Chapter 72

Use of Wild Triticeae Relatives for Stress Tolerance

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There are approximately 250 perennials among the 325 Triticeae species (Dewey, 1984) and relatively few of these have been hybridized with wheat. Those that have are predominantly included in the *Thinopyrum* group. Over the last decade and a half, phenomenal success has been achieved in the production of complex hybrids among the Triticeae, leading to a potential stock of invaluable alien genetic material introduced from distant hybridization.

Substantial information is available (Mujeeb-Kazi et al., 1991; Manyowa & Miller, 1991; Paull et al., 1991) relative to alien species contributions to stress tolerance. Many of these stress attributes would require situation specific improvement strategies because of local variation in stress patterns, climate, and user preferences. We have here selected three aspects: Al toxicity, Cu deficiency, and salinity; associating with these the potential contribution that alien variability may provide through classical or applied intergeneric and interspecific approaches. A few others are mentioned briefly. Keeping screening for the attributes as a routine prerequisite, the focus is heavily set upon incorporation of alien variation for *Triticum aestivum* L. involvement.

72-1 COPPER EFFICIENCY

Evaluation of Cu deficiency symptoms has been conducted at Cu levels ranging from 0 to 4.0 mg/pot (Graham, 1978) with an ultimate measure of grain yield. The reproductive phase is effected more than the vegetative (Graham, 1975). This screening led Graham to identify *Secale cereale* L. cv. Imperial as a Cu efficient source. Chromosome 5R from *S. cereale* disomically added to *Triticum aestivum* cv.

Chinese Spring (seed source: E. R. Sears) was further identified as being responsive and subsequently the 5RL rye arm of this chromosome addition was positively associated. CIMMYT obtained the 5AS/5RL translocation line from T. E. Miller (AFRC-IPSR, Cambridge) and used it as the male parent in crosses onto some CIMMYT spring wheat cultivars for generating the 5A, 5AS/5RL heterozygote F_1 combinations. Subsequent backcrossing (BC) of these F_1's with their respective recurrent parents up to BC VIII followed by an eventual selfing of the best heterozygote BC derivative results in elite *T. aestivum* near isogenic lines with the 5AS/5RL chromosome disomic. The 5AS/5RL heterozygote is identified at each BC through the morphological presence of the hairy peduncle (*hp*) marker mapped on 5RL, controlled by a dominant gene and effective in the hemizygous stage also. Differential C-banding checks on the heterozygote BC derivatives were integrated to ensure adequate advance accuracy. The Cu screening has been deferred until the BC program is completed, currently at BCIV.

72-2 COPPER TOXICITY

Since Cu is bound strongly to soil particles, occurrence of toxicity is rare. However, in acid soils over-fertilization and use in fungicide applications increase Cu toxicity. Though alternative remedial solutions exist, a mix with genetical inputs does have its advantage. Manyowa and Miller (1991) have identified *Th. bessarabicum* as a potent alien source to

contribute tolerant genes. *S. cereale* was another source identified, specifically chromosome 2R. Disomic additions allowed Manyowa and Miller to identify chromosomes 2J and 5J (also 2E^b and 5E^b) as tolerant contributing disomics. The potent 5J/6J (5E^bL/6E^bL) may well be a positive contributor because of 5E^bL. *Th. repens* has also been associated as a potential source; however, its hexaploid status may complicate its usage. Our focus will keep *Th. bessarbicum* at a priority, then utilize rye as a secondary source; clarification will emerge as we progress further into the paper.

72–3 ALUMINUM TOLERANCE

72–3.1 Screening

Direct observation of wheat seedling roots under Al stress was developed as a selection system by Polle et al. (1978), a methodology that has since been employed in CIMMYT and described (López-Cesati et al., 1986). The process is based on the fact that Al tolerance in wheat is largely a function of Al exclusion from the roots. Root tip growth, after immersion of the roots in a nutrient solution containing 46 ppm Al, followed by: (i) staining of the roots with 0.2% aqueous hematoxylin solution, (ii) observing continued root regrowth, and (iii) scoring on a 1 to 3 scale corresponded well with Al tolerance of the Triticeae germplasm.

Based upon the above screening schedule experiments were conducted using: (i) conventional germplasm, (ii) alien species with their wheat amphiploids, and (iii) some *S. cereale* cultivars (Table 72–1). The Al test levels were 0 and 46 ppm for (i) and (ii), and 0, 46, and 70 to 95 ppm for the *S. cereale* cultivars. Root regrowth scores after hematoxylin staining allowed for the estimation of the germplasms tolerance to Al at various concentration levels (Table 72–1).

Table 72–1. Triticeae germplasm screened for aluminum tolerance under laboratory conditions in hydroculture with percentage tolerance response.

Germplasm	Cultivars or accessions	Al concentration (mg/kg)			
		0	46	70	95
Conventional					
Triticum aestivum	Chinese Spring	100	24		
	CNT-1	100	100		
	Glennson 81	100	0		
	Maringa	100	100		
	Pavon	100	56		
Alien					
Parents and	Chinese Spring	100	20		
Amphiploids	*Aegilops variabilis*	100	90		
	T. turgidum cv Laru	100	0		
	CS/*Ae. variabilis*	100	82		
	Laru/*Ae. variabilis*	100	0		
Secale cereale	Short T–4776	100	100	95	65
	Sardev T–4777	100	100	100	90
	Doukala T–4778	100	100	100	95
	Turkey T–4779	100	100	100	90
	Prolific T–4781	100	100	100	90
	Blanco T–4783	100	100	95	95

72–3.2 Genetics and Wide Hybridization Studies

72–3.2.1 Genetic Studies

Earlier unpublished observations in our laboratory have provided information that cv. Glennson 81 is highly susceptible to Al at 46 ppm, cv. Chinese Spring is medium tolerant, with Maringa and CNT-1 being highly tolerant. Genes controlling Al tolerance in wheat have been reported to range from one to the additive effect of two or more genes, dominant in action, located genomically and chromosomally with variability across cultivars (see review and update by Manyowa & Miller, 1991). Since a monosomic series is now available in cv. Glennson 81, highly susceptible to Al, a monosomic study was designed using the CNT-1 cultivar as the tolerant parent. Glennson 81 monosomic plants with 41 chromosomes were cytologically identified and crossed with cv. CNT-1. The F_1 seed thus obtained is to form the basis of the subsequent monosomic analytical study.

72–3.2.2 Wide Hybridization Studies

With the effectiveness of the *ph1b* locus superbly demonstrated (Sears, 1977), its incorporation as the maternal parent in hybridization with *S. cereale* cultivars and *Aegilops variabilis* was considered as a practical route to improving wheat germplasm utilizing genetic variability from alien species. *S. cereale* cultivars are first being repeatedly screened, tolerant seedlings grown for controlled seed increase and after at least near homozygosity is achieved, hybridizations will be made to *T. aestivum* cv. Chinese Spring (*ph1b ph1b*). The *T. aestivum* × *Ae. variabilis* hybrid production, embryo excision, regeneration, transplanting, and cytological procedures for validation were identical to those described earlier (Mujeeb-Kazi & Miranda, 1985; Mujeeb-Kazi et al., 1987; 1989). The self-sterile F_1 hybrids were advanced by crossing with wheat and obtaining backcross (BCI) seed from which embryos had to be excised, presumably a consequence of the presence of the *ph* locus. Subsequent backcrosses formed reasonably well-filled seed, and embryo culture was not necessary. Cytological analysis of advanced BC derivatives was essential to facilitate selection of plants possessing 42 chromosomes and stable meiosis. Such normal BC selfed derivatives have not yet been achieved and even though somatic counts are 42 or close to it, the meiotic relationships are deviating highly from normalcy (Table 72–2). *Ae. variabilis* has also been hybridized with *T. aestivum* cv. Pavon with the *Ph* dominant locus. Backcrosses to Pavon and eventual selfings have resulted in numerous plants with 44 chromosomes with bivalent meiosis. The seed increase once completed will allow for Al screening to progress and hopefully identify alien chromosome/s associated with Al tolerance. Further incorporation, though time-consuming, will follow routine genetic manipulation procedures.

Alien species with the N genome have also been reported to possess Al tolerance (Berzonsky & Kimber, 1989) and though one could utilize *T. ventricosum* (DDNN) or *T. rectum* (UUMMNN) exploiting the diploid *T. uniaristata* (NN) is

Table 72-2. Meiotic metaphase I chromosomal pairing relationships in advanced derivatives of *T. aestivum* cv. Chinese Spring (*ph1b*)/*Aegilops variabilis*//CS (*ph1b*) n.

Chromosome no. of BCII selfed derivatives	Mean metaphase I chromosome associations					
	I	II Ring	II Rod	III	IV	V
40	6.6	13.3	2.4	0.4	0.2	—
41	3.0	16.8	1.9	0.2	—	—
41 (1 cell)	6.0	11.0	4.0	—	—	1.0
42	6.0	5.7	4.7	3.7	0.7	0.3
44	4.3	16.6	3.1	0.1	—	—
44	11.2	10.4	3.6	1.4	0.2	—

preferred. To the best of our information, no direct hybrids exist between *T. uniaristata* and *T. aestivum*, but with the current success of numerous divergent crosses, like wheat × maize (Riera-Lizarazu et al., 1992); achieving this hybrid combination should be relatively simple.

72–4 SALINITY TOLERANCE

Through a collaborative research program involving CIMMYT, AFRC-APSR, Cambridge Laboratory, and Bangor, University of Wales, several salt tolerant alien genera and conventional sources have been identified, and further substantiated by other literature reports (Table 72–3). This cumulative information has led to formulation of a comprehensive list of alien variability available for introgressing alien genes into wheat. Integration of alien variability requires

Table 72-3. Triticeae relatives with a promise for salinity tolerance based upon literature reports and collaborative research findings.

Germplasm designation	Polyploidy or origin	Reference
Conventional source		
T. aestivum cvs.		
Candeal	Mexico	
Kharchia 65	India	
KRL 1–4	India	
Lu 26S	Pakistan	
Pasban–90	Pakistan	
Sakha–8	Egypt	
Shorawaki	Pakistan	
SNH–9	India	
WH–157	India	
Yecora (Oasis)	Mexico	
Alien sources		
Th. elongatum† (*E. elongata*)	2n = 2x = 14	McGuire & Dvorak, 1981
Th. scirpea(*E. scirpea*)	2n = 2x = 28	McGuire & Dvorak, 1981
Th. elongatum(*E. pontica*)	2n = 10x = 70	McGuire & Dvorak, 1981
Th. junceiforme (*E. junceiformis*)	2n = 4x = 28	McGuire & Dvorak, 1981
Th. distichum (*E. disticha*)	2n = 4x = 28	McGuire & Dvorak, 1981
Th. bessarabicum†	2n = 2x = 14	Gorham et al., 1985
L. racemosus(*E. giganteus*)	2n = 4x = 28	McGuire & Dvorak, 1981
Aegilops squarrosa†	2n = 2x = 14	Gorham, 1990
Aegilops umbellulata	2n = 2x = 14	Gorham, 1990
Aegilops comosa	2n = 2x = 14	Gorham, 1990
Aegilops mutica	2n = 4x = 28	Gorham, 1990
Psathyrostachys junceа†	2n = 4x = 28	Dewey, 1984

†Of priority use in CIMMYT's Wide Crossing Program.

wheat × alien species hybridization as the initial step followed by a genetic integration methodology. The priority alien species include *Th. bessarabicum, Th. elongatum* (both diploids, $2n = 2x = 14$), and selected accessions of *T. tauschii* ($2n = 2x = 14$, DD). The former two species form the intergeneric hybridization category and the latter that of interspecific hybridization. Hybrid production and their advance procedures have been documented earlier (Mujeeb-Kazi et al., 1987; 1989; Mujeeb-Kazi & Asiedu, 1990). The hydroculture screening of advanced derivatives for salinity levels maintained by NaCl over regimes between 0 and 250 mol m⁻³, together with growth related parameters, and Na and K estimations for establishing K/Na discrimination values are identical to those adopted in the laboratory in Bangor, Wales (Gorham, 1990; Gorham et al., 1987) and closely followed at CIMMYT, Mexico.

72–5 TESTING OF CONVENTIONAL GERMPLASM

From the conventional wheat germplasm, we have established a testor set of cultivars that contains germplasm considered as salt tolerant with a few susceptible entries. Some of these entries have a long history of being classified as such—Chinese Spring, Kharchia 65, Lu26S, and have been extensively researched by several laboratories. One tolerant entry (Shorawaki) has been little publicized. Some still require rigid evaluations—Sakha 8, SNH-9, WH-157, Candeal, and the new Indian release (KRL 1–4), a derivative from a cross involving Kharchia 65, considered an elite cultivar for saline-sodic soils. It is reported to have superb growth and gives good yield even at pH 9.6 (K. N. Singh, 1991, personal communication). The susceptible cultivars included in the set were Yecora or Oasis and a durum PBW 34. In hydroculture tests conducted in Bangor (Table 72–4), Kharchia 65, Lu 26S, and Shorawaki exhibited desirable growth and ion content (K/Na) relationships. This trend was inconsistent for other cultivars.

It appears that with such a restricted conventional germplasm source available, additional genetic diversity occupies a significant place for wheat improvement. Even the promise that Kharchia 65 had for salinity and projections made from its use (Epstein et al., 1980), an impact leading to cultivar release from those derivatives did not occur. In an independent program, however, this has recently occurred. The KRL 1–4 cultivar is apparently the only cultivar that has

Table 72–4. Dry weight, Na and K content estimations from plant sap of some *Triticum aestivum* cultivars grown in 150 mol m⁻³ NaCl. Data measured after 50 d at full stress.

Cultivar	Dry weight	Na	K
	—g—	mol m⁻³	mol m⁻³
Shorawaki	2.69 ± 0.37	31 ± 3	198 ± 11
Lu 26S	2.04 ± 0.22	37 ± 5	227 ± 11
Kharchia 65	2.14 ± 0.23	71 ± 12	222 ± 14
Yecora	1.11 ± 0.19	69 ± 15	261 ± 18

been systematically bred using Kharchia 65 and released for cultivation. The acceptance of Lu 26S as a cultivar has still to gain a significant place for saline conditions, but it is inevitably an elite cultivar with superb attributes of the parental cultivar Lu 26. Its adoption may encounter competition from the release of PASBAN 90 in the same environment, a cultivar derived from *T. aestivum/Th. distichum//2* T. aestivum* after several selfings for normal duration planting in irrigated soils as well as saline sodic conditions. Though the pedigree reflects an alien species, its contribution is still undocumented.

There have been several reports on alien germplasm possessing salinity tolerance attributes. This germplasm provides optimism towards positive contribution of these resources for wheat improvement. The distant alien species that stand out as contributors for salt tolerance are *Th. elongatum* (2n = 2x = 14) and *Th. bessarabicum* (2n = 2x = 14). The former has been extensively investigated (Dvorak et al., 1988), with the promise of *Th. bessarabicum* well recognized (Gorham et al., 1985) but still removed from thorough utilization.

In hydroculture tests we re-evaluated some salt tolerant characteristics of these species and confirmed their positive attributes through amphiploids with *T. aestivum* cultivars (Table 72–5). The response at 200 mol m⁻³ confirmed tolerance. Even though diploid alien sources stand at a priority, we recognize that where diverse genomic distance prevails, the salt tolerant trait may not be simply inherited as evidenced from the observations of Dvorak et al. (1988) where three of the seven disomic additions of *Th. elongatum (Lophopyrum elongatum)* to wheat gave a positive salt tolerance response. This poses several constraints for introgressing genes from these three addition lines into wheat and a further constraint in transferring tolerance from Chinese Spring into a commercial cultivar that will contribute to agricultural productivity under global saline conditions. This inevitably will require an extended time frame to accomplish. We have added a different dimension in anticipation that the reciprocal cross (*Th. elongatum* × *T. aestivum*) may be better able to exploit the alien species cytoplasm, as well as give derivatives in an

agronomically superior plant type like Goshawk "S." With multiple alien chromosomes involved, the program is also designed to produce multiple disomics, incorporate the maize (*Zea mays* L.) mediated polyhaploid system and then manipulate the alien introgression by *Ph* locus suppression. There is much to be accomplished and an array of options could be infused in the methodology. For *Th. bessarabicum* (2n = 2x = 14), the current status has the disomic 5J addition to *T. aestivum* cv. Chinese Spring imparting salt tolerance. The 2J addition was susceptible and the amphiploid (2n = 8x = 56) salt tolerant (Forster et al., 1987; 1988). A wider acceptance of the reported positive effect of 5J is needed however, since results elsewhere have provided varied responses. We have proceeded to produce the complete addition set of seven chromosomes in a background superior to Chinese Spring. Additionally, since the species has also been considered as a source for Cu toxicity, and Al and Mn tolerance, completing the addition line set seems logical.

By backcrossing onto the F₁ hybrid (*T. aestivum* cv. Chinese Spring/*Th. bessarbicum*) with a commercial *T. aestivum* cultivar (Genaro 81) and selfing, several 44 chromosome derivatives have been selected. These meiotically stable (22 bivalents) derivatives possess superior agronomic characters, are highly fertile and tentatively encompass characteristics, based upon morphological, cytological, and biochemical diagnostics, that are associated with each of the seven wheat homoeologous groups (Table 72–6). Limited screening (Table 72–7) on some of these 44 chromosome derivatives (Mujeeb-Kazi, 1992) has identified a positive salt tolerance response for two disomic addition lines (3J and 7J) and a 3J/7J translocation derivative. These observations suggest the need for developing multiple disomic additions in

Table 72–6. *Thinopyrum bessarabicum* (2n = 2x = 14, JJ) disomic addition lines identified on the basis of cytological, morphological, and biochemical markers and tentatively assigned to seven homoeologous groups of *Triticum aestivum* L.

Tentative disomic line designation	Line characteristic		
	Cytological	Morphological	Biochemical
1J	44 (22 II)†		MDH and Glu
2J	44 (22 II)†	Tapering spike	SOD
3J	44 (22 II)†	Solid stem	EST
4J	44 (22 II)†	Blue aleurone	PGM (?)
5J	44 (22 II)†	Club shaped spike	β-AMY
6J	44 (22 II)†		GOT
7J	44 (22 II)†		α-AMY

†Mean relationships over 40 meiocytes estimated. Predominantly 22 bivalents observed.

Table 72–5. Dry weight, Na and K cell sap values in some wheat cultivars and their alien derivatives under hydroculture at 50 mol m⁻³, then at 200 mol m⁻³ NaCl. Growth data measured 50 d after reaching 50 mol m⁻³, Na + K measured in plants grown at 50 mol m⁻³ NaCl.

Cultivar and line	Dry Weight	Na plant sap	K plant sap
	-g-	mol m⁻³	mol m⁻³
Chinese Spring (CS)	4.42 ± 1.14	31 ± 3 (268 ± 21)	225 ± 5 (207 ± 4)†
CS/*Th. bessarabicum* (amphiploid)	2.30 ± 0.30	17 ± 2 (169 ± 28)	196 ± 7 (285 ± 8)†
Awnless + solid stem	3.42 ± 0.40	22 ± 2 (123 ± 15)	240 ± 9 (321 ± 9)†
CS/*Th. bessarabicum* line			
Goshawk (GH"S")	1.85 ± 0.26	20 ± 3 (220 ± 27)	243 ± 1 (270 ± 9)†
Th. elongatum/GH"S"	5.33 ± 0.86	17 ± 2 (105 ± 20)	233 ± 7 (285 ± 17)
CS/*Th. elongatum*	6.23 ± 0.86	18 ± 2 (99 ± 12)	263 ± 7 (290 ± 11)†

†Na and K measured in plants grown at 200 mol m⁻³ NaCl.

Table 72–7. Salinity hydroculture screening of some promising wheat/ *Thinopyrum bessarabicum (th)* disomic addition lines with 44 chromosomes at 150 mol m⁻³ NaCl measured after 50 days of full stress. Data tabulated for dry weight (g) and Na plus K from plant sap.

Amphiploid and addition lines	Chromosome no.	Dry weight, g	K/Na
CS	42	4.5	4.5
CS/*Th. bessarabicum*	56	3.7	9.2
+ 3J	44	1.0	7.9
+ 3J/7J	44	2.7	4.3
+ 7J	44	1.4	7.2
Yecora	42	1.1	3.7

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Chinese Spring  x  Th. bessarabicum
    (Ph Ph)
                              │
                              │
                              │
                    ┌─────────┘
                    ▼
     F₁ hybrid        x  Chinese Spring
(2n=4x=28, ABDJ)          (phib phib)
      (Ph)                     │
                              │
                    ┌─────────┘
                    ▼
Backcross I derivatives  x  (a) Chinese Spring
(2n=7x=49, AABBDDJ)              (phib phib)
     Ph ph
                              or

                         (b) Zea mays
                              │
                    ┌─────────┘
                    ▼
```

(a) Identify phib phib derivatives with J chromosomes

or

(b) Identify phib polyhaploid with J chromosomes
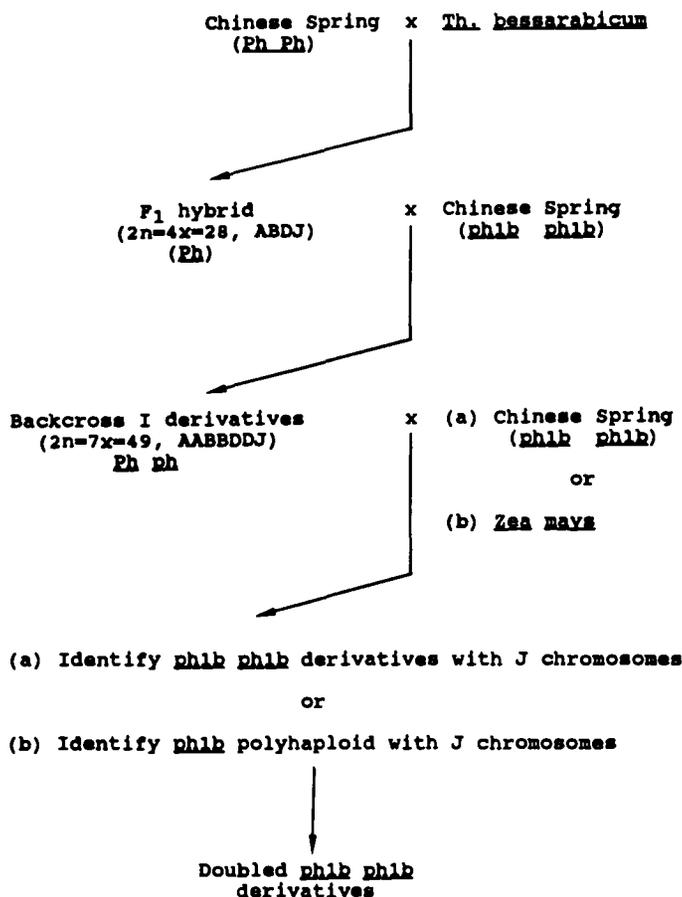
Doubled phib phib
derivatives

Fig. 72–1. Schematic showing genetic manipulation option using *phib* locus of *Triticum aestivum* cv. Chinese Spring by direct crossing or by maize mediated polyhaploid system.

order to unify the segregated salt tolerance effects. Multiple disomics arise from the selfing of BCI derivatives which possess 49 chromosomes (2n = 7x = 49; AABBDDJu). In the process of selfing, the alien chromosomes are paternally transmitted in a high enough frequency to give BCIF₁ derivatives with chromosomal complements of more than one disomic alien addition (e.g., 23 bivalents). Subsequent genetic manipulation procedures with desirable single chromosome disomic additions or multiple disomic additions will follow routine cytogenetic methodology.

Previously eluded to, but now being addressed is the use of the Chinese Spring *phib* genetic stock. Inevitably its role seems very crucial for complex characters like salt tolerance, and even though difficulties have been encountered in exploiting its full potential (Sharma & Gill, 1986) the merits v arrant more attention. Since that report, advance of *phib* × alien species has become possible (Rosas & Mujeeb-Kazi, 1990). An alternate route offers more promise and is being assessed with the Chinese Spring (*Ph*) × *Th. bessarabicum* hybrid (Fig. 72–1). Results from this backcross of the *phib* source and subsequent manipulation, promises to prove quite effective in handling alien transfers for salinity. More recently, through establishing the methodology of genomic in situ hybridization with *Th. bessarabicum*, the exploitation of the *phib* locus stands a logical extension for its application aimed at detecting subtle wheat/alien homoeologous exchanges.

Table 72–8. Growth data (dry weight), Na and K values at 50 mol m⁻³ NaCl measured after 50 d growth from some *Triticum turgidum* cultivars and synthetic hexaploids derived from them.

Cultivar and line	Dry Weight	Na plant sap	K plant sap
	—— g ——	mol m⁻³	mol m⁻³
Chinese Spring (CS)	4.42 ± 1.14	31 ± 3	225 ± 5
T. turgidum cultivars			
ROK"S"/KMLI"S"	1.07 ± 0.30	130 ± 4	150 ± 10
PBW 34	2.14 ± 0.35	139 ± 17	165 ± 22
CPT/GEDIZ/3/GOO/			
/JO"S"/CR"S"	1.80 ± 0.18	132 ± 1	141 ± 2
MEX/VIC/YAV	1.20 ± 0.36	123 ± 5	183 ± 3
DOY 1	2.29 ± 0.34	168 ± 13	111 ± 23
T. turgidum/T. tauschii (Synthetic hexaploids)			
W–20 Durum/#214	1.98 ± 0.93	26 ± 12	200 ± 10
W–42 PBW 114/*T. tauschii*†	2.28 ± 0.55	17 ± 7	226 ± 11
W–90 Durum 3/#206	3.13 ± 0.09	13 ± 4	213 ± 4
W–124 Durum 4/#434	1.13 ± 0.54	13 ± 8	230 ± 8
W–132 Durum 5/#510	6.87 ± 0.56	52 ± 28	183 ± 2

†Synthetic obtained from India (Dr. H. Dhaliwal). In absence of PBW 114 durum, we have used PBW 34 as an indicator. *T. tauschii* accession not known to us.

72–5.1 Interspecific Hybridization

Triticum tauschii (*Aegilops squarrosa;* 2n = 2x = 14, DD). Unequivocally recognized as the D genome donor to hexaploid wheat (2n = 6x = 42, AABBDD), the numerous accessions of *T. tauschii* offer a closely related gene pool that has enormous genetic diversity for biotic and abiotic factors. Direct screening of these accessions or through a bridge cross product involving susceptible durum wheat would lead to swift introgression of the alien D genome variability. These details have been reviewed and reported (Mujeeb-Kazi et al., 1993). The evidence that *T. tauschii* accessions with established agricultural attributes can be rapidly exploited by direct crosses to *T. aestivum* holds extensive promise for the near future. There exists a wide array of synthetic hexaploids (*T. turgidum* × *T. tauschii*) in CIMMYT that after a field screen led to selection of a few promising salt tolerance types, which were subsequently evaluated in hydroculture (Table 72–8). The expected differences in Na and K concentrations in the leaf sap caused by the presence of the enhanced K/Na discrimination character in the hexaploids but not the tetraploids was observed. From the dry weight and K/Na discrimination values of the synthetic hexaploids that are satisfactory, direct crosses of these *T. tauschii* accessions onto susceptible *T. aestivum* cultivars (e.g., Oasis or Yecora) is our immediate recourse. It is anticipated that further screening of *T. tauschii* accessions will facilitate our breeding for this complex trait and needs to be pursued at a priority level.

72–6 CONCLUSION

Alien genetic variability, whether close or distantly related to the *Triticum* crop species, provides an invaluable arsenal of genes that are a subject of elevated research interest (Mujeeb-Kazi & Kimber, 1985; Sharma and Gill, 1983).

Identification of these alien sources for stress tolerance has resulted in an array of germplasm from which those of priority usage have been selected. Genetic integration methodologies and sophisticated diagnostic techniques are going to be an asset for bringing about alien genetic introgression, the eventual success depending upon the complexity of the trait. From the prevailing evidence it appears that *Th. bessarabicum* will be the solution for salinity, Cu, Al, Mn, as well as a few fungal and insect related problems. Despite this promise, one does need to realize that the ultimate test of all research projections will be gains made through crop productivity. Exemplifying one aspect—salt tolerance: Will the tolerance response of the 4D substitution for chromosome 4A or 4B for durum wheats be a solution, or the dry weight plus K/Na discrimination level criteria express itself into desirable crop yields in saline lands or the transfers from salt tolerant *T. tauschii* accessions to *T. aestivum* produce elite cultivars, or will the *ph1b* wheat genetic manipulation system be so effective that the best can be introgressed from *Th. bessarabicum* and others, or a rye segment provide a genetic upheaval in wheat breeding like it has for the 1B/1R and to a lesser extent the 1A/1R translocated wheats. When such aspects are reflected upon, others envisioned and all placed in perspective over a time-frame the challenges of culminating at least some research promises or projections are magnified.

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