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ABSTRACT

Constraints due to global biotic and abiotic stress continue to exist in wheat germplasm. Novel genetic diversity resides in several annual/perennial Triticeae species that can be introgressed into wheat through intergeneric hybridization, of which *Thinopyrum curvifolium* is the principle source as it addresses the emphasis here for achieving wheat derivatives resistant to *Helminthosporium* leaf blight (*Cochliobolus sativus*). Some additional sources like *Th. elongatum* (2n=2x=14) and *Secale cereale* are also mentioned. The interspecific hybridization strategy offers alien genetic introgression opportunities, for which the closely related *Triticum* species have a priority. Of these sources, the D genome *T. tauschii (Aegilops squarrosa)* accessions and some of the A genome species *(T. boeoticum, T. monococcum and T. urartu)* are being exploited.

INTRODUCTION

During the past two decades, significant emphasis has emerged on utilization of alien genetic variation for wheat improvement. Methodologies have evolved that elucidate the usage of alien species attaching priority as to their choice of utilization. The species choice is based heavily upon the genomic relationship between the alien source and wheat, complexity of the character to be transferred, and the polyploidy status of the contributing species. With the wide array of annual and perennial Triticeae species existant, such alien genetic incorporation procedures are categorized under intergeneric and interspecific hybridization. The former route is generally more cumbersome to exploit, and practical outputs tend to be long-term. The interspecific approach in contrast, provides a swift means of introgressing alien genes from closely related sources and yields quality products more simplistically. A blend of both approaches provides the opportunity of pyramiding a more diverse genetic pool better adapted to combat biotic- and abiotic-stress constraints as they may associate with durability of resistance. In this presentation, the focus in on development of wheat germplasm that expresses enhanced resistance to *Helminthosporium sativum; Cochliobolus sativus* Ito and Kuribay or *Helminthosporium* leaf blight; compared to cultivar BH 1146, which is globally recognized as a superior resistant cultivar. The disease is widespread in several wheat production countries such as Bangladesh, Nepal, Thailand, India, Uganda, Brazil, Bolivia and Paraguay. The yield losses can be alarming, and losses up to 83.0% may occur. In Mexico, a naturally infectious field screening hot site exists in Poza Rica where we have encountered losses up to 58%. This has provided us the crucial input necessary to advance our alien genetic introgression program whose details relative to *Helminthosporium* leaf blight are described further.

BREEDING

The Intergeneric Hybridization Approach

Screening of the alien Triticeae species initially identified an ideal resistant source in *Thinopyrum curvifolium* (2n=4x=29) which was hybridized to *Triticum aestivum* cv Chinese Spring. The F_1 hybrid, 2n=5x=35, was advanced by crossing onto it the wheat cultivars Glennson 81, then Alondra/Pavon and eventually selfed. These selfed derivatives were screened for resistance under the severely infected natural field conditions of Poza Rica, Mexico, leading to selection of elite lines with superior resistance to *Helminthosporium* leaf blight. Following three years of yield testing, stability has persisted for all the selected characteristics. The five best resistant lines were agronomically characterized for registration as genetic stocks (Table 1) and were distributed to breeding programs. All five lines represent better *C. sativus* resistance than other wheat germplasm available in CIMMYT based upon evaluations for leaf/node damage at the milk and dough stage of development, as well as symptoms on spikes and mature grains (Table 2). Yield tests further demonstrated superiority of these lines as compared to susceptible and the existant resistant check (like BH 1146). The *Th. curvifolium* derived germplasm now figures in up to 89.8% of the 1994 selections made by

Table 1. Agronomic characteristics of *Cochliobolus sativus* resistant spring bread wheat germplasms grown at Poza Rica, Mexico, during the 1990-91 and 1991-92 field crop cycles.

Germplasm	Grain yield	Days to physiol. maturity	Plant height	1000-Grain weight	Test weight
	kg ha^{-1}		cm	g	kg hl^{-1}
Line -295-1	1997	102	87	29.4	73.4
Line -295-2	1564	106	88	27.4	73.9
Line -295-3	1431	108	87	25.4	74.2
Line -295-4	1580	105	88	26.4	69.5
Line -295-5	1461	110	91	25.3	72.4
BH 1146 (Res. check)	982	100	85	27.1	71.7
Ciano 79 (Susc. check)	166	103	63	16.7	38.8

Pedigree of lines 1 to 5: Chinese Spring/ *Th. curvifolium*//Glennson 81/3/Alondra/Pavon

Days from emergence

Table 2. Disease reactions of five spring wheat germplasm lines to *Cochliobolus sativus* at Poza Rica, Mexico during the 1990-91 field crop cycle.

Germplasm	Leaves † a	Leaves † b	Spike ‡ (1-9)	Grain § (1-5)
Line 295-1	93	94	2	2
Line 295-2	92	93	2	2
Line 295-3	93	93	2	2
Line 295-4	92	92	2	2
Line 295-5	92	94	3	2
BH 1146 (Resistant)	93	95	6	3
Ciano 79 (Susceptible)	99	99	9	5

† Two-digit scoring system: first digit = height of infection; 5 = up to mid-plant, and 9 = up to flag leaf; second digit = disease severity on infected leaves; 1 = low and 9 = total leaf destroyed; a = score at early milk stage, b = score at soft dough stage.

‡ 1 = low infection and 9 = high infection.

§ 1 = low grain infection and 5 = severely infected.

our wheat breeding program in Poza Rica. All lines have the euploid complement of 2n=6x=42 chromosomes and are satisfactory combiners with other wheat cultivars. Cytogenetic, biochemical, and molecular analyses have not enabled the detection of alien introgression from *Th. curvifolium*. However, through limited initial use of the A600 probe (courtesy CSIRO, Canberra, Australia) presence of alien DNA was apparent. This needs further validation.

Helminthosporium spot blight resistance was also observed in *Th. elongatum, Th. scirpeum, Th. intermedium, Leymus racemosus, Th. bessarabicum* and *Secale cereale*. Screening data supporting the resistance of *Th. elongatum* is evidenced from the field performance of its 2n-8x=56 chromosome amphiploid (Table 3) compared to a susceptible wheat cultivar Goshawk "S". Being a diploid, *Th. elongatum* is the next priority source being exploited other than *S. cereale*. In all such intergeneric hybrid based alien transfers, an infusion of the introgression manipulation methodology during initial stages of the program is preferable (Kimber, 1993), of which use of the *ph* loci is one approach (Mujeeb-Kazi et al., 1993).

The Interspecific Hybridization Approach

The interspecific route offers a rapid means of introgressing novel diversity from the closely related wild grasses because of their genomic proximity to the A. B and D genomes of *T. aestivum*. Several sources are being utilized, with the most extensive being that of the several

Table 3. Disease reactions of *Thinopyrum elongatum* based germplasm to *Cochliobolus sativus* at Poza Rica, Mexico, during the 1992-93 field crop cycle.

Test material	Leaves † a	Leaves † b	Spike ‡ (1-9)	Grain § (1-5)
Th. elongatum/GH"S"	92	92	2	2
CS/*Th. elongatum*	92	93	3	x
8A 206	92	93	3	3
GH"S"	94	96	7	4
CS	94	97	7	x
Cno 79 (Susceptible)	99	99	9	3
BH 1146 (Resistant)	93	95	6	3

† Two-digit scoring system: first digit = height of infection; 5 = up to mid-plant, and 9 = up to flag leaf; second digit = disease severity on infected leaves; 1 = low and 9 = total leaf destroyed; a = score at early milk stage, b = score at soft dough stage.

‡ 1 = low infection and 9 = high infection.

§ 1 - log grain infection and 5 = severely infected

Table 4. Disease reactions of AABBDD synthetic hexaploids and AAAABB hexaploids to *Cochliobolus sativus* during the Poza Rica, Mexico 1992-1993 field-crop cycle.

Germplasm	Leaves † a	Leaves † b	Spike ‡ (1-9)	Grain § (1-5)
GAN	96	96	7	5
GAN/*T. tauschii* (236)	92	92	3	x
DOY 1	95	97	7	5
DOY 1/*T. tauschii* (447)	92	92	3	x
DOY 1/*T. tauschii* (510)	92	92	3	x
SCOOP 1	97	97	8	5
----/3/*T. monococcum* (98)	92	92	3	x
----/3/*T. monococcum* (118)	92	93	3	x

† Two-digit scoring system: first digit = height of infection; 5 = up to mid-plant, and 9 = up to flag leaf; second digit = disease severity on infected leaves; 1 = low and 9 = total leaf destroyed; a = score at early milk stage, b = score at soft dough stage.

‡ 1 = low infection and 9 = high infection.

§ 1 = low grain infection and 5 = severely infected.

accessions of *T. tauschii (Aegilops squarrosa)* via the synthetic hexaploid bridge as a crossing step to *T. aestivum*. In all these aspects of genetic improvement, the durum and bread wheat cultivars are susceptible. Hence, when field resistance is observed either in the synthetic hexaploid or the advanced derivatives from *T. aestivum*/synthetic hexaploid crosses, it is attributed to a contribution of the *T. tauschii* accession. The accession contributing to resistance can then be utilized directly in crosses (Alonso and Kimber 1984) with susceptible bread wheats. We have adopted

this dual approach since the *T. tauschii* accessions field screening failed to provide conclusive data. In the same context the A genome species are utilized by producing the AAAABB hexaploids, which are screened for resistance and crossed further to their respective durum parents for relevant improvement of durums. The A genome accession, after it has been identified as resistant in the AAAABB hexaploid is next used in direct crosses to susceptible *T. aestivum* cultivars. Data from DD genome synthetics and A genome hexaploids for the *Helminthosporium* leaf blight screening is presented in Table 4. The three durum cultivars; GAN, DOY_1 and SCOOP_1 express a high degree of susceptibility as observed on leaves, spikes, and mature grains. The resistance of the AABBDD and AAAABB germplasm was highly expressive except for grain finish scores that were not recorded because of late maturity of these derivatives.

Alien genetic diversity from annual/perennial Triticeae species has significantly contributed to improvement of bread wheat germplasm and avenues now exist to further enhance the diversity of durum wheats through A genome exchanges. Though not yet exploited, D genome transfers to the A genome need further research inputs, and this may further enhance diversity for durums. In general, it appears that adequate genomic variations exist, which if pyramided into cultivated wheats could ensure a considerable level to resistance to *Cochliobolus sativus*. The transfer and diagnostic methodologies will contribute to such an outcome.

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