



Field Evaluation of Rice(*Oryza Sativa* L.) Genotypes for Resistance against Brown Spot Disease (*Drechslera Oryzae*)

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Received: August 28, 2025

Published: October 08, 2025

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Abstract

Rice (*Oryza sativa* L.) is a staple food crop for more than half of the world's population. It is cultivated in more than 100 countries with approx. 90 % production from Asia and nearly 3 billion people depends on rice for their 20 % of the daily calorie intake. Brown spot disease, incited by *Drechslera oryzae*, poses a major constraint to rice yield-especially in rainfed and humid agro-climatic zones. To promote durable resistance, identifying and screening resistant genotypes is imperative. In this pursuit, a field investigation was undertaken during the Kharif season of 2023 at Bihar Agricultural University, Sabour, involving 421 rice genotypes under the National Screening Nursery-1 (NSN-1). The genotypic evaluation revealed marked variation in disease response across entries. Among 421 genotypes in NSN-1, one genotype PR 124 was found immune (disease score '0') and only 55 genotypes having designation no. MTU 1382, BRR 0181-IR 93827-2-1-1-4, BRR 0180-IR14L157, WGL 1495, RP 6317-RMS-S35-BC2F4-49-25-12-18, Varadhan, Swarna, CR 4392-RGA-16, Rasi, RP Bio 4918-B-B-166-23, RP 6252-BV / RIL-BV202, CR 3562-2-1-1-3-1-1, CR 4387-RGA-271, RP 6689-PyF-111-23, CR 4075-1341-3-3-2-2-1 4-3, MTU 1390, AD 16124, PR 121, HRI-209, CR 4331-74-2-2-1, Naveen, Pusa 2090-17-20, JGL 38206, RNE-0456, RNE-0463, PR-121, RP 6741-RAF-2607-IJ-2, JGL 38105, CO-39, etc. were rated as resistant (disease score '1'). Furthermore, 131 genotypes were categories as moderately resistant, 114 as moderately susceptible, 92 as susceptible, and 28 as highly susceptible. These results offer critical insights into rice genotypic resistance against brown spot and highlight promising candidates for incorporation into breeding programs aimed at enhancing disease resilience and ensuring stable rice productivity.

Keywords: Rice; Brown Spot; *Drechslera Oryzae*; Field Evaluation

Introduction

Rice (*Oryza sativa* L.) continues to be a cornerstone of global food security, nourishing over 3 billion people and serving as the

primary dietary staple for nearly 60 % of the population across Asia and Africa. With the global population projected to exceed 9 billion by 2050, the demand for rice is expected to rise sharply, ne-

cessitating sustained improvements in productivity and resilience [1]. In India, rice cultivation spans approximately 51.5 million hectares, with a record production of 151 million tonnes forecasted for the 2025–26 season, supported by favorable monsoons and robust agronomic practices. The crop contributes over 40% to the national food grain output and supports the livelihoods of nearly 70 % of rural households [2]. Bihar ranks seventh among rice-producing states, with an estimated output of 7.02 million tonnes and a productivity of 24.53 quintals per hectare, predominantly under rainfed conditions [3]. Rice is primarily grown as a monocrop during the kharif season, occupying nearly 60% of the state’s cultivated land [4]. Despite its agronomic significance, rice productivity is severely constrained by biotic and abiotic stresses. Among biotic factors, fungal pathogens such as *Pyricularia oryzae* (blast), *Bipolaris oryzae* (brown spot), *Rhizoctonia solani* (sheath blight), and *Sarocladium oryzae* (sheath rot) are particularly detrimental [5,6]. Brown spot, caused by *Drechslera oryzae* (teleomorph: *Cochliobolus miyabeanus*), remains a persistent threat due to its seed-borne nature and widespread prevalence across rice-growing regions. Historical outbreaks, such as the Bengal famine of 1943, underscore its socio-economic impact [7]. Under favorable conditions for disease development particularly in rainfed areas with poor soil fertility yield losses attributed to brown spot can vary from as low as 6 % to exceeding 50% [8]. Recent field assessments in Bihar report disease incidence up to 31.39 % and severity reaching 46.60% [4].

Fungicidal control of *Bipolaris oryzae* could be one of the option for management of this disease; however, it remains a short-term solution and may lead to the buildup of toxic chemical residues, posing potential ecological risks [9]. The recurring nature and economic burden of brown spot, identifying resistant rice genotypes offers a sustainable alternative to chemical control. Genotypic screening enables the selection of resistant lines suitable for breeding programs and deployment in endemic zones [5,6]. Accordingly, the present study was conducted during the kharif season of 2023 at the Research Farm of Bihar Agricultural University, Sabour, to evaluate 421 rice genotypes under the National Screening Nursery-1 (NSN-1) framework for resistance to brown spot disease under field conditions for further utilization of resistant genotypes.

Materials and Methods

A field-based investigation was undertaken during the Kharif season of 2023 at the Research Farm of Bihar Agricultural College,

Sabour, located within zone III A agro-climatic zone of Bihar. The principal objective of the study was to evaluate the response of 421 rice genotypes from the National Screening Nursery-1 (NSN) segment against rice brown spot disease under natural epiphytotic conditions. Agronomic interventions were executed as per the standardized protocols of the All India Coordinated Rice Improvement Project (AICRIP). Each genotype was represented by a single row measuring 3.5 meters in length, and transplantation was conducted using an Augmented Block Design to effectively account for spatial heterogeneity and varietal divergence.

For percent disease severity assessment, twenty-five leaves per entry were randomly sampled fifteen days preceding harvest. The virulence of brown spot, incited by *Drechslera oryzae*, was quantified using the 0–9 disease rating scale [10]. Subsequently, the Percent Disease Index (PDI) was computed [11], facilitating uniform estimation of disease intensity across all evaluated genotypes (Figure 1).

Per cent Disease Index (PDI) =
$$\frac{\text{Sum of all individual disease ratings}}{\text{Total number of leaves observed} \times \text{Maximum disease grade}} \times 100$$

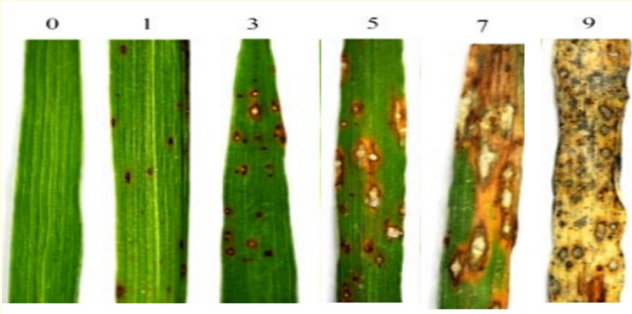


Figure 1: Pictorial scale for screening of brown spot disease of rice.

Based on the computed PDI values, all genotypes were categorized into five distinct disease reaction classes - Resistant (R), Moderately Resistant (MR), Moderately Susceptible (MS), Susceptible (S), and Highly Susceptible (HS) as per the criteria outlined in table 1.

Disease score	Disease Severity (% of leaf area diseased)	Disease Reaction
0	No incidence	Immune
1	Less than 1 %	Resistant (R)
3	1 - 10 %	Moderately resistant (MR)
5	11 - 25 %	Moderately susceptible (MS)
7	26 - 50 %	Susceptible (S)
9	More than 50 %	Highly Susceptible (HS)

Table 1: Disease scoring scale of brown spot of rice.

Results and Discussion

The findings from the current investigation reveal pronounced heterogeneity in disease response among the 421 rice genotypes evaluated using the 0–9 disease rating scale under naturally prevailing epiphytotic conditions of brown leaf spot. Based on the extent of symptom expression, the genotypes were stratified into six distinct reaction categories. The frequency distribution of genotypes across these categories is detailed in Tables 2 and 3, and visually represented in Figure 2. Among 421 genotypes in NSN-1, one genotype PR 124 was found immune (disease score ‘0’), only 55 having designation no. MTU 1382, Improved Samba Mahsuri, BRR 0181-IR 93827-2-1-1-4, BRR 0180-IR14L157, WGL 1495, RP 6317-RMS-S35-BC2F4-49-25-12-18, Varadhan, Swarna, CR 4392-RGA-16, Rasi, RP Bio 4918-B-B-166-23, Improved Samba, Mahsuri, RP 6252-BV / RIL-BV202, CR 3562-2-1-1-3-1-1, CR 4387-RGA-271, RP 6689-PyF-111-23, CR 4075-1341-3-3-2-2-1 4-3, MTU 1390, AD 16124, PR 121, HRI-209, CR 4331-74-2-2-1, Naveen, Pusa 2090-17-20, JGL 38206, RNE-0456, RNE-0463, PR-121, RP 6741-RAF-2607-IJ-2, JGL 38105, Improved Samba Mahsuri, BPT 5204, RP 6765-RAF 1012-30, MTU 1121, RP 6616-CGR 7, TRC GN 116-B-B-14-2, CRR 806-2, CR 4350-7-5-1-17, AD 18158, Pusa 1988-15-7-44-98-67, Pusa 1823-12-62, CSR 389-16-6, Pusa 44, RP 6755-RMS-1-23-65-83, Super 4400, JNPT 1058, AD 19050, RRX-3366, PR 113, ADVRH-162108, RP 6530-RMS-34-8-33 49, RP 6531-RMS-78-54-7 44, RP 6684-CGR 13, TN1 and CO-39 were rated as resistant (disease score ‘1’) and 28 genotypes having designation no. BRR 0181-IR 93827-29-1-1-4, TRC 185-B-B-82-2-11, RP Bio

4919-B2-NSR 5, RP 6522-MSA-16-24-16-1550, CR 4358-3-3-1-2-1, RP 6757-RMS-22-17-34-47, Pusa 2091-26, CB 18611, BRR 0156, CSR M1-4, RP 6166-47-1-23, RNR 28399, PHI-20106, MEPH-159, RP 6747-19484-1-1, RP 6686-CGR 22, WGL 14, CRHR-168, CSR BT-252-201, NWGR 17133, NVSR 929, CR Dhan 202, Improved Samba Mahsuri, Samba Mahsuri, GNV 2020-05, BRR 2177, RNC-0752 and Swarnadhan were found highly susceptible (maximum disease score ‘9’). Furthermore, 131 genotypes were categories as moderately resistant, 114 as moderately susceptible, 92 as susceptible, and 28 as highly susceptible. These outcomes are similar with the findings of [12] and they evaluated 142 rice genotypes under natural field conditions. The study revealed a predominance of susceptible responses, with only a limited number of genotypes showing moderate resistance. Notably, genotypes such as AD 17083, ADT 39, CB 16118, TPS 3, AD 18131, TRY 3, TR 05031, AD 16154, AD 18035, and Karuppukavuni exhibited moderate resistance. [13] examined 354 rice genotypes and reported the absence of highly resistant entries; however, 32 genotypes-including BPT 5204 and CSR 36-exhibited moderate resistance, emphasizing the relevance of intermediate resistance as a pivotal trait for breeding in scenarios lacking complete immunity. Similarly, in an earlier study, 244 genotypes evaluated and identified only three-namely IET-23403, 22876, and 23392-as resistant to brown spot disease [14]. Complementary findings by [15] reported eleven genotypes, such as Rasi, JGL-1798, and KMP-201, that remained free of disease symptoms throughout the cropping cycle, suggesting their value as potential candidates in resistance enhancement programs. Likewise, [16] screened 70 entries and recorded resistance in a single genotype, PK-3699-43, while the majority displayed moderate to high levels of susceptibility. A total of 639 rice genotypes were evaluated for resistance to brown spot disease. The findings indicated that none of the genotypes exhibited complete immunity. However, 23 genotypes—including CR 4396-1-13-11, CSR AP10, YNPK-7258, HURS 23-16-IR 143511-78-2-2 963-50-18, CSR 2018-43-16, CSR 2018-43-37, CSR 10, CCSRI/GRS11-4-283-34, CR 4084 1-B-1-B-1, MLD 214-IR16T1001, and KR 21001-demonstrated notable resistance, with disease severity limited to 1%. Furthermore, 170 genotypes were moderately resistant, 186 moderately susceptible, 184 susceptible, and 76 highly susceptible [17]. The fourteen rice varieties were screened against brown leaf spot disease and revealed that none of the varieties was immune [18]. Among them, only HJ-G1 and HJ-G2 were found moderately resistant and rest twelve varie-

ties were susceptible. 95 rice genotypes were evaluated for resistance to brown spot disease and found that 22 genotypes (23.16 %) exhibited resistance to moderate resistance, whereas the remaining 73 genotypes (76.84 %) were classified as moderately susceptible to susceptible [19]. Collectively, these studies denote that absolute resistance to brown spot is infrequent, with most genotypes falling within moderately resistant or susceptible categories. The differences in resistance levels observed among the NSN-1 entries

may be due to the diverse genetic makeup and varying activity of defense-related genes. These genetic factors influence how each genotype responds to brown spot infection. The identification of resistant and moderately resistant genotypes provides useful material for breeding programs. These genotypes can be used in crossing and selection efforts to develop new rice varieties with improved resistance to brown spot disease.

Disease score	Disease Severity (% of leaf area infected)	Disease Reaction	No. of genotypes	Frequency (%)
0	No incidence	Immune (I)	1	0.24
1	Less than 1 %	Resistant (R)	55	13.06
3	1 – 10 %	Moderately resistant (MR)	131	31.11
5	11 – 25 %	Moderately susceptible (MS)	114	27.08
7	26 – 50 %	Susceptible (S)	92	21.85
9	> 50 %	Highly Susceptible (HS)	28	6.65

Table 2: Frequency of NSN-1 genotypes showing different disease reaction against Brown spot disease of rice during *Kharif* 2023.

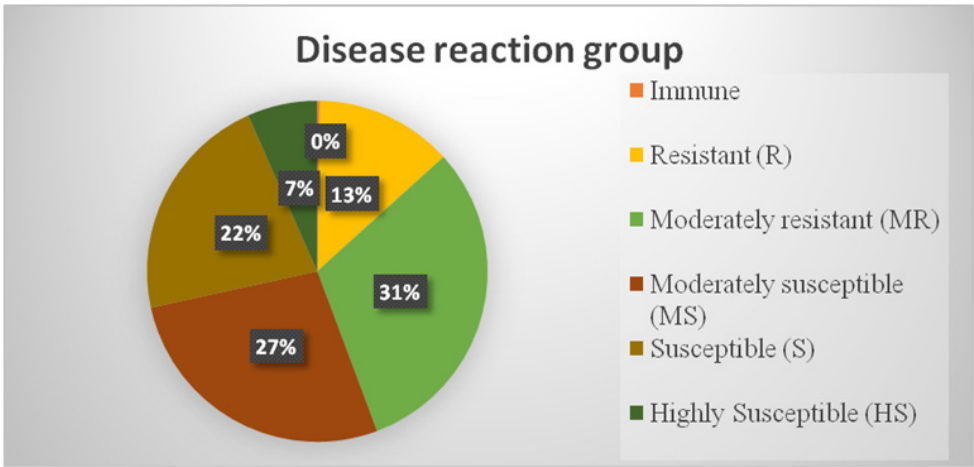


Figure 2: Frequency of NSN-1 genotypes showing different disease reaction against Brown spot disease of rice during *Kharif* 2023.

Rating scale	Genotypes
0 (Immune)	PR 124
1 (Resistant)	MTU 1382, Improved Samba Mahsuri, BRR 0181-IR 93827-2-1-1-4, BRR 0180-IR14L157, WGL 1495, RP 6317-RMS-S35-BC2F4-49-25-12-18, Varadhan, Swarna, CR 4392-RGA-16, Rasi, RP Bio 4918-B-B-166-23, Improved Samba, Mahsuri, RP 6252-BV / RIL-BV202, CR 3562-2-1-1-3-1-1, CR 4387-RGA-271, RP 6689-PyF-111-23, CR 4075-1341-3-3-2-2-1 4-3, MTU 1390, AD 16124, PR 121, HRI-209, CR 4331-74-2-2-1, Naveen, Pusa 2090-17-20, JGL 38206, RNE-0456, RNE-0463, PR-121, RP 6741-RAF-2607-IJ-2, JGL 38105, Improved Samba Mahsuri, BPT 5204, RP 6765-RAF 1012-30, MTU 1121, RP 6616-CGR 7, TRC GN 116-B-B-14-2, CRR 806-2, CR 4350-7-5-1-17, AD 18158, Pusa 1988-15-7-44-98-67, Pusa 1823-12-62, CSR 389-16-6, Pusa 44, RP 6755-RMS-1-23-65-83, Super 4400, JNPT 1058, AD 19050, RRX-3366, PR 113, ADVRH-162108, RP 6530-RMS-34-8-33 49, RP 6531-RMS-78-54-7 44, RP 6684-CGR 13, TN1 and CO-39
3 (Moderately Resistant)	CSR 189-11-122, NVSR 6361, CSR10, CSR 389-16-22, CSR 389-16-6, Pusa 44, CRU-BCKV-22-35, HRI-214, UPLRH-181325, VNR-228, CO-51, PAN-2150, UPLRH-162087, JGL 35085, NLR 3684, CSR 27 SM160, BPT 5204, OR 2674-14-6-2, CR Dhan 201, BRR 2184, RCPR 70-IR 84899-B-184-16-1-1-1, CRR 790-69, DRR Dhan 54, RP 5977-MS-M-112-1-9-22-4-6-3, Swarna (Positive Check), Vandana, RP 5977-MS-M-33-4-8-3-7-5-1, RP 6524-MSA-16-399 16-332, Improved Samba Mahsuri, Swarna (Positive Check), RP 5594-71-14-2-1, CR 3756-2-4-2-1-1-1, CR 3516 -1-1-1-1-1-1, RP 6529-RMS-1757-3-47-84, RP 6529- RMS-1708-65-97-14, RP 6714-MS-SS-8-4-7-2-11-5-3, RP 6252-BV/RIL-BV24, RP 6420-C10-21, RP 6252-BV/RIL-BV38, CR 4395-6-3-47, RP 6712-MS-SF-39-4-2 3-9-5-1, Swarna (Positive Check), RP 6690-MASC-12-46, RP 5405-JBB-631 (B)-B-BB-1-1-1-1, Rasi (Positive Check), Vandana (Positive Very Early Duration Check), RP 6499-MAID-93-12-9-2-1-1-1, RP Bio 4918-B-B-166-30, Pusa 5417-15-11-9-54-17, Pusa 44 (RP), RNR 35105, KNM 13557, CO-51 (NC), UPR 4304-12-1-1-1, RP 6680- RMS-1703-55 89-66, CRR 778-B-B-2-2, RP 6420-C10-269-12, IIABR-10 / IIAB-309/IR 13T144, CSR M1-5, R 1902-97-1-77-1, CR 4386-RGA-134, CRR - DH64, VNR-231, MEPH-167, US 314 (Hybrid Check), Bio-271, JKRH-1170, NWGR-16032, WGL 1720, KPS-10321, RP 6468-JB 396-9-7-2-1-1-1, KR 21001, KR 21003, JGL 34560, HRI 174, RP 6317-RMS-S35 BC2F4-49-25-12-24, Gontra Bidhan-3, MALI-348, PR 113-PHI-21103, KR 19011, KR 19015, ADT 39, CR 4331-85-1-1-1, TRC GTS 739-B-B-4-1, TTBD 106-2-4, NDR 359, RP 6743-RAF-0208-IJ-9, RP 6742-RAF-909-IJ-4, Jaya, NVSR 934, KAVERI-7623, RP 6765-RAF 999-41, RCPR 93-IR 106312-50 1-1-1, PAU 7592-366-1-1-B (RYT4009), IIABR-13/IIAB 4/IR15L1505, RP 5594-97-5-1 (PSV 222), RCPR 92-IR 97069-1-1 1-1, RP 6252-BV/RIL BV2024, CRR 790-43, CR 3561-5-2-1-1-1-1, IIRRH 160, PA-6129, MTU 1376, Swarna, Pusa 44, CR 3562-2-1-1-1-1-1, MEPH-173, CSR 389-16-22, Pusa 5417-15-11-9-54-17, CSR 389-16-19-15, Pusa 5417-15-11-9-50-27, CSR 389-16-23-42, Pusa 1823-12-82, RP 6750-RMS-2-23-67-91, RP 6751-RMS-1-13-34-42, RP 6757-RMS-22-17-34-17, RP 6532-RMS-13-15-6-24, RP 6284-Patho 6-1-1, BPT 3243, Super 4466, KNM 13584, Gotra Bidhan -3, MEPH-168, JKRH-1135, Pusa 44, NVSR 6494, CSR 141-11-112, CSR 103-10-2 PR 115 / FL 478 MS 405 5205 CSR 36, Benibhog and IR-50

5(Moderately Susceptible)	CSR 36 (Alkaline Check), NVSR 545, FL478, CR 4060-1318-5-2-2-2-1 5-3-4, Pusa RH-60, JKRH-1004, KPS 6251, UPLRH-180842, US 314, IIRRH-130, BRR 2152, RP 6528-RMS 1421-43 25-29, CR 3937-1-1-1-1-1-2-3, CSR PET 27, RP 5594-147-23-1, TRC 184-B-B-76-1-1, CRR 842-IR14L159, Rasi (Positive Check), RP 6255-BV / RIL / BPT / Varadhan / 1696, Rasi (Positive Check), CR 4418-4-1-2-1-3-1, CR 4340-6-1-GSR IR2-1- R6-N3-N4-N68-N35, RP 6328-218-B-29-1 (PSV 1103), CR 4383-RGA-35, RP 6715-MS-SS-999-11-6-2-5-4-2, RP Bio 4918-B2-175K-2, RP 6252-BV/RIL-BV1024, RP 6691-HWR 31, RP Bio 4919-B-B-13-7, RP 6500-MAID-90-9-2-1-1-1-1, RP Bio 5477-NH-663, RP 6166-47, RP 6750-RMS-2-23-67-91, Improved Samba Mahsuri, CR 4401-1-7-IR 117834-10-1-RGA-1, NVSR 3211, IIABR-9 / IIAB-54 / IR 16A3098, JGL 28639, RP 5599-240-B-7-3 (PS-56), HURS 19-9-IR 128773-4-3-1-4-B, CR 3745-3-2-1-2-1-1, KNM 12509, WGL 1719, RP 6529-1780-28-7-16, ORJ 1345 (TP 30531), RNR 35109, CR 3843-22-2, CR 3842-62-5-1-1-1, KR 21002, ADT 45 (Recurrent Parent), HURS 19-3, NDR 359 (NC), RP 6697-P.N.24-14, R 2454-1-R1-10, WGL 1355, RRX-271, Pusa 5358-3-1-1-1-1-1, RP 6488-MAID-1-180 119-1-1-1-1, PRNP 10027, NVSR 624, Indam 200-055, PNPG 114, ADVRH-191788, MEPH-170, RRX-3484, PHI-22108, PHI-22109, MALI-484, BPT 3284, CR 3741-1-1-2-1-1-2, RAL-LIS-20609, 27P63, TNTRH-99, RP 6764-BGIR-7-26-3, CR 4402-(1,2,3,4)-89-1-3 1, CR 3553-1-5-1-2-1-1, RNR 39027, CR 3516-11-2-2-1-1-1, CR 4338-2-1-1, CR 4121-142-36-24-1, Bangabandhu - 1 Plus, BRR 2110, PA 6444, Pusa 3039-16-4-2-5, RP 6753-RMS-4-52-77-81, RP 6533-RMS-3-45-9-18, RP 6533-RMS-1-12-19 28, Swarna, RP 6477-Patho-5-4-5, RP 6284-Patho 6-1-2, RP 6477-Patho-5-4-4, CR4388-RGA-202-1, RNR 29320, BRR 2151, ORJ 1313, RALLIS-21304, HRI-216, SRPH-123, KJTRH-2107, US 312, RP 6529-RMS-14-66-11 78, CSR 10, RNR 29325, CSR 104-10-2, NVSR 6526, RP Bio 4918-B2-24K, CSR 116-10-2, CSR-389-16-19-15, RP 6751-RMS-1-13-34-42, Improved Samba Mahsuri, Vikramarya, CH-45
7(Susceptible)	CSR 189-11-122, IIRRH 156 (Hybrid), IIRRH 155 (Hybrid), CSR YET 59, JKRH-1601, WGL-14, BRR 2183, HURS 21-2-IR15T1473, RP 6112-MS-M-92-11-5-7-33-6-2, Improved Samba Mahsuri (Susceptible Check), RP 6252-BV/RIL-BV181, CR 3549-3-5-2-1-1-1, RP 6459-C2-168-1, RP 5593-83-27-1 (PSV 2081), RP 6689-PyF 111-25, RP 6754-RMS 23 -65-78-90, Pusa 5417-15-11-9-50-27, RCPR 94-IR97030-7-2-2-2, AD (Bio) 13060, HKR 18-32, NWGR-16034, NVSR 750, RCPR 95-IR 97046-39-2 1-2, RRX-3276, MTU 1348 (MTU 2689 45-1-1), CR 3564-1-1-4-2-2-1, HRI-211, RRX-338, Gangavati Sona, ORJ 1342, OR 2517-8, PHI-21104, RNC-0457, US 312, KJT-2010-3, CRHR-175, RP 6747-19483-1-1, Telangana Sona, NWGR 17123, RP Bio 4918-NPS 58-1-2, Pusa 2070-22-1, CR 4375-1-4-1-1-2-2, WGL 1367, NWGR 17111, CR 4425-1-1-3-1-1, HRI-215, NVSR 911, RNR 28373, R 2220-39-1-4-1, RP 6327-13-171-3-2 (PSV-1128), CR 4403-5-1-IR117841 4-1 RGA-1 RGA-1 RGA 2, IIRRH 159, IIRRH 161, BRR 2162, MTU 1377, RP 6330-179-3-9-1, CR 3988-6-3-1-1, CN 1317-557-5-6-BNKR 42-2-5-1, R 2404-346-1-164-1, BRR 0225, R 2370-496-1-278-1, VNR - 233, CRHR 166, Pusa 1988-15-7-44-98-15, RP 6749-RMS-7-17-27-41, RP 6752-RMS-3-25-94-22, RP 6756-RMS-29-43-64-82, RP 6532-RMS-14-25-3-45, WGL 1533, Daftari-1, RP Bio 4918-NPS 58-1-8, RDR 3609, LG-90303, SRH-333, RP 6693-16-388, RP 6529-RMS-77-98-77 23, DST 2bp 20-4-14-14, DST 66bp 8-5-6-4, MTU-1010, RP 6744-19182-1-1, Krishna Hamsa, Gauri, CSR 36, CSAR 9-29-2021, CSR-389-16-23-42, Pusa 44, RP 6750-RMS-2-23-67-91, HR-12, IR-64, Rasi, Nidhi, Ajaya and Tetep

9(Highly Susceptible)	BRR 0181-IR 93827-29-1-1-4, TRC 185-B-B-82-2-11, RP Bio 4919-B2-NSR 5, RP 6522-MSA-16-24-16-1550, CR 4358-3-3-1-2-1, RP 6757-RMS-22-17-34-47, Pusa 2091-26, CB 18611, BRR 0156, CSR M1-4, RP 6166-47-1-23, RNR 28399, PHI-20106, MEPH-159, RP 6747-19484-1-1, RP 6686-CGR 22, WGL 14, CRHR-168, CSR BT-252-201, NWGR 17133, NVSR 929, CR Dhan 202, Improved Samba Mahsuri, Samba Mahsuri, GNV 2020-05, BRR 2177, RNC-0752 and Swarnadhan
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Table 3: Grouping of rice genotypes showing different disease reaction against Brown spot disease of rice during *Kharif* 2023.

Conclusion

This study revealed significant genetic variation among 421 rice genotypes from the NSN-1 segment in response to brown spot disease under field conditions. Only one genotype (PR 124) showed complete immunity (disease score ‘0’), while 55 genotypes were classified as resistant (score ‘1’), indicating strong potential for use in resistance breeding. Additionally, 131 genotypes were moderately resistant, followed by 114 moderately susceptible, 92 susceptible, and 28 highly susceptible entries. These findings confirm the rarity of absolute resistance and underscore the importance of moderately resistant genotypes in guiding breeding and disease management strategies. The resistant genotypes could be provides a solid basis for developing brown spot-resistant cultivars suited to Eastern India’s agro-ecological conditions for eco-friendly management of brown spot disease of rice.

Acknowledgement

The authors express their sincere gratitude to the Department of Plant Pathology, Bihar Agricultural University, Sabour, Bhagalpur, for providing the essential infrastructure and support necessary for the successful completion of this research. Acknowledgment is also extended to ICAR-IIRR, Hyderabad, for supplying planting materials and financial assistance, which substantially facilitated the execution of the study.

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