

IDENTIFICATION OF STABLE SOURCES OF MULTIPLE DISEASE RESISTANCE IN PIGEONPEA AGAINST FUSARIUM WILT AND STERILITY MOSAIC DISEASE

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ABSTRACT

Pigeonpea (*Cajanus cajan* (L.) Millsp.), locally known as *arhar* or *tur*, is a major pulse crop in India valued for its high protein content and nitrogen-fixing capacity. However, crop yield is severely constrained by Fusarium wilt (FW) and Sterility Mosaic Disease (SMD). In this study, 43 pigeonpea genotypes were evaluated for dual resistance against FW and SMD in a sick plot screening during *kharif* 2023–24 at the Regional Agricultural Research Station, Warangal. Based on percent disease incidence (PDI), 16 genotypes (WRGE-171, WRGE-173, WRGE-178, WRG-443, WRG-447, WRG-466, WRG-499, WRG-505, WRG-506, TDRG-1551, TDRG-1643, TDRG-1679, TDRG-1691, TDRG-1698, PRG-435, and ICPL-87119) demonstrated resistance (PDI $\leq 10\%$) to both Fusarium wilt and Sterility mosaic diseases. Nine genotypes (WRGE-150, WRGE-155, WRGE-160, WRGE-162, WRGE-176, WRGE-177, WRGE-180, WRG-464, and TDRG-1664) exhibited moderate resistance (PDI 10.01–30.0%). Additionally, 12 genotypes (WRGE-165, WRGE-167, WRGE-169, WRG-501, WRG-508, WRG-510, WRG-512, WRGE-174, WRG-523, TDRG-272, TDRG-1640, TDRG-1654) showed FW resistance while remaining moderately resistant to SMD. These identified resistant genotypes serve as promising donor parents for breeding disease-resistant, high-yielding pigeonpea cultivars to benefit the farming community.

Keywords: *Cajanus cajan*, Fusarium wilt, Sterility mosaic disease, Disease resistance, Genotypes, Sick plot screening

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is one of the most important grain legumes belonging to the family Fabaceae and serves as a major source of dietary protein for millions of people in the semi-arid tropics and subtropics. It is the second most important pulse crop after chickpea in India and is predominantly cultivated under rainfed conditions. Approximately 88% of the global pigeonpea production is consumed as split pulse (dal), making it an indispensable component of food and nutritional security in South Asia (Rao *et al.*, 2010). Besides its importance as a food crop, pigeonpea contributes significantly to sustainable agriculture through biological nitrogen fixation, soil fertility improvement, fodder production, fuelwood, and soil conservation. The seeds are rich in protein (about 21%), carbohydrates, dietary fiber, minerals, and essential amino acids such as lysine, methionine, and arginine, enhancing their nutritional value (Orwa *et al.*, 2009).

Globally, pigeonpea is cultivated on 6.36 million hectares, producing 5.48 million tonnes with an average productivity of 861 kg ha⁻¹. India is the largest producer, accounting for nearly 75% of the global area and production, where the crop occupies about 5.05 million hectares with a production of 4.34

million tonnes and an average productivity of 859 kg ha⁻¹ (Anonymous, 2024). Among the major pigeonpea-growing states are Maharashtra, Karnataka, Madhya Pradesh, Telangana, Andhra Pradesh, Gujarat, Tamil Nadu, and Uttar Pradesh. In Telangana, pigeonpea occupies approximately 1.79 million hectares, with an annual production of 1.45 million tonnes and an average productivity of 812 kg ha⁻¹ (Anonymous, 2025).

Despite its agronomic and nutritional importance, pigeonpea productivity remains considerably lower than its potential due to the combined effects of abiotic and biotic stresses. Among the biotic constraints, Fusarium wilt, caused by *Fusarium udum* Butler, and Sterility Mosaic Disease (SMD), caused by Pigeonpea Sterility Mosaic Virus (PPSMV), are the most destructive diseases affecting pigeonpea cultivation throughout India. Other important diseases include Phytophthora blight and dry root rot caused by *Macrophomina phaseolina* (Reddy *et al.*, 1998). Fusarium wilt is a soil-borne disease capable of causing severe plant mortality at different crop growth stages, leading to yield losses ranging from 30 to 100% depending on the genotype, pathogen race, and environmental

conditions. Similarly, SMD, popularly known as the “green plague” of pigeonpea, is characterized by excessive vegetative growth, mosaic mottling, reduced leaf size, and complete or partial sterility of infected plants, resulting in yield losses of up to 95% when infection occurs at the early stages of crop growth. (Gupta *et al.*, 2012; Saxena *et al.*, 2021).

Fusarium wilt may occur from the seedling stage to crop maturity, although the most severe losses are observed when infection occurs during flowering and pod development, frequently resulting in complete crop failure. The pathogen, *F. udum*, is both soil- and seed-borne and survives as chlamydospores in infected plant debris for up to six years, making disease management difficult through conventional means (Haware *et al.*, 1996). Likewise, Sterility Mosaic Disease is transmitted by the eriophyid mite *Aceria cajani* and is particularly devastating when infection occurs during the early vegetative stage (approximately 30 days after sowing), leading to complete sterility, cessation of flowering, and drastic yield reduction. Disease severity is generally greater in ratoon and perennial pigeonpea crops due to continuous inoculum build-up and vector persistence (Reddy *et al.*, 1993; Chandra *et al.*, 2019).

The occurrence of these two diseases either individually or simultaneously has become a major challenge in pigeonpea-growing regions of India. Although chemical and cultural management practices provide partial control, they are often uneconomical, environmentally undesirable, or ineffective under high disease pressure. The existence of multiple races of *F. udum* and the variability in PPSMV strains further complicate disease management. Therefore, the development and deployment of resistant cultivars remain the most economical, eco-friendly, and sustainable approach for managing these diseases.

Identification of stable and durable resistance sources is a prerequisite for breeding pigeonpea cultivars with broad-spectrum disease resistance. Stable resistance ensures consistent performance across diverse environments, seasons, and pathogen populations, thereby enhancing the reliability of resistant cultivars under farmers’ field conditions. Furthermore, incorporating resistance to both

Fusarium wilt and Sterility Mosaic Disease into a single genotype is highly desirable for achieving durable disease management and reducing production risks.

In this context, systematic screening of pigeonpea germplasm under artificial disease pressure provides an effective strategy for identifying stable sources of resistance. Such resistant genotypes can serve as valuable donors in breeding programs aimed at developing high-yielding cultivars possessing multiple disease resistance. Therefore, the present investigation was undertaken to identify stable sources of multiple disease resistance against Fusarium wilt and Sterility Mosaic Disease in pigeonpea, with the objective of identifying genotypes exhibiting consistent resistance to both diseases for their effective utilization in resistance breeding programs.

MATERIAL AND METHODS

A set of 43 pigeonpea genotypes, obtained from the Regional Agricultural Research Station, Warangal, and ARS, Tandur, were evaluated against Fusarium wilt disease under sick plot and Sterility mosaic disease through artificial screening separately during Kharif, 2023, at the Regional Agricultural Research Station, Warangal. Pigeonpea cultivars ICPL 2376 and ICP 8863 were used as susceptible controls for Fusarium wilt and sterility mosaic disease, respectively, and ICP87119 was used as a resistant control for both diseases. Each genotype was planted in two replicated rows, 5 m long, with 25 plants per row.

The susceptible check, viz., ICPL 2376 for wilt disease and ICP 8863 for SMD, was planted after every four test entries, respectively. PPSMV virus-infected leaves were used to inoculate all the test plants at the two-leaf stage (14-20 days after germination) (Nene and Reddy, 1976). In this, mite-infested (approximately 50-100 mites per trifoliate) leaflets obtained from SMD-affected plants (maintained at Regional Agricultural Research Station, Warangal) were stapled to the leaves of test plants. Mites from the stapled leaf migrate onto the test seedling, resulting in virus transmission. *Fusarium udum* multiplied on sorghum grains was added to the sick plot to screen against Fusarium wilt before sowing and 45 days after sowing to ensure high

disease pressure under the wilt sick plot, which is maintained with the optimum spore load of *Fusarium udum* 6-7 X 10⁵ spores/ml.

The test entries were graded as resistant, moderately resistant or susceptible based on per cent disease incidence as per the rating scale given by AICRP on Kharif Pulses, 2020. Observations on symptom type and severity were recorded at flowering and pod maturity stages, by which time 100% incidence was recorded in susceptible controls and all the plants showed severe symptoms.

Per cent disease incidence was calculated as follows:

Percent disease incidence = [(No. of Infected plants) / (Total no. of plants)] × 100

AICRP on Kharif Pulses Wilt and SMD disease scoring scale, 2020

Grade	Wilt incidence (%)
Resistant (R)	0-10
Moderately Resistant (MR)	10.01-30
Susceptible (S)	Above 30.0

RESULTS AND DISCUSSION

A total of 43 pigeonpea genotypes were evaluated under artificial epiphytotic conditions for their reaction against *Fusarium* wilt and Pigeonpea Sterility Mosaic Disease (SMD). The genotypes exhibited considerable variability in their response to *Fusarium* wilt and Sterility mosaic disease, indicating the presence of substantial genetic diversity for resistance to these economically important pathogens (Table1 & 2). Such variability offers valuable opportunities for identifying stable sources of resistance for utilization in pigeonpea improvement programmes.

Reaction of pigeonpea genotypes to *Fusarium* wilt

Based on the AICRP disease rating scale, the genotypes were classified as resistant (0–10% PDI), moderately resistant (10.01–30.0% PDI) and susceptible (>30% PDI). Among the 43 genotypes evaluated, 32 genotypes (72.7%) were resistant to *Fusarium* wilt, 12 genotypes (27.3%) were moderately resistant and only one genotype (ICPL-2376) exhibited a susceptible reaction (Fig1). The large proportion of

resistant entries demonstrates the successful incorporation of wilt resistance in the breeding material.

Among the tested entries, 31 genotypes exhibited a resistant (R) reaction with wilt incidence ranging from 0.00 to 9.65%, whereas 13 genotypes were categorized as moderately resistant (MR) with disease incidence ranging from 10.10 to 28.10%. Only one genotype (ICPL-2376) was found to be susceptible (S), recording the highest wilt incidence of 65.30% (Table 2).

Among the resistant entries, complete resistance (0.00% wilt incidence) was observed in WRGE-169, WRGE-173, WRGE-174, WRG-523, TDRG-272, TDRG-1551, TDRG-1640, TDRG-1691, TDRG-1693, PRG-434 and ICPL-87119, indicating their potential as valuable sources of resistance. Other promising resistant genotypes included WRGE-171 (5.60%), WRGE-178 (6.80%), WRG-443 (3.60%), WRG-447 (5.70%), WRG-466 (4.20%), WRG-499 (2.30%), WRG-505 (1.30%), WRG-506 (3.60%), WRG-508 (3.60%), PRG-435 (6.90%), TDRG-1643 (6.58%), TDRG-1654 (7.78%), TDRG-1679 (8.70%), TDRG-1695 (9.25%) and TDRG-1698 (9.65%) presented in Table 1.

Moderately resistant genotypes included WRGE-150, WRGE-155, WRGE-160, WRGE-162, WRGE-176, WRGE-177, WRGE-180, WRG-464, WRG-486, WRG-488, WRG-512, TDRG-1664 and TDRG-1722, with wilt incidence ranging from 10.10 to 28.10%. The susceptible check ICPL-2376 recorded the highest wilt incidence (65.30%), confirming the effectiveness of the artificial sick plot for disease screening.

The predominance of resistant genotypes observed in the present investigation agrees with earlier reports where extensive variability for wilt resistance was identified among pigeonpea germplasm. Screening studies by Ashitha *et al.* 2016 reported several resistant genotypes under wilt-sick plot conditions, emphasizing the effectiveness of field screening in identifying stable resistance sources. Similarly, Reddy *et al.* 2025 observed substantial variation among advanced breeding lines and identified resistant entries suitable for utilization in resistance breeding programmes.

Table 1. Evaluation of pigeonpea genotypes against Fusarium wilt and sterility mosaic disease at RARS, Warangal during Kharif, 2023

S.No	Name of the genotypes	Mean Percent disease incidence of Fusarium wilt	Host reaction	Mean Percent disease incidence of SMD	Host Reaction
1	WRGE-150	14.6	MR	11.47	MR
2	WRGE-155	10.7	MR	10.88	MR
3	WRGE-160	20.0	MR	16.67	MR
4	WRGE-162	28.1	MR	12.94	MR
5	WRGE-165	3.1	R	17.53	MR
6	WRGE-167	4.2	R	23.04	MR
7	WRGE-169	0.0	R	30.21	MR
8	WRGE-171	5.6	R	1.90	R
9	WRGE-173	0.0	R	10.00	R
10	WRGE-176	16.3	MR	22.40	MR
11	WRGE-177	10.1	MR	14.29	MR
12	WRGE-178	6.8	R	9.50	R
13	WRGE-180	21.5	MR	15.63	MR
14	WRG-443	3.6	R	0.00	R
15	WRG-447	5.7	R	9.25	R
16	WRG-464	12.4	MR	10.32	MR
17	WRG-466	4.2	R	8.19	R
18	WRG-486	13.9	MR	6.35	R
19	WRG-488	18.9	MR	5.56	R
20	WRG-499	2.3	R	9.32	R
21	WRG-501	2.4	R	19.17	MR
22	WRG-505	1.3	R	9.55	R
23	WRG-506	3.6	R	5.00	R
24	WRG-508	3.6	R	10.08	R
25	WRG-510	0.0	R	19.01	MR
26	WRG-512	6.0	R	28.28	MR
27	WRGE-174	0.0	R	16.52	MR
28	WRG-523	0.0	R	16.39	MR
29	TDRG-272	0.00	R	21.20	MR
30	TDRG-1551	0.00	R	7.45	R
31	TDRG-1640	0.00	R	13.46	MR
32	TDRG-1643	6.58	R	9.35	R
33	TDRG-1654	7.78	R	14.56	MR
34	TDRG-1664	13.85	MR	22.62	MR
35	TDRG-1679	8.70	R	5.61	R
36	TDRG-1691	0.00	R	0.00	R
37	TDRG-1692	6.12	R	32.92	S
38	TDRG-1693	0.00	R	40.78	S
39	TDRG-1695	9.25	R	42.93	S
40	TDRG-1698	9.65	R	0.00	R
41	TDRG-1722	19.10	MR	50.00	S
42	PRG-434	0.00	R	59.16	S
43	PRG-435	6.90	R	0.00	R
44	ICPL-87119 (R check)	0.00	R	2.50	R
45	ICPL-2376 (S check for wilt)	65.30	S	-	-
46	ICPL-8863 (S check for SMD)	-	-	100.00	S

Table 2. Grouping of pigeonpea genotypes based on their host reaction against Fusarium wilt disease.

Disease reaction	PDI range	Promising Genotypes against Fusarium wilt disease
Resistant (R)	0.0–10.0	WRGE-165, WRGE-167, WRGE-169, WRGE-171, WRGE-173, WRGE-178, WRG-443, WRG-447, WRG-466, WRG-499, WRG-501, WRG-505, WRG-506, WRG-508, WRG-510, WRG-512, WRGE-174, WRG-523, TDRG-272, TDRG-1551, TDRG-1640, TDRG-1643, TDRG-1654, TDRG-1679, TDRG-1691, TDRG-1692, TDRG-1693, TDRG-1695, TDRG-1698, PRG-434, PRG-435, ICPL-87119
Moderately Resistant (MR)	10.01–30.0	WRGE-150, WRGE-155, WRGE-160, WRGE-162, WRGE-176, WRGE-177, WRGE-180, WRG-464, WRG-486, WRG-488, TDRG-1664, TDRG-1722
Susceptible (S)	30.01–100.0	ICPL-2376

Table 3. Grouping of pigeonpea genotypes based on their host reaction against Sterility mosaic disease.

Disease reaction	PDI range	Promising Genotypes against Sterility mosaic disease
Resistant (R)	0.0–10.0	WRGE-171, WRGE-173, WRGE-178, WRG-443, WRG-447, WRG-466, WRG-486, WRG-488, WRG-499, WRG-505, WRG-506, TDRG-1551, TDRG-1643, TDRG-1679, TDRG-1691, TDRG-1698, PRG-435, ICPL-87119
Moderately Resistant (MR)	10.01–30.0	WRGE-150, WRGE-155, WRGE-160, WRGE-162, WRGE-165, WRGE-167, WRGE-169, WRGE-176, WRGE-177, WRGE-180, WRG-464, WRG-501, WRG-510, WRG-512, WRGE-174, WRG-523, TDRG-272, TDRG-1640, TDRG-1654, TDRG-1664
Susceptible (S)	30.01–100.0	TDRG-1692, TDRG-1693, TDRG-1695, TDRG-1722, PRG-434, ICPL-8863

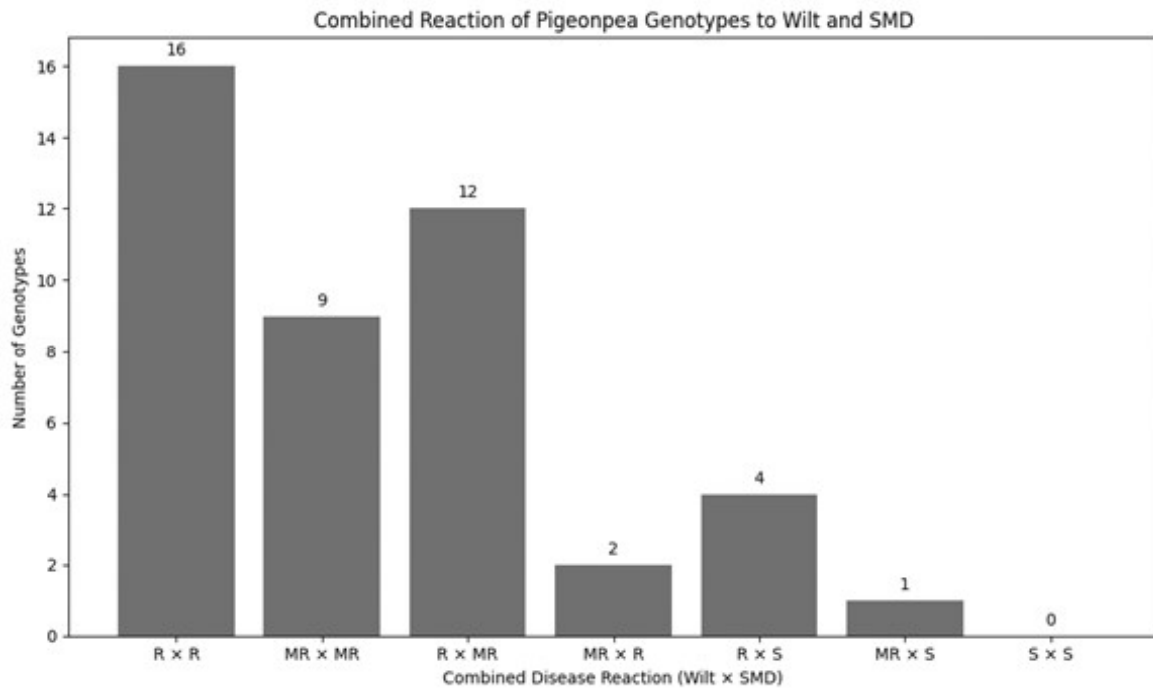


Fig 1. Reaction of pigeonpea genotypes against Fusarium wilt and sterility mosaic disease.

Reaction of pigeonpea genotypes to Sterility Mosaic Disease

The same set of 43 pigeonpea genotypes were evaluated under artificial epiphytotic conditions for resistance to Sterility Mosaic Disease (SMD) at RARS, Warangal. The disease incidence ranged from **0.00 to 59.16%**, demonstrating a wide variation in the response of the genotypes.

Among the evaluated entries, 18 genotypes were classified as resistant (R) with SMD incidence ranging from 0.00 to 10.00%, 21 genotypes exhibited moderately resistant (MR) reaction with disease incidence between 10.08 and 30.21%, while six genotypes were found to be susceptible (S) with disease incidence ranging from 32.92 to 59.16% (Table2).

Complete resistance (0.00% disease incidence) was recorded in WRG-443, TDRG-1691, TDRG-1698, PRG-435 and ICPL-2376. Other resistant genotypes included WRGE-171 (1.90%), WRGE-178 (9.50%), WRGE-173 (10.00%), WRG-447 (9.25%), WRG-466 (8.19%), WRG-486 (6.35%), WRG-488 (5.56%), WRG-499 (9.32%), WRG-505 (9.55%), WRG-506 (5.00%), WRG-508 (10.08%), TDRG-1551 (7.45%), TDRG-1643 (9.35%) and TDRG-1679 (5.61%) presented in Table 1.

Moderately resistant genotypes comprised WRGE-150, WRGE-155, WRGE-160, WRGE-162, WRGE-165, WRGE-167, WRGE-169, WRGE-176, WRGE-177, WRGE-180, WRG-464, WRG-501, WRG-510, WRG-512, WRGE-174, WRG-523, TDRG-272, TDRG-1640, TDRG-1654, TDRG-1664 and TDRG-1692, recording disease incidence between 10.08 and 30.21%. The susceptible reaction was observed in TDRG-1692 (32.92%), TDRG-1693 (40.78%), TDRG-1695 (42.93%), TDRG-1722 (50.00%) and PRG-434 (59.16%), indicating high susceptibility under artificial inoculation conditions.

Screening against SMD revealed relatively greater variability than Fusarium wilt (Fig1). Among the evaluated entries, 18 genotypes (40.9%) exhibited resistant reactions, 20 genotypes (45.5%) were moderately resistant, whereas six genotypes (13.6%) were susceptible. These observations indicate that resistance to PSMD is comparatively less common than resistance to wilt, reflecting the complex interaction among the virus, its eriophyid mite vector (*Aceria cajani*), and the host plant.

Comparable observations have been reported by Vijaya Bhaskar (2022), who evaluated pigeonpea germplasm under Telangana conditions and found fewer genotypes resistant to sterility mosaic disease

than to wilt, suggesting that identifying stable sources with combined resistance remains a major breeding objective.

Combined resistance to Fusarium wilt and Sterility Mosaic Disease

Simultaneous evaluation for both diseases enabled the identification of genotypes possessing multiple disease resistance. Sixteen genotypes (WRGE-171, WRGE-173, WRGE-178, WRG-443, WRG-447, WRG-466, WRG-499, WRG-505, WRG-506, TDRG-1551, TDRG-1643, TDRG-1679, TDRG-1691, TDRG-1698, PRG-435 and ICPL-87119) expressed resistance to both Fusarium wilt and PSMD. Nine genotypes exhibited moderate resistance to both diseases, while twelve genotypes were resistant to wilt but moderately resistant to PSMD. Only four genotypes that were resistant to wilt became susceptible to PSMD, and no genotype was susceptible to both diseases (Table4 & 5).

The identification of sixteen genotypes possessing combined resistance is particularly important because Fusarium wilt and sterility mosaic disease are the two most destructive diseases of pigeonpea, capable of causing severe yield losses individually and complete crop failure when they occur together under favorable conditions. Host plant resistance remains the most economical, environmentally safe, and sustainable strategy for their management. Similar efforts to identify combined resistance have been reported by Singh *et al.* (2024), who identified several pigeonpea genotypes possessing simultaneous resistance to both Fusarium wilt and sterility mosaic disease across multiple locations in Gujarat.

CONCLUSION

The resistant genotypes WRGE-171, WRGE-173, WRGE-178, WRG-443, WRG-447, WRG-466, WRG-499, WRG-505, WRG-506, TDRG-1551, TDRG-1643, TDRG-1679, TDRG-1691, TDRG-1698, PRG-435 and ICPL-87119 identified in the present study constitute valuable donor sources for resistance breeding and may be effectively utilized in hybridization programmes aimed against both pathogens. These genotypes also warrant further multilocation evaluation to determine the stability and durability of resistance across diverse agro-climatic conditions before their utilization in varietal development. The absence of any genotype susceptible to both diseases further highlights the improved disease resistance status of the breeding material and reflects the effectiveness of continuous selection under disease pressure.

Table 4. Combined expression of pigeonpea genotypes against Fusarium wilt and sterility mosaic diseases.

Category	Wilt Reaction	SMD Reaction	Genotypes	No. of Genotypes
Resistant to both diseases (R × R)	R	R	WRGE-171, WRGE-173, WRGE-178, WRG-443, WRG-447, WRG-466, WRG-499, WRG-505, WRG-506, TDRG-1551, TDRG-1643, TDRG-1679, TDRG-1691, TDRG-1698, PRG-435, ICPL-87119	16
Moderately Resistant to both diseases (MR × MR)	MR	MR	WRGE-150, WRGE-155, WRGE-160, WRGE-162, WRGE-176, WRGE-177, WRGE-180, WRG-464, TDRG-1664	9
Resistant to Wilt + Moderately Resistant to SMD (R × MR)	R	MR	WRGE-165, WRGE-167, WRGE-169, WRG-501, WRG-508, WRG-510, WRG-512, WRGE-174, WRG-523, TDRG-272, TDRG-1640, TDRG-1654	12
Moderately Resistant to Wilt + Resistant to SMD (MR × R)	MR	R	WRG-486, WRG-488	2
Resistant to Wilt + Susceptible to SMD (R × S)	R	S	TDRG-1692, TDRG-1693, TDRG-1695, PRG-434	4
Moderately Resistant to Wilt + Susceptible to SMD (MR × S)	MR	S	TDRG-1722	1
Susceptible to both diseases (S × S)	S	S	None	0
Total genotypes evaluated for both diseases				44

Table 5. Categorized the promising genotypes against Fusarium wilt and sterility mosaic disease.

Disease reaction	Genotypes	No.
R to both Wilt and SMD	WRGE-171, WRGE-173, WRGE-178, WRG-443, WRG-447, WRG-466, WRG-499, WRG-505, WRG-506, TDRG-1551, TDRG-1643, TDRG-1679, TDRG-1691, TDRG-1698, PRG-435, ICPL-87119	16
MR to both Wilt and SMD	WRGE-150, WRGE-155, WRGE-160, WRGE-162, WRGE-176, WRGE-177, WRGE-180, WRG-464, TDRG-1664	9

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