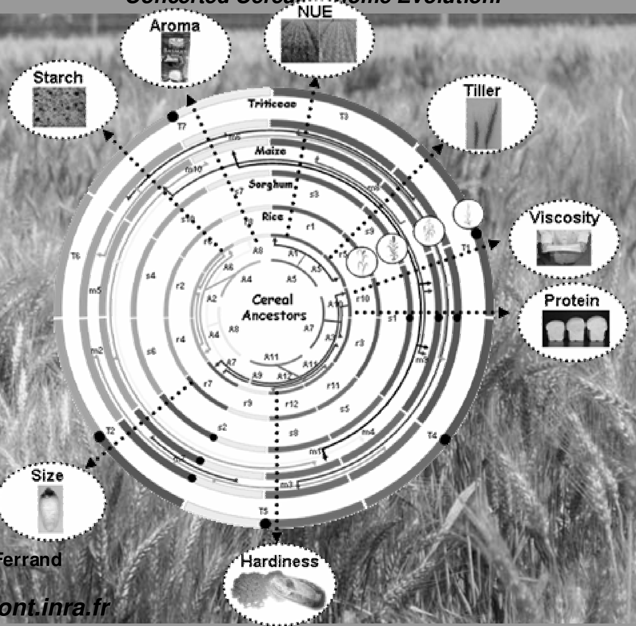
Cross-Genome Map Based Cloning of Ortho-metaQTL in Wheat Unravels New Evidence for Concerted Cereal Genome Evolution.



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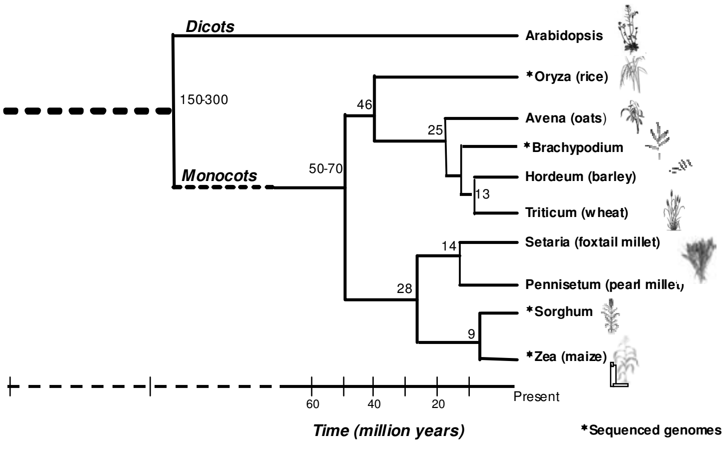
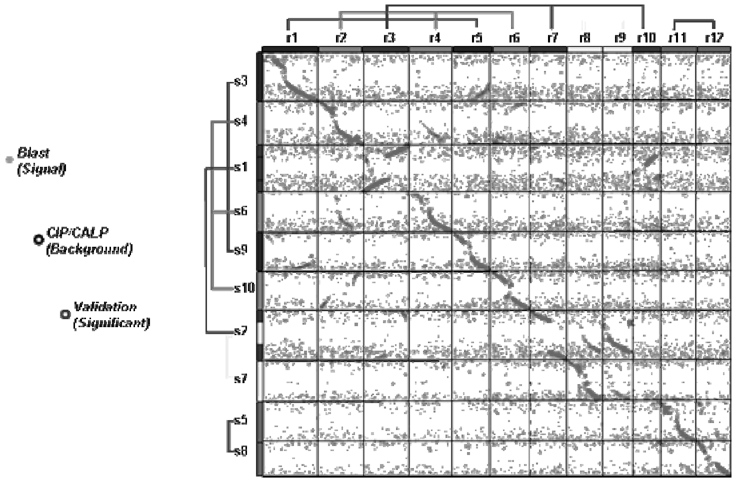
Cereal phylogeny



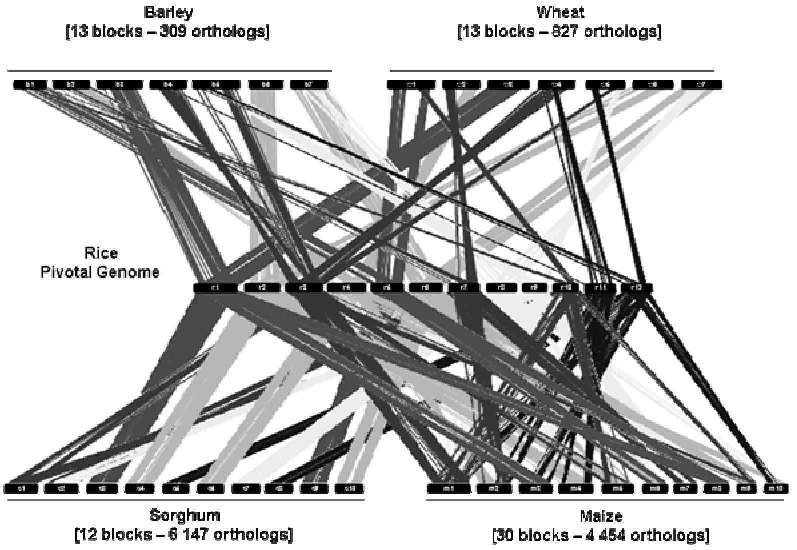
- **Cereals have diverged from a common ancestor 50-70 MYA**
- **Tools in bioinformatics, mathematics, statistics**

Standards for Comparative Genomics



Brief. In Bioinf. (2009) in press

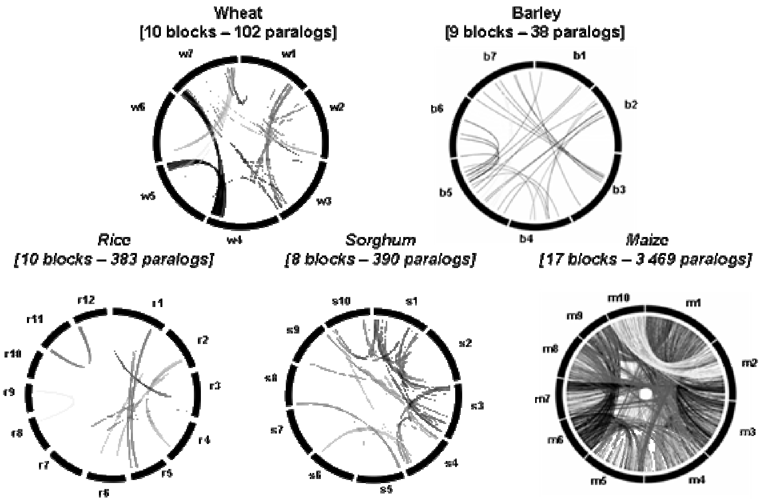
Synteny between Wheat, Barley, Rice, Maize, Sorghum



➥ 80% homologs – 50% single copy homologs – 20% orthologs

Plant Cell (2008) 20(1):11-24
PNAS (2009) in press

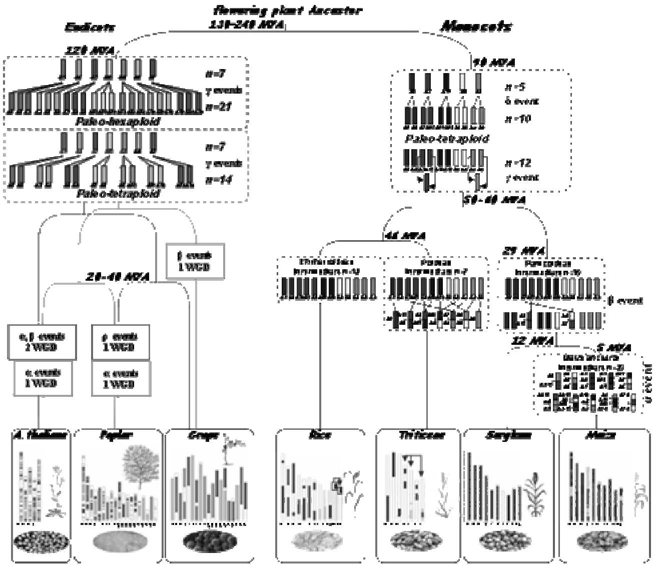
Duplications within Wheat, Barley, Rice, Maize, Sorghum



↳>50 % genome duplicated through polyploidy (WGD) (vs aneuploidy)

Plant Cell (2008) 20(1):11-24
PNAS (2009) in press

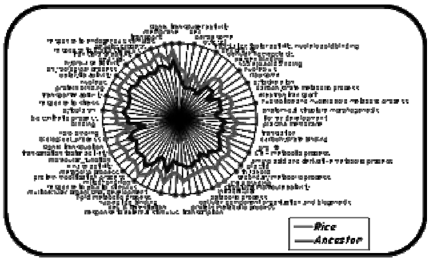
Toward an Angiosperm Ancestor Genome Structure

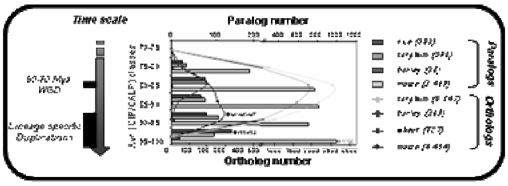


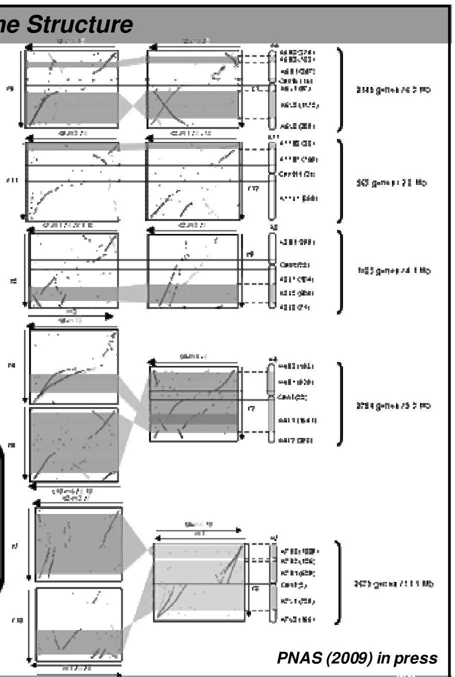
PNAS (2009) in press

Ancestor Genome Structure

9 138 genes
33 Mb

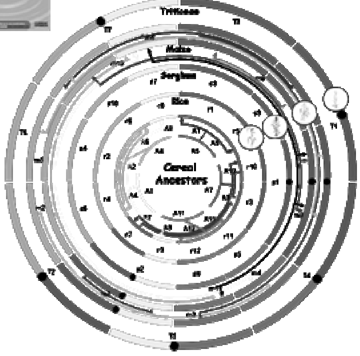






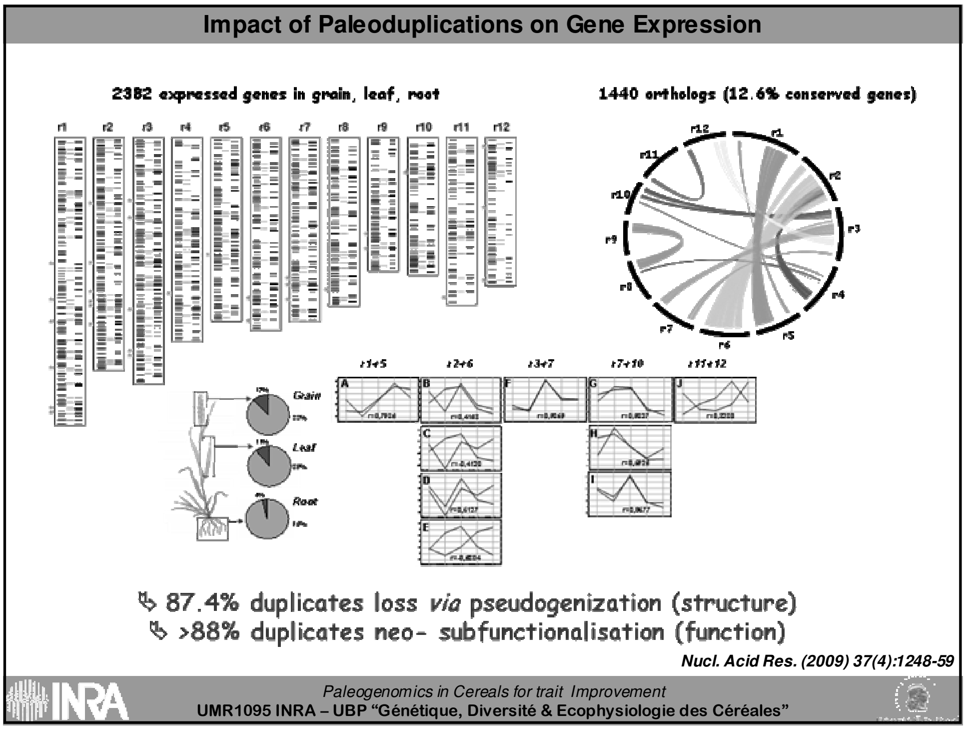
PNAS (2009) in press

The 'Inner Circle' of the Cereal Genomes



Salse J et al.
The 'inner circle' of the cereal genomes.
Curr Opin Plant Biol. 2009 12(1):1-7
Poster 8

Devos KM et al.
Updating the "crop circle".
Curr Opin Plant Biol. 2005 8(2):155-62



Impact of Paleoduplications on Gene Expression

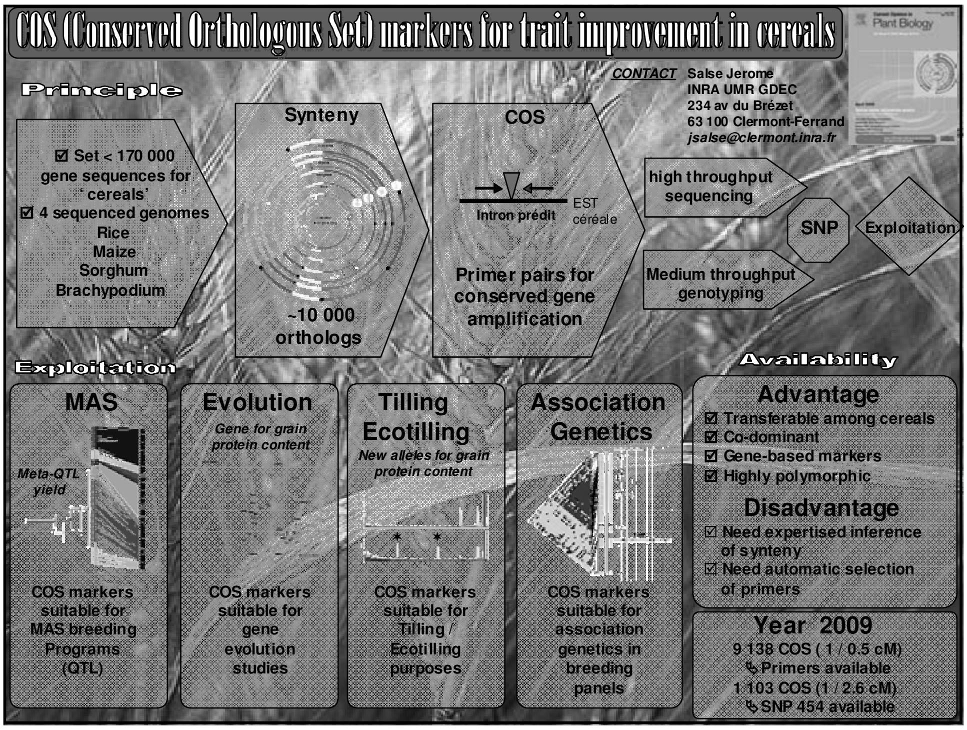
2382 expressed genes in grain, leaf, root

1440 orthologs (12.6% conserved genes)

↳ 87.4% duplicates loss *via* pseudogenization (structure)
↳ >88% duplicates neo- subfunctionalisation (function)

Nucl. Acid Res. (2009) 37(4):1248-59

Paleogenomics in Cereals for trait Improvement
UMR1095 INRA – UBP "Génétique, Diversité & Ecophysiologie des Céréales"



COS (Conserved Orthologous Set) markers for trait improvement in cereals

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Principle

☑ Set < 170 000 gene sequences for ' cereals'
☑ 4 sequenced genomes
Rice
Maize
Sorghum
Brachypodium

Synteny

~10 000 orthologs

COS

Primer pairs for conserved gene amplification

high throughput sequencing

Medium throughput genotyping

SNP

Exploitation

Exploitation

MAS

COS markers suitable for MAS breeding Programs (QTL)

Evolution

Gene for grain protein content

COS markers suitable for gene evolution studies

Tilling Ecotilling

New alleles for grain protein content

COS markers suitable for Tilling / Ecotilling purposes

Association Genetics

COS markers suitable for association genetics in breeding panels

Availability

Advantage

- ☑ Transferable among cereals
- ☑ Co-dominant
- ☑ Gene-based markers
- ☑ Highly polymorphic

Disadvantage

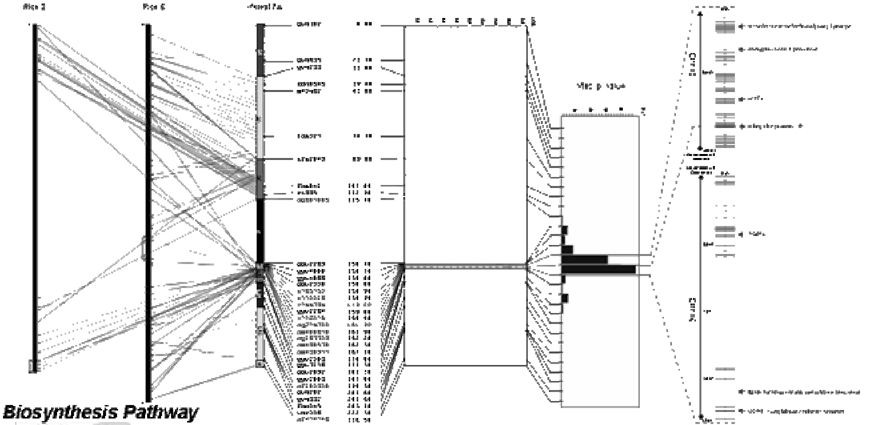
- ☑ Need expertised inference of synteny
- ☑ Need automatic selection of primers

Year 2009

9 138 COS (1 / 0.5 cM)
↳Primers available
1 103 COS (1 / 2.6 cM)
↳SNP 454 available

Synteny-based cloning

Topic: Pentosan Viscosity (PV) trait measured with capillary viscometer (AVS 310 Schott Garate, Germany) reflects the fraction of soluble pentosans (mainly Arabinoxylans, Ax) considered as dietary fibers.



Ax Biosynthesis Pathway

Funct. Int. Genomics (2009) in press

Paleogenomics in Cereals for Trait Improvement

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Umar Masood (Pdh)
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Stéphane Bénédit
Nicolas Guilhot

Gilles Charmet / Catherine Feuillet

Collaboratos:

- **Comparative Genomics (Rice)**
  Richard Cooke / Michel Delseny
- **Comparative Genomics (Barley)**
  Tim Close / Nils Stein / Robbie Waugh
- **Comparative Genomics (Maize, Sorghum)**
  Jo Messing
- **Comparative Genomics (Brachypodium)**
  Mike Bevan, Klaus Mayer
- **Comparative Genomics (Tools / Evolution)**
  Emmanuel Courcelle, Thomas Faraut, Eric Tannier