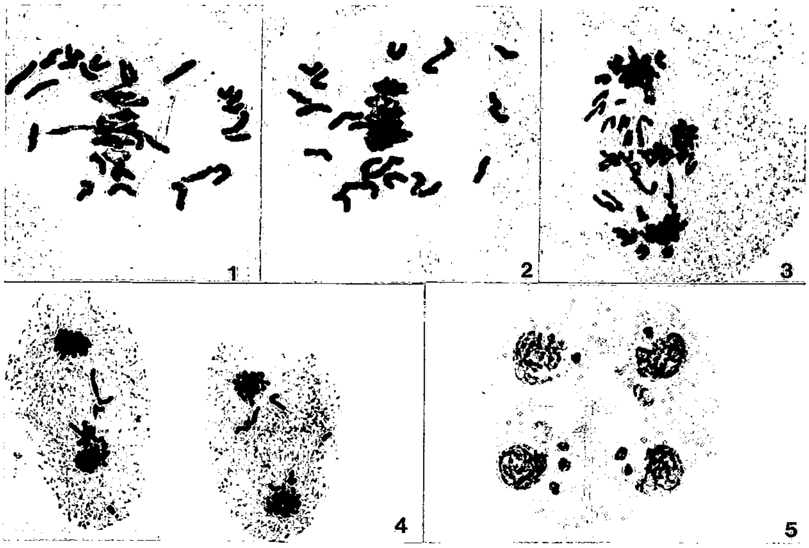
WHEAT INFORMATION SERVICE

ISSN 0510-3517



No. 78

June, 1994

Kihara Memorial
Yokohama Foundation for
the Advancement of Life Sciences
Yokohama, Japan

WHEAT INFORMATION SERVICE

Wheat Information Service (WIS) founded in 1954 is a biannual international journal on wheat genetics and its related fields, published by Kihara Memorial Yokohama Foundation for the Advancement of Life Science. WIS promotes the exchange of research information among wheat researchers all over the world.

Wheat Information Service publishes research articles regarding genetics, breeding and cytology, and lists of genetic stocks, gene and chromosome nomenclature, of *Triticum* and related genera, and records and announcement of meetings, and other information useful for wheat researches.

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Manuscript Instruction

1. Manuscripts should be typed double space in English on 20 × 29 cm bond papers with 3 cm margins. One original and one copy are required for submission.
2. One article, including figures and tables, should not be longer than five printed pages.
3. Research articles should include Title, Author's name(s) and address, Summary (300 words or less), Introduction, Materials and Methods, Results, Discussion, and References.
4. Scientific name and gene symbols should be underlined.
5. Tables and figures must be numbered with Arabic numerals.
6. Reference format should follow that shown below:
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Wheat Information Service
Number 78: 1 – 12 (1994)

I. Review

Genetic diversity in wheat — an international approach in its evaluation and utilization

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Introduction

In agreement with its mandate, the International Center for Agricultural Research in the Dry Areas (ICARDA) has been designated, in the global network coordinated by the International Plant Genetic Resources Institute, as a center for holding a global base collection of barley, faba bean and lentil and a regional base collection of wheat, chickpea and pasture and forage legumes. This mandate also includes wild relatives of the cultivated species.

ICARDA's location in the center of origin of most of its mandate crops provides a unique opportunity to explore, collect, conserve and evaluate germplasm. Barley, wheat, lentil, chickpea, pea, vetch and other forage legumes were domesticated in the Fertile Crescent some 8 - 10 000 years ago. However, Near East civilizations, as well as traditional subsistence agricultural systems in the region today, have been based on two major crops - wheat and barley (Harlan 1992).

Wild progenitors and relatives of wheat and barley still grow in the Near East region and during the long history of their evolution they became well adapted to the highly variable and stressful environment of the region. Wild progenitors of wheat, diploid *Triticum urartu* and tetraploid wild emmer, *Triticum dicoccoides*, are limited in its geographical distribution only to the Fertile Crescent and adjacent regions (Fig. 1 and 2). However, they can be found in very diverse environments within the region; ranging from –100 m bsl to 1700 m asl and 200 mm to 1000 mm of rainfall, with similar variations in temperature limits and soil fertility. Consequently, the wild wheats developed different ecotypes which display specific adaptation. Unpredictable fluctuation of weather conditions from year to year, so typical for the Near East region, resulted in the development of highly heterogenous populations composed of mostly homozygous individuals. This particular population structure provides for extraordinary buffering capacity. The high within-population diversity was found in different traits: spike characteristics, heading time, plant height, seed storage proteins and disease resistance. Recent research at ICARDA also revealed population heterogeneity in photoperiod and vernalization responses. Since both *T. urartu* and *T. dicoccoides* chromosomes are homologous with chromosomes of durum and bread wheat, their genetic diversity may be relatively easily exploited in breeding programs. These two wild wheats, as well as the related *Triticum boeoticum* and *Triticum araraticum* and some species of the genus *Aegilops* may be particularly useful in wheat breeding for tolerance to abiotic and biotic stresses.

What has been said above about wheat wild progenitors is equally valid for barley and its wild progenitor, *Hordeum spontaneum.*

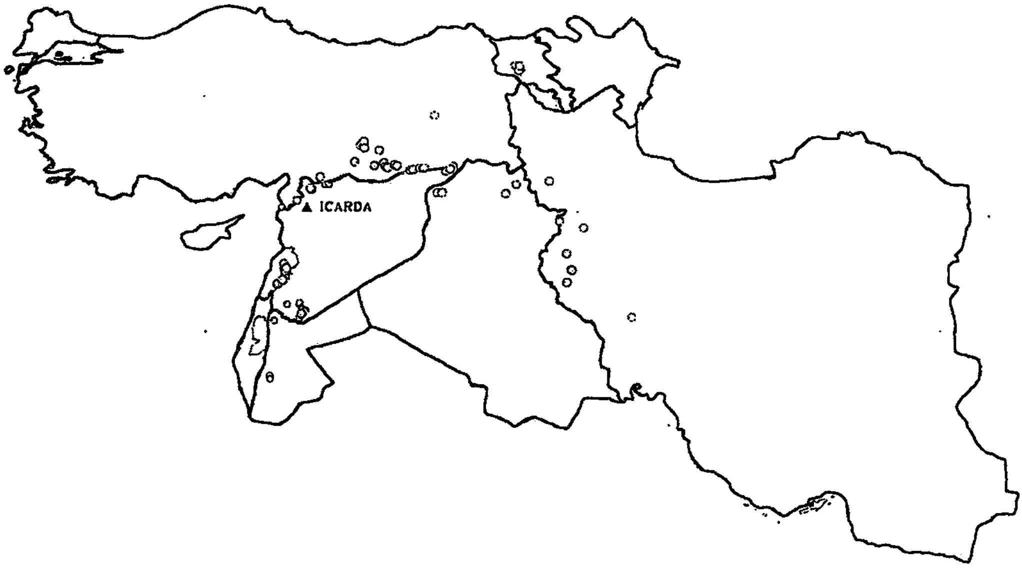


Fig. 1. Geographical distribution of *Triticum urartu* in WANA

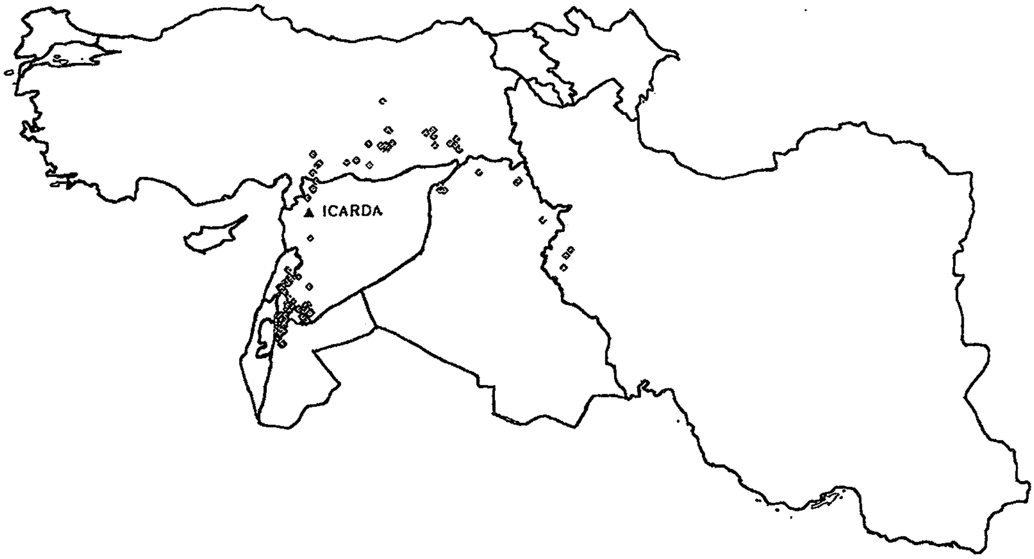


Fig. 2. Geographical distribution of *Triticum dicoccoides* in WANA

Table 1. Status of cereals collection at ICARDA by origin (December 1993)

	Barley	Wild Barley	Durum Wheat	Bread Wheat	Other Cult Wheat	Wild Wheat	Aeg.	Total
WANA	9510	1441	12543	6977	142	1131	1994	33738
Afghanistan	200	7	82	4	–	–	6	299
Algeria	127	12	1081	457	–	–	71	1748
Cyprus	7	4	102	1	–	–	51	165
Egypt	195	8	204	70	–	–	20	497
Ethiopia	2690	-	4896	2110	–	–	–	9696
Iran	209	64	98	95	8	5	304	783
Iraq	141	19	131	132	–	1	35	459
Jordan	134	127	270	17	1	508	198	1255
Lebanon	4	20	30	2	–	28	198	282
Libya	85	7	5	1	–	–	32	130
Morocco	743	4	237	208	–	–	62	1254
Oman	44	–	–	60	9	–	–	113
Pakistan	246	3	16	745	3	–	49	1062
Palestine	5	929	32	–	–	40	18	1024
Saudi Arabia	3	–	5	–	–	–	–	8
Syria	449	222	382	87	3	288	366	1797
Tunisia	601	–	1270	374	–	–	9	2254
Turkey	1186	15	1872	983	118	261	575	5010
UAE	6	–	–	–	–	–	–	6
Yemen	99	–	58	–	–	–	–	157
ICARDA lines	2336	–	1772	1631	–	–	–	5739
EUROPE	3891	41	3347	468	58	35	627	8467
ASIA	4285	92	202	241	3	4	121	4948
AFRICA	156	–	53	5	–	–	–	214
AMERICA	3189	21	634	25	–	–	–	3869
OCEANIA	84	–	44	5	–	–	–	133
Unknown	288	13	979	50	260	38	41	1669
TOTAL	21403	1608	17802	7771	463	1208	2783	53038

Collection priorities and strategy

Unfortunately, the valuable genetic diversity of the natural populations of wild relatives of cereals is subjected to severe genetic erosion, particularly in wild wheats. The most detrimental factor is overgrazing by small ruminants, which is ubiquitous in most parts of the Near East. The other negative factor is the loss of original habitats resulting from soil reclamation projects, changes in agronomic practices (fallow replacements) and urbanization.

Therefore, ICARDA gives high priority to collection and conservation of the wild relatives of wheat and barley. In the last six years, the Genetic Resources Unit at ICARDA has conducted more than 20 collection missions focused on the cereal wild relatives which yielded about 2500 new population samples. These and other accessions donated by other gene banks or institutions make the present total of ICARDA holdings as follows: 1608 accessions of wild barley, 1208 accessions of wild *Triticum* and 2783 accessions of *Aegilops* spp. (Table 1).

Recent research at ICARDA revealed that large natural populations of wild progenitors of wheat and barley consisting of millions of individuals display extremely high genetic diversity which cannot be adequately sampled and maintained in an *ex situ* collection in the gene bank. Therefore, ICARDA, in cooperation with national programs, has developed a proposal for conserving the most diverse populations on site (*in situ*). This dynamic method of germplasm conservation would complement the *ex situ* collections and allow further development in response to changing climatic and other conditions.

Landraces or farmers' varieties of cultivated wheat and barley originating from the West Asia and North Africa (WANA) region receive the highest priority in ICARDA's collection strategy. There are two main reasons for giving a special attention to this type of germplasm: i) genetic erosion caused by their replacement by improved varieties, and ii) good adaptation to the stressful and highly variable environments of the West Asia and North Africa region which is mandated to ICARDA.

It is estimated that landraces make up 80% of ICARDA cereal germplasm holdings.

The unpredictable year-to-year fluctuations of weather in the WANA region and the way in which the landraces are reproduced by the farmers resulted in high genetic diversity. Therefore, landraces are heterogenous in many characters and are composed of a number of genotypes and can, therefore, provide more genetic diversity for plant breeding programs than improved varieties. In fact, a number of improved varieties of cereals have been developed by ICARDA either as a direct single-plant selections from WANA landraces or from a cross in which a landrace or a line derived from it was used as a parent.

In the recent years, the Genetic Resources Unit at ICARDA focused on filling the gaps in the geographical representation of countries of the WANA region in its collections. This effort resulted in the collection of a good representation of most of the countries in barley, durum wheat and their wild relatives (Table 1).

All germplasm accessions of barley and durum wheat in the ICARDA collections have been characterized and/or evaluated for a number of descriptors and the results were published in a durum wheat catalog and barley catalog vol. I and II.

The cereal genetic resources are maintained at GRU/ICARDA in a medium-term active and long-term base collections and all unique accessions were safely duplicated at CIMMYT, Mexico in 1990.

As a contribution to a global effort, ICARDA is now developing a barley "core" collection of 300 accessions that will represent a species diversity for the WANA countries. A similar core collection will also be created by ICARDA for wheat.

ICARDA, as well as other CGIAR centers, favors the unrestricted access to genetic resources for all *bona fide* users. In the last four years, 1990-93, the Genetic Resources Unit of ICARDA distributed from its collections a total of 50036 seed samples of wheat, barley and their wild relatives to users all over the world. The major part, however, was distributed for utilization in the WANA region, either directly to national programs (11962 accessions) or indirectly through ICARDA germplasm improvement programs (18859). ICARDA's gene bank also serves as a backup to genetic resources programs of the WANA countries and, when possible, its collections are duplicated in the country of origin.

Evaluation and utilization

At ICARDA plant genetic resources conservation activity is not confined to its collection from the centers of diversity and safe storage in the gene bank. The approach, however, is to carry out detailed evaluation of the material preferably in its own habitat with close collaboration of the National Agricultural Research System (NARS) of the respective country to identify new sources of resistance to the biotic and abiotic stresses responsible for low and variable productivity of wheat. Though a very large amount of material was evaluated for more than 30 characters but here only a few traits which has direct effect on the adaptability (Growth habit) of the new germplasm or the most pertinent stresses (Thermal) are reported for the germplasm collected from WANA as well as developed at ICARDA (Table 2).

Growth habit

Growth habit (GH) and maturity plays vital role in the adaptation of wheat varieties in different agro-climatic situation which is influenced by temperature, photoperiod and genotypes. The growth habit studies were carried out in the green house in combination with field evaluation by planting in late spring. It is important to first study and evaluate the genetic variability in the germplasm originating from different regions of each country and then at ICARDA we target the new germplasm according to the needs of each region. In total 2045 lines/cultivars were studied for growth habit on a scale of 1 (spring) to 5 (strong winter type). Variability for GH was large and the germplasm from WANA showed a gradation from spring to pure winter type.

Growth habit data revealed that approximately 90% of the wheat germplasm from Morocco, Algeria, Syria and Ethiopia is of spring type and the remaining of facultative type (Fig. 3). On the other hand 75% of the germplasm from Iran, and Turkey was of winter/facultative type and only

Table 2. Wheat cultivars/lines evaluated

Origin	Growth Habit	Cold	Heat
Afghanistan	84	84	54+(12)
Iran	85	85	35+(12)
Pakistan	49	45	19+(3)
Turkey	425	675	53+(13)
Syria	45	40	8+(13)
Morocco	46	45	6+(10)
Algeria	31	35	11+(8)
Ethiopia	335	335	11+(10)
ICARDA	945	1462	44+(22)
TOTAL	2045	2806	241+(103)

Figures in ( ) are for Durum wheat.

Table 3. *Triticum* species used in durum wheat improvement at ICARDA

Species/Accession		Characteristics						
		G.H.	PH (cm)	DH	PROT. %	TKW (g)	YR	FROST Tol.**
T. turgidum Var. dic.	– SY 20017	P	100	156	20.2	19	R	1
" "	– SY 20101	SP	105	161	20.5	21	70S	1
" "	– SY 20021	P	115	160	21.0	26	5R	1
" "	– SY 20089	P	100	171	22.1	26	R	1
" "	– SY 20085	P	120	161	22.0	23	20MR	1
" "	– WR 33	P	90	155	21.0	28	5R	1
" "	– WR 42	P	87	150	20.5	27	20R	1
T. kotschyi	– SY 20224	P	50	145	18.0	25	R	1
T. zhukovski	– WR 13	SP	110	140	13.5	37	R	1

*) GH = Growth habit; P = Prostrates, & SP = Semi Prostrate, **) Highly Tolerant.

Table 4. Varieties released by NARS with the assistance of ICARDA

Species	No.	Countries
Bread Wheat	45	16 (Algeria, Egypt, Ethiopia, Greece, Iran, Jordan, Libya, Morocco, Pakistan, Portugal, Sudan, Syria, Tanzania, Tunisia, Yemen).
Durum Wheat	42	15 (Algeria, Cyprus, Egypt, Greece, Jordan, Lebanon, Libya, Morocco, Pakistan, Portugal,Saudi Arabia, Spain, Syria, Tunisia, Turkey).
Barley	44	22 (Algeria, Chile, China, Cyprus, Ecuador, Ethiopia, Iran, Jordan, Mexico, Morocco, Nepal, Pakistan, Peru, Portugal, Qatar, S. Arabia, Spain, Syria, Thailand, Tunisia, Vietnam, Yemen).

25% of spring type. Since at ICARDA the cereal improvement activity is divided into spring and winter wheat projects, the germplasm developed under winter and facultative wheat project was evaluated. The growth habit of germplasm developed at ICARDA ranged from pure spring types (15%) to winter and facultative types (85%) which is directed to serve the region with continental climate. These data clearly indicate that at ICARDA the genetic diversity for the important traits to serve the diverse needs of WANA is enhanced.

Cold tolerance

In several countries cold and frost cause serious damage to wheat in a number of ways, such as partial to complete killing of plants, foliar damage, partial to complete head damage and spike sterility. At ICARDA we are screening the materials in the field and employ the crown freezing test (Tahir et al. 1991) in the laboratory. In total 2806 lines/cultivars from different countries (Table 2) were evaluated at Haymana - Turkey under field conditions and in the freezing chambers at –11°C. Since the mortality under field conditions in the germplasm from Algeria, Ethiopia, Pakistan and Afghanistan was more than 80%, hence not evaluated in the freezing chambers. The data from the freezing chambers revealed that 30 and 45% of the material from Iran and Turkey, respectively, had more than 50% survival, however, 15 and 25% of the lines from these two countries showed high level of cold tolerance (75% survival) at –11°C, whereas from other countries (Syria and Morocco) none of the lines was found to have more than 50% survival (Fig. 4). To overcome the problem of massive cold damage in wheat in countries of West Asia and North Africa efforts were made to incorporate cold tolerance from other sources into the locally adapted germplasm. The breeding material is subjected to evaluation and screening at different stages of development. In the initial years of 1980-82 the cold tolerance was relatively very low, however in the subsequent years through continuous evaluation/testing significant progress was made to generate and develop cold tolerant wheat material. The new wheat germplasm (Fig. 5) shows very high level of cold tolerance and only a small proportion of the material had more than 50% damage at –11°C in comparison to local germplasm (Fig. 4). Majority of the segregating populations (IWFWSP) and International Winter/Facultative Wheat Observation Nursery (IWFWON) had 63 and 57% lines, respectively which had more than 75% survival. Only a very low percentage (<10%) of the new material was completely killed, inspite of the fact that 30% of the material was of facultative type and 15% of spring type. The results clearly show that cold tolerance level of spring/facultative wheats can also be improved without incorporating vernal or photoperiod sensitive gene(s) which are generally associated with cold tolerance.

Heat tolerance

High temperature is a major abiotic stress which severely damages wheat in WANA. Its effect is compounded in the presence of moisture stress after anthesis. It was, therefore, felt necessary to study and answer three questions, i.e., a) Is there enough genetic variability for this trait in wheat

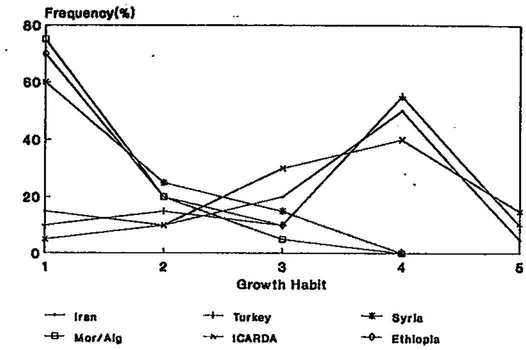


Fig. 3. Growth habit in wheat germplasm

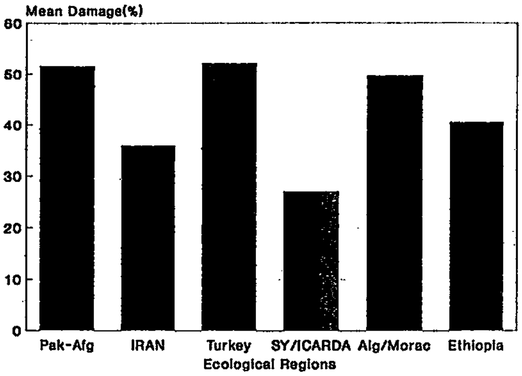


Fig. 6. Heat tolerance in wheat from different regions

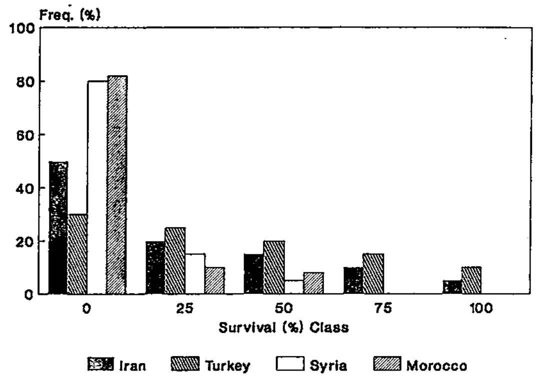
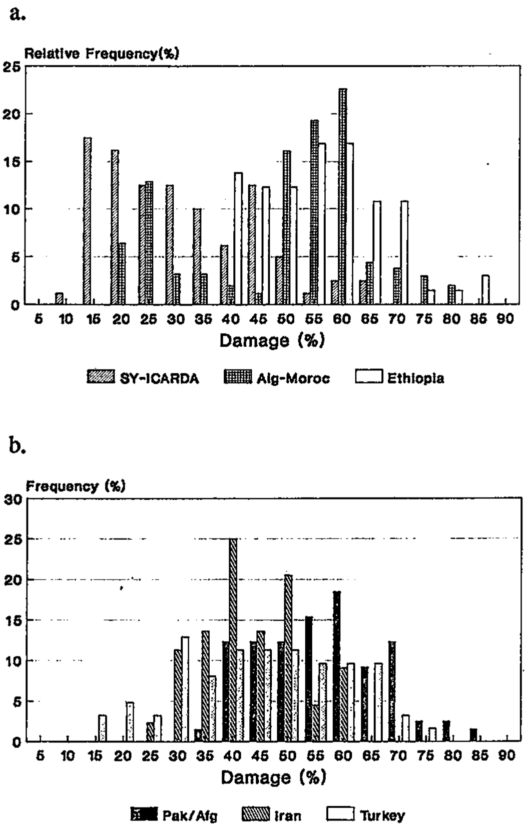


Fig. 4. Cold tolerance in wheat germplasm from WANA



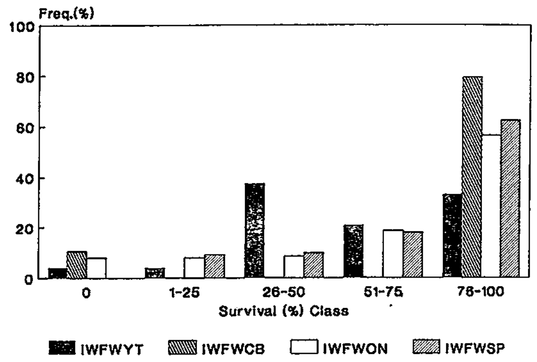


Fig. 5. Cold tolerance in ICARDA's wheat germplasm

Fig. 7. Relative frequency (%) of wheat lines for heat tolerance from different regions

germplasm of WANA; b) which species (bread or durum wheat) is more tolerant, and; c) is ICARDA/CIMMYT narrowing down genetic variability in wheat germplasm? Heat tolerance was studied on the basis of thermostability of the cell membrane which was estimated as the percent membrane injury (electrolyte leakage) (Blum and Ebercon 1981; Saadalla et al. 1990; Shanahan et al. 1990; Tahir and Singh 1993).

The heat tolerance of 241 bread wheat, 103 durum wheat lines/varieties, originating from WANA (Table 2) was studied along with a heat resistant check, Tam 107, and a susceptible check Nugains.

Data on the heat tolerance of 344 wheat lines/varieties are presented in Fig. 6. Percentage injury was classified into four groups: 1) 0-20% injury = resistant; 2) 21-40% injury = moderately resistant; 3) 41-60% injury = moderately susceptible and 4) more than 60% injury as susceptible. Eighteen percent of the lines were highly resistant to heat and better than the resistant check Tam 107 (25% injury). A fairly large number (53%) of the lines were found to be moderately resistant to heat. Heat tolerance data in Fig. 6 shows that on an over all basis ICARDA developed material had the lowest heat damage followed by Iran and Ethiopia. However, the mean heat damage (%) does not give true picture of the total genetic diversity for each country. The data presented in Fig. 7 a & b of each country revealed that Turkish wheat germplasm was the most diverse in which damage (%) ranged from 15 to 75%, whereas out of Iranian germplasm the minimum damage observed was 25%. The frequency distribution of heat tolerant lines shows that ICARDA generated material contained the most tolerant lines followed by Turkey, Algeria/Morocco and Iran, whereas Ethiopian, Pakistani/Afghanistan material was more susceptible to high temperature. The heat tolerant lines of these countries, in most of the cases, originated from heat prone areas, indicating that the possibility of identifying suitable sources of resistance to high temperature are higher where the problem of heat stress to the crop is severe. The ICARDA/CIMMYT lines were derived from selection under high temperature conditions. A great majority of the material developed at ICARDA is, therefore, much more heat resistant than the local germplasm from WANA.

Though cumulative frequency distribution data on heat tolerance shows that bread wheats are more heat tolerant but statistically no significant difference between *Triticum aestivum* and *T. durum* lines was observed (Fig. 8). Heat tolerance seems to be more related to the ecological origin and to selection pressure for high temperature tolerance. Therefore, we suggest that early breeding generations should be subjected to high temperature under field conditions, and field selected material should be rated on the basis of percent membrane injury to isolate any non-resistant lines or lines possessing avoidance mechanisms.

These studies indicate that ICARDA/CIMMYT is not reducing or narrowing down the genetic variability for the above mentioned traits. However, the narrowing down of genetic diversity can be seen in terms of lower frequency of material on the susceptible side and more on resistant side. But this kind of total diversity if narrowed down is a desirable development.

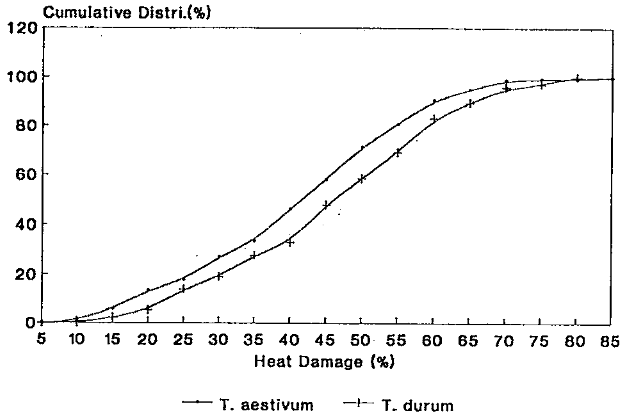


Fig. 8. Cumulative distribution of heat tolerant lines in *T. aestivum* and *T. durum*

Use of wild species and landraces

One of the objectives of wheat improvement at ICARDA is to evaluate the genetic diversity for desirable agronomic traits, especially biotic and abiotic stresses in the cultivated and wild *Triticum* species; and transfer those gene(s) into good agronomic background. The transfer of alien genes for the improvement of cultivated wheat has been carried out by many scientists (Riley and Kimber 1966; Sharma and Gill 1983; Islam and Shepherd 1988; Tahir 1983, 1985, 1986 and 1990).

Studies at ICARDA on the use of landraces and wild *Triticum* species were initiated in 1980. A very large number of germplasm was evaluated for a number of agronomic characteristics. The studies revealed that there is tremendous genetic variability among the landraces as well as wild *Triticum* species for the investigated traits (Tahir, 1983; Tahir and Damania, 1990; Damania et al. 1992). The selected germpalsm possessing the desirable gene(s) was employed in crossing program to develop genetic stocks for different traits to expand the base of available genetic diversity against factors depressing the productivity of wheat (Table 3).

The results on the use of three species - *Triticum turgidum* L. var. *dicoccoides* (AABB), *T. zhukovskyi* Men. and Er., and *T. kotschyi* (Bioss) Bowden are briefly discussed here. These species were used to transfer agronomic traits such as high protein, yellow rust resistance and cold/frost tolerance in durum wheat.

durum × *dicoccoides* derivatives

The agronomic data of selected yellow rust resistant lines from the *durum* × *dicoccoides* crosses showed an improvement over the check varieties for agronomic traits such as grain color and frost tolerance, as well as yellow rust resistance. Although none of the derived lines gave significantly higher yield than the improved check variety Sham 1, a number of them have the potential to do so. None of these lines gave significantly lower yield than the check cultivars. More than 50% of these lines had higher protein content, ranging from 13 to 20 per cent, compared to a protein content of 15.7 and 15.6 per cent, respectively, for Sham 1 and Haurani.

Significant differences in thousand-kernel-weight (TKW) were found. The TKW in the selected lines ranged from 29 to 54 g, compared to 42 and 48 g, respectively, for the two check varieties Sham 1 and Haurani. Eight lines showed significantly lower TKW compared to Sham 1, but all the lines had significantly higher protein content than the checks. Nine lines had significantly higher TKW than improved check variety Sham 1, whereas only one entry (Rubio Candeal/SY 20021/Ente//Stk = ICI 81-22-18) had significantly higher TKW (54 g) than the Haurani check and was equal in protein content compared to the check varieties. Two entries (BD 272/SY20101 and BD 1658/SY20089) had significantly higher TKW and protein content than the check varieties. At least five entries had equal or better TKW as compared to improved check variety Sham 1 and at the same time possessed significantly higher protein content than this check.

The TKW ranged from 33 to 44 g, against 41 g for the checks. There was a high degree of variation within and among derivatives of different cross combinations. No significant differences in days to maturity were observed. However, plant height of the derivatives ranged from 90 to 140 cm, compared to 90 cm and 130 cm for Sham 1 and Haurani, respectively. Statistically significant differences within and among different crosses were observed.

durum × *kotschyi* and *durum* × *zhukovskyi* derivatives

The agronomic data for derivatives from these two interspecific crosses showed that none of the derivatives was significantly superior in yield or TKW but all of them had much better protein content, especially the line derived from (Haurani/Kotschyi-SY 20224//Haurani,) cross which had a protein content of 16.1 per cent, compared to 11.8 per cent and 13 per cent for Waha and Haurani, respectively. This particular cross was also resistant to yellow rust, although one of its parents, Haurani, is not.

The *durum* × *kotschyi* derivatives also had far greater cold tolerance and were significantly taller than the parents, which is a desirable trait for sever moisture stress situations. The *durum* × *zhukovskyi* derivatives also showed a higher level of cold tolerance. There was a significant difference in plant height, which ranged from 110 to 130 cm compared to 90 cm for Waha's and 145 cm for Raspinegro, the two durum wheat parents employed in the cross.

Through the use of locally adapted germplasm of WANA and wild forms of *Triticum* a large number of cultivars (Table 4) in *Triticum aestivum*, *T. durum* and *Hordeum vulgare* have been released in a number of countries.

However, with the release of improved cultivars with better tolerance to prevalent biotic and abiotic stresses and with their wide adoption by the farmers in the stressed environments has put up a threat to the elimination of naturally occurring genetic diversity. This diversity is further threatened by the expansion of wheat cultivation to marginal areas to meet the ever increasing food demand due to high population growth in the WANA countries covering fertile crescent which is the primary center of genetic diversity.

The conservation of this immensely important natural resource for the future generations is beyond the concepts and means of any single nation. Therefore an international approach to conserve the biodiversity *in situ*, which ultimately will also help in preservation of fast deteriorating environments is urgently warranted.

Conclusions

1. West Asia and North Africa is still the richest source of genetic diversity in wheat.
2. Diversity is related to source of origin.
3. Significant differences occur between various traits at different evaluation sites.
4. Characters associated with stress tolerance are in high frequencies in certain regions.
5. Considerable diversity in certain traits was observed within a location.
6. Though there is still great unexploited diversity in cultivated forms but wild species provide a rich reservoir of desirable genes.
7. Modern agriculture is eroding naturally occurring diversity. There is a need to create safe havens to conserve biodiversity in its natural habitat.
8. International Networking in Conservation, Evaluation and Utilization of naturally occurring diversity will be the right approach to save the natural resource and conserve the environments.
9. Internationally coordinated efforts are needed to enhance and expand genetic diversity.

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Wheat Information Service
Number 78: 13 – 17 (1994)

II. Articles

Intervarietal polymorphism of heterochromatin in bread wheat, *Triticum aestivum* L.

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Summary

Polymorphism in banding patterns of somatic chromosomes in *Triticum aestivum* L. cultivars, Jauhar, M-143, Pavon, Sarsabz, Sindh-81, Mexipak, Sonalika, ZA-77 and Chinese Spring was studied by the Giemsa N-banding technique. Sixteen out of twenty one chromosomes exhibited distinct banding patterns, while no bands were observed in 1A and 3D to 6D. The banding polymorphism was observed mainly in the B-genome chromosomes, whereas the D-genome chromosomes revealed maximum consistency. The bands 1BL2. 7 and 6BL2. 5 reported by earlier workers in Chinese Spring were not observed in our material of the same cultivar, which however, showed the maximum number of bands per haploid genome. Thirteen of these bands were missing in different combinations in other cultivars. Four bands viz., 2BL2.41, 3BL2.41, 7BL2.61 and 2DL1.7 not present in the cv. Chinese Spring, were observed in M-143, Sarsabz, Mexipak; Jauhar, M-143, Pavon, Sarsabz; M-143, Sindh-81, Sarsabz, Mexipak; and Sindh-81, respecitively. On the basis of the banding pattern an homozygous reciprocal translocation involving 5A and 4B chromosomes was observed in a plant belonging to cv. M-143. This led to the formation of 5AL/4BL and 5AS/4BS instead of normal 5A and 4B chromosomes.

Introduction

The N-banding technoque has been shown to stain specific heterochromatic regions in many organisms, including cereal crops, such as barley (Islam 1980, Singh and Tsuchiya 1982), rye (Schlegel and Gill 1984) and wheat (Endo and Gill 1983, Gill 1987, Gerlach 1977). It has been employed for detecting translocations between wheat and barley chromosomes, for isolating lines possessing a pair of barley chromosomes substituted for a particular pair of wheat chromosomes (Islam 1980), and for detecting the 1B/1R translocation in many cultivars of wheat (Cai and Liu 1989, Jahan et al. 1990).

The aim of the present study was to explore the extent of band heteromorphy and chromosome polymorphism in several Pakistani wheat cultivars as compared to the check cultivar, Chinese Spring, utilizing Giemsa N-banding technique, and standard chromosome band nomenclature.

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Materials and methods

Nine cultivars viz., Jauhar, M-143, Pavon, Sindh-81, Sarsabz, Mexipak, Sonalika, ZA-77 and Chinese Spring of *Triticum aestivum* L. ($2n = 6x = 42$; AABBDD) were used in the present study. Chinese Spring was included as a check cultivar to make meaningful comparisons.

Seeds were germinated in the petri dishes, lined with moist filter paper, and kept in the dark at room temperature for about 72 hours. Root tips were harvested and transferred to another petri dish for the pretreatment, also kept in dark for 2.5 hours as described by Jahan and Vahidy (1989). The pretreatment solution used was a mixture of 10 mg colchicine, 5 mg 8-Hydroxy-quinoline and 5 drops of DMSO in 20 ml of distilled water. The root tips were fixed in 0.2% acetocarmine and stored for two days in the refrigerator at 4°C. The use of 0.2% acetocarmine helped in getting good spread of the chromosomes for N-banding. The cover glasses were removed by liquid nitrogen before further processing. The slides were treated for 10-15 minutes in 45% acetic acid at 60°C, air-dried and kept at room temperature for 2-3 days. Treatment of the slides in 2M phosphate buffer was similar to that descrided by Jahan et al. (1990). Slides were then washed 3-4 times in deionized water and stained in a liquid Giemsa solution, using 10 ml of prepared Giemsa (Fluka No. 48900) in 195 ml of 1/15 M Sorenson's phosphate buffer at pH 6.8 for about 45 minutes at room temperature. The slides were rinsed briefly in 1/15 M Sorenson buffer, air-dried for 2-3 days and mounted in the Canada balsam. From permanent slides at least five cells were selected for photomicrography and karyotyping. The identification of chromosomes was based upon diagnostic banding patterns as elucidated by Endo and Gill (1984) and Gill et al. (1991).

Results and discussion

Sixteen out of twenty one chromosomes exhibited distinct N-banding patterns. No bands were observed in chromosomes 1A, 3D, 4D, 5D and 6D. N-banding polymorphism was observed mainly in the B-genome chromosomes in all cultivars. The chromosomes 3A, 1B, 5B, 1D and 7D exhibited maximum banding pattern consistency. The overall banding pattern among cultivars was similar to that of Chinese Spring, though some differences described in Table 1 were observed.

The chromosome 2A consistently had faint proximal 2AL1.3 and terminal 2AL1.5 bands in the long arm and a prominent proximal 2AS1.3 band in the short arm. The chromosomes 2A and 3A can often be confused with each other and could be misidentified as both have a similar sized bands in the proximal region of the short arm (Endo and Gill 1984). The terminal band 2AL1.5 of Chinese Spring was not observed in Jauhar, Sindh-81 and Sarsabz cultivars. Proximal band 4AL1.3 was not observed in Jauhar, M-143, Pavon and Sarsabz. The terminal band 4AL2.7 was not observed in any cultivar except Sonalika and Chinese Spring (Table 1). The proximal band 5AL1.3 was darker in M-143 as compared to the other cultivars.

A reciprocal translocation was observed in M-143 cultivar. Instead of normal 5A and 4B chromosomes 5AL/4BL and 5AS/4BS translocated chromosomes were observed (Fig. 1). Gill and Kimber (1977) observed a translocation in 4A (later renamed as 4B) and the 6B chromosomes of cultivar Thatcher. The characteristic twin bands, 6AL1.3 and 6AL1.5 were not observed in Pavon

Table 1. Polymorphic N-Bands in nine cultivars of *Triticum aestivum* L. The + and – indicate presence and absence of dark bands, respectively.

Polymorphic N-bands	Cultivars* 1	2	3	4	5	6	7	8	9
2AL1.5	+	–	+	+	–	–	+	+	+
4AL1.3	+	–	–	–	+	–	+	+	+
4AL2.7	+	–	–	–	–	–	–	+	–
6AL1.3	+	+	+	–	–	+	+	+	+
6AL1.5	+	+	+	–	–	+	+	+	+
7AS1.5	+	+	+	+	+	–	+	+	–
7AL1.7	+	–	+	+	+	+	+	+	+
1BL2.7	–	–	–	–	–	–	–	–	–
2BL2.41	–	–	+	–	–	+	+	–	–
3BS2.7	+	–	+	+	+	–	+	+	+
3BL2.41	–	+	+	+	–	+	–	–	–
4BS1.7	+	+	–	+	–	–	–	+	+
4BL1.5	+	+	–	–	+	+	+	+	+
4BL2.5	+	+	–	+	+	+	+	+	+
4BL2.7	+	–	–	–	–	–	–	–	–
6BS3.6	+	+	+	+	+	+	–	–	–
6BL2.5	–	–	–	–	–	–	–	–	–
6BL2.7	+	–	–	–	–	–	–	–	–
7BL2.61	–	–	+	–	+	+	+	–	–
2DL1.7	–	–	–	–	+	–	–	–	–

* 1=Chinese Spring, 2=Jauhar, 3=M-143, 4=Pavon, 5=Sindh-81, 6=Sarsabz, 7=Mexipak, 8=Sonalika and 9= ZA-77.

and Sindh-81 (Table 1). Endo and Gill (1984) also did not observe these bands in pure lines and substitution lines of four wheat cultivars. The terminal band 7AS1.5 was missing in Sarsabz and ZA-77, while the terminal band 7AL1.7 was not observed in Jauhar.

The cultivars M-143, Sarsabz and Mexipak exhibited an additional band 2BL2.41, not observed in other cultivars including Chinese Spring. The terminal band 3BS2.7 was missing in Jauhar and Sarsabz. The band 3BL2.41 observed in Jauhar, M-143, Pavon and Sarsabz was absent in other cultivars. Jewell and Mujeeb-Kazi (1983) reported maximum differences in N-banding patterns of 3B chromosome in Chinese Spring and Veery. Proximal band 4BS1.7 was not observed in M-143, Sindh-81, Sarsabz and Mexipak, while the proximal band 4BL1.5 was missing in M-143 and Pavon. The terminal band 6BS3.6 of the satellite was not observed in Mexipak, Sonalika and ZA-77, while in the rest of cultivars this band was very faint. The terminal bands 1BL2.7 and

6BL2.5 observed in Chinese Spring by Gill et al. (1991) were not found in our material of the same cultivar. An extra terminal band 7BL2.61 was observed clearly in M-143, Sindh-81, Sarsabz (Fig. 2) and faintly in Mexipak, while it was not observed in rest of the cultivars. Chen et al. (1988) reported the differences in N-banding patterns of B genome in three endemic hexaploid wheats from western China.

Chromosomes 1D and 7D showed characteristic bands 1DS1.3 and 7DS1.5, respectively, in the interstitial regions, while the chromosome 2D exhibited bands 2DS1.3 and 2DL1.7. The

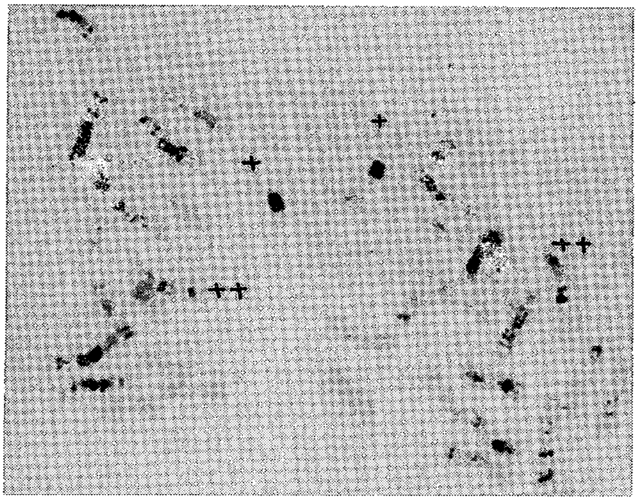

Fig. 1. A representative cell of cv. M-143 showing homozygous translocation 5AS/4BS (+) and 5AL/4BL (++).

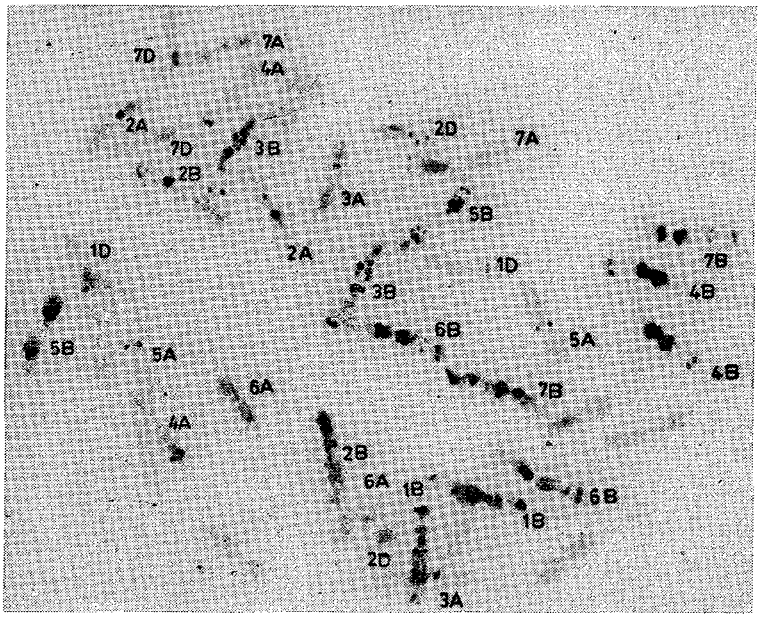

Fig. 2. A representative somatic cell of wheat, *Triticum aestivum* L. cv. Sarsabz, showing additional Giemsa N-bands such as 3BL2.41 and 7BL2.61 as compared to Chinese Spring.

terminal band 2DL1.7 was observed in cv. Sindh-81 only (Table 1). According to Endo and Gill (1984), chromosomes 3A, 5A, 2D and 7D showed the same banding patterns in their four cultivars as compared to the Chinese Spring. The bands reported earlier as 1BL2.7 and 6BL2.5 in cv. Chinese Spring were not observed in our material. Four bands viz., 2BL2.41, 3BL2.41, 7BL2.61 and 2DL1.7 not observed in the cv. Chinese Spring, were observed in some of the local cultivars (Table 1). Endo (1986) reported bands in all chromosomes except 1A of Chinese Spring by the C-banding and found the similar banding patterns in fourteen chromosomes as those found in the N-banded karyotype.

An intervarietal polymorphism of heterochromatin distribution was confirmed by the banding technique which may be used to study the pedigree, chromosomal aberrations like deletion, duplication, translocation and to differentiate among cultivars. Through DNA composition the heterogeneity of heterochromatin can be revealed further as specific DNA sequences are involved in the composition of heterochromatin (Gerlach and Peacock 1980). The differential DNA sequences and DNA protein composition may account for heterochromatic heterogeneity as observed by banding procedures.

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Wheat Information Service
Number 78: 18 –20 (1994)

Breeding behaviour of monosomics in hexaploid wheat

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All the monosomic lines of the wheat cultivar Chinese Spring, developed by E.R. Sears, and twenty monosomic lines (excluding 5B) of the Indian wheat variety Pb. C591, developed by Swaminathan et al. (1968) have been maintained at the Division of Genetics, Indian Agricultural Research Institute , New Delhi. These monosomic series have been utilized in genetical and cytogenetical studies (Joshi et al. 1968, Joshi and Singh 1979, Singh and Joshi 1979, Singh and Joshi 1986, Singh 1992).

Breeding behaviour of all the monosomic lines in the above two series was studied for a period of eighteen years. Data pertaining to variety Chinese Spring revealed that out of the 617 plants

Table 1. Chromosome constitution in the selfed progenies of Chinese Spring monosomics

Year	Total plants analysed	Disomic	Monosomic	Double Monosomic	Nullisomic and Trisomic
1970	70	30 (42.9)	39 (55.7)	1 (1.4)	–
1971	9	5 (55.5)	4 (44.5)	–	–
1972	37	13 (35.1)	24 (64.9)	–	–
1973	52	23 (44.2)	28 (53.8)	–	1 (1.9)
1974	24	7 (29.2)	17 (70.8)	–	–
1978	2 (only 5B)	1 (50.0)	1 (50.0)	–	–
1979	39	10 (25.64)	28 (71.8)	–	1 (2.6)
1980	38	11 (28.9)	27 (71.0)	–	–
1981	37	12 (31.6)	24 (63.2)	–	1 (2.7)
1982	43	18 (41.9)	24 (55.8)	1 (2.3)	–
1983	38	12 (31.6)	26 (68.4)	–	–
1985	39	15 (38.5)	24 (61.5)	–	–
1986	33	13 (39.4)	20 (60.6)	–	–
1987	24	6 (25.0)	18 (75.0)	–	–
1989	33	8 (24.2)	25 (75.8)	–	–
1990	3 (only 5B)	1 (33.3)	2 (66.7)	–	–
1991	54	26 (48.1)	28 (51.9)	–	–
1993	42	15 (35.7)	26 (61.9)	1 (2.3)	–
Total	617	226	405	3	3
Percentage	–	36.6	65.6	0.5	0.5

Table 2. Chromosome constitution in the selfed progenies of monosomics of Var. Pb. C591.

Year	Total plants analysed	Disomic	Monosomic	Double Monosomic	Nullisomic and Trisomic
1970	35	6 (17.1)	29 (82.9)	–	–
1971	27	7 (25.9)	20 (74.1)	–	–
1972	28	7 (25.0)	21 (75.0)	–	–
1973	40	14 (35.0)	25 (62.5)	–	1 (2.5)
1974	9	3 (33.3)	6 (66.6)	–	–
1978	30	8 (26.6)	20 (66.7)	1 (3.3)	1 (3.3)
1979	31	8 (25.8)	23 (74.2)	–	–
1980	91	37 (40.7)	53 (58.2)	–	1 (1.1)
1981	33	7 (21.2)	26 (78.8)	–	–
1982	27	7 (25.9)	20 (74.1)	–	–
1983	32	10 (31.3)	21 (65.6)	1 (3.1)	–
1985	38	14 (36.8)	24 (63.2)	–	–
1986	5 (only 5B and 3A)	–	5 (100.0)	–	–
1987	30	7 (23.3)	23 (76.6)	–	–
1989	43	17 (39.5)	25 (58.2)	1 (2.3)	–
1990	7 (only 3A)	–	7 (100.0)	–	–
1991	34	6 (17.6)	28 (82.4)	–	–
1993	33	10 (30.3)	23 (69.7)	–	–
Total	573	168	399	3	3
Percentage	–	29.3	69.6	0.5	0.5

analysed, 65.6% were monosomics (20”+1’), 36.6% disomics (21”), 0.5% double monosomics (19”+2’) and 0.5% were nullisomics and trisomics (20” and 20”+1”’ or 21”+1’) (Table 1). Similarly out of 573 plants analysed in variety Pb. C591, 69.6% were monosomics, 29.3% disomics, 0.5% double monosomics and 0.5% nullisomics and trisomics (Table 2). The frequencies of monosomics and disomics in the selfed progenies of monosomic lines in these varieties were well within the range (49 to 85% of monosomics and 11 to 29% of disomics) shown by Morris and Sears (1967). Low frequencies of nullisomics and trisomics obtained in the monosomic lines of the two varieties could be due to the fact that only healthy plants were selected for cytological analysis, expecting that identified monosomics could be effectively used in crossings and for maintenance of monosomic lines.

Person (1956) reported a low frequency of double monosomics (0.4%) in a population of 225 monosomics. A similar frequency of double monosomics was obtained by McGinnis and Campbell (1960). The frequency obtained in the present study is consistent with those reported by these workers. However, Joshi et al. (1968) reported a very high frequency of double monosomics (1.9%)

in the selfed progenies of Chinese Spring monosomic lines. Since the presence of double monosomics and trisomics may permit univalent shift, a rigid cytological check of monosomic plants used in selfing or in crossing programme, is essential, in order to maintain the purity of the monosomic lines.

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Wheat Information Service
Number 78: 21 – 23 (1994)

Identification of chlorophyll synthetic genes in three hexaploid wheat varieties

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Summary

Chromosome 3A of an Indian hexaploid wheat var. Pb. C591 carries a gene for chlorophyll synthesis (Singh and Joshi 1979). In the present study, F_2 segregation of green and albino seedlings was studied in crosses between Pb. C591 monosomic 3A (female) and varieties Kundan, Oligo and Rht-8 (male). Two dominant genes in Oligo and Rht-8 and one in Kundan regulated chlorophyll synthesis. One of the two genes in Oligo and Rht-8 and a single gene in Kundan were located on chromosome 3A.

Introduction

Austin et al. (1986) reported a high rate of photosynthesis (Pmax) in the flag leaves of diploid species of wheat. Necessity of identification of genes controlling Pmax in diploid, tetraploid and hexaploid species and their transfer to hexaploid wheats have been suggested. Since chlorophyll content has been implicated in Pmax, it becomes necessary to identify chlorophyll synthetic gene(s) in both donor as well as in recipients to facilitate their effective and selective transfer. In the present study we identified chlorophyll synthetic genes in three hexaploid wheat varieties.

Materials and methods

A variety Pb. C591 carries one gene or gene complex for chlorophyll synthesis that is located on chromosome 3A (Singh and Joshi 1979). In the selfed progenies of Pb. C591 monosomic 3A, Joshi et al. (1979) observed an unusally high frequency of nullisomics (12.0%) manifested as albino seedilings. To facilitate the identification of chlorophyll synthetic gene(s), monosomic 3A of Pb. C591 (female) was crossed with the varieties Kundan, Oligo and Rht-8. The F_1 hybrids were cytologically examined at first meiotic metaphase to determine the chromosome constitution. At maturity, F_2 seeds were taken from all the hydrids separately. Seeds were germinated in petri-dishes for observing the seedling traits.

Results and discussion

At 8th day after imbibition, seedlings were second for the presence of chlorophyll in the F_2 progenies obtained after crosses of monosomic 3A (Pb. C591) × three varieties. Data pertaining to

Table 1. Segregation of albino seedlings in the F_2 progenies of crosses between monosomic 3A (Pb. C591) and three varieties.

Cross	Number of plants	Seedlings		Albino
		Green	Albino	%
Disomics (Pb. C591)	6	1194	0	0.0
Monosomics 3A (Pb. C591)	6	1053	147	12.3
Kundan		995	0	0.0
Oligo		990	0	0.0
Rht-8		993	0	0.0
Mono 3A × Kundan				
Disomics	8	2385	0	0.0
Monosomics	3	780	103	11.7
Mono 3A × Oligo				
Disomics	5	1158	0	0.0
Monosomics	5	1037	45	4.1
Mono 3A × Rht-8				
Disomic	6	1422	0	0.0
Monosomics	2	412	13	3.0

the frequency of albino seedlings recorded (Table 1). All the disomic plants (2n = 42) from selfed monosomic 3A produced only green seedlings, while the monosomic plants (2n = 41) gave an albino frequency of 12.3%.

There were 11 F_1 hydrids in the cross of monosomic 3A (Pb. C591) × Kundan. Out of these, 8 hybrids were disomics and 3 were monosomics. The disomic hybrids produced only green seedlings, while the monosomics produced both green and albino seedlings with an overall albino frequency of 11.7%. The absence of albino seedlings in the F_2's of disomic hybrids suggests that the variety Kundan carries a chlorophyll synthesis gene allelic to that in variety Pb. C591. The frequency of albino seedlings (11.7%) in the F_2's of monosomic hybrids was very close to that (12.3%) observed in the selfed progeny of monosomic 3A, suggesting that variety Kundan carries a gene for chlorophyll synthesis which is located on chromosome 3A.

In the cross of monosomic 3A (Pb. C591) × Oligo there were 5 disomic and 5 monosomic hybrids. All the disomic hybrids produced only green seedlings, whereas monosomic hybrids segregated for albino seedlings with a frequency of 4.1%. The absence of albino seedlings in the F_2's of disomic hybrids indicates the presence of a gene allelic to the gene located on chromosome 3A of variety Pb. C591. The segregation of albino seedlings in the F_2 populations of monosomic hybrids confirmed this. Based on the frequency of albino seedlings (nullisomics) in the selfed progeny of monosomic F_1 hybrids involving chromosome 3A the observed albino frequency (4.1%), that fits in a monogenic ratio of 3 green : 1 albino among the nullisomics (cytologically confirmed), suggested the involvement of one more gene for chlorophyll synthesis besides the gene located on chromosome 3A in variety Oligo.

Table 2. Chlorophyll synthetic genes identified in hexaploid wheat.

Variety	No. of genes involved	Carrier chromosome	Source	
Pb. C591	One	3A	Singh and Joshi	1979
Chinese Spring	Two	3A and 3D	Singh and Joshi	1986
T. sphaerococcum	Two	3A and 3D	Singh	1990
Mara	Two	3A + 1 more	Singh	1991
Oligo	Two	3A + 1 more	Present study	
Kundan	One	3A	Present study	
Rht-8	Two	3A + 1 more	Present study	
Sel. 111	One	3A	In press	
Kalyansona	Two	3A + 1 more	In press	
Sonalika	Two	3A + 1 more	In press	

There were only 8 hybrid plants in the cross of monosomic 3A (Pb. C591) × Rht-8 among which 6 hybrids were disomics and 2 monosomics. Disomic hybrids of this cross produced only green seedlings indicating the presence of a chlorophyll synthetic gene allelic to the gene located on chromosome 3A in variety Pb. C591. However, the monosomic F_1 hybrids segregated for green and albino seedlings, confirming the presence of an allelic gene in variety Rht-8. The albino frequency observed in the F_2 generation of monosomic hybrids was 3.0%, fitting a monogenic ratio of 3 green : 1 albino among the nullisomic class. The result suggest that variety Rht-8 also carries two chlorophyll synthetic genes, one of which is located on chromosome 3A.

So far ten hexaploid wheat varieties involving old and new ones have been analysed for the presence of chlorophyll synthetic genes (Table 2). Of these, Pb. C591, Kundan and Sel. 111 carry only one gene or gene complex for chlorophyll synthesis whereas Chinese Spring, *T. sphaerococcum*, Mara, Oligo, Rht-8, Kalyansona and Sonalika have been found to carry two genes each. Interestingly enough, at least one of two genes is always present on chromosome 3A in all the varieties analysed so far.

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Wheat Information Service
Number 78: 24 – 27 (1994)

Incorporation of stripe rust resistant specific genes into Unnath Kalyansona carrying different gene complexes

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Summary

The wheat stripe rust resistant specific genes *Yr9*, *Yr11*, *Yr12*, *Yr13* and *Yr14* were incorporated into Unnath Kalyansona carrying different gene complexes for stem and leaf rusts by simple back cross. In BC_2S_4 and BC_3S_4 generations the genotypes with excellent resistant for all three rusts were selected. An increase in grain yield/plant and 1000-grain weight were noticed in the newly constituted lines.

Key words: Stripe rust, gene complexes, Unnath Kalyansona.

Introduction

The wheat yellow rust caused by *Puccinia striiformis* (Westend f.sp. *tritici*) is one of the important rust diseases in the wheat growing areas in India (Singh et al., 1990; Brahma et al., 1993; Reddy et al., 1993 a, b). It is confined to the cool climatic area of Indo-gangetic plains, foot hills of Himalaya, Himalayan mountains in North, Nilgiri and Palney hills in South. The high yielding wheat variety Kalyansona released in late 1960's (Rao, 1978) became susceptible to all the three rusts in the middle of 1970's. This variety was improved for stem and leaf rusts after incorporation of *Sr24* + *Lr24* linked genes from Australian wheat variety TR 360-147/3 Agl4 and *Sr26* + *Lr24* from Darf/3 Ag/Kite and *Sr27* + *Lr28* from rye back ground (Kochumadhavan et al., 1988).

All the lines of Unnath Kalyansona are however highly susceptible to stripe rust. The percentage of infection is more in Unnath varieties than the original variety and this may be due to less competition among other rust pathogen for spreading. The present paper reports the results of transfer of five stripe rust resistance genes into Unnath Kalyansona by back cross method.

Materials and methods

Five stocks both spring and winter growth habit of hexaploid wheat carrying genes *Yr9* (Verry's), *Yr11* (Joss Chambier) *Yr12* (Pride), *Yr13* (Guardian) and *Yr14* (Score W 119) were critically evaluated for eight seasons under natural and artificial epiphytotic conditions at IARI-Regional Station, Wellington, Nilgiris. This location is a 'Hot Spot' and 'Foci' for all the three rusts, therefore the genotype possessing complete rust resistance can be selected under heavy pathogen pressure in natural condition. The rust reactions were recorded by combining severity (Percentage

of infection) and response (type of infection). These potentially valued genes were transferred to the imporved Kalyansona by simple back cross method. Intensive plant selections were made in BC$_2$ and BC$_3$ and resistant plants were advanced to BC$_2$S$_4$ and BC$_3$S$_4$. Grain yield/plant (g) and 1000-grain weight (g) were recorded both on recurrent parents and costituted lines.
't' test was applied to test the means.

Results and discussion

The following fifteen lines were constituted in BC$_3$S$_4$ in Unnath Kalyansona background.

Sr24 + *Lr24* + *Yr9*
Sr24 + *Lr24* + *Yr11*
Sr24 + *Lr24* + *Yr12*
Sr24 + *Lr24* + *Yr13*
Sr24 + *Lr24* + *Yr14*
Sr26 + *Lr24* + *Yr9*
Sr26 + *Lr24* + *Yr11*
Sr26 + *Lr24* + *Yr12*
Sr26 + *Lr24* + *Yr13*
Sr26 + *Lr24* + *Yr14*
Sr27 + *Lr28* + *Yr9*
Sr27 + *Lr28* + *Yr11*
Sr27 + *Lr28* + *Yr12*
Sr27 + *Lr28* + *Yr13*
Sr27 + *Lr28* + *Yr14*

So far eighteen diverse specific genes conditioning resistance to *Puccinia striiformis* have been reported. Based on the critical field evaluation, all the incorporated genes were proved to be resistant to stripe rust (Table 1).

In the gene complex of *Sr24* + *Lr24* the appearance of black rust was noticed upto 40% which could be due to the deterioration of *Sr24* gene. The trace moderately resistance condition for black rust was only observed in the gene complexes of *Sr26* + *Lr24* and *Sr27* + *Lr28*. Since *Yr9* gene is linked with *Sr31* + *Lr26*, the resistance to black rust was also noticed along with yellow rust. Moreover a complete resistance condition was observed for leaf and stripe rusts in all the gene complexes. The disease free Kalyansona genotypes gave significant increase in grain yield/plant

Table 1. Rust reaction of improved Kalyansona carrying different gene complexes.

Parent/Yr gene	Resistance source	*Sr24* + *Lr24*			*Sr26* + *Lr24*			*Sr27* + *Lr28*		
		Bl	Br	Yl	Bl	Br	Yl	Bl	Br	Yl
Kalyansona	—	40S	F	60S	5MR	F	60S	TMR	F	60S
Yr9	Imperial rye	TMR	F	F	F	F	F	F	F	F
Yr11	Joss Chambier	40S	F	F	5MR	F	F	TMR	F	F
Yr12	Pride	40S	F	F	5MR	F	F	TMR	F	F
Yr13	Guaridian	40S	F	F	5MR	F	F	TMR	F	F
Yr14	Scire (W 119)	40S	F	F	5MR	F	F	TMR	F	F

F = Free, S = Susceptible, MR = Moderately resistant, TMR = Trace moderately resistant, Numericals (5, 40, 60) are the per cent of sevearity, Bl = Black rust, Br = Brown rust, Yl = Yellow rust.

Table 2. The grain yield and 1000-grain weight of parents and newly constituted lines.

Genotype/ Gene Complex	Grain yield (g) plant (mean)	't' test value		1000-grain Wt (g) (mean)	't' test value	
		+	++		+	++
+Kalyansona	8.2	—	—	28	—	—
++Unnath Kalyansona						
(*Sr24* + *Lr24*)	8.5	0.554	—	29	1.225	—
Sr24 + *Lr24* + *Yr9*	10.2	5.283**	2.656*	37	5.512**	4.902**
Sr24 + *Lr24* + *Yr11*	9.5	4.697**	1.708	35	8.573**	7.353**
Sr24 + *Lr24* + *Yr12*	8.9	2.941*	0.704	34	2.941*	2.451*
Sr24 + *Lr24* + *Yr13*	9.6	5.058**	1.879	36	4.899**	4.289**
Sr24 + *Lr24* + *Yr14*	9.8	4.226**	3.611*	36	9.798**	8.578**
++U.Kalyansona						
(*Sr26* + *Lr24*)	8.9	1.893	—	29	1.225	—
Sr26 + *Lr24* + *Yr9*	10.4	6.843**	3.249*	36	4.355**	3.813**
Sr26 + *Lr24* + *Yr11*	9.8	7.689**	2.299*	35	4.287**	3.676*
Sr26 + *Lr24* + *Yr12*	10.0	4.166**	2.044	36	9.798**	8.578**
Sr26 + *Lr24* + *Yr13*	9.4	4.385**	1.158	35	8.573**	7.353**
Sr26 + *Lr24* + *Yr14*	9.8	8.355**	2.351*	35	3.810**	3.268*
++U.Kalyansona						
(*Sr27* + *Lr28*)	8.7	2.101	—	29	1.225	—
Sr27 + *Lr28* + *Yr9*	10.3	5.044**	3.550*	37	2.756*	2.451*
Sr27 + *Lr28* + *Yr11*	9.6	3.362**	1.997	35	8.573**	7.353**
Sr27 + *Lr28* + *Yr12*	10.0	4.023**	5.465**	36	4.355**	3.813**
Sr27 + *Lr28* + *Yr13*	9.8	4.976**	2.015*	35	8.573**	7.353**
Sr27 + *Lr28* + *Yr14*	10.1	7.983**	4.759**	36	4.899**	4.289**

* Significant at 5% level

** Significant at 1% level

and 1000 grain weight over original and Unnath Kalyansona (Table 2). These stripe rust resistance genes have been successfully transferred into the number of commercial wheat varieties under cultivation in U.K.

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Wheat Information Service
Number 78: 28 – 33 (1994)

Morphology and cytology of intergeneric hybrids of *Kengyilia gobicola* and *K. zhaosuensis* crossed with *Roegneria tsukushiensis*

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Summary

Two intergeneric hybrids were obtained from *Kengyilia gobicola* Yen et J. L. Yang and *K. zhaosuensis* J. L. Yang, Yen et Baum crossed with *Roegneria tsukushiensis*. Chromosome pairings were studied at metaphase I in the two hybrids. Meiotic configurations were 18.69 univalents + 11.56 bivalents + 0.04 trivalents for *K. gobicola* × *R. tsukushiensis*, and 18.56 univalents + 11.73 bivalents + 0.04 trivalents for *K. zhaosuensis* x *R. tsukushiensis*. Lagging chromosomes at anaphase I and II, tetrads with micronuclei were observed in these two hybrids. Chromosome bridges were found at anaphase I and II in *K. zhaosuensis* × *R. tsukushiensis*. The results indicated that *K. gobicola* and *K. zhaosuensis* share two same basic genomes with *R. tsukushiensis*.

Introduction

Kengyilia Yen et J. L. Yang is a new genus found in west China (Yen and Yang 1989, 1990). *Kengyilia gobicola* Yen et J. L. Yang, a hexaploid (2n = 42) (Sun et al. 1989) perennial grass, is distributed in Gobi Desert at the foot of Muztagata Mt., Xinjiang, China. This species has short, rod-like leaves that form tube-like structures and much hair on the adaxial epidermis of leaf blade. The adaxial epidermal surface of the blade is covered with a thick cuticule layer and bears few stomata. The deep root with dense root hair holds sand around it in the form of a sand sheath. The hairy spike reduces evaporation to protect the physiological activity of this important reproductive organ. These characteristics make *K. gobicola* a good drought resistant plant (Yen and J. L. Yang 1990).

Kengyilia zhaosuensis J. L. Yang, Yen et Baum, a hexaploid (2n = 42) (Sun et al. 1989, 1993), perennial plant, is distributed in Zhaosu country, Xinjiang.

K. gobicola and *K. zhaosuensis* are new species which were found in recent years. The karyotypes of them were reported by Yen and J.L. Yang (1989), and Sun et al. (1993).

Roegneria tsukushiensis (Honda) B. R. Lu, Yen et J. L. Yang, a popular grass growing along the fields and road-sides, is widely distributed in China, Korea and Japan (Ohwi 1965, Lu et al. 1990). This species is allohexaploid (2n = 42), which comprises three different genomes (Sakamoto 1964, Dewey 1984, Lu et al. 1990).

In an attempt to explore the biosystematic relationships of *K. gobicola* and *K. zhaosuensis* with *R. tsukushiensis*, the artificial hybrids were made from *R. tsukushiensis* crossed with *K. gobicola* and *K. zhaosuensis*. The morphological and cytological analyses of these hybrids are reported in the present paper.

Materials and methods

The species used for morphological analysis and intergeneric hybridizations in the present study were collected in 1987. The experimental materials are listed in Table 1.

Table 1. The experimental materials

Species	2n	Collection site	Collector	Code No.
Kengyilia gobicola Yen et J. L. Yang	42	Tashiquerqan, Xinjiang	Yen et al.	Y665
K. zhaosuensis J. L. Yang, Yen et Baum	42	Zhaosu, Xinjiang	Yen et al.	Y803
R. tsukushiensis	42	Yaan, Sichuan	Yang et al.	Y83017

Roegneria tsukushiensis (Honda) Lu B. R., Yen et J. L. Yang was used as male parent. The spikes of *Kengyilia gobicola* Yen et J. L. Yang and *K. zhaosuensis* J. L. Yang, Yen et Baum were emasculated and covered with cellulose bag. The hand-emasculated spikes were pollinated two days later by brushing maternal stigmas with newly broken anthers of the paternal species. Caryopses showing enlargement at 14 days were excised for embryo culture. Seedlings at the three leaves stage were transplanted into sand culture pots, watered with complete nutrient solution, and kept in low temperature room over summer.

Morphological characters were compared between the the parents and their F_1 hybrids.

For cytological observation, the young spikes were fixed in Carnoy's I solution (alcohol:acetic acid = 3:1), and stored in a refrigerator. Chromosome pairings were observed at the MI of the pollen mother cells (PMCs) using the aceto-carmine smear method. Photographs were taken by Olympus AD-10 camera system.

Voucher specimen of the parents and the F_1 hybrids have been kept in the nursery and the herbarium of Triticeae Research Institute, Sichuan Agricultural University.

Results

Production and morphology of F_1 hybrids: *K. gobicola* and *K. zhaosuensis* were used as female parents in crossing with *R. tsukushiensis*. The results are shown in Table 2. One well growing seedling was obtained by means of embryo culture for *K. gobicola* × *R. tsukushiensis* and *K. zhaosuensis* × *R. tsukushiensis*, respectively.

Table 2. The results of crosses between the two *Kengyilia* species and *R. tsukushiensis*

Combinations	No. of spikes crossed	No. of florets pollinated	Seed set		No. of embryos cultured	No. of plants obtained
			No.	%		
K. gobicola × *R. tsukushiensis*	1	40	6	15	6	1
K. zhaosuensis × *R. tsukushiensis*	1	44	2	4.5	2	1

Eighteen morphological characters of the parents and the hybrids were observed and measured as shown in Table 3. Number of spikelets per spike and florets per spikelet in *R. tsukushiensis* are more than those in *K. gobicola* and *K. zhaosuensis*. Lengths of spike, spikelet, awn on lower and upper glumes, lemma and awn on lemma, and palea of *R. tsukushiensis* were longer than those of *K. gobicola* and *K. zhaosuensis*. The lower and upper glumes of *R. tsukushiensis* are as long as those of *K. gobicola*, while shorter than those of *K. zhaosuensis*. The lemmas and rachis of *K. gobicola* were pubescent, while those of *R. tsukushiensis* were glabrous. The lemmas of *K. zhaosuensis* was pubescent. The F_1 hybrids of *K. gobicola* x *R. tsukushiensis* and *K. zhaosuensis* × *R. tsukushiensis* were intermediate between their parents in morphology. Since *K. gobicola* and *K. zhaosuensis* are distributed in arid area of Xinjiang, they could not endure the summer of subtropic climate of Dujiangyan city, Sichuan, while *R. tsukushiensis* and its hybrids crossed with *K. gobicola* and *K. zhaosuensis* could adapt to this condition.

Cytology: The data of chromosome pairings at metaphase I of PMCs in the two cross combinations are shown in Table 4. The chromosome configurations are shown in Figures 1 to 10.

Both of the hybrids of *K. gobicola* × *R. tsukushiensis*, and *K. zhaosuensis* × *R. tsukushiensis* had 42 chromosomes. They had similiar meiotic pairing patterns. A large number of univalents were found in the two cross combinations, i. e., on average, 18.69 univalents per cell for *K. gobicola* × *R. tsukushiensis*, and 18.56 univalents per cell for *K. zhaosuensis* × *R. tsukushiensis*. The average number of bivalents were 11.56 with the range of 7 to 14 for *K. gobicola* × *R. tsukushiensis*, and 11.73 with the range of 8 to 14 for *K. zhaosuensis* × *R. tsukushiensis*. A low frequencies of trivalents were also observed in both combinations with the average of 0.04 per cell. The chiasmata frequencies in *K. gobicola* x *R. tsukushiensis* and *K. zhaosuensis* × *R. tsukushiensis* were 17.44 and 17.41, respectively. The lagging chromosomes at anaphase I and II, and tetrads with micronuclei were observed in both combinations. Chromosome bridges at anaphase I and II were found in the hybrid of *K. zhaosuensis* × *R. tukushiensis*.

Table 3. Morphological characteristics of *K. gobicola*, *K. zhaosuensis*, *R. tsukushiensis*, and their hybrids on eighteen characters

Character	*K. gobicola*	*K. gobicola* × *R. tsukushiensis*	*R. tsukushiensis*	*K. zhaosuensis* × *R. tsukushiensis*	*K. zhaosuensis*
No. spikes/plant	9.29±1.83	13.0±2.31	21.64±3.04	25.40±1.52	14.40±1.82
No. florets/spikelet	5.91±0.83	4.86±0.54	7.34±1.28	4.22±0.61	4.71±0.49
Length of spike (cm)	8.24±2.62	15.9±1.65	21.14±2.70	19.44±1.17	13.38±2.59
Length of spikelet (cm)	1.47±0.08	1.52±0.14	2.19±0.17	1.14±0.10	1.61±0.16
Length of the 1st glume (cm)	0.66±0.08	0.68±0.05	0.61±0.07	0.76±0.05	1.10±0.09
Breadth of the 1st glume (cm)	0.25±0.04	0.20±0.01	0.17±0.02	0.20±0.01	0.27±0.03
Length of awn on the 1st glume (cm)	0.07±0.03	0.07±0.03	0.80±0.39	0.21±0.05	0.10±0.05
No. nerves of the 1st glume	5.60±0.52	4.75±0.46	4.50±0.57	5.27±0.45	5.44±0.51
Length of the 2nd glume	0.57±0.10	0.57±0.04	0.53±0.06	0.66±0.06	1.03±0.07
Breadth of the 2nd glume	0.24±0.05	0.18±0.02	0.15±0.02	0.19±0.01	0.25±0.03
Length of awn on the 2nd glume (cm)	0.07±0.03	0.06±0.02	0.91±0.24	0.12±0.04	0.07±0.04
No. nerves of the 2nd glume	3.86±0.53	3.25±0.46	3.10±0.30	4.08±0.39	4.08±0.29
Length of the 1st lemma (cm)	0.80±0.06	0.86±0.03	0.93±0.05	0.86±0.03	0.96±0.13
Length of awn on the 1st glume (cm)	0.28±0.07	0.62±0.06	3.60±0.33	0.99±0.10	0.42±0.16
Length of palea (cm)	0.77±0.05	0.88±0.03	0.94±0.05	0.89±0.03	0.85±0.05
Hair on palea*)	++	++	––	––	+
Hair on rachis*)	+	+	––	––	––
Form of palea	truncate	truncate	obtuse	truncate	truncate

*) ++: dense hair, +: sparse hair, ––: hairless

Table 4. The average meiotic pairings at metaphase-I in the intergeneric hybrids of *K. gobicola* × *R. tsukushiensis* and *K. zhaosuensis* × *R. tsukushiensis*

Cross combinations	No. of cells observed	I	II			III	Xta
			Total	Rod	Ring		
K. gobicola × *R. tsukushiensis*	55	18.69 (13–28)	11.56 (7–14)	5.76 (1–10)	5.80 (0–10)	0.04 (0–1)	17.44
K. zhaosuensis × *R. tsukushiensis*	104	18.56 (14–26)	11.73 (8–14)	6.13 (0–10)	5.60 (1–10)	0.01 (0–1)	17.41

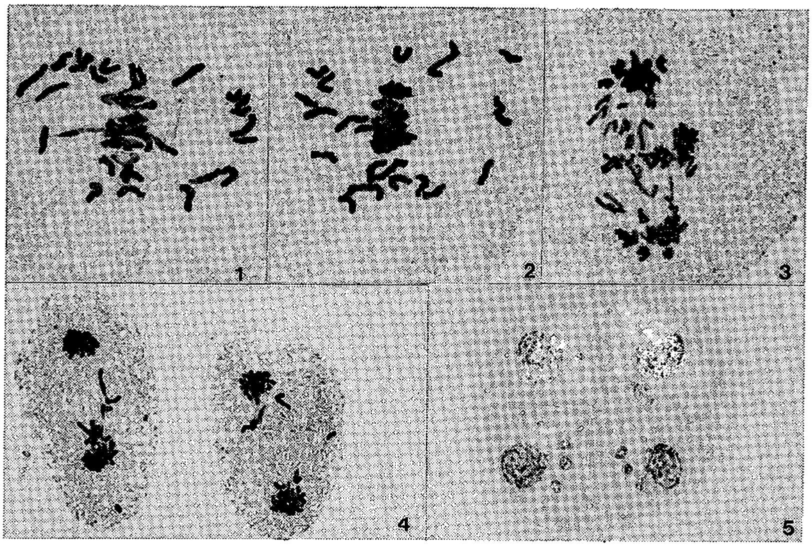

Fig. 1-5. Meiosis in the hybrid of *Kengyilia gobicola* × *Roegneria tsukushiensis*. 1: 23 univalents + 8 bivalents + 1 trivalent at MI. 2: 20 univalents + 11 bivalents at MI. 3: Lagging chromosomes at anaphase I. 4: Lagging chromosomes at anaphase II. 5: Tetrad with micronuclei

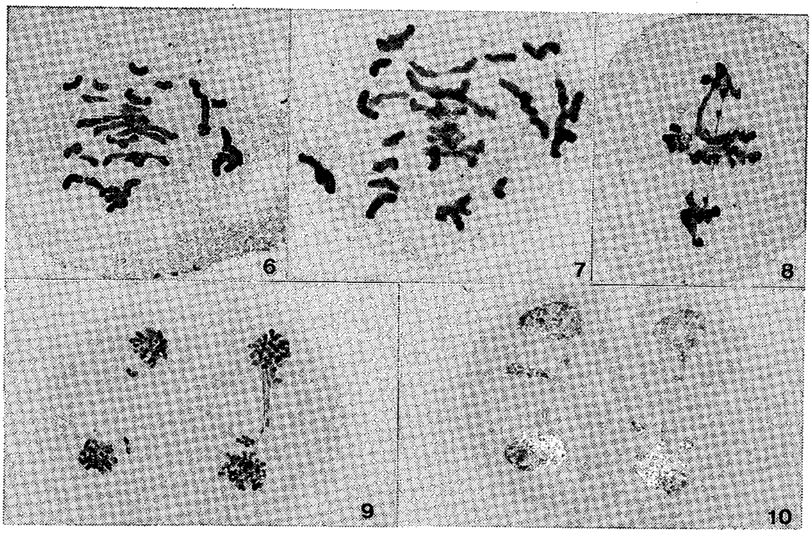

Fig. 6-10. Meiosis in the hybrid of *Kengyilia zhaosuensis* × *Roegneria tsukushiensis*. 6: 22 univalents + 10 bivalents. 7: 24 univalents + 9 bivalents. 8: Lagging chromosomes and chromosome bridge at anaphase I. 9: Lagging chromosome and chromosome bridge at anaphase II. 10: Tetrad with micronuclei

Discussion

K. gobicola and *K. zhaosuensis* are new species which were found in west China in recent years. Their genomes were not analysed. Their karyotypes showed that they possess a set of long chromosomes, which can be distinguished clearly from H, S, and Y genomes. The fourth and sixth chromosomes of karyotypes were satellite chromosomes which were similiar to those of P genome of *Agropyro*n (Yen et al. 1989, 1990). According to the karyotypes, Yen and J. L. Yang (1989, 1990) infer that *K. gobicola* and *K. zhaosuensis* have the P genome and two sets of other genomes.

R. tsukushiensis has the S, H and Y genomes (Sakamoto 1964, Dewey 1984, Lu et al. 1990). The frequencies of 11.56 and 11.73 bivalents per cell were found in the hybrids of *K. gobicola* and *K. zhaosuensis* crossed with *R. tsukushiensis* respectively. The results indicated that *K. gobicola* and *K. zhaosuensis* share two sets of genomes of *R. tsukushiensis* and the two genomes of *K. gobicola* and *K. zhaosuensis* have high homology with the two genomes of *R. tsukushiensis*.

Chromosome bridges at anaphase I and II were found in meiosis of *K. zhaosuensis* × *R. tsukushiensis*. It showed that paracentric inversion probably occurred between the genomes of *K. zhaosuensis* and *R. tsukushiensis*.

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Wheat Information Service
Number 78: 34 – 38 (1994)

Crossability percentages of bread wheat landraces from Hunan and Hubei provinces, China with rye

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Introduction

Our previous papers (Luo et al. 1992, 1993a, 1993b) reported the crossabilities of landraces from Sichuan, Shaanxi and Henan Provinces and the Tibet Region, China and their geographical distribution, and revealed that landraces with high crossability widely exist in the regions of Sichuan, Shaanxi and Henan, but rare in Tibet region. As the extendence of the previous ones, the present paper reports the crossabilities of landrace accessions from Hunan and Hubei Provinces, China.

Materials and methods

Ninety-four accessions of wheat landraces (*Triticum aestivum* L.) were grown from seeds, of which 44 landraces from Hunan Province and 50 landraces from Hubei Province, China were kindly provided by Mr. Shiqiang Yun of Crop Institute of Hunan Academy of Agricultural Sciences and Mr. Qichang Zhang of Institute of Modernization of Hubei Academy of Agricultural Sciences, respectively. The inbred line of Qinling rye (*Secale cereale* L.) was used as male tester in the crosses. The emasculation and pollination techniques were as reported earlier (Luo et al. 1992). Thirty days after pollination, the number of florets with and without seeds were recorded for each spike. The data are expressed as the percentage of successful crosses over the total number of florets pollinated. The *t*-test was adopted to detect the crossability differences between a wheat landrace and the control (Chinese Spring).

Results and discussion

As the landraces were tested separately in 1991-1992, the crossability percentage of Chinese Spring in the year was applied in the *t*-test.

1. The crossabilities of wheat landraces from Hunan Province: The crossability percentages with rye of 44 wheat landraces from Hunan Province, China were investigated in 1991 (Table 1). The crossability percentages of Chinese Spring with rye in 1991 (73.0%) was used for comparison with those of landraces.

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Table 1. Crossability percentages of wheat landraces from Hunan Province, China with rye

	Landrace	Crossability percentage	No. florets pollinated	Locality
	Chinese Spring	73.0	100	(Sichuan)
***	Fangmai (HN 11)	81.8	99	Yongxing
****	Youmang Hingkemai (HN 7)	95.0	99	Rucheng
*	Baikemai (HN 9)	0.0	100	Rucheng
****	Baikemai (HN 1)	95.0	100	Linwu
****	Huangkemai (HN 5)	95.0	100	Jiahe
****	Duanzuimai (HN 6)	94.0	100	Jiahe
****	Linwu Fangmai (HN 2)	93.0	100	Yizhang
**	Chimianmai (HN 3)	54.0	100	Yizhang
***	Chimian Xiaomai (HN 4)	82.0	100	Yizhang
**	Hongke Youmangmai (HN 10)	32.3	99	Zixing
***	Bendi Xiaomai (HN 15)	76.0	100	Jiangyong
***	Hongke (HN 30)	81.0	100	Qiyang
***	Mimai (HN 51)	77.0	100	Chaling
*	Heshangmai (HK 53)	0.0	100	Liling
**	Taijiang Xumai (HN 56)	23.0	100	Taojiang
**	Yangxiaomai (HN 54)	11.0	100	Xiangtan
**	Beni Heshangmai (HN 63)	12.0	100	Qianyang
***	Huangmai (HN 62)	70.0	80	Huitong
**	Wugang Xiaomai (HN 64)	58.0	100	Wugang
**	Guanglaomai (HN 66)	22.0	100	Mayang
****	Hongkemai (HN 20)	85.0	100	Xintian
*	Yangmai (short-awned) (HN 70)	1.0	99	Mayang
***	Yukamai (HN 67)	63.0	100	Mayang
*	Yangmai (HN 68)	0.0	100	Mayang
**	Fangmai (HN 12)	15.2	99	Leyang
***	Hongnianmai (HN 17)	75.0	100	Lanshan
***	Hongkemai (HN 19)	76.0	100	Ningyuan
***	Jianghua Xiaomai (HN 14)	77.8	99	Jianghua
**	Guichuyimai (HN 18)	30.0	100	Lanshan
****	Hongke Xumai (HN 21)	90.0	100	Xintian
**	Dazhong (HN 22)	13.1	99	Hanling
*	Hongkemai (HN 27)	2.0	100	Qiyang
**	Daoshimai (HN 36)	54.0	100	Xinning
***	Sifangmai (HN 28)	70.0	100	Qiyang
***	Heshangmai (HN 35)	82.0	100	Hengyang
*	Heshangmai (HN 42)	1.3	80	Shaodong
*	Yangmai (awnless) (HN 69)	4.0	100	Mayang
**	Heshangmai (HN 37)	5.0	100	Wugang
***	Hongkemai (HN 29)	68.0	100	Qiyang
**	Baiyang Mianmai (HN 50)	16.3	80	Lianyuan
**	Hongxumai (HN 43)	10.0	100	Shaodong
**	Heshangmai (HN 39)	6.0	100	Shaodong
*	Heshangmai (HN 40)	0.0	100	Longhui
***	Hongxu Xiaomai (HN 41)	63.0	100	Longhui

Note: *: No or very low crossability; **: low crossability, significantly lower than CS; *** same level of crossability as CS; ****: significantly higher crossability than CS.

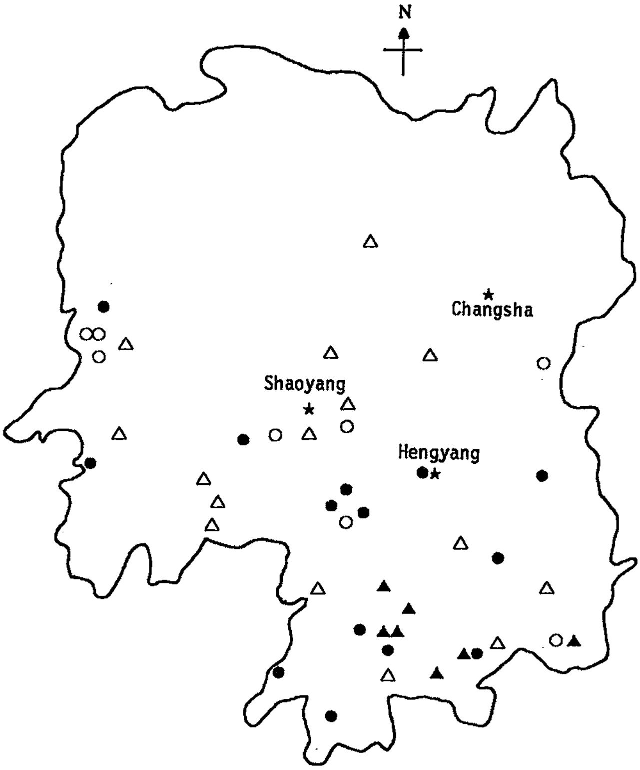

Fig. 1. The geographical distribution of crossability of wheat landraces in comparison with Chinese Spring (73%) in Hunan, China
○ <5%, △ ≥5%<73%, ● ≒73% (Chinese Spring), ▲ >73%

Of the 44 landraces involved in this investigation, seven showed much higher crossabilities than Chinese Spring, 14 had similar crossabilities to Chinese Spring, and 23 presented lower or no crossabilities with rye. The landraces with much higher crossabilities than or similar to Chinese Spring frequently occurred in the central and southern parts of the Province (Fig. 1).

2. The crossabilities of wheat landraces from Hubei Province: The crossability percentages with rye of 50 wheat landraces from Hubei Province, China were investigated in 1992 (Table 2). The crossability percentages of Chinese Spring with rye in 1992 (77.0%) was used for comparison with those of landraces.

Among 50 landraces from Hubei Province, four accessions showed much higher crossability than the Chinese Spring, seven had similar crossability to Chinese Spring and 39 presented lower or no crossabilities with rye. The landraces with much higher crossabilities than and similar to

Table 2. Crossability percentages of wheat landraces from Hubei Province, China with rye

	Landrace	Crossability percentage	No. florets pollinated	Locality
	Chinese Spring	77.0	100	(Sichuan)
**	Huoshaotou	27.0	100	Yingshan
**	Baimang Dazi	58.3	60	Yingcheng
*	Jinda	2.0	100	Xiangning
**	Zhaoliang	13.8	80	Jiayu
***	Shuibianzhi	78.3	106	Tongshan
*	Gulao Bianzhongxiaomai	2.5	80	Chongyang
***	Heshangtou	86.0	100	Tongcheng
***	Qitoumai	87.5	80	Yangxin
*	Changxumai	1.0	100	Daye
*	Baixiaomai	2.0	100	Huanggang
*	Bagutao	2.0	100	Xishui
*	Paomai	2.0	100	Hong'an
**	Jiyupuo	48.0	100	Macheng
****	Changshamai	96.0	100	Luotian
****	Bagutao	90.0	100	Huangmei
**	Hongmaoqiu	55.0	60	Xincun
****	Hongxu	92.2	102	Guangji
***	Baimang Guangtoumai	85.0	100	Zhongxiang
***	Honghuazao	88.2	102	Jianli
**	Heshangmai	49.0	100	Yichang
*	Xiaoganmai	1.3	80	Dangyang
*	Sanli Yicun	3.0	100	Yidu
**	Bendixiaomai	55.0	100	Wufeng
*	Maogan	0.0	100	Xingshan
*	Baimangmai	3.0	100	Zigui
**	Dabaimang	28.0	100	Xiangyang
*	Sanyuehuang	0.0	100	Zhaoyang
*	Wuyuezao	1.0	100	Yicheng
**	Qianjinbudao	38.4	86	Guanghua
**	Huoliaotou	10.0	100	Gucheng
*	Yixishi	0.0	80	Nanzhang
***	Baiyumai	33.9	112	Yunxian
**	Hongmangmai	17.0	100	Baokang
**	Baimangmi	6.3	80	Zigui
**	Erchiban	40.6	106	Yunxi
**	Baimaizi	11.0	100	Yunxian
**	Maiyumai	14.3	98	Yunxian
**	Heshangtou	52.0	100	Zhushan
*	Dahongmang	2.0	100	Zhuxi
**	Baodijia	6.0	100	Fangxian
***	Quanmangmai	72.0	100	Shennongjia
**	Nanshan Xiaomai	5.8	104	Shennongjia
**	Hongmangmai	54.0	100	Shennongjia
**	Wuojiaomai	39.0	100	Enshi
**	Baimang Guangtoumai	49.0	100	Zhongxiang
*	Hongpimai	0.0	100	Jianshi
*	Sanyuehuang	0.0	100	Xuan'en
**	Heshangtou	44.0	100	Lichuan
***	Jiyubao	67.7	100	Xiangfeng
*	Baikejiang	6.7	104	Laifeng

Note: The star(s) refer to the crossability as shown in the footnote in Table 1

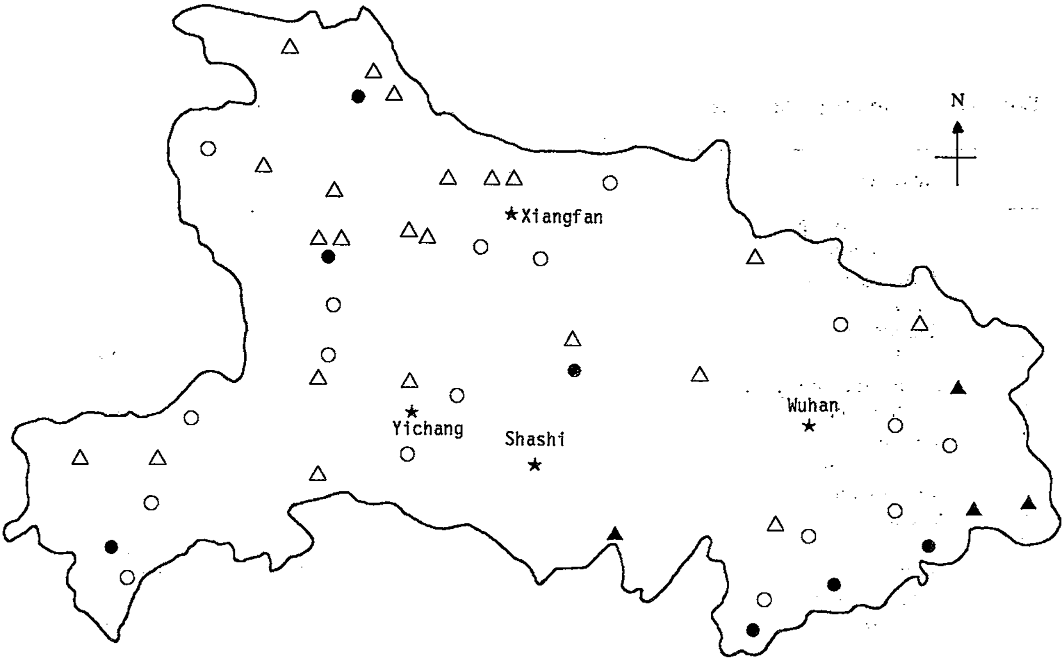

Fig. 2. The geographical distribution of crossability of wheat landraces in comparison with Chinese Spring (77%) in Hubei provice, China
○ <5%, △ ≥5%<77%, ● =77% (Chinese Spring), ▲ >77%

Chinese Spring were widely distributed in the Hubei Province, China (Fig. 2).

From the investigation, it is clear that the distribution of high crossability landraces in Hunan and Hubei provinces is geographically continuous with that in Sichuan, Shaanxi and Henan Provinces, China (Luo et al. 1992, 1993a).

Acknowledgments

The authors are highly thankful to the National Science Foundation of China and IBPGR, FAO, UN, for their financial supports. The helps of Mr. S. Q. Yun and Mr. Q. C. Zhang in providing landraces samples, and Ms K. H. Peng, Mr. S. H. Han, Mr. B. Shuai and Ms. Z. Jiang in emasculation work are gratefully acknowledged.

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Luo MC, Yen C and Yang JL (1993a) Crossability percentages of bread wheat landraces from Shaanxi and Provinces, China with rye. Euphytica 67: 1-8.

Luo MC, Yen C and Yang JL (1993b) Crossability percentages of bread wheat collections from Tibet, China with rye. Euphytica 70: 127-129.

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III. Record

The 24th wheat genetics symposium Japan

On 29th of March, 1994, at Kyoto, the 24th Wheat Genetics Symposium Japan had been held, organized by Dr. Kozo Nishikawa (Kihara Memorial Foundation), where about 50 Japanese wheat geneticists and breeders had discussed on the subject of genetic stock conservation and its network construction in wheat and its related species. Because of the tradition of wheat researches in Japan, they are proud of conserving various genetic stocks including wild spcecies accessions, artifical amphiploids, aneuploids, cytoplasmic substitution lines, and chromosome deletion lines. The symposium concluded that these genetic stocks were common properties for plant reserchers of the world, and should be maintained cooperatively under an international network system. They agreed to organize a working group for initiating the construction of a network for wheat genetic stock conservation.

The program of the symposium was as follows;

Special Lectures.

I. Preservation of barley genetic stocks in Okayama University.
   Dr. Shozo Yasuda (Okayama Women's College).
II. Cereal improvement at ICARDA — An international approach.
   Dr. Muhammad Tahir (ICARDA)
III. On the concept and practise of networking.
   Dr. Hirotoyo Ishii (University of Library Science)

Reports

1. Wheat genetic resources conservation in Ministry of Agriculture, Forestry and Fishery of Japan: Toshiaki Yamada (Agriculture Research Center)
2. A declaration on genetic stocks by Japan Academy: Koichiro Tsunewaki (Kyoto University)
3. Function of Germplasm Institute, Kyoto University: Sadao Sakamoto (Kyoto University)
4. Problems concerning conservation of aneuploid series: Yoshihiko Furuta (Gifu University)
5. Short reports on the present status of genetic stock and DNA clone conservation
   (1) Oversea: Wheat Germ Resource Center (Kansas State Univ.) by T. R. Endo (Nara Univ.).
   (2) Domestic: DNA clones by Y. Ogihara (Yokohama City Univ.), T. Terachi (Kyoto Sangyo Univ.), Seeds by T. Shimada and K. Murai (Ishikawa Agri. Coll.), K. Tsunewaki (Kyoto Univ.), T. Sasakuma and H. Tsujimoto (Yokohama City Univ.), N. Nakata (Tottori Univ.), C. Nakamura (Kobe Univ.), J. Fujigaki (Tokyo Agri. Univ.), K. Kato (Kochi Univ.), A. Yanagisawa (Hokkaido Pref. Genetic Resource Center), T. Morikawa (Osaka Pref. Univ.), K. Nishikawa (Kihara Memorial Found.)

The content of Dr. Tahir's lecture is literated as shown in the review article of WIS 78. The summaries of lectures by Drs. Yasuda and Yamada are outlined in the follwing pages.

Preservation of Barley Genetic Stocks in Okayama University

Shozo Yasuda

Okayama Women's College
Ariki 787, Kurashiki 710, Japan

Cultivated barley ranks fourth in world cereal production. Barley is also known to be the most progressing crop for gene analysis after maize and tomato. Many morphological and physiological characters of barley are rather easy to distinguish, and are governed by major gene or genes. Sogaard et al. (1982), as a master list of barley genes, have cited more than 900 genes including about 400 genes of which are evident in their related chromosomes. These traits will prove the usefulness of barley as an experimental organism for genetics, mutation, molecular biology and so on.

I will here introduce outlines of the Barley Germplasm Center of Research Institute for Bioresources, Okayama University, which was established in 1979. About 4,000 barley varieties collected from around the world by Dr. R. Takahashi, Emeritus Prof. of Okayama University, were preserved as the base of the collection. The contents of the collection at present and the activities of the Center are as follows:

1. Cultivars (ca. 5,300: *Okayama University accession code)

Country, Region	Code*	No.	Country, Region	Code*	No.
Japan	(OUJ)	781	Turkey	(OUT)	835
Korea	(OUK)	491	Europe	(OUU)	523
China	(OUC)	205	Africa	(OUB)	313
Nepal	(OUN)	438	Ethiopia	(OUE, F)	976
India & S.W. Asia	(OUI)	556	Others	(OUA)	151

2. Wild species (OUH): 274 strains of 25 species, including *H. spontaneum*, *H. bulbosum*, *H. murinum* and so on.

3. Mutants (OUM): 421 spontaneous and induced mutants.

4. Linkage testers (OUL): 172 lines including those from barley geneticists overseas and from the genetic analyses made at the Institute. Two sets of trisomic lines (*H. spont.* transcaspicum and Shin Ebisu 16) which were identified by Dr. T. Tsuchiya.

5. Near-isogenic lines: A total of 403 near-isogenic lines made by two methods of repeated selfing for heterozygotes and of repeated backcrossings. These lines are isogenic to so-called genetic

backgrounds, except for any of the genes, *uz* (semi-brachytic growth), *n* (naked kernal), *v* (six-row), *l* (dense spike), lk_2 (short awn), *K* (hooded appendage), *sh*, Sh_2, Sh_3 (spring growth habit), *dw*'s (dwarfness), etc.

6. Tetraploid lines: 22 lines from around the world.

7. Principal materials under investigation: 500 cvs from the Hokkaido Pref. Agr. Sta., Japan. 350 cvs and 450 mutants from Agr. Res. Center, Japan. 400 naked landraces from Tribhuwan Univ., Nepal.

8. Storage of the materials: (a) short-term storage of active seeds in polyethylene bottles (15°C), (b)medium-term storage of active seeds in metal cases (15°C), and (c)long-term storage of original seeds in polyethylene boxes (–18°C).

9. Activities: The database has been established for about 5,300 cvs with 30 items for morphological, physiologial and genetic characteristics. As for 4023 of those cultivars, detailed information has been published in the "Catalogue of Barley Germplasm Preserved in Okayama University, 1983". The Center has been updating the system to the software 'UNIFY' in workstation to allow users in other facilities connection to the computer network.

Conservation of Wheat and Barley Genetic Resources in MAFF

Toshiaki Yamada

National Agriculture Research Center
Kanondai 3-1-1, Tsukuba 305, Japan

The current number of germplasm of wheat, barley, oats, rye, triticale and their relatives preserved in the Center Bank of the National Institute of Agrobiological Resources, Tsukuba, is shown in Table 1. A part of them is also preserved in the Sub-Banks of the National Agricultural Experiment Stations including the National Agriculture Research Center. Some dozens of *Elytrigia* and *Elymus* clones are preserved in the Sub-Bank of the Kyushu National Agricultural Experiment Station. Almost two hundred clones of *Hordeum bulbosum* L. are preserved in the Sub-Banks of National Agriculture Research Center, Shikoku National Agricultural Experiment Station, National Center for Seeds and Seedlings, etc. They have been collected mainly by collecting missions and international exchange.

Table 1. Number of accessions of wheat, barley, oats, rye, triticale and their relatives preserved in the Center Bank of National Institute of Agrobiological Resources of Japan (March 31, 1993)

Species	No. of accessions	
	Base collection	Active collection
Triticum aestivum (L.) Thell.	18274	13433
Triticum compactum Host.	48	48
Triticum dicoccoides Koern.	1	1
Triticum dicoccum (Schrank.) Schubl.	6	6
Triticum durum Desf.	4781	272
Triticum monococcum L.	1	1
Triticum polonicum L.	1	1
Triticum spp.	998	0
Triticum spelta L.	13	13
Triticum turgidum L.	5	5
Hordeum agriocrithon E. Aberg	2	2
Hordeum leiorrhynchum Koern.	1	1
Hordeum spontaneum C. Koch	31	31
Hordeum vulgare L.	10364	6292
Hordeum vulgare L. var. *distichon*	1838	1831
Aegilops aucheri Boiss.	56	56
Avena abyssinica Hochst	1	1
Avena barbata Pott	2	2
Avena brevis Roth	1	1
Avena byzantina C. Koch	3	3
Avena fatua L.	9	9
Avena hirtula Lag.	1	1
Avena longiglumis Dur.	1	1
Avena magna Murphy et Terrell	2	2
Avena murphyi Ladizinsky	1	1
Avena nuda L.	1	1
Avena orientalis Schreb.	1	1
Avena sativa L.	1086	1086
Avena sp.	15	15
Avena sterilis L.	4	4
Avena wiestii Schreb.	2	2
Secale cereale L.	44	44
Triticum sp. × *Secale* sp.	52	52

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IV. Information

1. **Seventh International Symposium, Pre-harvest Sprouting in Cereals** (July 2-7, 1995; Abashiri, Japan)
See details in WIS No. 77. To receive the first announcement, contact the Secretariat or Dr. Walker-Simmons.

Secretariat; Kitami Agricultural Experiment Station, Kunneppu, Hokkaido 099-14, Japan; telephone +81-157-47-2146, fax +81-157-47-2774.

Dr. M. K. Walker-Simmons: USDA-ARS, 209 Johnson Hall, Washington State University, Pullman, WA 99164-6420; telephone +1-509-335-8696, fax. +1-509-335-8674, e-mail simmons@wsuvml.edu.

2. **Agri-Food Quality '95** (June 25-28, 1995; University of East Anglia, UK)
There are increasing opportunities for improving the quality of plant-derived foods by exploiting conventional and molecular biological approaches to plant breeding. Effective responses to this challenge, which address complex scientific problems, are best tackled by the development and exploitation of integrated interdisciplinary research activities. The aim of this meeting is to bring together those involved in R and D across the plant-, food- and biological sciences, consumer scientists, representatives of the agro-food industries, and regulatory agencies to evaluate progress at interface of agriculture and food, to identify research opportunities and to discuss possibilities for extending effective interdisciplinary collaboration. These issues will be addressed through a programme of plenary sessions, contributed papers and posters, and workshops. In finalizing the programme, emphasis will be placed on contributions which cross disciplines.

Programm Topics to be covered will include: Manipulation of crop to improve the quality of plant foods; nutritional quality, fitness for storage and processing, organoleptic/texture quality. Manipulation of storage components (starch, protein, lipid) for food. Consequences for food quality of improving "natural resistance" of crops. Improvement of plant food quality in less-favoured regions. Opportunities for "adding value" - nutriceuticals, functional foods, novel foods. Consumer attitudes to improving crop and food quality. To receive first announcement and detailed information, contact to the secretariat:
Agri-Food Quality '95, Institute of Food Research, Norwich Research Park, Colney, Norwich NR47UA, UK. Telephone: +44(0)603 255000, Fax: +44(0)603 507723

3. **Catalogue of Wheat Experimental Strains maintained in the universities and institutes in Japan** (pp. 150)
The catalogue listing 2547 wheat experimental strains can be now available from;
Dr. Y. Tateno, Laboratory of Genetic Resources, National Institute of Genetics, Mishima, Shizuoka-ken 411, Japan. Telephone: +81-559-75-0771, Fax: +81-559-71-3651, Cable: GENETICS MISHIMA.

4. **Seventh European Congress on Biotechnology** (February 19-23, 1995; Nice, France) Second announcement of this congress is available from; ECB 7, c/o Societe de Chimie Industielle, 28, rue Saint-Dominique, F75007, Paris, France.

   This congress includes scientific aspects of plant biotechnology, agronomy, food and feed sciences other than microorganisms and animal biotechnology, and socio-economic studies. Persons wishing to present a poster communication are invited to send before September 15, 1994 a summary of their presentation, on the attached form of the second circular.

V. Editorial remarks

Last September, from the replies submitted to a questionnaire, we realized that in addition to those preserved in Plant Germplasm Institute, Kyoto University, not less than 1,000 lines and accessions of various kinds of genetic stocks and DNA clones in wheat and related genera have been preserved in universities and institutes in Japan. The fact encouraged us to organize the 24th Wheat Genetics Symposium Japan, "Genetic stock conservation and its network construction", held on March 29, 1994, in Kyoto. The report of the symposium was made in this issue.

For articles for information, including meeting notice, book advertisement, or announcement, you can use facsimile to send the manuscripts through the number, 45-743-2833 (Country code of Japan is 81).

The next issue (No. 79) will be published in December, 1994. Your further contributions will be very appreciated.

The mailing list for subscription is, now, being renewed. Please see the attached sheet in No. 77.

Letter to Editor

Oeiras, May 9 1994

Dear Editor:

It is with great pleasure that I add a few lines to my "Renewal of Registration".

I would like to congratulate you for the 40th anniversary of WIS and for the article on Prof. Kihara, on the occasion of his centennial, in the November 1993 issue.

I remember well, among other pleasant memories of Prof. Kihara, a lunch I had with him and Dr. Flora Lilienfeld, a few days after the excellent International Genetics Symposium, in 1956. And I treasure the autographed copy on his 1924 work on "Cytologische und genetische Studien ..." he offered me on that occasion.

I believe WIS is such a good and well known name that no change is necessary for its prestige. However, "Wheat Science" or "Journal of Wheat Research" are also very good names.

I certainly agree that any papers on molecular analysis concerning wheat and its relatives should be included, as all the other subjects.

Once more, my congratulations and the best wishes of continuation of success.

Yours sincerely
Prof. Miguel Mota
Department of Genetics, Estação Agronómica Nacional
P-2780 Oeiras, Portugal

International Advisory Board

Editional Board

Explanation of the picture on the cover

Meiosis in the hybrid of *Kengyilia gobicola* × *Roegneria tsukushiensis*. See the articile by G. L. Sun et al. for the details.

WIS No.78

編集　国際小麦研究連絡会議
西川浩三

発行所　木原記念　横浜生命科学振興財団
〒232　横浜市南区六ツ川3–122–20
Tel. (045) 721–0751

発行日　1994年　6月　27日

印刷　株式会社　野毛印刷
Tel. (045) 252–2511

Wheat Information Service No. 78

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