

**CYTOGENETICS OF INTERGENERIC HYBRIDS INVOLVING
GENERA WITHIN THE TRITICEAE**

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SUMMARY

The cytogenetics of intergeneric hybrids between Agropyron elongatum ($2n=2x=14$, $2n=4x=28$, $2n=10x=70$), A. junceum ($2n=6x=42$), Elymus canadensis ($2n=4x=28$, SSHH), E. giganteus ($2n=4x=28$, J₁J₁X₁X₁), Hordeum vulgare ($2n=2x=14$, HH), Secale cereale ($2n=2x=14$, RR), Triticum timopheevii ($2n=4x=28$, AAGG), T. turgidum ($2n=4x=28$, AABB) and T. aestivum ($2n=6x=42$, AABBDD) is presented. Mention is made of backcross I and II progeny resulting from (H. vulgare - T. turgidum) x T. turgidum, (H. vulgare - T. aestivum - T. aestivum) x T. aestivum, and (T. aestivum - E. giganteus - T. aestivum) x T. aestivum combinations. The production of some trigeneric hybrids is reported. Somatic cytology confirms the amphiploid status of T. aestivum x A. junceum plants to be $2n=12x=84$.

INTRODUCTION

Intergeneric hybridization may facilitate a transfer to wheat (Triticum aestivum L.) of high lysine content, barley yellow dwarf resistance, drought tolerance, rust resistance, salt tolerance and scab resistance from related or distant genera that are so characterized, Mujeeb-Kazi and Rodriguez 1980a. The sources of genetic transfer identified by testing or species habitat reside in Agropyron species, Elymus species, Hordeum vulgare, or amphiploids of Triticum turgidum x Agropyron elongatum.

This paper presents the cytogenetic data obtained from intergeneric hybrids, trigeneric hybrids, backcross I and II progenies, or amphiploids between Agropyron species, Elymus species, Hordeum vulgare, Secale cereale, T. turgidum, T. timopheevii and T. aestivum.

MATERIALS AND METHODS

The crossing between the various genera was carried out in the field at El Batan, and Ciudad Obregon, Mexico. Additional crossing dictated by pollen availability was done in the greenhouses or growth chambers in El Batan, Mexico. The genera and species included in the program were:

<u>Agropyron elongatum</u>	$2n=14$, $2n=4x=28$, $2n=10x=70$
<u>A. junceum</u>	$2n=6x=42$
<u>Elymus canadensis</u>	$2n=4x=28$, SSHH
<u>E. giganteus</u>	$2n=4x=28$, JJXX
<u>Hordeum vulgare</u> cv. Manker	$2n=14$, HH
<u>Secale cereale</u> cv. Prolific	$2n=14$, RR
<u>Triticum timopheevii</u>	$2n=4x=28$, AAGG
<u>T. turgidum</u> cv. (i) Cocorit	$2n=4x=28$, AABB
(ii) Cr"S" - T. pol. x G ²	$2n=4x=28$, AABB
<u>T. aestivum</u>	$2n=6x=42$, AABBDD cvs. Bonza, Chinese Spring, Pavon, Zaragoza, Tobarí
<u>T. turgidum</u> cv. Stewart x <u>A. elongatum</u>	($2n=6x=42$)

The greenhouse conditions were 20°C day/12°C night, 60%/45% RH with natural day-light of approximately 15 hours. The growth chambers were maintained under 14 h. day, 15°C day/10°C night, and 45% RH. The pollination and embryo culture procedure has been reported in MUJEEB-KAZI and RODRIGUEZ 1980a. Somatic counts were according

to the schedule of MUJEEB et al. 1978a. Feulgen or 2% propionic orcein staining was adopted for meiotic analyses.

The colchicine treatment concentration was 0.2% + 2.0% dimethylsulfoxide (DMSO). This was applied to the tillers by the capping method for 4 hours, or for 6 hours when done by the aerated root treatment.

RESULTS AND DISCUSSION

I. INTERGENERIC HYBRIDS

Diploid and tetraploid *A. elongatum* formed hybrids with *T. turgidum*, *H. vulgare* and *S. cereale*. Homeology and autosyndetic pairing for the tetraploid *A. elongatum* were lacking, which gave chiasmata frequencies of 0.32 and 0.38 with *T. turgidum* and *H. vulgare*. Pollen mother cells of *A. elongatum* x *S. cereale* were entirely empty, but the pubescence marker common of *Secale* in x *Triticum-Secale* was morphologically visible at the base of the sterile spikes. Somatic cytology indicated presence of seven *Secale* chromosomes by chromosome banding. The *H. vulgare* x *T. turgidum* hybrid expressed meiotic instability with pollen mother cells possessing a cumulative chromosome number of greater than or less than the normal 21, HAB composition. The observations are consistent with similar variations earlier recorded by FEDAK 1977, 1980; and MUJEEB et al. 1978b; they were not observed by MARTIN and LAGUNA 1980 where the *H. chilense* germ-plasm may be a factor. The low chiasmata frequency of 0.81/cell in the *E. canadensis* x *H. vulgare* hybrid sheds a different light upon the pairing of the H genome of the two genera. A higher bivalent frequency was to be expected from interpretations derived from the H genome relationships and evolution as presented by DEWEY 1970, 1971. The variation obtained is being studied in greater detail. Amongst the hybrids obtained from *A. junceum* ($2n=6x=42$) those with *T. aestivum* produced five seeds after colchicine treatment. All seeds germinated and were somatically confirmed to be $2n=12x=84$. The cytogenetic details are in Table I.

II. BACKCROSS PROGENIES

- A. BACKCROSS I. The backcross I plants that grew vigorously are listed in Table II. For the *H. vulgare* - *T. aestivum* x *T. aestivum* combinations the chromosome range was from 28 to 50. The expected number was $2n=7x=49$. The plant with 28 chromosomes was presumably a product of pseudogamopomixis, while that with 50 chromosomes a consequence of an unreduced egg cell carrying 29 chromosomes being fertilized by *T. aestivum* pollen. Chromosome elimination from 56 to 55 was observed in *T. aestivum* - *E. giganteus* x *T. aestivum*. This was for an *Elymus* chromosome since the meiotic relationship was $21_{II} 13_I$ for this plant, and $21_{II} 14_I$ for the second backcross hybrid of the same combination. The JX genomes of *Elymus* failed to exhibit pairing in the *T. aestivum* x *E. giganteus* hybrid and also maintained their specificity in the backcross, (MUJEEB-KAZI and RODRIGUEZ 1980b).
- B. BACKCROSS II (BCII). Difficulties were observed in obtaining BCII seed because of the *Hordeum* cytoplasm in barley x wheat hybrids, ISLAM et al. 1975. These difficulties were overcome by (i) two early pollinations followed by (ii) two gibberellic acid applications, see MUJEEB-KAZI and RODRIGUEZ 1980a. Seed set was obtained in all combinations with *T. aestivum* cultivars. The BCII seed are expected to possess a somatic count of $42_w + 0$ to 7_H chromosomes, unless an apomictic plant was involved in the crossing where either apomictic or heptaploid combinations would be recovered. A total of 167 BCII plants are being maintained for cytological study and for furthering the objective of developing disomic barley addition and substitution lines,

TABLE 1: Cytogenetic data of some intergeneric hybrids involving Agropyron, Elymus, Hordeum, Secale and Triticum species

INTERGENERIC HYBRID		SOMATIC CHROMOSOME NUMBER	MEIOTIC CHROMOSOME RELATIONSHIP					CHIASMATA (x^{2a}) FREQUENCY/CELL	
♀ PARENT	♂ PARENT		I	II	II(.)*	III	IV		OTHER
<u>A. elongatum</u>	<u>T. turgidum</u>	2n=3x=21	20.38	0.28	0.02				0.32
<u>A. elongatum</u>	<u>H. vulgare</u>	2n=3x=21	20.19	0.34	0.01	0.03	0.01		0.38
<u>A. elongatum</u>	<u>S. cereale</u>	2n=3x=21	POLLEN MOTHER CELLS TOTALLY EMPTY						-
<u>H. vulgare</u>	<u>T. turgidum</u>	2n=3x=21	19.26	0.39	0.46	0.02			1.21
<u>E. canadensis</u>	<u>H. vulgare</u>	2n=3x=21	19.51	0.49	0.04	0.12	0.01		0.81
<u>T. turgidum</u>	<u>A. junceum</u>	2n=5x=35	21.19	6.15	0.28	0.27	0.01	0.01 (VIII)	7.35
<u>T. aestivum</u>	<u>A. junceum</u>	2n=6x=42	20.65	8.58	1.38	0.40	0.10		12.38

*

II(.)* = Ring bivalent

TABLE 2: Chromosomal constitution of backcross I plants, and backcross II seed obtained

LAB NUMBER	BACKCROSS I PLANTS		CHROMOSOME NUMBER	BACKCROSS II		FLORETS POLLINATED	SEED SET
	♀ PARENT	♂ PARENT		♂ PARENT			
1120B*	cv. Manker - cv. Pavon	cv. Pavon	47	cv. Pavon	52	4	
				cv. Chinese Spring	225	25	
1123 *	cv. Manker - cv. Bonza	cv. Bonza	28	cv. Chinese Spring	26	2	
1124A*	cv. Manker - cv. Bonza	cv. Bonza	49	cv. Pavon	104	15	
				cv. Chinese Spring	98	2	
1124D*	cv. Manker - cv. Bonza	cv. Bonza	49	cv. Pavon	248	82	
				cv. Zaragoza 75	26	15	
1125B*	cv. Manker - cv. Chinese Spring	cv. Chinese Spring	48	cv. Bonza	97	4	
				cv. Chinese Spring	222	27	
1125E*	cv. Manker - cv. Chinese Spring	cv. Chinese Spring	49	cv. Pavon	20	2	
				cv. Chinese Spring	128	21	
1125F*	cv. Manker - cv. Chinese Spring	cv. Chinese Spring	48	cv. Pavon	18	1	
				cv. Chinese Spring	40	4	
*	cv. Manker - cv. Pavon	cv. Pavon	28	cv. Pavon	66	1	
				cv. Chinese Spring	62	3	
*	cv. Manker - cv. Pavon	cv. Pavon	50	cv. Pavon	41	9	
				cv. Chinese Spring	108	17	
1512 *	cv. Chinese Spring-E. <u>giganteus</u>	cv. Chinese Spring	56 55	cv. Chinese Spring	168	11	
				cv. Pavon	50	4	
1513 *	cv. Chinese Spring-E. <u>giganteus</u>	cv. Chinese Spring	56	cv. Pavon	98	7	

* Manker = H. vulgare cultivar; Bonza, Chinese Spring, Pavon and Zaragoza 75 = T. aestivum cultivars.

TABLE 3: New backcross I hybrids, F₁ hybrids, and trigeneric hybrid combinations obtained and maintained in El Batan, Mexico

♀ PARENT	HYBRID COMBINATION	♂ PARENT	FLORETS POLLINATED	SEED SET	EXPECTED CHROMOSOME NUMBER	EXPECTED CHROMOSOME DETAIL	OBSERVED SOMATIC COUNT
BACKCROSS I HYBRIDS							
<u>T. aestivum</u> - <u>E. giganteus</u>		x <u>T. aestivum</u> cv. Pavon	24	1	2n=8x=56	42 _W 14 _E	56
<u>T. aestivum</u> - <u>E. giganteus</u>		x <u>T. aestivum</u> cv. Chinese Spring	40	4	2n=8x=56	42 _W 14 _E	56
<u>T. aestivum</u> - <u>E. giganteus</u>		x <u>T. aestivum</u> cv. Zaragoza	24	4	2n=8x=56	42 _W 14 _E	56
<u>H. vulgare</u> - <u>T. turgidum</u>		x <u>T. turgidum</u> cv. Cocorit 71	72	8	2n=7x=35	28 _W 7 _H	35
F₁ HYBRIDS							
(<u>T. turgidum</u> - <u>A. elongatum</u> C-1)		x <u>A. elongatum</u> (2n=10x=70)	124	9	2n=8x=56	14 _W 7 _A 35 _A	56
(<u>T. turgidum</u> - <u>A. elongatum</u> C-1)		x <u>T. aestivum</u> cv. Bonza	66	30	2n=6x=42	35 _W 7 _A	42
(<u>T. turgidum</u> - <u>A. elongatum</u> C-1)		x <u>T. aestivum</u> cv. Chinese Spring	47	5	2n=6x=42	35 _W 7 _A	42
(<u>T. turgidum</u> - <u>A. elongatum</u> C-1)		x <u>T. aestivum</u> cv. Pavon	94	11	2n=6x=42	35 _W 7 _A	42
(<u>T. turgidum</u> - <u>A. elongatum</u> C-1)		x <u>T. aestivum</u> cv. Zaragoza	286	104	2n=6x=42	35 _W 7 _A	42
<u>T. aestivum</u> cv. Bonza		x <u>A. elongatum</u> (2n=10x=70)*	300	0	2n=8x=56	21 _W 35 _A	56
cv. Chinese Spring		x <u>A. elongatum</u> (2n=10x=70)	196	130	2n=8x=56	21 _W 35 _A	56
cv. Pavon		x <u>A. elongatum</u> (2n=10x=70)	203	2	2n=8x=56	21 _W 35 _A	56
cv. Zaragoza		x <u>A. elongatum</u> (2n=10x=70)	82	70	2n=8x=56	21 _W 35 _A	56
<u>T. timopheevii</u>		x <u>A. elongatum</u> (2n=10x=70)	253	129	2n=7x=49	14 _W 35 _A	49
<u>T. turgidum</u> cv. Cocorit 71		x <u>A. elongatum</u> (2n=10x=70)	128	85	2n=7x=49	14 _W 35 _A	49
TRIGENERIC HYBRIDS							
<u>T. aestivum</u> - <u>E. giganteus</u>		x <u>A. elongatum</u> (2n=10x=70)	76	12	2n=10x=70	21 _W 14 _E 35 _A	-
(<u>T. aestivum</u> - <u>E. giganteus</u> - <u>T. aestivum</u>)		x <u>A. elongatum</u> (2n=10x=70)	100	12		21 _W 0 to 14 _E 35 _A	-
(<u>H. vulgare</u> - <u>T. aestivum</u> - <u>T. aestivum</u>)		x <u>S. cereale</u> (2n=14)	3 plants via embryo culture			21 _W 0 to 7 _H 7 _R	-

* The reciprocal cross required embryo culture after 20 days of pollination and gave 7 plants, each with 56 chromosomes

MUJEEB-KAZI and RODRIGUEZ 1980c.

III. NEW BCI HYBRIDS, F₁ HYBRIDS, AND TRIGENERIC HYBRIDS

A. BCI HYBRIDS. All seed (BCI) from *T. aestivum* - *E. giganteus* x *T. aestivum* cvs. Pavon, Chinese Spring, Zaragoza had the expected 56 chromosomes. Pseudogamopomixis appeared commonly in the *H. vulgare* - *T. turgidum* x *T. turgidum* backcross. Of eight seeds obtained, seven germinated, five had 21 chromosomes (2n=3x=21, HAN), one had 35 (HAABB) and one has yet to be analyzed (Table III). This is a reflection upon the frequency of euploids that so commonly arise in intergeneric hybridization, and that generally are attributed to other mechanisms (MUJEEB et al. 1978b).

B. F₁ HYBRIDS. The *T. turgidum* x *A. elongatum* (2n=6x=42) amphiploid is a tall plant, late, but rust resistant. It has been crossed to several *T. aestivum* cultivars to facilitate the rust resistance transfer, limited at this stage to homeologous pairing of the *Triticum* pentaploid component with complementation from the *A. elongatum* genomes. Cultivar Chinese Spring combined poorly with the amphiploid under the crossing conditions.

Several cultivars of *T. aestivum*, *T. timopheevii*, and *T. turgidum* have been crossed with a salt tolerant *Agropyron* species (*A. elongatum*, 2n=10x=70), seed of which was obtained from Argentina. Tolerance was based upon the species soil habitat. No seed set with *T. aestivum* cv. Bonza, but seven F₁ plants were obtained from the reciprocal cross (Table III) with embryo culture. A total of 173 plants are being grown and await meiotic analyses.

C. TRIGENERIC HYBRIDS. The trigeneric hybrids between *T. aestivum* - *E. giganteus* x *A. elongatum* (2n=10x=70) were developed for incorporating the salt tolerance of *A. elongatum* via possible homeologous transfer to *T. aestivum* and complement the tolerance present in *E. giganteus* that may presumably be expressed when disomic additions are produced. The salt or drought tolerance data for either *A. elongatum* or *Elymus* is not available although, the soil habitat provides this indication. Producing the hybrid combinations has been fairly convenient, and advanced progeny will be tested in these habitats. The trigeneric (*Hordeum* - *T. aestivum* - *T. aestivum*) x *S. cereale* required embryo culture and is a cytological curiosity. The *H. vulgare* - *T. aestivum* x *S. cereale* trigeneric was obtained by FEDAK and ARMSTRONG 1980; and KIMBER and SALLEE have reported one for *T. timopheevii* - *H. bogdanii* x *S. cereale*. The one reported here had a BCI maternal composition and should have the 21W 0 to 7H 7R chromosomal detail (Table 3).

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