

Inheritance of Newly Identified Asiatic Rust Resistance Source EC 242104 in Soybean

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ABSTRACT: An experiment was carried out at ARS., Kasbe Digraj, Sangli to study the inheritance of Asiatic rust resistance in a newly identified resistant source (EC 242104) of soybean in *Kharif* 2022. For this purpose, two crosses were made viz., Cross I JS 2098 x EC 242104 and Cross II KDS 753 x EC 242104 and various generations (F₁ & F₂) of these crosses were evaluated along with their parents (P₁ and P₂) and susceptible check (JS 335). In order to spread infection, susceptible check JS 335 was sown on the border row and in between the lines. The distribution of rust grade, on a scale of 0 to 7, was noted for lesion types that were immune, reddish brown (RB) or resistant and TAN lesion or susceptible. The study revealed that in cross-I JS 2098 x EC 242104, the F₂ progenies segregated in 3 resistant: 1 susceptible ratio indicating monogenic dominant inheritance of resistance to soybean rust. In cross-II KDS 753 x EC 242104, the F₂ progenies segregated in 15 resistant: 1susceptible ratio indicating duplicate gene interaction, when presence of either of dominant gene/allele ensures rust resistance.

Keywords: Soybean, Rust, Inheritance, *Phakospora pachyrhizi*, EC 242104.

INTRODUCTION

Asian soybean rust caused by *Phakospora pachyrhizi* Syd. is one of the most significant barriers to the production of soybeans worldwide (Chander *et al.*, 2019). Although there are many effective management strategies in place to control the disease, breeding resistance is the most effective method. Some studies have shown that rust resistance is qualitatively inherited and controlled by single dominant gene. Bromfield and Hartwig (1980) determined the inheritance of soybean rust resistance in two F₂ populations with PI 230970 and PI 230971 as the resistant parents. Their analysis of F₂'s showed that rust resistance was dominant and qualitatively (simply) inherited. Monogenic dominant inheritance has been also reported by Bhor *et al.* (2014); Parhe *et al.* (2017); Aoyagi *et al.* (2020). Quantitative inheritance has also been reported to control inheritance to soybean rust resistance. Ribeiro *et al.* (2007) reported that soybean rust resistance was quantitatively inherited, which was predominantly controlled by additive gene action. This finding was supported by Maphosa *et al.* (2012) who found that soybean rust resistance was predominantly controlled by additive gene action. To date six dominant genes have been identified: *Rpp1*, *Rpp2*, *Rpp3*, *Rpp4*, *Rpp5*

and *Rpp6*. These genes are not effective against all populations of *P. pachyrhizi* (Bonde *et al.*, 2006; Pham *et al.*, 2009; Miles *et al.*, 2011). More resilient resistance to Asiatic rust can be achieved by pyramiding resistance genes within a single cultivar as *Rpp* genes provides resistance against specific isolates of *P. pachyrhizi* (Bhor *et al.*, 2014).

Previously identified sources of rust resistant lines (Ankur and EC 241780) in soybean that have been widely utilized in breeding programme reported resistant breakdown. The transfer of resistance genes through classical breeding or through marker-assisted selection allows the development of resistant varieties and their use as an efficient and cost effective method for soybean rust control (Rosa *et al.*, 2015). Therefore, studies on the inheritance of resistance in soybean to *P. pachyrhizi* are very important for varieties development.

MATERIAL AND METHODOLOGY

An experiment was carried out to study the inheritance of newly found Asiatic rust resistance source (EC 242104) of soybean in *kharif* 2022 at Agricultural Research Station, Kasbe Digraj, Sangli. Parents, F₁ and F₂ of two crosses (JS 2098 x EC 242104 and KDS 753 x EC 242104) were planted at spacing of 60 x 20cm

(Plate 1). Out of the two conventional parent used for study JS 2098 is rust susceptible and KDS 753 is rust resistance. Susceptible check JS 335 was sown in between lines and on border row to spread infection. The leaves from rust infected fields were collected and in the morning uredospores were oozed out and the uredospore suspension was sprayed on all population at 45 days after sowing. Use of fungicide was avoided.

The severity of rust was scored between 65-90 days after sowing based on percent leaf area infected by using 0-7 scale. Observation on around 500 to 600 F₂ plants were taken for the inheritance study in response to rust under artificial epiphytotic condition. Chi square analysis (Fisher, 1941) was done for testing the segregation ratio of rust resistance genes.



Plate 1. Experimental plot.

RESULTS AND DISCUSSION

A. Lesion types with disease grades in cross I JS 2098 × EC 242104 (Plate 2)

Out of the total 40 plants of P₁ (JS 2098), 4 plants (10%) recorded 7 grade and 15 plants (37.5%) recorded 5 grade while 21 plants (52.5%) recorded 3 grade severe susceptibility to rust showing TAN lesions. Out of 40 plants of P₂ (EC 242104), 4 plants (10%) recorded 5 grade, 11 plants (27.5%) recorded 3 disease grade, 25 plants (62.5%) recorded 1 diseases grade. These plants showed RB lesions with resistant reaction. Out of 31 F₁ of cross JS 2098 × EC 242104 plants, 6

plants (19.35%) were of 1 grade and 18 plants (58.06%) recorded 3 disease grade while 7 (22.58%) plants recorded 5 grade RB lesions showing resistant reaction (Table 1).

In F₂ generation, 42 plants (6.25%) exhibited 1 grade resistant reaction, 311 plants (46.34%) recorded 3 grade resistant reaction. 145 plants (21.60%) recorded 5 grade resistant reaction (RB lesions). 30 F₂ plants (4.47%) recorded 3 grade TAN reaction, 101 plants (15.05%) plants recorded 5 grade TAN lesions and 42 plants (6.25%) recorded 7 grade TAN lesions showing susceptible reaction.

Table 1: Distribution of rust grades in cross I: JS 2098 × EC 242104 to soybean rust in Kharif 2022.

Generations	Number of plants	Immune	RB lesions			TAN lesions			
			Disease grade			Disease grade			
		0	1	3	5	1	3	5	7
P ₁ JS 2098	40	0	0	0	0	0	21	15	4
P ₂ EC 242104	40	0	25	11	4	0	0	0	0
F ₁	31	0	6	18	7	0	0	0	0
F ₂	671	0	42	311	145	0	30	101	42
% of total plants									
Generations	Number of plants	Immune	RB lesions			TAN lesions			
			Disease grade			Disease grade			
		0	1	3	5	1	3	5	7
P ₁ JS 2098	40	0	0	0	0	0	52.5	37.5	10
P ₂ EC 242104	40	0	62.5	27.5	10	0	0	0	0
F ₁	31	0	19.35	58.06	22.58	0	0	0	0
F ₂	671	0	6.25	46.34	21.60	0	4.47	15.05	6.25



Plate 2. Distribution rust lesions in parents and F₁ along with susceptible check in cross I JS 2098 × EC 242104.

B. Lesion types with disease grades in cross II KDS 753 × EC 242104 (Plate 3)

Out of the total 40 plants of P₁ (KDS 753), 22 plants (55%) recorded 1 grade and 14 plants (35%) recorded 3 grade while 4 plants (10%) recorded 5 grade RB lesions showing resistant reaction to rust. Out of 40 plants of P₂ (EC 242104), 4 plants (10%) recorded 5 grade, 11 plants (27.5%) recorded 3 disease grade, 25 plants (62.5%) recorded 1 diseases grade RB lesions showing resistant reaction. Out of 34 F₁ of cross KDS 753 × EC 242104 plants, 8 plants (23.53%) recorded 1 disease grade showing resistant reaction. 24 plants (70.59%)

were of 3 grade and 2 plants (5.88%) were of 5 grade (RB lesions) showing resistant reaction (Table 2). In F₂ generation, 72 plants (12.46%) exhibited 1 grade (RB lesions) resistant reaction, 374 plants (64.71%) recorded 3 grade (RB lesions) resistant reaction. 96 plants (16.61%) recorded 5 grade (RB lesion) resistant reaction. Amongst TAN lesion grades 23 plants (3.97%) recorded 3 grade susceptible reaction. 10 F₂ plants (1.73%) recorded for 5 grade susceptible reaction, while 3 plants (0.32%) showed 7 grade susceptible reaction.

Table 2: Distribution of rust grades in cross II: KDS 753 × EC 242104 to soybean rust in Kharif 2022.

Generations	Number of plants	Immune	RB lesions			TAN lesions			
			Disease grade			Disease grade			
		0	1	3	5	1	3	5	7
P ₁ KDS 753	40	0	22	14	4	0	0	0	0
P ₂ EC 242104	40	0	26	9	5	0	0	0	0
F ₁	34	0	8	24	2	0	0	0	0
F ₂	578	0	72	374	96	0	23	10	3
% of total plants									
Generations	Number of plants	Immune	RB lesions			TAN lesions			
			Disease grade			Disease grade			
		0	1	3	5	1	3	5	7
P ₁ KDS 753	40	0	55	35	10	0	0	0	0
P ₂ EC 242104	40	0	65	22.5	12.5	0	0	0	0
F ₁	34	0	23.53	70.59	5.88	0	0	0	0
F ₂	578	0	12.46	64.71	16.61	0	3.97	1.73	0.52



Plate 3: Distribution rust lesions in parents and F₁ along with susceptible check in cross II KDS 753 × EC 242104.

C. Genetics of resistance to soybean rust

The genetics of soybean rust resistance observed in the present finding is presented cross-wise (Table 3).

Cross-I JS 2098 × EC 242104. The F₁ generation of the cross-I JS 2098 × EC 242104 produced all rust resistant (Immune/RB) plants. This indicated that the resistance to soybean leaf rust was controlled by dominant gene in this cross. In the segregating F₂ generation of the cross JS 2098 × EC 242104, out of the 671 plants studied, 498 were rust resistant (Immune/RB) and 173 were rust susceptible (TAN). The data represent non-significant Chi-square value (0.24) for the expected ratio of 3:1. The observed ratio of 2.88:1.12 closely fitted with the ratio of 3:1 indicating presence of monogenic dominant gene interaction for the inheritance of leaf rust of soybean. Monogenic inheritance controlling rust resistance was also reported by Rahangdale and Raut (2004); Kiryowa *et al.* (2005); Kim *et al.* (2012); Iwo *et al.*, (2012); Aoyagi *et al.* (2020).

Cross II KDS 753 × EC 242104. The F₁ generation of the cross KDS 753 × EC 242104 produced all rust resistant (Immune/RB) plants. This indicated that the resistance to soybean leaf rust was controlled by dominant gene in this cross. In the segregating F₂ generation of the cross KDS 753 × EC 242104, out of the 578 plants studied, 542 were rust resistant (Immune/RB) and 36 were rust susceptible (TAN). The data represent that non-significant Chi-square value (0.10) for the expected ratio of 15:1. The observed ratio of 15.05:0.95 closely fitted with the fitment 15:1 indicated presence of duplicate gene interaction for the inheritance of leaf rust of soybean. This is because KDS 753 (Phule Kimaya) already has dominant rust resistance gene from EC 241780. Thus, presence of two dominant genes resulted into duplicate gene interaction. Duplicate gene action controlling rust resistance in soybean was also reported by Pierozzi *et al.* (2008); Parhe *et al.* (2017).

Table 3: Summarized data on inheritance of rust resistance under field condition in two soybean crosses in Kharif 2022.

Crosses	Generations	Number of observed plants			Expected ratio		Observed ratio		Number of plants expected		CHI square	P value	Gene action
		R	S	Total	R	S	R	S	R	S			
Cross I JS 2098 × EC 242104	P ₁	0	40	40	-	-	-	-	-	-	-	-	-
	P ₂	40	0	40	-	-	-	-	-	-	-	-	-
	F ₁	31	0	31	-	-	-	-	-	-	-	-	-
	F ₂	498	173	671	3	1	2.88	1.12	503.5	167.5	0.24 (NS)	0.62	Monogenic
Cross II KDS 753 × EC 242104	P ₁	40	0	40	-	-	-	-	-	-	-	-	-
	P ₂	40	0	40	-	-	-	-	-	-	-	-	-
	F ₁	34	0	34	-	-	-	-	-	-	-	-	-
	F ₂	542	36	578	15	1	15.05	0.95	541.8	36.12	0.10 (NS)	0.75	Duplicate

CONCLUSIONS

From above findings it is clearly evident that Asiaticrust resistance in cross I JS 2098 × EC 242104 was controlled by single dominant gene. In cross II KDS 753 × EC 242104, two dominant genes controlling resistance reaction resulted into duplicate gene interaction. This is because KDS 753 already contain rust resistance gene from parent EC 241780. Identified exotic germplasm line EC 242104 showed highly resistance reaction.

FUTURE SCOPE

New identified source of Asiatic rust resistance line EC 242104 of soybean can be used in gene pyramiding in combination with previously identified sources of rust resistance lines to develop elite rust resistant soybean.

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