

## Botanical and ethnobotanical considerations for Wheat

- Taxonomic designation: *Triticum spp*
- Botanical description: it is a summer or winter annual grass. Monocotyledons
- Growth habit: Cold winter, comparatively hot summer and moderate precipitation (annual rainfall average between 15- 45 inches).
  - generation time has important implications for genetic analysis: Wheat requires 4 month approx from seed planted to seed harvested.
  - genetic conservation strategies: Germplasm collections (national and international)
- Economic value: 2005 North America production: 82.7 millions tons. 2005 World production: 618 millions tons. 2006 592 millions tons. Second cereal most important after maize and preferred in industrialized countries.
  - importance drives private/public research:
- Public research centers (International: CIMMYT or National Research Programs (USDA) in cooperation with Universities (Wheat Breeding Program in Oregon by OSU ). There are many International and Nationals research centers worldwide for wheat research and breeding.
- Public companies, governments, and universities are the big players in breeding/genetics on wheat. There are private companies such as Monsanto, Syngenta, but it is difficult to recover the research investment looking for profits.
- End use: Food principal
  - Driver for genetic analysis: Protein Content, Protein Quality, Starch and Pigment content are the most important quality components.
- Center of origin and/or genetic diversity Fertile Crescent
  - Wild and ancestral species are a source of useful genes: as *Eikon*, *Aegilops*. *Leymus racemosus*, a wild relative of wheat that grows on sea shores and which, in addition to exuding nitrification inhibitors, carries tolerance to saline soils and resistance to fungal diseases of wheat.
  - Strategies for collecting/ conserving genetic diversity: plant explorations and seed exchanges, the individual collections. The National Small Grains Collection (NSGC) USDA-ARS
  - Maintaining genetic diversity: he National Small Grains Collection (NSGC) USDA-ARS

## Genetics considerations

.Some wheat species are diploid, with two sets of chromosomes, but many are polyploids, with four sets of chromosomes (tetraploid) or six (hexaploid).<sup>[13]</sup>

- Einkorn wheat (*T. monococcum*) is diploid.
- Durum wheat is tetraploid.
- Hexaploid wheats. Resulted from the hybridization of a wild diploid grass (*Aegilops tauschii*) and a tetraploid (Durum wheat).

- Genome size: Most wheat is hexaploid
  - (Megabases Mb) = 13,500 megabases in size
    - Model species and crop plants 130–140 Mb in the model experimental plant, *Arabidopsis thaliana* or 400 Mb for the model cereal, rice
- Chromosome number:
  - $n = 7$  chromosome per genome. Bread Wheat has 6 copies genome.
  - $2n = 6x = 42$  AABBDD
- Ploidy level
  - tetraploid =  $4x$ , Durum wheat;  $2n = 4x = 28$
  - hexaploid =  $6x$ , Bread wheat;  $2n = 6x = 42$
  -
- **Genetic implications of sexual reproduction**
  - Sexual differentiation: Monoecious (Hermaphrodite).
  - Asexual reproduction: No
  - Sexual reproduction:
    - Self-pollinated by nature
    - Cross pollinated: To improve wheat varieties on breeding programs.
  - Degree of heterozygosity in cultivars: 3.125% heterozygosity, 96.87% homozygosity and after 5 self pollinations.

## Biotechnology

Molecular breeding tools: The size and structure of the wheat genome makes it one of the most complex crop species for genetic analysis. The development of molecular techniques for genetic analysis, in particular the use of molecular markers to monitor DNA sequence variation between varieties, landraces, and wild relatives of wheat and related grass species, has led to a dramatic expansion the understanding of wheat genetics and the structure and behaviour of the wheat genome. The most comprehensive collection of wheat genetic data is on (<http://wheat.pw.usda.gov/>).

- Linkage maps: By studying how often two genes are transmitted together scientists can estimate how close they are on the chromosome and create what is called a linkage map. Results: Molecular linkage map of Einkorn wheat (diploid): mapping of storage-protein and soft-glume genes and bread-making quality QTLs. (The 3 genomes also translate into 21 linkage groups in wheat, again adding to the complexity of mapping work.)
- Quantitative Trait Loci (QTL):. Goal: QTL for yield and yield components, for disease and quality. Results: QTL controlling grain dormancy on chromosome 4A of wheat.
- Marker Assisted Selection (MAS): Emerging MAS targets are necessarily programme-dependent, but the broad focus is on quantitative trait locus (QTL) targets that could have a major impact on breeding efficiency. Larger number of markers usually needs to be screened on

wheat than is the case for rice, maize, or barley. Molecular markers widely used are RAPD, AFLP, SSR, Hybridisation based methods (DArT). Wheat market value is low, and this impedes the ability of the industry to invest in MAS infrastructure to the extent that is possible for crops such as maize. MAS use will be directed towards specific purposes such as accelerated selection of a few traits that are difficult to manage by conventional phenotyping, for the maintenance of recessive alleles in backcrossing programmes, for the pyramiding of disease resistance genes and for guiding the choice of parents to be used in crossing programmes.

**Table 3. Comparison of the most widely used marker systems for wheat**

Marker System	Loci detected per assay	DNA amount needed	Advantages	Disadvantages
RFLP	3	5 µg	Highly reliable, co-dominant, serve as reference to other cereal maps, large number available, target specific regions	Technically difficult, slow, requires large amount of DNA. Detect low level of polymorphism
SSR	1	0.2 µg	Reliable, co-dominant, often genome-specific, target specific regions, amenable to automation	High development cost
AFLP	50	0.2 µg	Reliable, detect large number of loci simultaneously, amenable to automation	Random, dominant
RAPD	10	0.2 µg	Cheap, technically simple	Unreliable, dominant

**Table 6. Recent publications describing the association of molecular markers with traits in bread wheat**  
CAPS, cleavage amplified polymorphic sequence; SCAR, sequence characterised amplified region; STS, sequence tagged site

Locus	Trait	Source	Marker type	Location	Reference
<i>Rusts</i>					
Lr47	Adult plant resist.	<i>T. speltoides</i>	CAPS	7A	Helguera <i>et al.</i> 2000
Lr35			STS	2B	Seyfarth <i>et al.</i> 1999
Lr21		<i>Ae. tauschii</i>	RFLP	1DS	Spielmeier <i>et al.</i> 2000
Yr10, YrVav			RFLP	1BS	Spielmeier <i>et al.</i> 2000
Yr28	Adult plant resist.	<i>Ae. tauschii</i>	RFLP	4DS	Singh <i>et al.</i> 2000
Yr18			RFLP	7DS	Singh <i>et al.</i> 2000
Yrns-B1		Lgst. 79–74	RFLP	3BS	Borner <i>et al.</i> 2000
YrH52		<i>T. dicocoides</i>	SSR	1B	Peng <i>et al.</i> 2000
Yr17		<i>Ae. ventricosa</i>	RAPD/SCAR	2A	Robert <i>et al.</i> 1999
Yr17, Lr37, Sr38		<i>Ae. ventricosa</i>	STS, RFLP	2AS	Seah <i>et al.</i> 2000
<i>Powdery mildew resistance</i>					
Pm1c and Pm4a			AFLP		Hart <i>et al.</i> 1999
Pm21		<i>H. villosa</i>	SCAR	6VS	Liu <i>et al.</i> 1999
Pm26		<i>T. turgidum</i>	RFLP	2BS	Rong <i>et al.</i> 2000
Pm13		<i>Ae. longissima</i>	STS	3S	Cenci <i>et al.</i> 1999
<i>Other disease resistances</i>					
	Wheat streak mosaic by movirus		RFLP	2D	Khan A.A. <i>et al.</i> 2000
Dn5	Diuraphis noxia resist.		SCAR		Venter and Botha 2000
Rkn-mn1	Root-knot nematode	<i>Ae. variabilis</i>	RAPD		Barloy <i>et al.</i> 2000
<i>Stress</i>					
	Boron tolerance		RFLP	7B, 7D	Jefferies <i>et al.</i> 2000
	Sprouting resistance			5AL, 6A, 3B, 7B	Zanetti <i>et al.</i> 2000
	Cold tolerance		RFLP	5A	Vagujfalvi <i>et al.</i> 2000
	Preharvest sprouting		STS, SSR	6B, 7D	Roy <i>et al.</i> 1999
<i>Quality</i>					
	Flour colour	STS	7A		Parker and Langridge 2000
	Milling yield		RFLP	3A, 7D, 5A	Parker <i>et al.</i> 1999
	Grain protein content		SSR	2DL	Prasad <i>et al.</i> 1999
Wx-A1	Waxy		SSR	7D	Shariflou and Sharp 1999
	High grain protein	<i>T. turgidum</i>	RFLP	6B	Mesfin <i>et al.</i> 1999
	HMW glutenins		STS	Group 1	Ahmad 2000

- Genetically Modified Organisms (GMOs):
  - a) HMW glutenin (high molecular weight glutenin) genes in transgenic wheat.
  - b) Monsanto, the agricultural biotechnology company, genetically modified a variety of hard red spring wheat to resist the company's Roundup herbicide.
    - The genes : *Glu-1D-1* is (HWW glutein gene).
    - The techniques: <http://www.biotech-info.net/felsot1.html> wheat to resist the company's Roundup herbicide.
    - The issues: Legal, Social, Environment.

## Referentes

### **Australian Journal of Agricultural Research**

[http://www.publish.csiro.au/?act=view\\_file&file\\_id=AR01082.pdf](http://www.publish.csiro.au/?act=view_file&file_id=AR01082.pdf)

**CIMMYT** <http://www.cimmyt.org/english/wps/news/2007/oct/wildGrasses.htm>

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