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IDENTIFICATION OF GENES FOR RESISTANCE TO STEM RUST AND THEIR DIVERSITY IN EIGHT BREADWHEAT VARIETIES. I. CROSSES WITH SUSCEPTIBLE PARENTS AND Sr LINES

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ABSTRACT

A set of eight sources of stem rust resistance, viz., HD 2009, HD 2177, HD 2189, WH 169, HW 142, TzPP, Marco Juarez Inta, and Pj $62-Gb^2 \times TzPP \times Knott#2$ (E 8643), were crossed to two susceptible parents and Sr lines. Tests in the seedling stage were carried out with races 40 and 295 of stem rust. The F₂ and F₃ investigations indicated the presence of 2–3 genes in different sources. These were dominant, recessive or complementary in nature. Modification of gene action from complementary to dominant duplicate factors in different genetic backgrounds was observed. The genes Sr6, Sr11 and Sr26 against race 40 were detected in some sources. There were indications of the presence of gene Sr9e against race 295. F₃ analysis indicated different genes for the two races, except Sr26 present in E 8643 causes resistance against both the races.

Key words: Wheat, rust resistance, race-specific genes.

Basic studies are required for the identification of genes for resistance to rusts, so that they could be introduced into agronomically adapted cultivars. Genes for durable field resistance are few and introduction of specific genes against the potential races may prove to be a durable solution for different agroclimatic zones. In the central parts of India, stem rust is a common occurrence. Race 40 and its biotypes occur most frequently. Race 295 affects *dicoccum* wheats grown in the coastal and mountaneous regions of Gujarat, Maharashtra and the southern states of the Indian peninsula and is a potential race for the region. The studies carried out until 1977 were summarised by Chopra and Kulkarni [1]. Nathawat et al. [2] and Sawhney et al. [3] further investigated various sources of resistance and identified Sr6, 8, 9b, 11 and some other genes in dwarf wheats.

MATERIALS AND METHODS

The study was carried out with a few popular resistant cultivars like HD 2009, HD 2177 and HD 2189 [4] along with Wh 169 and HW 142 which showed resistance to as many as 20

pathotypes of Indian origin (RRL reports 1974–76) [4]. Tezanos Pintos Precoz (TzPP), Marco Juarez Inta (MJI) and Pj62-Gb² x TzPP x Knot#2 (E 8643) are reported to be good sources of resistance on international scale. Pissi Local and NP 4 were used as susceptible and the Sr lines 6, 9d, 9e, 11, 21 and 26 were utilised as resistant parents. Sr 9d (susceptible) was wrongly used in place of Sr 9b, which was resistant to race 295. Sr 6, 11 and 21 were resistance to race 40 and SR 26 to both. Sr 9e was resistant only to race 295.

The standard procedure for inoculation and recording of reactions was followed as described by [5]. Plants with intermediate reactions $2 \pm$ and 3 with necrosis or chlorosis were included in the resistant class. Lines with predominance of susceptible plants were classified as S:R. Race relationship studies were carried out on the same F₃ lines for the two races.

RESULTS AND DISCUSSION

The data on F_2 and F_3 studies in the crosses with susceptible parents are presented in Table 1, while those on race relationship in F_3 are given in Table 2, and for F_2 of the crosses with Sr lines in Tables 3 and 4.

The variety HD 2009 (Lerma Rojo 64A x Nainari 60) showed presence of a pair of dominant complementary genes and a dominant factor (Table 1). For race 40, Sr6 and Sr11 were present while Sr 9 was observed to operate for race 295 (Tables 3, 4). Independent genes for the two races were operative (Table 2). However, with Sr6 and Sr11, it was difficult to explain, the presence of complementary gene action and one dominant factor for race 40. Studies with Sr21 indicated that the complementary gene action was modified to duplicate dominant factors. With Sr 9d (susceptible) operation of one dominant factor indicated the presence of a common complementary gene. This indicated modification of gene action in different genetic backgrounds. Sr6 seems to have been incorporated from Kentana and Sr11 from Gabo, which appear in the pedigree of HD 2009. Jha [6] also reported change in mode of inheritance from dominant to complementary gene action, due to rise in temperature.

The variety HD 2177 possessed a dominant and two recessive genes for race 40 and a pair of complementary genes against race 295 (Table 1). Sr11 for race 40 was present. Modification of gene action due to the Sr lines 9d and 9e against race 295 was noticed in this variety, when complementary genes behaved as duplicate dominant (Tables 3, 4). The variety HD 2177 had Safed Lerma, K 338, Frontana, K 58 and Gabo 55 as parents. Sr11 seems to have been incorporated from Gb 55. The genes for the two races were independent (Table 2).

HD 2189 showed high resistance in peninsular India. It possesses one dominant and one recessive genes each operating independently against the two races (Table 2). Sr11 was active against race 40 and contributed from Gabo or Timstein (Table 3). Recessive factors have been reported by Jha [7], Jag Shoram and Rao [8] Sawhney et al. [9].

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Cross	Race 40					Race 295			
resistant X suscep- parent tible parent	gene- ration	No. of plants	expected ratio R:S R:Seg:S R:S:S:R	χ ²	Р	No. of plants	expect- ed ratio R:S R:Seg:S R:S:S:R	χ2	Р
HD 2009 x PL	F2	377	57:7	0.28	0.7-0.5	418	9:7	2.45	0.20.1
	F3	102	19:38:7	2.05	0.5-0.3	102	1:8:7	1.94	0.50.3
HD 2009 x NP4	F2	396	57:7	0.13	0.8–0.7	442	9:7	0.85	0.5–0.3
	F3	111	19:38:7	2.25	0.5–0.3	111	1:8:7	1.04	0.7–0.5
HD 2177 x PL	F2	379	55:9	1.88	0.2–0.1	828	9:7	0.55	0.5–0.3
	F3	80	37:18:8:1	0.11	0.99	80	1:8:7	1.34	0.7–0.5
HD 2177 x NP4	F2	424	55:9	0.62	0.5–0.3	563	9:7	0.92	0.5–0.3
	F3	126	37:18:8:1	0.73	0.9–0.8	126	1:8:7	1.17	0.7–0.5
HD 2189 x PL	F2	382	13:3	1.27	0.3–0.2	276	13:3	3.01	0.1–0.05
	F3	106	7:6:2:1	0.16	0.99–0.95	106	7:6:2:1	0.82	0.90.7
HD 2189 x NP4	F2	358	13:3	0.06	0.080.7	504	13:3	0.73	0.5–0.3
	F3	111	7:6:2:1	0.09	0.99	111	7:6:2:1	1.42	0.7–0.5
E 8643 x PL	F2	355	55:9	3.15	0.10.05	304	55:9	2.75	0.1-0.05
	F3	107	37:18:8:1	2.02	0.70.5	107	37:18:8:1	0.42	0.95-0.9
HD 8643 x NP4	F2	413	55:9	0.33	0.7–0.5	231	55:9	2.00	0.2–0.1
	F3	88	37:18:8:1	3.73	0.3–0.2	88	37:18:8:1	1.14	0.9–0.8
WH 169 x PL	F2	381	3:1	1.59	0.3–0.2	348	3:1	0.06	0.8–0.7
	F3	113	1:2:1	0.09	0.99–0.95	113	1:2:1	1.57	0.5–0.3
WH 169 x NP4	F2	398	3:1	2.62	0.2–0.1	315	3:1	0.31	0.7–0.5
	F3	120	1:2:1	1.93	0.7–0.5	120	1: 2 :1	0.60	0.8–0.7
HW 142 x PL	F2	439	55:9	0.10	0.80.7	229	13:3	3.43	0.1–0.05
	F3	120	37:18:8:1	0.47	0.950.9	120	7:6:2:1	2.31	0.7–0.5
HW 142 x NP4	F2	264	55:9	1.16	0.30.2	426	13:3	0.002	> 0.99
	F3	107	37:18:8:1	0.16	0.990.95	107	7:6:2:1	2.80	0.050.3
TzPP x PL	F2	412	57:7	0.21	0.7–0.5	1008	43:21	2.68	0.2–0.1
	F3	92	19:38:7	1.76	0.5–0.3	92	19:24:14:7	5.58	0.2–0.1
TzPP x NP4	F2	387	57:7	0.35	0.7–0.5	590	43:21	0.003	0.99–0.95
	F3	100	19:38:7	2.38	0.2–0.1	100	19:24:14:7	1.59	0.7–0.5
MJI x PL	F2	137	13:3	0.65	0.50.3	294	55:9	0.003	0.950.9
	F3	100	7:6:2:1	1.17	0.80.7	100	37:18:8:1	2.53	0.50.3
MJI × NP4	F2	277	13:3	2.45	0.20.1	178	55:9	0.43	0.7-0.5
	F3	100	7:6:2:1	2.20	0.70.5	100	37:18:8:1	2.51	0.5-0.3

 Table 1. Inheritance pattern of eight breadwheat varieties against the stem rust races 40 and 295

The percentage of WH 169 had much in common with HD 2177, i.e. E 4870 and V 18 (sister lines from the cross Kalyan Sona \times S 227) had common pedigree but only one dominant and one recessive gene for race 40 (Sr 6, Sr 11, Sr 21 and Sr 26 being absent) operated (Table 1). For race 295, a single dominant gene was observed, which was different from Sr 9e (Table 4). It appears that genes different from those of HD 2177 got selected.

In the variety HW 142, parents like Timgalen and HW 113 with complex pedigree were involved. There were many parents having resistance genes. This variety had shown resistance at Wellington to the race complex of Southern Hills. However, three genes, one dominant and two recessive, against race 40 and one dominant and one recessive genes against race 295 were identified. Only Sr11 was present. Other genes were different from Sr 6, Sr 21, Sr 26, Sr 9e etc. and were independent for the two races (Tables 2, 4). Perhaps Sr 9b might have been incorporated from Timgalen [10] which is effective against race 295.

Tezanos Pintos Precoz. An early maturing tall variety, selected in South America, shows high resistance in many countries. It carries two complementary dominant genes each for the two races. Apart from this, one dominant gene against race 40 and one recessive gene against race 295 caused resistance (Table 1). Sr6 was present (Table 3). All the six genes were

Response to different races		Number of lines in the cross with different varieties							
40	295	HD 2009	HD 2177	HD 2189	WH 169	HW 142	TzPP	MJI	E 8643
Resistant	Resistant	2	1	18	14	32	9	22	36
Resistant	Segregating	18	28	30	24	34	21	19	25
Resistant	Susceptible	9	16		11	3	2	1	1
Segregating	Resistant	7	4	24	13	24	7	35	24
Segregating	Segregating	33	16	21	35	25	38	17	18
Segregating	Susceptible	26	14	7	9	1	8	2	1
Susceptible	Resistant	_		1	_	1		3	2
Susceptible	Segregating	3	1	4	4	_	6	1	
Susceptible	Susceptible	4		1	3	-	1		_
Total		102	80	106	113	120	92	100	107
χ ²		6.90	5.97	1 2.26	6.72	4.04	11.71	. 5.42	8.77
P at 8 d.f.		0.7-0.5	0.7-0.5	0.2-0.1	0.7-0.5	0.9–0.8	0.2-0.1	0.80.7	0.5-0.3
No. of genes	-independent common	5	5	4	3	5	6	5	4 1

Table 2.	Race relationship studies in F3 for the stem rust races 40 and 295 in the crosses of
	eight varieties with Pissi Local

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Table 3. S ei	egregation ight varieti s	pattern es witl tem roc	nonlinked (Tal resistance of TzPI many genes inclu				
Parent	F ₂ Segre	gation	Ratio	Р	Mar	co Iuarar	
	R	S			in Arconting for		
			Sr6 (R)		Klien R	endidor.	
	004	1			recessiv	e oenes a	
HD 2009	934		No. segr.		100051	c genes a	
HD 2177	192	10	247:9	0.3-0.2	Table 4	Consection	
HD 2189	868	52	61:3	0.2-0.1	i abie 4.	segregand	
WH 169	559	20	61:3	0.10.5		cigitt vali	
HW 142	336	8	247:9	0.3-0.2			
TzPP	223		' No Segr.	—	Paront	Se	
MJI	115		No Segr.	—	ratem		
E 8643	478	—	No Segr.			K	
		II. S	Sr 11 (R)				
HD 2009	1416		No Segr.		HD 2009	704	
HD 2177	1757		No Segr.		HD 2177	1052	
HD 2189	621	_	No. Segr.		HD 2189	668	
WH 169	687	141	13:3	0.2-0.1	WH 159	Hybr	
HW 142	401		No Segr.		HW 142	73	
TzPP	791	17	247:9	0.30.2	TzPP	706	
MII	Necrosis				MII	Hybr	
E 8643	832	7	253 : 3	0.5-0.3	E 8643		
		ш.	Sr 9e (S)				
HD 2009		_			HD 2009	102	
HD 2177	101	18	55 : 9	08-07	HD 2177	1749	
HD 2189	194	48	13.3	0.7-0.5	HD 2189	72	
WH 160			10.0		WH 169	254	
HW 142	_	_			HW 142	810	
Т ₇ рр	350	35	57 . 7	03_02	T ₇ PP	879	
MI	000		<i></i>	0.0-0.2	MI	1044	
E 8643	_	_		-	E 8643	Hybr	
		IV. 9	Sr 21 (R)			•	
HD 2009	912	2	255 : 1	0.5-0.3	HD 2009	Hybr	
HD 2177	Necrosis				HD 2177	,	
HD 2189	651	25	61:3	0.3-0.2	HD 2189		
WH 169	832	8	253:3	0.8-0.7	WH 169		
HW 142	331	9	247:9	0.5-0.5	WH 142		
TzPP	779	30	249 : 7	0.1-0.5	TzPP		
MII	591	26	61:3	0.7-0.5	MII		
E 8643	073	28	247.0	03.02	F 8643		

nonlinked (Table 2). The high field resistance of TzPP indicated involvement of many genes including minor factors [11].

Marco Juarez Inta. A variety developed in Argentina from the cross Sonora 64 x Klien Rendidor. One dominant and two recessive genes against race 40 independent

Table 4.	Segregation pattern in the F2 of crosses of							
	eight varieties with Sr lines against the							
	stem rust race 295							

_	Parent	Segreg	gation	Ratio	P Value		
		R	s				
			I. Sr	9d (S)			
	HD 2009	704	209	3:1	0.2-0.1		
	HD 2177	1052	83	15:1	0.2-0.1		
	HD 2189	668	1 66	13:3	0.50.3		
2-0.1	WH 159	Hybrid n	ecrosis				
	HW 142	738	160	13:3	0.5-0.3		
30.2	TzPP	706	317	43:21	0.3-0.2		
	MJI	Hybrid n	ecrosis				
5–0.3	E 8643	"					
			II. Sr	9d (S)			
	HD 2009	1021		No. segr			
8-0.7	HD 2177	1749	116	15:1	0.99-0.95		
70.5	HD 2189	725	34	61 : 3	0.99-0.95		
	WH 169	254	16	15:1	0.99-0.95		
	HW 142	819	43	61:3	0.90.8		
3-0.2	TzPP	878	15	253:3	0.2-0.1		
	MJI	1046	46	247:9	0.30.2		
	E 8643	Hybrid n	ecrosis				
			III. Sr	26 (R)			
5-0.3	HD 2009	Hybrid n	ecrosis				
	HD 2177						
30.2	HD 2189	"					
80.7	WH 169	"					
5-0.5	WH 142	"					
10.5	TzPP	"					
7-0.5	MJI	"					
30.2	E 8643			1387	No Segr.		

of one dominant and one recessive genes against 295 were detected (Tables 1, 2). Sr6 was identified in this variety. Cross with Sr11 line, showed hybrid necrosis. Other genes (Sr 21, 26 and 9e) were not detected. Sr 6 was contributed by Kl. Rendidor (Tables 3, 4).

E 8643 (Pj62-Gb² x TzPP x Knott#2) had cv. Kenya 58, Gabo as parents and the *Agropyron* gene, Sr 26, in its background. This variety possessed one dominant and two recessive factors for the two races (Table 1). Sr6 for race 40 and Sr26 for both races were detected (Tables 3, 4).

Segregation for the gene Sr11 was close to 253 : 3, indicating three dominant genes and one recessive factor. This showed reversal of gene action from recessive to dominant in certain backgrounds. Such modification was also reported by [12]. Crosses with other Sr lines proved necrotic and further studies were not possible. Kerber [13] reported Lr32 in *T. tauschi*, a partially dominant gene acting as recessive in hexaploid background depending on change of environment.

The studies on specific resistance in eight cultivars indicated operation of 1 to 3 genes in different varieties. Among these, Sr 6, Sr11, Sr9e and Sr 26 were the already identified genes. A number of other genes confering resistance may be responsible for avirulance to most of the Indian pathotypes. The independence of all the genes, except Sr 26 for the races 40 and 295, indicates that in present breeding programme in the various countries, are pyramiding specific genes for resistance to specific races present in any region.

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