

Differential Response of F₄ and F₅ Recombinant Inbred Lines (RILs) to Powdery Mildew Infection of Green Gram [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Green gram [*Vigna radiata* (L.) Wilczek] being a predominant legume crop of India is severely affected by the devastating foliar disease viz., powdery mildew which is caused by the fungus *Erysiphe polygoni* D.C. In this context, the present investigation was formulated involving F₄ and F₅ generations of RILs of two crosses viz., Chinamung × BL-849 and Chinamung × LM-1668 which has contrasting features for powdery mildew resistance with 146 and 155 Recombinant Inbred Lines (RIL's), respectively. All the RILs in both the crosses have shown variable responses to the powdery mildew screened under field condition. Out of 146 F₄ RILs of the cross Chinamung × BL-849 screened for powdery mildew, one of them was found to be highly resistant (R₀) viz., C1-34-23 and seventy five RILs were found to be moderately resistant (R₂). While, similar lines of 146 F₅ population RILs screened in Rabi season showed fourteen RILs to be highly resistant (R₀). Whereas in cross Chinamung × LM-1668, out of 155 F₄ RILs screened for powdery mildew under field condition, thirty nine RILs were found to be moderately resistant (R₂), while similar 155 F₅ RILs screened in *rabi* season showed one hundred and four moderately resistant (R₂). Some of the lines in both the populations were showing similar responses in both the seasons. The RIL C1-34-23 has shown R₀ response in the cross Chinamung × BL-849, whereas C2-14-11, C2-16-13 RILs has show R₂ response in cross Chinamung × LM-1668 in both seasons, which clearly indicates that these lines have become stable for the disease response. Such lines can be screened for yield related traits to develop highly resistant breeding lines with high yielding ability in green gram.

Keywords: Differential response, RILs, Green gram

GREEN GRAM [*Vigna radiata* (L.) Wilczek] a legume crop predominantly grown in South and South East Asia belongs to the family Fabaceae, with a diploid chromosome number of $2n=2x=22$, is an economically important *Vigna* crop species of Asia (Kang *et al.*, 2014). It is native to the Indo-Burma region with India, Burma, Thailand and Indonesia contributing almost 90 per cent of the world's production (Raturi *et al.*, 2015). In South East Asia, India is the largest produces with a production of 1.5-2 MT from 3-4 m ha area with a productivity of 0.5 t/ha (Pandey *et al.*, 2018). Well drained loam to sandy loam soils are the most suitable soils for green gram cultivation, while saline and alkaline soil or waterlogged soils are not suitable for cultivation. Green gram is considered as the Golden bean because of its nutritional values and suitability for increasing fertility of the soil. The nutritional profile of green gram reveals that it has 24 per cent protein, 10-15 per cent fat, 56-63 per cent carbohydrates and

also minerals and vitamins (Meena Neeraj Kumar *et al.*, 2016). Mature seeds are low in anti-nutritional factors and are highly digestible. It causes less flatulence as compared to other pulses, making it suitable for consumption, especially for children and old people. Green gram starch is considered to have a low glycaemic index and hence, the most suitable source of food for diabetic patients (Swaminathan *et al.*, 2012). In spite of the best efforts for improving the green gram varieties, the yield potential of this crop remains low owing to both biotic and abiotic factors. Powdery mildew caused by the fungus *Erysiphe polygoni* D. C., an obligate pathogen with a wide host range is the most devastating foliar disease of green gram. It is favoured by dry season and cool weather conditions which in turn results in yield reduction ranging from 9-50 per cent. Yield loss due to powdery mildew was reported to be 20-100 per cent in different regions of India (Pandey *et al.*, 2018). Severe infection

can reduce the yield between 20-40 per cent and a complete 100 per cent if infected at the seedling stage (Bainade *et al.*, 2014). The pathogen survives in conidial form on various hosts in the off season. The disease is secondarily spread through air by conidia produced in the season. Breeding for disease resistance is the strategy to avoid severe losses. Considering all the premises, an investigation was carried out to evaluate F₄ and F₅ recombinant inbred lines of green gram for resistance to powdery mildew under field conditions.

MATERIALS AND METHODS

In the study, F₄ and F₅ recombinant inbred lines (RILs) population of two crosses *viz.*, Chinamung × BL-849 and Chinamung × LM-1668, were screened for powdery mildew. The parents utilized in both the crosses were contrasting to powdery mildew resistance were scored for powdery mildew responses. 146 RILs of F₄ of the cross Chinamung × BL-849 and 155 RILs of F₄ of the cross Chinamung × LM-1668, were screened for resistance to powdery mildew. The parents differ for powdery mildew response as shown in Table 1.

TABLE 1

The characteristic features of parents and check varieties (*) of green gram

Parents	Disease reaction	Disease Score
Chinamung (Female)	Susceptible	4
BL 849 (Male)	Highly Resistant	0
LM 1668 (Male)	Highly Resistant	0
*Pusa Baisakhi	Moderately Susceptible	3
*KKM-3	Moderately Susceptible	3

The experiment was conducted during *kharif* 2015 and *rabi* 2015 in Augmented Design with two checks *viz.*, Pusa Baisakhi, KKM-3 and parents *viz.*, Chinamung, BL-849 and LM-1668. Each genotype was grown with a spacing of 30 cm × 10 cm. All the RILs of both the crosses were evaluated under natural field condition for powdery mildew infection in both the seasons. Seeds from randomly selected single plant of every recombinant inbred lines were taken and forwarded to next generation of RILs. Powdery

mildew disease intensity was recorded from the day of infection till harvest at weekly interval and the disease was scored on 0-5 scale as recommended by Reddy *et al.* (1994) (Table 2). The score recorded based on the scale was converted into per cent disease index (PDI) and used for screening. Disease severity

TABLE 2

Powdery mildew scale (Reddy *et al.*, 1994)

Score	Per cent of leaf area infested	Disease reaction
0	0	Highly resistant (R0)
1	0.1-5	Resistant (R1)
2	5.1-30	Moderately Resistant (R2)
3	30.1-65	Moderately susceptible (MS)
4	65.1-90	Susceptible (S)
5	90.1-100	Highly susceptible (HS)

was calculated as PDI to know the extent of damage caused by the disease by following formula :

$$\text{Per cent disease index} = \frac{\text{Sum of all disease rating} \times 100}{\text{Total number of ratings} \times \text{Maximum score}}$$

The one-way analysis of variance (ANOVA) was also used to verify the efficiency of scale, used for powdery mildew disease scoring into different classes based on per cent disease index (PDI) values (Table 3).

RESULTS AND DISCUSSION

Although, green gram is a major pulse crop of India, significant yield reduction upto 40-60 per cent was observed (Pandey *et al.*, 2018). This was attributed to the major fungal disease powdery mildew which is infecting about 90 per cent of green gram production. In addition, powdery mildew is a very serious problem in all areas having rice based cropping systems of India. Powdery mildew is caused by obligate bio-trophic fungus *Erysiphe polygoni* D. C., which is an air borne disease with being particularly important in climates with warm dry day and cool nights. Powdery mildew is one of the economically important disease which reduced the grain yield upto 20-100 per cent (Meena Neeraj Kumar *et al.*, 2016).

TABLE 3
Single factor analysis of variance for powdery mildew to check the significance of scale in F₄ and F₅ RILs of the cross Chinamung × BL 849 of green gram

Source of variation	Chinamung × BL 849							
	F ₄				F ₅			
	Df	Mean sum of squares	F	P-vale	Df	Mean sum of squares	F	P-vale
Between Groups	4	6306.27 **	132.53	9.63E-47	2	7881.09 **	271.66	1.97E-49
Within Groups	141	47.58**			143	29.01 **		
Total	145				145			

Use of host resistant sources is an effective and economical eco-friendly method for managing fungal disease. Hence, identification of sources of resistance to powdery mildew is the quint essential need of the hour. Thus the present investigation was carried out to identify resistant lines from different sources which could be further utilizes as donors for developing resistant varieties.

Recombinant Inbred Lines (RILs) make it possible to screen for powdery mildew resistance and enable to select the best parents for future use. In the present study, an attempt was made to identify recombinant inbred lines resistant to powdery mildew disease in green gram. The results revealed considerable amount of variability among RILs for powdery mildew resistance. Out of 146 F₄ RILs screened for powdery mildew under field condition, one of them was found to be highly resistant (R0) *viz.*, C1-34-23. Seventy five RILs were found to be moderately resistant (R2). Sixty four were found to be moderately susceptible (MS), four were susceptible (S) and two were highly susceptible (HS) *viz.*, C1-451-247 and C1-501-292 in

the cross Chinamung × BL 849. While similar 146 F₅ RILs screened in *rabi* season showed fourteen RILs to be R0, one hundred and nine were R2 and twenty three were found to be MS (Table 5). Whereas, in cross Chinamung × LM 1668, out of 155 RILs screened for powdery mildew in field condition, thirty nine RILs were found to be R2. Eighty five were found to be MS and thirty one found to be S. While similar 155 F₅ RILs screened in *rabi* season showed one hundred and four to be R2. Forty seven were MS and four were found to be S type (Table 6). The varying responses of each RIL screened for powdery mildew over two seasons are presented in Fig.1 and Fig.2. One-way analysis of variance revealed that the scale used for classification is highly significant thus conferring the reliability of scale suggested by Reddy *et al.*, 1994 (Table 3 and Table 4).

The results speculate the different RILs of both the crosses present variable response to powdery mildew in two seasons due to quantitative nature of disease. As shown in Fig.3 and Fig.4, RILs have variable response per disease score in two seasons. Thus, the

Table 4
Single factor analysis of variance for powdery mildew to check the significance of scale in F₄ and F₅ RILs of the cross Chinamung × LM 1668 of green gram

Source of variation	Chinamung × LM 1668							
	F ₄				F ₅			
	Df	Mean sum of squares	F	P-vale	Df	Mean sum of squares	F	P-vale
Between Groups	2	23631.36 **	327.09	8.5E-56	2	13958.27 **	344.98	3.15E-57
Within Groups	152	72.25 **			152	40.46 **		
Total	154							

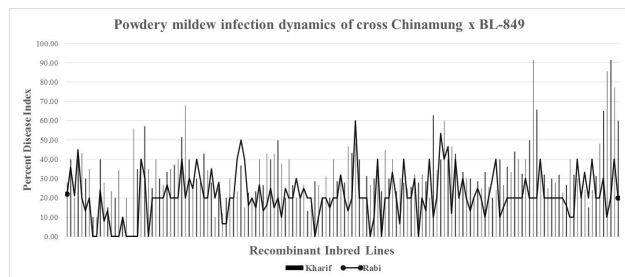


Fig. 1: Powdery mildew infection dynamics of cross Chinamung × BL-849 in green gram.

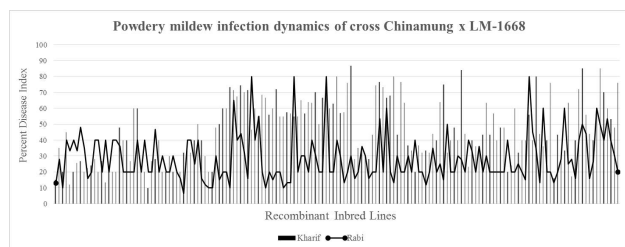


Fig. 2: Powdery mildew infection dynamics of cross Chinamung × LM-1668 in green gram.

population can be used for QTL mapping for dissecting the nature of gene action controlling the disease. However, there is possibility of the RIL populations to be unstable so both the populations should be advanced for further generation so that they become stable. Some of the lines in two populations are showing

similar response in both the seasons (Table 5 and Table 6) which clearly indicates that these lines have

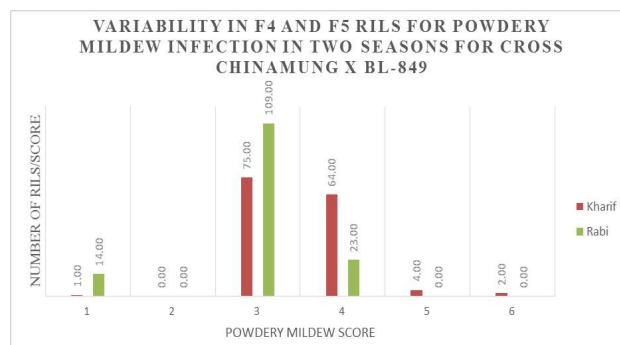


Fig. 3: Varying response of F₄ and F₅ RILs for powdery mildew infection in two seasons for cross Chinamung × BL-849

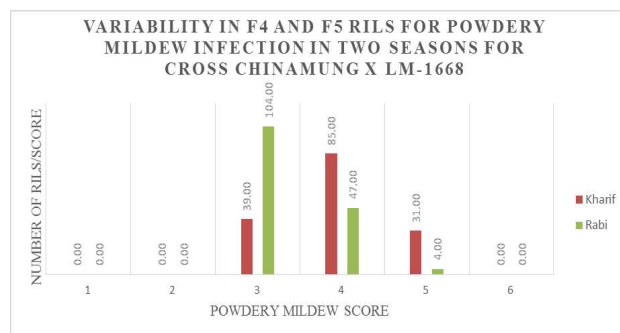


Fig. 4: Varying response of F₄ and F₅ RILs for powdery mildew infection in two seasons for cross Chinamung × LM-1668

TABLE 5
Field screening of 146 F₄ and F₅ RILs for powdery mildew resistance of the cross Chinamung × BL 849 in green gram

Grade	Leaf Area Infected (%)	Disease Reaction	RILs		Total RILs (146)		RILs showing same disease response in F ₄ and F ₅
			F ₄	F ₅	F ₄	F ₅	
0	0	Highly Resistant (R0)	C1-34-23	C1-15-10, C1-15A-11, C1-21A-17, C1-25-19, C1-28-20, C1-32-22, C1-37-23, C1-38-27, C1-41-28, C1-44-31, C1-175-111, C1-236-152, C1-246-159, C1-275-177	1	14	C1-34-23
1	1.1-5	Resistant (R1)	0	0	0	0	
2	5.1-30	Resistant (R2)	C1-9-6, C1-15-10, C1-15A-11, C1-16A-13, C1-17A-14, C1-21A-17, C1-25-19, C1-30-21, C1-32-22, C1-46-32, C1-50A-35, C1-51A-36, C1-78-56, C1-83-58, C1-84-59,	C1-1-1, C1-9-6, C1-13-7, C1-16-12, C1-16A-13, C1-17A-14, C1-30-21, C1-43-30, C1-46-32, C1-48-34, C1-50A-35, C1-51A-36, C1-52-37, C1-65-49, C1-63-47, C1-72-51,	75	109	C1-9-6, C1-16A-13, C1-17A-14, C1-30-21, C1-46-32, C1-50A-35, C1-51A-36, C1-78-56, C1-84-59, C1-91-64, C1-98-65, C1-102-66, C1-

1	2	3	4	5	6	7	8
			C1-89-62, C1-91-64, C1-98-65, C1-102-66, C1-124A-67, C1-104-68, C1-106-69, C1-112-73, C1-122-79, C1-123-80, C1-132-87, C1-135-89, C1-128-85, C1-158-99, C1-161-101, C1-165-102, C1-168-105, C1-169-106, C1-172-109, C1-173-110, C1-175-111, C1-182-116, C1-185-119, C1-195-126, C1-205-132, C1-208-134, C1-214-137, C1-229-148, C1-236-152, C1-241-155, C1-246-159, C1-251-163, C1-260-168, C1-266-170, C1-267-171, C1-268-172, C1-270-174, C1-275-177, C1-283-182, C1-284-183, C1-404-205, C1-408-209, C1-410-211, C1-412-213, C1-413-214, C1-414-215, C1-416-217, C1-417-218, C1-422-221, C1-428-227, C1-463-258, C1-467-262, C1-470-265, C1-472-267, C1-474-268, C1-479-273, C1-481-275, C1-482-276, C1-487-281, C1-488-282	C1-75-54, C1-77-55, C1-78-56, C1-84-59, C1-86-60, C1-88-61, C1-91-64, C1-98-65, C1-102-66, C1-124A-67, C1-104-68, C1-109-69, C1-123-80, C1-132-87, C1-135-89, C1-131-86, C1-128-85, C1-145-93, C1-147-94, C1-148-95, C1-149-96, C1-154-98, C1-158-99, C1-160-100, C1-161-101, C1-165-102, C1-168-105, C1-169-106, C1-172-109, C1-173-110, C1-182-116, C1-185-119, C1-187-120, C1-195-126, C1-196-127, C1-206-132, C1-212-137, C1-217-139, C1-218-140, C1-226-146, C1-229-148, C1-232-150, C1-241-155, C1-247-160, C1-251-163, C1-260-168, C1-266-170, C1-268-172, C1-270-174, C1-274-176, C1-279-179, C1-283-182, C1-289-187, C1-295-190, C1-301-196, C1-404-205, C1-406-207, C1-408-209, C1-410-211, C1-412-213, C1-413-214, C1-414-215, C1-415-216, C1-416-217, C1-417-218, C1-423-222, C1-428-227, C1-429-228, C1-430-229, C1-435-233, C1-445-241, C1-446-242, C1-448-244, C1-450-246, C1-451-247, C1-454-250-, C1-461-256, C1-463-258, C1-467-262, C1-470-265, C1-471-266, C1-472-267, C1-474-268, C1-477-271, C1-478-272, C1-481-275, C1-487-281, C1-489-283, C1-490-284, C1-497-289, C1-500-291, C1-501-292, C1-510-296	124A-67, C1-104-68, C1-106-69, C1-123-80, C1-132-87, C1-135-89, C1-128-85, C1-158-99, C1-161-101, C1-165-102, C1-168-105, C1-169-106, C1-172-109, C1-173-110, C1-182-116, C1-185-119, C1-195-126, C1-205-132, C1-214-137, C1-229-148, C1-241-155, C1-251-163, C1-260-168, C1-266-170, C1-268-172, C1-270-174, C1-283-182, C1-404-205, C1-408-209, C1-410-211, C1-412-213, C1-413-214, C1-414-215, C1-416-217, C1-417-218, C1-428-227, C1-463-258, C1-467-262, C1-470-265, C1-472-267, C1-474-268, C1-481-275, C1-487-281		
3	30.1-65	Moderately Susceptible (MS)	C1-1-1, C1-13-7, C1-16-12, C1-28-20, C1-38-27, C1-41-28, C1-42-29, C1-43-30, C1-44-31, C1-48-34, C1-52-37, C1-65-49, C1-63-47, C1-72-51, C1-36A-53, C1-77-55, C1-86-60, C1-88-61, C1-120-78, C1-131-86, C1-	C1-42-29, C1-36A-53, C1-83-58, C1-89-62, C1-112-73, C1-120-78, C1-122-79, C1-208-134, C1-220-142, C1-242-156, C1-256-165, C1-267-171, C1-284-183, C1-296-191, C1-298-193, C1-300-195, C1-302-197, C1-422-221, C1-	64	23	C1-42-29, C1-36A-53, C1-120-78, C1-220-142, C1-242-156, C1-256-165, C1-457-252

1	2	3	4	5	6	7	8
			145-93, C1-147-94, C1-148-95, C1-149-96, C1-154-98, C1-160-100, C1-187-120, C1-196-127, C1-217-139, C1-218-140, C1-220-142, C1-226-146, C1-232-150, C1-242-156, C1-247-160, C1-256-165, C1-274-176, C1-279-179, C1-289-187, C1-295-190, C1-296-191, C1-298-193, C1-300-195, C1-301-196, C1-302-197, C1-406-207, C1-415-216, C1-423-222, C1-429-228, C1-430-229, C1-435-233, C1-445-241, C1-446-242, C1-448-244, C1-450-246, C1-457-252, C1-461-256, C1-471-266, C1-477-271, C1-478-272, C1-489-283, C1-490-284, C1-497-289, C1-510-296	457-252, C1-479-273, C1-482-276, C1-488-282, C1-506-295			
4	65.1-90	Susceptible (S)	C1-75-54, C1-454-250, C1-500-291, C1-506-295	0	4	0	
5	90.1-100	Highly Susceptible (HS)	C1-451-247, C1-501-292	0	2	0	

TABLE 6
Field screening of 155 F₄ and F₅ RILs for powdery mildew resistance of the cross Chinamung × LM-1668 in green gram

Grade	Leaf Area Infected (%)	Disease Reaction	RILs		Total RILs (155)		RILs showing same disease response in F4 and F5
			F ₄	F ₅	F ₄	F ₅	
0	0	Highly Resistant (R0)	0	0	0	0	
1	1.1-5	Resistant (R1)	0	0	0	0	
2	5.1-30	Resistant (R2)	C2-8-6, C2-9-7, C2-10-8, C2-12-9, C2-13-10, C2-14-11, C2-16-13, C2-19-14, C2-22-16, C2-23-17, C2-33-24, C2-35-26, C2-45-30, C2-50-33, C2-59-41, C2-69-47, C2-75-49, C2-79-51, C2-1289A-53, C2-82-54, C2-87-57, C2-88-58, C2-89-59, C2-90-60, C2-91-61, C2-92-62,	C2-14-11, C2-16-13, C2-23-17, C2-35-26, C2-55-38, C2-58-40, C2-59-41, C2-63-43, C2-69-47, C2-79-51, C2-1289A-53, C2-86-56, C2-87-57, C2-88-58, C2-89-59, C2-90-60, C2-91-61, C2-92-62, C2-93-63, C2-112-79, C2-118-85, C2-119-86,	39	104	C2-14-11, C2-16-13, C2-23-17, C2-35-26, C2-59-41, C2-69-47, C2-79-51, C2-1289A-53, C2-87-57, C2-88-58, C2-89-59, C2-90-60, C2-91-61, C2-92-62, C2-119-86, C2-1584-93, C2-136-95, C2-98-68, C2-103-73, C2-104-

1	2	3	4	5	6	7	8
			C2-119-86, C2-1584-93, C2-136-95, C2-98-68, C2-103-73, C2-104-74, C2-1417-188, C2-1453-212, C2-1483-235, C2-1489-238, C2-1540-255, C2-1547-257, C2-1560-261	C2-1584-93, C2-136-95, C2-150-101, C2-1587-102, C2-153-104, C2-1586-105, C2-1203-108, C2-1215-115, C2-1224-123, C2-1225-124, C2-1229-127, C2-1230-128, C2-1232-130, C2-1233-131, C2-1234-132, C2-1236-134, C2-1237-135, C2-1253-142, C2-1255-144, C2-1256-145, C2-1257-146, C2-1259-148, C2-1260-149, C2-1261-150, C2-1268-155, C2-1269-156, C2-1278-161, C2-1280-163, C2-1281-164, C2-1284-167, C2-98-68, C2-1582-69, C2-103-73, C2-104-74, C2-105-75, C2-1290-169, C2-1294-172, C2-1296-174, C2-1297-175, C2-1406-179, C2-1409-181, C2-1412-184, C2-1413-185, C2-1416-187, C2-1418-189, C2-1419-190, C2-1421-191, C2-1432-196, C2-1438-199, C2-1439-200, C2-1444-203, C2-1447-206, C2-1448-207, C2-1449-208, C2-1451-210, C2-1452-211, C2-1455-214, C2-1457-216, C2-1458-217, C2-1460-219, C2-1462-220, C2-1469-225, C2-1480-233, C2-1482-234, C2-1489-238, C2-1490-239, C2-1492-241, C2-1493-242, C2-1494-243, C2-1531-249, C2-1533-251, C2-1537-253, C2-1540-255, C2-1541-256, C2-1547-257, C2-1557-259, C2-1560-261, C2-1561-262, C2-1572-267, C2-1573-268, C2-1580-274, C2-1581-275			74, C2-1540-255, C2-1541-256, C2-1547-257, C2-1560-261, C2-1572-267, C2-1573-268
3	30.1-65	Moderately Susceptible (MS)	C2-54-37, C2-55-38, C2-58-40, C2-63-43, C2-65-44, C2-86-56, C2-93-63, C2-106-76, C2-108-77, C2-112-79, C2-1585A-82, C2-118-85, C2-150-101, C2-	C2-8-6, C2-9-7, C2-10-8, C2-12-9, C2-13-10, C2-19-14, C2-22-16, C2-33-24, C2-45-30, C2-50-33, C2-54-37, C2-65-44, C2-75-49, C2-82-54, C2-106-	85	47	C2-54-37, C2-65-44, C2-106-76, C2-108-77, C2-1585A-82, C2-1220-119, C2-1221-120, C2-1258-147, C2-102-72, C2-

1	2	3	4	5	6	7	8	
			1587-102, C2-153-104, C2-1586-105, C2-1219-118, C2-1220-119, C2-1221-120, C2-1229-127, C2-1230-128, C2-1233-131, C2-1234-132, C2-1236-134, C2-1237-135, C2-1242-139, C2-1253-142, C2-1255-144, C2-1256-145, C2-1257-146, C2-1258-147, C2-1260-149, C2-1268-155, C2-1269-156, C2-1278-161, C2-1280-163, C2-1582-69, C2-102-72, C2-105-75, C2-1406-179, C2-1412-184, C2-1413-185, C2-1416-187, C2-1418-189, C2-1419-190, C2-1421-191, C2-1432-196, C2-1433-197, C2-1438-199, C2-1439-200, C2-1446-205, C2-1447-206, C2-1448-207, C2-1449-208, C2-1452-211, C2-1454-213, C2-1455-214, C2-1456-215, C2-1457-216, C2-1458-217, C2-1460-219, C2-1462-220, C2-1469-225, C2-1480-233, C2-1482-234, C2-1490-239, C2-1492-241, C2-1493-242, C2-1494-243, C2-1498-245, C2-1499-246, C2-1531-249, C2-1532-250, C2-1533-251, C2-1541-256, C2-1556-258, C2-1557-259, C2-1561-262, C2-1567-265, C2-1572-267, C2-1573-268, C2-1574-269, C2-1578-272, C2-1579-273, C2-1580-274	76, C2-108-77, C2-1585A-82, C2-1207-110, C2-1208-111, C2-1210-112, C2-1212-113, C2-1220-119, C2-1221-120, C2-1258-147, C2-1270-157, C2-102-72, C2-1291-170, C2-1295-173, C2-1417-188, C2-1433-197, C2-1446-205, C2-1453-212, C2-1454-213, C2-1456-215, C2-1483-235, C2-1499-246, C2-1530-248, C2-1532-250, C2-1556-258, C2-1565-263, C2-1566-264, C2-1567-265, C2-1574-269, C2-1575-270, C2-1577-271, C2-1578-272, C2-1579-273				1433-197, C2-1446-205, C2-1454-213, C2-1456-215, C2-1499-246, C2-1532-250, C2-1556-258, C2-1578-272, C2-1579-273
4	65.1-90	Susceptible (S)	C2-1203-108, C2-1207-110, C2-1208-111, C2-1210-112, C2-1212-113, C2-1215-115, C2-1224-123, C2-1225-124, C2-1232-130, C2-1259-148, C2-1261-150, C2-1263-152, C2-1270-157, C2-1281-164, C2-1284-167, C2-1290-169, C2-1291-170, C2-1294-172, C2-1295-173, C2-1296-174, C2-1297-175, C2-1409-	C2-1219-118, C2-1242-139, C2-263-152, C2-1498-245	31	4	C2-1263-152	

1	2	3	4	5	6	7	8
			181, C2-1444-203, C2-1451-210, C2-1530-248, C2-1537-253, C2-1565-263, C2-1566-264, C2-1575-270, C2-1577-271, C2-1581-275				
5	90.1-100	Highly Susceptible (HS)	0	0	0	0	

become stable for the disease response. Such lines which are showing stable resistant response to the powdery mildew can be screened for yield related traits and should be recommended for the development of highly resistant breeding lines for powdery mildew disease with high yielding ability in green gram.

Broadening the genetic base by selection of parents from diverse and interspecific background is of paramount importance to achieve productivity gains. Recombinant inbred lines (RILs) facilitate the selection of best possible parents to create mapping populations and further be utilized in marker assisted selection and thus make the breeding programme more efficient. Hence use of resistant varieties in combination with other components of managements is a the most effective integrated methodology to combat with devastating fungal disease powdery mildew.

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