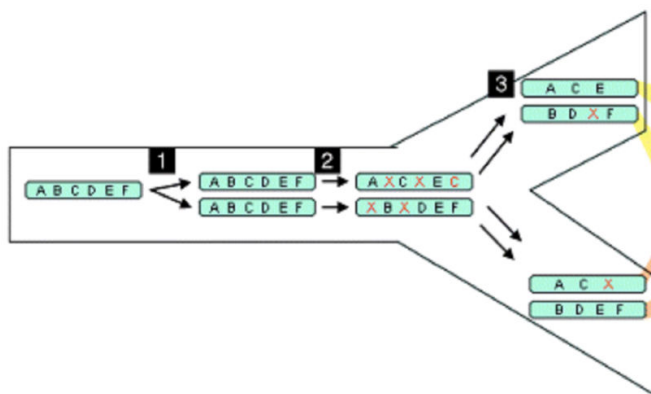


Figure 2. Bird et al, 2018 (Edger lab)



Gene loss through intra-strand recombination

Woodhouse et al., 2010

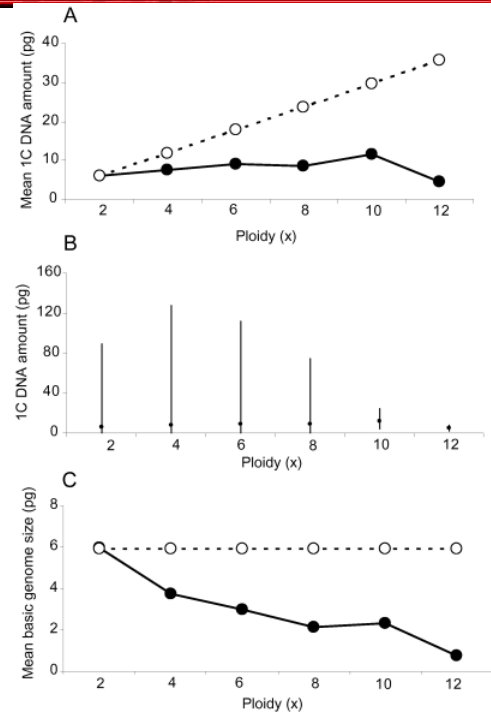


Creation of new genes

Fan et al., 2008

Genome downsizing

Leitch & Bennett, 2004

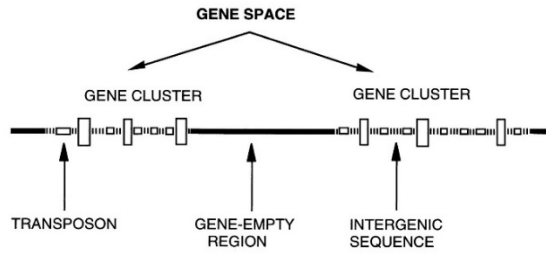


Genome sequence summary & caveats

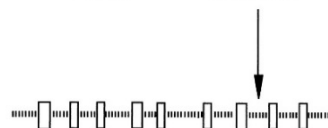
Gene space in the plant genome

Barakat, Matassi, & Bernardi, 1998

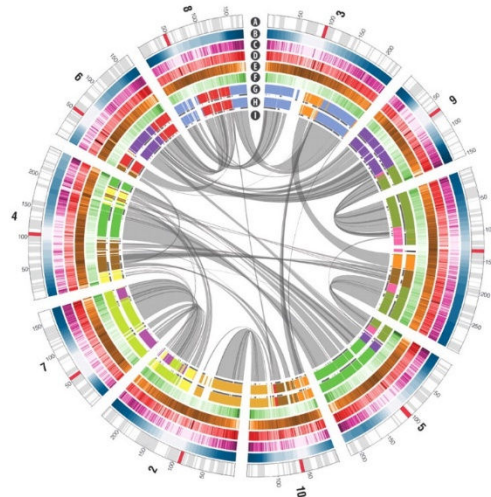
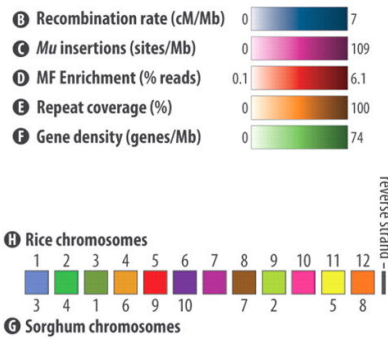
Gramineae (415-5,300 Mb)



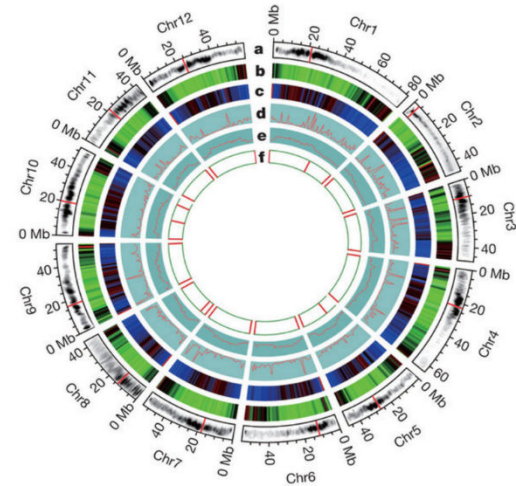
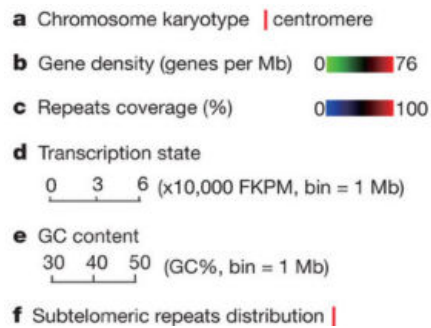
Arabidopsis (120 Mb)



Schnable et al, 2009



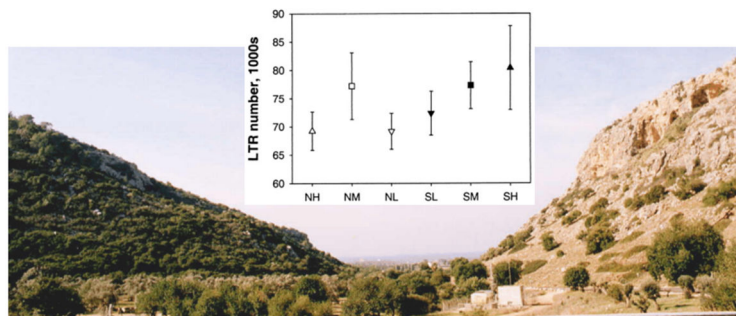
The Potato Genome Sequencing Consortium, 2011



Adaptive Value of DNA Content

Environmental effects on genome size

Kalendar et al, 2000



Cell size vs DNA content

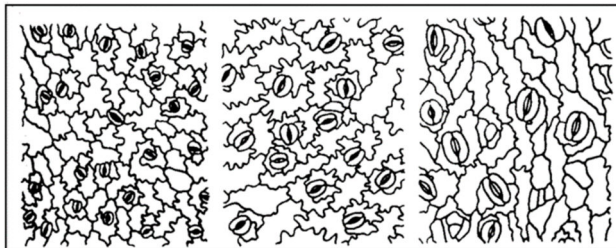
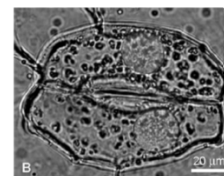
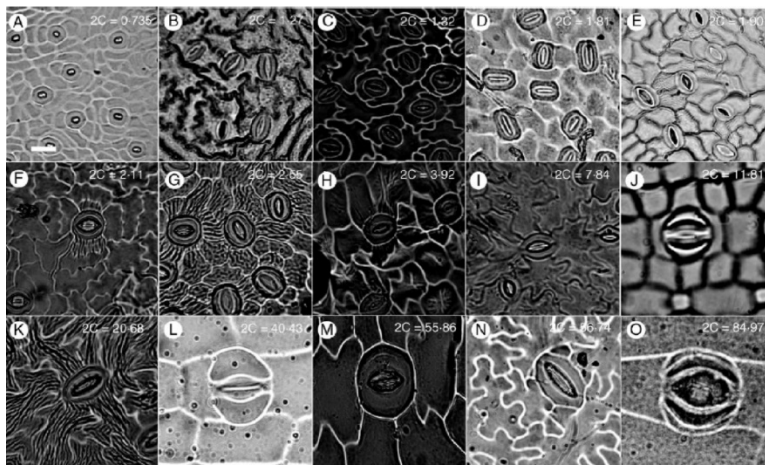


Figure 3. Epidermal cells of 2x, 4x and 8x Nicotiana. Greenleaf, 1938

Knight & Beaulieu, 2008; Pellicer et al, 2010

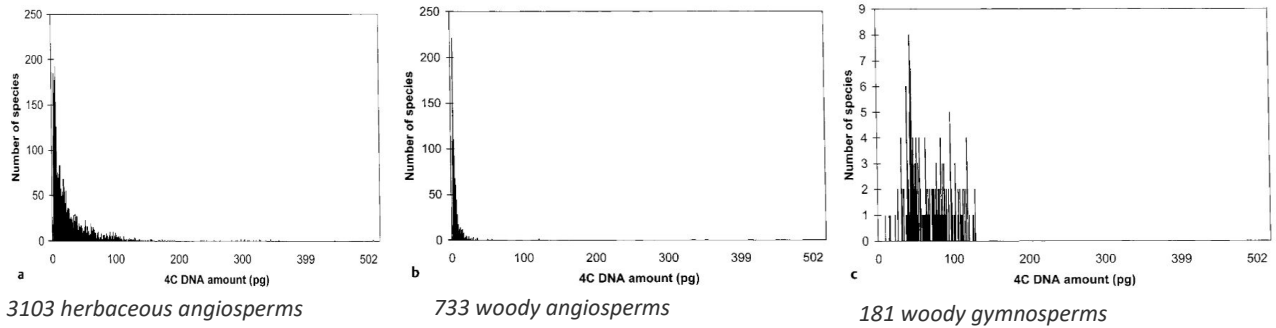


Paris japonica
2C = 304.46

White scale bar in (A) = 20 μ m. (A) *Citrus aurantifolia*, (B) *Rosa acicularis*, (C) *Origanum vulgare*, (D) *Quercus robur*, (E) *Fraxinus excelsior*, (F) *Ligustrum vulgare*, (G) *Platanus orientalis*, (H) *Cypripedium irapeanum*, (I) *Capsicum annuum*, (J) *Zingiber officinale*, (K) *Sambucus racemosa*, (L) *Tradescantia paludosa*, (M) *Cypripedium formosanum*, (N) *Paeonia clusii*, (O) *Tradescantia virginiana*.

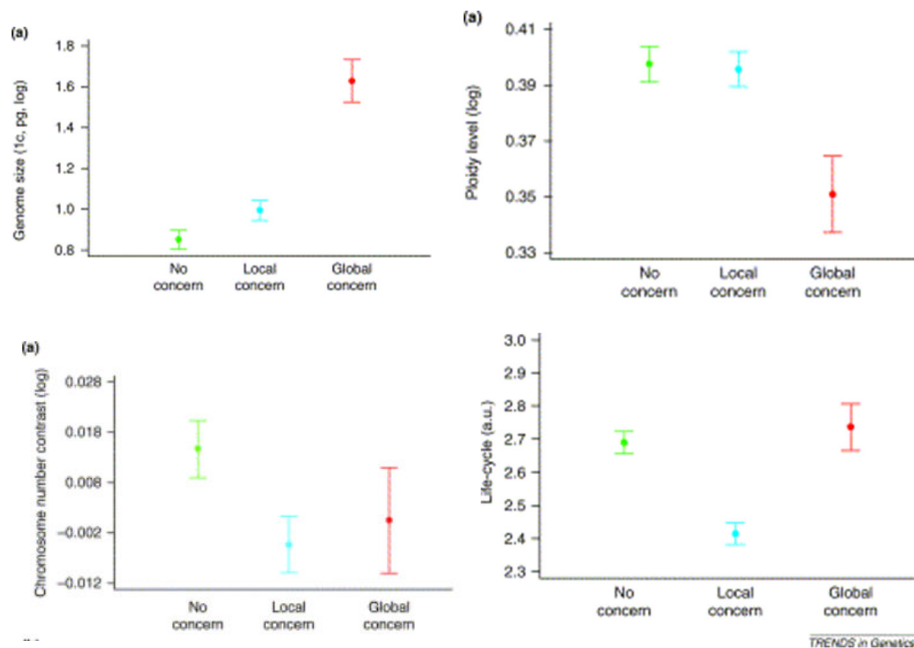
Constraints on cell size

Ohri, 2008



DNA content vs fitness

Vinogradov 2003

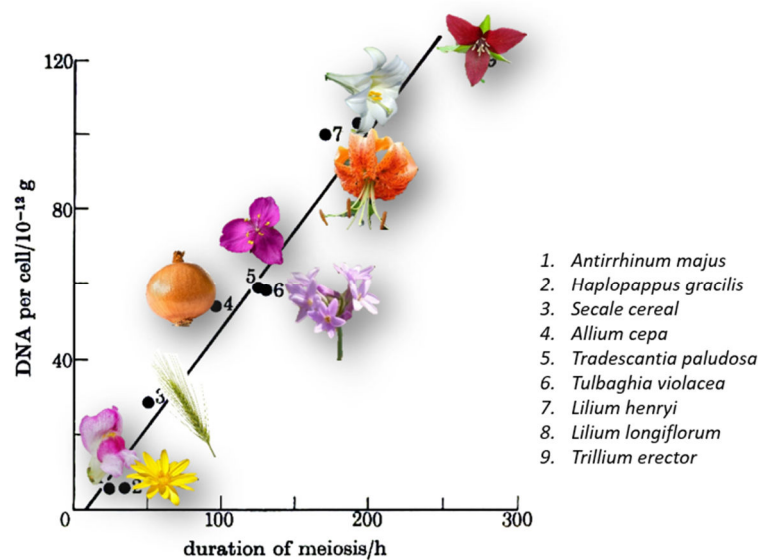
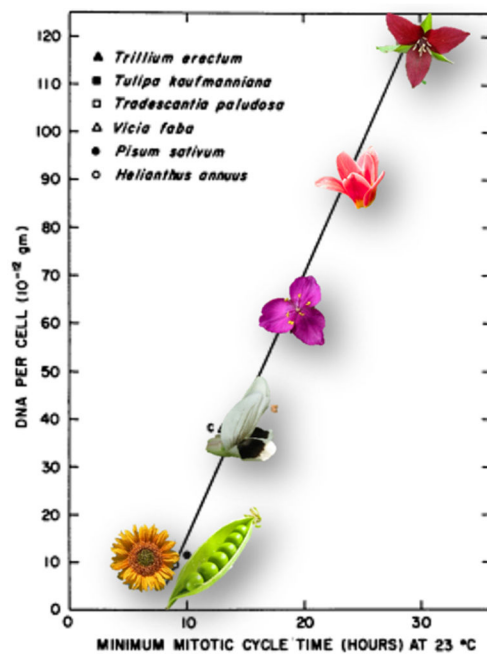


The nucleotype

Bennett, 1972

DNA content vs cell cycle time

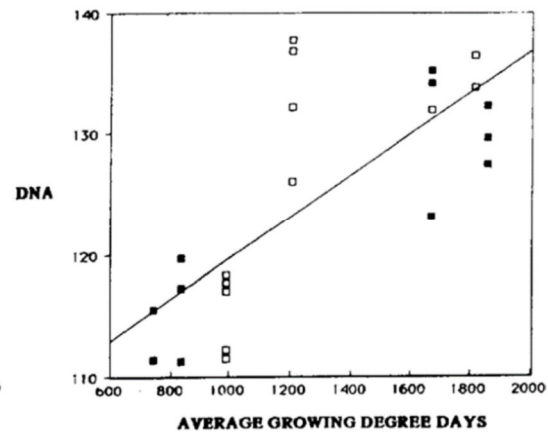
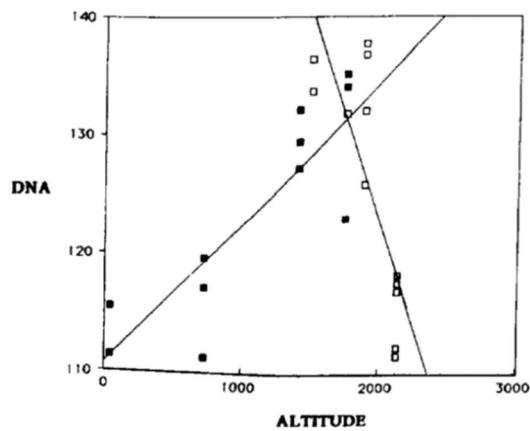
Van't Hopf and Sparrow, 1963; Bennett, 1971



DNA content vs growth

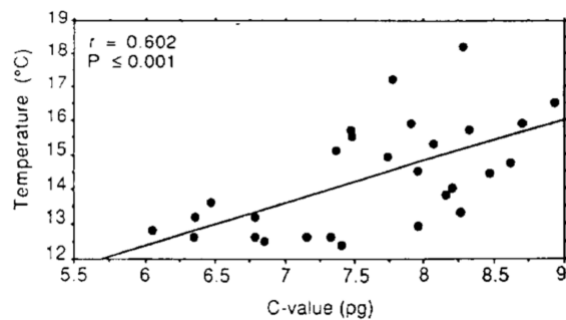
Corn vs altitude

Bullock and Rayburn, 1991; McMurphy and Rayburn, 1992



Tall fescue in Italy

Ceccarelli et al, 1992



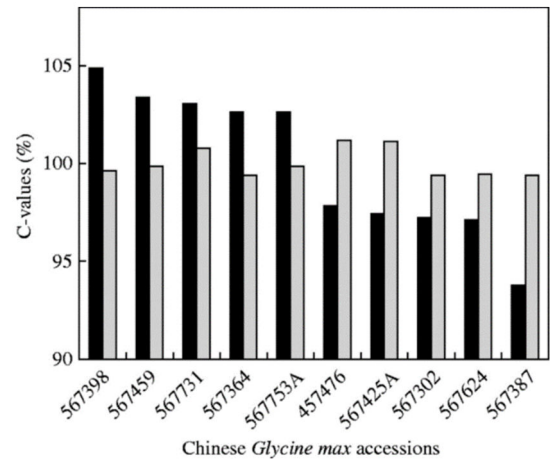
Knight et al., 2005

Variable	# Studies Showing		
	+ Correlation to 2C DNA Content	- Correlation to 2C DNA Content	Non-linear or Non-significant Correlation
Altitude	8	9	7
Latitude	5	8	6
Temperature	4	9	2
Precipitation	4	3	1
Seed Mass	11	0	1
Generation Time	12	3	4
Relative Growth Rate	5	4	2

Measurement errors

Greilhuber 2005

Figure 4. Greilhuber 2005 data in grey, superimposed on Rayburn data (black)



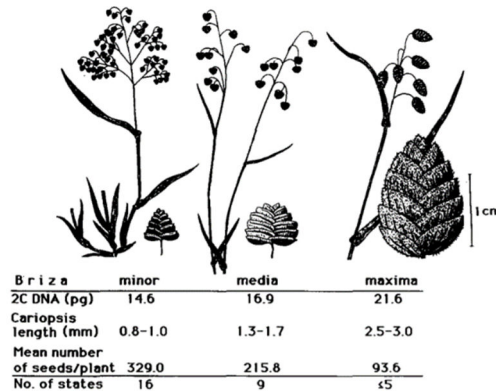
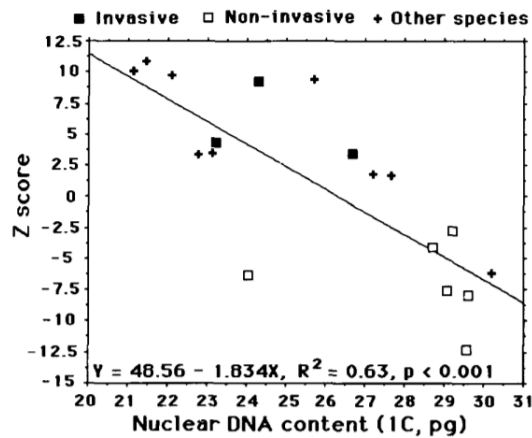
Rayburn et al, 2004

Line	# Plants	Relative mean	Standard deviation
PI 266085	22	2.847	0.093
PI 227324	22	2.825	0.064
PI 437088	22	2.814	0.071
PI 253666	22	2.814	0.076

DNA content vs invasiveness

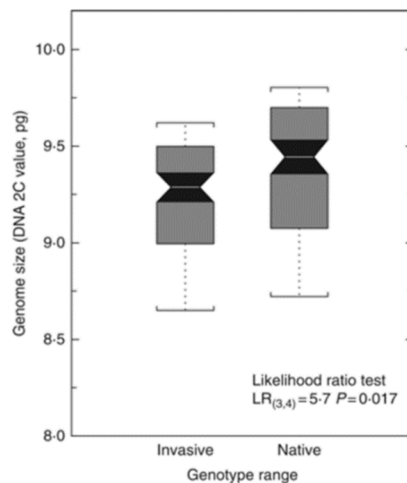
Rejmánek, 1996

Review by Suda et al, 2014

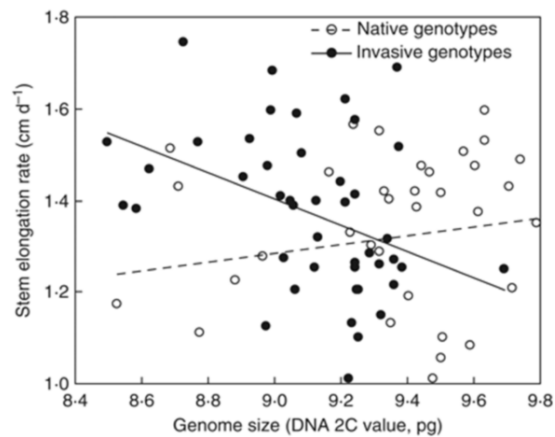


Reed canarygrass

Lavergne et al., 2010



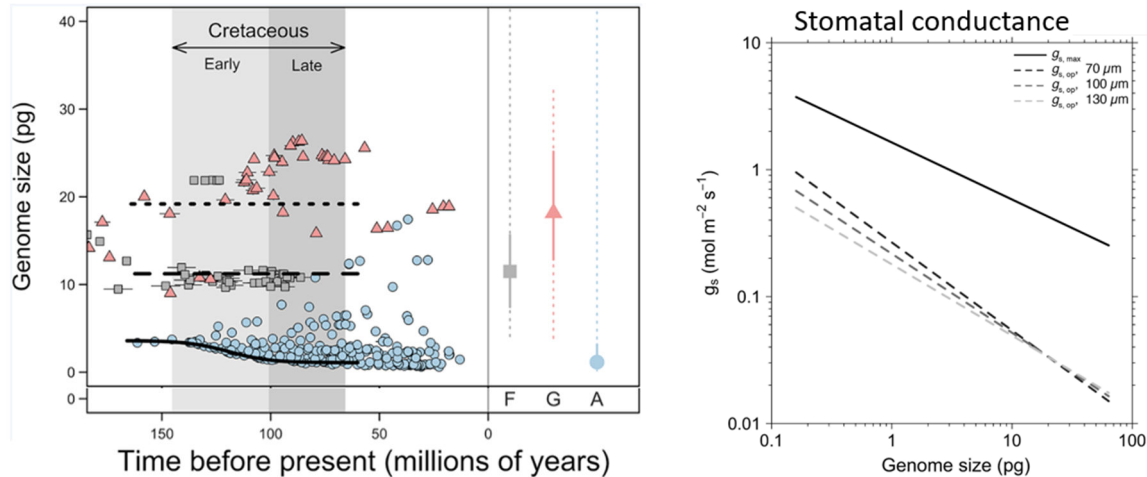
Average DNA content of invasive and non invasive genotypes



Correlation between stem growth rate and DNA content. These parameters were not significantly correlated in native (non invasive) genotypes, but very negatively correlated with invasive genotypes.

DNA content vs rise of angiosperms

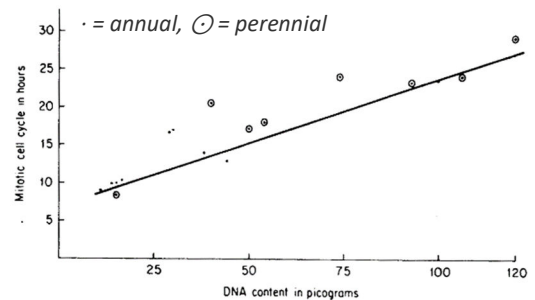
Simonin & Roddy, 2018



DNA content vs life cycle

Swanson, Merz, & Young, 1981

Species	pg/haploid genome	Mitosis (hours)	Meiosis (hours)	Plant habit
<i>Crepis capillaris</i>	1.20	10.8	--	Annual
<i>Haplopappus gracilis</i>	1.85	10.5	36.0	Annual
<i>Pisum sativum</i>	3.9, 4.8	10.8	--	Annual
<i>Ornithogalum virens</i>	6.43	--	96.0	Perennial
<i>Secale cereale</i>	8.8, 9.6	12.8	51.2	Annual
<i>Vicia faba</i>	13.0, 14.8	13.0	72.0	Annual
<i>Allium cepa</i>	14.8, 16.25	17.4	72.0	Perennial
<i>Tradescantia paludosa</i>	18.0	18.0	126.0	Perennial
<i>Endymion nonscriptus</i>	21.8	--	48.0	Perennial
<i>Tulipa kaufmanniana</i>	31.2	23.0	--	Perennial
<i>Lilium longiflorum</i>	35.3	24.0	192.0	Perennial
<i>Trillium erectum</i>	40.0	29.0	274.0	Perennial



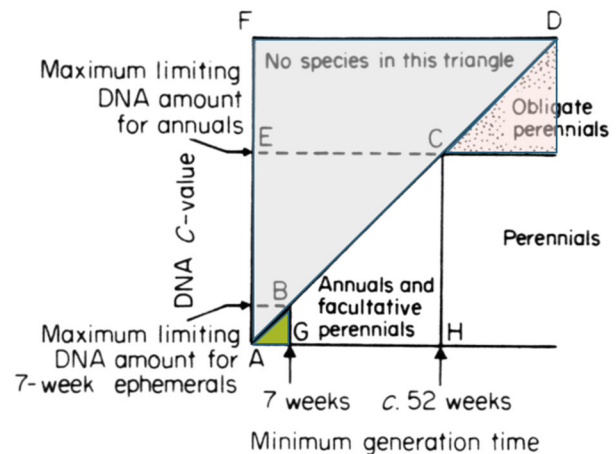
Definitions

Bennett, 1987

- **Annual**
 - Sets seed and completes life cycle within one year (52 weeks) or shorter growth season.
 - Hence, a fast growth rate is essential
- **Perennial**
 - Does not complete life cycle within 1 year
- **Facultative perennial**
 - Sets seed within 1 year
- **Nucleotypically determined obligate perennial**
 - The DNA content slows down the cell cycles to where the plant cannot set seed or complete its life cycle within one year
- **Genotypically determined obligate perennial**
 - Long life cycle not determined by DNA content, such as juvenility in trees
- **Temperature-determined obligate perennials**
 - Extreme environments with growing seasons too short to complete a life cycle in 1 year

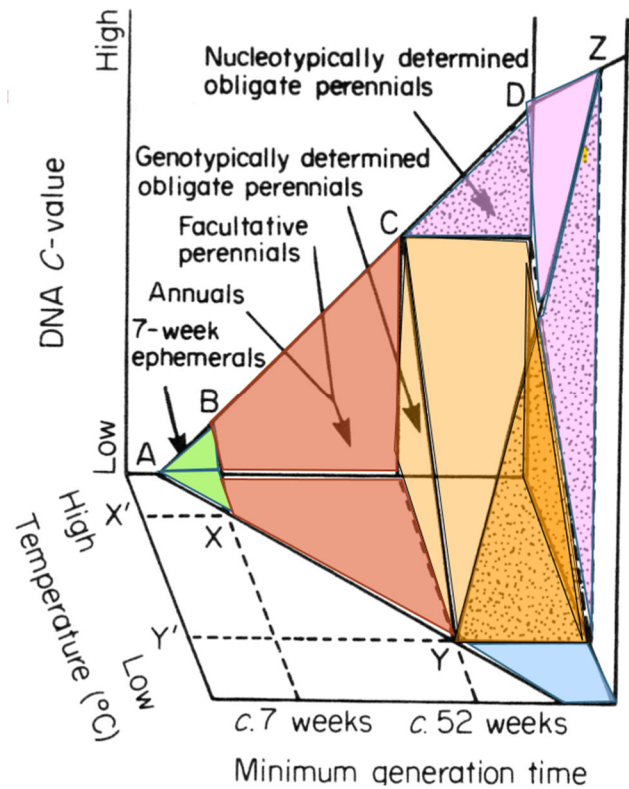
Effect of DNA @ constant temperature

Bennett, 1987



Effect of DNA considering temperature

Bennett, 1987



Category of Plant	DNA C-value is below the segment:	Minimum generation time is:	The plants can exist at temperatures:
Ephemerals	AB	≤ 7 weeks	> X'
Annuals and Facultative Perennials	BC	≤ 52 weeks but > 7 weeks	> Y'
Genotypically- determined obligate perennials	C	> 52 weeks	> Y'
Nucleotypically- determined obligate perennials	CD	> 52 weeks	> Y'
Temperature-determined obligate perennials	can be as great as CD but tends to be lower	> 52 weeks	< Y'