

Species and genetic diversity  
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Wild genetic diversity of some important crops  
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## Genetic diversity and center of diversity of crops

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## Section 1

### Species and genetic diversity

# Genetic diversity

- Is reliant on the heritable variation within and between populations of organisms.
- Genetic variation (new) arises by gene and chromosome mutations, and through recombination.
- It has been estimated that in humans and fruit flies alike, the number of possible combinations of different forms of each gene sequence exceeds the number of atoms in the universe.
- Genetic variation enables both natural evolutionary change and artificial selective breeding to occur.
- Only a small fraction (<1%) of the genetic material of higher organisms is outwardly expressed in the form and function of the organism; the purpose of the remaining DNA and the significance of any variation within it are unclear.

- Before initiating a (molecular/marker-assisted) breeding program an assessment of genetic diversity of the available germplasm is necessary.
- The goal is to select parents that are genetically diverse enough that you can identify differences - polymorphisms - in the progeny.
- Of several, few of the measures of genetic diversity are:
  - Based on the number of variants among the alleles
  - Polymorphism or rate of polymorphism ( $P_j$ )
  - Proportion of polymorphic loci
  - Number of alleles (A) and allelic richness ( $A_s$ )
  - Average number of alleles per locus
  - Based on the frequency of variant alleles
  - Average expected heterozygosity ( $H_e$ ; Nei's genetic diversity)
- Clearly the use of markers is needed for these measures of genetic diversity.

A study of 26 accessions of groundnut (consisting of interspecific derivatives, land races and released cultivars) and 8 primers of a 10-mer were selected for RAPD DNA assay. The genetic similarity ( $S_{ij}$ ) ranged from 59.0% to 98.8%, with an average of 86.2%. Both multidimensional scaling and unweighted pair-group method with arithmetic averages (UPGMA) dendograms revealed the existence of five distinct clusters. However, this classification could not be related to known biological information about the accessions falling into different clusters. Some accessions with diverse DNA profiles (ICG 1448, 7101, and 1471, and ICGV 99006 and 99014) were identified for mapping and genetic enhancement in groundnut. [Dwivedi et al., 2001].

Accession <sup>1</sup>	Pedigree	Origin	Biological status <sup>2</sup>	Botanical variety	Seeds per pod	Seed colour <sup>3</sup>	Reaction to abiotic and biotic stresses
ICGV 99001	'Robut 33-1' × <i>A. villosa</i>	India	ID	<i>vulgaris</i>	2-1-3	DR	Resistant to rust and late leaf spot
ICGV 99002	'Chico' × ('Shulamit' × <i>A. correntina</i> × <i>A. batizocoi</i> )	India	ID	<i>hypogaea</i>	2-3-1	DR	Resistant to rust
ICGV 99003	<i>A. hypogaea</i> × ( <i>A. cardenasi</i> × <i>A. stenosperma</i> )	India	ID	<i>hypogaea</i>	2-1-3	DR	Resistant to rust
ICGV 99004	TMV 2 × ( <i>A. hypogaea</i> × <i>A. cardenasi</i> )	India	ID	<i>vulgaris</i>	2-1	DR	Resistant to rust and late leaf spot
ICGV 99005	TMV 2 × ( <i>A. hypogaea</i> × <i>A. batizocoi</i> × <i>A. duranensis</i> )	India	ID	<i>hypogaea</i>	2-1-3	DR	Resistant to rust
ICGV 99006	<i>A. hypogaea</i> × <i>A. cardenasi</i>	India	ID	<i>vulgaris</i>	2-1-3	DR	Resistant to rust and late leaf spot
ICGV 99007	<i>A. hypogaea</i> × <i>A. cardenasi</i>	India	ID	<i>hypogaea</i>	2-1	DR	Resistant to rust
ICGV 99008	'Robut 33-1' × <i>A. villosa</i>	India	ID	<i>hypogaea</i>	2-1-3	DR	Resistant to rust
ICGV 99009	<i>A. hypogaea</i> × <i>A. cardenasi</i> × ICG 4751	India	ID	<i>hypogaea</i>	2-3-1	DR	Resistant to rust
ICGV 99010	<i>A. hypogaea</i> × <i>A. cardenasi</i> × ICG 4751	India	ID	<i>hypogaea</i>	2-1	DR	Resistant to late leaf spot
ICGV 99011	ICGMS 42 × ( <i>A. hypogaea</i> × <i>A. cardenasi</i> )	India	ID	<i>hypogaea</i>	2-3-1	T	Resistant to late leaf spot
ICGV 99012	ICGMS 42 × ( <i>A. hypogaea</i> × <i>A. cardenasi</i> )	India	ID	<i>hypogaea</i>	2-3-1	T	Resistant to rust
ICGV 99013	<i>A. hypogaea</i> × <i>A. cardenasi</i>	India	ID	<i>vulgaris</i>	2-1-3	DR	Resistant to rust and late leaf spot
ICGV 99014	<i>A. hypogaea</i> × <i>A. cardenasi</i>	India	ID	<i>vulgaris</i>	2-1	T	Resistant to rust and late leaf spot
ICGV 99015	TMV 2 × ( <i>A. hypogaea</i> × <i>A. batizocoi</i> × <i>A. duranensis</i> )	India	ID	<i>hypogaea</i>	2-1-3	DR	Resistant to rust
ICGV 99016	TMV 2 × ( <i>A. hypogaea</i> × <i>A. batizocoi</i> × <i>A. duranensis</i> )	India	ID	<i>hypogaea</i>	2-3-1	DR	Resistant to rust
ICG 10021		Peru	LR	<i>peruviana</i>	3-2-1	DP	Resistant to rust and cold tolerant
ICG 4751		USA	—	<i>vulgaris</i>	2-1	T	
ICG 1448		USA	—	<i>vulgaris</i>	2-1	T	Resistant to aflatoxin
ICG 7101		India	LR	<i>vulgaris</i>	2-1	T	Resistant to aflatoxin
ICG 4749		Argentina	LR	<i>vulgaris</i>	2-1	T	Resistant to seed colonization
ICG 1326	AH 4218 × AH 4354	India	RC	<i>vulgaris</i>	2-1	T	Resistant to seed colonization
ICG 1471	Selection from exotic germplasm from Argentina	Senegal	RC	<i>vulgaris</i>	2-1	T	Resistant to seed colonization
ICG 799	Selection from 'Robut'	India	RC	<i>hypogaea</i>	2-1	T	Resistant to seed colonization
ICG 3042	Selection from 'Kadiru 2'	Nigeria	RC	<i>hypogaea</i>	2-1	T	Tolerant to peanut bud necrosis disease
ICG 5285		Israel	RC	<i>hypogaea</i>	2-1	R	

<sup>1</sup> ICG, ICRISAT groundnut; ICGV, ICRISAT groundnut variety.<sup>2</sup> LR, land race; RC, released cultivar; ID, interspecific derivatives.<sup>3</sup> DR, dark red; T, tan; DP, dark purple; R, rose.

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A study conducted in **Ghana** evaluated 142 soybean accessions, genotyped with 34 SSR markers. 5 quantitative and 2 qualitative traits were concurrently evaluated. 29 of the SSR markers were polymorphic with mean allele number of 5.3, PIC of 0.51 and gene diversity of 0.55. UPGMA clustering and Principal Coordinate Analysis was similar in explaining the extent of diversity within the accessions. Structure analysis placed most of the accessions into two subpopulations with 18 (12.7%) as admixtures. Both UPGMA clustering-based SSR data and PCA from phenotypic data showed similar results[Denwar et al., 2019].

Marker	Major allele frequency	Allele number	Allele diversity	Heterozygosity	PIC
sat_280	0.88	6	0.22	0.08	0.21
satt612	0.38	8	0.71	0.73	0.66
GMES4591	0.50	3	0.59	1.00	0.51
GMES2891	0.34	9	0.80	0.54	0.77
Satt244	0.26	11	0.81	0.77	0.79
Satt545	0.32	7	0.79	0.99	0.76
GMES6224	0.50	4	0.62	0.99	0.55
GMES3177	0.94	3	0.11	0.00	0.10
GMES3757	0.89	2	0.20	0.00	0.18
GMES6842	0.68	2	0.43	0.00	0.34
GMES0676	0.96	4	0.07	0.01	0.07
CSSR18	0.40	11	0.71	0.97	0.65
CSSR438	0.50	4	0.55	0.99	0.45
GMES0707	0.73	3	0.41	0.08	0.35
GMES2038	0.50	3	0.53	1.00	0.42
GMES2036	0.99	2	0.03	0.00	0.03
GMES6270	0.43	5	0.62	0.91	0.55
GMES3941	0.82	3	0.30	0.00	0.26
Sat_210	0.36	8	0.72	0.83	0.68
AW781285	0.51	4	0.60	0.07	0.52
Sat_142	0.35	4	0.73	0.46	0.68
Sat_038	0.40	5	0.66	0.82	0.60
AW310961	0.32	5	0.75	0.38	0.70
Sat_305	0.89	2	0.19	0.00	0.17
Sat_205	0.23	9	0.83	0.70	0.80
Sat_254	0.57	5	0.59	0.11	0.54
Sat_105	0.30	7	0.78	0.80	0.75
Sat_125	0.18	9	0.86	0.54	0.84
Sat_171	0.26	5	0.79	0.85	0.75
Mean	0.53	5.3	0.55	0.50	0.51

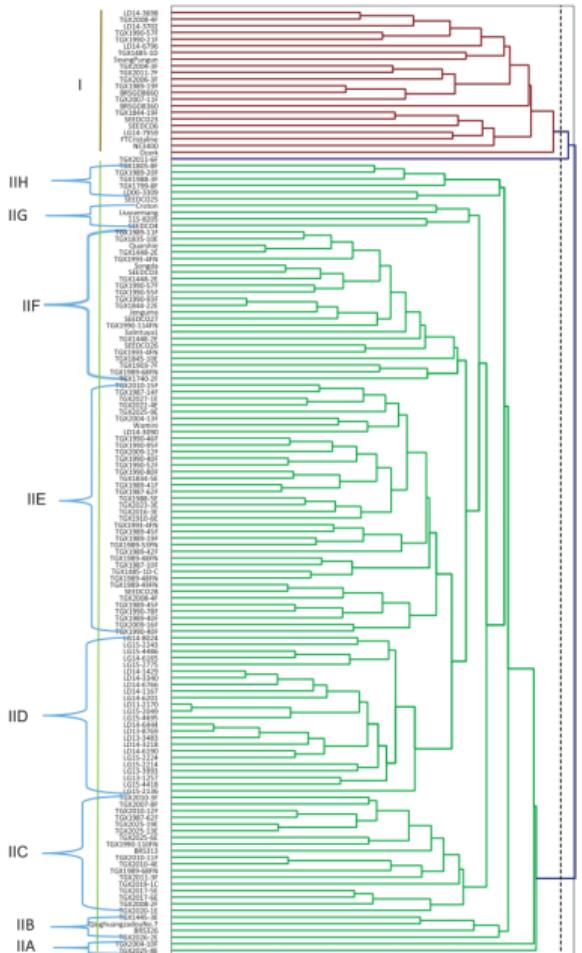
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# Retrotransposable Elements: DNA Fingerprinting and the Assessment of Genetic Diversity

Ruslan Kalendar, Alexander Muterko, and Svetlana Boronnikova

## Abstract

Retrotransposable elements (RTEs) are highly common mobile genetic elements that are composed of several classes and make up the majority of eukaryotic genomes. The “copy-out and paste-in” life cycle of replicative transposition in these dispersive and ubiquitous RTEs leads to new genome insertions without excision of the original element. RTEs are important drivers of species diversity; they exhibit great variety in structure, size, and mechanisms of transposition, making them important putative components in genome evolution. Accordingly, various applications have been developed to explore the polymorphisms in RTE insertion patterns. These applications include conventional or anchored polymerase chain reaction (PCR) and quantitative or digital PCR with primers designed for the 5' or 3' junction. Marker systems exploiting these PCR methods can be easily developed and are inexpensively used in the absence of extensive genome sequence data. The main inter-repeat amplification polymorphism techniques include inter-retrotransposon amplified polymorphism (IRAP), retrotransposon microsatellite amplified polymorphism (REMAP), and Inter-Primer Binding Site (iPBS) for PCR amplification with a single or two primers.

**Key words** Retrotransposon, Molecular marker, IRAP, REMAP, iPBS

For the extensive discussion and protocol outline, refer to Kalendar et al. [2021].

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# Genetic Diversity of Cultivated Tropical Plants

*Scientific editors*

Perla Hamon

Marc Seguin

Xavier Perrier

Jean Christophe Glaszmann

# Species diversity

- Species are the fundamental descriptive units of the living world and this is why biodiversity is very commonly, and **incorrectly**, used as a synonym of species diversity, in particular of “species richness”.
- When considering species numbers alone, life on earth appears to consist mostly of insects and microorganisms.
- The greater the interspecific differences (e.g., by an isolated position within the taxonomic hierarchy), then the greater contribution to any overall measure of global biological diversity – implicit by the term “biodiversity”.
- The ecological importance of a species can have a direct effect on community structure, and thus on overall biological diversity. For example, a species of tropical rain forest tree that supports an endemic invertebrate fauna of a hundred species makes a greater contribution to the maintenance of global biological diversity than does a European alpine plant that may have no other species wholly dependent on it.
- In a seminal work on the measurement of diversity, Whittaker (1972) introduced the concepts of alpha, beta, and gamma diversity. The measurements with

# Germplasm

- Germplasm refers to the genetic material that can be used to perpetuate a species or population
- Germplasm provides the material used to initiate a breeding program
- Sometimes only germplasm screening and evaluation is practiced for introduction of improved variety in a region
- Certain institutional sets-ups such as gene banks are charged with the responsibility of assembling, cataloguing, storing and managing large number of germplasm. This allows for quick retrieval.

# Gene pool

J.R. Harlan and J.M.J. de Wet proposed a categorization of gene pools of cultivated crops according to the feasibility of gene transfer or gene flow from those species to the crop species.

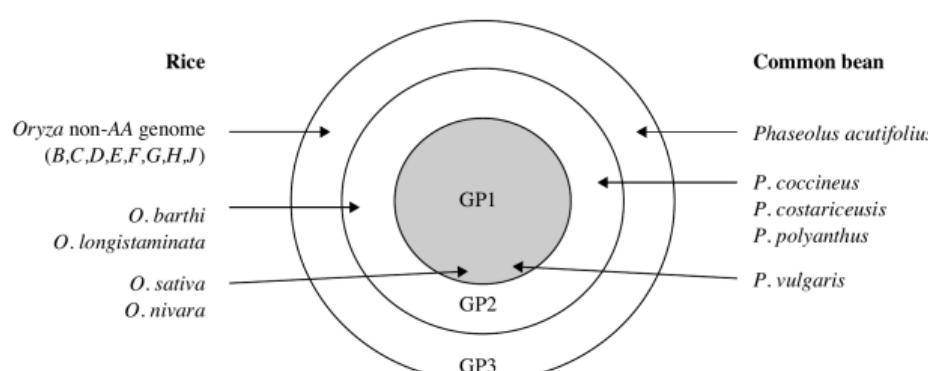


Figure 1: Crop gene pools; A system proposed by Harlan



Figure 2: The embryo rescue of grape seeds. Increasing diversity by introgression from wild relatives can be complicated by the existence of crossing barriers or poor hybrid fertility.

# Types of gene pool

- *Primary gene pool (GP1)*
  - GP1 consists of biological species that can be intercrossed easily (interfertile) without any problems with fertility of the progeny. That is, there is no restriction to gene exchange between members of the group. This group may contain both cultivated and wild progenitors of the species.
- *Secondary gene pool (GP2)*
  - Members of this gene pool include both cultivated and wild relatives of the crop species. They are more distantly related and have crossability problems. Nonetheless, crossing produces hybrids and derivatives that are sufficiently fertile to allow gene flow. GP2 species can cross with those in GP1, with some fertility of the F1, but more difficulty with success.
- *Tertiary gene pool (GP3)*
  - GP3 involves the outer limits of potential genetic resources. Gene transfer by hybridization between GP1 and GP3 is very problematic, resulting in lethality, sterility, and other abnormalities. To exploit germplasm from distant relatives, tools such as embryo rescue and bridge crossing may be used to nurture an embryo from a wide cross to a full plant and to obtain fertile plants.

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## Section 2

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# Domestication

a plant population has been domesticated when it has been substantially altered from the wild state and certainly when it has been so altered to be unable to survive in the wild

N.W. Simmonds

- Domestication is the process by which genetic changes (shifts) in wild plants are brought about through a selection process imposed by humans.

# Domestication syndrome (Changes in plant species under domestication)

Table 1: Changes in plants under domestication

General effect	Specific traits altered
<b>Increased seedling vigor (more plants germinating)</b>	Loss of seed or tuber dormancy Large seeds
<b>Modified reproductive system</b>	Increased selfing Reduced complexity of reproductive organs Vegetatively reproducing plants
	Altered photoperiod sensitivity Shift in sex form of species Promotion of asexual reproduction
<b>Increased number of seeds harvested</b>	Non-shattering Reduced number of branches (more fruits per branch)

Table 2: Changes in plants under domestication<sup>1</sup> (...continued)

General effect	Specific traits altered
<b>Increased appeal to consumers</b>	Attractive fruit/seed colors and patterns Enhanced flavor, texture, and taste of seeds/fruits/tubers (food parts) Reduced toxic principles (safer food) Larger fruits Reduces spikiness
<b>Altered plant architecture and growth habit</b>	Increase in economic yield (HI) Compact growth habit (Determinacy, reduced plant size, dwarfism) Reduced branching Decreases in variability within a variety
<b>Change in developmental phenology</b>	Change in life cycle (normally from perennial to annual for seed crops, and from annual to biennial for vegetable crops)

<sup>1</sup>For a detailed contrast between wild and domestication traits, refer to Lecture on 'Domestication, plant introduction, and acclimatization' of Introductory Plant Breeding course.

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## Section 3

### Origin and diversity

## Law of homologous series of variation

- Nikolai I. Vavilov (1887-1942), the Russian botanist and plant breeder, demonstrated the existence of 'centres of origin' of cultivated plants (more correctly named today as 'centres of diversity'), in which can be found the highest level of genetic variability of a species. This variability, which arises in nature by mutation spontaneous hybridization, introgression and changes in chromosome form and number, provides the means by which adaptation to heterogenous environments can occur.
- It allows the breeder to identify sources of variation for specific characteristics. The extension of this principle to related species was formulated by Vavilov in his 'law of homologous series of variation'. This law allows the prediction of the appearance of a given type of mutation in a plant species when such a type has been found in another species phylogenetically related to the first.
- Defined plant breeding as 'plant evolution directed by man'; concept of 'applied plant genetics'.

## Defining center of origin and center of diversity

- CBD takes the “centre of origin” and the “centre of crop diversity” as references referring to the scientific rather than political connecting points for the definition of origin. [Rights to plant genetic resources and traditional knowledge]
- It defines “centre of origin” as “a geographical area where a plant species, either domesticated or wild, first developed its distinctive properties”, and “centre of crop diversity” as “the geographic area containing a high level of genetic diversity for crop species in in-situ conditions” (Articles 2.8 and 2.9).
- On the basis of sovereignty of states over their natural resources, CBD takes “country” as starting point for defining the origin of genetic resources.
- Accordingly, “the country of origin of genetic resources” is defined as the country that possesses the genetic resources in in situ conditions (Article 2.4).

# Domestication and origin of major crop species

Table 3: Estimated time of domestication and centre of origin of major crop species; Brown and Campos [2014], Page 23.

Crop category	Crop	Length of time domesticated (years)	Possible region of origin
Cereals	Maize, <i>Zea mays</i>	7000	Mexico, Central America
Cereals	Rice, <i>Oryza sativa</i>	4500	Thailand, Southern China
Cereals	Wheat, <i>Triticum</i> spp.	8500	Syria, Jordan, Israel, Iraq
Cereals	Barley, <i>Hordeum vulgare</i>	9000	Syria, Jordan, Israel, Iraq
Cereals	Sorghum, <i>Sorghum bicolor</i>	8000	Equatorial Africa
Oilseeds	Soybean, <i>Glycine max</i>	2000	North China
Oilseeds	Oil palm, <i>Elaeis guineensis</i>	9000	Central Africa
Oilseeds	Coconut palm, <i>Cocos nucifera</i>	100	Southern Asia
Oilseeds	Rapeseed, <i>Brassica napus</i>	500	Mediterranean Europe
Oilseeds	Sunflower, <i>Helianthus annus</i>	3000	Western United States
Pulses	Beans, <i>Phaseolus</i> spp	7000	Centra America, Mexico
Pulses	Lentil, <i>Lens culinaris</i>	7000	Syria, Jordan, Israel, Iraq
Pulses	Peas, <i>Pisum sativum</i>	9000	Syria, Jordan, Israel, Iraq
Root crops	Potato, <i>Solanum tuberosum</i>	7000	Peru
Root crops	Cassava, <i>Manihot esculenta</i>	5000	Brazil, Mexico

Table 4: Estimated time of domestication and centre of origin of major crop species; Brown and Campos [2014], Page 23 (...continued).

Crop category	Crop	Length of time domesticated (years)	Possible region of origin
<b>Root crops</b>	Sweet potato, <i>Ipomoea batatas</i>	6000	South Central America
<b>Root crops</b>	Sugar beet, <i>Beta vulgaris</i>	300	Mediterranean Europe
<b>Vegetables</b>	Tomato, <i>Lycopersicum esculentum</i>	3000	Western South America
<b>Vegetables</b>	Cabbage, <i>Brassica oleracea</i>	3000	Mediterranean Europe
<b>Vegetables</b>	Onion, <i>Allium</i> spp.	4500	Iran, Afganistan, Pakistan
<b>Fruit</b>	Orange, <i>Citrus sinensis</i>	9000	South-east Asia
<b>Fruit</b>	Apple, <i>Malus</i> spp.	3000	Asia Minor, Central Asia
<b>Fruit</b>	Grape, <i>Vitis</i> spp.	7000	Eastern Asia
<b>Fruit</b>	Banana, <i>Musa acuminata</i> , <i>M. balbisiana</i>	4500	South-east Asia
<b>Others</b>	Cotton, <i>Gossypium</i> spp.	4500	Centra America, Brazil
<b>Others</b>	Coffee, <i>Coffea</i> spp.	500	West Ethiopia
<b>Others</b>	Rubber, <i>Hevea brasiliensis</i>	200	Brazil, Bolivia, Paraguay
<b>Others</b>	Alfalfa, <i>Medicago sativa</i>	4000	Iran, Northern Pakistan

# Rice: History and origin

- Probably originated 130 MYA (Virmani and Ilyas-Ahmed, 2007)
- Spread as wild grass in Gondwanaland.
- Domesticated independently in Asia and Africa.
  - *O. sativa* (derived from *O. rufipogon* in China and in India)
    - Asian wild progenitor called *O. rufipogon* has also perennial to annual types
    - Annual types of the wild progenitor called *O. nivara* resulted in present day asian rice
  - *O. glaberrima* (derived from *O. barthii* in the Niger river delta)
- Both cultivated species – *O. sativa* and *O. glaberrima* (tropical West african rice) originated from common ancestor.
- Alternative hypotheses: two distinct subspecies of rice ( *indica* and *japonica*) arose from different wild variants of *O. rufipogon*.

Group ID	Subpopulation	Varietal group	Reference
Group I	<i>indica</i>	<i>Indica</i>	Glaszmann 1987, Garris <i>et al.</i> 2005
Group II	<i>aus</i>	<i>Indica</i>	Glaszmann 1987, Garris <i>et al.</i> 2005
Group III	<i>deep water</i>	<i>Indica</i>	Glaszmann 1987
Group IV	<i>rayada</i>	<i>Indica</i>	Glaszmann 1987
Group V	<i>aromatic</i>	<i>Japonica</i>	Glaszmann 1987, Garris <i>et al.</i> 2005
Group VI	<i>temperate japonica</i>	<i>Japonica</i>	Garris <i>et al.</i> 2005
Group VII	<i>tropical japonica</i>	<i>Japonica</i>	Garris <i>et al.</i> 2005

Figure 3: The recognized subpopulations of *Oryza sativa*Figure 4: *Oryza rufipogon* panicle.Figure 5: Undehusked seeds of African Oryza species. (a) *Oryza longistaminata* (b) *Oryza glaberrima* 1 (c) *Oryza glaberrima* 2 (d) *Oryza brachyantha* (e) *Oryza eichingeri* (f) *Oryza punctata* (g) *Oryza barthii*.

# Rice phylogeny and history in literatures

- Phylogeny of the genus *Oryza* as revealed by molecular approaches, Volume IV, Rice Genetics, 2001.
- Evolution and domestication of Rice, Volume IV, Rice Genetics, 2001.

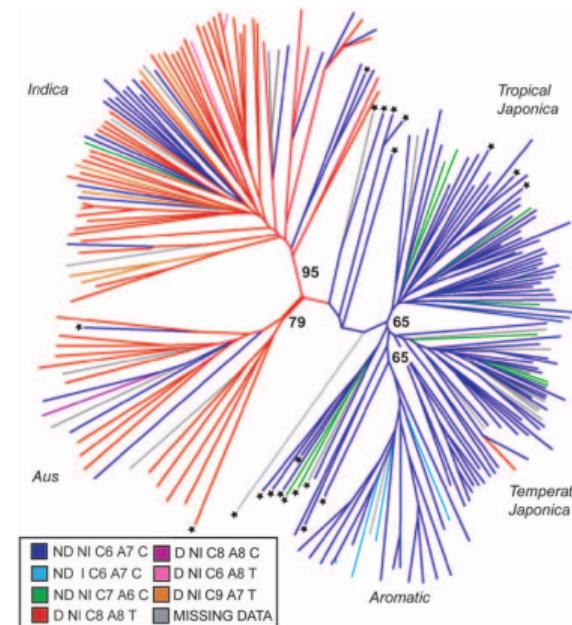


Figure 6: Unrooted neighbor-joining tree based on C.S. Chord (1967) based on 169 nuclear SSRs. The key relates the color of the line to the chloroplast haplotype based on ORF100 and PS-ID sequences. Admixed individuals are identified with an asterisk. Bootstrap values (out of 100) are indicated at the branch points. Source: Garris et al. [2005].

- First archaeological evidence of rice cultivation leads to Yangtze valley of eastern China.
- Domestication has resulted in alterations to a large array of morphological traits:
  - Seed shattering behavior
  - Grain coloration
  - Grain size enlargement
  - Prostrate to erect growth habit
  - Reduced seed dormancy
- Genetic factors contributing to domestication syndrome *Shattering4 (Sha4)* on chromosome 4 and black hull by *Black hull (Bh4)* on chromosome 4.

# Maize: History and origin

- Domestication history based on 7100 year old maize pollen from San Andres.
- Initially cultivated in seasonal tropical forest of southwestern mexico.
- Originated from annual teosinte (*Zea mays* subspecies *parviglumis*) around 9000 years ago in mid to lowland regions.
- Later on admixture occurred among *parviglumis* and *mexicana* (highland type) subspecies.

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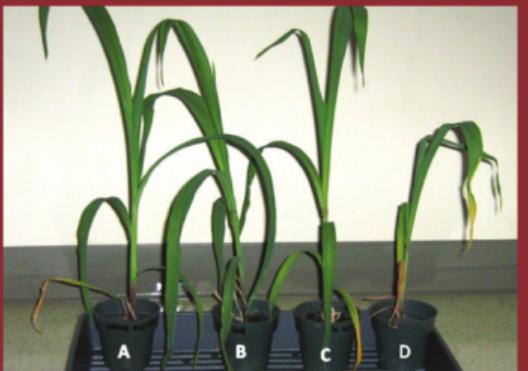
References

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**Genetics, Genomics and Breeding of Crop Plants**

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# Genetics, Genomics and Breeding of Maize

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# Wheat: History and origin

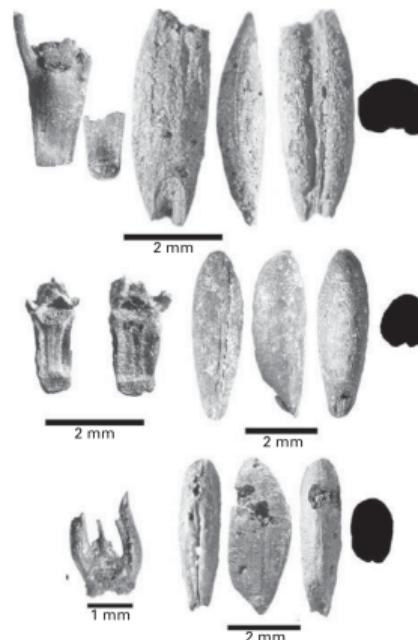


Figure 7: Charred wild cereal spikelet bases (left) and grains (right). Top, *Hordeum spontaneum* (wild barley) from Jerf el Ahmar. Middle, *Secale* sp. (rye) from Jerf el Ahmar. Bottom, *Triticum boeoticum* (single-grain einkorn) from Tell Qaramel. Note the basal abscission scar seen in the barley (top row, second from the left) and for rye the lower end of the rye spikelet bases (second row, first and second from left) is more reliable than the upper scar for distinguishing between wild and domestic.

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References

## Section 4

### Megacentres of cultivated plants

Species and genetic diversity  
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Wild genetic diversity of some important crops  
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Origin and diversity  
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Megacentres of cultivated plants  
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References



Figure 8: Megacentres of cultivated plants (Zeven and Zhukovsky, 1975); Hayward et al. [2012], Page 37

Table 5: Cultivated plants and their regions of diversity. Based on Zeven and Zhukovsky (1975) and Zeven and de Wet (1982); Hayward et al. [2012], Page 54, 55.

SN	Region	Crops
1	Chinese-Japanese region	Prosomillet, Foxtail millet, Naked oat Soybean, Adzuki bean Leafy mustard Orange/Citrus, Peach, Apricot, Litchi Bamboo, Ramie, Tung oil tree, Tea
2	Indochinese-Indonesian region	Rice Rice bean, Winged bean Cucurbits/Ash gourd Mango, Banana, Rambutan, Durian, Bread fruit, Citrus/Lime, Grapefruit Bamboos, Nutmeg, Clove, Sago-palm, Ginger, Taros and Yams, Betel nut, Coconut
3	Australian region	Eucalyptus, Acacia, Macadamia nut
4	Hindustani region	Rice, Little millet Black gram, Green gram, Moth bean, Rice bean, Dolichos bean, Pigeonpea, Cowpea, Chickpea, Horsegram, Jute Eggplant, Okra, Cucumber, Leafy mustard, Rat's tail radish, Taros and Yams Citrus, Banana, Mango, Sunhemp, Tree cotton

Table 6: Cultivated plants and their regions of diversity. Based on Zeven and Zhukovsky (1975) and Zeven and de Wet (1982); Hayward et al. [2012], Page 54, 55.

SN	Region	Crops
5	Central Asian region	Sesame, Ginger, Turmeric, Cardamom, Areca nut, Sugarcane, Black pepper, Indigo
		Wheat (Bread/Club/Shot), Rye
		Allium/Onion, Garlic, Spinach, Peas, Beetroot, Faba bean
		Lentil, Chickpea
6	Near Eastern region	Apricot, Plum, Pear, Apple, Walnut, Almond, Pistachio, Melon, Grape, Carrot, Radish
		Hemp/Cannabis, Sesame, Flax, Safflower
		Wheat (Einkorn, Durum, Poulard, Bread), Barley, Rye/Secale
		Faba bean, Chickpea, French bean, Lentil, Pea
7	Mediterranean region	Brassica oleracea, Allium, Melon, Grape, Plum, Pear, Apple, Apricot, Pistachio, Fig, Pomegranate, Almond
		Safflower, Sesame, Flax
		Lupins, Medics
		Wheat (Durum, Turgidum), Oats
		Brassica oleracea, Lettuce, Beetroot, Colza
		Faba bean, Radish
		Olive, Trifolium/Berseem, Lupins, Crocus, Grape, Fennel, Cumin, Celery, Linseed

Table 7: Cultivated plants and their regions of diversity. Based on Zeven and Zhukovsky (1975) and Zeven and de Wet (1982); Hayward et al. [2012], Page 54, 55.

SN	Region	Crops
8	African region	Wheat (Durum, Emmer, Poulard, Bread) African rice, Sorghum, Pearl millet, Finger millet, Teff Cowpea, Bottle gourd, Okra, Yams, Cucumber Castor bean, Sesame, Niger, Oil palm, Safflower, Flax Cotton, Kenaf, Coffee
9	European-siberian region	Kola, Bambara, Groundnut, Date palm, Ensete, Melons Peach, Pear, Plum, Apricot, Apple, Almond, Walnut, Pistachio, Cherry Cannabis, Mustard (black), Chicory, Hops, Lettuce
10	South American region	Potato, Sweet potato, Xanthosoma Lima bean, Amaranth, Chenopodium, Cucurbita, Tomato, Tobacco, Lupin
		Papaya, Pineapple Groundnut, Sea island cotton
		Cassava, Cacao, Rubber tree, Passion fruit
11	Central American and Mexican region	Maize, French bean, Potato, Cucurbita, Pepper/Chilli, Amaranth, Chenopodium, Tobacco, Sisal hemp, Upland cotton
12	North American region	Jerusalem artichoke, Sunflower, Plum, Raspberry, Strawberry

# Bibliography |

Peter Brown, Jack Caligari and Hugo A. Campos. *Plant breeding*. Wiley Blackwell, 2014.

Nicholas Ninju Denwar, Frederick J Awuku, Brian Diers, Francisca Addae-Frimpongmaah, Godfree Chigeza, Richard Oteng-Frimpong, Doris K Puozaa, and Michael T Barnor. Genetic diversity, population structure and key phenotypic traits driving variation within soyabean (*glycine max*) collection in ghana. *Plant Breeding*, 138(5):577–587, 2019.

SL Dwivedi, S Gurtu, S Chandra, W Yuejin, and SN Nigam. Assessment of genetic diversity among selected groundnut germplasm. i: Rapd analysis. *Plant Breeding*, 120 (4):345–349, 2001.

Amanda J Garris, Thomas H Tai, Jason Coburn, Steve Kresovich, and Susan McCouch. Genetic structure and diversity in *oryza sativa* I. *Genetics*, 169(3):1631–1638, 2005.

## Bibliography II

Michael D Hayward, Nils Olöf Bosemark, and T Romagosa. *Plant breeding: principles and prospects*. Springer Science & Business Media, 2012.

Ruslan Kalendar, Alexander Muterko, and Svetlana Boronnikova. Retrotransposable elements: Dna fingerprinting and the assessment of genetic diversity. *Molecular Plant Taxonomy: Methods and Protocols*, pages 263–286, 2021.