

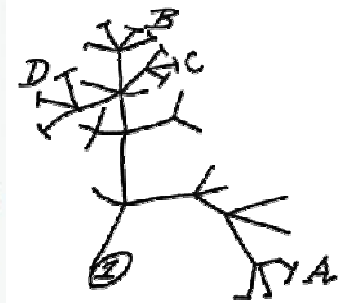
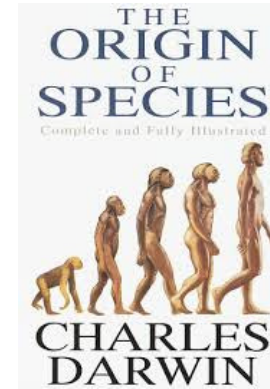
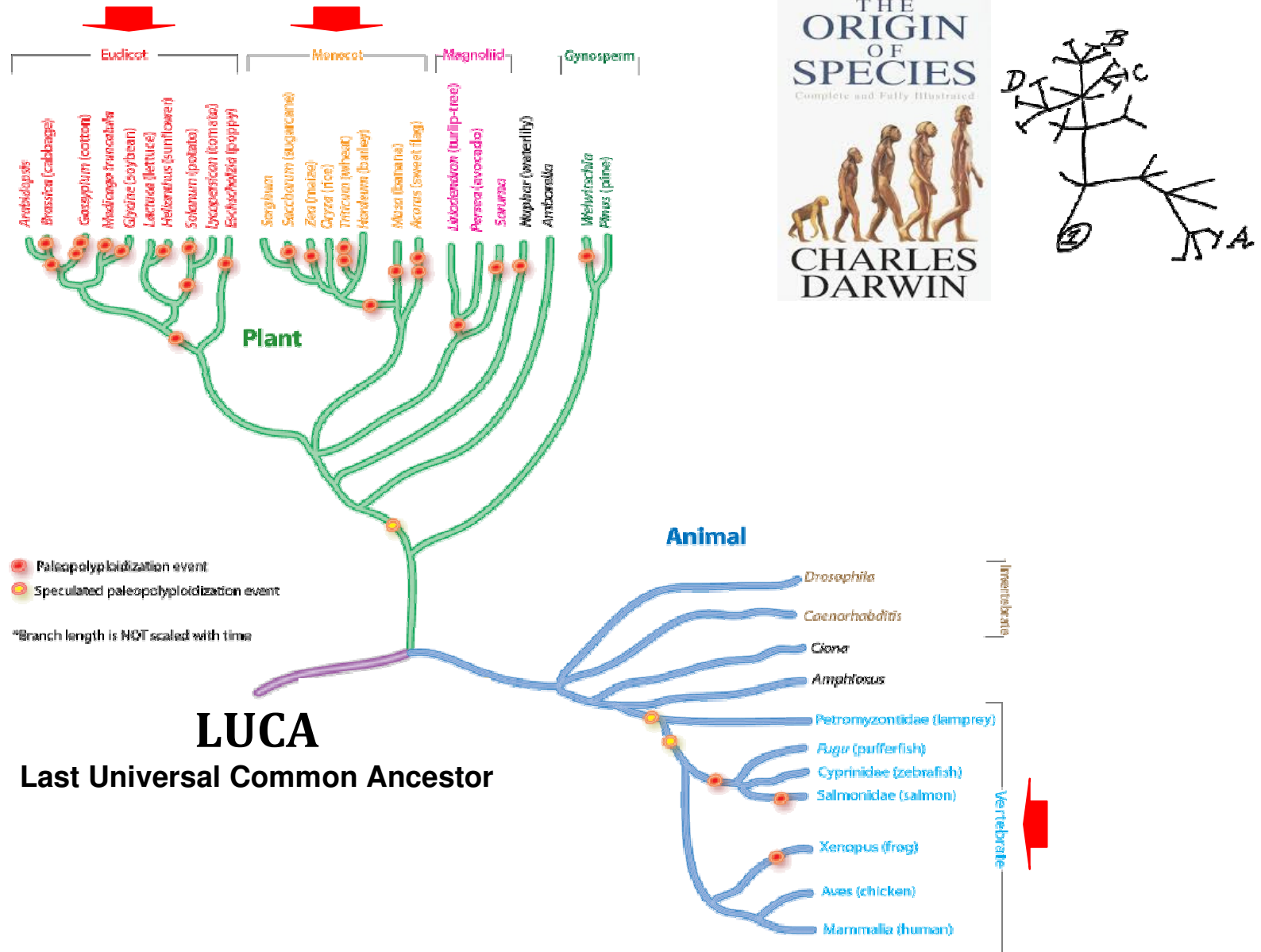
Les plantes modernes : origine, nouvelles espèces et amélioration variétale



Paleogenomics and Evolution

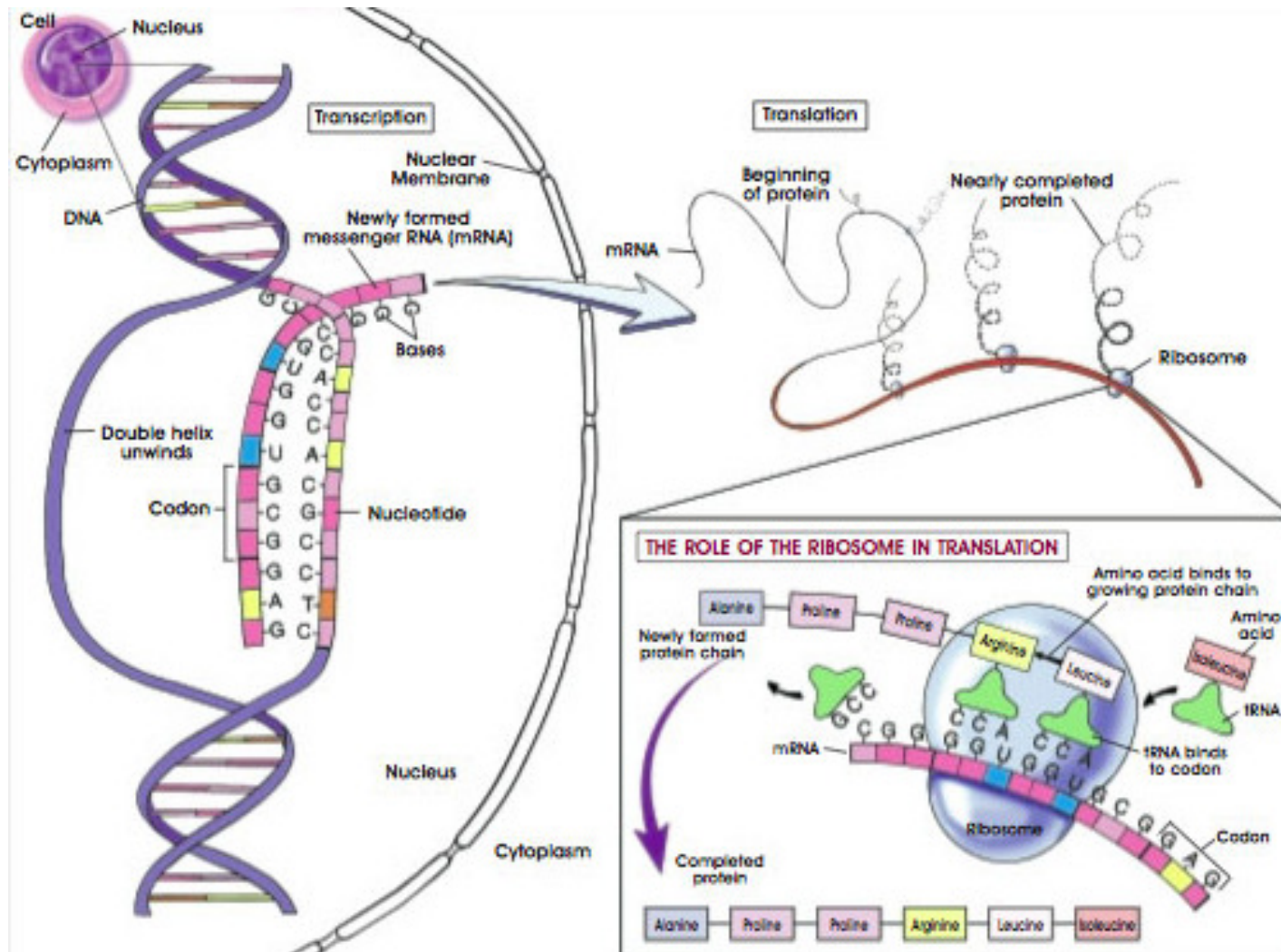


Background – Evolution.





Background – Genomes / Chromosomes.

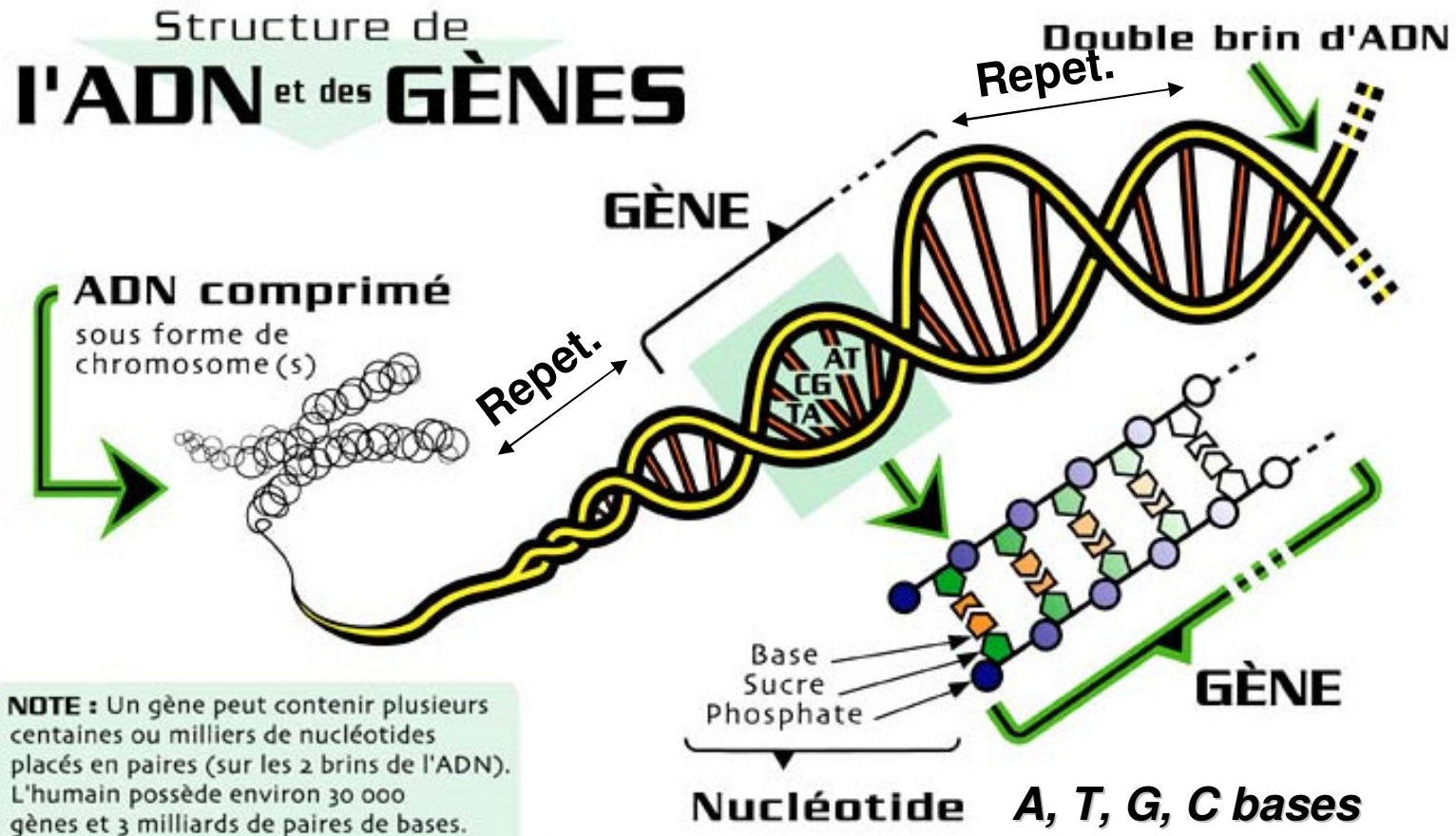


Genome = chromosome containing genes + TEs

Masella and Chung 2008



Background – Genes / Repeats.



Genome = genes and intergenic sequence (repeat)

@ <http://www.mddep.gouv.qc.ca>



Comparative Genomics 80'-90'.

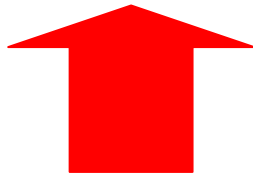
1980

2000-2005

x10-100 markers
Unit = cM

x10-100 genes
Unit = bp

Genomes (rice/At)
20 000-40 000 genes
Unit = bp

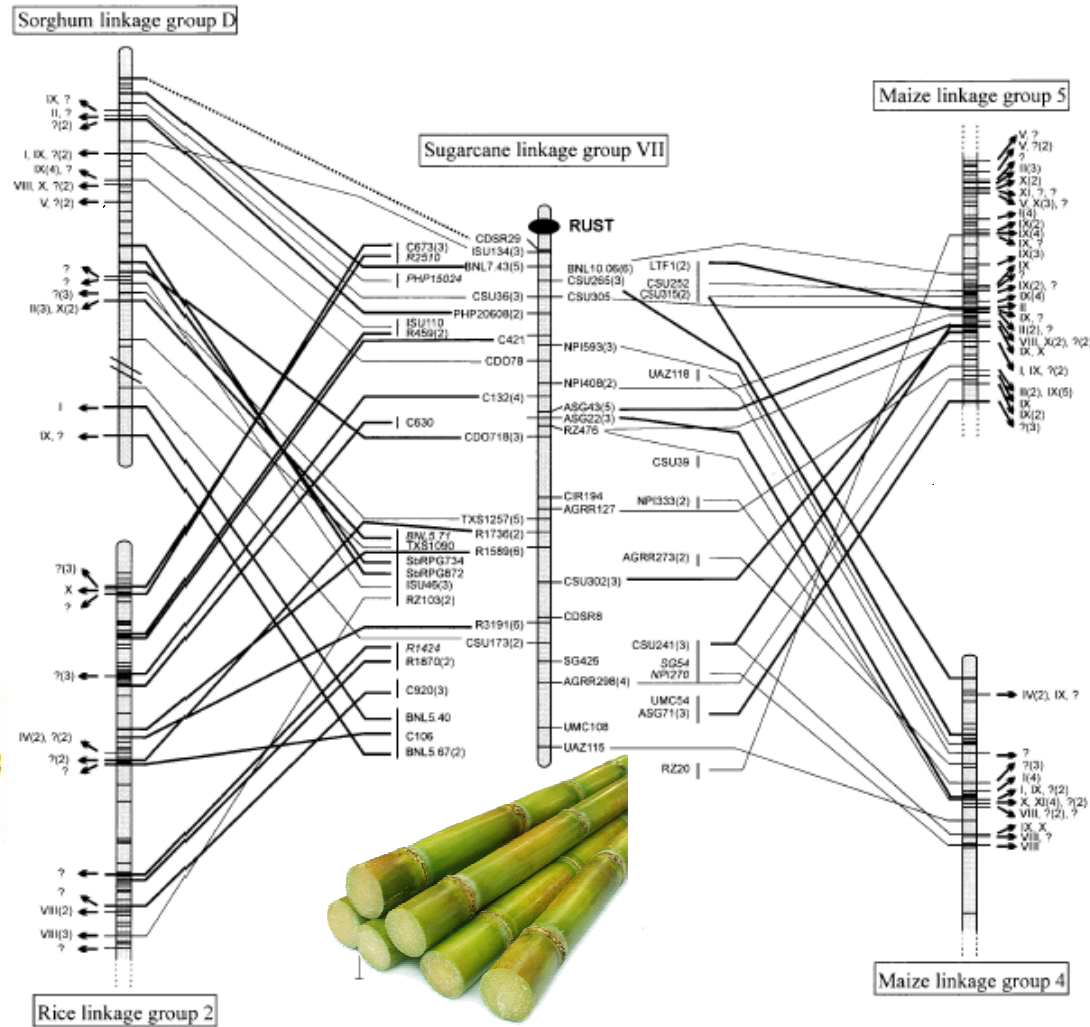
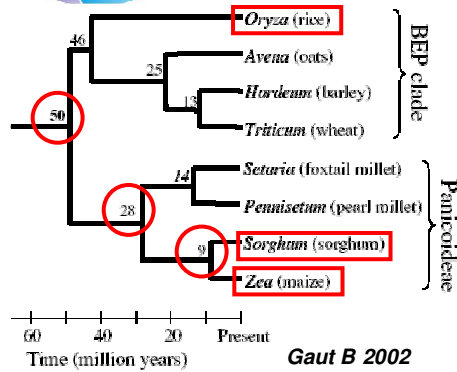




Background – Comparative Genomics (1999).

C. Asnagli · F. Paulet · C. Kaye · L. Grivet · M. Deu
J.C. Glaszmann · A. D'Hont

Application of synteny across Poaceae to determine the map location of a sugarcane rust resistance gene



Results:

- ☞ Common markers (184 loci)
- ☞ Resistance gene locus
- ☞ 60 MYA speciation
- ☞ Conserved synteny





Comparative Genomics 80'-90'.

1980



2000-2005

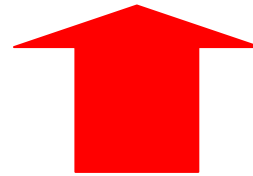
x10-100 markers
Unit = cM



x10-100 genes
Unit = bp

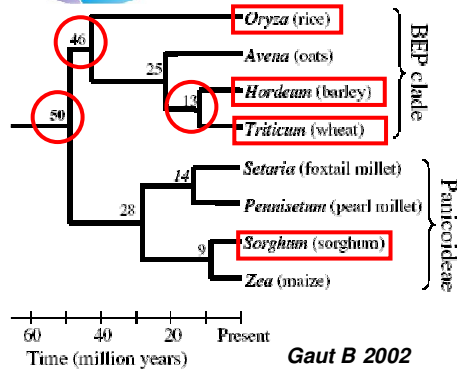


Genomes (rice/At)
20 000-40 000 genes
Unit = bp



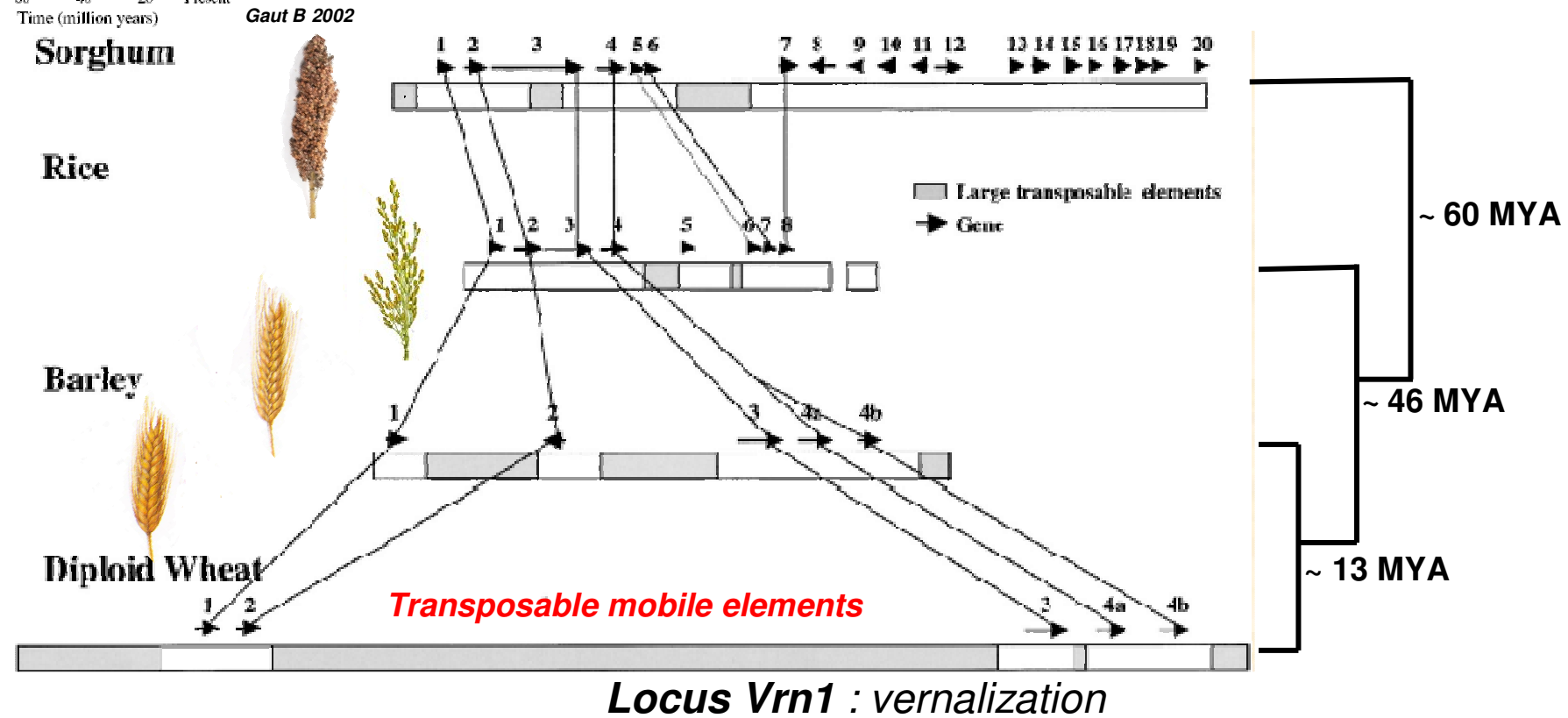


Background – Comparative Genomics (2000).



Different Types and Rates of Genome Evolution Detected by Comparative Sequence Analysis of Orthologous Segments From Four Cereal Genomes

Wusirika Ramakrishna,* Jorge Dubcovsky,[†] Yong-Jin Park,^{*1} Carlos Busso,[†] John Emberton,* Phillip SanMiguel[‡] and Jeffrey L. Bennetzen^{*2}





Comparative Genomics 80'-90'.

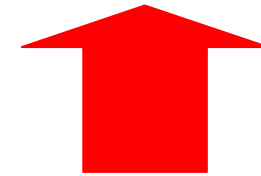
1980

2000-2005

x10-100 markers
Unit = cM

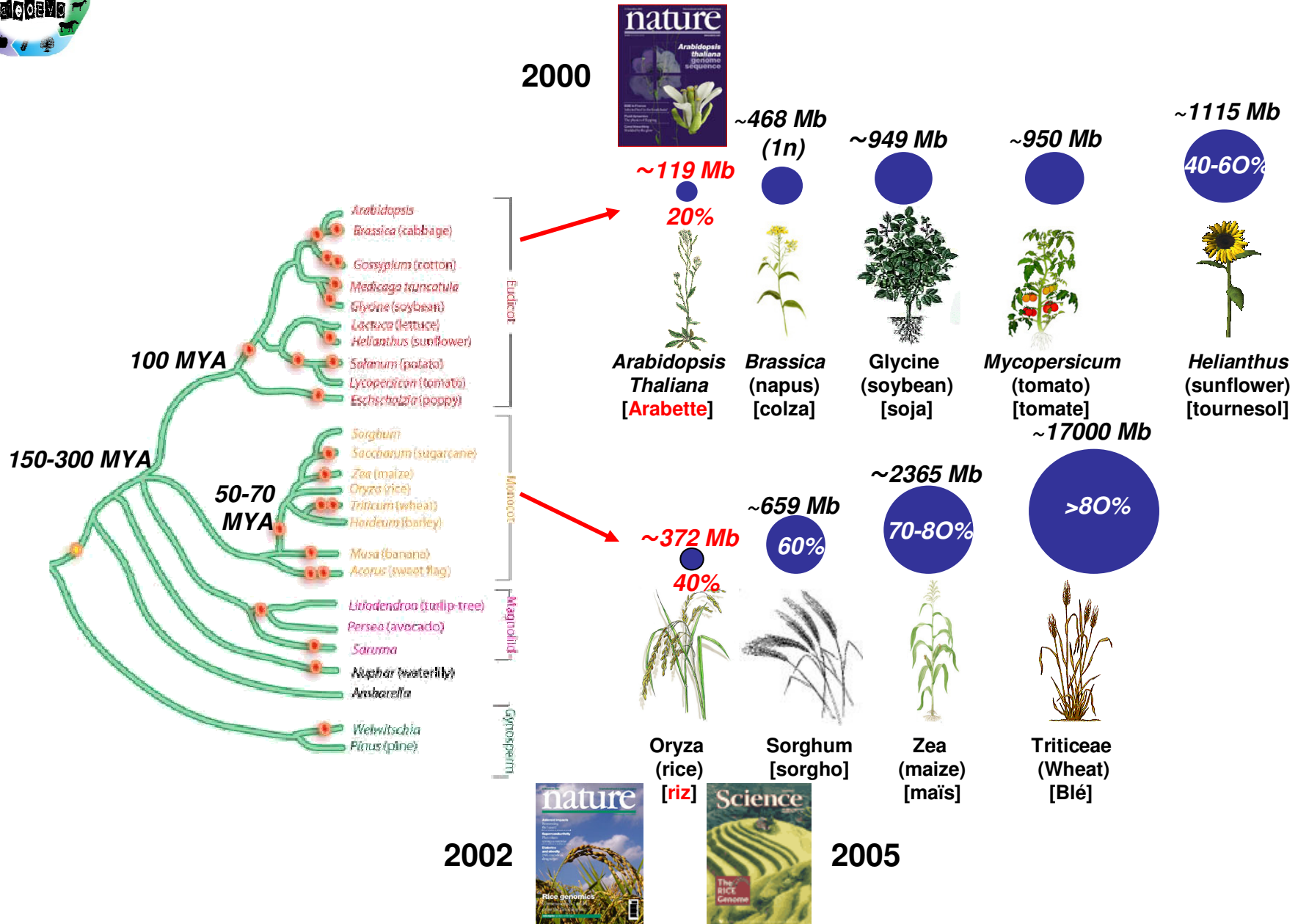
x10-100 genes
Unit = bp

Genomes (rice/At)
20 000-40 000 genes
Unit = bp





Background – Genome Size





Comparative Genomics 80'-90'

1980

2000-2005

x10-100 marqueurs
Unité cM

x10-100 gènes
Unité bp

Génomes (riz/At)
20 000-40 000 gènes
Unité bp

MAIN CONCLUSIONS:

- ↪ Conserved Syntenie : monocots > dicots;
- ↪ Duplicated Genomes : old/recent polyploïds;
- ↪ Genome Size Differences: proportion TE ≠;
- ↪ Since 2009: numerous genomes available.....



Plant & Animal Genomes.

12 genomes

SPECIES	COMMON NAME	CHROMOSOMES	GENOME (MB)	ANNOTATED GENES	SYNTENY	DUPLICATION	WGD
PLANTS							
<i>Oryza sativa</i>	Rice	12	372	41046	RG	448-10-73	1R
<i>Sorghum bicolor</i>	Sorghum	10	659	34008	6147-12-99	409-10-84	1R
<i>Zea mays</i>	Maize	10	2365	32540	4454-30-82	3454-17-99	2R
<i>Brachypodium distachyon</i>	Brachypodium	5	271	27601	8533-12-99	642-13-79	1R
<i>Vitis vinifera</i>	Grape	19	302	21189	RG	543 - 23 - 71	1R
<i>Arabidopsis thaliana</i>	Cress	5	119	33198	2389 - 80 - 99	1630 - 55 - 83	3R
<i>Populus trichocarpa</i>	Poplar	19	294	30260	4555 - 87 - 92	4164 - 46 - 73	2R
<i>Glycine max</i>	Soybean	20	949	46194	4013 - 164 - 97	9533 - 89 - 55	3R
<i>Fragaria</i>	Strawberry	7	208	32630	3289 - 94 - 70	114 - 27 - 19	1R
<i>Theobroma cacao</i>	Cacao	10	218	27814	4472 - 21 - 81	370 - 19 - 66	1R
<i>Malus x domestica</i>	Apple	17	528	58984	3498 - 104 - 70	2845 - 69 - 59	2R
Total					27135-695-81	19559-396-57	

8 genomes

ANIMALS							
<i>Homo sapiens</i>	Human	23	3059	18794	RG*	128-29-33	2R
<i>Mus musculus</i>	Mouse	20	2635	19380	10088-143-75	48-21-13	2R
<i>Canis familiaris</i>	Dog	39	2445	42626	5551-97-71	76-26-19	2R
<i>Equus caballus</i>	Horse	32	2360	18838	10195-83-83	134-24-26	2R
<i>Monodelphis domestica</i>	Opposum	9	3502	31265	3413-79-78	16-7-4	2R
<i>Gallus gallus</i>	Chicken	33	1032	30077	2311-41-91	41-17-25	2R
<i>Oryzias latipes</i>	Medaka	24	721	17117	2124-238-60	830-125-39	3R
<i>Pan troglodytes</i>	Chimpanzee	24	3175	40460	5091-56-62	43-11-15	2R
Total					38773-737-74	1316-260-22	

GBE (2012) 4(9):917-28

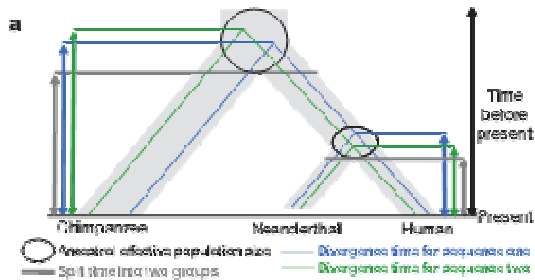


Paleogenomics... genome of extinct ancestors.

ARTICLES

Analysis of one million base pairs of Neanderthal DNA

Richard E. Green¹, Johannes Krause¹, Susan E. Pääbo¹, Adrian W. Briggs¹, Michael T. Ronan¹, Jan F. Simons², Lei Du¹, Michael Eichler¹, Jonathan M. Rothberg¹, Maja Paunovic¹ & Svante Pääbo¹

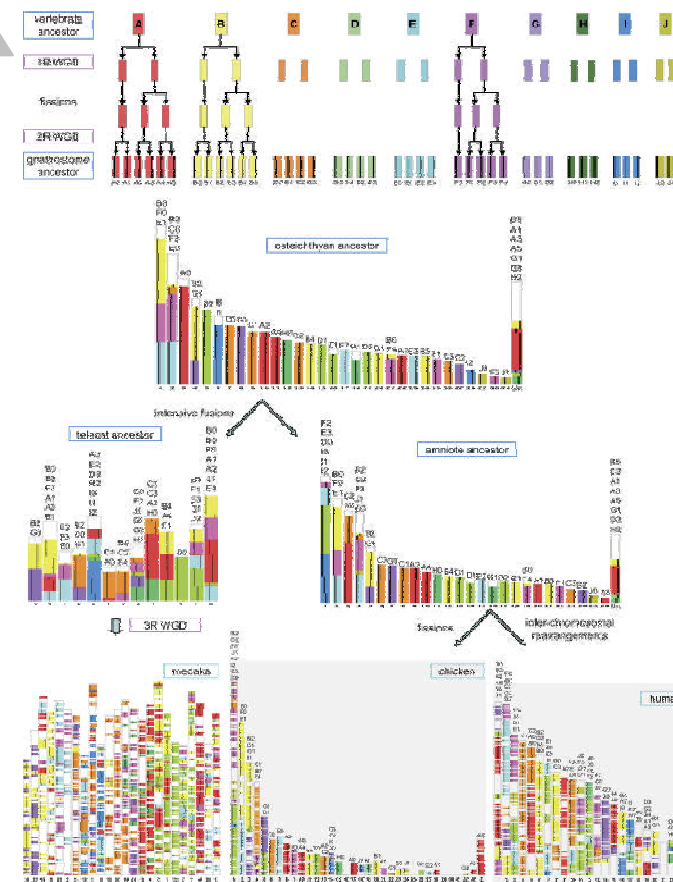


Sequenced fossil DNA



Reconstruction of the vertebrate ancestral genome reveals dynamic genome reorganization in early vertebrates

Yoichiro Nakatani, Hiroyuki Takeda, Yuji Kohara, et al.



Modern species genome sequences



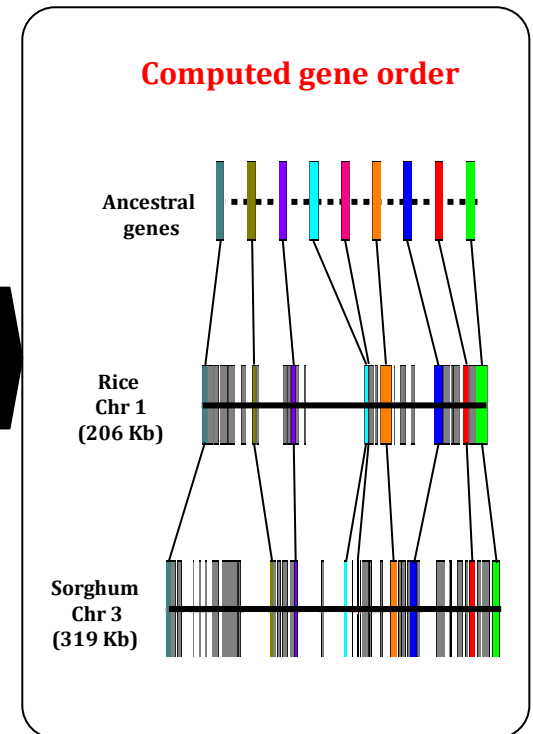
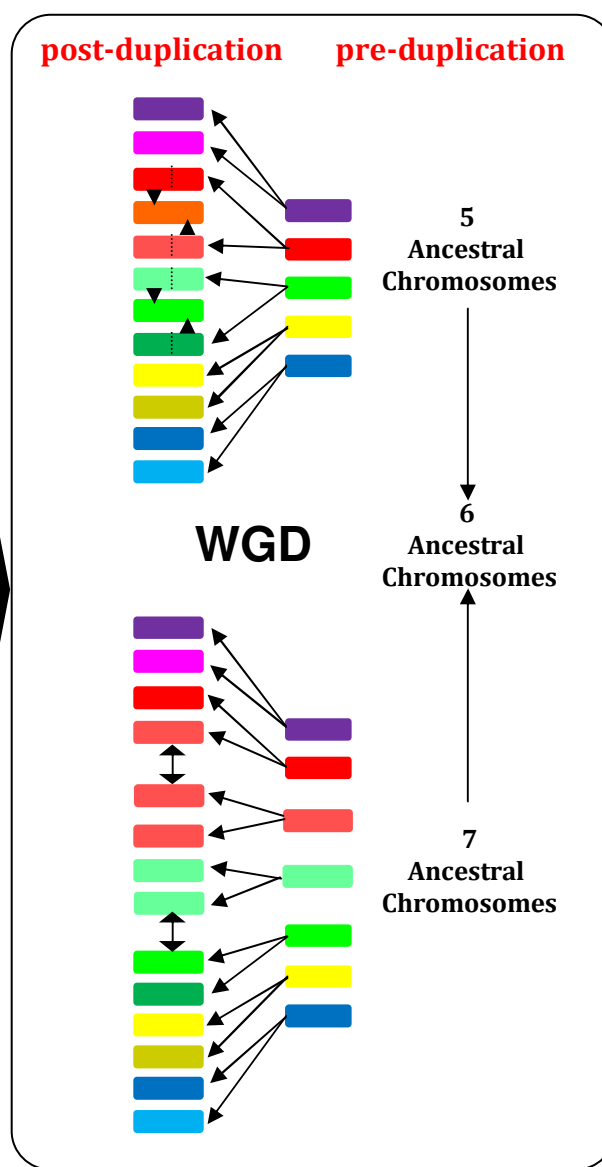
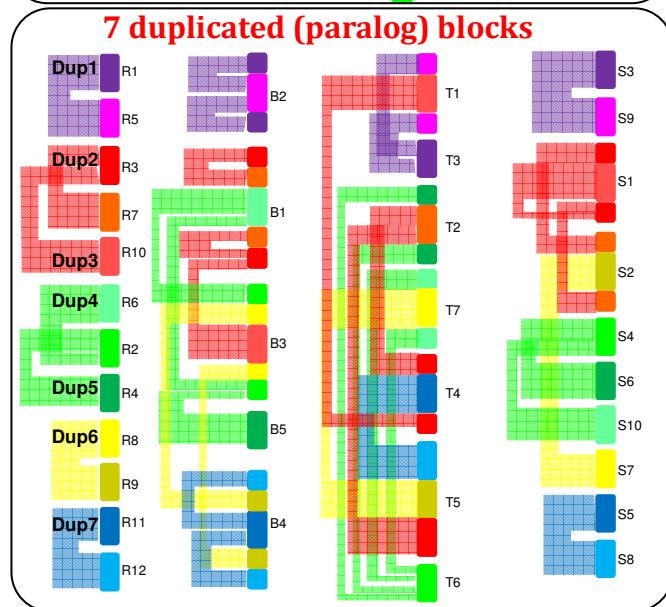
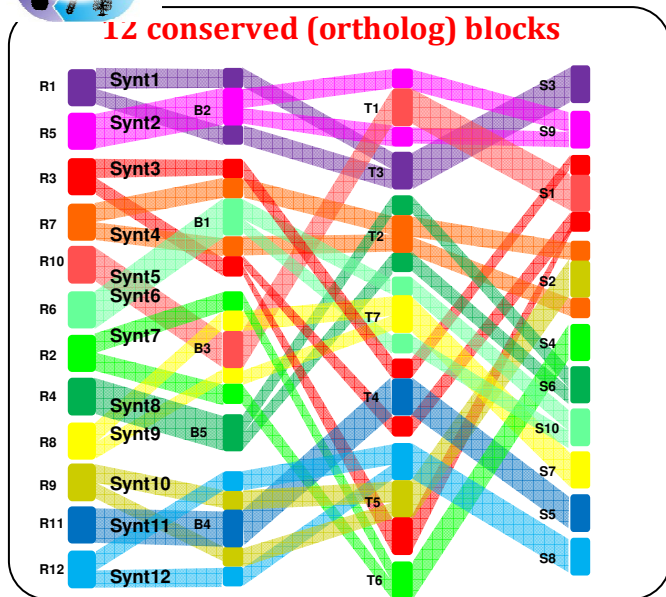


Strategy for Comparing Genomes and Reconstruct Ancestors.

Modern genome comparison

→ Pre- post-WGD ancestor reconstruction

→ Ancestral gene order modeling

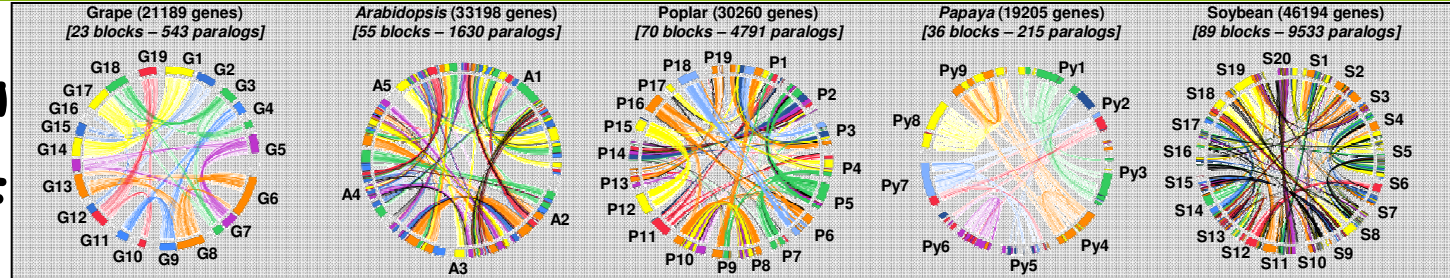


Plant Cell (2008) 20(1):11-24
 Brief. In Bioinf. (2009) 10(6):619-30
 PNAS (2009) 106(35):14908-13
 TPS (2010) 15(9):479-87
 Genome Research (2010) 20(11):1545-1557
 Nat Genet (2011) 43(2):101
 CRAS (2011) 334:205-211
 COPB (2012) 15(2):122-30



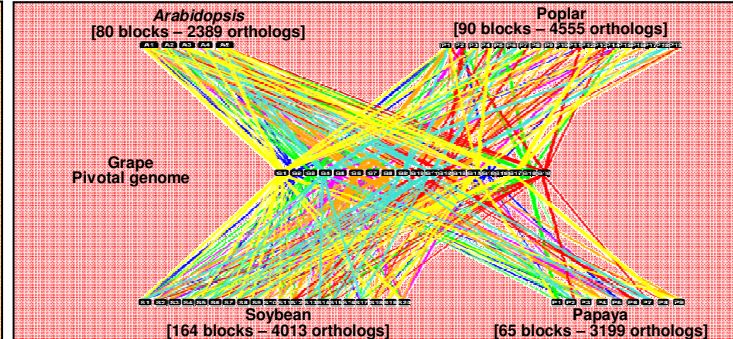
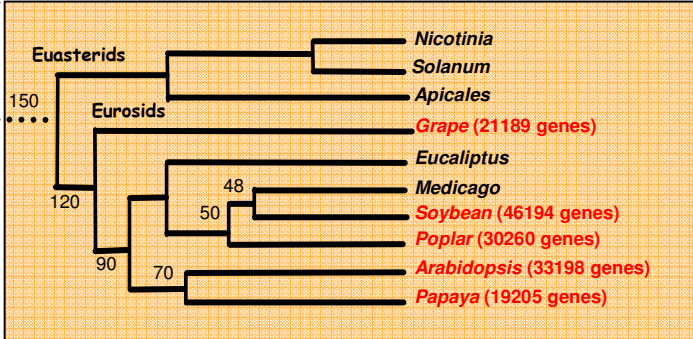
Comparing Plant Genomes and Reconstruct Ancestors.

Eudicots



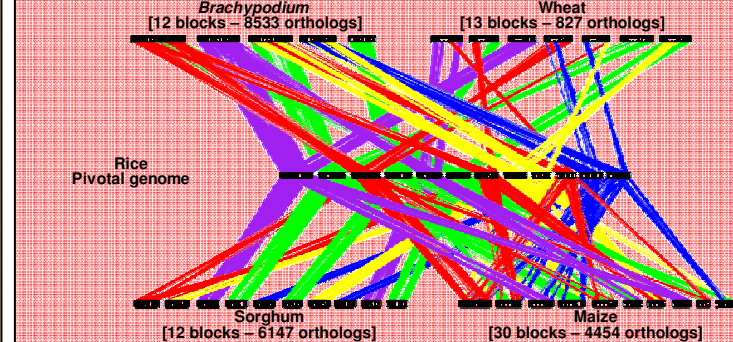
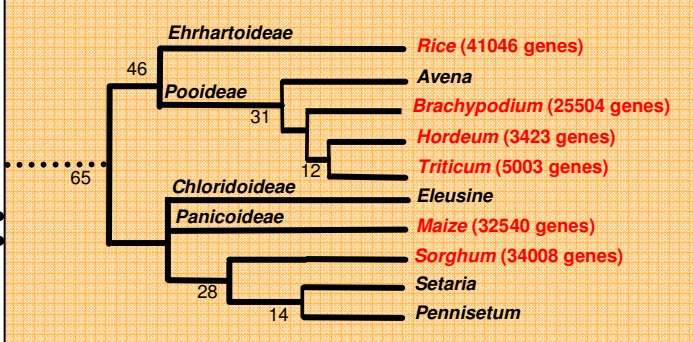
>50% duplicated

Flowering plants

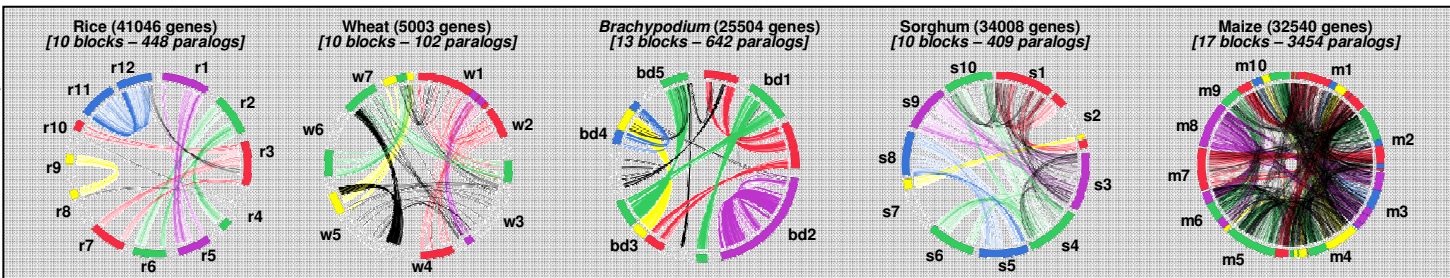


80% conserved

Monocots

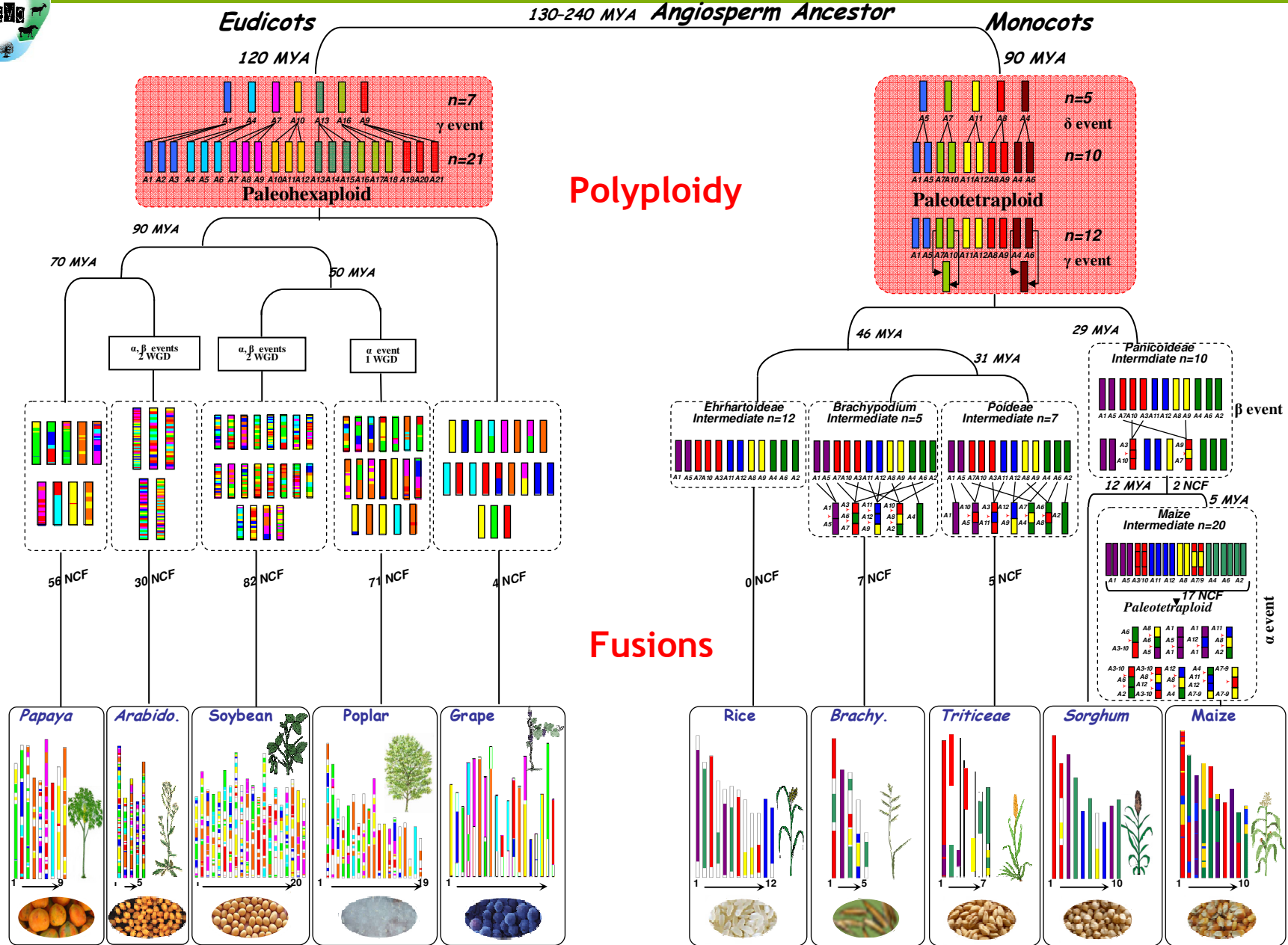


>50% duplicated



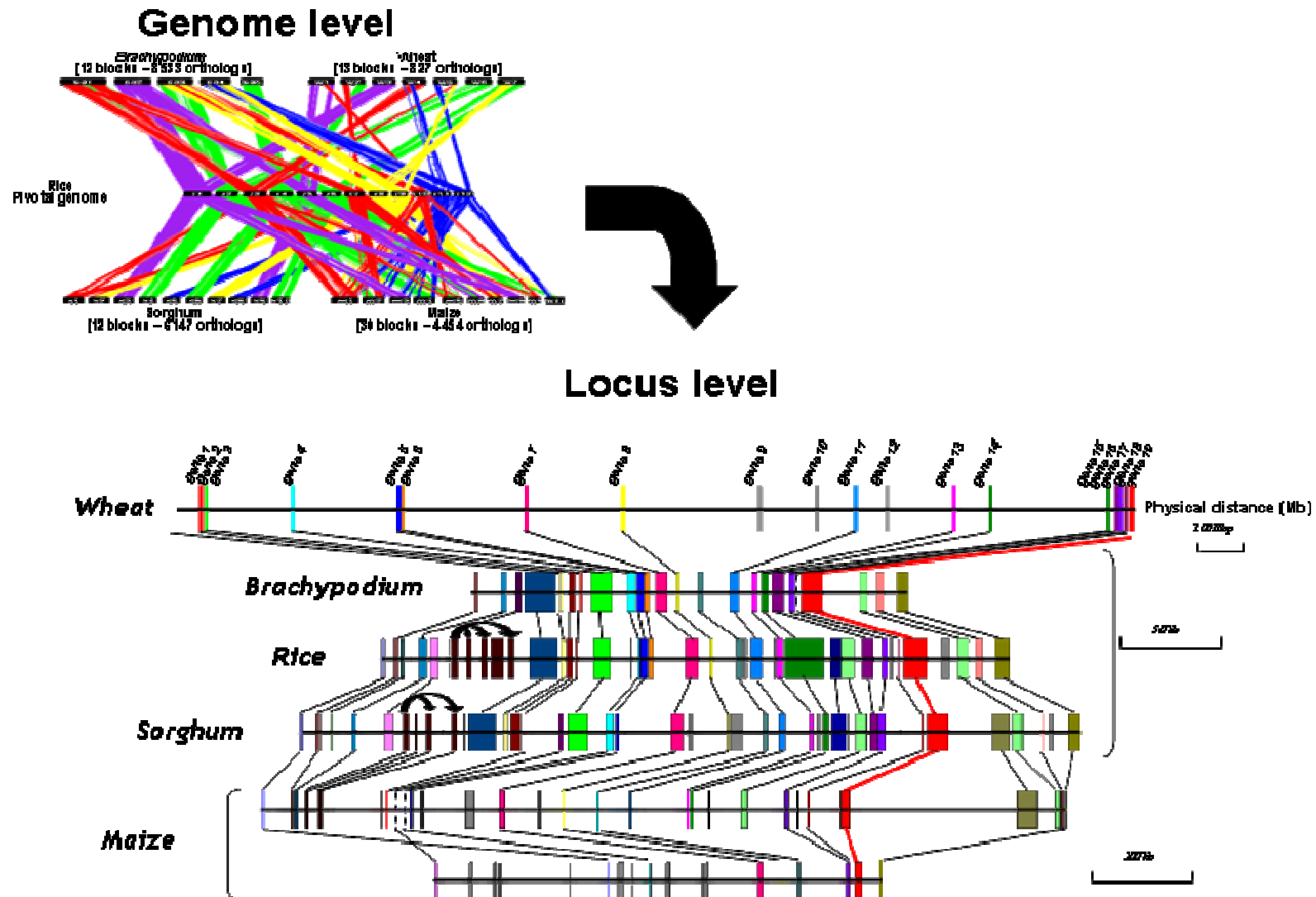


Toward an Angiosperm Ancestor Genome Structure.





Strategy for Comparing Genomes and Reconstruct Ancestors.

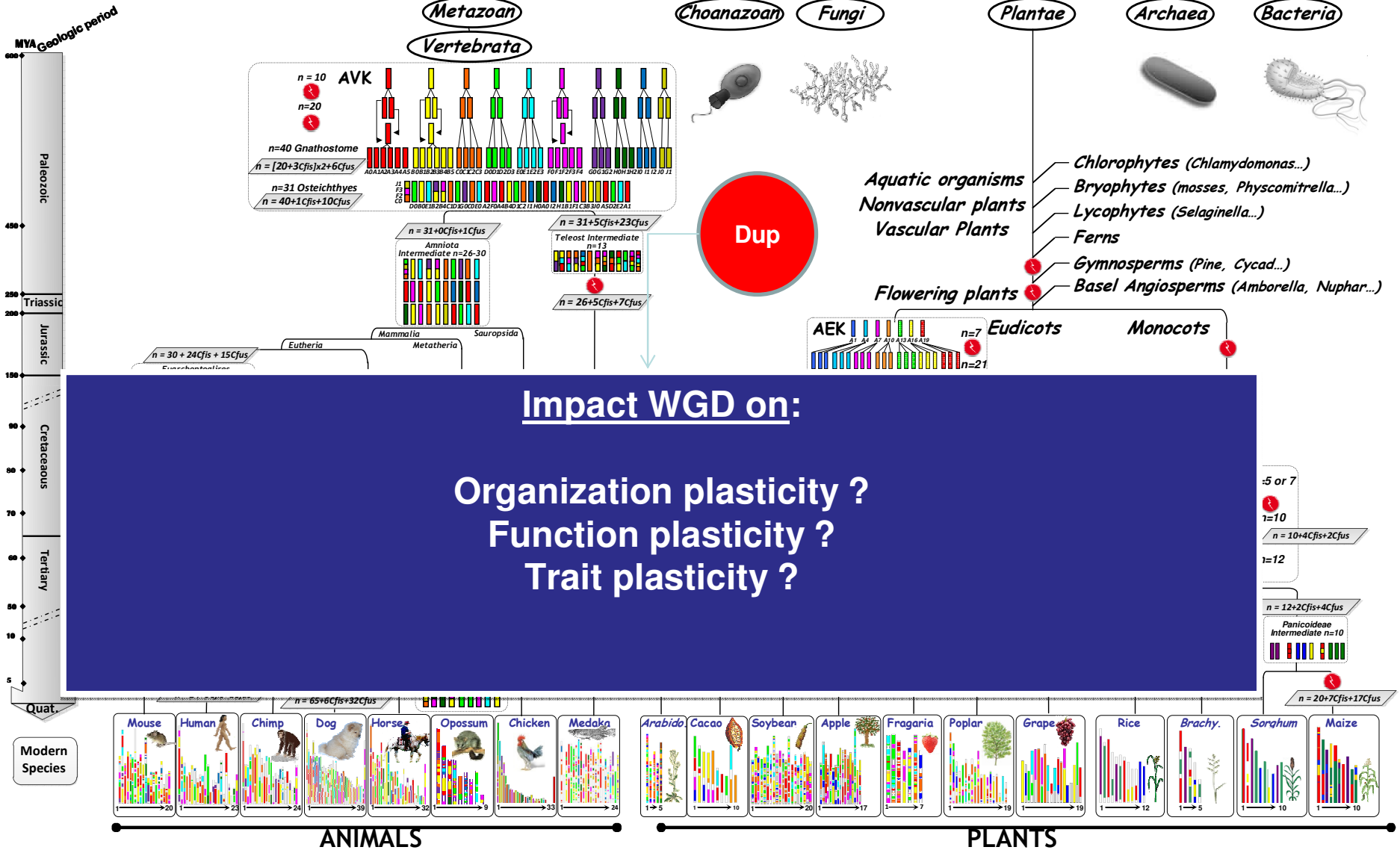




PaleoEVO – Evolutionary Scenario.

Duplication/Polyploidy

TREE OF LIFE

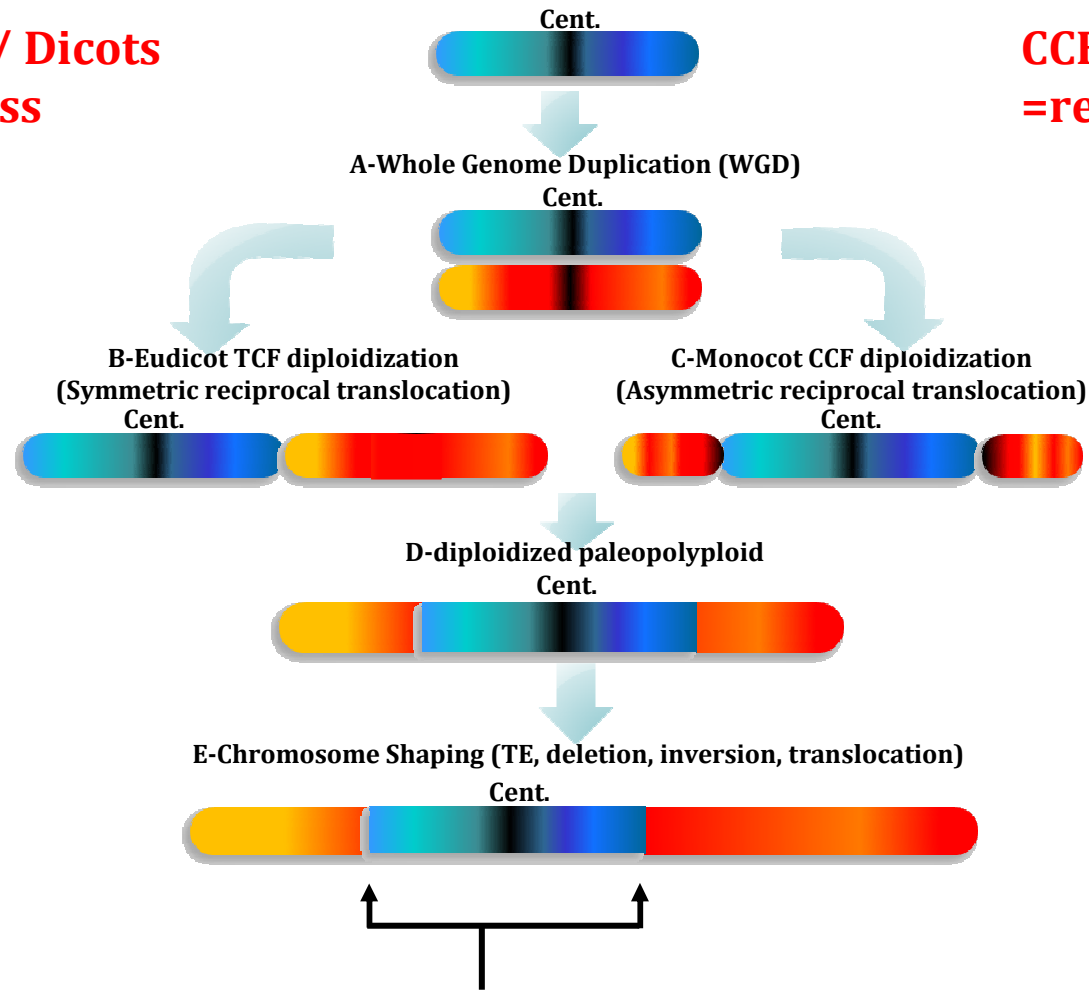




PaleoEVO – Chromosome Plasticity.

**TCF in Animal / Dicots
=ancient process**

**CCF in Monocots
=recent process**

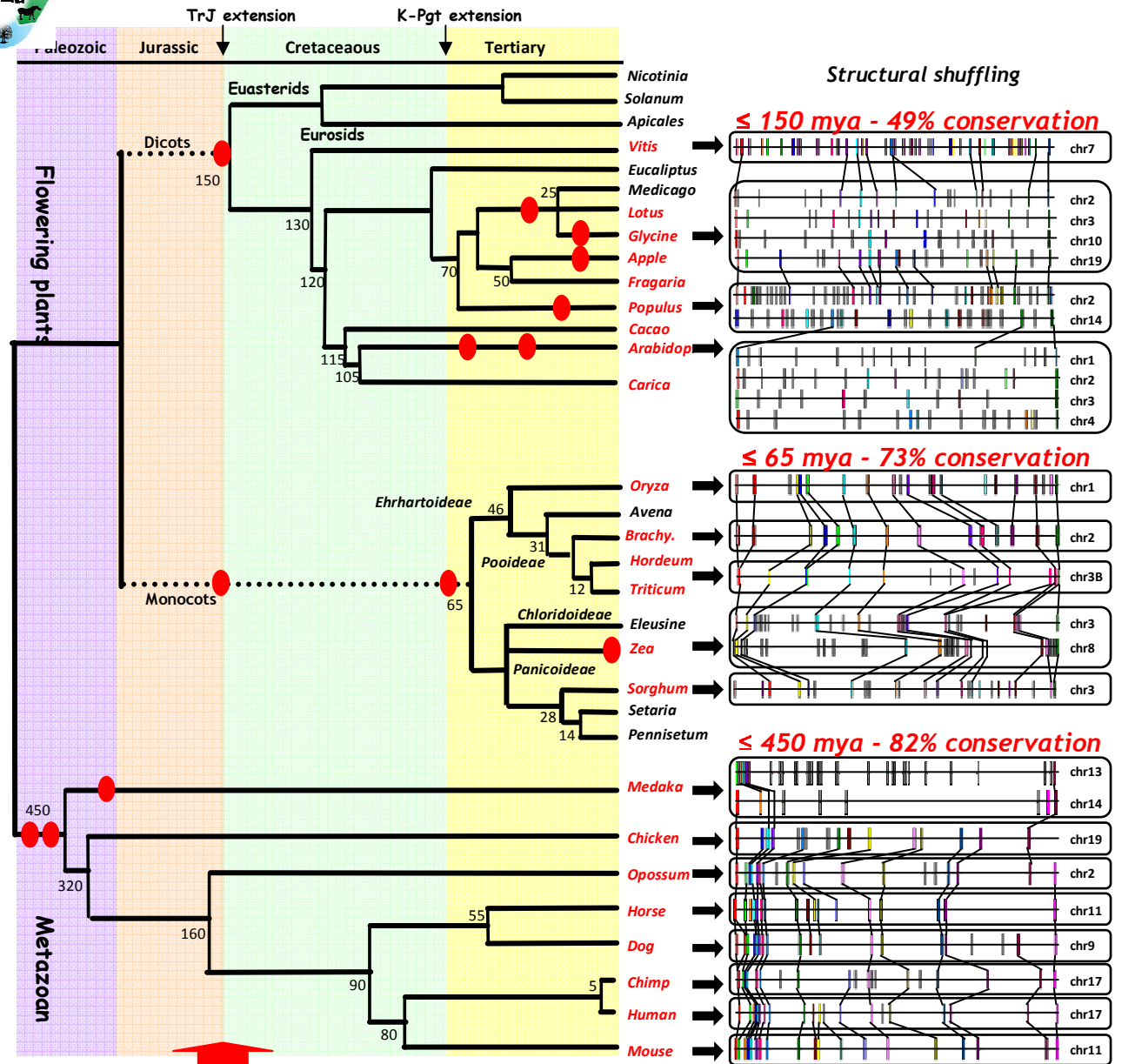


SBP / CF, evolutionary hot spots

COPB (2012) 15:1-9



PaleoEVO – Conservation Plasticity.



Up to 3R recent
= Low conservation

3R ancient
= High conservation

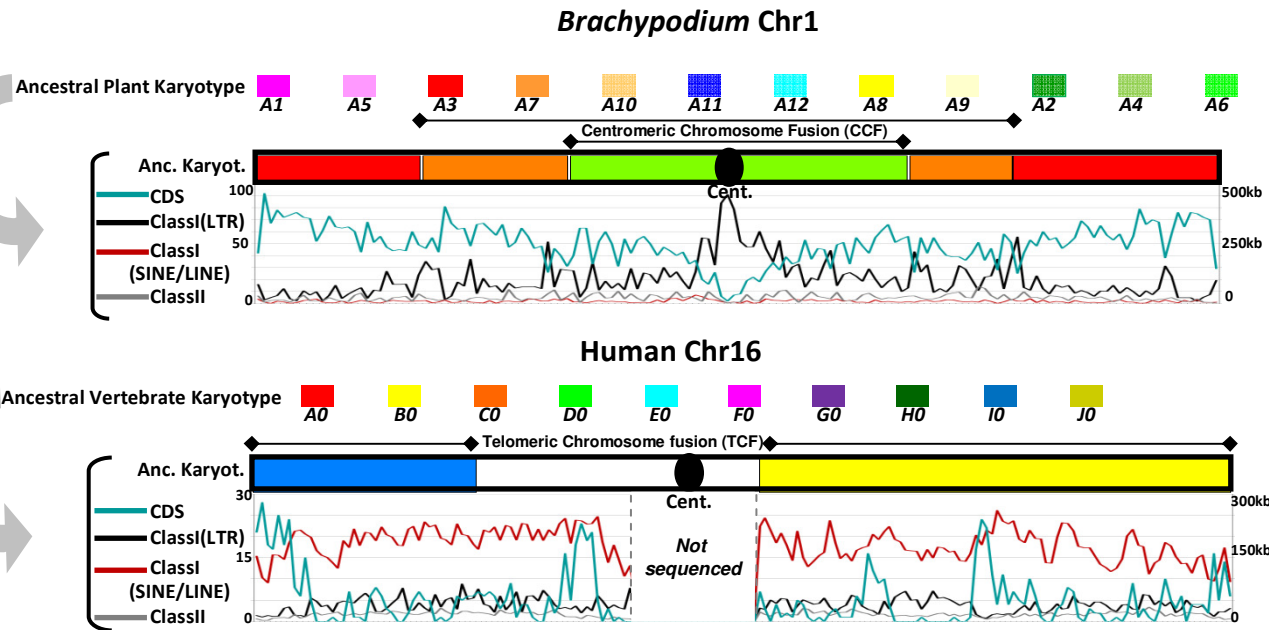
GBE (2012) 4(9):917-28



Plant vs. Animal Genome Architectures.

**PLANTS
=
PLASTIC**

**ANIMALS
=
STABLE**



↪ Duplications

- ☒ Frequent and recent in plants ➤ Adaptation by WGD.
- ☒ Rare and ancient in animals ➤ Adaptation by CNVs.

↪ Genes

- ☒ Enriched in telomeres in plants / Local islands in animals.
- ☒ Longer genes in animals, variable intergenic spaces in plants.

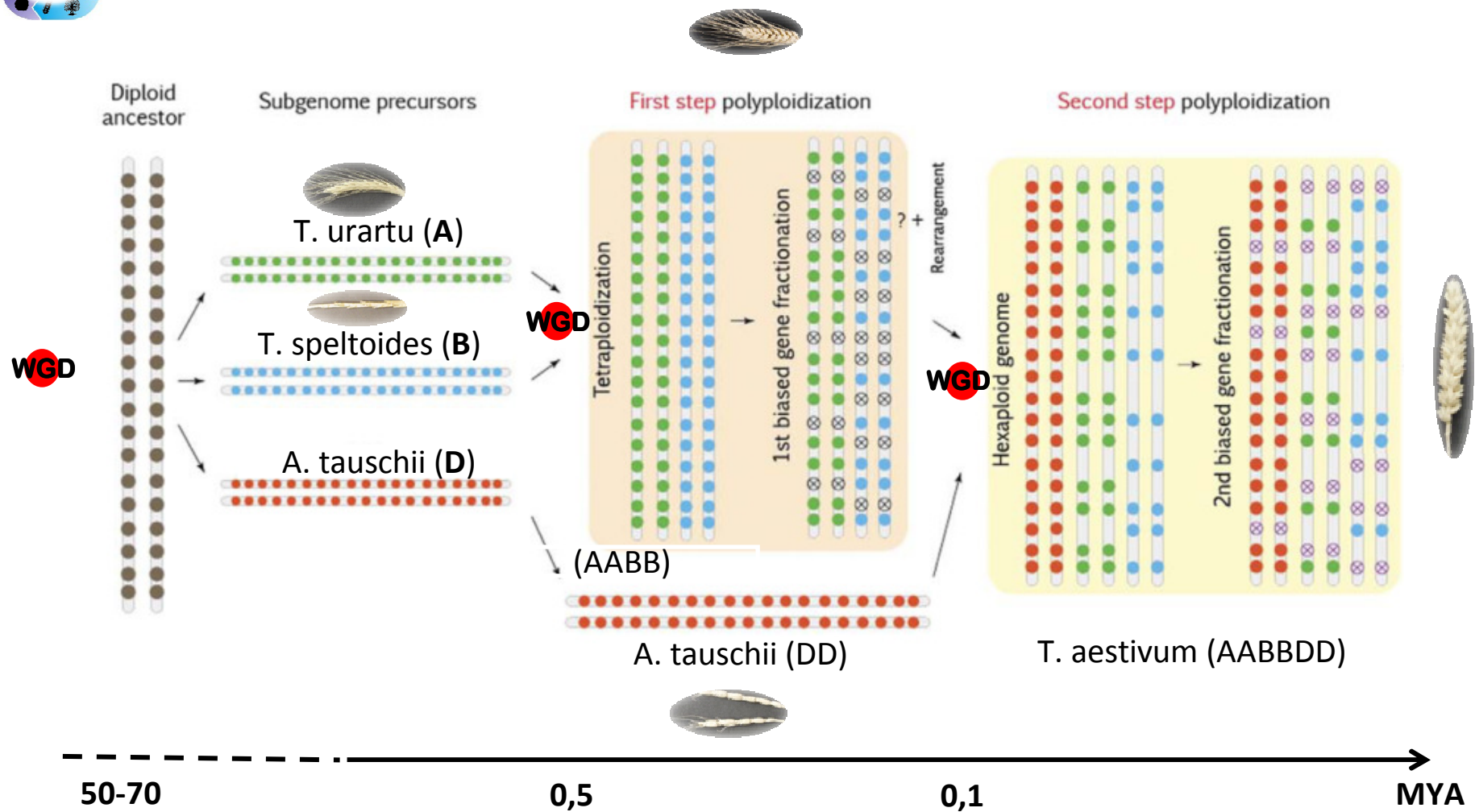
↪ TEs

- ☒ Mainly recent class I in plants.
- ☒ Mainly ancient burst of class II (SINE and LINEs) in animals.

COPB (2012) 15(2):122-30
GBE (2012) 4(9):917-28

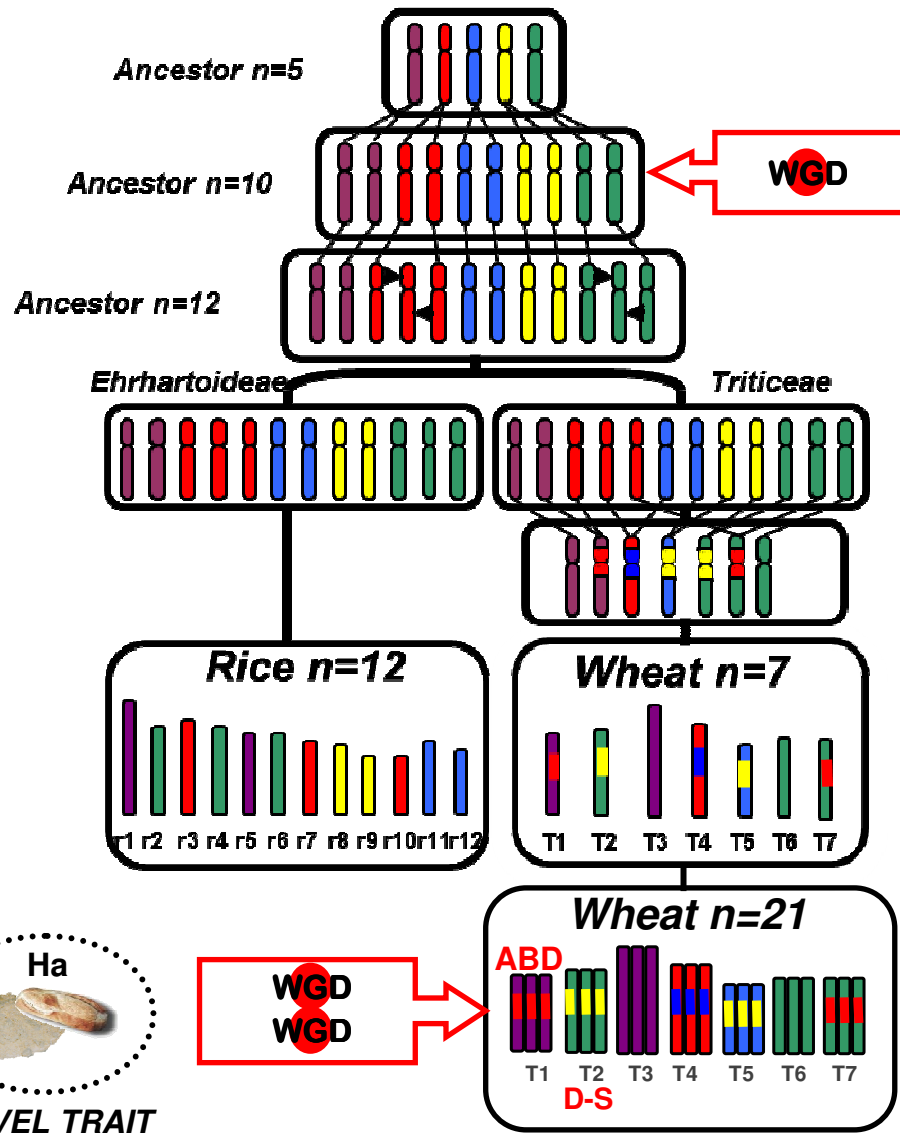
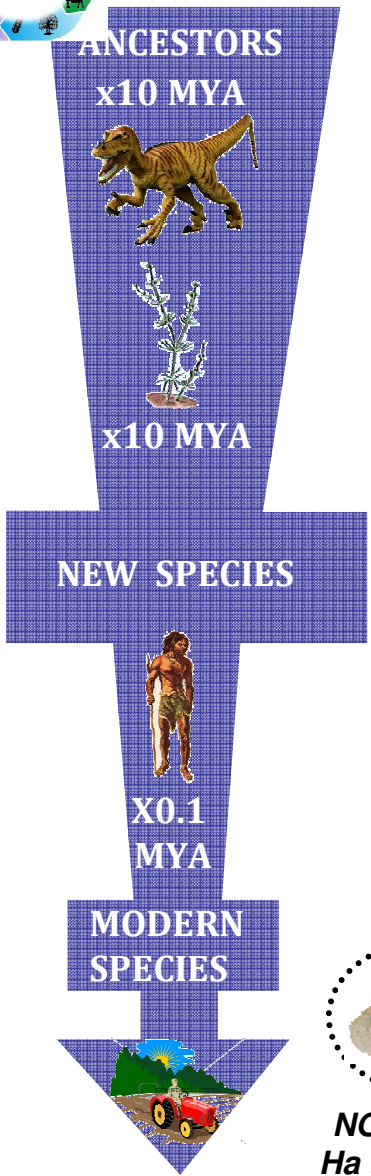


Evolutionary History of Recent Polyploid Genomes (Bread Wheat).

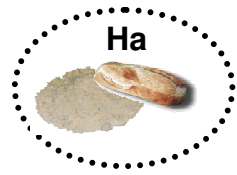


Cheng et al 2012

Impact of Duplication on Traits.



NOVEL FUNCTION
PSY = 'Carotenoid content'

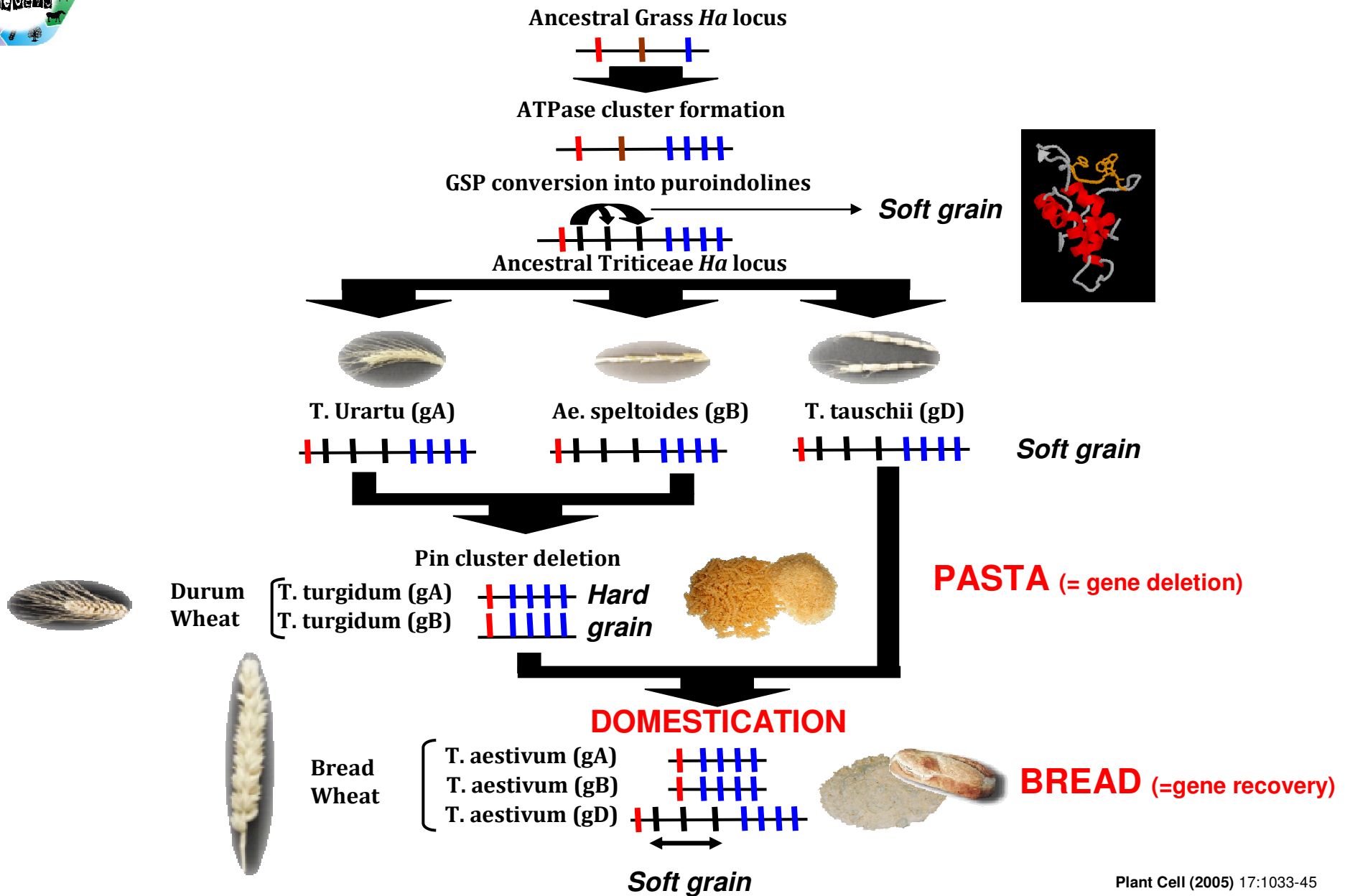


NOVEL TRAIT
Ha = 'Hardness'





Soft Grain (bread making) Recovered by Hexaploidization

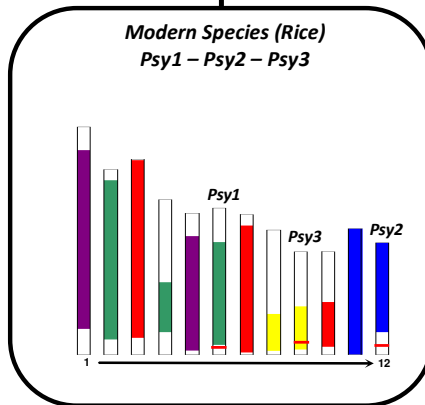
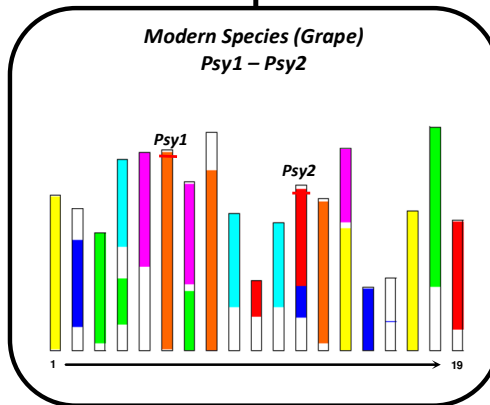
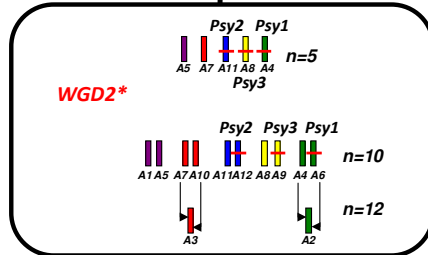
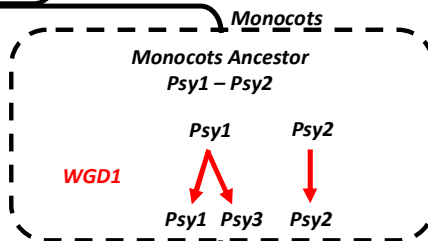
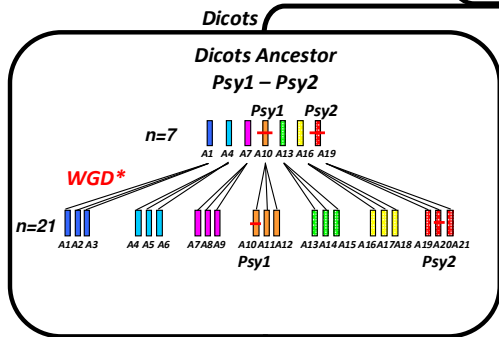


Plant Cell (2005) 17:1033-45

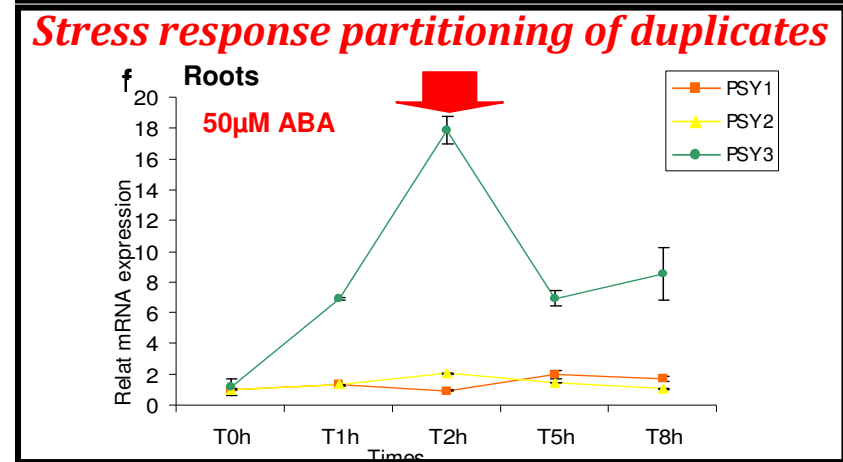
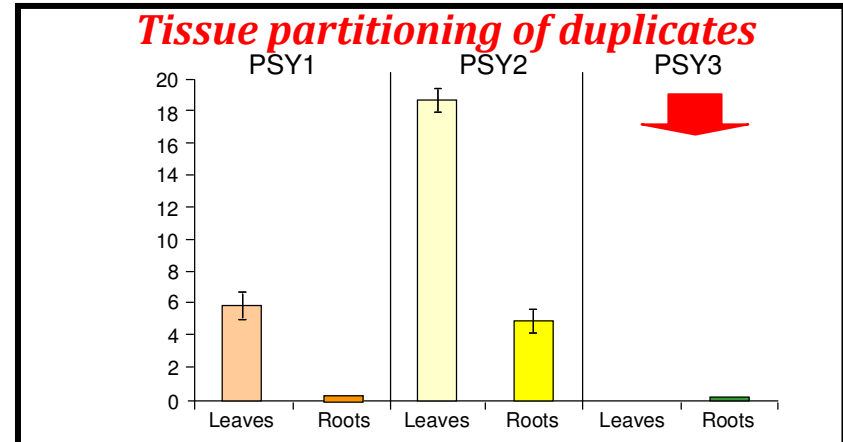
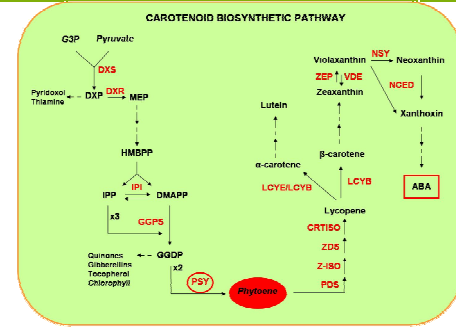


Stress (ABA) Response Acquired by Tetraploidization

Monocots-Dicots
Ancestor
Psy1 – Psy2



PSY duplicates



BMC Genomics (2012) 13:221.



Impact of Duplications (WGD-SD-CNV) on Traits

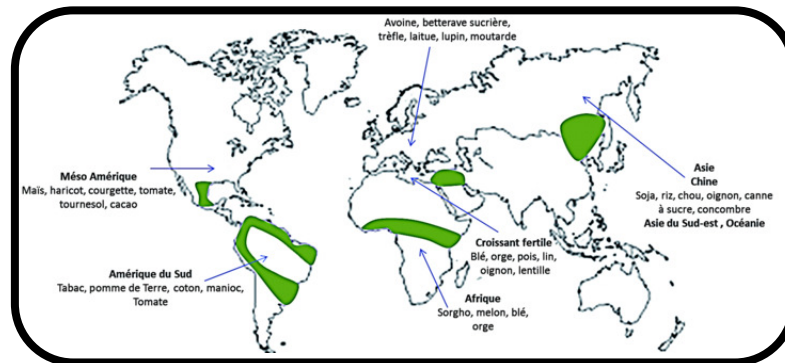
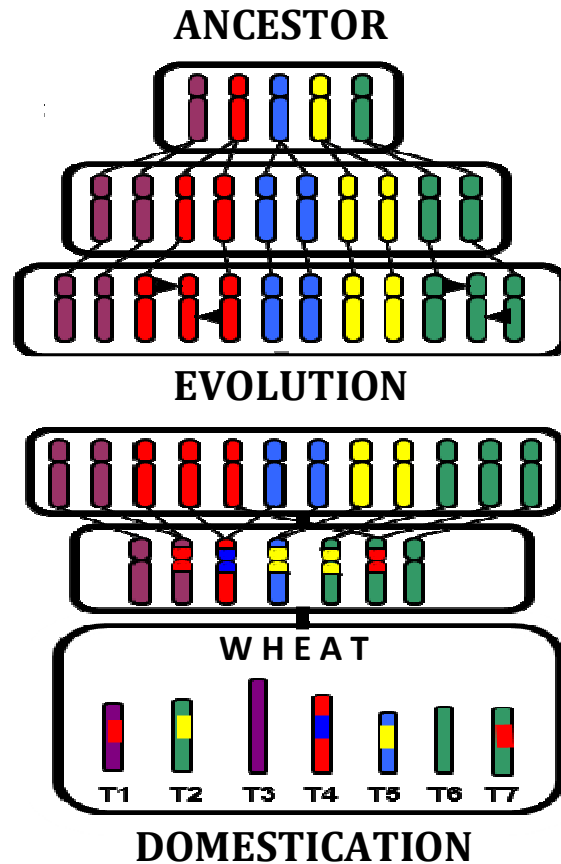


Locus	Function	plant species	(WGD) (SD) (CNV)	References
<i>Terminal flower</i>	Flowering time	Sunflower	WGD	Blackman et al. 2011
<i>CONSTANS</i>	Flowering time	Barley	WGD	Cockram et al. 2010
<i>NA</i>	Fiber	Cotton	CNV	Rong et al 2010, Zhu et al. 2011
<i>FLC</i>	Flowering time	Arabidopsis	SD	Nah et al. 2010 Rosloski et a. 2010
<i>FLT</i>	Flowering time	Brassica	SD	Wang et al. 2099
<i>Rxp</i>	-	Soybean	WGD	Kim et al. 2009
<i>Ha</i>	Grain quality	Wheat	CNV	Chantret et al. 2005
<i>S locus</i>	Self incompatibility	Brassica	CNV	Zhang et al. 2011
<i>Oak</i>	Incompatibility	Arabidopsis	CNV	Smith et al. 2011
-	Incompatibility	Arabidopsis	WGD	Bikard et al. 2009
-	Etiolation	Rice	WGD	Mao et al. 2011
<i>GW2</i>	kernel size and weight	Maize	WGD	Li et al. 2010
<i>SUN</i>	Fruit shape	Tomato	SD	Xiao et al. 2008
<i>P</i>	Pigmentation	Maize	CNV	Chopra et al. 1998
<i>C3/C4</i>	Photosynthesis	Sorghum - Maize	WGD - CNV	Wang et al. 2009
<i>CDPK</i>	Stress response	Wheat - Rice	WGD	Geng et al. 2011

☑ Numerous traits driven by genome duplications (large-scale & local-based)

GPGR2 (2013) in press

EVOLUTION & DOMESTICATION.



Gene mutations:

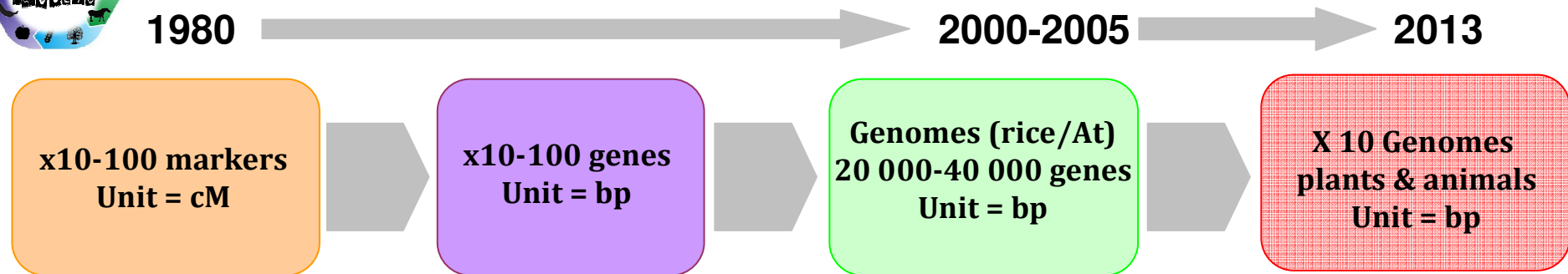
- **Ramification/Tiller**
(genes *Tb1* maize, *MOC* rice)
- **Seed shattering**
(gene *Sh1* rice, maize)
- **Flowering/earliness**
(gene *VRN* wheat)
- **Compact kernel**
(gene *Q* wheat)



*Favour growing
and harvesting*



Comparative Genomics from 80' to 2013

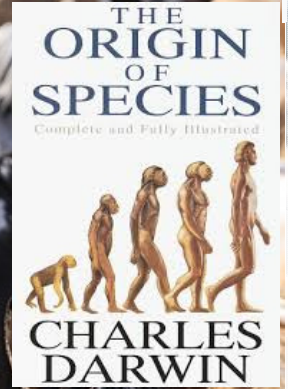
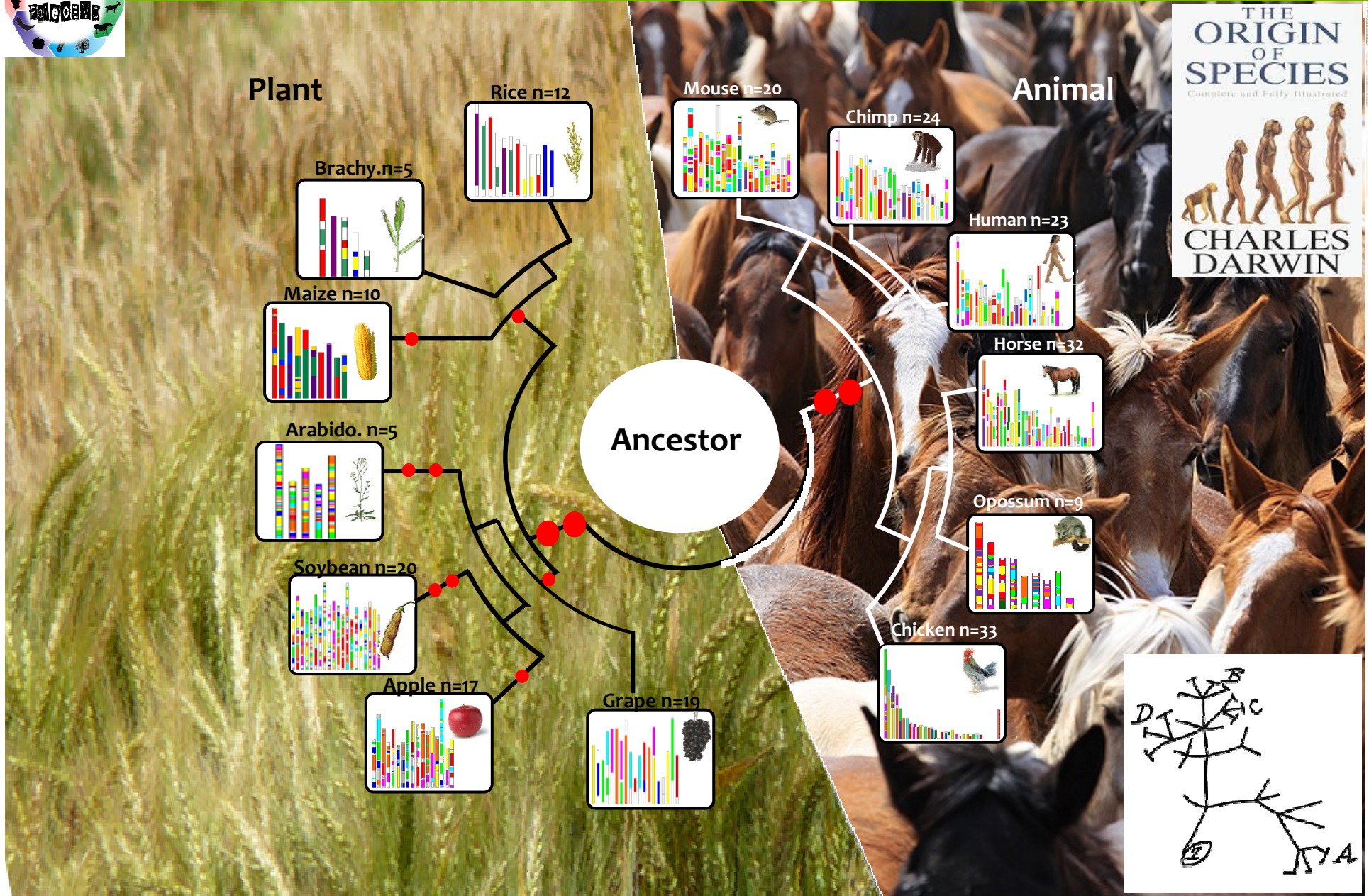


MAIN CONCLUSIONS:

- **Ancestor** : Structure identification (reduced in chr and genes);
- **Duplications**: Common/ancestral and recent in plants;
- **Modern species** : Specific shuffling of ancestor;
- **Plasticity**: Duplicated gene redundancy eroded;
- **Function**: Duplicates as a matrix for new function;
- **Traits**: Duplicates as a matrix for novel/adapted traits.



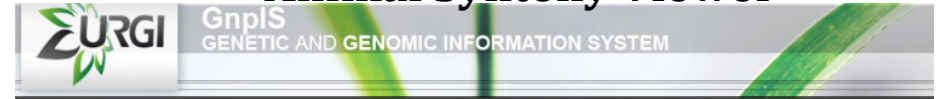
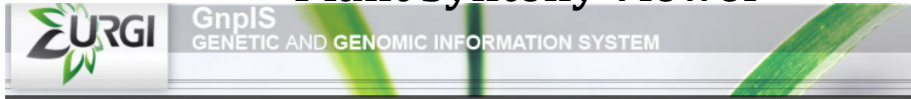
From Darwin (1859) to PaleoGenomics (2013).





Plant Synteny Viewer

Animal Synteny Viewer



- Bienvenue murat
Déconnexion
- Principal
 - ACCUEIL
 - A PROPOS
- Recherches globales
 - CONTACTS
 - ORGANISMES
- Documentation
 - GUIDE DE L'UTILISATEUR
 - FAQ
 - NOUVEAUTÉS
 - NOTES DE VERSION
- GnplS
 - SOUMISSION
 - GNPIS
 - EPHESIS
 - GNPARRAY
 - GNPGENOME
 - GNPMAP
 - GNPPROT
 - GNPSEQ
 - GNPSEQNGS
 - GNPSNP
 - SIREGAL
 - SYNTENY

Synteny / Plant Synteny Viewer

▼ Search parameters

Search by gene name:

Search by ancestral chromosome:

Search by modern chromosome:

▼ Display parameters

Enable/disable the complementary search of homolog genes along reference chromosome

Change modern chromosome window size:

Change ancestral chromosome window size:

Synteny / Animal Synteny Viewer

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- GNPIS
- EPHESIS
- GNPARRAY
- GNPGENOME
- GNPMAP
- GNPPROT
- GNPSEQ
- GNPSEQNGS
- GNPSNP
- SIREGAL
- SYNTENY

▼ Search parameters

Search by gene name:

Search by human chromosome:

Search by modern chromosome:

▼ Display parameters

Enable/disable the complementary search of homolog genes along reference chromosome

Change modern chromosome window size:

Change Human chromosome window size:



Collaboration Network.

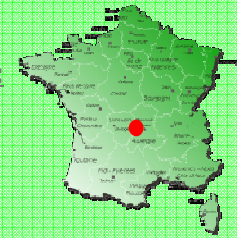
PaleoEVO group



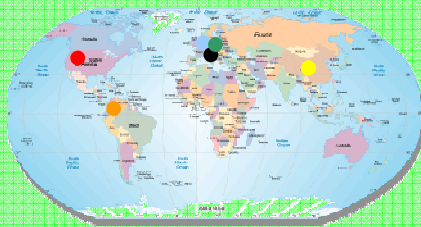
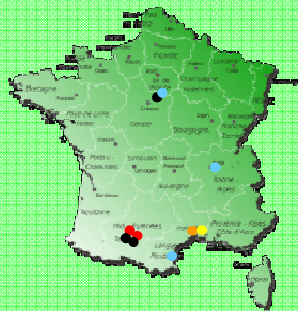
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Fundings



PaleoGenomics & Evolution (group PaleoEVO). J.Salse.
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THANK
YOU
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