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Effect of infection types of selected wheat cultivars and differentials, set A and B against six pathotypes of *Puccinia striiformis* under environmental conditions

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ABSTRACT

Wheat (Triticum aestivum L.) is the second most important cereal crop next to rice in India. Green revolution has changed India from importer to exporter of wheat. Rust is one of the most devastating diseases of wheat worldwide and are known historically for causing plant disease epidemics. Stripe or yellow rust caused by Puccinia striiformis Western f.sp. tritici Eriks. is a specialized pathogen consisting of races with different virulence spectra. Hence present studies were conducted at SKUAST-J, Research Farm, Chatha with objectives to generate genetic back ground information of selected wheat cultivars to pathotypes of P. striiformis.The pattern of host pathogen interaction between selected cultivars (RSP 561, JAUW 584, JAUW 598 and RAJ 3765) and six pathotypes 78S84, 46S119, 46S103, 47S102, 70S69 and 67S8 of P. striiformis was revealed that only 4 pathotypes(46S103, 47S102, 70S69 and 67S8) permitted for postulation of host resistance gene(s). Effect of Agra Local (AL) back ground on Yr expression in selected wheat cultivars, direct and reciprocal crosses were made between above bread wheat cultivars with susceptible AL to generate F_1 and F_2 seeds. F_1 population of RSP 561 showed dominant nature of resistance against all the selected pathotypes and F_2 population showed the presence of two dominant genes confirming resistance against 46S103 and 47S102 but one dominant and one recessive gene confirming the resistance against 70S69 and 67S8.F_1 population of JAUW 584 revealed the dominant nature of resistance against 46S103, 70S69 and 67S8 pathotypes. F_2 population showed the presence of two dominant genes confirming resistance to 46S103 and 67S8. While one dominant independent gene confirming the resistance to 70S69.F_1 population of JAUW 598 revealed dominant nature of resistance against all the test pathotypes. F_2 population showed the presence of one dominant and one recessive gene against the 46S103 and 67S8 while three dominant independent genes and two dominant genes confirming the resistance against 47S102 and 70S69 respectively. F_1 population of RAJ 3765 showed dominant nature of resistance and F_2 segregation showed the presence of one dominant genes confirming resistance against 47S102.

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INRODUCTION

Wheat is a major staple food for mankind in many parts of the world with 729 million tons produced during 2014 (FAO STAT, 2015). It is cultivated on 15.4% of the arable land in the world in almost all countries, except the humid and high-temperature areas in the tropics and high-latitude environments. Increasing wheat yield potential in the developing world is a primary aim for food security concern (Duveiller *et al.,* 2007). Due to consistent increase in the world population, there is a need of 60% increase in wheat production to meet the requirement of developing world till 2050 (Singh and Trethowan, 2007; Singh *et al.*, 2007; Rosegrant and Agcaoili, 2010).Wheat(*Triticum aestivum* L.) is one of the most important cereal crops of India. In India wheat is cultivated over an area of 31.34 million hectares (2014-15) and is second largest wheat producing country after China. In Jammu and Kashmir, wheat is grown over an area of 291 thousand hectares with a production and productivity of 582 thousand quintals and 20 quintals per hectares (Anonymous, 2015). Today, the most challenging task for wheat breeders is to increase grain yield as well as to improve the grain quality of crop for end products (Goutam *et al.*, 2013). Biotic stresses such as diseases, rust (leaf, stem, and stripe), powdery mildew and karnal bunt have been reported to produce devastating consequences on wheat quality and production

(Keller *et al.,* 2008; Goyal and Prasad, 2010). The rusts of wheat is caused by fungal pathogens that can be disseminated thousands of kilometers by wind and are capable of causing considerable economic loss throughout the world (Kolmer, 2005; Goyal and Prasad, 2010). Cultivation of susceptible cultivars coupled with very early infection of the disease causes 100 per cent yield losses (Afzal *et al*., 2007). Yield reduction varies depending upon the time of infection, severity of disease, and the duration of infection in the major grain-producing parts of the wheat plant (Murray *et al.*, 1994; Line, 2002).

MATERIAL AND METHOD

Recording of host-pathogen interaction

Theinoculated seedlings were ready for observation after 14-15 days of incubation. The infection types were recorded according to the classification of Jonston and Mains (1932) against different pathotypes. For an easy categorization of resistant and susceptible reaction types, the following table was used.

Recording of host-pathogen interaction

Reaction type	Category	Description of symptoms
0; (naught fleck)	**Immune**	No visible infection
; - (fleck minus)	**Nearly immune**	Slight necrosis
; (fleck)	**Very resistant**	No uredia but hypersensitive fleck
1 (one)	**Very resistant**	Uredia minute, surrounded by distinct necrotic area
2 (two)	**Moderately resistant**	Uredia small to medium , surrounded by chlorotic or necrotic border
3 (three)	**Moderately susceptible**	Transverse banding is visible sometime
33+ (three three +)	**Susceptible**	Uredia profusely sporulating
3+/4 (three plus/ four)	**Highly susceptible**	Uredia profusely sporulating and form stripes in adult plants
X	**Heterogeneous**	Variable type of uredia
Y	**Heterogeneous**	Susceptible type of uredia at the tip and resistant towards the base of leaf
Z	**Heterogeneous**	Resistant type of uredia at the tip and susceptible type towards the leaf base

Genetic stock and cultivars

In the present study the seeds of four promising bread wheat cultivars *i.e*, RSP 561, JAUW598, JAUW584, and RAJ3765, susceptible line Agra Local (AL) and including two sets of isogenic lines/differentials (Set A & B), with known genes for resistance to yellow rust, were obtained from Division of Plant Breeding & Genetics, SKUAST-Jammu.

RSP 561: The variety is double dwarf with medium early maturity and awned ears. Showing resistance to all the three wheat rusts. It was released in 2015 by SKUAST of Jammu.

JAUW 584: The variety is semi-dwarf, timely sown, irrigated condition with medium early maturity . It was showing resistance to all the three wheat rusts. It is an advance line under release by the State Varietal Release Committee (proposal submitted).

JAUW 598: The variety is semi-dwarf, late sown for unirrigated condition and showing resistance to all the three wheat rusts. It is an advance line under release by the State Varietal Release Committee (proposal submitted).

RAJ 3765: The variety is double dwarf with medium early maturity, showing resistance to all the three wheat rusts and recommended for North Western plain zone.It was released in 1994/95.

Agra Local: It is a tall wheat cultivar, which was in past grown in western Uttar Pradesh. Grains are red, hard and bold with good chapatti making quality. It is highly susceptible to all the Indian pathotypes of stripe and leaf rust, in the seedling and adult stages. Mehta used this cultivar in 1923 for maintaining the rust cultures on Agra Localat Regional Research Station (IIW&BR) Shimla. It is used as a susceptible parent for inheritance studies in India.

The pedigree of selected cultivars.

Cultivar	Pedigree	Year of release
RSP 561	HD 2637/*Ae. crassa* / HD 2687	2015
JAUW 584	PDW 233/*Ae. crassa*/ PBW 343	Advance Line
JAUW 598	HD 4702/*Ae. sharonemsis*/ HD 2687	Advance Line
RAJ 3765	HD2402/VL639	1994-95
Agra Local	----------	------

Pathotypes

Six pathotypes 78S84, 46S119, 46S103, 47S102, 70S69 and 67S8 of *Puccinia striiformis* were used for the seedling evaluation. Pure, viable urediospores of eachpathotype was obtained from Regional Research Station (IIWBR) Shimla (HP).

RESULTS

Infection types of selected wheat cultivars and differentials, set A and B against six pathotypes of *Puccinia striiformis.*

Four improved bread wheat cultivars *i.e*, RSP 561, JAUW 584, JAUW 598, RAJ 3765 and near isogenic wheat genotypes included in sets of differential Set A and B, were evaluated against host pathogen interaction*viz., six* pathotypes (78S84, 46S119, 46S103, 47S102, 70S69 and 67S8) of *Puccinia strifformis* causing stripe rust, at seedling stage in poly house. Infection types (ITs) of cultivars and Agra Local to the six pathotypes are presented in table 1. The reaction pattern of cultivar RSP 561 showed resistance (ITs ;, 2) to all pathotypes except 78S84,which was susceptible (IT 3+). JAUW 584 showed resistance (ITs ;, 0;) to three pathotypes, 46S103, 70S69 and 67S8, whereas 78S84, 46S119 and 47S102 pathotypes exhibited susceptible reaction (ITs 3, 3+). The interaction of JAUW598 was resistant (IT 0;) against most of the pathotypes (46S103, 47S102, 70S69 and 67S8), however 78S84 and 46S119 having susceptible reaction (IT 3). RAJ 3765 showed high degree of susceptibility (ITs 3, 3+, 3-) to most of the pathotypes except 47S102, which showed resistance (IT 0;). Susceptible check Agra Local showed susceptible reaction (IT 3+) to all the pathotypes. The pattern of host pathogen interaction did not permit postulation of genes for resistance in test cultivars with pathotypes 78S84 and 46S119, because these pathotypes were having high degree of susceptibility with test cultivars. Therefore, only four pathotypes (46S103, 47S102, 70S69 and 67S8) were selected for further studies.

Reaction pattern of six pathotypes (78S84, 46S119, 46S103, 47S102, 70S69 and 67S8) on differential, set A and set B is depicted in Table 1. The data reveal that *Yr9+* was resistant (IT 0;) to all the test pathotypes, *Yr9* showed resistant reaction (IT 0;) against four pathotypes (46S103, 47S102, 70S69 and 67S8) and susceptible reaction (IT 3+) against 78S84 and 46S119 pathotypes. *Yr2+* was resistant (IT ;) against three pathotypes (78S84, 70S69 and 67S8) but susceptible to other three pathotypes (46S119, 46S103 and 47S102). *Yr2KS* was susceptible (ITs 3, 3+) against most of the pathotypes except 70S69 and 67S8 (ITs 1+, 2+). Reaction of these pathotypes was always compared before recording the inoculated sets to ensure purity of the above virulence.

The reaction pattern of cultivar RSP 561 showed resistance to all pathotypes except 78S84. JAUW 584 demonstrated resistance to three pathotypes 78S84, 46S119 and 47S102. The interaction of JAUW 598 was resistant against most of the pathotypes 46S103, 47S102, 70S69 and 67S8 except 78S84 and 46S119. RAJ 3765 showed high degree of susceptibility against most of the pathotypes except 47S102. The most important and widely used yellow rust resistance genes *Yr*9, became susceptible in India during 1996 by the emergence of new pathotype 46S119 and in 2001 with the emergence of new pathotype 78S84, having an additional virulence on *Yr*27, rendered the most popular mega-wheat variety PBW 343 susceptible (Prashar *et al.,* 2007).The pattern of host pathogen interaction did not permit postulation of gene(s) for resistance in test cultivars having susceptible type of reaction.

Table 1. Infection types of selected wheat cultivars and differentials, set A and B against six pathotypes of *Puccinia striiformis.*

Cultivar	Pathotypes					
	78S84	**46S119**	**46S103**	**47S102**	**70S69**	**67S8**
RSP 561	3+	2	;	;	;	;
JAUW 584	3	3	;	3+	0;	0;
JAUW 598	3	3	0;	0;	0;	0;
RAJ 3765	3+	3+	3-	0;	3-	3+
Agra Local	3+	3+	3+	3+	3+	3+
Differential set A						

Chinese 166 (*Yr1*)	0;	;	;	3+	;	3-
Lee (*Yr7*)	3+	3+	3+	3+	3+	3+
Heines Kolben (*Yr6*)	3+	2,3	2,3	2,3	2,3	2+
Vilmorin 23 (*Yr3*)	3+	2,3	2,3+	2,3+	2+	2+
Moro (*Yr10*)	0;	0;	0;	0;	0;	0;
Strubes Dickkopf	0;	3+	3+	3+	;1	;1,2
Suwon 92 X Omar	3+	0;	0;	0;	3+	3+
Riebesel 47/51 (*Yr9+*)	0;	0;	0;	0;	0;	0;
Differential set B						
Hybrid 46 (*Yr4*)	0;	3+	3+	2	1,2	0;
Heines VII (*Yr2+*)	0;	3+	3+	3+	;	0;
Compare (*Yr8*)	0;	2,3	3	3	2,3	2+
T. seelta album (*Yr5*)	0;	0;	0;	0;	0;	1,.2
Tc* 6/*Lr26* (*Yr9*)	3+	3+	0;	0;	0;	0;
Sonalika (*Yr2+*)	;	3+	3+	3+	;	;
Kalyansona *Yr2(KS)*	3+	3	3+	1+	3+	2+

Inheritances of resistance studies

To investigate the effect of Agra Local (AL) back ground on *Yr* expression in selected four cultivars, RSP 561, JAUW 584, JAUW 598 and RAJ 3765 were crossed with susceptible cultivar AL and its reciprocal crosses were also made to develop F_1 population. F_1 populationwas multiplied to F_2 generation for F_2 seeds. F_1 and F_2 seeds were analyzed for resistance against four selected pathotypes 46S103, 47S102, 70S69 and 67S8 at seedling stage. The infection types obtained in F_1 were considered to determine dominanceor recessiveness of resistance. The Chi-square (**χ^2**) was calculated on the basis of two classes namely resistant and susceptible in F_2 generation. Seedling studies were done in the polyhouse.

Genetic analysis of resistance in RSP 561

Infection types on RSP 561, AL, F_1 and F_2 generation of RSP 561 x AL cross and its reciprocal cross at seedling stage against the pathotypes 46S103, 47S102, 70S69 and 67S8 has been presented in Table 2.

Genetic analysis of segregating F_2 seedlings to pathotype 46S103

The data presented in table 2 indicated that infection type of parental line RSP 561 was resistant (IT ;) while Agra Local had susceptible type of reaction (IT 3+). The F_1 seedlings of cross RSP 561 X AL showed resistance (IT ;). This indicated that the resistance in RSP 561 against above pathotype was dominant in nature. F_2 seedlings of the above cross segregated for 247 resistant and 18 susceptible reactions, reflecting the ratio of 15R:1S (**χ^2 = 0.1336, p= 0.7147**). In reciprocal crosses, the resistance in F_1 was dominant and F_2 seedlings segregated as 222 resistant and 15 susceptible reactions, deriving the ratio of 15R:1S (**χ^2 = 0.0026, p= 0.9593**). Identical F_2 segregation of the reciprocal cross ruled out any cytoplasmic effect in controlling resistance. Results obtained from direct and reciprocal crosses of parents indicated the presence of two dominant independent genes conferring resistance to these pathotypes.

Table 2:Segregation pattern in F_2 seedlings of crosses RSP 561 x Agra local and reciprocal cross against pathotypes (46S103, 47S102, 70S69 and 67S8) of *Puccinia striiformis.*

Cross	Parent /Gen.	ITS	Total seedlings	Reaction		Expected ratio	(χ^2)	P. value
				R	S			
Pathotype 46S103								
RSP 561 x AL	RSP 561	;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	;	5	5	0	-	-	-
	F_2	;,1,3+	265	247	18	15R:1S	0.1336	0.7147
AL x RSP 561	F_1	;	6	6	0	-	-	-
	F_2	;,1,2,3+	227	222	15	15R:1S	0.0026	0.9593
Pathotype 47S102								
RSP 561 x AL	RSP 561	;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	;	7	7	0	-	-	-
	F_2	;,1,2,3+	215	201	14	15R:1S	0.0249	0.8746
AL x RSP 561	F_1	;	6	6	0			
	F_2	;,1,2,3+	205	193	12	15R:1S	0.0546	0.8152
Pathotype 70S69								
RSP 561 x AL	RSP 561	;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	;	6	6	0	-	-	-

	F_2	;,1,2,3+	197	164	33	13R:3S	0.5172	0.4720
AL x RSP 561	F_1	;	6	6	0	-	-	-
	F_2	;,1,2,3+	208	172	36	13R:3S	0.2840	0.5941
Pathotype 67S8								
RSP 561 x AL	RSP 561	;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	;	6	6	0	-	-	-
	F_2	;,1,2,3+	228	183	45	13R:3S	0.1457	0.7024
AL x RSP 561	F_1	;	4	4	0	-	-	-
	F_2	;,1,2,3+	217	179	38	13R:3S	0.2189	0.6398

Genetic analysis of segregating F_2 seedlings to pathotype 47S102

The table 2 further indicated that the parent RSP 561 showed resistant reaction (IT ;), while Agra Local (AL) had susceptible reaction (IT 3+) against the pathotype 47S102. Seeds of F_1 cross of RSP 561 x AL and AL x RSP 561 were resistant (IT **;)** showing dominant nature of resistance against above pathotype. The segregation of seedlings in F_2 showed 201 resistant and 14 susceptible reactions and 193 resistant and 12 susceptible outcomes in direct and reciprocal cross, respectively, in the ratio of 15R : 1S (**χ^2 = 0.0249, p= 0.8746 & χ^2 = 0.0546, p= 0.8152,** respectively). Data of reciprocal cross revealed that cytoplasm did not play any role in the inheritance of resistance to this pathotype and seedlings segregated in the ratio of 15R : 1S indicated that two dominant independent genes conferring resistance to this pathotype.

Genetic analysis of segregating F_2 seedlings to pathotype 70S69

The data presented in table 2 indicate that RSP 561 was resistant (IT ;) while Agra Local had susceptible type of reaction (IT 3+). The F_1 of RSP 561 x Agra Local cross and its reciprocal cross showed resistant type of reaction (IT ;). This indicates that the resistance in RSP 561 to above pathotype is dominant. F_2 seedlings of the above cross segregated for 164 resistant and 33 susceptible results, showing the ratio of 13R:3S (**χ^2 = 0.5172, p= 0.4720**). Analysis of reciprocal cross also sported the above study. The resistance in F_1 was dominant and F_2 seedlings segregated as 172 resistant and 36 susceptible types, deriving the ratio of 13R:3S (**χ^2 = 0.2840, p= 0.5941**). Identical F_2 segregation of the reciprocal cross ruled out any cytoplasmic effect in controlling the resistance. Results from direct and reciprocal crosses indicated the presence of one dominant and one recessive genes, conferring resistance to this pathotypes.

Genetic analysis of segregating F_2 seedlings to pathotype 67S8

The data presented in table 2 indicate that interaction type of 67S8 pathotype on RSP 561 was resistant type of reaction (IT ;), while Agra Local had susceptible (IT 3+) and F_1 of RSP 561 x AL cross and its reciprocal cross was (IT ;), showed dominant nature of resistance against above pathotype. The segregation of seedlings in F_2 showed 183 resistant and 45 susceptible in the direct cross and 179 resistant and 38 susceptible types in reciprocal cross and seedlings segregated in the ratio of 13R:3S (**χ^2 = 0.1457, p= 0.7024 and χ^2 = 0.2189, p= 0.6398, respectively**) indicated that the presence of one dominant and one recessive genes conferring resistance to this pathotype.

Genetic analysis of resistance in JAUW 584

Infection type of parental line JAUW 584, AL, F_1 and segregation pattern of F_2 generation from direct and reciprocal crosses at seedling stage against pathotypes viz., 46S103, 47S102, 70S69 and 67S8 have been presented in Table 3.

Genetic analysis of segregating F_2 seedlings to pathotype 46S103

The data presented in table 10 indicate thatparental line JAUW 584 was resistant (IT ;) while Agra Local had susceptible type of reaction (IT 3+). The F_1 of JAUW 584 x AL cross showed (IT ;) identical to its parent against the pathotype 46S103. Resistance in F_1 generation of the above cross showed dominant nature of gene expression in both direct and reciprocal cross. F_2 generation of direct cross segregated for 245 resistance seedlings and 19 susceptible seedlings, which fitted in the ratio of 15R:1S (**χ^2 = 0.4040, p= 0.5250**). Reciprocal cross of AL x JAUW 584 also followed the same pattern of inheritance and the segregation of seedlings in F_2 showed 185 resistant and 12 susceptible seedlings and segregated in the ratio of 15R:1S (**χ^2 = 0.0083, p= 0.9287),** which ruled out any cytoplasmic effect in controlling the resistance. The analysis confirmed the presence of two dominant independent genes governing JAUW 584 against the above pathotype.

Genetic analysis of segregating F_2 seedlings to pathotype 47S102

The table 3 further indicated thatboth parents JAUW 584 and AL showed susceptible type of reaction (ITs 3, 3+). The direct and reciprocal crosses also showed susceptible reaction in F_1 generation against pathotype 47S102, therefore, the F_1 generation was discarded.

Table 3:Segregation pattern in F_2 seedlings of crosses JAUW 584 x Agra local and reciprocal crosses against pathotypes (46S103, 47S102, 70S69 and 67S8) of *Puccinia striiformis*.

Cross	Parent/ Gen.	ITs	Total seedlings	Reaction		Expected ratio	(χ^2)	P. value
				R	S			
Pathotype 46S103								
JAUW 584 x AL	JAUW 584	;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	;	7	7	0	-	-	-
	F_2	;,1,2,3+	264	245	19	15R:1S	0.4040	0.5250
AL x JAUW 584	F_1	;	6	6	0			
	F_2	;,0;,1,3+	197	185	12	15R:1S	0.0083	0.9287
Pathotype 47S102								
JAUW 584 x AL	JAUW 584	3	10	0	10	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	3+	5	0	5	-	-	-
	F_2	-	-	-	-	-	-	-
AL x JAUW 584	F_1	3	6	0	6	-	-	-
	F_2	-	-	-	-	-	-	-
Pathotype 70S69								
JAUW 584 x AL	JAUW 584	0;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	0;	5	5	0	-	-	-
	F_2	;,0;,2,3+	270	207	62	3R;1S	0.5975	0.4395
AL x JAUW 584	F_1	0;	6	6	0	-	-	-
	F_2	0;,1,2,3+	255	198	57	3R;1S	0.9529	0.3290
Pathotype 67S8								
JAUW 584 x AL	JAUW 584	0;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	0;	7	7	0	-	-	-
	F_2	0;,1,2,3+	240	226	14	15R:1S	0.0711	0.7899
AL x JAUW 584	F_1	0;	6	6	0	-	-	-
	F_2	;,1,2,3+	265	249	16	15R:1S	0.0202	0.8875

Genetic analysis of segregating F_2 seedlings to pathotype 70S69

The data presented in table 3 indicate thatinfection types of parental line JAUW 584 was resistant (ITs 0;) while Agra Local showed susceptible type of reaction (IT 3+). The F_1 seedlings of JAUW 584 x AL cross and its reciprocal cross showed resistant reaction (IT 0;). This indicated that the resistance in RSP 561 against above pathotype is dominant in nature. F_2 seedlings of the above direct cross segregated for 207 resistant and 62 susceptible seedlings depicted the ratio of 3R:1S (**χ^2 = 0.5975, p= 0.4395**). In reciprocal cross of F_2 seedlings segregated as 198 resistant and 57 susceptible types, exhibited the ratio of 3R:1S (**χ^2 = 0.9529, p= 0.3290**) and confirmed the above findings. Identical F_2 segregation of the reciprocal cross ruled out any cytoplasmic effect in controlling resistance. Results obtained from direct and reciprocal crosses of parents indicated that the presence of a dominant gene against above pathotype in JAUW 584.

Genetic analysis of segregating F_2 seedlings to pathotype 67S8

The data presented in table 10 indicate that JAUW 584 was resistant (IT 0;) while Agra Local showed susceptible type of reaction (IT 3+) against the 67S8 pathotype. Seedlings reaction of F_1 JAUW 584 x AL cross was resistant (IT 0;) and showed dominant nature of resistance against the above pathotype. The segregation of seedlings in F_2 showed 226 resistant and 14 susceptible results in the direct cross and 249 resistant and 16 susceptible outcomes in the reciprocal cross inheritance of resistance to this pathotype and seedlings segregated in the ratio of 15R:1S (**χ^2 = 0.0711, p= 0.7899 and χ^2 = 0.0202, p= 0.8875, respectively**). Seedlings segregation of reciprocal cross revealed that cytoplasm played no role in the inheritance of resistance to this pathotype. The analysis confirmed the presence of two dominant independent genes governing in JAUW 584 against the above pathotype.

Genetic analysis of resistance in JAUW 598

Infection types of parental lines JAUW 598, AL, F_1 and segregation pattern of F_2 generation of direct and reciprocal crosses against pathotypes 46S103, 47S102, 70S69 and 67S8 have been presented in Table 4.

Table 4: Segregation pattern in F_2 seedlings of cross JAUW 598 x Agra local and reciprocal cross against pathotypes (46S103, 47S102, 70S69 and 67S8) ***Puccinia striiformis.***

Cross	Parent/ Gen.	ITs	Total seedlings	Reaction		Expected ratio	(χ^2)	P. value
				R	S			
Pathotype 46S103								
JAUW 598 x AL	JAUW 598	0;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	0;	4	4	0	-	-	-
	F_2	;,0;,3+	270	216	54	13R:3S	0.2761	0.5993
AL x JAUW598	F_1	0;	5	5	0	-	-	-
	F_2	;,1,2,3+	254	210	44	13R:3S	0.3387	0.5604
Pathotype 47S102								
JAUW 598 x AL	JAUW 598	0;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	0;	4	4	0	-	-	-
	F_2	0;,1,2,3+	262	258	4	63R:1S	0.0020	0.8875
AL x JAUW598	F_1	0;	6	6	0	-	-	-
	F_2	0;,1,2,3+	270	265	5	63R:1S	0.1465	0.7019
Pathotype 70S69								
JAUW 598 x AL	JAUW 598	0;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	0;	6	6	0	-	-	-
	F_2	0;,1,2,3+	208	194	14	15R:1S	0.0821	0.7746
AL x JAUW598	F_1	0;	5	5	0	-	-	-
	F_2	0;,1,2,3+	192	181	11	15R:1S	0.0889	0.7655
Pathotype 67S8								
JAUW 598 x AL	JAUW 598	0;	10	10	0	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	0;	4	4	0	-	-	-
	F_2	0;,1,2,3+	280	233	47	13R:3S	0.7092	0.3998
AL x JAUW598	F_1	0;	6	6	0	-	-	-
	F_2	0;,1,2,3+	216	180	36	13R:3S	0.6154	0.4329

Genetic analysis of segregating F_2 seedlings to pathotype 46S103

The data presented in table 4 indicate thatparental lines of JAUW 598 were resistant (IT ;) while Agra Local had susceptible type of reaction (IT 3+). The F_1 of JAUW 598 x AL cross and its reciprocal cross showed resistance (ITs ;). This indicates the presence of dominant nature of resistance against the above pathotype. F_2 of the above cross segregated for 216 resistant and 54 susceptible seedlings presented the ratio of 13R:3S (**χ^2 = 0.2761, p= 0.5993**). Analysis of reciprocal cross also sported the above study. F_2 from reciprocal cross segregated as 210 resistant and 44 susceptible seedlings, resulted in deriving the ratio of 13R:3S (**χ^2 = 0.3387, p= 0.5604**). Identical F_2 segregation of the reciprocal cross ruled out any cytoplasmic effect in controlling resistance. Results from direct and reciprocal crosses indicated the presence of one dominant and one recessive genes, conferring resistance to this pathotype.

Genetic analysis of segregating F_2 seedlings to pathotype 47S102

The table 4 further indicated that JAUW 598 was resistant (IT ;), while, Agra Local had susceptible type of reaction (IT 3+). The F_1 of JAUW 598 x AL cross showed resistant (IT ;). This indicated that the resistance in JAUW 598 to above pathotypes is dominant. F_2 seedlings of the above cross segregated for 258 resistant and 4 susceptible seedlings showed the ratio of 63R:1S (**χ^2 = 0.0020, p= 0.8875**). Analysis of reciprocal cross also sported the above study. The resistance in F_1 was dominant and F_2 seedlings segregated as 265 resistant and 5 susceptible deriving the ratio of 63R:1S (**χ^2 = 0.1465, p= 0.7019**). Identical F_2 segregation of the reciprocal cross ruled out any cytoplasmic effect in controlling the resistance. Result from direct and reciprocal crosses indicated the presence of three dominant independent genes conferring resistance to this pathotype.

Genetic analysis of segregating F_2 seedlings to pathotype 70S69

The data presented in table 4 indicate thatparent line JAUW 598 was resistant (IT 0;), while, Agra Local had susceptible type of reaction (IT 3+). The F_1 of JAUW 598 x AL cross showed resistant (IT ;) identical to its parent JAUW 598 on inoculation with pathotypes 70S69. Resistances in F_1 generation of above cross showed dominant nature of gene expression. F_2 generation of above crosses segregated for resistance in 194 seedlings and susceptibility in 14 seedlings, which fitted in the ratio of 15R:1S (**χ^2 = 0.0821, p= 0.7746**). Reciprocal cross AL x JAUW 598 also followed the same pattern of inheritance and the segregation of seedlings in F_2 showed 181 resistant and 11 susceptible types. These seedlings segregated

in the ratio of 15R:1S (**χ^2 = 0.0889, p= 0.7655)** which ruled out any cytoplasmic effect in controlling resistance. The analysis confirmed the presence of two dominant independent genes governing in JAUW 598 against the above pathotype.

Genetic analysis of segregating F_2 seedlings to pathotype 67S8

The table 4 further indicated that JAUW 598 was resistant (IT 0;) while Agra Local had susceptible type of reaction (IT 3+). The F_1 of JAUW 598 x AL cross showed resistance (IT 0;). This indicates that the resistance in JAUW 598 to above pathotypes is dominant. F_2 seedling of the above cross segregated for 233 resistant and 47 susceptible seedlings showing the ratio of 13R:3S (**χ^2 = 0.7092, p= 0.3998**). Analysis of reciprocal cross also sported the above study. The resistance in F_1 was dominant and F_2 seedlings segregated as 180 resistant and 36 susceptible results, deriving the ratio of 13R:3S (**χ^2 = 0.6154, p= 0.4329**). Identical F_2 segregation of the reciprocal cross ruled out any cytoplasmic effect in controlling resistance. Result from direct and reciprocal crosses revealed that the presence of one dominant and one recessive genes, conferring resistance to 67S8 pathotype.

Genetic analysis of resistance in RAJ 3765

Infection type of parental line RAJ 3765, AL, F_1 and segregation pattern of F_2 generation of RAJ 3765 x AL cross and its reciprocal cross at seedling stage against pathotypes 46S103, 47S102, 70S69 and 67S8 have been presented in Table 5.

Genetic analysis of segregating F_2 seedlings to pathotype 46S103

The data presented in table 5 indicate thatboth the parents RAJ 3765 and Agra Local were susceptible (ITs 3, 3+) against pathotype 46S103. F_1 population of direct and reciprocal cross also showed susceptible reaction against the above pathotypes. So F_1 population was not multiplied for further analysis.

Table 5:Segregation pattern in F_2 seedlings of cross RAJ 3765 x **Agra local and reciprocal cross against pathotypes (46S103, 47S102, 70S69 and 67S8) of *Puccinia striiformis.***

Cross	Parent/ Gen.	Infection type	Total seedlings	Reaction		Expected ratio	(χ^2)	P. value
				R	S			
Pathotype 46S103								
RAJ 3765 x AL	RAJ 3765	3	10	0	10	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	3+	6	0	6	-	-	-
	F_2	-	--	-	-	-	-	-
AL x RAJ 3765	F_1	3+	5	0	5	-	-	-
	F_2	-	--	-	-	-	-	-
Pathotype 47S102								
RAJ 3765 x AL	RAJ 3765	0;	10	10	0	-	-	-
	AL	3+	6	0	6	-	-	-
	F_1	0;	5	5	0	-	-	-
	F_2	0;,2,3+	224	177	47	3R:1S	1.9286	0.1649
AL x RAJ 3765	F_1	0;	6	6	0			
	F_2	0;,2,3+	192	149	43	3R:1S	0.6944	0.4048
Pathotype 70S69								
RAJ 3765 x AL	RAJ 3765	3-	10	0	10	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	3	6	0	6	-	-	-
	F_2	-	--	-	-	-	-	-
AL x RAJ 3765	F_1	3+	6	0	6	-	-	-
	F_2	-	-	-	-	-	-	-
Pathotype 67S8								
RAJ 3765 x AL	RAJ 3765	3	10	0	10	-	-	-
	AL	3+	10	0	10	-	-	-
	F_1	3	4	0	4	-	-	-
	F_2	-	-	-	-	-	-	-
AL x RAJ 3765	F_1	3+	5	0	5	-	-	-
	F_2	-	-	-	-	-	-	-

Genetic analysis of segregating F_2 seedlings to pathotype 47S102

The table 5 further indicated thatwheat cultivar RAJ 3765 was resistant (IT 0;) while AL had susceptible type of reaction (IT 3+) and F_1 seedlings of RAJ 3765 x AL cross showed resistance (ITs 0;) . This indicates the dominant nature of RAJ 3765 to above pathotype. F_2 seedlings of the above cross segregated for 177 resistant and 47 susceptible seedlings reflected the ratio of 3R:1S (**χ^2 = 1.9286, p= 0.1649**). F_2

seedlings of reciprocal cross also sported the above study and segregated as 149 resistant and 43 susceptible types, deriving the ratio of 3R:1S (χ^2 **= 0.6944, p= 0.4048**) and confirmed the above findings. The cytoplasm has no effect in controlling resistance. The data confirmed the presence of a dominant gene against above pathotype in RAJ 3765.

Genetic analysis of segregating F_2 seedlings to pathotype 70S69

The table 5 further indicated thatboth parents RAJ 3765 and AL were susceptible (IT 3 & 3+) against pathotype 70S69, F_1 population of direct and reciprocal cross also showed susceptible reaction against the above pathotypes. So, F_1 population was not multiplied for further analysis.

Genetic analysis of segregating F_2 seedlings to pathotype 67S8

The data presented in table 5 also indicate thatboth parents RAJ 3765 and AL were susceptible (ITs 3, 3+) against pathotype 67S8, F_1 population of direct and reciprocal cross also showed susceptible type of reaction against the above pathotypes. Therefore, F_1 population was not multiplied for further analysis

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