Agropolis Resource Centre
for Crop Conservation,
Adaptation & Diversity

Comparative population genomics in crops and their wild relatives : assessing the impact of domestication on crop diversity

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& ARCAD research teams

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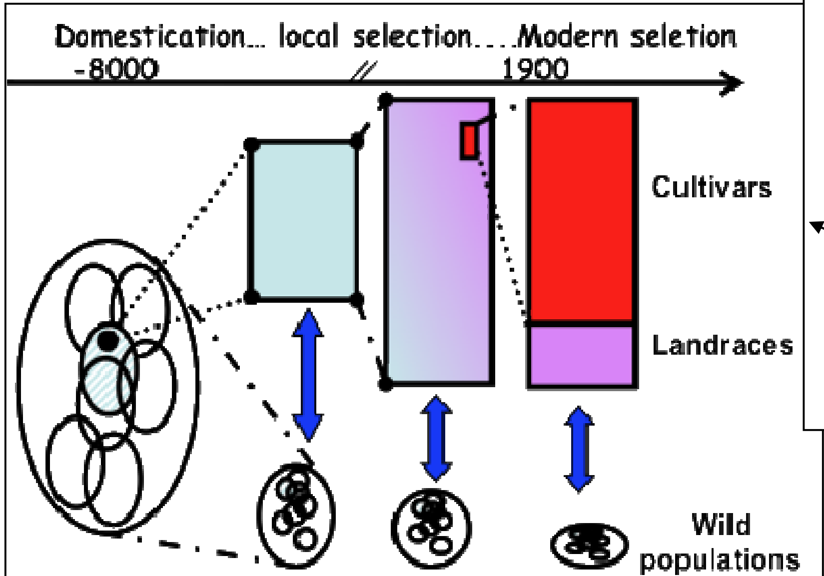
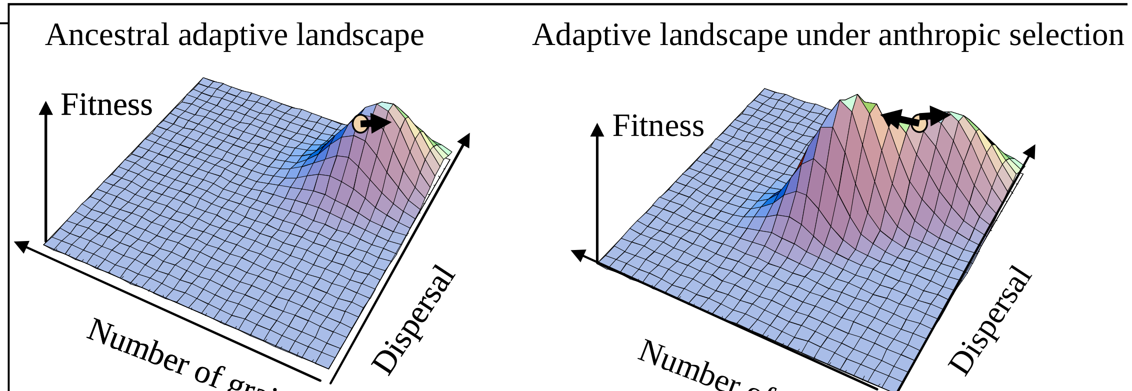
PGR Secure-Eucarpia Conference, Cambridge, 17 June 2014

Why studying domestication ?

- A long-term evolutionary experiment



(Glémin & Bataillon 2009)



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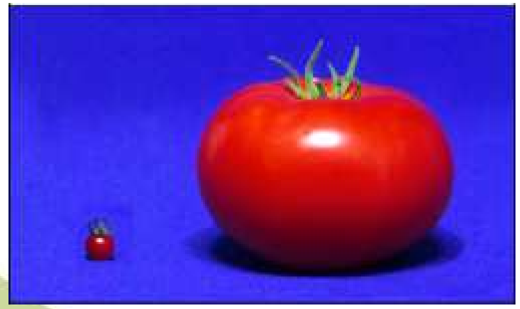
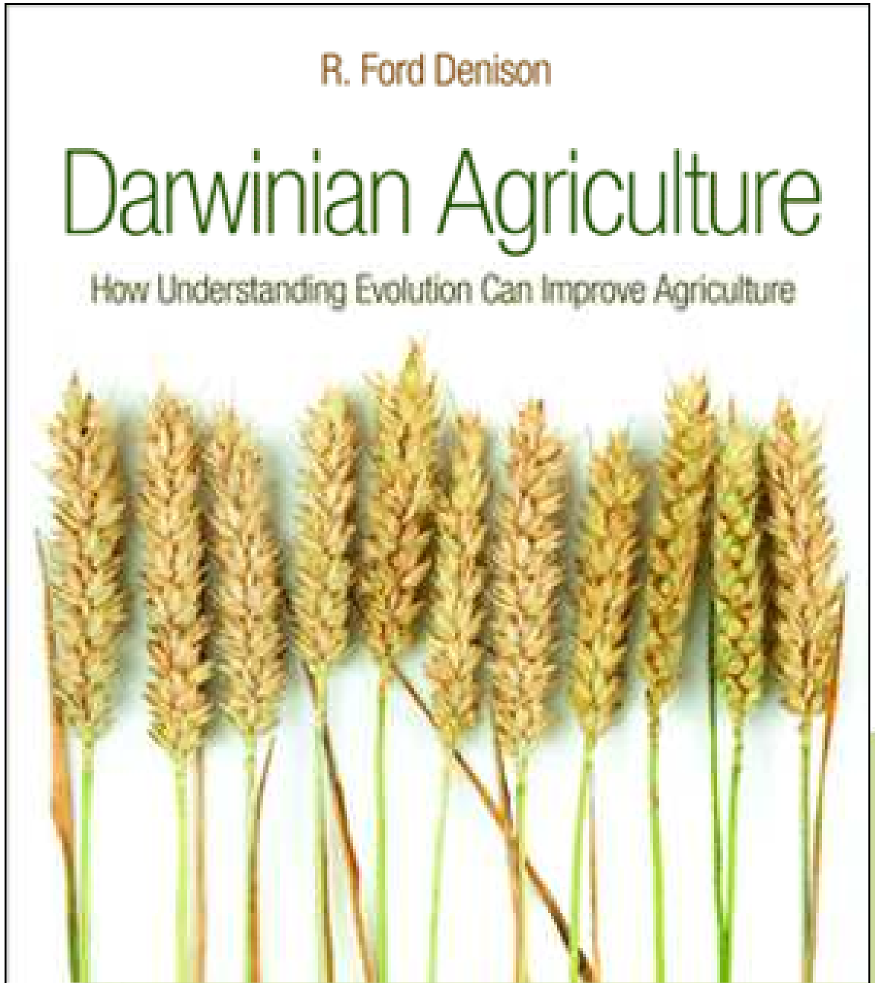


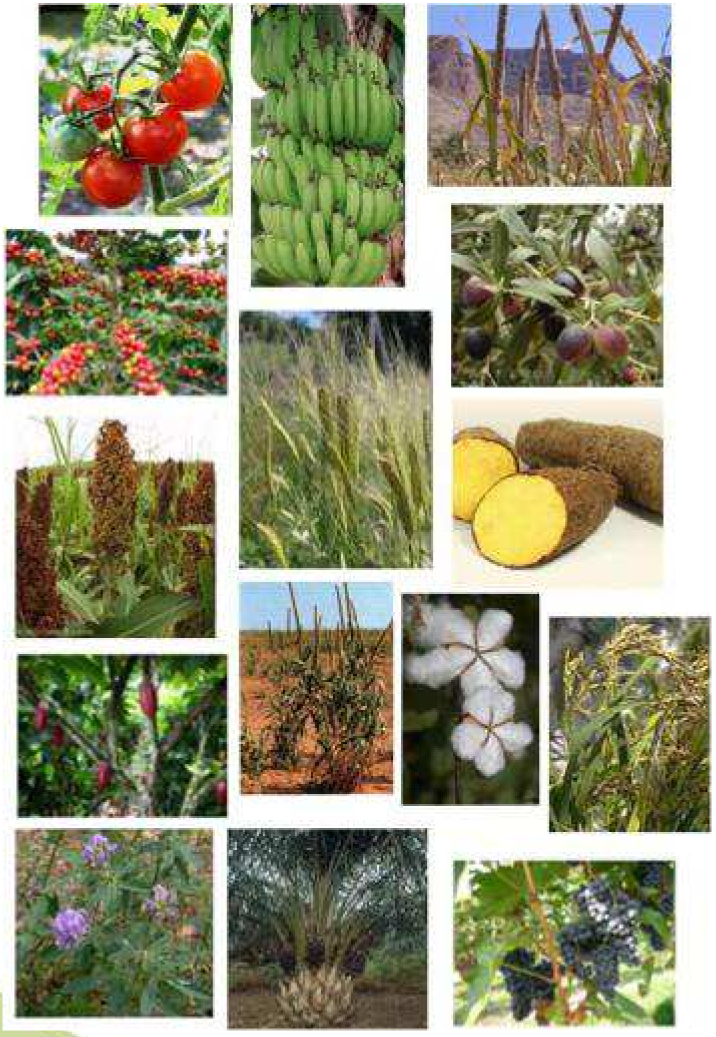
Why studying domestication ?

- A long-term evolutionary experiment

- Understand where the crops come from and draw lessons



Comparative population genomics of crops and their wild relatives



- Evolution of genetic diversity
  - Loss and recovery
  - Domestication scenarios
- Selection during domestication
  - Domestication genes
  - Cost of domestication
- Comparative approaches
  - Effects of life history traits
  - Convergent evolution
- Comparative evolution of gene families

Target crops

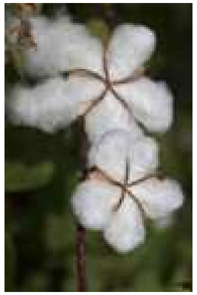
Banana	Monocot	Perennial	Outcrossing
Palm tree	Monocot	Perennial	Outcrossing
Yam	Monocot	Annual	Out/clonal
Einkorn	Monocot	Annual	Selfing
Pearl millet	Monocot	Annual	Outcrossing
African rice	Monocot	Annual	Selfing
Sorghum	Monocot	Annual	Selfing
Fonio millet	Monocot	Annual	Selfing
Cocoa	Dicot	Perennial	Outcrossing
Coffee	Dicot	Perennial	Outcrossing
Cotton	Dicot	Perennial	Selfing
Olive tree	Dicot	Perennial	Outcrossing
Alfalfa	Dicot	Perennial	Outcrossing
Grapevine	Dicot	Perennial	Outcrossing
Tomato	Dicot	Annual	Selfing



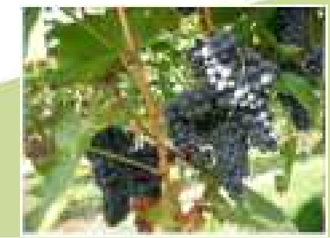




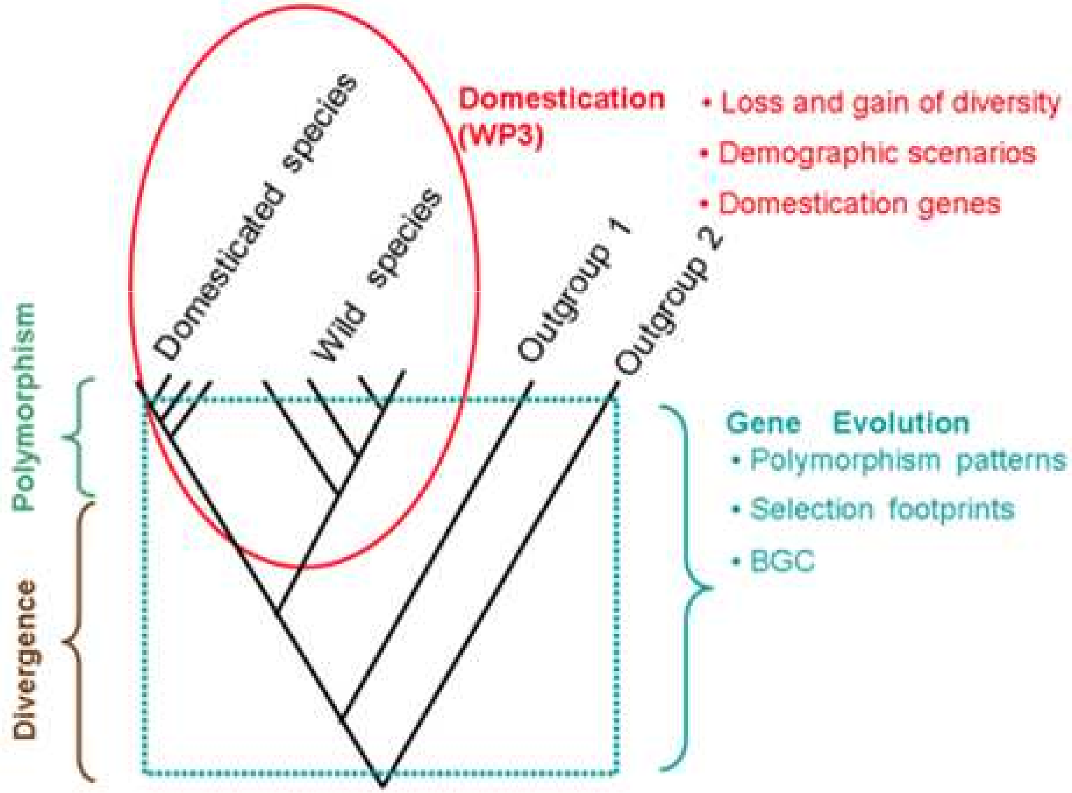




A single sampling strategy



Technical choices

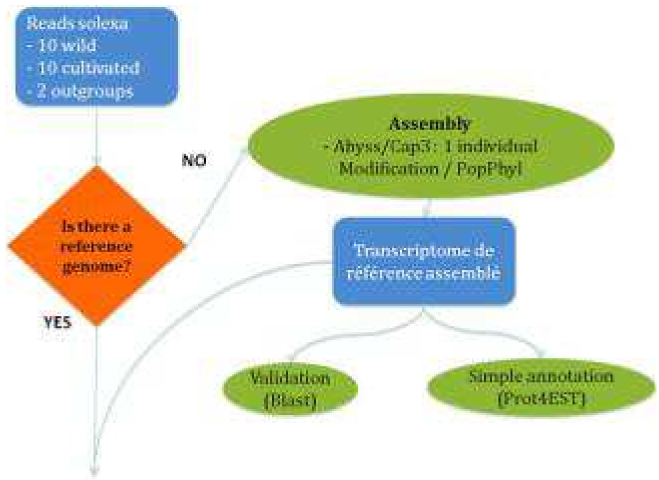
- Goals
  - Reduce complexity
  - Access to coding sequences
  - Access to expression levels

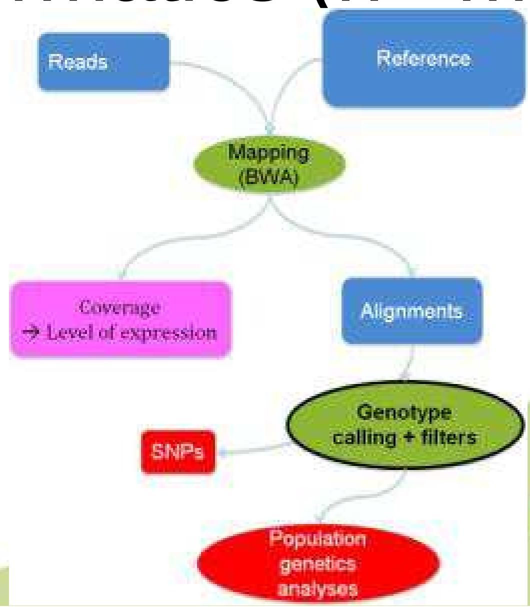
    ➔ Transcriptome sequencing
  - Be able to use local technological platforms (GenoToul, MGX Montpellier)
    - From 454 Roche to Solexa High-seq
    - Standardization of protocols
    - Development of "pre NGS" skills and know-how

→ Attractivity, Connectivity

Some figures

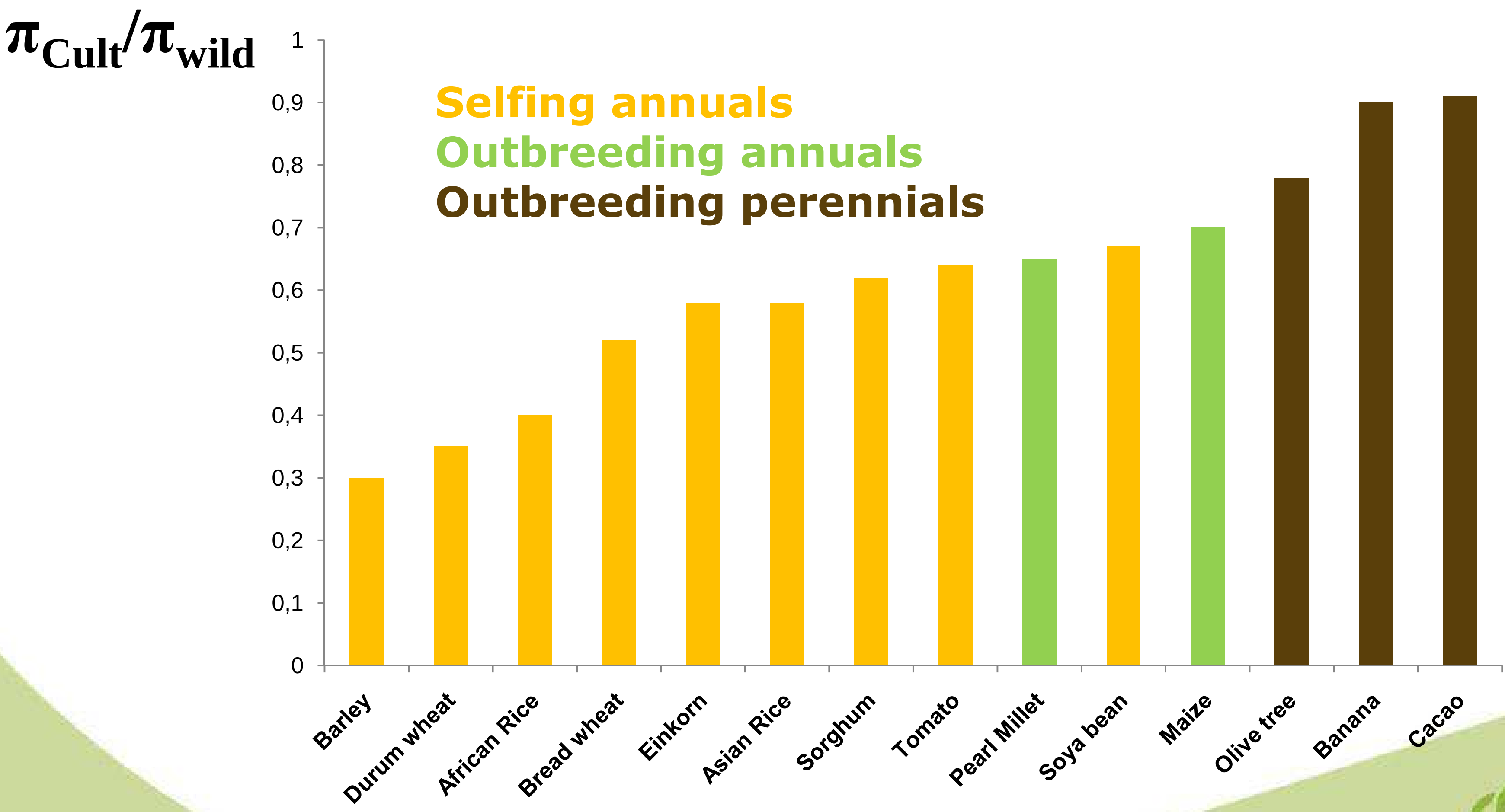
- 332 RNAseq banks
- 45 species
- 35 lanes High-Seq 2000
- 13.3 billions reads (75-100bp)
- n months of work in bioinformatics (n= many)





Comparison across crops of diversity loss over domestication

Impact of life history traits



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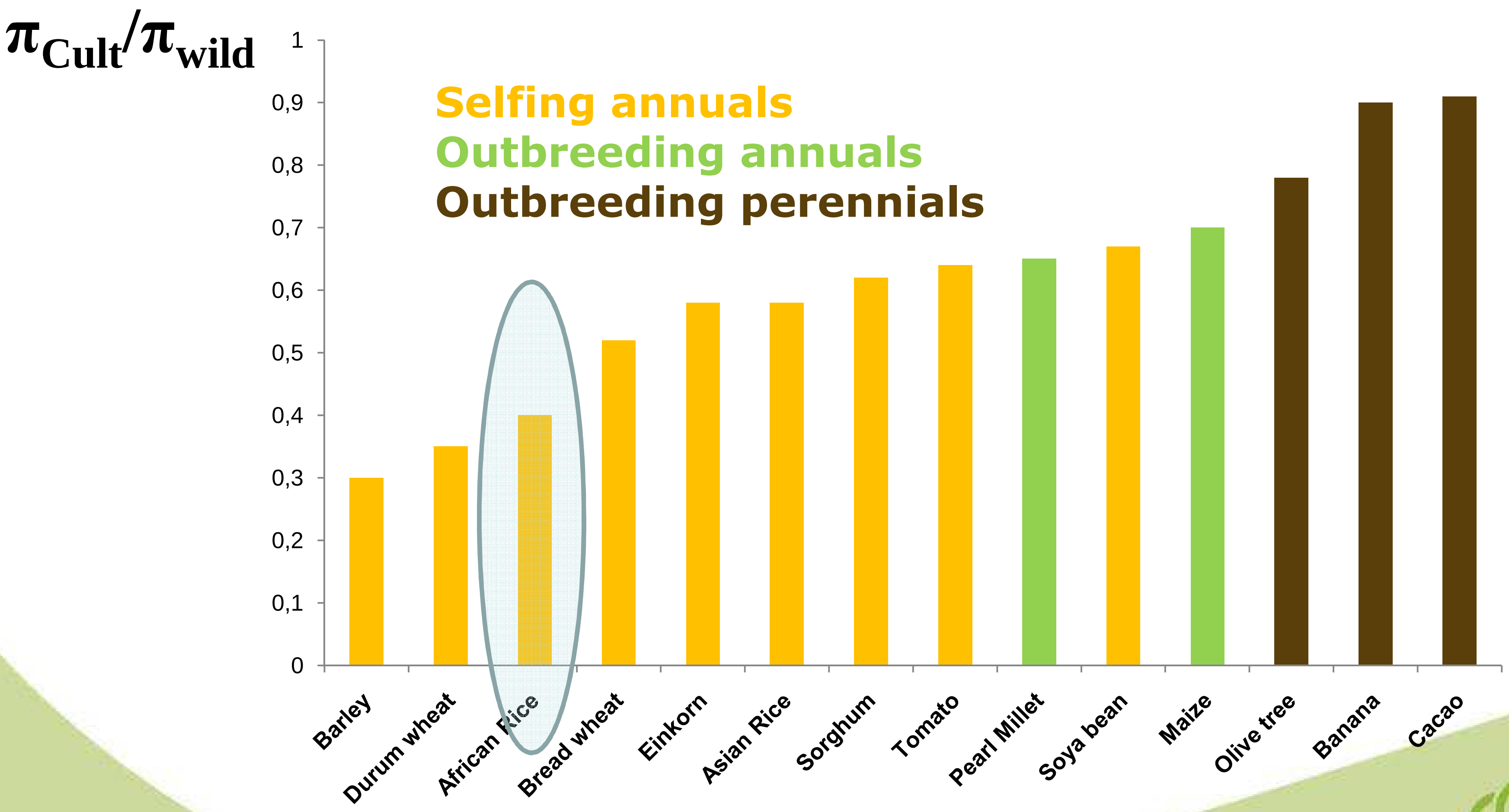
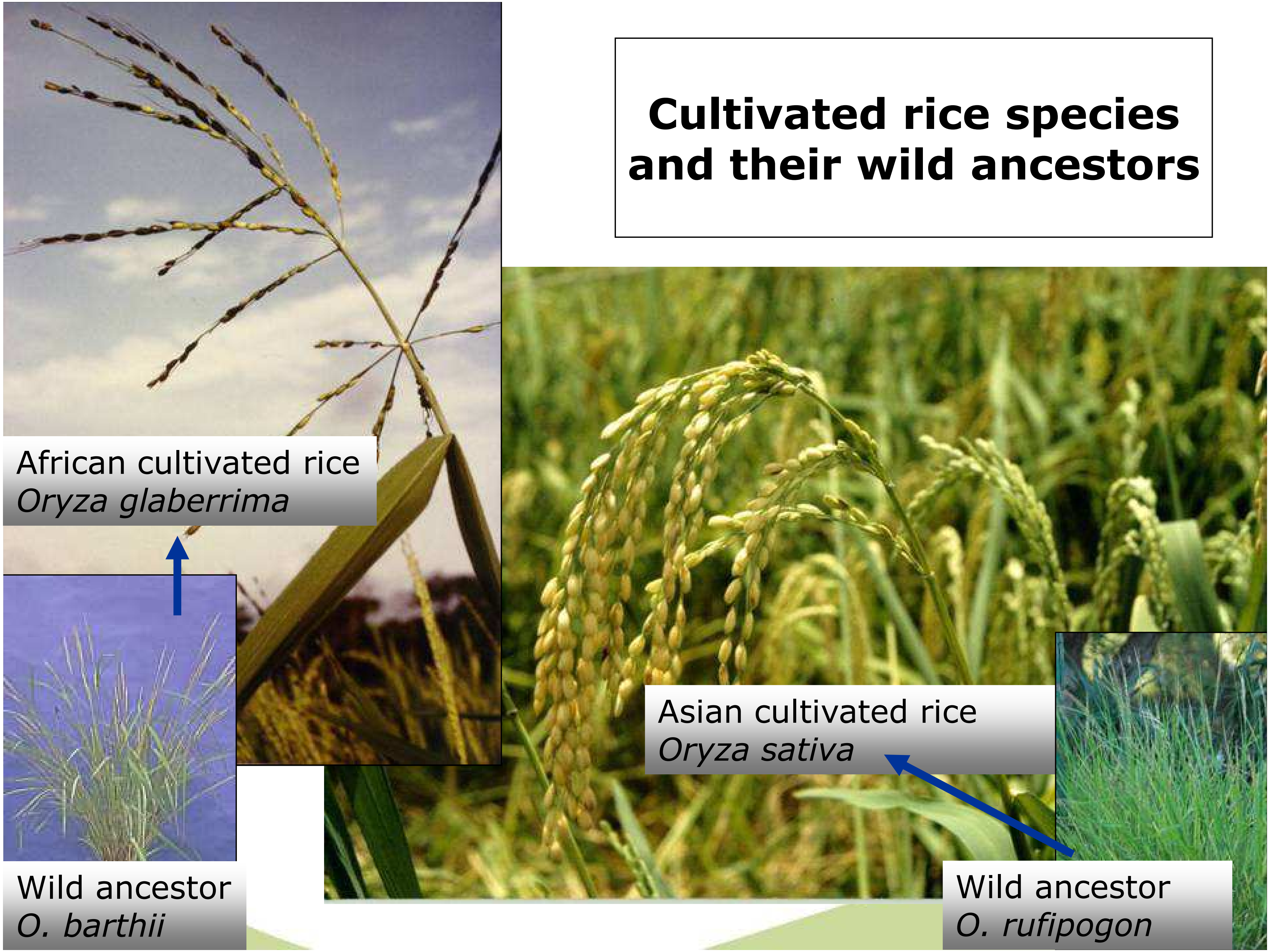
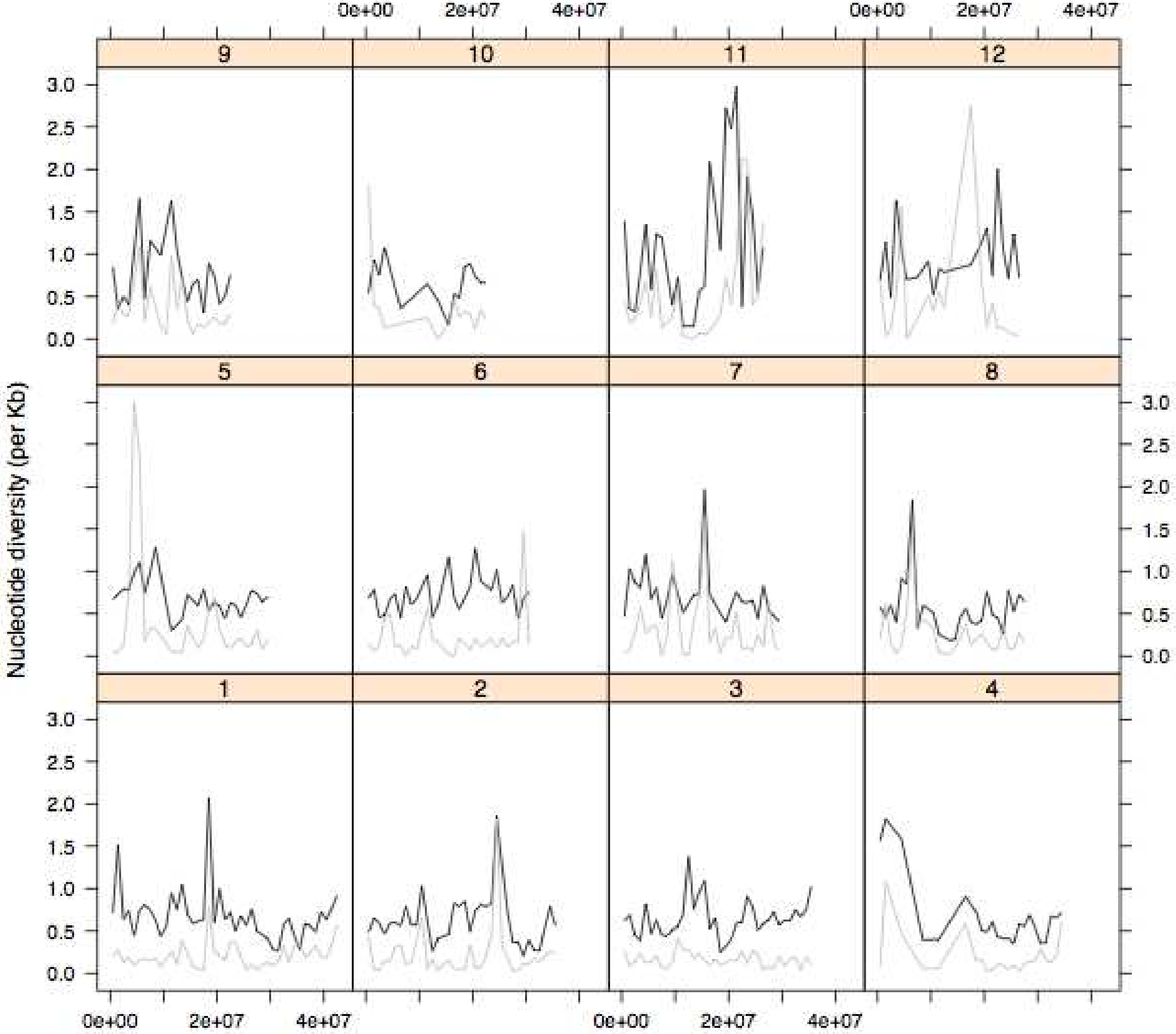


Cultivated rice species and their wild ancestors



Domestication of the African rice

Loss of diversity



$$\frac{\pi_S(Cult)}{\pi_S(Wild)} = 0.41$$

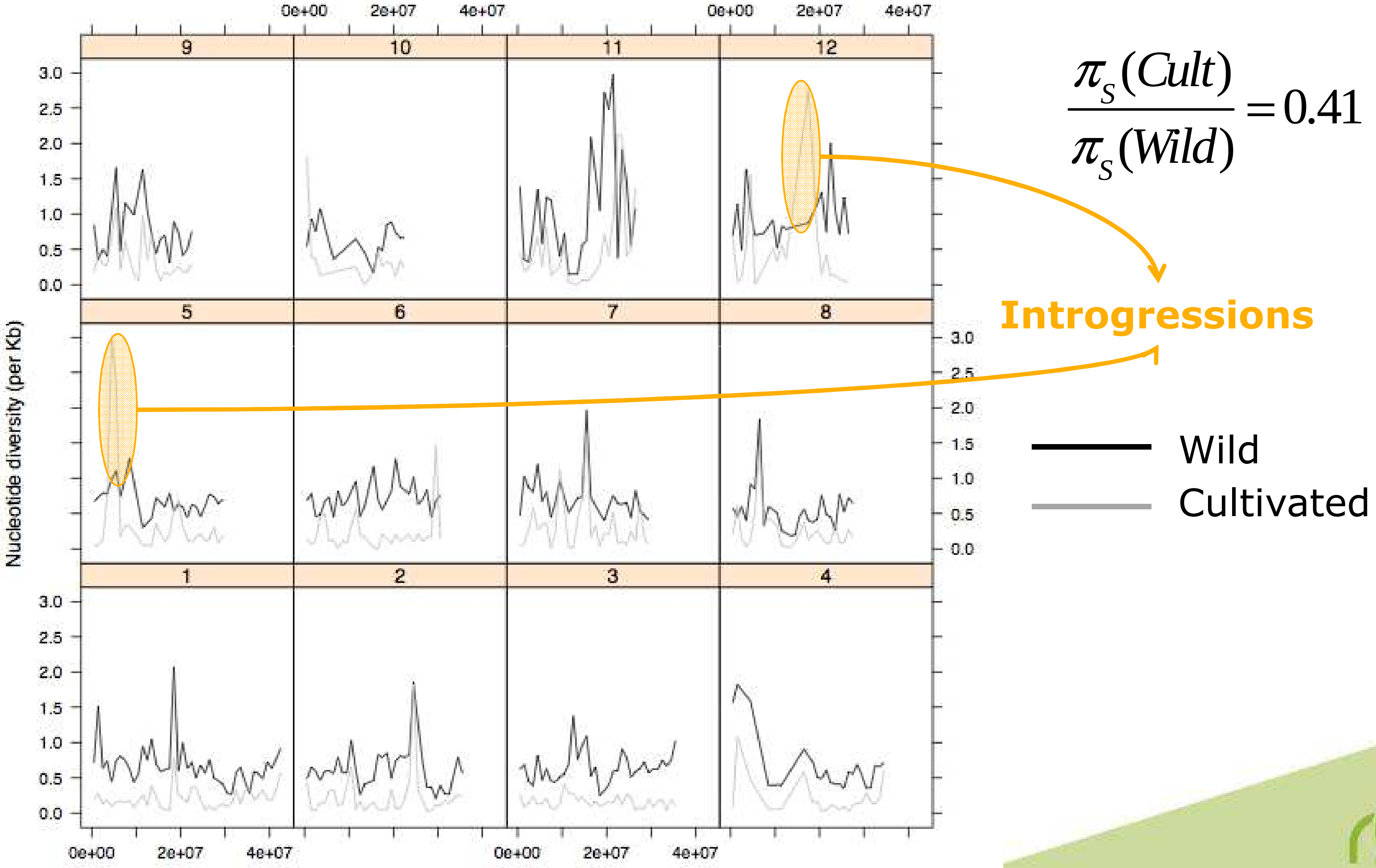
Wild

Cultivated

Nabholz et al. Mol Ecol 2014

Domestication of the African rice

Loss of diversity



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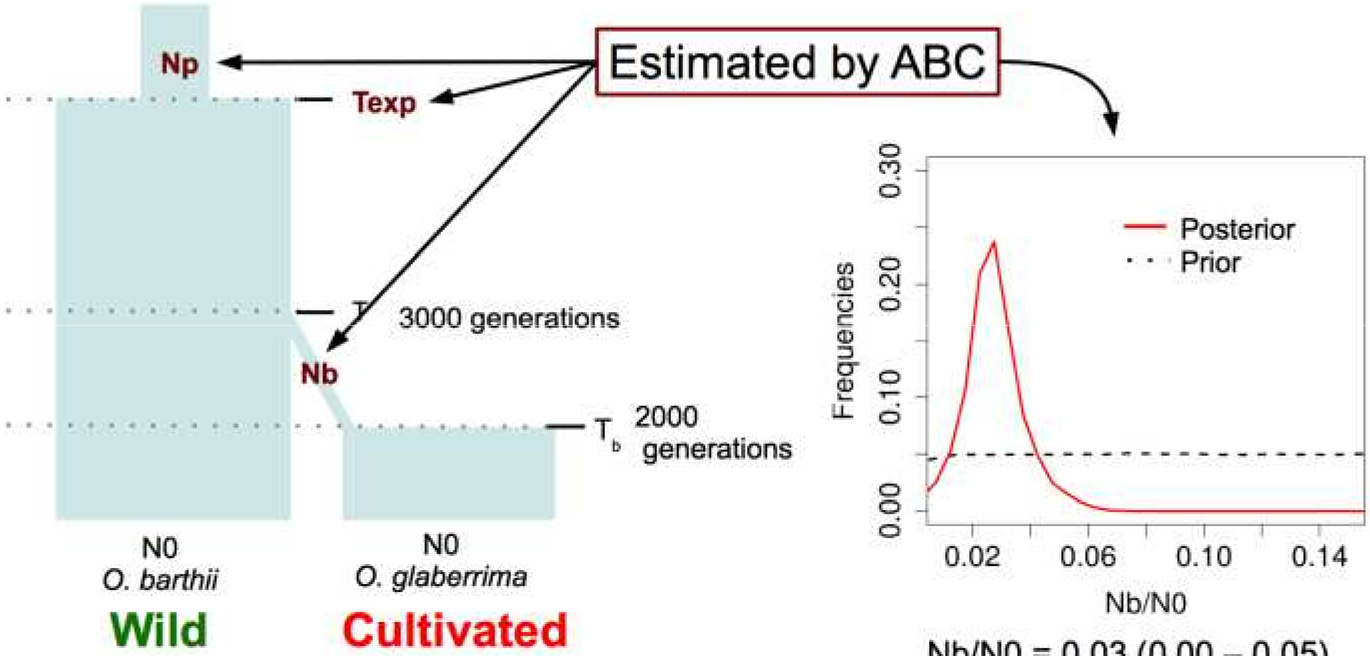
Domestication of the African rice

Estimation of the bottleneck intensity by ABC



Nb/N0 = 0.03 (0.00 – 0.05)

After Nabholz et al. Mol Ecol 2014

Domestication of the African rice

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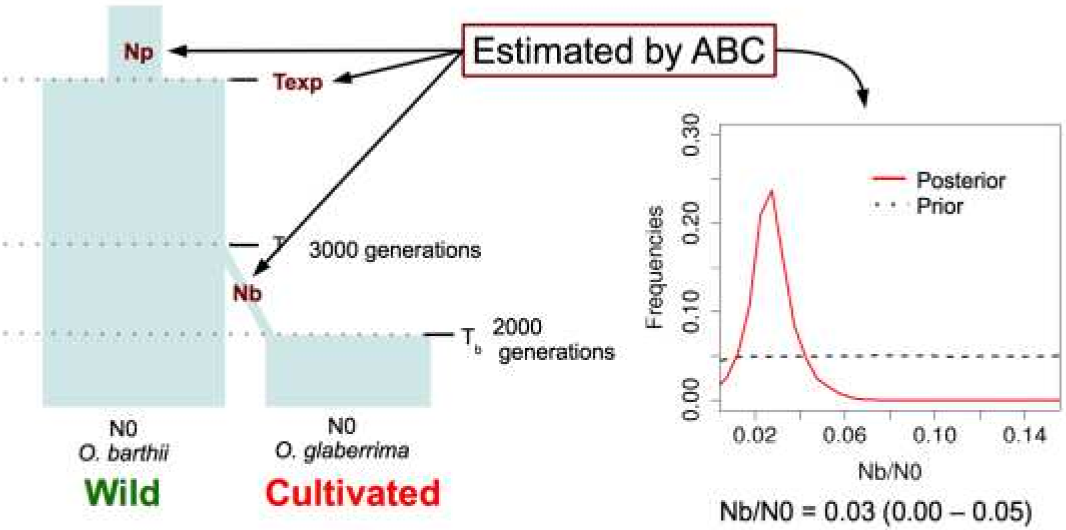
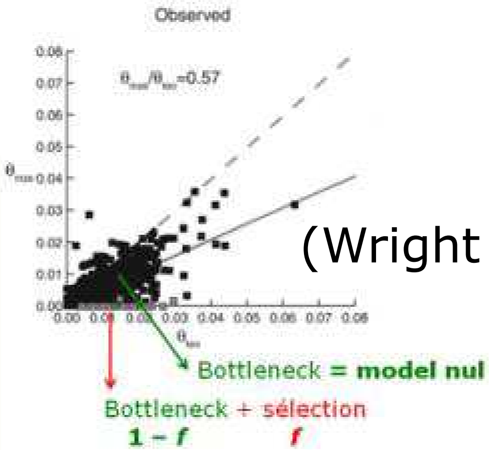


→ No outlier !

Very strong bottleneck → lack of power for detecting outliers



(Wright et al. 2005)

After Nabholz et al. Mol Ecol 2014

Domestication of the African rice

Comparison of bottleneck intensity in some cereals

Population	# genes	# sites	πs wild	π s crop	π total wild	π total crop	Ratio πwild/ πCrop	References
O. barthii / glaberrima	**12,169**	**11,987,421**	**1.40**	**0.56**	**0.69**	**0.26**	**0.41**	**This study**
T. t. dicocoides / dicoccum	21	21,720	3.60	1.20	2.70	0.80	0.33	(Haudry et al. 2007)
O. rufipogon / japonica	111	54,541	5.19	1.47	3.57	1.11	0.28	(Caicedo et al. 2007)
O. rufipogon / sativa (jap. + ind.)	111	54,541	5.19	3.20	3.57	2.29	0.61	(Caicedo et al. 2007)
Z. m. mays / parviglumis	774	230,638			9.74	6.51	0.67	(Wright et al. 2005)

African Rice

- A poorly diverse wild ancestor
- A very intense bottleneck

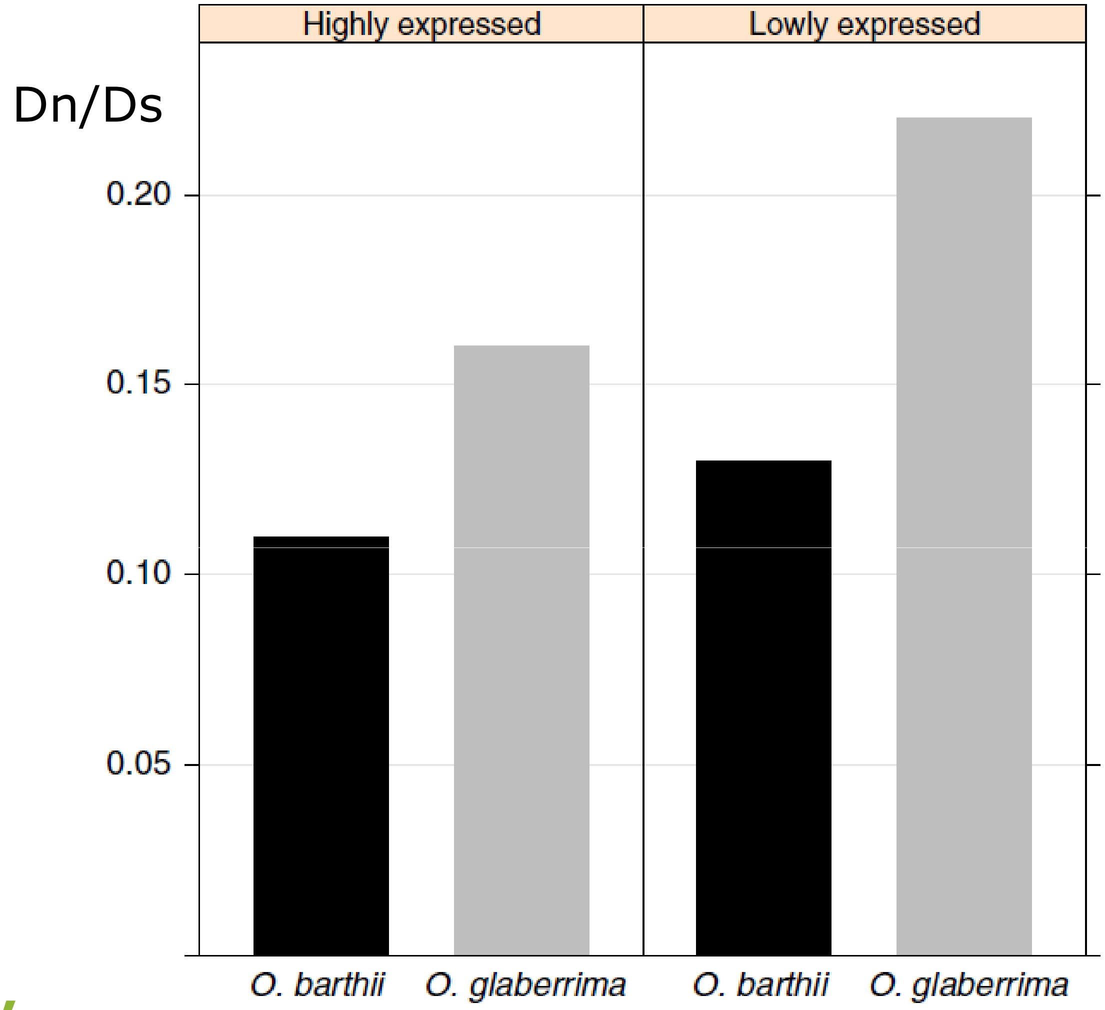
After Nabholz et al. Mol Ecol 2014

Domestication of the African rice

<u>Assumption :</u>
non synonymous mutations are mostly deleterious

➔Likely fixation of weakly deleterious alleles in the cultivated rice

➔Use wild diversity



The ratio of non synonymous (Dn) over synonymous (Ds) divergence *in O. glaberima* and *O. barthii* in highly and lowly expressed genes

Nabholz et al. Mol Ecol 2014

Conclusions

- Comparative population genomics
  - Domestication
    - Loss of diversity depends on life history traits
    - Cost of domestication in African rice
      - Very strong bottleneck during domestication
      - Likely fixation of weakly deleterious alleles
      - Usefulness of the wild ancestor diversity and wide-hybridization approcahes
  - Many advantages to having a shared conceptual approach + a standardized operational approach

Credits

- *« Comparative population genomics » leaders :* Sylvain Glémin, Jacques David
- All teams that contributed samples
- National and International partners: Guinea, Kenya, Mali, Burkina Faso, Madagascar, Morocco, Brazil, Bioversity International
- *Data production team :* Laure Sauné, Morgane Ardisson, Sylvain Santoni, Ange-Marie Risterrucci, Fabienne Morcillo
- *Bioinformatics :* Manuel Ruiz, Gautier Sarah, Jean-François Dufayard, Nicolas Galtier (for kindly providing access to the PopPhyl pipeline)
- *Post docs :* Benoit Nabholz, Yves Clément, Iris Fisher, Jacques Dainat, Concetta Burgarella
- *Students :* Emmanuel Reclus, Julia Morosini
- *Data analysis :* David Pot, Yves Vigouroux, Christopher Sauvage
- *Arcad technical coordination* : Jean-Pierre Labouisse

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www.arcad-project.org

More information

- Nabholz B, Sarah G, Sabot F, Ruiz M, Adam H, Nidelet S, Ghesquière A, Santoni S, David J, Glémin S (2014) Transcriptome population genomics reveals severe bottleneck and domestication cost in the African rice (*Oryza glaberrima*). *Molecular Ecology 23* : 2210–27

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