Paleogenomics in Cereals for trait Improvement

UMR1095 INRA – UBP “Génétique, Diversité & Ecophysiologie des Céréales”

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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

80% homologs - 50% single copy homologs - 20% orthologs

Synteny between Wheat, Barley, Rice, Maize, Sorghum

60% homologs - 50% single copy homologs - 20% orthologs
Duplications within Wheat, Barley, Rice, Maize, Sorghum

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

PNAS (2009) in press

Toward an Angiosperm Ancestor Genome Structure

PNAS (2008) in press
Ancestor Genome Structure

9 136 genes
33 Mb

The ‘Inner Circle’ of the Cereal Genomes

Boiza J et al.
The ‘inner circle’ of the cereal genomes.

Demas K et al.
Updating the ‘snap shot’.

PNAS (2009) in press

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Impact of Paleoduplications on Gene Expression

PER expressed genes in grain, leaf, root
1600 orthologs (2.2% conserved genes)

- 57.4% duplicates loss due pseudogenization (structure)
- 58.5% duplicates neo-functionalization (function)


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COS markers suitable for breeding programs

Tilling: New allele for grain protein content

Association Genetics

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

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

Year: 2009
- 186 COS (1.5% C)
- Primers available
- 45 COS (1% C)
- SNP array available