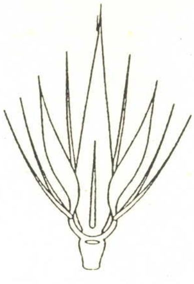
International Triticeae Symposium
Summary proceedings

4-8 May 1997
Aleppo, Syria

Compiled by

A. Bari and A. A. Jaradat

Organized by
The Triticeae Consortium
The International Center for Agricultural Research in the Dry Areas (ICARDA)
The International Plant Genetic Resources Institute (IPGRI)



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Content

Introduction

Summary proceedings
3rd International Triticeae Symposium
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The International Center for Agricultural Research in the Dry Areas (ICARDA)
The International Plant Genetic Resources Institute (IPGRI)

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Introduction

At the Second International Triticeae Symposium in 1994, the participants unanimously accepted a proposal for the Third International Triticeae Symposium to be held in Aleppo, Syria. The International Plant Genetic Resources Institute, West Asia and North Africa Regional Office (IPGRI-WANA) and The International Center for Agricultural Research in the Dry Areas (ICARDA) are serving as hosts.

The purposes of the symposium are:

(1) to exchange the latest scientific information and advancements related to annual and perennial Triticeae species; and
(2) to promote the exchange of ideas for developing coordinated or collaborative research.

In preparation for the symposium the first announcement was distributed in print and electronically through the Internet. An electronic form was also provided on the Internet so that people could register via E-mail.

During the symposium, plenary lectures will be delivered by leading scientists in their field of expertise. Scientific papers will be presented by participants orally or as posters. There will be five sessions:

Session I.	Evolutionary Genomic Relationships in the Triticeae
Session II.	Biodiversity and Biogeography
Session III.	Genetic Resources and Core Collections in Breeding and Research
Session IV.	Evaluation and Pre-breeding of Cereals and Forages
Session V.	Quality and Utilization

Session I

Evolutionary Genomic Relationships in the Triticeae

Chromosome Pairing in Some Synthetic Hybrids Between Bread Wheat and *Thinopyrum* Species: Breeding Implications

A.B. Almouslem, P.P. Jauhar, V.R. Bommineni and T.S. Peterson
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Fargo, North Dakota 58105, USA.

Hybridization with perennial grasses of the wheatgrass genus *Tinopyrum A.* Love has contributed substantially to the genetic improvement of bread wheat, *Triticum aestivum* L. ($2n = 6x = 42$; AABBDD genomes). *Thinopyrum bessarabicum* ($2n = 2x = 14$; JJ genome), *Th. curvifolium* ($2n = 4x = 28$; $J_1J_1J_2J_2$) and *Th. nodosum* ($2n = 2x = 28$) are valuable reservoirs of genes for resistance to stem rust and barley yellow dwarf virus. We synthesized hybrids with these perennial grasses using a highly crossable cultivar, Fukuhokomugi (Fukuho), as female parent. Several pentaploid hybrids ($2n = 5x = 35$) of Fukuho with *Th. curvifolium* and *Th. nodosum* were produced. Hybridization between Fukuho and *Th. bessarabicum* produced both tetraploid ($2n = 4x = 28$., ABDJ) and pentaploid ($2n = 5x = 35$; ABDJJ) hybrids. The latter arose as a result of functioning of the unreduced gamete of the male parent *Th. bessarabicum*. Unlike the female wheat parent, the F_1 hybrids were perennial. Morphologically, They were essentially intermediate between the parental species. Even in the presence of *Ph1b*, several hybrids showed some homoeologous chromosome pairing. Thus, in the tetraploid ABDJ hybrids, 17.7 to 23.5% of the complement showed association. Details of chromosome pairing will be described and its implications in plant breeding discussed.

* * *

Analysis of 5S rDNA units in the Triticeae: the potential to assign sequence units to haplomes

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Experimental Farm, Ottawa, Ontario, Canada.

In the Triticeae, 5S rRNA genes are organized into tandem repeats of 5S rDNA sequence types or units. We have postulated that some 5S DNA units may be useful for the detection of haplomes. The assignment of these units to different haplomes can be demonstrated using examples from several genera, including *Elytrigia* (with respect to *Pseudoroegneria*), *Hordeum, Roegneria* (mostly *Elymus*) and *Kengyilia*. The purpose of this paper is to summarize our recent progress in using sequence information from cloned 5S rDNA genes to define rDNA repeat units and our attempts to correlate the presence of several rDNA units to various genome/haplome carriers.

Efficient techniques for polyhaploid production in hexaploid wheat using pearl millet crosses

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A methodology for producing wheat polyhaploids using wide crosses followed by embryo rescue has been developed over the last two decades. Significant technical advances have been achieved by using pollen selected from different subfamilial species and applying plant growth regulators. Efficient crossing techniques were developed in pearl millet crosses using stored pollen and detached-tiller culture, and resulted in considerable savings in terms of labor and space required for growing parent plants. They will also accelerate the production of doubled haploids from hybrid progenies that tare used as recombinant inbred lined with favorable uniformity in breeding selection and genetic analyses.

Production and Meiotic Analysis of Some intergeneric Hybrids Between Durum Wheat and *Thinopyrum* Species

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The wheatgrass genus *Thinopyrum* A. Love is a valuable source of genes for durum wheat (*Triticum turgidum* L., 2n = 4x = 28; AABB genoumes) improvement. *Thinopyrum bessarabicum* (2n = 2x = 14; JJ genoume) and *Th. curvifolium* (2n = 4x = 28; $J_1J_1J_2J_2$) have a host of genes for superior agronomic traits such as resistance to stem and leaf rusts and barley yellow dwarf virus. These grass species were crossed with Langdon (LDN), a superior cultivar of durum wheat, as female, and several hybrids with and without the homeologous pairing suppresser gene, *Ph1*, were synthesized. Hybrids without *Ph1* were produced by using a Langdon substitution line LDN-5D(5B) (in which chromosome 5B carrying the *ph1b* gene was substituted by chromosome 5S) as the female parent. The F_1 hybrids were perennial and phenotypically intermediate between the parental species. The hybrids lacking *Ph1b* showed extensive homoeologous chromosome pairing. Thus, in two triploid F_1 hybrids (2n = 3x = 21; ABJ) between LDN-5D (5B) and *Th. bessarabicum,* 58.4 % of the chromosome complement showed chiasmatic association. Similarly, in hybrids between LDN-5D (5B) and *Th.* curvifolium almost 48.2 % of the complement showed pairing. Relatively high pairing (varying from 18.9 to 36.1 %) was also observed in the presence of *Ph1* in some durum x *Th.* curvifolium hybrids, presumably because of the partial inactivation of *Ph1b*. Data on chromosome pairing will be presented and possibility of gene transfer into durum wheat will be discussed.

Translocations of rye chromosome 2R in wheat to study water-use efficiency

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Recent research of J.G. Waines and co-workers has shown that rye (*Secale cereale* L.) chromosome 2R improves water use efficiency and drought tolerance of wheat (*Triticum aestivum* L.). To determine which chromosome arm and which segment of an arm is responsible for this effect, centric translocations 2RS.2BL and 2BS.2RL were produced in Chinese Spring wheat and transferred by backcrosses to Pavon wheat. Pairs of lines: translocation homozygotes and their normal sibs were produced for field trials. To identify small segments of chromosome 2R responsible for water use efficiency, the centric translocations were recombined with chromosomes of Pavon using the ph1b mutation. So far, 63 recombinants of 2RL and 5 recombinants of 2RS were isolated. Recombination frequency was 16.3% for 2RL and 0.24% for 2RS. Of the 2RL recombinants, four involve 2DL, two 2AL, and 57 2BL; of the 2RS recombinants, three involve 2BS and one each, 2AS and 2DS. All recombinant chromosomes resulted from single cross-overs; the cross-overs were concentrated in the distal regions of the chromosome arms. The DNA of the 2RS.2BL and 2BS.2RL translocation homozygotes of Pavon were screened with 489 OPERON primers and 79 RAPD markers of the translocated arms were identified. Of these, 39 seem associated with the presence of the 2RS and 40 with 2RL. However, presence of the proximal regions of chromosome 2B from CS introduces a certain level of ambiguity into this analysis. Once the work is completed and sets of translocation homozygotes are developed in the genetic background of Pavon, it should be possible to identify the segment of rye chromosome 2R responsible for water-use efficiency in wheat

* * *

Inheritance and the effect of a gene for long glume: A key character for taxonomy

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Triticum turgidum var. *polonicum*, is a primitive wheat for traditional agriculture. It is characterized by a long empty outer glume, which is one of the key characters for taxonomy in *Triticum*. The long glume is controlled by the P gene, the location of which was confirmed on chromosome 7A. At ICARDA, several traits (earliness, long vitreous kernels and tolerance to high temperature during the grain-filling period) have been transferred to a durum wheat cultivar, "Sebou", from *T.*

polonicum. However, "Sebou" does not have a long glume. Near isogenic pairs for the P gene have been established in the genetic backgrounds, tetraploid cultivar, LD222 and hexaploid cultivars, Prins and Saratovskaya 29. We assessed the effect of the P gene (1) on spike and gross morphology and (2) on kernel yield plants with the P gene that have several sterile basal spikelets. The entire glume of the tetraploid with the P gene was longer than those of hexaploids with the P gene. Spikes of hexaploid with the P gene were longer than those of the tetraploid with P. The spike density and kernel yield/plant were also influenced by the P gene, although there was no consistent trend on the kernel yield/plant.

Session II

Biodiversity and Biogeography

Biodiversity and Biogeography

Diversity of the *Triticeae* in the Near East

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The most important species of the tribe *Triticeae* are found in the Near East. The particularities of the Mediterranean climate in the semi-arid regions of the Near East, i.e. the long period of drought and high temperature in summer, favored the evolution of annuals from ancestral perennial species. Species richness and the high proportion of annuals in the Near East indicates that the region is a center of annual *Triticeae* diversity. Spreading of annual species into specific habitats resulted in the evolution of diploid species with well-defined phytogeography. Wide hybridization and subsequent polyploidization within the *Triticum/Aegilops* complex lead to the evolution of more broadly adapted polyploids. Some annual species have relatively large grains and are rich in nutrients, to facilitate a vigorous growth at the onset of the cool and rainy winter season. Such species were predisposed to domestication which occurred in the Near East arc some 10 000 years ago. Currently, wheat and barley account for 36% of the world's total cereal hectarage and wheat alone provides one third of human food. As the wild relatives are an important source of genes or gene complexes in wheat and barley improvement programs, solid knowledge of the species geographic distribution may indicate presence of distinct ecotypes adapted to specific environments. Development of the global wheat wild relatives database by IPGRI and ICARDA, and recent collection and survey missions by ICARDA, has contributed to better knowledge of the wheat and barley wild relatives phytogeography and habitat. Analyses of diversity in natural populations of wild *Triticum* spp. revealed large variation in a number of important traits such as disease resistance, cold tolerance, seed storage proteins and photothermal response. Partitioning of variation in four wild *Triticum* spp. demonstrated that diversity in some adaptive traits is distributed mostly among species (number of spikelets per spike, waxiness, awn length, earliness *per se*, low-temperature vernalization response), while in other traits most of the variation is among populations within species (photoperiod response, days to heading) or within populations (awn color, glume color). Similar to wild relatives, a recent study of phenotypic diversity in cultivated barley collection held at ICARDA, which included more than 18,000 accessions, demonstrated that cultivated barley germplasm from the Near East countries (Turkey, Syria) was a rich source of variation for twelve agro-morphological traits. To safeguard the rich but rapidly eroding genetic diversity of WANA wheat and barley gene pool, ICARDA assembled and is holding in its gene bank large *ex situ* collections comprising 25,000 accessions of landrace origin and 5,500 wheat and barley wild relatives accessions. The genetic richness of the wild part of the crop gene pool is now becoming more accessible with the recent advances of biotechnology, therefore these genetic resources may be essential for the development of improved germplasm meeting future needs of sustainable agriculture. As the high genetic diversity of cereal wild relatives and landraces may not be adequately conserved in *ex situ* collections, ICARDA has been involved in the identification of natural populations for conservation *in situ* and has started, in collaboration with the Syrian national program, three pilot experiments simulating cereal wild relatives *in situ* conservation. The Germplasm Program of ICARDA has developed a new strategy for a dynamic on-farm conservation of cereal landraces through participatory breeding.

What is *Elymus komarovii* (Nevski) Tzvelev?

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Elymus komarovii is a poorly studied taxon native to the mountains of Southern Siberia, Mongolia, and North-Western China. Morphologically it is closely linked to the boreal group of *Elymus* species possessing the SH genomes and the most similar species are found in the *Elymus alaskanus-kronokensis* complex and in the *Elymus mutabilis-transbaicalensis* complex. The aims of this investigation are to elucidate its taxonomic status and whether it is distinctly delineated from the other taxa. The methods used for this purpose are to analyze the morphological variation and a biosystematic analysis through intraspecific and interspecific hybridizations and measurement of sterility barriers in F1 and F2 generations together with molecular studies like isozyme variation analysis and storage protein variation analysis. These will finally be complemented with a study of micro satellite variation. The preliminary results will be presented and discussed.

* * *

Locating diversity using germplasm passport data and herbarium records: *Case of wild wheat in Cyprus*

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Botanical information and germplasm collecting data available on *Aegilops* spp. at the Agricultural Research Institute in Cyprus were used to create dot distribution maps. These maps in turn were used as raw data to carry out data analysis (regression line, diversity indices, cluster analysis). Prior to the analysis of dot distribution maps, the country was split into equal areas to compare these areas in terms of species richness and diversity. The results suggest that further collecting is still needed of *Aegilops* in Cyprus. The diversity is estimated on the basis of the information collected "*a priori*" (geographic origin, genomic variation, taxonomy). The geographical origin provides, although partially, information on the genetic diversity (M. Lefort-Buson *et* al., 1988). Information such as passport data is important in the prediction of high diversity sites. This type of information, in combination with other information *collected a posteriori* (evaluation), can provide the potential diversity for the species under study.

The Triticeae in the Manual of North American Grasses

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The generic treatment of the Triticeae has been the most controversial aspect of the *Manual of North American Grasses*. Fourteen genera are recognized as occurring in Canada and the continental U.S.A. Five genera (*Elymus, Hordeum, Leymus, Pascopyrum, Pseudoroegneria*) are represented by native species, *Pascopyrum* being restricted to the *Manual* region. The completely introduced genera are *Aegilops, Agropyron, Dasypyrum, Eremopyrum, Psathyrostachys, Secale, Taeniatherum, Thinopyrum,* and *Triticum*. Many North American taxonomists, particularly those that are more floristically inclined, strongly support a much broader interpretation of *Elymus*, in some instances including *Psathyrostachys, Leymus,* and *Taeniatherum* in addition to *Pseudoroegneria* and *Psathyrostachys*. Many of the same individuals also recognize both *Aegilops* and *Triticum*. Both *Sitanion* and *Hystrix* are recognised in *Genera Graminum*, a position that is defensible on morphological grounds. A few species of the extreme northwest have been transferred to *Roegneria*. The focus on the generic controversy has obscured the real need for basic systematic studies of individual species.

Host reactions of Triticeae to different cereal cyst nematode species

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Three species of the cereal cyst nematodes *Heterodera avenae, Heterodera latipons* and Gotland strain, closely related to *Heterodera filipjevi* on morphological and molecular criteria, occur more or less commonly in Europe, North Africa and West Asia. According to their geographical location, they could severely damage cereal production, especially barley, bread and durum wheats. For environmental and economical reasons, control of these pests is planned on the use of resistant cultivars. The aims of this study were to find in the Triticeae candidate germplasm which could be further used in breeding and/or biotechnology programs to improve the resistance of bread and durum wheats to the three nematode species. Nine populations of *H. avenae* originating from 7 countries or continents (Algeria, France, Morocco, Spain, Australia, India, West Asia), one population of *H. filipjevi* from Bulgaria and one population of *H. latipons* (West Asia) were studied for their development capability on diploid (genomes A,Sl ,U,D), tetraploid (genomes AB, UM, DvMv,USv) and hexaploid wheats. Data are given on the virulence and fitness of the nematode populations and the resistance levels of the germplasm tested.

Accumulation of proline in relation to abiotic stresses in wheat

M. Benlaribi and G. Chaib
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Proline accumulation in the vegetative parts of the plant is considered as an indicator of drought, salinity and other abiotic stresses. Proline accumulation was studied in durum wheat seeds during germination, young leaves (stages 2 and 3) under ample moisture and drought conditions. It was possible to identify two groups in the durum wheat genotypes in this study. A North-African group of genotypes, selected from landrace populations was found to accumulate high proline levels, and another group, mainly introduced from countries with favorable rainfall, was found to accumulate less amounts of proline when subjected to drought.

* * *

The use of DNA markers in the study of biodiversity in barley

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A core collection is a subset of the total collection representing the genetic diversity with a minimum of repetitiveness. It has many roles to play in the management and use of genetic resources. The objective of this study is to evaluate the genetic diversity of a barley core collection covering the WANA region using molecular markers. The core collection was provided by GRU, ICARDA. A total of 323 accessions out of 396 was analyzed using one plant from each accession. For Syria and Afghanistan ten plants per accession were analyzed. The RAPD technique was used. Four Operon primers were used: OP-B01, OP-G08, OP-K16 and OP-S09. The amplified fragments of the same molecular weight were scored for presence and absence. The results showed a high level of genetic diversity between accessions. Accessions collected from specific areas revealed unique patterns as well as patterns which were in common with other collection areas. The accessions from Syria and Afghanistan showed intra accession variability. In this study the RAPD technique proved to be very useful to estimate biodiversity in a barley core collection. More detailed analysis is needed to estimate the total biodiversity of barley existing in WANA countries to be represented within the core collection.

Isozyme characterisation of genetic diversity in species of the genus *Elymus*

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Elymus L. is the largest and most widely distributed genus in the tribe Triticeae and comprises about 150 species throughout the world. Over the last decade, a number of research programmes have been carried out on many *Elymus* species and a great amount of information have been obtained. However, there is a general lack of knowledge about the population genetic structure of the majority of the *Elymus* species. This information is an important prerequisite for conservation and utilisation of these taxa as well as to understand the phylogenetic and evolutionary relationships in this genus. The present investigation is part of a research program aimed to study the population genetic structure of four *Elymus* species, namely, *E. caninus*, *E. alaskanus*, *E. mutabilis* and *E. fibrosus*, mainly from the Nordic region. We also wanted to investigate the patterns of genetic variation from other species (more than 25) from Central Asia and North and South America. The results presented here constitute the preliminary data obtained from this investigation. The aim was to compare the electrophoretically detectable genetic variation obtained in the Nordic *Elymus* species with the other *Elymus* species. The results are discussed with regard to six enzyme systems, namely, Diaphorase (DIA), Aconitase (ACO), Malate dehydrogenase (MDH), Phophoglucomutase (PGM), Shikimate dehydrogenase (SKD) and Glucose phosphate isomerase (GPI).

* * *

High molecular weight (HMW) glutenin subunits polymorphisms present in the Syrian durum wheat landrace Haurani

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Variability for High Molecular Weight (HMW) glutenin subunits in the Syrian durum wheat landrace Haurani, originated from Hauran plateau, southern Syria, was investigated using SDS-PAGE. Haurani is found throughpout the Middle East region with an excellent adaptability to different dryland conditions. A survey of several populations collected from different locations in Syria was conducted in terms of HMW-gs composition. Multiple allelic forms at the Glu-A1 and Glu-B1 loci located on the long arms of chromosomes 1A and 1B have been reported.The HMW-gs frequencies were also studied. A large variation for HMW glutenin subunits was detected.

Isoenzyme data on the autochthonous and independent origin of the North American allotetraploid *Elymus* species

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The genus *Elymus* L. comprises amphiploids of intergeneric hybrids that unite the pivotal S genome of *Pseudoroegneria* with the H genome of *Hordeum* subgen. Stenostachys (= genus *Sitanion*), the Y genome of unestablished taxonomy, and the P genome of *Agropyron* in various combinations (Dewey 1984). The SH genome group is of widest distribution extending throughout the Europe, Asia, North and South America. Cytogenetic studies of meiotic pairing in F1 hybrids between some Asian and N. American SH genome species have shown (Hodgson 1964, Dewey 1974) a high degree of chromosome homology, suggesting a possibility of common Asian origin of the whole SH genome group with the following migration of some colonizing founders through the ancient Beringian bridge to N. America and subsequent adaptive radiation and diversification at the tetraploid level. Previous isoenzyme studies (Jaaska 1974,1992), however, showed that the Eurasian and N. American SH genome species have distinctly different esterase isoenzyme EST-A fixed heterozygosities, evidencing their separate allopolyploid origin from different diploid precursors. In this report new data on the isoenzyme diversity among the N. American SH genome *Elymus* species in comparison with the indigenous S genome species *Pseudorogneria spicata* and the H genome species *Hordeum brachyantherum* s.l. and *H. jubatum* will be presented. It will be shown that fixed heterozygosities of diagnostic isoenzymes in the SH genome species combine allozymes found in the indigenous S and H genome species, indicating their suitability as putative diploid progenitors and genome donors. The isoenzyme data strongly support the hypothesis of the autochthonous origin of the N. American SH genome allotetraploids from the indigenous S and H genome progenitors. The observation of different fixed heterozygosities at some isoenzyme loci in different allotetraploids indicates their apparently independent origin from different genotypes of diploids. The data on the intraspecific variability of some isoenzymes in auto- and allogamous allotetraploids will be discussed with respect to possibilities of their multiple origin and further diversification at the tetraploid level.

* * *

Micromorphological patterns of some amphiploids in the tribe Triticeae

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Natural and artificial hybrids commonly resemble one (or both) parental species. This is visible in gross morphology. Bennett (1993) proved that such a uniparental dominance is correlated with a spatial arrangement of component genomes of the hybrid. For the present study the quantitative characters describing glumes, lodicules as well as morphology and meristematic activity of lemma and palea epidermis were analyzed. This was made for two groups of amphiploids: of intergeneric (*Leymus, Elymus, Pseudoroegneria, Critesion, Triticum, Aegilops, Thinopyrum, Secale)* and of interspecific (*Aegilops, Triticum*) origin. Within intergeneric hybrids the most pronounced maternal dominance was found in *Elymus canadensis* x *Critesion bogdanii* and *Elymus canadensis* x *Pseudoroegneria libanotica*. The paternal dominance was a little weaker in *Pseudoroegneria libanotica* x *Elymus yezoensis*. In reciprocal amphiploids between *Triticum boeoticum* and *Aegilops uniaristata* the dominance of wheat was stronger. In interspecific hybrids of the genus *Aegilops* the dominance of wheat was stronger. In interspecific hybrids of the genus *Aegilops* the dominance of *Ae. umbellulata* was distinct in reciprocal amphiploids after crossing with *Ae. uniaristata* and *Ae. sharonensis* as a mother plant. The amphiploids having *Aegilops squarrosa* as a paternal plant show biparental dominance. Their epidermal characters are of a paternal pattern. The biparental dominance was also found in *Triticum fungicidum*, *Triticum kiharae* and *Triticale*. An autoamphiploid, *Triticum timonovum*, is very distant from its parental species, *Triticum timopheevi*. Characters of lodicules were arranged in three cluster dimensions, shape, hairiness and lobe. Characters describing the morphology of epidermis were included in two clusters, of lemma and palea. However, the characters of papillae and hairs in lemma and palea were set in common clusters. Meristemoid activity in inflorescence bracts was described by the number of different types of cells. The papillae of bracts (lemma and palea) were in a distant cluster when compared with duplexes (silica and cork cells). When selected amphiploids were stressed by malnutrition, deficit of water and high temperature they changed generally in a similar way. The above results make possible the selection of forms appropriate for looking for the spatial arrangement of genomes. This purpose may be well attained by *in situ* hybridization of the genomic DNA.

* * *

A comparative study of durum wheat and its progenitor wild emmer wheat

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Ten accessions of wild wheat (*Triticum dicoccoides*) and accessions of cultivated durum wheat were characterized by random amplification of polymorphic DNA (RAPD) profiles using 10-mer, oligonucleotides with diverse GC content. All tested primers yielded arrays of amplified DNA products ranging in size from 50bp to 800bp. Application of the RAPD analysis to ten samples within each accession of the above mentioned wild and cultivated wheat showed polymorphism and variation within the same accession and there were also great variations in the amplification DNA banding pattern from one accession to another in the wild and cultivated wheat.

Variation of high molecular weight glutenin subunits in tetraploid wheat *T. timopheevii*

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High molecular weight glutenin subunits present in several accessions of tetraploid wheats with genomic formula AAGG, *T. timopheevii* (cultivated) and subsp. *araraticum* (wild), were analyzed by sodium dodecylsulfate polyacrylamide gel electrophoresis (SDS-PAGE) and reversed phase high performance liquid chromatography (RP-HPLC). Combination of these techniques permitted us to associate different type of subunits to the A or the G genome and assess the extent of allelic variation present at corresponding encoding loci. Results also revealed that in both subspecies accessions are present possessing expressed y-type subunits at the Glu-A1 locus. This is in contrast with what was observed in tetraploid wheats of genomic formula AABB, where only in the wild species *T. turgidum* subsp. *dicoccoides* such subunit is expressed. Electrophoretic and chromatographic behaviour of x-and y-type subunits, present at the Glu-A1 locus in both subspecies, is very similar to the one observed in the wild diploid wheat relative *T. urartu*. This result supports the role of this species in the formation of polyploid wheats of the *timopheevii* group.

Present-day distribution of hulled wheats (einkorn, emmer and spelt) in Spain: the contribution of archaeoethnobotany

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Hulled wheat species (einkorn, emmer and spelt) are amongst the oldest plants cultivated in the Near East. In Spain, it is still possible to find, today, the three species under cultivation in isolated areas. Research based on archaeobotanical studies, and literary sources indicates that the three species were under cultivation during both prehistoric and historic times. Pesent-day distribution within Spain is concentrated in mountain areas of Andalucia (einkorn) and Asturias (emmer and spelt) where traditional farming systems still survive. These are the last relicts of much larger scale cultivation in the past. For millennia farmers have grown different crops which were adapted to different cultivation techniques and grown under different cropping systems. This valuable knowledge is part of people's cultural and genetic heritage and a priceless element in any attempt to conserve and manage genetic resources. The changes occurring in rural areas have led to the abandonment of traditional farming practices and these crops that once played an important role within the domestic economy. Both germplasm and traditional knowledge are highly threatened and urgent efforts should be made to safeguard this heritage before it is lost.

Phylogenetic analysis of *Hordeum*

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Though extensively studied for years the phylogeny of *Hordeum* is still largely unknown. Genome analysis has defined four major groups of species carrying the I, H, X, and Y genomes, respectively, but has failed to reveal any relationships between the groups. The phylogenetic relationship between the four groups is being explored using both morphological and molecular data. The molecular data include plastid RFLPs and DNA sequences (rbcL and rpoA) as well as nuclear DNA sequences (Adh1). Congruence between the different data sets is investigated.

Genetic variability of a hulled wheats collection evaluated in different agronomic environments in Italy

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The renewed economic interest in the hulled wheats species (*Triticum monococcum* L., *T. dicoccum* Schubler and *T. spelta* L.) stimulated several Italian institutions to collect, characterize and safeguard the germplasm of the still cultivated landraces. Sixty accessions of *T. dicoccum* and *T. spelta* were collected in the traditional Italian cultivation areas and evaluated for two years (1994/95 and 1995/96) in unreplicated plots at S. Angelo Lodigiano LO (North Italy) and Tolentino MC (Central Italy). The accessions were evaluated for different traits such as growth habit, plant height, heading date, spike length, number of seeds per spikelet, 1000-kernel weight and SDS sedimentation volume of flour. Eight accessions, were compared in agronomic replicated trials carried out in 1995/96 at S. Angelo Lodigiano LO, Bologna (Central Italy), Tolentino MC and Ururi FG (South Italy). Hulled and dehulled grain yield, yield-related traits and qualitative parameters were measured. A high level of variability was detected in some traits such as yield, height, heading date, kernel weight, lodging resistance. The mean hulled grain yield was 3.44 t ha^{-1} for *T. dicoccum* and 3.63 t ha^{-1} for *T. spelta*. Significant differences of several traits were observed among accessions and environments. The characterization of still cultivated landraces could bring to a rational utilization of the final product, to a most efficient commercialization and to an increase of the farmers' income. Therefore, this action could support in the future "on farm" conservation of hulled wheats.

Exploiting genetic diversity of old wheats for a new millennium

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Although high inputs and high yielding wheats have played a significant role in reducing hunger the loss of indigenous and heritage varieties has become recognized as a serious problem. Agricultural biodiversity conservation must become an action statement, not just a policy concept. Old varieties grow in low input systems and increasing genetic diversity within the selection of seed planted by the farmers makes ecological sense. NGO work with traditional, heritage and landrace wheats has helped increase the profile of the value of these wheats for their own merit, not just as gene bank stock for plant breeding and biotechnology use. Some new uses for older crops may provide some answers for food security in the next millennium. The impact of NGO wheat conservation efforts in two very different countries, Canada and Ethiopia will be discussed. NGO groups have worked in collaboration with national gene banks as well as farmers to keep old wheats in cultivation. These programs show that each individual can take an active role in seed conservation activities and become globally responsible for genetic resource conservation.

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Characterization of microsatellite markers and microsatellite polymorphism in Elymus species

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Microsatellites, also known as simple sequence repeats (SSRs) are a subset of the tandemly repeated DNA family represented by extremely short nucleotide sequence repeats (less than 5 base pairs (bp)) that are abundantly present and interspersed in eukaryotype genomes. Microsatellites are highly variable DNA sequences that can be used as markers for the genetic analysis of plants. The potential of microsatellite markers for use in genetic diversity study in *Elymus* species was evaluated. Genomic library of *Elymus caninus* was constructed. The library was screened with two dinucleotide and two trinucleotide repeats. Positive clones were found for two dinucleotide repeats, no positive clone was found for trinucleotide repeats. Positive clones were sequenced to validate the presence of microsatellite to generate polymerase chain reaction (PCR) primers based on the sequences of flanking the microsatellite. In addition, eighteen microsatellite-specific primers developed in the Triticum aestivum were tested on 27 accessions of 19 species. Four primer pairs failed to reveal any variation in the accessions tested, four primers revealed polymorphism on part of tested accessions. Ten primers did reveal polymorphism, detecting between 2 and 32 alleles at each locus, indicating the potential of 'cross species amplication' is highlighted as an additional source of microsatellite markers for genetic research in Elymus species. Phenetic analysis of the derived information allowed a dendrogram to be constructed depicting the similarity between these accessions.

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Genetic diversity as revealed by RAPD in *Triticum aestivum*, *Triticum aestivum* subsp. *tibeticum* and *Triticum spelta*

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In order to improve the heterosis of hybrid wheat, it is necessary to establish a new heterotic group. This study was undertaken to evaluate the genetic diversity within and between wheat species and subspecies as revealed by random amplified polymorphic DNA (RAPD), to assess the possibility of establishing a new heterotic group in hybrid wheat breeding. Twenty two common wheat (*Triticum aestivum* L.) cultivars, seven accessions of *T. aestivum* subsp. *tibeticum* Shao and seventeen spelt wheat (*T. spelta* L.) introduced from Germany, Switzerland and Canada were used for RAPD analysis. Of the 26 10- mer arbitrary primers tested against the 46 genotypes, a total of 279 products were amplified, among which 182 (65%) products were found to be polymorphic. The polymorphic products amplified by each primer ranged from 2 to 18, with an average of 7. RAPD polymorphism was found to be much higher in *T. spelta* (58%). RAPD polymorphism in spring and winter common wheat was only 18% and 33%, respectively. The 182 polymorphic products were used to calculate genetic distance (G.D.). Mean genetic distance was two times larger in spring and winter spelt (0.4043; 0.3820) and *T. aestivum* subsp. *tibeticum* (0.4319) than in spring and winter common wheat (0.1214; 0.2164) .The mean genetic distance between spring and winter common wheat was 0.2355, but the genetic distance was doubled between spelt and common wheat and between *T. aestivum* subsp. *tibeticum* and common wheat. The result of cluster showed that the 46 genotypes were distinctly classified into two groups. Group 1 include all spelt wheat, in which spring spelt was distinctly separated from winter spelt. Group 2 included all common wheat; *T. aestivum* subsp. *tibeticum* was clearly separated. This indicate that *T. aestivum* subsp. tibeticum is more closely related to common wheat than to spelt. Spring and winter common wheat could be also separated distinctly in the lower hierarchy. It was concluded that T. *spelta* and *T. aestivum* subsp. *tibeticum* show much higher genetic diversity within their population and were more distantly related to common wheat, which could be used to diversify the genetic basis for hybrid wheat breeding and to improve heterosis. The RAPD marker method can be used to establish wheat heterotic groups.

Ecogeographical distribution and seed drying characteristic of native grasses of Morocco

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The native grass species occurring in the semi arid zones of Morocco offer a valuable genetic diversity that can serve in the selection of adapted materials to be used in range improvement and desertification projects. Selection of promising materials requires a knowledge of the ecology and the species in relation to edaphic, climatic and biotic factors. Germplasm collecting missions have been undertaken in different regions of the country since 1983. A total of 276 accessions, representing more than 25 genera of grasses were made over 128 sites. The most frequent genera represent three subfamilies: the *Festucoideae*, the *Panicoideae* and the *Eragrostoideae*. The *Festucoideae* are represented by 4 tribes (*Aveneae, Festuceae, Stipeae* and *Triticeae*) and 10 main genera, the Eragrostoideae with 3 tribes (*Aristideae, Eragrosteae* and *Chlorideae*) and 3 genera and the Panicoideae with 2 tribes (*Andropogoneae* and *Paniceae*) and 4 genera. The ecology of these genera according to the environmental factors has been studied and their distribution in relation to altitude, rainfall and soil are reported. Furthermore, the seed-drying curves of the most frequent genera at 20% relative humidity and 17°C were established.

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Biodiversity in barley, oat and triticale: development and applications of molecular markers

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Molecular markers are able to reveal genetic variation among different genotypes directly at the nucleotide sequence level (Pecchioni *et al.*, in press). The aim of this work was to study via molecular markers the inter-varietal biodiversity, as well as genetic variation among cultivated and wild forms in Triticeae. RFLP analysis of highly polymorphic loci applied to 50 barley cultivars allowed us to identify probes useful for investigating genetic variability in cultivated barley (Pecchioni *et al.*, 1993). These RFLP markers were translated into more user-friendly STS markers and their effectiveness to detect genetic variability among European winter and spring barley cultivars was compared with traditional morpho-physiological descriptors as well as biochemical markers, such as hordeins (Faccioli *et al.*, 1995). RAPD marker suitability and reliability were assessed for fingerprinting barley, oat and triticale varieties and genetic distances were calculated via cluster analysis for the considered varieties of each species. Biodiversity inside the *Hordeum* genus was investigated by the use of RAPD and STS markers on a set of European cultivars, Italian and Nepalese landraces, *Hordeum spontaneum*, *Hordeum bulbosum* and several accessions of wild barley species from the tertiary genepool. Two phylogenetic trees generated by UPGMA cluster analysis were substantially in agreement with classifications based on morphological and physiological observations (von Bothmer, 1992). The whole set of molecular markers developed could be usefully utilized to detect genetic variability in Triticeae for breeding purposes, for phylogenetic studies as well as to complement varietal discriminations for plant variety rights.

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Variation for isozymes and agronomic traits in tetraploid wheat (*Triticum turgidum* L.) landraces of Ethiopian origin

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Tetraploid wheats (*Triticum turgidum*) L. are the predominant wheat species cultivated in Ethiopia since long ago and due to the high diversity observed in these wheats, the country is considered as a center of diversity for these wheats. They are mainly landraces consisting of mixtures of different types and the occurrence of botanical forms makes these wheats interesting both from the botanical and agronomic points of view. The wealth of diversity available in these wheats needs to be utilized in crop improvement and as part of an effort to sue it, studies are underway to assess their diversity and extent of their variation for agronomic traits. The evaluations for agronomic traits were conducted locally in Ethiopia where better expressions for agronomic potentials could be realized. These wheats contain high diversity as estimated based on isozymes, the within population diversity. Similarly, agronomic evaluations revealed that they vary considerably for the desirable traits which can be exploited both for the short term and long term improvement work. It has been possible to select types with good yields from these landraces through phenotypic mass selection and achieve yield increment at the farmers level.

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Diversity in wild wheats from northern Syria

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Several species of wild wheats grow abundantly in northern Syria. They include *Aegilops speltoides*, *Triticum urartu*, *T. monococcum* subsp. *aegilopoides* and *T. turgidum* subsp. *dicoccoides*. Populations of these species were sampled in 1994 at several locations in Aleppo, Raqqah and Hasakah Provinces. Genetic diversity was assessed using starch gel electrophoresis. The results of this study will be presented and inferences made on the population biology of the species.

Triticeae Research in Afghanistan

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In the 1960s the agricultural production system of Afghanistan was subsistence and not much attention was paid to provision of inputs (improved seed, fertilizer and plant protection services) to the farmers. Therefore the food production potential of the country was not fully realized. Wheat constitutes the major part of the diet in Afghanistan, with a 180-200 kg per capita consumption annually. The cataclysmic drought of 1969-1972 brought an awareness in the authorities to pay attention to agriculture research to facilitate increased agriculture production. With the advent of the Green Revolution, crop improvement activities on Triticeae (wheat, barley and rye) were initiated and improved in the decade of 1970s. An accelerated wheat varieties introduction program was initiated and 19 research stations were established covering a wide range of agroclimatic conditions. A number of wheat varieties such as Mexipak, Indus 66, Kalyan 227, Besoztaya, Afghanistan-14, Bakhtar, Darulaman-I, Durum Ciano's D27617; Darulaman-2, Herat-I, Balkh-66, Bamyan-I, Darulmanan-4 and Nangrahar-64 were introduced to the farmers in the country, along with fertilizers and plant protection. As a result of this the average yield of wheat grew from 832 kg/ha to 1,150 kg/ha in 1977-78 and the country was approaching self-sufficiency. A number of yield trials and observation nurseries of wheat (bread and durum), triticale, and barley were received from CIMMYT and ICARDA and tested on farmer fields by the Swedish Committee for Afghanistan (SCA) through their research program. The varieties Pirsabak-85 and Pak-81 for warmer areas and Atay-85 for cooler areas were found to perform well in Afghanistan. The results of wheat yield trials from 1991-1996 have been compiled and a number of lines identified as possible candidates for release under irrigated and rainfed conditions. The results of this work indicate that these lines have out yielded Pirsabak-85 by 6 to 38% and have the potential to yield more than 6 tonnes per hectare.

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Study of the Bulgarian *Aegilops* genetic resources

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The species of *Aegilops* genus possess a number of valuable traits, such as disease and pest resistance and adaptation to environmental stresses, which make them a precious genetic base for wheat breeding. Bulgaria presents a great diversity of *Aegilops* species. During the expeditions realized by the IIPGR in various regions of Bulgaria, nine of the 22 species which constitute the *Aegilops* genus were identified and about 300 local accessions collected. A study of these genetic resources has been initiated with the following objectives: a better understanding of the relationships between *Aegilops* species and their environment, an identification of potential sources of resistance to diseases and abiotic stresses, and a better knowledge of the structure of diversity of the species allowing more efficient germplasm management. The relationships established between ecological characteristics of the prospected sites and the presence of the species have permitted to precise the nature of environmental factors determining the distribution of each one of them. Consequently, the collected accessions were evaluated for agronomic traits such as resistance to rusts and powdery mildew and frost tolerance. The respective roles of the constitutive genomes of the different species and the geographical origin of the populations are analyzed. The interest of each species for the genetic improvement of wheat is discussed and potential progenitors of biotic and abiotic stress resistance for wheat improvement are proposed. A diversity structure analysis was performed for *Aegilops geniculata* Roth on the basis of morphological traits and on randomly amplified polymorphic DNA markers (RAPD). The study revealed an important infraspecific diversity for morphological traits, as well as for molecular markers. Differences between ecological regions were observed and regions characterized with higher interpopulation diversity were identified. This result allow one to orientate the future collections and to initiate the constitution of a core collection of Bulgarian *Aegilops* genetic resources. The integration of different approaches presented in this study would permit a more efficient use of *Aegilops* germplasm in the future.

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Session III

Genetic Resources and Core Collections in Breeding and Research

Genetic Resources and Core Collections in Breeding and Research

Evolving Issues in Crop Genetic Resources Conservation

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The issues in crop genetic resources (CGR) conservation may be grouped in three main categories: (a) biological, (b) socio-economic, and (c) legal and political. The current emphasis appears to be shifting from the first to the latter two categories. Recently, some of the social and political issues, such as the ownership of crop genetic resources, equitable compensation system and farm-based conservation, have received considerable attention. On the other hand, important biological issues, such as comprehensive and reliable evaluation of CGR preserved *ex situ*, assessment of genetic loss in semi-natural and agricultural habitats, and devising practical alternatives to maintaining landrace populations of crop species in traditional agroecosystems, have received little attention. Under the inspiring leadership of Harlan and Frankel in the early 1970s, when conscious and concerted efforts to preserve CGR began, CGR were perceived as the common heritage of humankind. Today, CGR are widely recognized as "national heritage". The long-term impacts of this genetic isolation is far from certain. An understanding of the nature and magnitude of genetic diversity in comprehensive *ex situ* collections of CGR appears to be matter of far less concern today than developing core collections of CGR and establishing their relative merits. The core collection strategy was originally proposed by Frankel in 1984 as a means of increasing the use of CGR preserved in *ex situ* collections. It is now being promoted as a practical approach to gene bank management, as well as an efficient strategy for the conservation of CGR. However, the gains in efficiency and usefulness of core collections relative to large reserve collections appear to be largely conjectural. The implications of this strategic shift for long-term conservation of crop genetic diversity will be discussed. Another important evolving issue is the in situ conservation of CGR. Contrary to the earlier views that *in situ* conservation is appropriate for wild crop relatives, it is now emerging as a viable approach to conserving genetic diversity in crop species. However, several important questions concerning in situ conservation of crop species; such as optimal number of farms, farm and population size, farm management to minimize genetic erosion and maximize genetic gains, utilization of CGR and cost-effectiveness; remain unresolved. On-farm conservation of CGR is an interactive ecological, genetic and ethno-cultural process. The success of this complex method of CGR conservation requires a harmonious integration of indigenous knowledge systems and modern scientific knowledge systems into a combined sources of wisdom. The compelling issue is, how agricultural production systems can be intensified without increasing the risk of further loss of genetic diversity in crop plants. The importance of pursuing multidisciplinary fundamental research in this complex area CGR conservation cannot be over-emphasized. Unfortunately, however, with the current emphasis on legal, political and economic issues, the fundamental agro-biological issues in CGR conservation are sadly overlooked.

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DNA fingerprinting of divergent landraces of wheat for grain filling rate

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The development of molecular markers has revolutionized many areas of plant breeding and biology. DNA polymorphisms that are revealed by e.g. RFLP analysis, DNA fingerprinting and PCR-based techniques are now being applied to the marker-assisted breading of crops, the development of linkage maps, and other uses. The main objective of this study is to use the AP-PCR (arbitrarily primed polymerase chain reaction) to differentiate between high grain filling rate (HFR) and low grain filling rate (LFR) wheat landrace genotypes as an initial step for using that techniques in our breeding program to develop a high filling rate line. The results indicated that this technique is a powerful one and can separate the two groups perfectly, therefore we can use this technique in our breeding programs.

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Sources of resistance in *Triticum* and *Aegilops* species to Hessian fly (*Diptera cecidomyiide*) in Morocco

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Hessian fly, *Mayetiola destructor* (Say), is a destructive wheat pest in Morocco. Genetic resistance has been the most practical means of controlling this pest. A total of 372 accessions of *Triticum* and *Aegilops* species were evaluated for Hessian fly resistance in the field and in the greenhouse. Several accessions of *Ae. geniculata, Ae. triuncialis, Ae. neglecta, Ae. ventricosa, Ae. cylindrica, Ae. caudata, Ae. squarrosa* and one *T. boeoticum* were homogeneously resistant, and Two *T. monococcum* accessions showed heterogenous reactions to this pest. This is the first resistance to the Moroccan Hessian fly identified in *T. boeoticum* and *T. monococcum*. Antibiosis is the mechanism responsible for the resistance in

Aegilops species and *T. monococcum*, whereas *T. boeoticum* seems to have tolerance. These sources of resistance are being used by CIMMYT/ICARDA and Moroccan wheat breeders to develop resistant varieties to Hessian fly in North Africa.

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Creation of genetic variability in wheat through *Aegilops* species and its role in sustainable production

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The Nuclear Institute for Agriculture and Biology (NIAB) has a sizable program on wide hybridization aiming at creation of genetic variability for stress tolerance in wheat. Numerous accessions of different *Aegilops* species have been acquired from different germplasm centers of the world. These species have been screened continuously for the last 6-8 years. During the year 1995-96 we tested about 159 different accessions of *Ae. tauschi, Ae. cylindrica, Ae. geniculata, Ae neglecta, Ae. speltoide* and *Ae. variabilis* for wheat diseases and tolerance of salinity. The salt-tolerant and disease-resistant accessions are being hybridized with wheat cultivars used for general cultivation. The wheat material selected so far through this hybridization has been tested rigorously for all the prevalent diseases of wheat including all type of rusts, powdery mildew and karnal bunt. The finished material is being distributed to different organizations of the world and is of two fold significance. It has resistance against salinity and has out-yielded all the existing salt-tolerant wheat germplasm, and it can be grown on large tracks of salt-affected land in the country and abroad. It is also disease-resistant and therefore, be grown on normal soils for general cultivation. Since the disease resistance has been incorporated from the wild species, the material can also serve as a source of resistance to be incorporated in high yielding but susceptible wheat cultivars. In this program, a large number of *Aegilops* species/accessions are being tested every year. It is anticipated that through wide hybridization, material tolerant to newly emerging stresses like powdery mildew and barley yellow dwarf virus would be available which could be used in breeding programs to get sustainable productivity provided the wild germplasm be continuously screened, identified for their variability and utilized in the crossing program for the production of the germplasm to be used in any emergency.

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Wild barley germplasm evaluation and use in breeding for grain yield and pasture improvement

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Wild barley, *Hordeum vulgare* subsp. *spontaneum* is widespread in uncultivated fields and edges of cropped land in all the WANA countries and it is adapted to the harsh conditions, (heat and drought) of the Region. It crosses readily with subsp. *vulgare* cultivated barley. Over 10,000 spikes of wild barley, subsp. *spontaneum* and subsp. *agriocrithon* , were selected in Cyprus and their progenies were evaluated in nurseries. The best of these genotypes were used in breeding programs with subsp. *vulgare* cultivars. The result was to produce the highest grain-producing line, named Trachonas, in 1995/96, a relatively dry season. Traits improved by the wild barley genes include grain yield, tillering capacity, earliness, increased spike fertility, test weight of the grain and harvest index. Selection for "Reverse evolution" in the segregating populations of crosses between wild barley and subsp. *vulgare* cultivars resulted in the development of brittle rachis populations of leafy plants having the wild type of seed dispersing and seed dormancy genotypes. These genotypes have been tested to establish self-regenerating pasture barley in permanent pasture lands. Such pastures have regenerated each year for 10 year, without the need to reseed. Two varieties have been released, Mia Milia, a bulk of selected genotypes from the crosses, and Achera, a mixture of selected genotypes from natural out crosses between subsp. vulgare and subsp. *spontaneum* wild barley.

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Wild Triticeae as genetic resources of aphid, rust and powdery mildew resistance

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The Czech wild Triticeae germplasm collection includes over 1200 accessions of annual and perennial species. Within the annuals *Aegilops* and wild cereals are prevelent. Other, rather neglected annuals and perennial species were chosen for a basic evaluation as a secondary or tertiary genepool for cereal improvement or as a primary genepool for fodder crops breeding. About 200 accessions of *Agropyron, Dasypyrum, Eremopyrum, Elymus, Hordeum, Hordelymus, Leymus, Pseudoroegneria, Secale, Thinopyrum*, and *Taeniatherum* collected from Russia, Transcaucasia, Mongolia or Central Asia or received from various sources were evaluated. Resistance to the most virulent races for Czech conditions of stem rust *Puccinia graminis* f.sp. *tritici* Erikss. et Henn, brown rust *P. recondita* Rob. ex Desn., stripe rust *P. striiformis* Westend and powdery mildew *Erysiphe graminis* f.sp.*tritici* (DC.) Marchall was tested on adult plants in infected fields or on seedlings in the greenhouse. A very high percentage of completely resistant accessions was found within the perennial species. Infestation of cereal aphids *Sitobion avenae* (F.), *Metopolophium dirhodum* (Walk.), *Rhopalosiphum padi* (L.) and *Sipha elegans* del Guer. was observed during several years. Relatively lower aphid occurrence in 1990, 1991, 1995 and 1996 show rather an aphid preference for individual Triticeae species. Wild cereals and related species are much more infested than distantly related perennial grasses. A correlation was found between rust and aphid infestation.

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Relationship between seed storage proteins and gluten strength in durum wheat

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At ICARDA the electrophoresis and sodium dodecylsulphate (SDS)-sedimentation tests are used as routine for grain quality studies. To determine the relationship between seed storage proteins and gluten strength, a multilocation trial of 8 durum wheat varieties in 20 locations-years has been continuing in the dryland zone of Syria. Low molecular weight (LMW) type 2 glutenin subunits coded at the Glu-B3 locus have been reported to be responsible for pasta-making quality in durum wheat. However, the present study indicates that LMW type 2 is correlated but variable in gluten strength. The varieties showed no differences for gliadin components and LMW glutenin subunits; all of them carrying -45 and LMW-2. However, large differences and variation was shown for high molecular weight (HMW) glutenin subunits and grain quality traits related to gluten strength, such as protein content, SDS-sedimentation value, and SDS-sedimentation index. In this paper, the relationship between the electrophoretic patterns and gluten strength will be discussed.

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Suitability of wild genera and species of the tribe Triticeae as ovipositional and larval hosts of the hessian fly and the barley stem gall midge

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The Hessian fly (*M. destructor* (Say)), and the barley stem gall midge (*M. hordei* Keiffer) are the most serious insect pests of wheat and barley in Morocco. Wild genera and species of the tribe Triticeae were evaluated in a laboratory to determine their antixenosis and antibiosis levels and define the ovipositional and larval host ranges of the two insects. Results showed that of genera in the tribe Triticinae, Hessian fly females preferred *Triticum*, *Secale* and *Haynaldia* for oviposition. However, there was no association between the antixenosis level of a species and its antibiosis level. Two of the most preferred species (*T. tauschii* and *H. villosa*) were homogeneously resistant (antibiosis); one (*T. monococcum*) was heterogeneous. Species of the least preferred genera were all homogeneously susceptible, except for *Agropyron cristatum*. The level of antixenosis was affected by leaf width and stem-leaf angle. *Secale*, *Haynaldia*, and *Triticum*, the most preferred genera, had the largest stem-leaf angles and the widest leaves. Species of these genera also had the lowest leaf pubescence densities, although other species that were less preferred also had low pubescence density. Of genera in the subtribe Hordeinae, *H. spontaneum*, and *H. bulbosum* were the most preferred for oviposition by Hessian fly. Although there were large difference, all genera were suitable ovipositional and larval hosts. Unlike Triticinae species, Hordeinae species that had low levels of antixenosis also had low levels of antibiosis and were suitable larval hosts, except for H. bulbosum. Also, ovipositional preference was positively associated with stem-leaf angle and leaf width. The most preferred species had the widest leaves and the largest stem-leaf angles. The most preferred species also had low leaf pubescence density, whereas less preferred species had high pubescence density. However, some species with low pubescence density were less preferred for oviposition. Within *Triticum*, species with the A genome (*T. monococcum, T. boeticum*), the AB genomes (*T. turgidium, T. dicoccoides*), the C genome (*T. dichasians*), the D genome (*T. tauschii*), the AG genomes (*T. timopheevii, T. araraticum*), the DMcr genomes (*T. crassum*), and the UMo genomes (*T. ovatum*) were the most preferred. Cultivated wheat *T. aestivum* (ABD genomes), however, was significantly more preferred than the wild species. In general, the most preferred species for oviposition were also suitable larval hosts. However, *T. tauschii*, *T. cylindricum*, and *T. ventricosum* were resistant (antibiosis). *T. monococcum*, *T. boeticum*, *T. dichasians*, *T. longissium*, and *T. timopheevii*, *T. araraticum* were heterogeneous for resistance. There was low variability in the leaf morphological characters of Triticum species; however, the most preferred species had significantly larger stem-leaf angles, wider leaves, and lower leaf pubescence than the other species. Most species of *Hordeum* were suitable ovipositional hosts for the barley stem gall midge, but H. agriocrithon, *H. spontaneum*, *H. bulbosum*, and *H. chilense* were the most preferred. These species were also suitable as larval hosts, except for *H. bulbosum*. Other species were less suitable as larval hosts; several were heterogeneous for resistance. In most species, leaf morphological characters, such as high leaf pubescence density, extremely upright or prostrate leaves, and narrow leaves, increased the level of antixenosis. In conclusion, this study identified the range of host and non host grass species on which Hessian fly and barley stem gall midge can survive and reproduce in Morocco. New sources of resistance (antibiosis and antixenosis) to these two insects were also identified for potential use in wheat and barley breeding programs.

Promoting better conservation and use of hulled wheats

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Hulled wheat species (*Triticum monococcum*, *T. dicoccum* and *T. spelta*) are among the most ancient cereal crops of the Mediterranean region. These cereals were popular for hundreds of years, and long represented a staple food within the region. At a certain point in history however, the introduction of higher-yielding-free-threshing wheats caused hulled wheats to fall into a state of neglect, to such an extent that they even become a relic crop (as in the case of einkorn). For social, cultural or simply economic reasons, hulled wheats are becoming popular once again. This is the case for instance of Italy, where they have become an exclusive and fashionable food for which discerning consumers are prepared to pay a higher price than for any other wheat product. The 'underutilized' aspect of hulled wheats is being widely recognized, and this acts as a further incentive to farmers to grow them. What should we be doing however to safeguard hulled wheat species such as einkorn, or to ensure that landraces of this crop will be still grown, in spite of the possible spreading of new improved types? What is the distribution of these species in the world, and what is the actual situation regarding their use and commercialization? What role could national and international communities be playing to secure the remaining diversity of these species whilst promoting their sustainable use. A concrete contribution for addressing these issues is represented by the Hulled Wheat Genetic Resources Network, an IPGRI initiative created in 1994 in the framework of the Institute's efforts aiming at the better conservation and use of underutilized species. Among the outputs of this collaborative group, there is a recently published monograph on hulled wheats, resulted from the proceedings of an international Conference organized by IPGRI in July 1995 in Italy.

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Assessment of genetic variability in Ethiopian germplasm of Durum wheat by RFLP analysis

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About 270 genotypes belonging to nine populations of *Triticum durum* collected from three Ethiopian regions (Tigray, Gonder and Shewa) were analyzed by RFLP in order to define (i) the extent and distribution of genetic variability, (ii) the population structure, (iii) the relationship among population, and (iv) the presence of rare genotypes. Moreover, the genetic variability was divided into its component: (i) among regions within country (Ethiopia), (ii) among populations within regions, and (iii) among genotypes within populations. Fourteen non-radioactive probes, one for each chromosome arm, identifying a total of 132 bands, were used. The hybridization bands were characterized by different frequencies and distributions among populations and among regions. Some of them did not detect any polymorphism, having a coefficient of heterozygosity equal to zero, while others were extremely variable, having the maximum heterozygosity value.

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Variation in old landraces of Rye, *Secale cereale* L., with isoenzyme electrophoresis

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Rye, *Secale cereale* L., is an important grain crop today in many areas of northern and eastern Europe because of its winter hardiness, resistance to drought and its ability to grow on acid and sandy soils. The crop reached the Nordic area from SE Europe and cultivation started about 2000 years ago. From the beginning, rye was a crop of the slash-and-burn agricultural system. The first record of rye in Sweden is from the province of Smaland, 100-200 AD. Early, each village had its own locally adapted variety isolated from material from other areas. These very local forms later developed into landraces with a wider adaptation. After the commercial agriculture started the old landraces disappeared rapidly, few are preserved in gene banks, and the few remaining ones are not very well preserved. Today we realize how important landraces are as a genetic resources for future plant improvement. The genetics variation and relationship between the different landraces in Sweden and with other countries have not been research. In order to investigate the genetic diversity in Swedish landraces of rye and their relations to material from other areas we have carried out an investigation based on isoenzyme electrophoresis. Twenty populations of Swedish landraces, some populations from the other Nordic countries and material from Central Europe were used in this investigation. Six different enzyme systems were studied, namely Aconitase (ACO), Diaphorase (DIA), Glucose phosphate isomerase (GPI), Malate dehydrogenase (MDH)Phosphpoglucomutase (PGM) and Phosphogluconate dehydrogenase (PGD).

The Wheat Genetics Resource Center: current status-future direction

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The collection of wheat germplasm maintained by the Wheat Genetic Resource Center (WGRC) at Kansas State University is a composite of collections from existing sources. In total, over 2,600 accessions of wild wheat species and 2,300 genetic stocks currently are maintained in the WGRC gene bank. Collection and characterization information is maintained and accessible through Internet access via GrainGenes, the small grains database for wheat and sugarcane, and from the WGRC. As there may be as much as three-fold duplication worldwide in the collection of Triticeae, it is now more important than ever that we begin to assess the world's wheat germplasm. There have been several efforts initiated in Europe and Asia, but none that we are aware of in the U.S. We have surveyed the USDA collection in the United States and have cross-referenced a significant percent of our collection. This survey also has enabled us to discover previously undetected duplication in the WGRC collection. We now want to coordinate this effort with other major gene banks (in the U.S. and around the world), especially those with germplasm holdings of wild Triticeae species.

Utilization of selected germplasm in Iraq's wheat-breeding program

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Low production per unit area is a serious constraint on wheat production in Iraq. Both genetic (suitable varieties) and cultural practices factors are responsible for this problem. A breeding program was initated to release new adapted varieties with high yield, good quality, and tolerance of biotic and abiotic stresses. Introduced germplasm of spring wheat as well as local varieties and landraces were used. Germplasm representing world collection of spring wheat as well as local varieties and landraces were used. These were evaluated for different characters such as yield, yield components, quality characteristics, disease reaction, and other characters. Some promising germplasm was selected. Hybridization between a number of the selected samples and local varieties was made to improve these varieties. A number of promising lines were selected and are under evaluation. Some of these selected varieties will be released soon. The result of this program will be discussed in detail.

The *Elymus* Core Collection

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The creation of an "*Elymus* Core Collection" has recently been proposed and this paper will discuss the background to this proposal. A very important task for a core collection is that it provides readily available standards for research. Often it is difficult to get access to adequate material. The E.C. should have a hierarchic structure with two sets of accessions. One set includes one entry per species. These entries will be fixed to ensure comparability. A second, larger set is chosen which includes at least two further entries of each species. This set should be dynamic with respect to both size and content. As a start, we propose that one-third of the about 150 species comprise the major core. The hierarchical levels encompass 1, 5, 15, and 50 taxa, respectively. The selection of species is based primarily on taxonomic, ecogeographic, and cytogenetic data. When supporting data is available, it will be included in the decision. The final choice of species will be reached by consensus between all available data.

* * *

Location of genes conferring drought resistance in bread wheat and rye

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Little is known of genes that influence rooting and drought resistance in bread wheat or rye. The evapotranspiration efficiency (ETE = ratio of total dry weight to total water used) of bread wheat tall landrace 'Chinese Spring" is relatively high. We used 42 ditelosomic and dimonotelosomic lines of Chinese Spring to identify chromosome arms that influence plant characters and ETE. Multiple regression analysis indicated that 95% of the variation observed in ETE was explained by variation in total dry weight and total water used. Variation in plant height, number of spikes (tillers), root dry weight, number of grains, and grain weight together explained 90% of the variation observed in plant total dry weight. Chromosome arms involved in expression of days to heading and maturity, plant height, number of spikes, root dry weight, shoot dry weight, number of grains, grain weight, and carbon isotope discrimination were identified, Specifically, both arms of chromosome 2A, the long arm of chromosome 2B, and the short arm of chromosome 2D might carry genes with positive effects on number of spikes, root dry weight, and shoot dry weight. None of the anuelpoids produced grain yield greater than Chinese Spring. The short arms of chromosomes 6A and 4D might carry genes that suppress carbon isotope discrimination. The chromosome arms belonging to homoeologous group 2 might carry genes with positive effects on

ETE. In rye the long arm of chromosome 2R also carries genes that control water use efficiency in a Chinese Spring background. The genetic basis of ETE in modern wheats could be broadened by substituting specific chromosome arms and translocations of landrace genotypes or relatives such as rye, that carry desired characters, into their genomes.

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Session IV

Evaluation and Pre-breeding of Cereals and Forages

Evaluation and Pre-breeding of Cereals and Forages

Use of locally adapted germplasm to enhance yield and yield stability in dry areas

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In most developing countries barley is often a poor man's crop, and the only crop able to give some yield in environments unfavorable to other field crops. Thus, in most developing countries, it is a typical crop of marginal environments where yields are limited by abiotic, biotic and nutritional stresses. One of the main objectives of the barley breeding program at ICARDA is to develop a conceptual framework to improve efficiency of breeding in different environments with emphasis on low-input, stressful environments. The breeding philosophy of the project, which evolved during the last ten years, is based on two closely related concepts, namely (1) the exploitation of specific adaptation through direct selection in the target environments, and (2) the use of locally adapted germplasm. From a collection of landraces made in 1981, and a systematic evaluation of both landraces and *Hordeum spontaneum* which began in 1984, throughout the routine use of landraces in pure-line selection as well as in mixtures, and of landraces and of *Hordeum spontaneum* in crosses, the paper describes the rational for, the methodologies of, and the results achieved by, the use of landraces and of the wild progenitor of barley, *Hordeum vulgare* ssp. *spontaneum*. Results from farmers fields indicate that this strategy, based on using landraces mainly as recipient of desirable traits and *Hordeum spontaneum* as donor of genes for adaptation to extremely stress conditions, increases yield by about 2% a year in environments previously considered too marginal for breeding to be successful.

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Utilization of primitive tetraploid wheat species to improve drought tolerance in durum wheat

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Use of alien tetraploid wheat species for drought tolerance improvement of durum wheat appeared to be promising not only for morphophysiological traits related to drought tolerance, but also for resistance to biotic stress and grain quality. Some accessions of tetraploid species (*T. dicoccum, T. carthlicum, T. polonicum,* and *T. umopheevi*) identified for their potential in the improvement of drought tolerance, were used in a physiology-based crossing program. The embryo rescue (*in vitro*) method was used for the crosses. Direct selection for yield and indirect selection

for various drought tolerance related traits were applied under water stress in the F_2 population. Divergent selection and genetic studies for drought adaptive attributes showed that selection for relative water content (RWC), proline content (PC), and carbon isotope discrimination (D) in the F_2 population was effective. These results also revealed that these traits are under complex genetic control; broad and narrow sense heritability were found to be high. In the case of photochemical quenching of chlorophyll fluorescence (q QS/q QT) and root parameters, narrow sense heritability and response to selection were low. Evaluation of the F_4 and F_5 lines obtained in this program for different morphological traits, yield and yield components have been effect under field conditions. The group selected for RWC, q Q, and D showed a greater drought tolerance under field conditions (early growth vigor, high harvest index, grain yield and biomass production) than the low group. These materials are now under evaluation in different environmental conditions. Direct selection for yield using the F_2 progeny method confirmed that early selection in F_2 and F_3 progenies produced some lines which performed better then their parents (durum wheat) under different conditions (Aleppo, Syria; Constantine, Algeria; Montpellier, France and Yemen). Evaluation for grain quality showed that high SDS values, protein content, and kernel yellowberry had been incorporated into advanced interspecific lines. Improvement of total biological and grain yield was demonstrated to be possible, both through direct or indirect selection. High number of lines F_4 and F_5 derived from interspecific crosses have been selected for traits related to drought tolerance. These lines will be used in breeding programs. Some back-crosses with durum wheat varieties will be however necessary particularly in the case of crosses with *T. timopheevi* and *T. carthlicum* for a better use in wheat breeding.
Key words: wheat tetraploid species, interspecific crosses, drought tolerance, divergent selection, direct selection, physiological criterion, grain quality, response to select.

Diversity in Pakistani wheat germplasm as revealed by RAPD analysis

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Accurate, reliable, fast and cost effective identification of species and landraces is essential for crop improvement as well as in pure and applied plant research. Thirty wheat accessions originating from different agro-ecological regions of Pakistan were studied to estimate the genetic diversity with the help of genetic markers. Thirty five scorable bands were generated with the help of 3-5 polymorphic bands ranging from 0.36 kb to 1.7 kb. The polymorphism for the RAPD markers was used to depict phylogenetic relationship among 30 accessions. The study revealed that accession originating from the same region did not clustered in to a particular group, which indicated that diversity among the accessions was not related to its area of origin.

Methods of evaluating germplasm, and their applicability to wheat genotypes

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The objectives of this study were to evaluate Lebanese wheat germplasm and also evaluate several methods of germplasm characterization and identification. 104 wheat genotypes were collected from several locations around Lebanon. The collection was characterized using physiological, morphological, and molecular techniques. Physiological evaluations included tests for drought, salinity and high temperature tolerance during different phases of development, and yield potential. Morphological characterization included describing the different morphological traits of the genotypes from planting until yield, such as plant height, number of fertile tillers, seed number, etc. Molecular evaluation included DNA fingerprinting of the different genotypes as well as storage protein analysis using polyacrylamide gel electrophoresis. Germplasm identification techniques were evaluated based on their sensitivity, ease of use, applicability, cost and reproducibility.

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Genetic diversity of seed storage proteins in Triticum boeoticum and T. urartu from Turkey, Iraq, Iran and Lebanon

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Variation of seed storage proteins at the Glu-A1, Glu-A2 and Glu-A1 loci was studied electrophoretically in 30 populations of *T. boeoticum* (49 accessions) and 16 populations of *T. urartu* (74 accessions), from Turkey, Iraq, Iran and Lebanon. A total of 69 and 49 allelic variants were found at the three loci, in *T. boeoticum* and *T. urartu*, respectively. Seed storage protein patterns in these species were quite distinctive from each other and allowed us to distinguish *T. boeoticum* from *T. uaratu*. In three above mentioned loci for each population (He), the mean number of alleles per locus (A) and the average effective number of alleles per locus (Ne) were equal to 0.135, 1.38, 1.23 and in 16 populations of *T. Urartu*. These estimations were equal to 0.264, 2.27 and 1.60, respectively. The low estimations of variability within populations in both species in this study was probably due to uniformity within populations of the accessions analyzed. However a high polymorphism was observed between accessions in both species in this study. The number of alleles at the gliadin loci in *T. boeoticum* was 61 and 40 in *T. urartu*. The high polymorphism observed at gliadin loci in these species may provide the possibility of unambiguous differentiation and identification of genotypes in these species. The degree of genetic differentiation between populations was evaluated, using Manhattan distance. The distribution of alleles at these loci was studied to determine association between seed storage protein polymorphism and ecogeographical conditions of collecting sites. The results showed that in both species the different populations were highly independent of distance between them and ecogeographic characters.

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Evaluation of the adaptation of durum wheat varieties to Mid Atlas mountains and Sais plateau of Morocco

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Eight widely grown durum wheat varieties were grown under different environmental conditions; in the Mid Atlas mountains during one season, and in the Sais plateau during two different seasons. The performance of the wheat varieties was evaluated for each environment and genotype x environment interactions assessed. Principal component analysis was used to classify the varieties into a group which performed well in the mountains area, group which performed better under the more favorable conditions of the Sais plateau, and finally a group of intermediate performance under both environments

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Preservation and utilization of wheat genetic resources for breeding purposes at the Cereal Research Institute, Hungary

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In the Germplasm Conservation Programme the Wheat Department of the Cereal Research Institute (CRI) preserves 3000 *Triticum* genotypes with the support of the Hungarian Ministry of Agriculture. In the last season 500 among the 3000 stored entries were evaluated according to the International Plant Genetic Resource Institute (IPGRI) system of characterization using descriptors to focus on morphological and highly heritable agronomic characters. The larger part of our collection is a basic collection, while the 500 entries are included in an active collection where we evaluate and multiply them. Our working collection (ca. 200 entries per year) is our crossing block which we select from the active collection on the basis of the entries' evaluation results. The main goals of the genebank program are the preservation and maintenance of the local old varieties, variety candidates or the lines selected by the institute carrying important characteristics which could be useful for breeding. We also conserve important genetic resources for disease and pest resistance, and for quality from all over the world. The evaluation of the active collection mostly concentrates on morphological and phenological characters, but characterizes quality, gliadin composition (HPLC), tolerance to abiotic stresses and resistance to plant diseases too. On the basis of the results of the detailed evaluation we selected genotypes from the active collections and included them in our crossing program. Seed samples are stored in the cold chamber (in glass containers, at 5°C temperature) of the Institute's breeding station, while the evaluation data are stored both in fieldbooks and in electronic files. The most frequent breeding goals are abiotic stress resistance, quality, and disease resistance. 50% of the parent materials originated from own or other Hungarian advanced lines, 30% from released cultivars varieties, 15% from other advanced lines from other countries and about 5% from exotic materials. Intergeneric hybrids (triticale, hybrids of *T. aestivum* and *T. tauschii*, triticale and *T. durum*) also produced resistance for biotic and abiotic stresses.

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Comparative anatomy of *Aegilops* species from Jordan

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Over 400 samples belonging to the genus *Aegilops* (wild wheat) were collected from different localities in Jordan in 1996. Taxonomic study showed that *Aegilops* L. comprises eight species as follows: *Ae. geniculata, Ae. kotschyi, Ae. peregrina, Ae. biuncialis, Ae. triuncialis, Ae. longissima, Ae. crassa* and *Ae. searsii. Aegilops* is considered as one of the most common genera of annual grasses in Jordan. Analysis of variance for a number of quantitative characters of the inflorescence indicated that variability between *Aegilops* L. species is highly significant which can be used to differentiate species from each other except for: length and width of glumes, lemmas and paleas which are less significant. The SEM micrographs of glume and awn outer surfaces show important features which could be used to identify *Aegilops* species. Three kinds of epidermal features have been shown: siliceous papillae, forward-pointing prickles, and stomata. Culm anatomy has been examined for Jordan *Aegilops* species using LM. Internode anatomy showed that the vascular bundles are arranged in two circles and restricted to the profile of the culms. The individual bundle is collateral, surrounded by sclerenchymatous sheath and well defined with two prominent metaxylem vessels and one protoxylem vessel lying in an endarch direction.The anatomy of the regions near the nodes (pulvinus) showed the presence of a leaf sheath enclosing the internode part of the culm. The leaf sheath consists of mesophyll cells containing large and oval-shaped bundles with reduced vascular tissues. The vascular bundles in the enclosed internode are arranged in two circles and restricted to the profile of the culm. Variations in the number and arrangement of xylem vessels of the vascular bundles between *Aegilops* species have been observed. Three types of vascular bundles were distinguished in the vegetative nodes of *Aegilops* species; Nodal plate bundles, elliptical bundles and diffuse bundles. Little variation between Aegilops species were provided by its nodal anatomy. Protein determination by spectrophotometer and SDS-PAGE of the grain proteins of *Aegilops* species were found to be reliable methods for species identification. Differences in the electrophoretic banding patters of *Aegilops* at the same ploidy level or different levels were found to be helpful in differentiation of *Aegilops* species from each other.

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Water use of different genotypes of wheat

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Water use of 2 varieties of bread wheat and 2 varieties of durum wheat was studied in the semi-arid area of Algeria. Water use of varieties of durum wheat is 1.05 mm/day for the variety "Oued Zenati" and 1.7 mm/day for "INRA 69". Water use for bread wheat is 1.9 mm/day for both varieties "Anza" et "Florence X Aurore". Water absorption for bread wheat is limited to the top layer of the soil (between 20-40 cm), while water absorption for durum wheat occurs deeper in the soil, at a depth of 70 to 80 cm.

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The cascade mechanism of redox regulation of mitochondrial genome expression in Triticeae species

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The elucidation of molecular mechanisms of regulation of mitochondrial genome activity under varying metabolic conditions of the organism is of primary importance for development of biotechnological strategy of purposeful manipulation of energy transforming mitochondrial functions. The paper presented demonstrates the existence of the cascade mechanism of redox regulation of mitochondrial genome expression in Triticeae species under changes of redox potential created by an addition of potassium ferricyanide as an oxidising agent and sodium dithionite as a reducing agent to the organelles. Under oxidising conditions the transcription was observed to be activated, while under reducing

conditions it was markedly repressed (1). The study of the activity of protein synthesis under different redox conditions in mitochondria of *Zea mays* and *Elymus sibiricus* showed that mitochondrial translation was also subjected to redox control. Since the effects of redox conditions on translation were preserved when the transcription was inhibited by ethidium bromide, several levels of redox control of genetic functions can be assumed to exist in mitochondria. Additionally, we showed that the mitochondrial genome activity depends upon the redox state of the respiration chain of *Elymus sibiricus* mitochondria. A scheme of the cascade redox regulation of mitochondrial genome functions is presented suggesting the presence of special redox sensors and redox regulators of a protein nature for main genetic processes in mitochondria. The presence of such mechanism of regulation of genetic processes in the mitochondria can provide, in our opinion, an efficient integration of the two main functions (energetic and genetic) of these organelles.

The systems of RNA and DNA synthesis in organelles used in genetic population studies of perennial wild grass *Elymus sibiricus*

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Recently genetic investigations of forage perennial grasses have been primarily performed at the nuclear genome level. The heredity and variability provided by cytoplasmic genomes and their genetic role in the biology and evolution of populations and species of forage grasses remain obscure. The paper presents results of the studies of RNA- and DNA-synthesizing systems of mitochondria of seedlings of different geographical populations of *Elymus sibiricus*. The reciprocal dependence between the RNA- and DNA-synthesizing activities was revealed in the genetic system of mitochondria of the *E. sibiricus* populations examined. It can be seen in the relative prevalence of one or another types of mitochondrial DNA template activity. A possible application of the characteristics of RNA and DNA syntheses in isolated mitochondria is given for assessment of agriculturally valuable traits in cereals. As a whole, the results obtained suggest a promising use of the characteristics of RNA- and DNA-synthesising system as genetic markers in genetic, breeding and biotechnological studies of perennial wild grass populations.

The potential of *Hordeum chilense* in breeding Triticeae species

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Hordeum chilense (Critesion chilense) is a wild species which crosses readily with diploid, tetraploid and hexaploid wheats and the intergeneric amphiploids obtained from them, named Tritordeum, have been under a breeding program on the past 15 years with the aim of creating a new crop. *H. chilense* crosses, also, readily with species of other Triticeae genera; *Secale, Haynaldia, Hordeum (vulgare* and *bulbosum*) and *Agropyron*. Amphiploids have been obtained between *H. chilense* and *S. cereale*, *H. bulbosum* and both *A cristatum* and *A. desertorum.* Tritordeum and the other *H. chilense* amphiploids can be used as bridge species to introgress genetic material from this wild barley into Triticeae species of agronomical interest. *H. chilense* is a native to Chile and a small area in Argentina. Collecting expeditions to the natural habitats of the species have been carried out by our group. The *H. chilense* collection has been evaluated at Córdoba (Spain) for morphological traits and resistance to biotic and abiotic stresses. Aphids and diseases reactions have been tested on *H. chilense* and amphiploids. *Hordeum chilense* is resistant to the barley and wheat brown rusts (*Puccinia hordei* and *P. recondita* f.sp. *tritici*, respectively). Some lines may be susceptible to *P. recondita* f.sp. *agropyrina*, to wheat and barley yellow rusts (*P. striiformis* ff.spp. *tritici* and *hordei*, respectively) and to the wheat stem rust (*P. graminis*). *H. chilense* is resistant to the wheat powdery mildew (*Erysiphe graminis tritici*), to some barley and rye powdery mildew (*E. graminis* ff.subsp. *hordei* and *secalis*, respectively) isolates and to *Septoria tritici. H. chilense* is also known to possess resistance to the aphids *Diuraphis noxia* and *Schizaphis graminum*, to the nematode *Meloidogyne naasi*, to the smuts *Ustilago nuda* and *U. tritici*, to *Drechslera teres*, to *Rhynchosporium secalis* and tolerance to salt. The cytoplasm of *H. chilense* is a new source of wheat male sterility, preliminary results suggest that restoring fertility gene are present in two different *H. chilense* chromosomes. Trisomics of two genetically distant accessions have been obtained which could facilitate the genetic mapping of any trait of interest. As well, addition lines on hexaploid and tetraploids wheat of three different accessions have been obtained. RAPDs and SCARs are been developed to be used in marked assisted selection. Also, *in situ* hybridization with pAs1 repetitive sequence have been found to be valuable for *H. chilense* chromosome identification. Chromosome variants plus molecular markers will help on the chromosome manipulation.

Diversity in *Aegilops* species for physiological traits related to abiotic stress tolerance

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Aegilops germplasm has been widely used by wheat breeders as a source of genes for disease resistance. Their utilization for improving abiotic stress tolerance of durum (or bread) wheat is however considerably lesser developed. For more efficient use of *Aegilops* germplasm, a better knowledge of its potential usefulness in the improvement of abiotic stress is needed. Osmotic adjustment is recognized as an important mechanism of drought tolerance and its contribution in maintaining high grain yield in drought prone environments has been clearly established in cereals. It is why osmotic adjustment has been particularly concerned by this study. For this purpose 77 *Aegilops* accessions (belonging to 19 species) have been first screened for relative water content (RWC) and leaf water potential (LWP) under water stress: large interspecific and intra population variations were observed for these traits. This screening has been completed by measurements of water loss rate of excised leaves and by a morphological study of the epidermis (epicuticular waxes and stomata) using scanning electron microscopy. On the basis of all these results 30 accessions were assessed for osmotic adjustment related traits (relative water content, leaf osmotic potential) as well as for chlorophyll fluorescence parameters allowing to identify accessions with high osmotic adjustment capacity and high photosynthetic resistance to water stress. Both low and high temperatures are known to strongly impair the photochemical apparatus of photosynthesis, with photosystem II (PSII) being the primary target. As far as thylakoïd membranes are concerned, screening for chilling and heat susceptibility have been achieved through *in vivo* measurements of chlorophyll fluorescence in leaves of accessions of six *Aegilops* species, five durum wheat varieties and one *T. dicoccoïdes* being used as checks. The critical break-point temperature (Tc) corresponding to the temperature at which initial level of chlorophyll fluorescence (Fo) starts to rise in leaf sample heated at a rate of 1°C min^{-1} was used to estimated the relative heat tolerance as described by Havaux (1993). On the other hand, chilling tolerance was measured by the quantum yield of photosynthetic electrons transport (fp) and reduction level of the primary electron acceptors of PSII (V) at a constant temperatures of 25 °C or 6 °C. The relation beyond all measured criteria is analyzed and the potential interest of *Aegilops* germplasm as a source of abiotic stress tolerance for durum wheat is discussed.

Yield components and yield stability of bread wheat in water limited environments

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Grain yield and its components of twelve imported wheat genotypes from ICARDA, in addition to four local wheat cultivars Sakha 92 and 69 as well as Giza 69 and 163 grown under 15 environmental conditions were evaluated. The fifteen environmental conditions are the combinations between 5 treatments of water regime and 3 diverse environments representing the old Egyptian lands (Om El Zain Sharkia) during 1991/1992 and 1992/1993 seasons as well as the new lands (ElArish-Senai) during 1992/1993 seasons. The results revealed that the genotype/environments interaction component accounted the most part of the total variation for grain yield and its components, i.e. number of spikes/m^2, number of grains/spike and 1000-grain weight. Regression coefficient (b) value varied among the studied genotypes from 0.68 to 1.9 for grain yield, 0.67 to 1.29 for spike/m2, o,74 to 1.22 for grain/spike and 0.46 to 1.48 for 10000 grain weight . Wheat genotypes No 5.7 and 12 showed a consistent performance over environments and could be considered the stable ones. significant correlation between the mean value and b was detected for train yield and spike/.m2. indicating that the performance of genotypes could be predicted from its mean value. However insignificant correlations were observed for grain/spike and 1000-grain weight, showing the independence of genes controlling the inheritance of these characters and the possibility of breeding new stable wheat recombinants over different environments and having high yielding ability.

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Accelerated generation advancement: More generations within a year

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In Europe, the breeding of new varieties of cereals takes 10-15 years, even more, particularly if genetically distant forms are used as donors of economically important characters. There are a few possibilities to shorten the breeding process, for instance by utilization of biotechnology. One of most accessible for the majority of practical breeders is cultivation of more generations within a year at the beginning of the breeding process. There is a possibility for European spring barley breeders to multiply second generations in geographically distant areas such as New Zealand, Chile, Uruguay etc. in the period September to February. This system is extensively used particularly by many West European spring barley breeders. Nevertheless, there are still many breeders preferring to keep the genetic resources during the period of their incorporation into new varieties in their own facilities. Utilization of climatic chambers or glasshouses represents very high energy consumption, particularly for artificial illumination. For example, cultivation of one generation of spring barley in climatic chambers requires 3.600 - 5.200 Kwh/m^2 or in glasshouses 850-1.500 k Wh/m^2 The basic perquisite to reduce energy consumption in cultivation of two generations within a year is the hybridization of genetic resources. The harvesting of matured hybrid grains in June and multiplication of the second generation in the field, under plastic films or glasshouse etc. in the period July to October, still provides basic conditions for the growing and development of cereals. Particular attention must be devoted to artificial vernalization of winter cereals from the point of view of temperature, day length and intensity of illumination. Twenty years experience with the incorporation of resistance genes to powdery mildew, rust resistance, winter hardiness for creation of commercially most important spring and winter barley varieties in Czech Republic will be presented and compared with other systems used in Europe.

Barley breeding for diverse growth habit and vernalization response to develop cold and drought- tolerant germaplsm

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Genetic variation in cold tolerance, growth habit, vernalization requirement and photoperiod response play a vital role in the adaptation of germplasm. The germplasm needs of major barley growing areas are different and should be met by tailoring material with growth phonology fitting to the local agroclimatic conditions. The growth habit, cold tolerance and drought tolerance of locally adapted barley cultivars such as Tokak, Bulbol (Turkey), Zarjau, Star, Walfajer (Iran), Baluchistan (Pakistan), Cycloneand Monolit (Russia) were studied and employed as checks to generate suitable material for different regions. The results on growth habit, vernalization requirements earliness, cold and drought tolerance beside stable high yield of improved winter and facultative barley germplasm are discussed.

Evaluation of Irrigation and Nitrogen Levels on Yield and Yield Components in Durum Wheat by Using Response Surface Methodology

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A quadratic response surface model (RSM) was used to study the effects of supplementary irrigation and nitrogen levels on grain yield and yield components. Two durum wheat varieties Cham 1 and cham 3 were studied for two successive years 1993-94 and 1994-95 under field conditions at Tel Hadya, ICARDA, Aleppo, Syria. The experiment was conducted using a split-plot design with 3 irrigations as main plots and nitrogen levels as sub-plots and varieties as sub-sub-plots replicated 3 times. Representative polynomial equations and contour lines describing the interactive effects of these treatments on yield and yield components were investigated . The RSM was very effective for estimating the optimum combinations of irrigation and nitrogen levels for maximizing the grain yield and its components. Contour plots displayed effects of irrigation and nitrogen levels on yield and its components in both seasons. Grain yield increased as irrigation and nitrogen increased in both seasons. Spikes / m^2 increased as irrigation increased in both seasons whereas, nitrogen was less important in the second year. Nitrogen had significant effects on kernels per spike whereas, irrigation was less important than nitrogen on this character. Linear and quadratic effects of nitrogen on kernels weight TKW were observed, nitrogen levels were slightly affected by this character in both seasons.

Barley Landraces : Source of Stress Tolerance

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A serious limitation to increasing yields under the harsh environments of the semi-arid regions (SAR) is the narrow germplasm base of many high yielding varieties. National as well as international programs have developed varieties that perform well under optimal growing conditions. But the potential of the newly developed germplasm cannot be realized in the SAR due to the lack of appropriate management practices. Landraces will consistently deliver at least some yield, despite inherent stress factors. They have an excellent adaptation to local conditions and a wide spectrum of resistance to diseases. In the semi-arid regions of Tunisia, about 40% of the barley growing area is occupied by landraces. Farmers in these areas are compelled to keep their landraces because of the useful qualities they posses and yield stability. Landrace cultivar collecting in Tunisia showed adequate disease resistance, but high variability in heading dates, ranging from 136 to 169 days. Barley accessions from the cold steppe region have the narrowest range of heading days, from 156 to 158. The level of disease resistance varied according to the specific disease. Fourteen out of 196 accessions screened showed multiple resistance to the major diseases. Seventy eight entries showed moderate to good resistance to scald, thirty accessions showed moderate resistance to powdery mildew. New sources for resistance to leaf rust were identified among Tunisian barley landraces. The low productivity of the landrace cultivars can be improved by extracting by individual cultivars or by crossing them to high yielding lines. Improved landrace cultivars have been tested at different locations in the SAR of Tunisia. A number of selected lines and populations out yielded the local check, Rihane, during both favorable and unfavorable crop seasons.

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Use of salinity tolerance in barley breeding programmes

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Utilization of local barley varieties as a source for salinity tolerance in crosses is common. Due to the fact that salinity-tolerant barley lines are susceptible to different diseases and there is a need to utilize these sources to cover other climatic zones comprising different photoperiods, a special hybridization program and management is required. In this direction, single and double crosses are produced by using the sources as the parental lines. Using special techniques, the segregating-populations will be screened under naturally saline soils. To shorten he breeding cycle, a shuttle breeding strategy evaluating two generations per year will be utilized.

Session V

Quality and Utilization

Quality characteristic of some wheat genotypes

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Different wheat genotypes of both spring and winter growth habit from local and world collections were evaluated for some quality characteristics. Significant differences among the studied genotypes were observed for the whole characters. The 1000-kernel weight ranged from 34 to 52 g. The Tunisian spring genotypes "2112-19" had the highest weight. The protein content in wheat flour ranged from 10.5 to 16.8. Most of the genotypes showed high protein content. The winter genotypes had the highest. Flour extraction ranged from 48.2 to 64.7. The spring genotypes were higher than winter genotypes in this character. The high flour extraction was in most cases associated with high kernel weight. The falling number ranged from 241 to 676. This test indicates amylase enzyme activity. The winter genotypes showed higher values. Wet gluten ranged from 19.2 to 37.4 and dry gluten from 6.8 to 13.2. SaberBeg showed the highest values among the spring genotypes. This genotype is still the best in quality among the local genotypes. Among the world collection. some spring genotypes and all the winter genotypes were promising.

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Seed yield and composition of field-grown wheat under arid and semi-arid environmental conditions in Jordan

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The relationship was studied between grain protein, lipid, sugars and starch content of wheat (*Triticum durum* L.) with grain yield under arid and semiarid Mediterranean environments. Twenty two wheat cultivars were grown at an arid (JUST) and semiarid (Maru) locations in northern Jordan. Except for sucrose and glucose, the variations in protein, lipid, fructose and starch conditions were significant. Wheat grown at the semiarid location exhibited higher yield and lower lipid, protein, sucrose, glucose and fructose contents but higher starch content than those grown at the arid location. Except for sugars and starch, high grain yields of cultivars were associated with low contents of protein and lipid, indicating that one-sided selection for high grain yields tends to reduce the nutritional quality of wheat grain.

Variability and genetic control of breadmaking quality in Einkorn (*Triticum monococcum*)

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In a previous study of 25 Einkorn accessions we found seven lines with acceptable gluten strength, yielding Chopin alveograph values and Brabender farinograph stability indices similar to those of bread wheat. Therefore, another 1099 additional accessions were screened for SDS sedimentation volume. Some of the accessions having SDS sedimentation volumes above 60 ml were included in a replicated plot trial at three locations in two years (1994-95 and 1995-96), and they underwent standard rheological and baking tests. Five new accessions, characterized by high breadmaking quality (bread volumes in the range 700-800 cc and SDS sedimentation volumes above 80 ml) were identified. Two lines, one extracted from accession ID1351, characterized by poor quality, and the other from accession IB1348, characterized by good quality, were crossed. Seed of 168 F2 plants was analysed for protein content and SDS sedimentation volume. The protein profile of each plant (high and low molecular weight glutenin composition) was determined by one dimensional SDS-PAGE. SDS sedimentation volume among F2 progenies ranged from 10 to 62 ml, protein content from 11.5 to 19.9% and specific sedimentation volume from 0.7 to 3.3 ml. The parental lines did not differ in high molecular weight (HMW) glutenins composition, but differences in low molecular weight (LMW) glutenins patterns occurred. The 10 best F2s showed the same LMW glutenins patterns as of the ID1348 parent, suggesting the involvement of two major recessive genes controlling the expression of this trait. Identification of additional baking quality related QTLs in this cross as well as in other two crosses *via* DNA markers (like AFLPs) is in progress. Our results clearly demonstrate the existence of a large genetic variability for breadmaking quality in Einkorn. Moreover, preliminary data from the segregating populations involving high and low quality parents suggest a relatively simple genetic control of the breadmaking quality in *T.monococcum*. According to our data, Einkorn could become an important crop for the production of new baked foods.

Selecting for noodle quality in Iranian hexaploid landrace wheat

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Considerable recent research has focused on defining the physicochemical basis for Asian noodle quality in common wheat. Past selection focused on bread baking quality is expected to have reduced the useful variation available in most breeding programs for noodle quality. Noodles are a very diverse product class, including white-salted and yellow-alkaline formulations, and fresh, dried, or steamed-and-fried (instant) processing steps. Noodle quality is affected by starch, protein and color factors, and wheat landraces or wild relatives may possess useful diversity in these traits that could be useful in breeding for improved noodle quality. A subset of 252 hexaploid accessions from a large collection of Iranian landraces held at the University of California, Davis, was intensively University of Hong Kong. The flour swelling volume (FSV) and peak viscosity (using a Rapid Visco-Analyzer, RVA) were highly correlated ($r=0.72^{***}$, $n=252$). FSV values in the landraces ranged from 30 to 56 ml g-1 and peak viscosities from 139-305 RVU. The upper ranges in these values represent desirable types for good quality Japanese noodles. SDS-sedimentation test and most of the major mixograph parameters were highly correlated. Most of the lines possessed known HMW glutenin subunit combinations, but a novel band was detected. Geographical concentrations within Iran of maximum starch and protein variation were quite different. Screening for polyphenoloxidase activity revealed significant variation for gray color development. These results will be discussed in relation to general strategies for genetic resource screening for new and complex objectives such as noodle quality.

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Five-year yield and yield components analysis of hulled wheat landraces from Italy

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Hulled wheats cultivation has been recently resumed in Italy, for the alternative foods market. In the absence of selected varieties, local landraces have been largely employed to plant new crops. The native emmer and einkorn wheat populations still grown in mountain areas of the Appenine range (Mediterranean Italy) were sampled. Field trials were established in Viterbo (central Italy), in 1989-91 and Bologna (northern Italy), in 1994-96, comparing ten emmer wheat and one einkorn wheat landraces with durum wheat and spelt tests. Additional experimental treatments were: two sowing dates (fall and spring), in the first two experiments at Viterbo, and three nitrogen dressings (0, 40 and 80 kg ha^{-1}), in the first year at Viterbo and in the two Bologna experiments. Detailed analyses on the effect of sowing dates, which results have already been published, allowed the discrimination of the emmer landraces in winter and alternative populations. Maximum yield in Bologna was almost double that in Viterbo. Grain yield of emmer landraces was always lower than the durum wheat tests, but comparable or higher than spelt. At Viterbo, yield potential between winter and spring emmers, as well as within each of these groups was not very different, whereas at Bologna winter emmers were more productive than spring types, with larger variation within groups. The only einkorn wheat landrace always had lower yield. Winter emmers were clearly differentiated from spring types by their higher seed size, often comparable to that of durum wheat. Seed number per unit area was the major constraint to emmer grain yield, especially for winter emmers and in the poorer environment of Viterbo. Among its determinants, the low number of spikes per unit area proved to be critical. Despite the profuse tillering, culm mortality was in fact very high, revealing a high degree of intra-plant competition and sensitivity to self-crowding.

Characterization and Assessment of Genetic Variability for High Molecular Weight Glutenin Subunits in a World Collection of Durum Wheat Landraces

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A world collection of durum wheat landraces was analyzed for the high molecular weight (HMW) glutenin subunits by sodium dodecylsulphate polyacrylamide gel electrophoresis (SDS-PAGE). High levels of variation were found: 5 allelic variants at the *Glu-A1* and 9 at the *Glu-B1* loci, with 19 *Glu-A1/Glu-B1* combinations. The null form was the most frequent variant at the *Glu-A1*, constituting almost 90%. The *Glu-B1* locus had greater variability than the *Glu-A1*; the variant carrying subunit 20 was the most frequent at 55%. Within the 9 variants, 2 had not been previously identified. The HMW electrophoretic pattern null with subunit 20 was the most common, at 49.2%. Our present knowledge of the diversity of HMW glutenin subunits in durum wheat is still limited and the lack of relationship with pasta-making properties could be due to the narrow range of variation recorded in variability studies to date for this class of seed storage proteins.

Inheritance of Straw Quality Characteristics in three Crosses of Barley (*Hordeum vulgare* L.)

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Three experiments were carried out during successive seasons, 1992/93 and 1993/94, at two ICARDA experimental stations, in Tel Hadya and Breda to study the inheritance of barley straw quality, and of important agronomic characters in barley crosses. The crosses were as follows: Cross 1:RIHANE-03/3/ ARIZONA 5908/ATHS/MAR/ ATHS*2 Cross 2: MO.B1337/W1291/ZAMBAKA Cross 3: SLB 62-68/TADMOR. Families were evaluated for different agronomic and quality characters for both the grain and straw. In the first season, genotypes within and among crosses differed significantly for biological (3511-11377 kg/ha) and, grain yield (1382-5435 kg/ha), for heading date, for dry matter intake (16.1-23.6 g/day), and for digestible organic matter (44.8-58.2%). In the second season, significant differences among families were generally found for biological and grain yield (ranging, respectively from 3250 kg/ha - 12333 kg/ha and from 2533 - 6193 kg/ha at Tel Hadya; and from 1866 kg/ha to 5500 kg/ha and from 916 -2291 kg/ha at Breda). Differences were also observed this season for heading date, dry matter intake (11.8-21.7 g/day at Tel Hadya and 20.3 - 28.6 g/day at Bread), and for digestible organic matter (36.6 - 49.7% at Tel Hadya and 41.8 - 53.6 % at Breda). Straw quality parameters generally and low heritability. Higher heritability values were recorded for digestible organic matter and lignin fiber. It is found that most families with low crude fiber content were characterized by high digestibility of organic matter and other desirable traits of straw quality. In addition, some families were found to posses high grain yield and good quality straw. Dry matter intake and digestibility of organic matter were positively correlated with protein percent in the straw. These characters may be considered as indicators of high nutritive value of the straw especially in rainfed areas. Nutritive value of straw was negatively correlated with grain yield a, straw yield, harvest index, plant height, acid detergent fiber (ADF), neutral detergent fiber (NDF), and lignin fiber in the straw. Grain yield was positively correlated with harvest index, number of spikes/unit area and plant height, and negatively correlated with grain protein percent and heading date. The genetic advance from selection was high for some characters such as protein content while it was low for other characters. This expected grain from selection varied among crosses and seemed to be affected by environmental factors. Cross 2 had families which were more stable for their production and quality characteristics. It is also noted from the results of this investigation that drier conditions lead to improving the nutritive value of straw in addition to high yielding ability. They also indicate the possibility of adopting agronomic characters having high heritability and correlated with quality characters as parameters for selection of genotypes with high straw quality.

Use of Biotechnology tools in durum wheat breeding programmes: Genetic map and gene markers

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The ICARDA biotechnology group is developing a genetic map to allow marker-assisted selection for durum wheat. For this purpose, several populations of recombinant inbred lines were developed using the Single Seed Decent (SSD) method. The work was conducted using the population Jenneha khetifa x Cham1. The techniques used consist of RFLPs, RAPD, STS markers and microsatellites markers. Actually, 27 RAPD markers, 2 STS markers and 6 microsatellite markers are mapped in this population. To improve durum pasta quality, PCR amplification using specific primers is adopted in the durum wheat-breeding program. Primers for low molecular weight (LMW) glutenin (types 2 and 1) and primers for gamma-gliadin (45 and 42) are used in PCR amplification. These two proteins have two different allelic forms. Glutenin LMW type 2 is associated with gliadin 45 and glutenin LMW type1 is associated with gliadin 42. The presence of low molecular weight (LMW) glutenin type 2 and gliadin 45 is associated with good pasta quality and the presence of low molecular weight (LMW) glutenin type1 and gliadin 42 is associated with poor pasta quality. PCR amplification shows two bands with a higher band specific for LMW glutenin type2 or for LMW glutenin type1. The higher band specific for LMW glutenin 2 is larger by 50 bp than the band for LMW glutenin type1. For the gliadin, the PCR amplification shows four bands. The second higher band is specific for gliadin 45 or gliadin 42. The band for gliadin 45 is larger by 50 bp than the band for gliadin 42. In heterozygote genotypes the band for glutenin LMW2 and glutenin LMW1 and bands for gliadin 45 and 42 are present. The screening of ICARDA ADYT 94, 95 and 96, show that more than 90% of cultivated genotypes in this area have glutenin LMW type2 and gliadin 45, less than 10% have glutenin LMW type1 and gliadin 42, and about 2.5% are recombinants or heterozygote lines.

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Electrophoretical identification base for hulled wheats exploitation as new food crops in Italy

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Until few years ago emmer wheat was a relict crop, grown as human food or animal feed in restricted areas of central Italy. Recently its popularity has increased enormously in the natural and health foods market. Grain supply from the native growing areas was not sufficient to match increased demand and new cultivations were therefore established. Emmer production in Italy is however still completely based on local landraces, since new varieties are not yet available. The availability of a knowledge base and methodology for genotype identification is therefore needed. A study was carried out on the electrophoretic characterisation of the Italian native emmer populations that represent the basic genetic material for the cultivation of this species, with the aim of establishing a knowledge base for the identification of the available genetic material. 50 single seeds from the 10 accessions representing the range of the Italian *Triticum dicoccum* landraces were individually ground. Two durum wheat varieties were included as tests. Electrophoresis analysis of glutenins allowed a good characterization of Italian emmer wheat landraces. Variability was found within each accession, with HMW (40 kD to 120 kD) subunits showing higher level of polymorphism than the LMW (14 kD to 40 kD) subunits. SDS-PAGE glutenin pattern of spring landraces resulted more polymorphic than the one of winter populations. This fact seemed related to morphological heterogeneity observed during field trials of the same material. The two groups of populations were characterised by specific bands and band patterns. Further analyses are being carried out to assess the possibility of application of these results to the detection of the presence of alien material in emmer wheat flour. The sensitivity of this method for the detection of different percentage of contamination is also being studied.

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Baking quality traits in a durum wheat x barley hybrid

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Tritordeum (XTritordeum Ascherson et Graebner) is the amphiploid derived from the cross between a South American wild barley (*Hordeum chilense* Roem. et Schult.) and wheat. Because this amphiploid has shown the agronomic characteristics of a new crop, we decided to evaluated the possible uses of this new cereal and its role in agriculture. For this reason, in the last five years, several lines of tritordeum have been evaluated, along with some lines of durum. The results have indicated that both hexa- and octoploid tritordeum exhibit quality characteristics similar to those of bread wheat and very different to those of durum wheat. Likewise, a wide range for quality characters has been shown between the tritordeum-tested lines. Several works, also, have suggested that the *H. chilense* line seems be to associated with the storage proteins from both parents. Although the hexaploid tritordeum have exhibited baking properties slightly poorer that those of bread wheat, any of the lines analyzed had been improved for quality. On this basis, we think that the role of tritordeum and *H. chilense* in the food industry could be similar to that of bread wheat, although the end-use and potential cultivated-zone are yet to be determined.

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Optimization of Phosphorus Nutrition of Dryland Cereal Crops by Developing New P Placement Strategies

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Optimization of phosphorus nutrition is a critical component of dryland cereal production. Soil moisture is an especially crucial factor that limits P mobility in arid and semi arid soils. Field experiments were conduced to determine if subsoil P placement, alone or in combination with shallow P placement provides better P availability than seed or shallow placement to dryland wheat in semi-arid environments. Deep and intermediate P placements increased grain yield compared with the seed placement. The deep placement and the split P between the deep and shallow depths increased the grain yield more than the placement alone. These increases were generally related to favorable effects on plant growth, number of heads per plant, and on P uptake during the later growth stages. Soil moisture in the subsoil may increased P mobility and thus the P utilization efficiency. The plant density was decreased by the seed-placed P which could be attributed to early salt injury. The tiller density was enhanced at anthesis but not at tillering by splitting P between deep and shallow depths. This may suggest that more tillers survived due to deep placement of P and late P uptake, which was also enhanced by the deep placement. The wheat roots were the highest at the depth of P placement which enhanced the uptake of water, P and other nutrients especially during the later growth stages when the soil surface become drier than the subsoil. It can be concluded that the deep placement of P can increase the late-season P availability. This enhances the shoot growth, root growth in the subsoil and increases the shoot growth, root growth in the subsoil and increases the grain yield.

Production and Quality of Barley/Sudan Grass Forage Irrigated by Treated Wastewater Under Dryland Conditions

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Field experiments are conducting at Ramtha Treatment Plant Station to evaluate the effect of irrigation of barley/sudan grass by wastewater on production and quality parameters of these forages. Different rates of wastewater were applied with or without fertilization. Soil and plant samples will be taken during the growing season and analyzed for dry weight, yield and yield components and for nutrient uptake. At the end of the experiment the forages will be fed to animals to evaluate the digestibility and nutritional parameters. Wastewater will also be analyzed for the major chemical, microbiological and natural characteristics.

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Use of landraces and wild relatives of durum wheat to improve durum stress tolerance and grain quality

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During the last 15 years, several crosses were made between improved genotypes and landraces of durum wheat as well as wild relatives to incorporate additional resistance sources to biotic and abiotic stresses and to broaden the genetic base of the crop. Studies were also carried out on the genetic variability of durum landraces and wild relatives to identify sources of resistance to abiotic and biotic stresses; and of variability in seed storage proteins and DNA markers associated with improved grain quality. Mediterranean landraces were found to possess desirable traits lacking in other materials, such as resistance to drought and cold, early plant vigor, long peduncle and high tillering. The results on the use of durum wheat landraces in the hybridization program show that substantial progress can be achieved in developing improved cultivars for dry areas. Besides landraces, wheat relatives, e.g. *Triticum dicoccoides*, *Triticum monococcum*, *Aegilops*, etc.), can provide valuable sources for widening the genetic base of durum wheat and for improvement of important economic traits including stress tolerance.

Variation of High Molecular Weight Glutenin Subunits in Durum Landraces of Turkey

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The high molecular weight (HMW) glutenin of durum landraces comprise an important source of seed storage proteins for improvement of pasta-and bread-making quality. We have analyzed 945 samples from 91 Turkish landraces of *Triticum durum* for their HMW glutenin subunits using SDS PAGE. Nine different genotypes and a total of 14 HMW glutenin alleles (including null-alleles) were identified: In genome A (*Glu*-A1 locus), there alleles were found in *Glu*- A1-1 (encoding x-type subunits) and one in *Glu*-A1-2 (encoding y-type subunits), ranging in MW from 110 to 116 KD. At this locus, null alleles were detected in very high frequency (66.3% in *Glu*-A1-1 and 100% in *Glu*- A1-2). The alleles at this locus formed three intragenomic combinations with only two different band patterns. In genome B (*Glu*- B1 locus), five alleles were found in *Glu*- B1-1 encoding (x-type subunits) and five in *Glu*- B102 (encoding y-type subunits), ranging in MW from 84 to 104 KD. In contrast to the high frequency of null alleles in *Glu*- A1, no such alleles were detected in *Glu*- B1. The different subunits encoded by *Glu*- B1-1 and *Glu*- B1-2 genes formed six different intragenomic combination (i.e., nine genotypes). Comparing the HMW glutenin alleles of Central and Southeast Anatolia, we found that some alleles, such as *Glu*- A1-1c, *Glu*- B1-1c, *Glu*- B1-1d, *Glu*- B1-2d and *Glu*- B1-2c were found in both regions, whereas *Glu*- A1-1b, *Glu*- A1-1e and *Glu*- B1-1d were restricted to Southeast Anatolia.

Triticale: Industrial Quality and Agronomic Performance of Substitution lines

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Triticale's (X *triticosecale wittmack*) comparative advantages over other cereals is its ability to produce high grain and biomass yields under both low and high input conditions. However, for grain quality of triticale, in general, remain the main obstacle for its adoption and expansion, particularly in developing countries. In order to overcome this, several substituted lines of "Rhino"cultivar with one D chromosome exchanged for the homeologous A,B, or R chromosome were developed. This study was conducted to assess the performance and quality of these substituted lines under field conditions in Yaqui Valley (North-West Mexico) in 1994-95 and 1995-96 crop cycles. Results from this study showed significant differences between substituted lines and their Rhino controls foremost agronomic

and industrial quality traits. Rhino lines with 6D (6A), for instance, showed significantly higher yields under both irrigated and drought conditions as well as better seed quality than Rhino. Similarly, several other substituted Rhino lines of other groups, such as group 1, had substantial improvement in their quality and/or agronomic performance.

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