

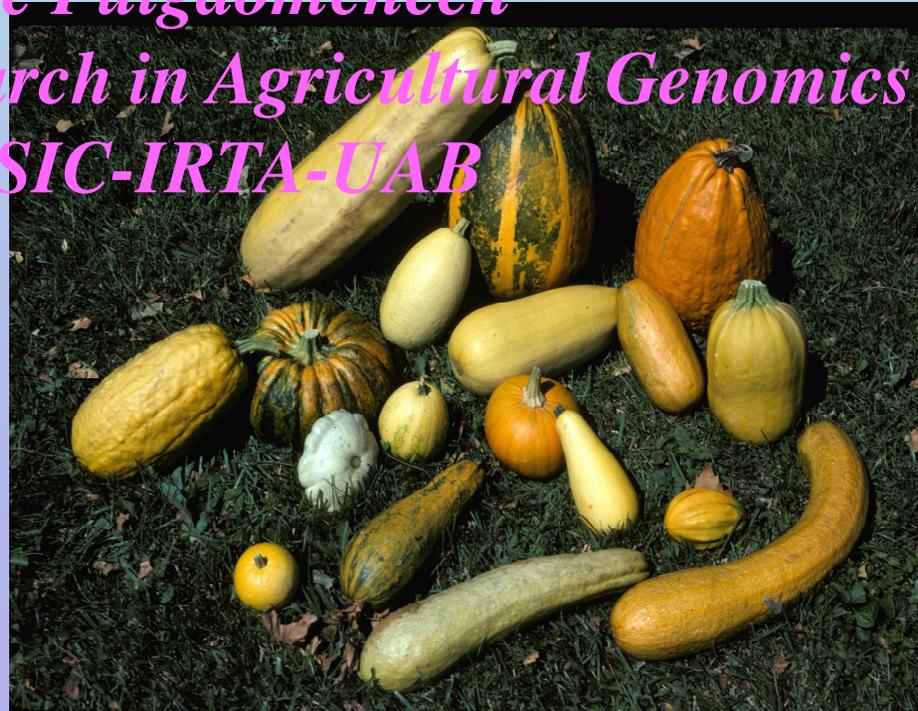


*Roundtable. The Future of Food  
Venezia 2008*

*Pere Puigdomènech*

*Centre for Research in Agricultural Genomics*

*CSIC-IRTA-UAB*



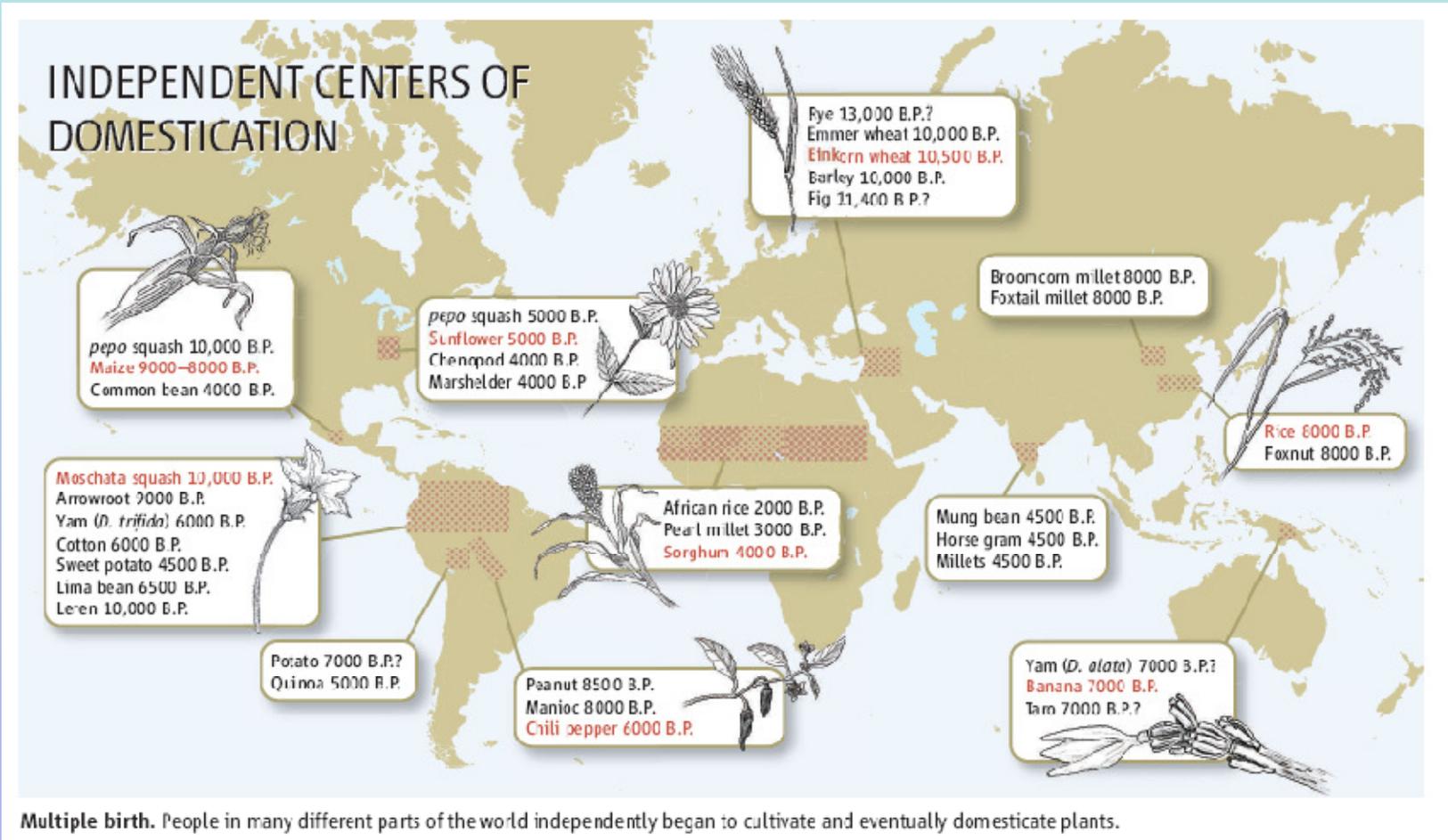
# What do we eat?

- We eat what is nutritious
- We eat what we choose as a function of our needs, our possibilities, our believes and our tastes

But also:

- We eat what we can cultivate
- We eat now what a complex industrial chain provides to us

# Plant domestication centres



**Multiple birth.** People in many different parts of the world independently began to cultivate and eventually domesticate plants.

# Maize, the gift of gods



**All in the family.** Maize and its wild ancestor teosinte (*left*) are closely related despite their differences.

## ***fw2.2*: A Quantitative Trait Locus Key to the Evolution of Tomato Fruit Size**

Anne Frary,<sup>1\*</sup> T. Clint Nesbitt,<sup>1\*</sup> Amy Frary,<sup>1†</sup>  
Silvana Grandillo,<sup>1‡</sup> Esther van der Knaap,<sup>1</sup> Bin Cong,<sup>1</sup>  
Jiping Liu,<sup>1</sup> Jaroslav Meller,<sup>2</sup> Ron Elber,<sup>2</sup> Kevin B. Alpert,<sup>1</sup>  
Steven D. Tanksley<sup>1§</sup>



*L. pimpinellifolium*

*L. esculentum*

# Plant domestication



# Rice domestication



## Rice Domestication by Reducing Shattering

Changbao Li, Ailing Zhou, Tao Sang\*

Crop domestication frequently began with the selection of plants that did not naturally shed ripe fruits or seeds. The reduction in grain shattering that led to cereal domestication involved genetic loci of large effect. The molecular basis of this key domestication transition, however, remains unknown. Here we show that human selection of an amino acid substitution in the predicted DNA binding domain encoded by a gene of previously unknown function was primarily responsible for the reduction of grain shattering in rice domestication. The substitution undermined the gene function necessary for the normal development of an abscission layer that controls the separation of a grain from the pedicel.

# Melon as a vegetable

*var tibish*



*var flexuosus*



*var chate*

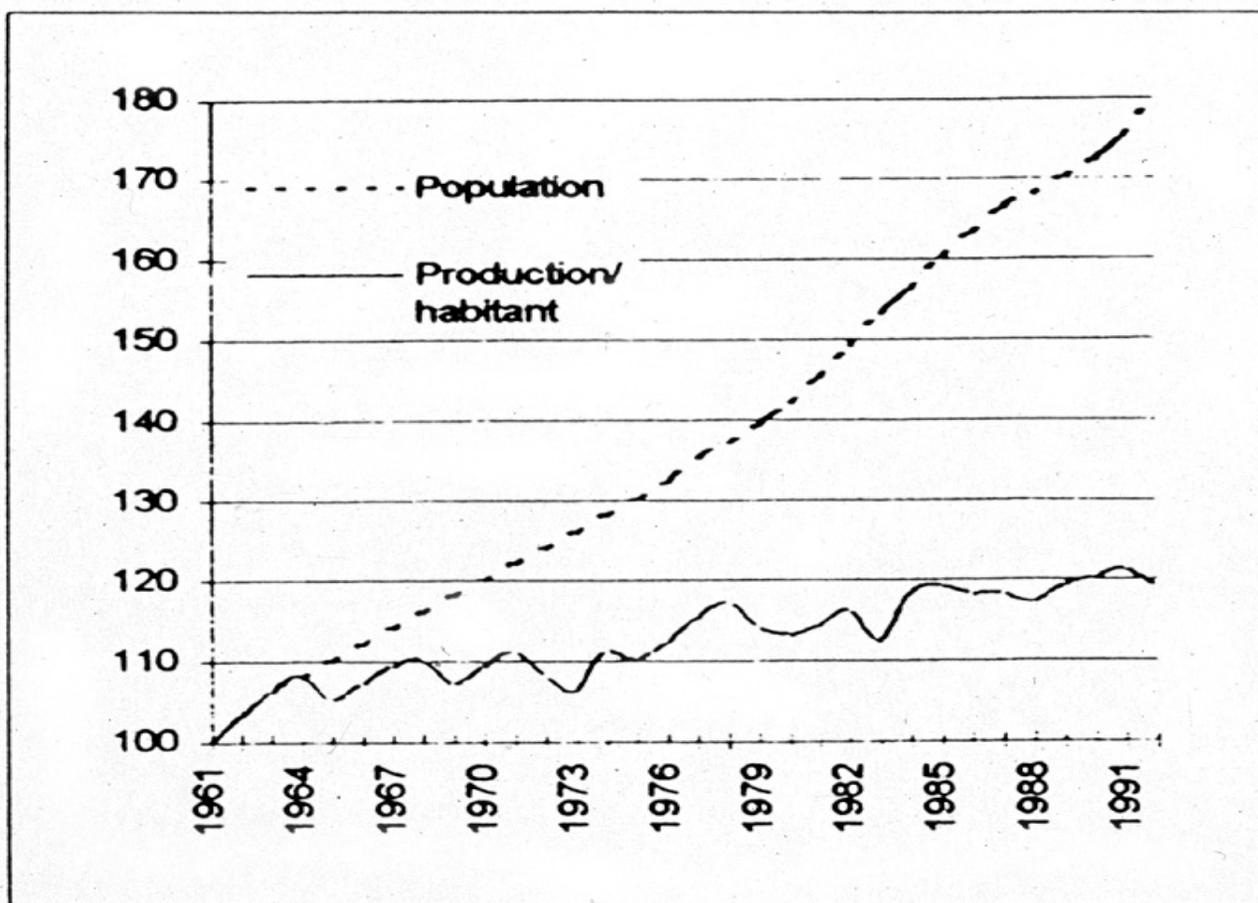


## **Domestication**

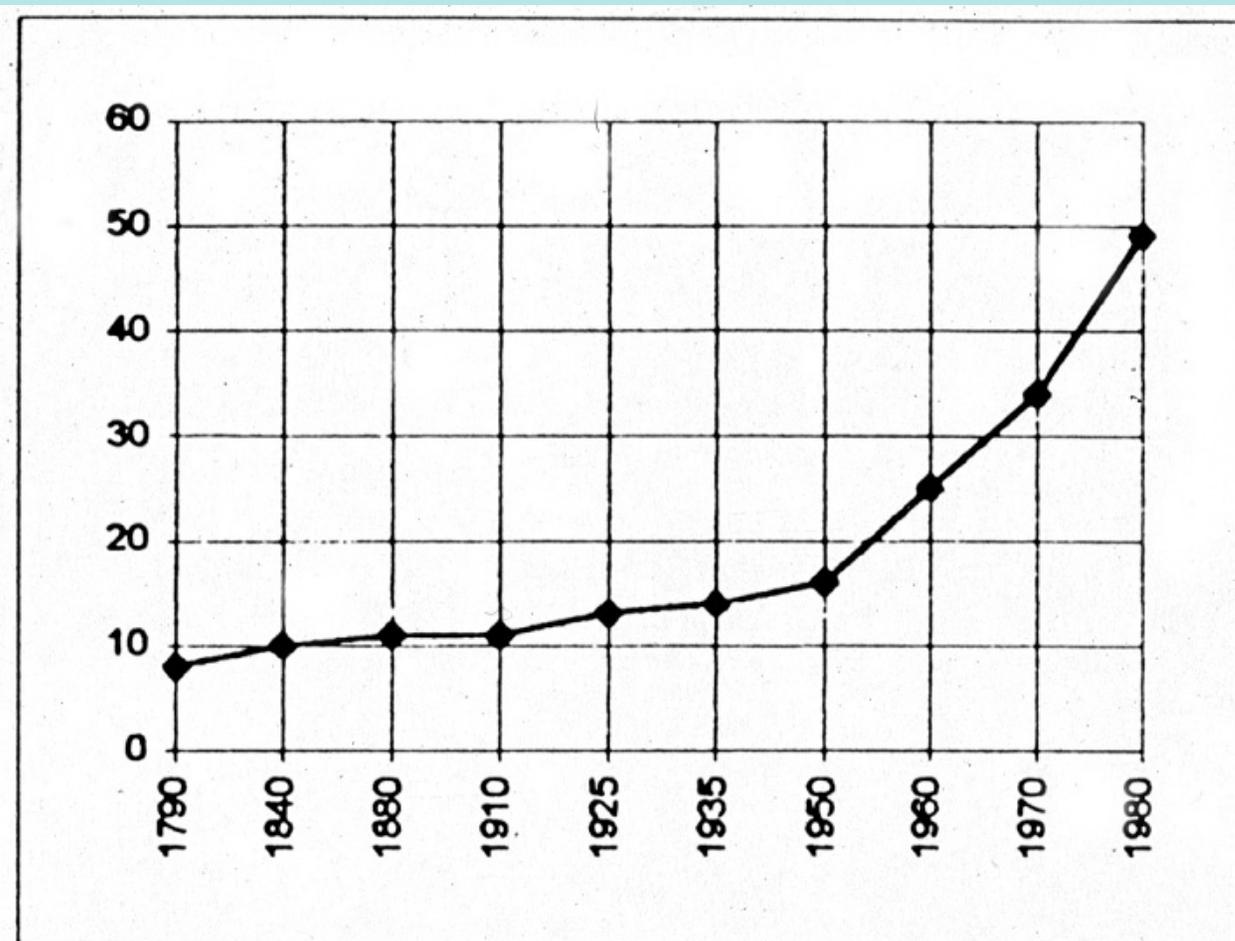
- 1. Plants cultivated in new habitats  
(less adapted – more variability)**
- 2. Absence of natural selection pressure**
- 3. Selection by man of characters non-beneficial to plants  
in natural situations**

# XXth century contradicts Malthus

- The birth of Genetics
- Fertilizers, pesticides, fungicides and herbicides
- Agronomic techniques (including mechanization, irrigation, etc.)
- Green revolution

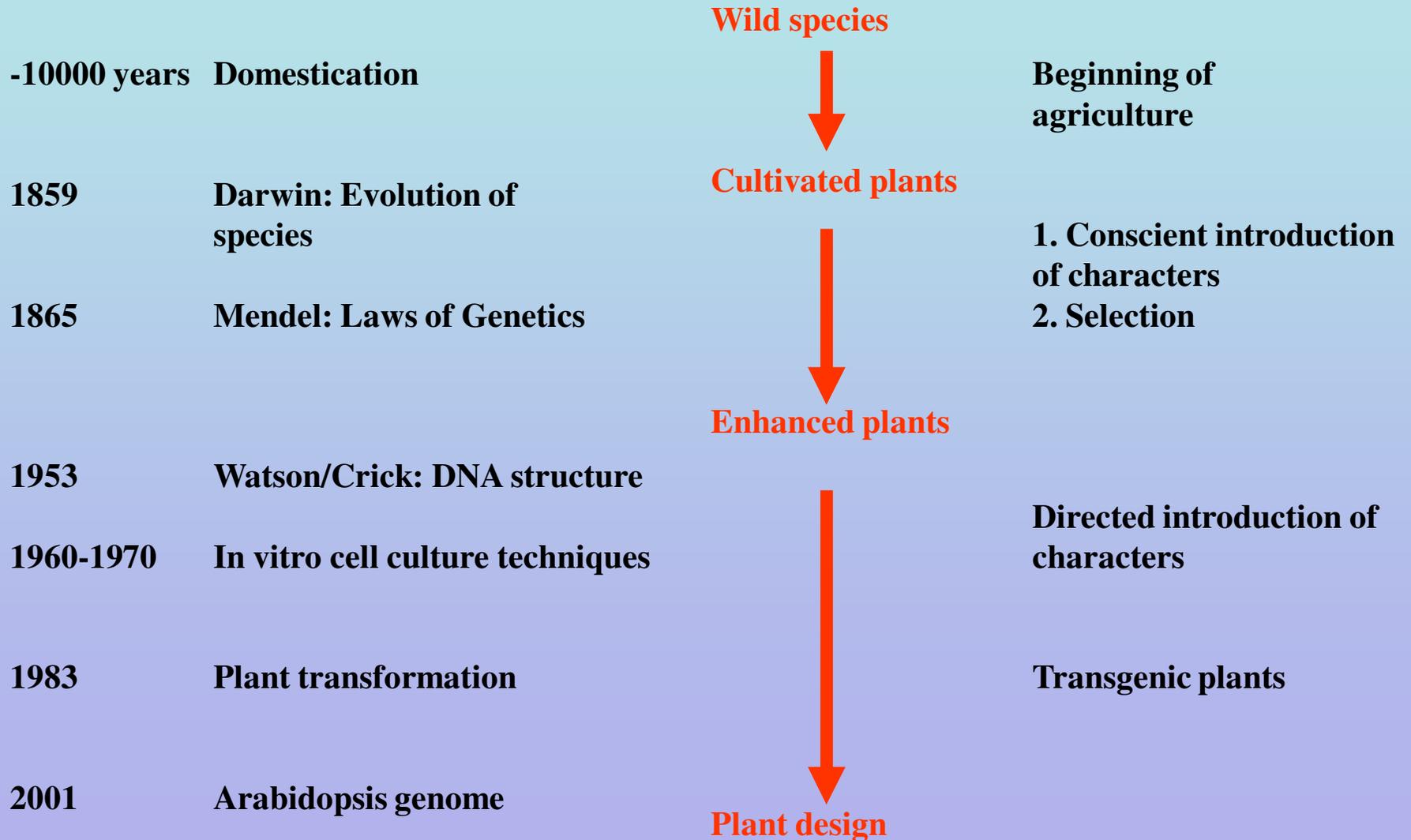


**Figure 4.** Évolution globale de la production agricole et de la population de 1961 à 1992 (indice 100 en 1961) [11].



**Figure 5.** Évolution des rendements moyens en céréales en France de 1790 à 1980 (Rdt. q/ha) [12].

# History of plant modification



# Genetics appears in decisive moments

- In plant and animal domestication
- In the applications of Mendel's laws during XXth century
- When Molecular Biology is applied since 1970
- Genomics appears at the end of XXth century

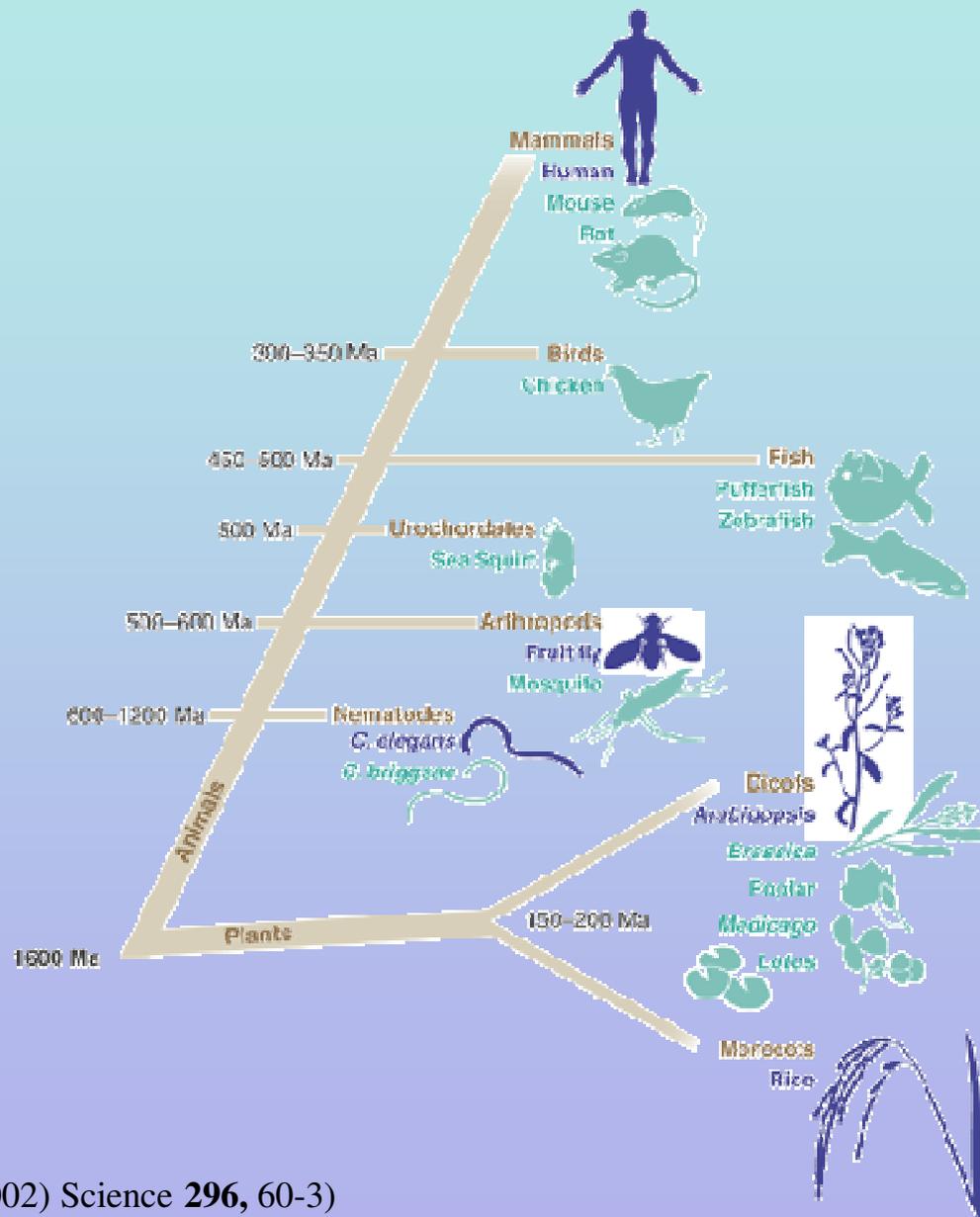




*Arabidopsis thaliana*

Chromosomes	5
DNA molecules length	115 Mb
Genes	25.498
Genes with EST	60 %
Gene density	4,5 Kb/g
Gene length	2 Kb

# Phylogenetic relations in multicelular organisms



(J. Bennetzen, (2002) Science **296**, 60-3)

## ARTICLES

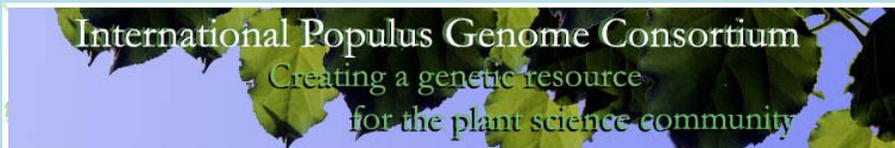
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# The map-based sequence of the rice genome

International Rice Genome Sequencing Project\*

Rice, one of the world's most important food plants, has important syntenic relationships with the other cereal species and is a model plant for the grasses. Here we present a map-based, finished quality sequence that covers 95% of the 389 Mb genome, including virtually all of the euchromatin and two complete centromeres. A total of 37,544 non-transposable-element-related protein-coding genes were identified, of which 71% had a putative homologue in *Arabidopsis*. In a reciprocal analysis, 90% of the *Arabidopsis* proteins had a putative homologue in the predicted rice proteome. Twenty-nine per cent of the 37,544 predicted genes appear in clustered gene families. The number and classes of transposable elements found in the rice genome are consistent with the expansion of syntenic regions in the maize and sorghum genomes. We find evidence for widespread and recurrent gene transfer from the organelles to the nuclear chromosomes. The map-based sequence has proven useful for the identification of genes underlying agronomic traits. The additional single-nucleotide polymorphisms and simple sequence repeats identified in our study should accelerate improvements in rice production.

# Populus genome



- About the Consortium
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- Steering Committee
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*Populus trichocarpa* v1.0

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With a genome of just over 500 million letters of genetic code, *Populus trichocarpa* was sequenced eight times over to attain the highest quality standards. Poplar was chosen as the first tree DNA sequence decoded because of its relatively compact genetic complement, some 50 times smaller than the genome of pine, making the poplar an ideal model system for trees.

The poplar genome, divided into 19 chromosomes, is four times larger than the genome of the first plant sequenced four years ago, *Arabidopsis thaliana*.

Thus far, researchers have revealed poplar's genome to be about one-third heterochromatin, that is, regions of chromosomes thought to be genetically inactive, which should provide shortcuts to important regulatory features.

## Genome Project Notes

The *Populus* genome assembly 1.0 is a preliminary release as part of the ongoing *Populus* genome project. A final draft sequence will be released in early 2005. The current assembly includes approximately 7.5X in small insert end-sequence coverage. Additional mapping and sequencing is ongoing.

Our goal is to make the genome sequence of Poplar widely and rapidly available to the scientific community. We endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this project in a timely fashion and we welcome collaborative interaction on the project and analyses as appropriate.

# The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla

The French-Italian Public Consortium for Grapevine Genome Characterization\*

*Nature* advance online publication 26 August 2007 | doi:10.1038/nature06148;  
Received 5 April 2007; Accepted 7 August 2007; Published online 26 August 2007



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**The European Group on Ethics in Science and New  
Technologies  
to the European Commission**

The group is an independent, pluralist and multidisciplinary body which advises the European Commission on ethical aspects of science and new technologies.

Web site address:

[http://ec.europa.eu/european\\_group\\_ethics/index\\_en.htm](http://ec.europa.eu/european_group_ethics/index_en.htm)

# Questions addressed to the Group (2005-2009)

- Ethical aspects of Nanomedicine (December 2006)
- Ethical criteria for the approval of european research projects using embryo stem cells of human origin (June 2007)
- Ethical aspects of consumption of meat from cloned animals (January 2008)
- Ethical aspects of new developments in agriculture (December 2008?)

# Concerns at the beginning of XXIst century

- Concerns related to food production: hunger divide, safe and healthy food
- Concerns related to the effects of agriculture on the environment: Biodiversity loss. Degradation of the environment. Habitat loss, deforestation, water use and water pollution, contribution to climate change

# Concerns at the beginning of the XXIst century

- Concerns related to social and political conditions: Political instability. Disruption of social structures and massive urbanisation. Control over food supply. Conflicts around food in the international trade
- Concerns related to the changing global situation: Population growth, globalisation of threats (pests, etc.), climate change, reducing oil reserves

# General criteria

- **Food security.** The right to food, distributive and social justice, beneficence and non-malificence
- **Sustainability.** Antropo- and ecocentric approaches: human beings, environment and future generations
- We have to use all the tools available to secure sufficient, safe and healthy food for people in all places and in the future and, as we have done in the past, science will be a key factor in the future.