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Research paper

Estimation of Disease Severity and Screening of Sheath Blight Resistant Cultivar among Indigenous Rice Genotypes

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Abstract

Sheath blight of rice caused by *Rhizoctonia solani* is a major disease that causes substantial yield loss of production globally. Development and use of resistant cultivars is a cost-effective strategy to manage the disease. The present study encompasses 43 rice germplasms that were evaluated for sheath blight resistance during 2022-2024 in Ranadevi farm of Centurion University of Technology and Management, Paralakhemundi, Odisha. Evaluation was conducted under natural field conditions supplemented with artificial inoculation of the pathogen. Disease severity was measured using a 0-5 disease grading scale. The classification of genotypes was carried out using Percent Disease Index (PDI), Area Under Disease Progress Curve (AUDPC), and Genotypic Category (GC). Disease modeling was established through the Gompertz model, RF (Random Forest), and ANN (Artificial Neural Network) models. Some of the genotypes like Swarna Subhagya, CR 1017, and NLR 33892 indicated consistent resistance or moderate resistance between seasons, having lower AUDPC value (<400), whereas, number of famous varieties (>15), such as IR 64, MTU 1010 and CR Dhan 308, recorded high susceptibility with AUDPC of more than 1500 and GC score of 5. Also, disease progression was well fitted within the different categories of resistance (R2 = 0.9747 - 0.9963) using the Gompertz model where whereas in the machine learning model, resistance responses were categorized. Further, compared to the test accuracy of the (Random Forest) RF classifier, which was 76.92 per cent, the ANN (Artificial Neural Network) model produced an accuracy of 81 per cent.

Keywords: *ANN (Artificial Neural Network); AUDPC; Gompertz Model; RF (Random Forest) and Sheath Blight.*

1. Introduction

Rice (*Oryza sativa L.)* is the most important cereal crop in the Graminae family, produced in 113 countries all over the world. Nearly 40 percent of the entire food grain production is contributed by rice [1]. At least half of the global population (3.5 billion) depends on rice as a staple food [2], [3]. India produces 129 mt of rice annually with a productivity of about 3.86 t ha-1 on the rice cultivation area of 44 mha [4]. Karnataka has a rice area of 1.4 mha that yields about 3.5 mt of rice at a productivity of 2.5 t ha-1. There are a large number of pathogens that induce stress on rice, hence rendering it unable to achieve its maximum production potential. The sheath blight agent, *Rhizoctonia solani*, has the potential to cause yield loss equal to or less than 4-45% depending on the crop growth stage, time of infection, and environment [5]. Sheath blight disease is considered the second most dangerous disease after blast in regard to the loss in seasonal production of rice [6], [7]. It has been a major production constraint in high-yielding-fertilizer-responsive-hybrid and highly tillered varieties in intensive rice production systems [8], [9]. *Rhizoctonia solani* Kuhn AG1-IA (anamorph) and *Thanatephorus cucumeris* (teleomorph) are facultative parasites and saprotrophs that exist in the soil. With the contact of the pathogen to the plant parts, such as tillers and leaves, it spreads rapidly via sclerotia that can survive in the soil and water within three years [10], [11]. The disease inhibits various parts of the plants, including leaf sheaths, upper leaves, as well as panicles, and its initial symptoms become evident at about the late tillering stage. It becomes aggressive at the stage of panicle differentiation [12]. The identification of the disease is usually assisted by one or several broad, rectangular or irregularly elongated lesions on the leaf sheath [13]. The disease is difficult to manage due to the wide host range of the virus as well as the sclerotia persistence in response to adverse environmental conditions. The primary instrument in managing the illness is chemical fungicides. However, such fungicides are often not commercially or environmentally feasible. The sheath blight (ShB) losses in rice can be minimized through developing resistant cultivars, as the rice landraces are described as genetic wealth, highly vigorous, and invaluable sources of sheath blight resistance [14]. However, little success has been achieved in developing resistant cultivars through genetically modifying them with defense-related genes [15]. To date, no entirely resistant rice germplasm has been identified, despite intense breeding pressure, large-scale germplasm resistance screens, and wild rice species resistance gene studies [16 - 18]. Even after decades of screening, there has been no release of a rice cultivar with full resistance to sheath blight. Notable limitations are (i) the high genetic and ecological adaptability of *Rhizoctonia solani*--especially AG1-IA--that maintains inoculum through long-lived sclerotia and can survive in a wide range of conditions; (ii) the predominantly quantitative and polygenic nature of host resistance, in which most QTLs have small to moderate effects and are influenced by environment-genotype interactions; and (iii) breeding trade-offs and linkage drag that make it difficult to introgress desirable alleles without affecting agronomic performance. Recent syntheses repeat that resistant germplasm is still rare and that field-level protection over a range of microclimates has been hard to sustain. [19], [20]. Breeders use their knowledge of genetic diversity to choose the parents in a hybridization program. New genes and pathways involved in defense responses against *R. solani* could be identified by screening popular landraces against resistance. The information attained in these studies can be used in developing high-yielding rice cultivars that are more resistant to sheath blight. To help address these problems, scientific approaches based on data to integrate phenotypic, environmental, and molecular data to define resistance and help with breeding decisions have increased interest. Random Forests (RF) and Artificial Neural Networks (ANN) machine learning (ML) models have demonstrated high promise in the classification of resistant and susceptible lines and prioritization of candidate loci. Their methods complement traditional QTL mapping and multi-omics research since they allow identifying more useful genetic material faster and more accurately. ML frameworks are also considered useful decision-support tools in breeding pipelines because they can process non-linear and complex datasets [21]. In rice, full resistance against sheath blight has never been achieved; the majority of cultivars have shown only partial resistance. Computational techniques such as RF and ANN present novel avenues to understand the quantitative characteristics of sheath blight resistance, combine multi-environmental data, and develop promising genotypes to be further bred. This justification is the foundation of the current study that assesses RF and ANN models to classify sheath blight resistance and stratifies rice genotypes to be used in improvement programs [22]. Therefore, the study had an aim of testing 43 common landraces of rice in the field against sheath blight.

2. Materials and Methods

2.1. Survey and surveillance

Our planned research survey and surveillance will take place in the southeastern coastline region of Odisha and Andhra Pradesh. A survey will be conducted to determine the various anastomosis groups, hosts, and disease severity across the region. The survey and surveillance study includes several data such as symptomatological fluctuation, part of infection, types of infection, percent disease incidence (PDI), disease severity (DS), yield/production, and loss percentage detection.

2.2. Experimental site and experimental design

The experiment was conducted at Ranadevi farm of Centurion University of Technology and Management, Parlakhemundi, Odisha, during the 2022-2024 cropping season. The experiment was conducted in 43 germplasms, 3 replications, and one check with Swarna (MTU-7019). The land was plowed twice crosswise by tractor-drawn harrow, and weeds were removed thoroughly from the field. Nurserybed was raised and sowing was done main field was prepared in an area of (22.2 x 3.4) m^2, along with a 0.5 m irrigation channel. (Figure 1) Thirty-day-old seedlings were transplanted into the main field with a spacing of 4.35 x 0.8 m^2. (Figure 2,3) The gap between plants was 10 cm, and the row-to-row distance was 20 cm. Seedlings that were 30 days old were transferred from the nursery to the main field (Figures 4,5,6).

Fig. 1: Rice Nursery Bed with Uni-form Growth of Seedlings Before Transplantation.

Fig. 2: Feld Screening Plot That was Put Under Natural Conditions to Determine Varietal Response Against Sheath Blight.

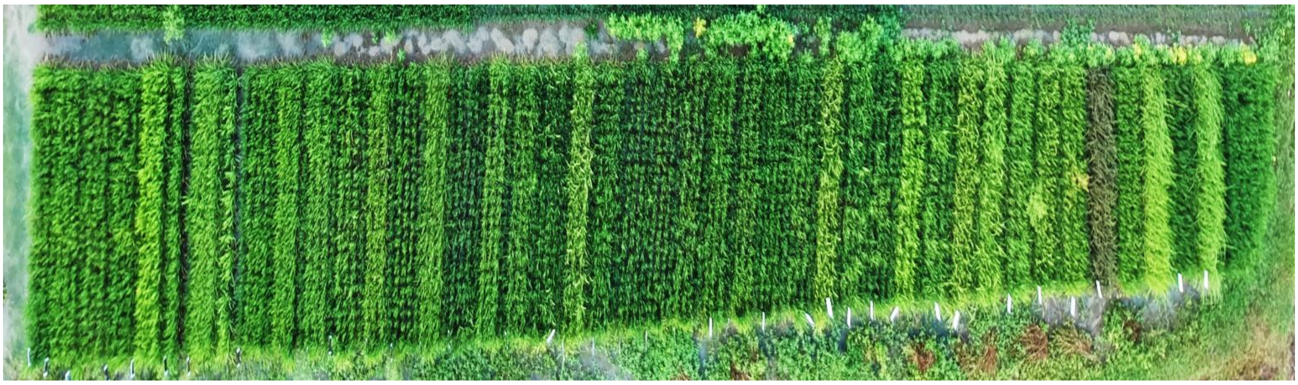

Fig. 3: Overview of Experimental Field Plan Taken by Drone to Indicate Plot Distribution and Uniformity.

Fig. 4: Field View at Crop Maturity Stage.

Fig. 5: Artificial Infection of *R. Solani* Sclerotia/Mycelial Discs in the Field in Tillering Stage.

Fig. 6: Three Replications with Swarna as the Susceptible Check were Demonstrated in the Experimental Design.

2.3. Experimental materials

Treatment consisted of 43 genotypes, out of which were collected from the Agricultural research station, Ragolu, Andhra Pradesh, Baghusala farm, and Ranadevi farm of Centurion University of Technology and Management, Parlakhemundi, Odisha.

2.4. Symptomatic characterization

The symptoms of sheath blight were systematically observed in field conditions (Figure 7) and their photographs recorded (Figure 8). First symptoms presented were small, water-soaked oval to irregular lesions on the plant leaf sheath along the waterline (Figure 8a). The lesions developed at a slow pace with a greyish center and brown margins (Figure 8b) and expanded in vertical direction along the sheath (Figure 8c) and to leaf blades (Figure 8d). As the disease progressed, several lesions were formed and they coalesced into large necrotic patches (Figure 8e), and in the severe condition, the sheath and leaves were highly affected and causing the plant to wilt and lodge (Figure 8f). Those are the symptoms of sheath blight brought about by *Rhizoctonia solani*.

Fig. 7: Symptomatic Representation of Sheath Blight Disease of Rice Caused by *R. Solani*.

(a) (b) (c) (d) (e) (f)

Fig. 8: Symptomatic Development of Sheath Blight in Rice by *R. Solani*: The Sheath Blight Lesions Develop Gradually into Irregular and Elongated Lesions with Grayish Foci and Dark Brown Periphery, Starting as Small Water-Soaked Spots Along the Waterline. The Lesions Gradually Fuse, Causing Girdling of the Sheath, Tiller Weakening, And Severe Cases Result in Lodging of Plants

2.5. Disease severity estimation

Disease severity is a “area of a sampling unit (plant surface) affected by disease expressed as a percentage or proportion of the total area” Nutter Jr *et al*., 1991). Disease severity data were started taking from the emergence of the disease; data is taken for a 10-day interval of time up to 9 observations. (Figure 9) The disease was scored by using 0-5 scale based on lesion character and lesion area, where 0 represented no lesion characteristics and 5 represented lesions in more than 75% leaf area. Disease severity was calculated by the formula given by Shrestha and Mishra (1994).

$$\text{Diseaese severity(DS)} = \frac{\text{Total lesion length}}{\text{Total length of sheath}} \times 100$$

$$\text{Percent disease index (PDI\%)} = \frac{\text{Sum of all individual disease ratings}}{\text{Total no.of plant assessed} \times \text{maximum ratings}} \times 100$$

Fig. 9: Level of Sheath Blight Disease Severity of Susceptible Swarna Rice.

2.6. Area under disease progress curve (AUDPC)

The area under the disease progress curve (AUDPC) is a common method for combining several observations of disease progression into a single number. Our research reveals that this method significantly underestimates the impact of the first and final observations [23].

AUDPC = $\sum^{n}$ $[(+ xi + 1)/2] *$

i=1

The AUDPC was estimated using the method provided by Das *et al*. (1992). The Area under Disease Progress Curve (AUDPC) is a quantitative indicator of disease intensity across time. It is used in plant pathology to identify and compare disease resistance levels among crop cultivars.

$$\text{AUDPC}=\sum_{i=1}^{n-1}\left(\frac{y_i+y_{i+1}}{2}\right)(t_{i+1}-t_i)$$

Where,
y_i= Disease Severity % on the i^{th} scoring
t_i = Number of days from sowing to i^{th}scoring
n = Total number of scorings
Among all the forty-three genotypes of rice that include one check variety, Swarna, were screened under field epiphytotic conditions for the occurrence of disease reaction to sheath blight.

2.7. Screening of resistance cultivar through field trial

The screening of rice cultivars against sheath blight disease under natural field conditions was done in the form of a field trial. Cultivar responses were assessed into five categories as Resistant (R), Moderately Resistant (MR), Moderately Susceptible (MS), Susceptible (S), and Highly Susceptible (HS) depending on the severity of the disease. The experiment was designed in a randomized block using three replications, and normal agronomic practices were utilized during the cropping season (Kharif 2022-24). The severity of the disease was measured every 10 days till 90 days of inoculation, and the Area Under Disease Progress Curve (AUDPC) was calculated to determine the progression of the disease. The cultivars were classified based on the AUDPC values as follows: Resistant (0-300%), Moderately Resistant (301-600%), Moderately Susceptible (601-900%), Susceptible (901-1100%), and Highly Susceptible (above 1100%) [24]. This classification was useful in the discovery of cultivars differing in the degree of resistance against sheath blight of rice.

2.8. Isolation of pathogen and morphocultural characterization

At first, washing the tissues thoroughly in sterile water, the causal fungi are isolated from plant tissues exhibiting clear symptoms. The infected tissues, along with adjacent small unaffected tissue, are cut into small pieces (2-5 mm squares) and by using flame-sterilized forceps, they are transferred to sterile petri dishes containing 0.1% mercuric chloride solution used for surface sterilization of plant tissues, for a period of 30-60 sec. Alternatively, Clorox (10%), sodium hypochlorite (1%), or hydrogen peroxide (50%) may be used for surface sterilization of plant tissues. The sterilized pieces will be aseptically transferred to petri dishes containing standard medium like potato dextrose Agar (PDA) supplemented with streptomycin sulfate, at the rate of 3-5 pieces of tissue per petri plate and incubated at room temperature (25±1^{0}C) that may favor the pathogen development. The sclerotial transfer technique is also effective for maintaining the culture for long-term basis. In this method, surface sterilization of the sclerotia is done with a 1% NaCl solution for 30 seconds, then washed three times with sterile distilled water. The sclerotia were transferred to the fresh PDA medium and incubated at 25±1^{0}C °C for 2-3 days. The initial fungal growth is further transferred to another fresh PDA plate to get a pure culture of the pathogen. Morphological and cultural variability of the pathogen is planned to be determined through various microscopic observations (Figure 10).

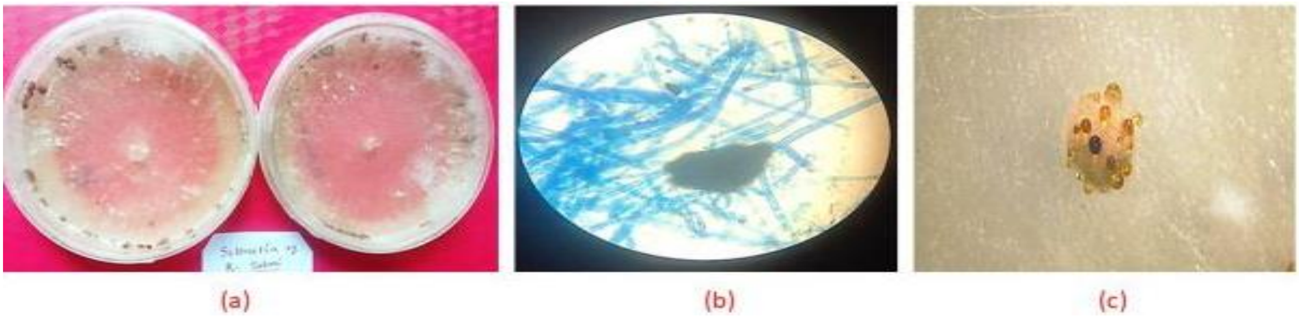

Fig. 10: Morphological Characteristics of *R. Solani*. (A) Pale White Mycelium Colony & Sclerotia Formation in the Periphery of Petri Plate on PDA Media.(B) Mycelium is Septate, branched right-angled under microscopic view. (C) Sclerotia Formation Observed Under Stereoscopy Microscope.

2.9. Pathogenicity test through detached leaf assay

Uniform-sized rice leaves were collected and thoroughly washed under running tap water to remove surface contamination. The cleaned leaves were then blotted dry using sterile blotter paper. Subsequently, the leaves were placed in sterile Petri plates lined with moist blotting paper to maintain adequate humidity. Sterile distilled water was added to ensure proper soaking and hydration of leaf tissues. For inoculation, a small wound was made on the surface of each leaf using a sterile needle to facilitate pathogen entry. Mycelial bits of the test pathogen *R. solani* were aseptically transferred into the wounded area of the leaves using sterile forceps. The inoculated Petri plates were incubated under a BOD incubator, and disease progression was observed and recorded (Figure 11).

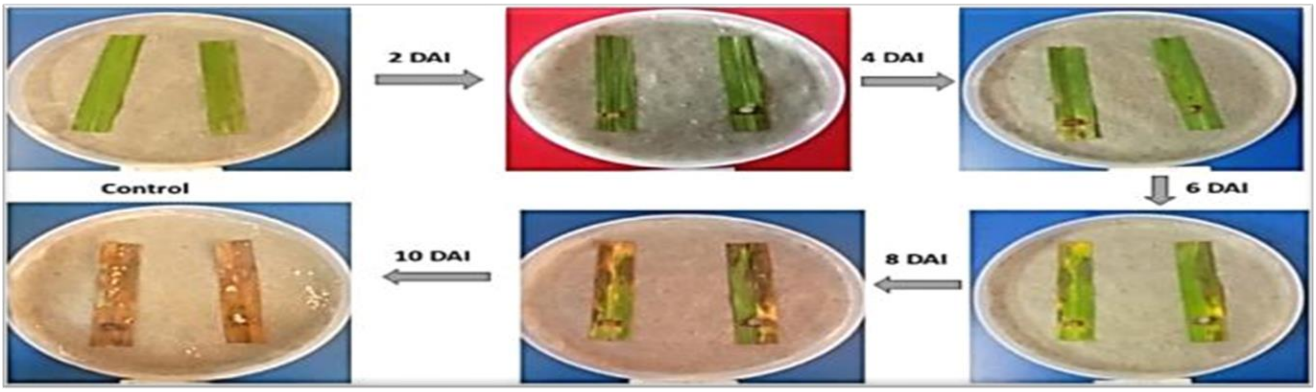

Fig. 11: Temporal Pathogenicity Test of *R. Solani* on Rice by Detach Leaf Assay. 2DAI- Initial Infection Starts at the Point of Inoculation. 4DAI- Turn Light Green Appearance with Increased Lessons. 6DAI- Gradual Increasement of Infection Locus.8DAI- Gradual Increasement of Infection Locus. 12DAI- Totally Destructed Tissue Along with Sclerotia Formation

2.10. Virulence detection through the seed mortality test

For the seed mortality test, six different rice germplasm lines were selected to evaluate their response to pathogen-induced mortality under in vitro conditions. Sterile petri plates were prepared by pouring 2% water agar and allowed to solidify under aseptic conditions. Ten healthy seeds from each germplasm were surface sterilized using 1% sodium hypochloride solution for 2-3 times, followed by rinsing with sterilized distilled water. The sterilized seeds were then placed evenly along the periphery of each petri plate in three replications. After seed germination, which typically occurred within 48-72 hrs., a mycelial bit of *R. solani* was inoculated at the center of the agar plate. The plates are incubated at 27 ± 2 ^{0}c. Seedling mortality was recorded at 2-day intervals. Mortality percentage was calculated for each germplasm based on the no. of dead seedlings relative to the total no. of germinated seeds (Figure 12).

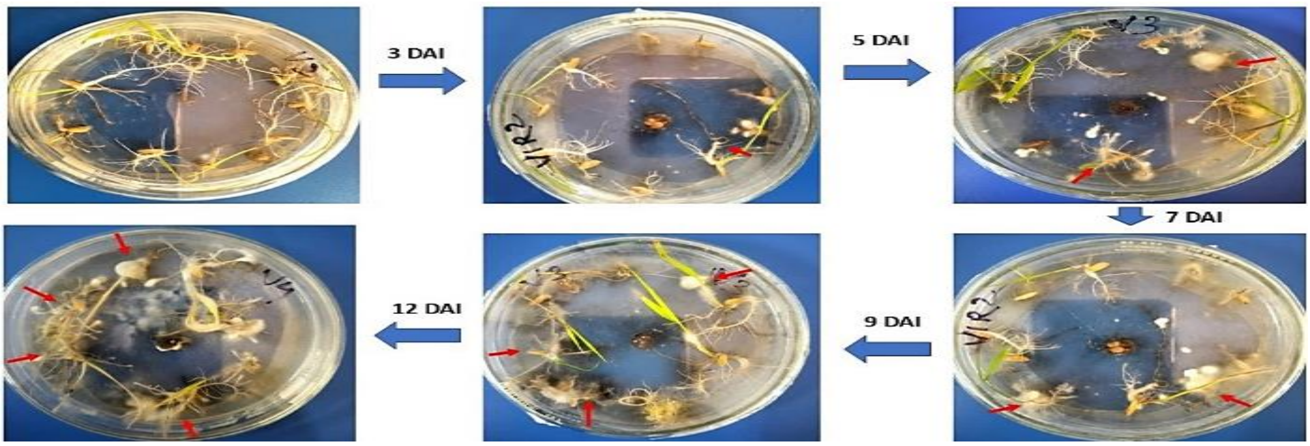

Fig. 12: Seed Mortality Test in Different Germplasm of Rice by Sheath Blight Disease of Pathogen *R. Solani*.

2.11. Statistical analysis

2.11.1. Artificial neural network (ANN)

A model called Artificial Neural Network (ANN) was then developed to categorize the rice cultivars into the five classes of disease resistance, such as Resistant (R), Moderately Resistant (MR), Moderately Susceptible (MS), Susceptible (S), and Highly Susceptible (HS), based on the traits evaluated in the field. AUDPC values were used to present labeled data, which was used to train this model, and accuracy was tested via the confusion matrix. The ANN was able to discern with high levels of susceptibility and highly susceptible categories, having a level of misclassification at the level of moderately resistant and moderately susceptible. In this direction, the usefulness of ANN in aiding disease-resistance screening rice breeding programs is brought out.

2.11.2. Random forest (RF) model

Random Forest (RF) model was employed to categorize rice cultivars into five resistance vectors, viz. Resistant, Moderately Resistant, Moderately Susceptible, Susceptible, and Highly Susceptible, expected based on AUDPC-based field outcome. A confusion matrix was utilized to train and test the model, and its high accuracy was observed in terms of classifying most cultivars, especially those belonging to the Highly Susceptible and Susceptible categories. The findings illustrate the possibility of RF as a helpful instrument in resisting disease in rice.

2.11.3. Gompertz model

The Gompertz model was applied to analyze the progress of sheath blight disease among rice cultivars in five resistance classes, including HS, S, MS, MR, and R. The data measured the disease severity (DS) against time (DAI). This was to provide the growth pattern of the disease by fitting the model. The curves demonstrated the different patterns of progression of each category, being quite effective in depicting the differences in the development of the disease within the cultivars.

3. Result

3.1. Survey and monitoring of sheath blight in varied geographical locations

The survey was taken in five locations to determine the level of sheath blight infestation in rice. Isolates of *Rhizoctonia solani* were noted, and their virulence was assessed. The most severe sheath blight infestation was found in different locations that were surveyed. A peak virulence level (****) was found at Gania and Daspalla (80-90%), where it shows 70-80 per cent infestation levels in Khandapada and Katalkaitha had somewhat lower severity (***), whereas Ranadevi registered the lowest levels of infestation (**), namely 50-60%. The isolates were mostly obtained using the leaf sheath sample (Table 1).

Table 1: Survey and Surveillance of Sheath Blight Infestation in Different Geographical Locations

Sl. No	Location	Longitude and Latitude	Crop	Inflectional plant part	Isolate No.	Virulence Level
1	Ranadevi	18.7973° N, 84.1499° E	Rice	Leaf sheath	RS IV	**
2	Khandapada	20.2630^{0}N, 85.1737^{0}S	Rice	Leaf	RS V	***
3	Gania	20.4029° N, 85.0435° E	Rice	Leaf sheath	RS I	****
4	Katalkaitha	18.7899° N, 84.1560° E	Rice	Leaf sheath	RS III	***
5	Daspalla	20.3356° N, 84.8490° E	Rice	Leaf sheath	RS II	****

***** is Indicating 80-90% Infestation, **** Indicating 70-80% Infestation, *** Indicating 60-70% Infestation, ** Indicating 50-60% Infestation.

3.2. Resistance screening germplasm collection

Forty-three varieties of rice were gathered in various research and field stations, such as the Agricultural Research Station in Ragolu (Andhra Pradesh), CUTM farms in Ranadevi and Baghusala (Paralakhemundi). Popularly grown lines, Swarna Subhagya, MTU 1156, IR 64, BPT 2782, MTU 1010, and some locally significant ones, include Manipuri Local and Juvraj Dhano. They are a broad diversity of genetic inheritance, and their resistance screening was done against various virulence levels of *R. solani* isolates (Table 2).

Table 2: Germplasm Used for the Screening and their Place of Collection

Sl. No.	Varieties	Variety name	Place of collection
1	V1	Swarna swoubhagya	Agricultural research station, Ragolu, Andhra Pradesh
2	V2	NLR 33892	Agricultural research station, Ragolu, Andhra Pradesh
3	V3	MTU 1156	Agricultural research station, Ragolu, Andhra Pradesh
4	V4	CR 411	Ranadevi Farm, CUTM, Paralkhrmundi
5	V5	CR 311	Agricultural research station, Ragolu, Andhra Pradesh
6	V6	MTU 1016	Agricultural research station, Ragolu, Andhra Pradesh
7	V7	Govindbhog	Baghusala farm, CUTM, Paralkhemundi
8	V8	CR 1017	Ranadevi Farm, CUTM, Paralkhrmundi
9	V9	MTU 1318	Agricultural research station, Ragolu, Andhra Pradesh
10	V10	MTU 1075	Agricultural research station, Ragolu, Andhra Pradesh
11	V11	RGL 2537	Agricultural research station, Ragolu, Andhra Pradesh
12	V12	KNMM 1638	Agricultural research station, Ragolu, Andhra Pradesh
13	V13	MTU 1061	Agricultural research station, Ragolu, Andhra Pradesh
14	V14	MTU 5204	Agricultural research station, Ragolu, Andhra Pradesh
15	V15	RGL 1880	Agricultural research station, Ragolu, Andhra Pradesh
16	V16	MTU 1121	Agricultural research station, Ragolu, Andhra Pradesh
17	V17	GRGL 11226	Baghusala farm, CUTM, Paralkhemundi
18	V18	RGL 2538	Agricultural research station, Ragolu, Andhra Pradesh
19	V19	NLR 34449	Agricultural research station, Ragolu, Andhra Pradesh
20	V20	MTU 1156	Agricultural research station, Ragolu, Andhra Pradesh

21	V21	IR 64	Agricultural research station, Ragolu, Andhra Pradesh
22	V22	BPT 2782	Baghusala farm, CUTM, Paralkhemundi
23	V23	MTU 1224	Agricultural research station, Ragolu, Andhra Pradesh
24	V24	BPT 3082	Agricultural research station, Ragolu, Andhra Pradesh
25	V25	MTU 1210	Agricultural research station, Ragolu, Andhra Pradesh
26	V26	RNR 15048	Agricultural research station, Ragolu, Andhra Pradesh
27	V27	NLR 3354	Agricultural research station, Ragolu, Andhra Pradesh
28	V28	CR1	Baghusala farm, CUTM, Paralkhemundi
29	V29	Marvel 1011	Agricultural research station, Ragolu, Andhra Pradesh
30	V30	CR 315	Baghusala farm, CUTM, Paralkhemundi
31	V31	RNR Marvel	Ranadevi Farm, CUTM, Paralkhrmundi
32	V32	MTU 101	Agricultural research station, Ragolu, Andhra Pradesh
33	V33	Soubhagya	Ranadevi Farm, CUTM, Paralkhrmundi
34	V34	CR Dhan 308	Ranadevi Farm, CUTM, Paralkhrmundi
35	V35	Mohani	Ranadevi Farm, CUTM, Paralkhrmundi
36	V36	CR Dhan 319	Agricultural research station, Ragolu, Andhra Pradesh
37	V37	MTU 1010	Baghusala farm, CUTM, Paralkhemundi
38	V38	RGL 2624	Agricultural research station, Ragolu, Andhra Pradesh
39	V39	Manipuri local	Baghusala farm, CUTM, Paralkhemundi
40	V40	RNR 15048	Agricultural research station, Ragolu, Andhra Pradesh
41	V41	Juvraj Dhano	Ranadevi farm, CUTM, Paralkhrmundi
42	V42	Puja	Ranadevi Farm, CUTM, Paralkhrmundi
43	V43	Lal Basmati	Ranadevi Farm, CUTM, Paralkhrmundi

3.3. Screening of resistance cultivar through field trial

The research trial was carried out during the three sequential Kharif seasons (2022, 2023, and 2024) in order to assess the resistance of 43 rice genotypes to sheath blight disease of *Rhizoctonia solani*. The severity of the disease was rated 10 days apart up to 90 days post-inoculation, and the changes in disease progression were measured by the Area Under Disease Progress Curve (AUDPC). Genotypes were defined as Resistant (R: 0-300), Moderately Resistant (MR: 301- 600), Moderately Susceptible (MS: 601-900), Susceptible (S: 901-1100), and highly susceptible (HS: >1100) based on the values of AUDPC. A Genotypic Category (GC) was also used to display genotypic performance on a scale of 1 (resistant) to 5 (highly susceptible). Swarna Subhagya, CR 1017, and NLR 33892 recorded resistant (R) or moderately resistant (MR) reactions under all three seasons, and there was a range of AUDPC values of 194.95 to 407.71 and 1 to 2 GC scores. Some of these entries were CR 311, MTU 1016, MTU 5204, and MTU 1318 with moderate resistant (MR) and moderate susceptible (MS) responses, AUDPC values range between 500 and 900, and GC score range between 2 and 3. Many of the genotypes, including Govindbhog, RGL 2537, KNMM 1638, and GRGL 11226, fell under moderately susceptible (MS) and susceptible (S), having an AUDPC of 900-1100 and GC measure of 3-4. Among the genotypes tested, the number of genotypes that were highly susceptible (HS) was more than 15 and included (IR 64, MTU 1010, CR Dhan 308, RGL 2624, Juvraj Dhano, and Puja) with Area under Disease Progress Curve of the pathogen (AUDPC) values above 1500 and GC scores to 5 in more than half, or in all the seasons. In 2024, the disease was severe, and the AUDPC values were highest in RGL 2624, IR 64, and Puja, which were 1986.35, 1892.14, and 1932.95, respectively.

This three-year field report demonstrated there were considerable genotypic differences in sheath reaction. Although the tested entries reveal that a small percentage of the population has a stable resistance and thus can be used as potential sources of resistance during the breeding phase of resistance, most of the genotypes exhibited moderate to high susceptibility, and hence the importance of using durable resistance to develop rice in the future improvement program (Table 3).

Table 3: Popular Cultivars and Land Races of Rice Reaction Against Sheath Blight (*PDI- Percent Disease Index, AUDPC- Area Under Disease Progress Curve, GC- Germplasm Category)

		2022 Kharif				2023 Kharif				2024 Kharif			
Sl. No.	Genotypes	Mean PDI	AUDPC	GC	Score	Mean PDI	AUDPC	GC	Score	Mean PDI	AUDPC	GC	Score
1	Swarna swoubha-gya	3.73	299.78	R	1	3.65	297.56	R	1	4.89	407.71	MR	2
2	NLR 33892	7.83	599.93	MR	2	7.55	599.85	MR	2	2.42	198.46	R	1
3	MTU 1156	11.53	984.52	MS	3	11.15	862.63	MS	3	12.38	994.72	S	4
4	CR 411	12.99	1124.93	HS	5	15.63	1238.73	HS	5	22.06	1783.90	HS	5
5	CR 311	5.62	595.61	MR	2	4.91	406.44	MR	2	7.36	592.94	MR	2
6	MTU 1016	6.77	529.71	MR	2	3.77	303.45	R	1	4.89	398.54	MR	2
7	Govindbhog	10.77	896.53	MS	3	10.77	860.65	MS	3	9.83	788.24	S	4
8	CR 1017	3.96	298.72	R	1	5.09	418.53	MR	2	2.37	194.95	R	1
9	MTU 1318	8.55	754.56	MS	3	5.90	476.70	MR	2	11.04	885.84	MS	3
10	MTU 1075	15.21	1160.84	HS	5	15.04	1178.48	S	4	11.09	903.90	S	4
11	RGL 2537	11.22	1059.70	S	4	11.44	894.71	MS	3	7.57	619.82	MS	3
12	KNMM 1638	11.88	1025.34	S	4	12.31	956.36	MS	3	17.20	1392.83	S	4
13	MTU 1061	9.54	921.20	S	4	9.48	738.15	MS	3	11.89	959.51	S	4
14	MTU 5204	9.54	797.56	MS	3	5.59	435.92	MR	2	11.18	900.18	MS	3
15	RGL 1880	8.55	723.69	MS	3	8.98	684.91	MS	3	11.84	961.60	S	4
16	MTU 1121	10.00	769.70	MS	3	11.71	905.03	MS	3	6.89	568.32	MR	2
17	GRGL 11226	9.71	819.19	MS	3	10.77	827.58	MS	3	9.73	779.49	MS	3
18	RGL 2538	9.47	806.84	MS	3	11.69	903.50	MS	3	9.96	799.10	MS	3
19	NLR 34449	10.38	863.69	MS	3	11.74	904.95	MS	3	9.93	795.54	MS	3
20	MTU 1156	11.86	1011.84	S	4	14.22	1104.38	HS	5	16.49	1332.57	HS	5
21	IR 64	10.22	926.29	S	4	12.94	1000.59	S	4	23.48	1892.14	HS	5
22	BPT 2782	11.46	975.68	S	4	12.92	997.47	S	4	10.19	821.32	MS	3
23	MTU 1224	10.65	946.62	S	4	12.14	934.49	S	4	21.52	1735.10	HS	3
24	BPT 3082	11.39	983.65	S	4	13.36	1032.39	S	4	12.20	988.34	S	4
25	MTU 1210	11.89	1039.21	S	4	13.53	1045.08	S	4	21.06	1700.32	HS	5

26	RNR 15048	13.37	1162.67	HS	5	15.80	1227.89	HS	5	23.37	1883.56	HS	5
27	NLR 3354	12.88	1162.34	HS	5	15.41	1196.96	HS	5	20.83	1681.73	HS	5
28	CR	10.41	965.13	S	4	11.57	926.96	S	4	18.51	1495.43	HS	5
29	Marvel 1011	12.38	1051.55	S	4	14.52	1124.90	HS	5	12.43	1000.68	S	4
30	CR 315	12.63	1119.46	HS	5	15.81	1230.33	HS	5	17.57	1420.29	HS	5
31	RNR Marvel	11.89	1070.07	S	4	14.43	1118.23	HS	5	18.17	1467.81	HS	5
32	MTU 101	12.24	1089.27	S	4	14.77	1144.13	HS	5	22.44	1810.01	HS	5
33	Soubhagya	12.37	1125.83	HS	5	13.70	1099.59	S	4	19.39	1566.30	HS	5
34	CR Dhan 308	10.65	996.00	S	4	14.40	1121.95	HS	5	21.76	1756.01	HS	5
35	Mohani	11.15	964.99	S	4	13.71	1063.43	S	4	17.34	1402.01	HS	5
36	CR Dhan 319	11.15	977.48	S	4	13.50	1046.89	S	4	19.71	1590.93	HS	5
37	MTU 1010	14.11	1199.70	HS	5	16.64	1297.62	HS	5	18.76	1515.28	HS	5
38	RGL 2624	12.88	1174.23	HS	5	15.13	1176.16	HS	5	24.65	1986.35	HS	5
39	Manipuri local	14.11	1242.91	HS	5	17.92	1403.68	HS	5	19.32	1559.76	HS	5
40	RNR 15048	11.15	1044.46	S	4	13.63	1084.38	S	4	23.49	1893.32	HS	5
41	Juvraj Dhano	14.11	1199.70	HS	5	16.67	1300.13	HS	5	18.79	1517.76	HS	5
42	Puja	13.37	1211.78	HS	5	15.74	1225.30	HS	5	23.98	1932.95	HS	5
43	Lal Basmati	10.90	1014.52	S	4	12.73	984.36	S	4	15.23	1213.30	HS	5

3.4. Correlation analysis

The analysis of correlation involved three-year data of three Kharif seasons (2022, 2023, and 2024) to determine the connections between Percent Disease Index (PDI), Area Under Disease Progress Curve (AUDPC), and Genotypic Category (GC) among the genotypes of rice under the research. During the season 2022, a strongly positive correlation was established between PDI and AUDPC, and a moderate negative correlation between GC and PDI/AUDPC (Table 4, Figure 13). The correlation of PDI with AUDPC reached 0.68 in the 2023 season, whereas the correlation of GC was 0.83 with AUDPC and 0.63 with PDI (Table 5, Figure 14). Once again, the values of correlation between all three parameters were proven to be significantly positive in the 2024 season, with the strongest correlation occurring between GC and AUDPC (Table 6, Figure 15). The correlation analysis pooled on the three seasons showed consistency and significant positive correlation between PDI, AUDPC, and GC, showing a stable trend in the development of the disease and a stable trend of genotypic grouping under field conditions (Figure 16). Range correlation plot, Yearly correlation plots, Pooled correlation plot. These were evidently confirmed in statistical relationships by the yearly and pooled correlation plot.

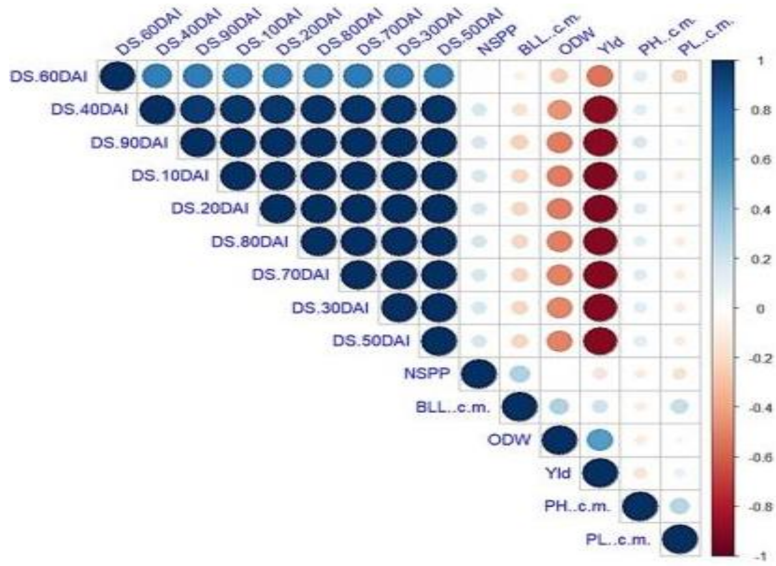

Fig. 13: Correlation Matrix for the Kharif Season 2022.

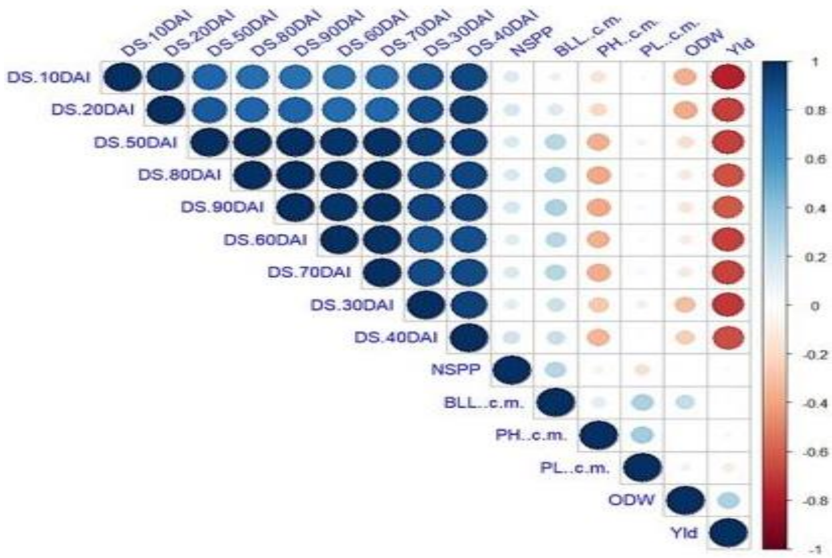

Fig. 14: Correlation Matrix for the Kharif Season 2023.

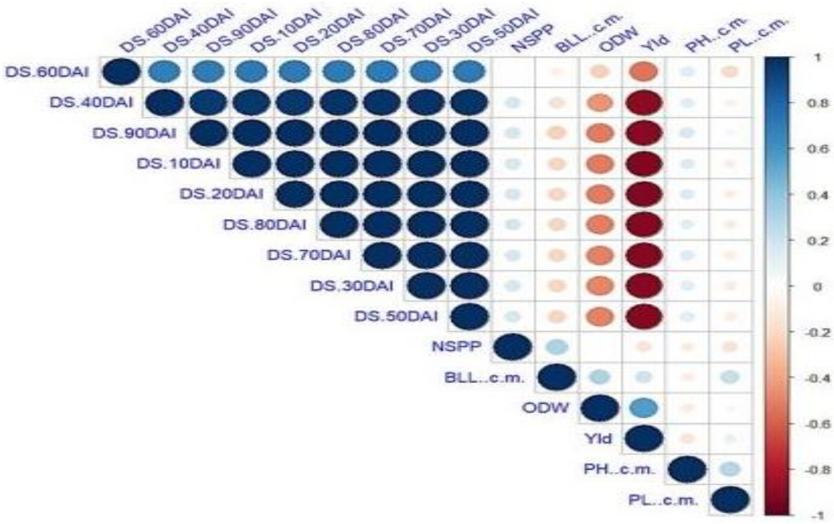

Fig. 15: Correlation Matrix for the Kharif Season 2024.

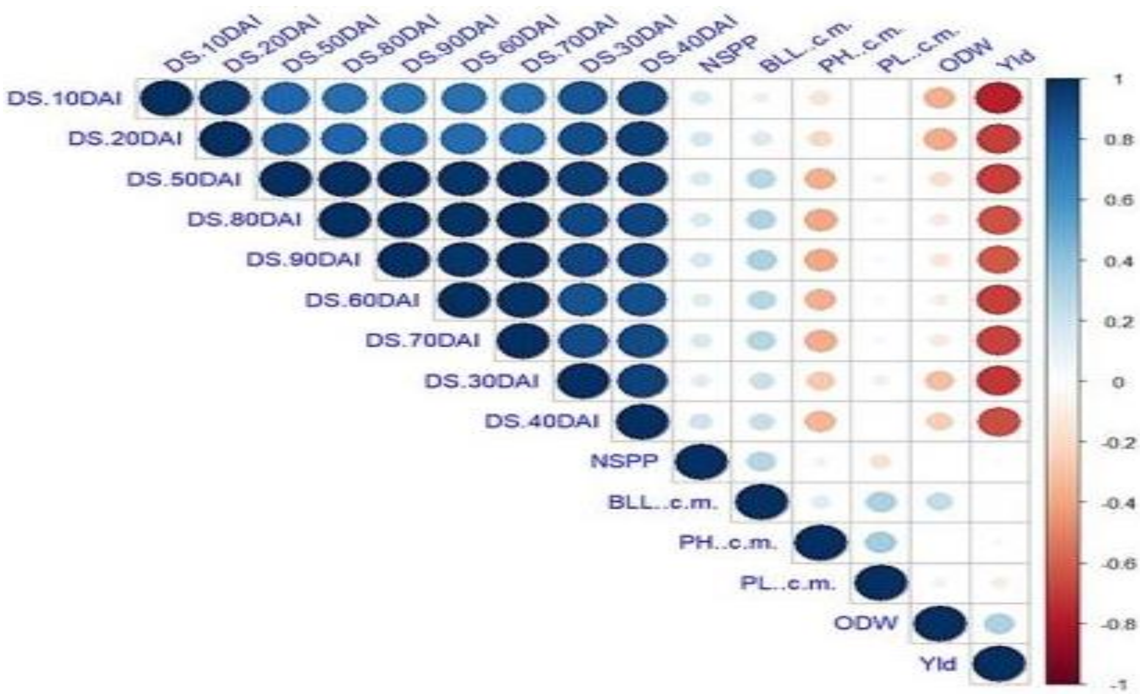

Fig. 16: Correlation Matrix for the All Three Kharif Season.

Table 4: Correlation Among Agronomic Traits (PH- Plant Height, NSPP- No. of Seed Per Panicle, BLL- Boot Leaf Length, ODW- Oven Dry Weight, YLD- Yield), Disease Severity (DS) and Percent Disease Index (PDI) At Different Days After Inoculation (DAI) For the Season 2022

	PH (c.m)	NSPP	BLL (c.m)	PL (c.m)	ODW	YLD	DS 10 DAI	DS 20 DAI	DS 30 DAI	DS 40 DAI	DS 50 DAI	DS 60 DAI	DS 70 DAI	DS 80 DAI	DS 90 DAI	PDI 10 DAI	PDI 20 DAI	PDI 30 DAI	PDI 40 DAI	PDI 50 DAI	PDI 60 DAI	PDI 70 DAI	PDI 80 DAI	PDI 90 DAI
PH (c.m)	1.00																							
NSPP	-0.06	1.00																						
BLL (c.m)	0.23	0.28	1.00																					
PL (c.m)	0.38	-0.15	0.35	1.00																				
ODW	0.06	-0.09	0.23	0.13	1.0																			
Yld	-0.13	-0.05	-0.04	-0.18	0.4	1.00																		
DS 10 DAI	-0.26	0.28	0.13	-0.30	-0.3	-0.52	1.00																	
DS 20 DAI	-0.31	0.29	0.24	-0.19	-0.45	-0.45	0.87	1.00																
DS 30 DAI	-0.39	0.12	0.35	0.12	-0.34	-0.64	0.62	0.68	1.00															
DS 40 DAI	-0.52	0.30	0.29	-0.20	-0.28	-0.41	0.82	0.88	0.82	1.00														
DS 50 DAI	-0.53	0.19	0.45	0.07	-0.20	-0.42	0.57	0.68	0.95	0.86	1.00													
DS 60 DAI	-0.60	0.22	0.46	0.03	-0.12	-0.28	0.52	0.65	0.88	0.85	0.99	1.00												
DS 70 DAI	-0.58	0.22	0.48	0.04	-0.12	-0.30	0.52	0.65	0.89	0.85	0.99	1.00	1.00											
DS 80 DAI	-0.58	0.22	0.48	0.05	-0.12	-0.30	0.52	0.65	0.90	0.84	0.99	1.00	1.00	1.00										
DS 90 DAI	-0.58	0.22	0.48	0.04	-0.12	-0.30	0.52	0.65	0.89	0.85	0.99	1.00	1.00	1.00	1.00									

PDI 10 DAI	0.18	0.05	0.12	0.09	-0.34	-0.77	0.43	0.45	0.54	0.35	0.35	0.23	0.25	0.25	0.25	1.00								
PDI 20 DAI	0.20	0.05	0.11	0.09	-0.35	-0.77	0.43	0.45	0.53	0.35	0.34	0.22	0.23	0.24	0.24	1.00	1.00							
PDI 30 DAI	0.20	0.00	0.10	0.08	-0.32	-0.75	0.43	0.44	0.51	0.32	0.32	0.20	0.22	0.22	0.22	0.98	0.99	1.00						
PDI 40 DAI	0.17	-0.05	0.10	0.06	-0.24	-0.70	0.43	0.40	0.49	0.30	0.31	0.20	0.21	0.21	0.21	0.94	0.95	0.98	1.00					
PDI 50 DAI	0.16	-0.05	0.09	0.05	-0.25	-0.70	0.43	0.40	0.49	0.30	0.31	0.20	0.21	0.22	0.21	0.94	0.94	0.98	1.00	1.00				
PDI 60 DAI	0.18	-0.05	0.08	0.07	-0.32	-0.75	0.47	0.44	0.50	0.32	0.31	0.19	0.21	0.21	0.21	0.94	0.94	0.98	0.99	0.98	1.00			
PDI 70 DAI	0.20	-0.05	0.08	0.08	-0.33	-0.75	0.46	0.45	0.50	0.33	0.31	0.19	0.21	0.21	0.21	0.94	0.95	0.98	0.98	0.98	1.00	1.00		
PDI 80 DAI	0.19	-0.08	0.08	0.09	-0.33	-0.73	0.47	0.45	0.49	0.33	0.31	0.19	0.20	0.21	0.21	0.90	0.91	0.96	0.96	0.95	0.99	0.99	1.00	
PDI 90 DAI	0.24	-0.11	0.05	0.11	-0.34	-0.68	0.45	0.43	0.43	0.30	0.25	0.14	0.15	0.15	0.15	0.78	0.81	0.85	0.84	0.83	0.89	0.90	0.94	1.00

Table 5: Correlation Among Agronomic Traits (PH- Plant Height, NSPP- No. of Seed Per Panicle, BLL- Boot Leaf Length, ODW- Oven Dry Weight, YLD- Yield), Disease Severity (DS), and Percent Disease Index (PDI) At Different Days After Inoculation (DAI) For the Season 2023

	NSPP	BLL (c.m)	PL (c.m)	ODW	YLD	DS 10 DAI	DS 20 DAI	DS 30 DAI	DS 40 DAI	DS 50 DAI	DS 60 DAI	DS 70 DAI	DS 80 DAI	DS 90 DAI	PDI 10 DAI	PDI 20 DAI	PDI 30 DAI	PDI 40 DAI	PDI 50 DAI	PDI 60 DAI	PDI 70 DAI	PDI 80 DAI	PDI 90 DAI
NSPP	1.00																						
BLL (c.m)	0.28	1.00																					
PL (c.m)	-0.17	0.36	1.00																				
ODW	0.10	0.21	0.06	1.00																			

Yld	0.01	-0.03	-0.17	0.43	1.00											
DS10DAI	0.07	0.25	0.14	-0.33	-0.84	1.00										
DS20DAI	0.11	0.31	0.12	-0.28	-0.77	0.99	1.00									
DS30DAI	0.14	0.37	0.10	-0.23	-0.68	0.96	0.99	1.00								
DS40DAI	0.17	0.41	0.08	-0.17	-0.58	0.91	0.96	0.99	1.00							
DS50DAI	0.21	0.46	0.04	-0.10	-0.44	0.83	0.90	0.95	0.99	1.00						
DS60DAI	0.23	0.48	0.01	-0.04	-0.32	0.75	0.84	0.90	0.95	0.99	1.00					
DS70DAI	0.23	0.48	0.02	-0.04	-0.32	0.74	0.83	0.90	0.95	0.99	1.00	1.00				
DS80DAI	0.23	0.48	0.02	-0.04	-0.32	0.75	0.83	0.90	0.95	0.99	1.00	1.00	1.00			
DS90DAI	0.23	0.48	0.02	-0.04	-0.32	0.75	0.83	0.90	0.95	0.99	1.00	1.00	1.00	1.00		
PDI10DAI	0.12	0.15	0.08	-0.21	-0.76	0.62	0.57	0.51	0.45	0.35	0.27	0.27	0.27	0.27	1.00	
PDI2	0.14	0.16	0.08	-0.	-0.	0.62	0.57	0.51	0.44	0.35	0.26	0.26	0.26	0.26	1.00	1.00

0 DAI				22	76																		
PDI 30 DAI	0.13	0.16	0.06	-0.23	-0.75	0.62	0.57	0.51	0.45	0.35	0.27	0.27	0.27	0.27	0.99	0.99	1.00						
PDI 40 DAI	0.10	0.22	0.20	-0.15	-0.64	0.53	0.48	0.42	0.36	0.27	0.20	0.19	0.20	0.20	0.86	0.87	0.88	1.00					
PDI 50 DAI	0.05	0.17	0.19	-0.23	-0.69	0.51	0.45	0.39	0.32	0.21	0.14	0.13	0.13	0.13	0.90	0.90	0.90	0.95	1.00				
PDI 60 DAI	0.06	0.18	0.19	-0.23	-0.70	0.52	0.46	0.39	0.32	0.22	0.14	0.13	0.13	0.13	0.90	0.90	0.90	0.95	1.00	1.00			
PDI 70 DAI	0.07	0.18	0.21	-0.25	-0.71	0.53	0.48	0.41	0.33	0.23	0.15	0.14	0.14	0.14	0.89	0.89	0.89	0.95	0.99	0.99	1.00		
PDI 80 DAI	0.06	0.19	0.21	-0.29	-0.70	0.55	0.49	0.42	0.35	0.25	0.17	0.16	0.16	0.16	0.86	0.87	0.88	0.94	0.97	0.98	0.98	1.00	
PDI 90 DAI	-0.04	0.18	0.13	-0.36	-0.67	0.59	0.55	0.49	0.43	0.34	0.27	0.26	0.26	0.27	0.78	0.78	0.80	0.87	0.88	0.89	0.89	0.94	1.00

Table 6: Correlation Among Agronomic Traits (PH- Plant Height, NSPP- No. of Seed Per Panicle, BLL- Boot Leaf Length, ODW- Oven Dry Weight, YLD- Yield), Disease Severity (DS), and Percent Disease Index (PDI) At Different Days After Inoculation (DAI) For the Season 2024

	PH (c.m)	NSPP	BLL (c.m)	PL (c.m)	ODW	YLD	DS 10 DAI	DS 20 DAI	DS 30 DAI	DS 40 DAI	DS 50 DAI	DS 60 DAI	DS 70 DAI	DS 80 DAI	DS 90 DAI	PDI 10 DAI	PDI 20 DAI	PDI 30 DAI	PDI 40 DAI	PDI 50 DAI	PDI 60 DAI	PDI 70 DAI	PDI 80 DAI	PDI 90 DAI
PH (c.m)	1.00																							
NSPP	-0.10	1.00																						

BLL (c.m)	-0.10	0.30	1.00															
PL (c.m)	0.28	-0.15	0.24	1.00														
ODW	-0.11	-0.01	0.30	0.05	1.00													
Yld	-0.14	-0.15	0.20	0.10	0.55	1.00												
DS10DAI	0.14	0.18	-0.22	-0.09	-0.51	-0.92	1.00											
DS20DAI	0.14	0.18	-0.22	-0.09	-0.51	-0.92	1.00	1.00										
DS30DAI	0.13	0.17	-0.22	-0.10	-0.49	-0.92	1.00	1.00	1.00									
DS40DAI	0.13	0.18	-0.17	-0.07	-0.44	-0.90	0.97	0.97	0.97	1.00								
DS50DAI	0.13	0.17	-0.22	-0.10	-0.49	-0.92	1.00	1.00	1.00	0.97	1.00							
DS60DAI	0.13	0.02	-0.08	-0.20	-0.23	-0.54	0.70	0.70	0.71	0.69	0.71	1.00						
DS70DAI	0.13	0.18	-0.22	-0.10	-0.50	-0.92	1.00	1.00	1.00	0.97	1.00	0.70	1.00					
DS80DAI	0.12	0.18	-0.22	-0.11	-0.50	-0.92	1.00	1.00	1.00	0.97	1.00	0.70	1.00	1.00				
DS90DAI	0.16	0.17	-0.23	-0.06	-0.51	-0.91	1.00	1.00	0.99	0.96	0.99	0.69	0.99	0.99	1.00			
PDI10DAI	0.24	0.13	0.02	0.04	-0.28	-0.52	0.59	0.59	0.56	0.52	0.56	0.41	0.57	0.57	0.61	1.00		
PDI20DAI	0.23	0.13	0.04	0.07	-0.31	-0.54	0.62	0.62	0.59	0.54	0.59	0.42	0.60	0.60	0.64	0.98	1.00	
PDI30DAI	0.23	0.13	0.03	0.07	-0.32	-0.55	0.63	0.63	0.60	0.56	0.60	0.44	0.61	0.61	0.65	0.97	1.00	1.00

PDI 40 DAI	0.23	0.13	0.03	0.08	-0.32	-0.55	0.64	0.64	0.61	0.57	0.61	0.45	0.62	0.62	0.66	0.96	0.99	1.00	1.00					
PDI 50 DAI	0.23	0.12	0.03	0.08	-0.32	-0.55	0.64	0.64	0.61	0.57	0.61	0.45	0.62	0.62	0.66	0.95	0.99	1.00	1.00	1.00				
PDI 60 DAI	0.24	0.08	0.00	0.07	-0.34	-0.58	0.66	0.66	0.64	0.59	0.64	0.48	0.65	0.65	0.68	0.94	0.98	0.99	0.99	0.99	1.00			
PDI 70 DAI	0.24	0.08	0.01	0.06	-0.35	-0.58	0.66	0.66	0.63	0.59	0.64	0.48	0.65	0.64	0.67	0.93	0.97	0.98	0.99	0.99	1.00	1.00		
PDI 80 DAI	0.24	0.07	0.01	0.06	-0.35	-0.58	0.66	0.66	0.64	0.60	0.64	0.48	0.65	0.65	0.67	0.92	0.96	0.98	0.98	0.99	1.00	1.00	1.00	
PDI 90 DAI	0.25	0.07	0.01	0.06	-0.36	-0.58	0.66	0.66	0.63	0.59	0.64	0.48	0.64	0.64	0.67	0.91	0.96	0.97	0.98	0.98	0.99	1.00	1.00	1.00

3.5. Assessment of rice genotypes on sheath blight resistance basis in kharif seasons on the basis of PDI, AUDPC, and statistical parameters

An extensive field trial of rice genotypes resistant to sheath blight was carried out in three (3) back-to-back Kharif seasons, i.e., 2022, 2023, and 2024. The outcomes were that there was significant genotypic difference in disease responsiveness as shown by percent disease index (PDI), area under disease progress curve (AUDPC), and yield-related qualities. In 2022 (Table 7,) distinct genetic differences between genotypes occurred, as some lines had lower PDI and AUDPC values, which is a sign of possible resistance. Thstatisticalic values of the coefficient of variation (CV), and critical difference (CD) justifthe ied existence of statistically significant variations among the genotypes. The same tendency was observed in 2023 (Table 8), when the environmental factors had a minor effect on the expression of the diseases, and some genotypes retained their resistance status and performed under all parameters. The 2024 (Table 9) showed an even greater distinction genotypically, where some lines were found suitable as having certain stability and low disease incidences under the field environment. The stability in measuring the CV and CD values in all the three years indicates the reliability of data and the accuracy of the experiment. On the whole, the outcomes allowed dividing the genotypes into resistant, moderately resistant and susceptible categories on the basis of the progression of the disease and agronomic performance.

Table 7: Coefficient of Variation (CV) and Critical Difference (CD) of the Rice Genotypes Tested in the Analysis of Resistance to Sheath Blight in Kharif Season 2022

Variety Name	PH (c.m)	NSPP	BLL (c.m)	PL (c.m)	ODW	Yld	DS 10 DAI	DS 20 DAI	DS 30 DAI	DS 40 DAI	DS 50 DAI	DS 60 DAI	DS 70 DAI	DS 80 DAI	DS 90 DAI	PDI 10 DAI	PDI 20 DAI	PDI 30 DAI	PDI 40 DAI	PDI 50 DAI	PDI 60 DAI	PDI 70 DAI	PDI 80 DAI	PDI 90 DAI
Swarna swoubha-gya	59.16	165.00	25.93	26.17	1041.00	2.15	0.00	3.97	7.00	12.78	20.38	31.85	33.89	37.45	39.48	0.00	1.34	2.18	2.97	3.81	4.46	5.45	6.19	7.16
NLR 33892	62.55	142.67	31.40	27.50	1123.00	1.76	7.30	8.48	11.67	17.78	25.79	37.89	39.93	43.49	45.52	7.30	5.23	6.12	7.24	7.97	8.54	8.96	9.61	12.64
MTU 1156	64.62	209.00	33.50	26.93	1031.00	1.51	14.43	15.55	18.58	24.37	31.98	43.46	45.49	49.05	51.09	14.43	7.43	9.34	10.74	11.40	12.43	13.42	15.39	17.97
CR 411	71.68	279.	38.37	30.20	1123.	1.53	10.70	11.82	14.87	20.67	28.29	39.80	41.83	45.39	47.43	10.	8.17	10.08	11.48	12.14	14.18	15.17	17.14	22.21

		00			00											70								
CR 311	82.36	214.67	37.47	32.23	1030.00	2.15	0.00	2.90	5.12	9.34	14.90	23.28	25.31	28.87	30.91	0.00	2.35	3.91	5.31	5.97	6.13	6.94	8.19	11.79
MTU 1016	82.39	114.00	25.27	39.23	843.00	1.73	4.93	5.56	7.26	10.50	14.76	21.20	23.23	26.79	28.83	4.93	1.97	3.88	5.28	5.94	7.98	8.97	10.94	16.01
Govind bhog	88.35	131.00	25.43	42.33	873.00	1.51	5.92	6.50	8.09	11.12	15.11	21.12	23.15	26.71	28.75	5.92	5.95	7.86	9.26	9.92	11.96	12.95	14.92	19.99
CR 1017	80.49	319.33	36.30	36.20	679.00	1.72	5.94	6.75	8.95	13.16	18.68	27.02	29.05	32.61	34.65	5.94	1.41	1.98	2.09	2.49	4.53	5.16	6.45	11.52
MTU 1318	63.73	126.67	28.43	23.43	811.00	1.76	5.81	6.84	9.64	14.98	22.00	32.60	34.63	38.19	40.23	5.81	3.73	5.64	7.04	7.70	9.74	10.72	12.69	17.76
MTU 1075	76.07	121.67	31.53	26.53	584.00	1.46	11.57	12.36	14.52	18.62	24.02	32.16	34.20	37.76	39.80	11.57	10.39	12.30	13.69	14.36	16.40	17.38	19.35	24.42
RGL 2537	73.67	238.33	29.73	32.50	863.00	1.68	6.17	6.99	9.19	13.40	18.94	27.29	29.32	32.88	34.92	6.17	6.40	8.31	9.70	10.37	12.41	13.39	15.36	20.43
KNMM 1638	69.07	219.33	29.97	26.50	578.00	1.21	13.61	14.52	17.01	21.75	27.98	37.38	39.41	42.97	45.01	13.61	7.89	9.56	10.72	12.09	13.89	14.15	15.04	17.29
MTU 1061	72.58	152.33	39.80	28.17	905.00	1.71	9.30	10.34	13.15	18.51	25.55	36.17	38.21	41.77	43.80	9.30	4.72	6.62	8.02	8.69	10.72	11.71	13.68	18.75
MTU 5204	63.89	132.33	22.33	17.23	559.00	1.23	14.80	15.71	18.17	22.88	29.07	38.41	40.45	44.01	46.04	14.80	4.72	6.61	8.01	8.69	10.72	11.71	13.68	18.75
RGL 1880	72.09	161.00	34.63	33.40	1175.00	1.82	5.80	6.78	9.44	14.51	21.18	31.25	33.28	36.84	38.86	5.80	3.73	5.64	7.04	7.70	9.74	10.72	12.69	17.76
MTU 1121	66.58	141.00	27.60	26.40	768.00	1.48	12.35	13.27	15.76	20.51	26.75	36.16	38.20	41.76	43.77	12.35	5.17	7.08	8.48	9.14	11.18	12.17	14.14	19.21
GRGL 11226	69.36	149.33	28.30	29.20	513.00	1.83	5.95	12.38	9.22	13.78	19.78	28.83	30.86	34.42	36.44	5.95	5.49	7.40	7.91	8.57	10.61	11.60	13.57	18.64

RGL 2538	81.10	90.33	32.47	24.27	837.00	1.69	5.66	5.47	8.43	12.29	17.36	25.01	27.05	30.61	32.62	5.66	5.24	7.15	7.66	8.32	10.36	11.35	13.32	18.39
NLR 34449	67.69	265.00	28.10	25.07	708.00	1.32	14.46	7.52	17.88	22.64	28.90	38.35	40.39	43.95	45.96	14.46	6.72	7.81	8.31	8.98	11.18	12.17	14.14	19.21
MTU 1156	71.11	294.67	31.57	27.57	659.00	1.43	10.98	14.61	14.66	19.30	25.40	34.61	36.65	40.21	42.22	10.98	8.21	9.29	9.80	10.46	12.66	13.65	15.62	20.69
IR 64	71.07	327.67	50.63	31.27	623.00	1.62	15.72	22.66	20.83	29.71	41.37	58.98	61.02	64.58	66.59	15.72	6.48	7.56	8.07	8.73	10.93	12.20	14.17	19.24
BPT 2782	62.39	131.67	29.43	27.53	772.00	1.48	5.63	10.22	17.25	23.12	30.83	42.47	44.50	48.06	50.08	5.63	7.71	8.79	9.30	9.97	12.17	13.44	15.40	20.47
MTU 1224	62.11	242.67	32.10	26.70	645.00	1.42	9.54	14.33	21.02	27.16	35.22	47.39	49.42	52.98	55.00	9.54	6.97	8.05	8.56	9.23	11.42	12.69	14.37	19.44
BPT 3082	62.37	201.67	37.53	31.40	738.00	1.32	15.19	21.00	27.51	34.96	44.73	59.49	61.53	65.09	67.10	15.19	7.71	8.79	9.30	9.97	12.17	13.44	15.11	20.18
MTU 1210	67.60	217.33	28.60	29.67	716.00	1.40	11.19	14.98	16.86	22.64	28.07	37.67	39.71	43.27	45.28	11.19	8.21	9.29	9.80	10.46	12.66	13.93	15.61	20.68
RNR 15048	78.11	179.67	25.67	37.50	912.00	1.14	7.43	10.21	14.46	15.82	22.67	29.71	31.75	35.31	37.32	7.43	9.69	10.77	11.28	11.94	14.14	15.41	17.09	22.16
NLR 3354	69.86	205.00	31.40	30.07	553.00	1.32	12.95	16.71	19.36	24.34	30.51	40.06	42.09	45.65	47.74	12.95	9.19	10.27	10.78	11.45	13.65	14.92	16.60	21.67
CR	77.72	299.33	31.17	26.60	526.00	1.18	10.77	13.96	10.02	20.42	19.48	27.58	29.61	33.17	35.26	10.77	6.72	7.81	8.31	8.98	11.18	12.45	14.13	19.20
Mar-vel 1011	69.48	108.67	33.67	53.37	569.00	1.16	5.90	10.22	23.43	18.97	36.22	47.18	49.22	52.78	54.86	5.90	8.70	9.78	10.29	10.95	13.15	14.42	16.10	21.17
CR 315	70.68	180.00	26.07	25.53	515.00	1.54	11.72	15.24	17.64	21.44	27.16	35.31	37.35	40.91	42.99	11.72	8.95	10.03	10.54	11.20	13.40	14.67	16.35	21.42
RNR Mar-vel	72.	148	18.43	23.	583.	1.	11.15	12.99	9.97	18.20	17.96	24.81	26.85	30.41	32.49	11.	8.21	9.29	9.80	10.46	12.66	13.93	15.61	20.68

	76	.33		67	00	47										15								
MTU 101	75.95	170.00	41.13	34.37	692.00	1.45	9.30	12.03	15.83	19.72	27.64	37.77	39.80	43.36	45.45	9.30	8.13	9.75	10.78	11.45	13.65	14.92	16.60	17.57
Soubhagya	77.50	299.00	32.40	26.40	621.00	1.26	8.38	10.58	16.09	16.78	25.60	33.75	35.79	39.35	41.43	8.38	9.69	10.77	11.28	12.03	13.47	14.74	15.03	16.48
CR Dhan 308	74.33	91.67	29.60	36.07	562.00	1.25	12.34	14.65	16.71	21.18	26.73	35.32	37.36	40.92	43.00	12.34	6.97	8.05	8.56	9.23	11.42	12.69	14.37	19.44
Mo-hani	93.18	185.67	24.37	25.63	637.00	1.63	7.58	9.03	6.95	13.12	13.22	18.60	20.63	24.19	26.28	7.58	7.47	8.55	9.05	9.72	11.92	13.19	14.87	19.94
CR Dhan 319	92.59	145.67	22.30	25.47	791.00	1.53	4.03	5.47	7.18	9.52	13.40	18.74	20.77	24.33	26.42	4.03	7.47	8.55	9.06	9.72	11.92	13.19	14.87	19.94
MTU 1010	72.14	160.00	27.33	31.60	549.00	1.11	6.74	8.99	18.47	15.32	28.19	36.52	38.55	42.11	44.20	6.74	10.43	11.51	12.02	12.68	14.88	16.15	17.83	22.90
RGL 2624	78.78	237.33	34.10	27.03	818.00	1.48	14.20	16.47	12.06	22.89	21.90	30.35	32.38	35.94	38.03	14.20	9.19	10.27	10.78	11.45	13.65	14.92	16.60	21.67
Ma-ni-puri local	91.26	134.00	53.00	40.47	903.00	1.17	8.56	11.46	20.83	18.97	32.34	42.22	44.25	47.81	49.90	8.56	10.43	11.51	12.02	12.68	14.88	16.15	17.83	22.90
RNR 15048	77.87	158.67	22.30	33.57	793.00	1.51	10.17	12.10	9.02	17.09	16.68	23.24	25.28	28.84	30.92	10.17	7.47	8.55	9.06	9.72	11.92	13.19	14.87	19.94
Ju-vraj Dhano	99.50	180.33	42.50	41.47	846.00	1.10	5.33	7.26	14.37	12.24	22.02	28.58	30.62	34.18	36.26	5.33	10.43	11.51	12.02	12.68	14.88	16.15	17.83	22.90
Puja	76.95	179.00	27.33	25.13	731.00	1.26	12.14	14.32	14.28	19.99	22.97	30.41	32.45	36.01	38.09	12.14	9.69	10.77	11.28	11.94	14.14	15.41	17.09	22.16
Lal Bas-mati	88.02	179.33	49.23	32.63	853.00	1.46	12.80	15.57	13.97	22.73	24.97	34.40	36.43	39.99	42.08	12.80	7.22	8.30	8.81	9.47	11.67	12.94	14.62	19.69
SEm	0.56	1.66	0.15	0.21	0.58	0.00	0.07	0.14	0.19	0.18	0.20	0.51	0.25	0.38	1.78	0.07	0.06	0.07	0.07	0.07	0.07	0.07	0.07	0.08

SEd	0.80	2.35	0.22	0.29	0.81	0.00	0.10	0.20	0.27	0.26	0.28	0.72	0.35	0.53	2.51	0.10	0.09	0.10	0.10	0.10	0.09	0.09	0.10	0.11
CD 5%	1.58	4.67	0.43	0.58	1.62	0.01	0.19	0.40	0.54	0.51	0.56	1.44	0.70	1.06	5.00	0.19	0.18	0.20	0.19	0.19	0.19	0.19	0.20	0.21
CD 1%	2.10	6.19	0.57	0.76	2.14	0.01	0.26	0.54	0.72	0.68	0.75	1.91	0.93	1.41	6.63	0.26	0.24	0.27	0.26	0.25	0.25	0.25	0.26	0.28
Mean	49.53	133.96	21.96	20.95	541.19	1.06	6.32	7.86	9.94	13.29	17.98	24.82	26.30	28.61	30.20	6.32	4.34	5.35	5.98	6.46	7.78	8.50	9.70	12.94
SD	9.40	62.41	7.46	6.42	179.59	0.25	3.90	4.40	5.10	5.45	7.08	9.11	9.11	9.11	9.10	3.90	2.44	2.37	2.30	2.33	2.54	2.66	2.78	3.32
CV	18.97	46.59	33.98	30.67	33.18	####	61.74	56.04	51.28	40.97	39.40	36.71	34.65	31.85	30.15	61.74	56.23	44.28	38.52	36.03	32.69	31.26	28.67	25.63

Table 8: Coefficient of Variation (CV) and Critical Difference (CD) of the Rice Genotypes Tested in the Analysis of Resistance to Sheath Blight in Kharif Season 2023

Variety Name	PH (c.m)	NSPP	BLL (c.m)	PL (c.m)	ODW	Yld	DS 10 DAI	DS 20 DAI	DS 30 DAI	DS 40 DAI	DS 50 DAI	DS 60 DAI	DS 70 DAI	DS 80 DAI	DS 90 DAI	PDI 10 DAI	PDI 20 DAI	PDI 30 DAI	PDI 40 DAI	PDI 50 DAI	PDI 60 DAI	PDI 70 DAI	PDI 80 DAI	PDI 90 DAI
Swarna swou bhagya	58.32	164.67	23.77	26.07	1033.00	2.14	0.00	3.28	7.15	11.62	19.67	29.80	31.78	34.41	37.03	0.00	1.48	2.14	3.06	19.67	4.65	5.32	5.86	6.17
NLR 33892	62.21	141.00	31.40	27.43	1098.00	1.82	4.49	8.29	12.78	17.97	27.30	38.03	41.02	43.61	46.41	3.95	4.32	5.19	5.87	27.30	8.46	10.15	10.76	12.06
MTU 1156	63.58	208.33	33.47	26.87	1013.00	1.42	12.55	16.28	20.69	25.78	34.94	45.47	48.45	51.04	53.76	5.43	6.91	8.64	9.12	34.94	10.59	11.55	15.82	22.77
CR 411	70.34	278.33	38.23	30.13	1140.00	1.53	7.79	11.21	15.26	19.93	28.34	38.73	40.91	43.48	46.22	9.85	11.52	13.67	14.12	28.34	15.65	16.61	20.88	23.83
CR 311	82.27	211.00	37.40	32.33	1022.00	2.07	0.00	2.45	5.35	8.69	14.71	21.29	24.26	26.86	29.52	0.00	1.48	3.21	4.94	14.71	6.19	7.16	8.99	7.10
MTU 1016	82.49	113.67	25.50	39.63	834.00	1.64	3.33	5.26	7.54	10.18	14.91	20.58	22.86	25.52	28.14	0.00	1.16	1.35	2.09	14.91	5.26	6.22	6.46	7.23
Govind bhog	87.29	130.	25.43	42.43	867.00	1.49	4.36	6.14	8.24	10.67	15.03	20.43	22.51	25.17	27.70	3.95	5.43	7.16	8.89	15.03	12.16	13.12	17.39	17.69

CR 1017	80.40	67316.00	36.23	35.13	686.00	1.73	3.85	6.34	9.28	12.68	18.79	26.39	28.47	31.13	33.82	0.00	1.98	2.36	3.48	18.79	6.23	7.19	11.46	7.98
MTU 1318	63.25	125.00	28.30	23.27	802.00	1.85	3.15	6.30	10.02	14.31	22.03	30.76	33.74	36.40	39.13	1.73	3.21	4.94	5.69	22.03	6.96	6.25	8.29	9.16
MTU 1075	76.14	119.00	31.40	26.90	573.00	1.34	9.61	12.07	14.97	18.33	24.36	31.76	33.94	36.53	39.29	8.40	9.88	11.60	9.27	24.36	16.12	17.08	21.35	26.59
RGL 2537	71.42	235.33	29.10	32.13	855.00	1.68	4.25	6.85	9.92	13.47	19.85	27.82	29.86	32.45	35.21	4.44	5.93	7.65	9.38	19.85	11.98	12.95	17.22	22.46
KNMM 1638	68.80	217.00	29.80	26.40	573.00	1.13	11.28	14.10	17.44	21.28	28.21	35.92	38.90	41.53	44.25	7.65	9.14	10.86	6.54	28.21	12.20	13.17	17.44	22.67
MTU 1061	72.38	150.67	39.77	28.20	893.00	1.60	7.05	10.42	14.41	19.01	27.29	36.71	39.69	42.13	45.04	2.72	4.20	5.93	7.65	27.29	9.85	10.81	15.08	20.32
MTU 5204	62.09	133.00	22.30	17.17	566.00	1.22	12.31	15.08	18.34	22.11	28.90	37.24	39.42	42.09	44.77	2.72	4.20	5.93	2.62	28.90	5.26	6.23	8.47	10.70
RGL 1880	72.25	160.67	34.40	33.23	556.00	1.85	3.17	6.08	9.51	13.48	20.61	29.48	31.57	34.23	36.92	1.73	3.21	4.94	6.67	20.61	9.05	10.01	14.28	22.98
MTU 1121	66.41	139.33	27.53	26.63	1180.00	1.40	10.03	12.86	16.20	20.06	27.01	35.54	37.73	40.32	43.08	3.21	4.69	6.42	9.14	27.01	12.57	13.53	17.80	26.50
GRGL 11226	69.11	148.00	28.10	29.20	754.00	1.81	3.66	6.34	9.51	13.17	19.75	27.04	30.02	32.70	35.37	3.46	4.94	6.67	8.40	19.75	10.87	11.84	16.11	24.80
RGL 2538	81.36	89.00	32.33	24.60	503.00	1.69	3.67	5.92	8.57	11.63	17.13	24.10	26.04	28.64	31.39	3.21	4.69	6.42	9.14	17.13	12.53	13.50	17.77	26.46
NLR 34449	66.68	263.33	27.83	25.30	521.00	1.26	12.10	14.93	18.28	22.14	29.09	37.81	39.82	42.50	45.17	4.69	6.17	7.90	9.63	29.09	11.63	12.60	16.87	25.56
MTU 1156	71.67	290.33	31.53	27.27	831.00	1.42	8.97	11.71	14.95	18.68	25.41	33.78	35.86	38.45	41.21	6.17	7.65	9.38	11.11	25.41	14.91	15.88	20.15	28.84

IR 64	71.81	325.33	50.43	31.20	696.00	1.61	9.82	14.97	21.05	28.06	40.69	55.59	58.57	61.06	63.92	4.44	5.93	7.65	9.06	40.69	13.45	15.44	19.71	28.41
BPT 2782	61.94	127.00	29.43	27.50	662.00	1.45	9.84	13.23	17.23	21.84	30.15	40.22	42.58	45.18	47.93	5.68	7.16	8.89	10.62	30.15	12.35	14.34	18.61	27.30
MTU 1224	62.27	244.67	32.00	26.13	610.00	1.37	13.54	17.18	21.47	26.43	35.35	45.58	48.56	51.21	53.91	4.94	6.42	8.15	9.88	35.35	11.39	13.37	18.07	26.77
BPT 3082	62.57	202.67	37.63	31.37	767.00	1.30	18.44	22.85	28.07	34.08	44.91	58.54	60.52	63.20	65.87	5.68	7.16	8.89	10.62	44.91	12.99	14.98	19.68	28.37
MTU 1210	67.25	215.67	28.63	29.17	636.00	1.36	10.88	13.72	17.09	20.98	27.97	36.57	38.75	41.34	44.10	6.17	7.65	9.38	11.11	27.97	12.89	14.88	19.57	28.27
RNR 15048	78.01	181.33	25.17	37.30	725.00	1.13	10.03	12.11	14.57	17.41	22.52	28.76	30.93	33.52	36.28	7.65	9.14	10.86	12.41	22.52	15.84	17.83	22.53	31.22
NLR 3354	69.81	207.33	31.07	30.10	702.00	1.16	13.42	16.26	19.61	23.49	30.45	38.23	41.20	43.87	46.56	7.16	8.64	10.37	12.10	30.45	15.50	17.48	22.18	30.88
CR	77.53	298.67	31.13	26.13	890.00	1.53	4.96	7.33	10.13	13.36	19.18	26.31	28.49	31.15	33.84	4.69	6.17	7.90	10.62	19.18	12.90	14.89	16.98	18.16
Mar-vel 1011	68.84	106.33	34.23	53.17	541.00	1.11	16.18	19.36	23.11	27.45	35.25	44.07	47.05	49.64	52.40	6.67	8.15	9.88	11.60	35.25	14.28	16.27	20.96	29.66
CR 315	70.50	178.67	26.07	25.53	502.00	1.06	12.83	15.30	18.23	21.60	27.68	35.23	37.31	40.00	42.66	6.91	8.40	10.12	13.00	27.68	16.18	18.16	22.86	31.55
RNR Mar-vel	72.81	147.33	18.13	23.20	570.00	1.47	5.67	7.68	10.06	12.80	17.74	23.76	25.93	28.52	31.28	6.17	7.65	9.38	11.11	17.74	14.51	16.50	21.20	29.89
MTU 101	75.13	168.00	41.03	34.17	680.00	1.42	10.26	13.49	17.30	21.70	29.62	39.55	41.57	44.16	46.92	7.16	8.64	10.37	11.64	29.62	14.42	16.41	21.11	29.80
Soubhagya	77.44	301.67	33.00	26.23	607.00	1.21	11.25	13.73	16.65	20.03	26.10	32.76	35.73	38.42	41.08	7.65	9.14	10.86	11.76	26.10	15.14	17.13	18.52	19.07

CR Dhan 308	73.90	90.33	29.57	36.07	563.00	1.25	11.05	13.53	16.47	19.85	25.94	33.41	35.58	38.26	40.94	4.94	6.42	8.15	11.85	25.94	15.20	17.18	21.88	29.87
Mohani	93.43	181.67	24.20	25.67	621.00	1.59	3.61	5.20	7.08	9.24	13.15	18.03	20.03	22.71	25.38	5.43	6.91	8.64	10.37	13.15	13.95	15.94	20.64	28.62
CR Dhan 319	92.56	144.00	22.00	25.10	780.00	1.49	3.83	5.39	7.23	9.35	13.18	17.64	19.97	22.67	25.33	5.43	6.91	8.64	10.37	13.18	13.58	15.57	20.27	28.25
MTU 1010	71.65	158.67	27.13	31.00	530.00	1.02	13.25	15.73	18.65	22.02	28.08	35.22	37.70	40.36	43.05	8.40	9.88	11.60	13.66	28.08	16.77	18.75	23.45	31.55
RGL 2624	77.68	238.33	33.97	27.17	806.00	1.49	6.86	9.38	12.35	15.79	21.96	29.59	31.72	34.41	37.07	7.16	8.64	10.37	12.10	21.96	15.10	17.09	21.79	29.88
Manipuri local	91.12	135.00	52.90	40.10	892.00	1.15	14.39	17.27	20.67	24.59	31.66	40.35	42.53	45.12	47.88	8.40	9.88	11.60	15.56	31.66	18.70	20.69	25.39	33.48
RNR 15048	78.03	162.33	22.60	33.13	813.00	1.49	5.05	7.04	9.38	12.09	16.96	23.04	25.07	27.66	30.42	5.43	6.91	8.64	10.37	16.96	15.17	17.15	21.85	23.09
Juvraj Dhano	99.33	177.67	42.03	41.10	841.00	1.05	10.12	12.04	14.31	16.93	21.64	26.57	29.55	32.24	34.90	8.40	9.88	11.60	13.33	21.64	16.89	18.88	23.58	31.68
Puja	76.59	184.00	27.10	25.43	705.00	1.23	9.70	11.92	14.55	17.58	23.04	29.77	31.88	34.57	37.23	7.65	9.14	10.86	12.59	23.04	15.81	17.80	22.49	30.59
Lal Basmati	88.16	182.67	49.13	32.17	860.00	1.46	8.20	11.02	14.35	18.19	25.11	33.42	35.80	38.45	41.15	5.19	6.67	8.40	10.12	25.11	12.37	14.36	19.06	27.16
SEm	1.05	2.09	0.12	0.13	0.91	0.00	0.07	0.07	0.07	0.07	0.07	0.36	0.07	0.35	0.36	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
SEd	1.48	2.96	0.17	0.19	1.29	0.01	0.10	0.10	0.10	0.10	0.10	0.50	0.11	0.49	0.51	0.09	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
CD 5%	2.95	5.89	0.33	0.38	2.57	0.01	0.20	0.20	0.20	0.21	0.21	1.00	0.21	0.98	1.01	0.19	0.21	0.20	0.21	0.21	0.20	0.20	0.21	0.20
CD 1%	3.91	7.80	0.44	0.50	3.41	0.02	0.26	0.26	0.26	0.27	0.28	1.32	0.28	1.29	1.34	0.25	0.28	0.27	0.27	0.28	0.26	0.26	0.27	0.27
Mean	49.28	133.	21.85	20.88	535.41	1.05	5.71	7.77	10.21	13.02	18.08	24.14	25.83	27.66	29.56	3.10	4.12	5.22	6.00	18.08	7.93	8.81	11.38	15.18

SD	9.54	0762.38	7.51	6.38	180.88	0.27	4.37	4.68	5.15	5.80	7.16	8.95	9.06	9.05	9.07	2.52	2.54	2.78	3.16	7.16	3.50	3.91	4.86	7.78
CV	19.36	46.88	34.36	30.54	33.78	25.59	76.53	60.21	50.45	44.54	39.58	37.07	35.08	32.70	30.69	81.30	61.71	53.31	52.63	39.58	44.11	44.44	42.70	51.29

Table 9: Coefficient of Variation (CV) and Critical Difference (CD) of the Rice Genotypes Tested in the Analysis of Resistance to Sheath Blight in Kharif Season 2024

Vari-ety Name	PH (c.m)	NSPP	BLL (c.m)	PL (c.m)	ODW	YLD	DS10DAI	DS20DAI	DS30DAI	DS40DAI	DS50DAI	DS60DAI	DS70DAI	DS80DAI	DS90DAI	PDI10DAI	PDI20DAI	PDI30DAI	PDI40DAI	PDI50DAI	PDI60DAI	PDI70DAI	PDI80DAI	PDI90DAI
Swarna swoubha-gya	58.36	161.80	27.67	25.07	1044.99	2.88	0.00	3.24	5.92	9.58	12.27	15.23	18.41	23.58	26.74	0.00	2.99	4.97	5.13	5.91	6.09	6.16	6.26	6.51
NLR 33892	61.39	139.47	33.13	26.40	1126.99	2.50	0.00	3.29	5.97	9.71	12.32	15.31	18.46	23.66	26.79	0.00	1.27	1.65	1.77	3.09	3.19	3.42	3.54	3.81
MTU 1156	63.99	205.80	35.23	25.84	1034.99	2.26	3.94	7.18	9.86	13.51	16.21	19.16	22.35	27.53	30.68	9.53	10.43	11.23	11.97	12.73	13.09	13.99	14.11	14.32
CR 411	71.39	275.80	40.10	29.10	1126.99	2.27	3.79	7.03	9.71	13.32	16.06	19.05	22.20	27.41	30.53	15.18	18.17	20.16	22.14	23.22	24.21	25.10	25.23	25.15
CR 311	83.32	211.47	39.20	31.14	1033.99	2.89	0.00	3.24	5.92	9.78	12.27	24.25	18.41	23.58	26.74	4.65	5.75	6.35	7.12	7.95	8.17	8.43	8.55	9.29
MTU 1016	83.54	110.80	27.00	38.14	846.99	2.47	0.00	3.26	5.94	9.68	12.29	15.19	18.43	23.61	26.76	0.00	1.66	3.42	4.31	5.24	6.21	7.38	7.50	8.26
Go-vindbhog	88.34	127.80	27.17	41.24	876.99	2.25	4.13	7.37	10.05	13.76	16.40	19.35	22.54	27.19	30.87	5.80	6.16	6.79	7.98	9.06	12.87	13.09	13.21	13.53
CR 1017	81.45	316.13	38.03	35.10	682.99	2.45	0.00	3.27	5.96	9.71	12.31	5.30	18.45	23.65	26.77	0.00	1.95	2.05	2.26	2.42	2.54	3.04	3.43	3.61
MTU 1318	64.29	123.47	30.17	22.34	814.99	2.51	0.00	3.24	5.92	9.55	12.27	15.24	18.41	23.56	26.74	8.74	9.17	9.84	10.56	11.04	11.87	12.58	12.70	12.90
MTU 1075	77.19	118.	33.27	25.44	587.99	2.20	5.15	8.39	11.07	14.79	17.42	20.41	23.56	28.75	31.89	0.00	5.76	7.52	9.78	10.78	13.72	15.71	17.73	18.78

		47																						
RGL 2537	72.47	235.13	31.47	31.40	866.99	2.42	0.00	3.26	5.94	9.70	12.29	15.29	18.43	23.63	26.76	0.00	2.94	5.63	7.62	8.69	9.68	10.58	10.74	12.21
KNMM 1638	69.85	216.13	31.70	25.40	581.99	1.95	7.52	10.76	13.44	17.21	19.79	22.74	25.93	31.03	34.26	10.27	13.25	15.24	17.23	18.30	19.29	20.19	20.31	20.69
MTU 1061	73.43	149.13	41.53	27.07	908.99	2.44	1.12	4.36	7.04	10.78	13.39	16.27	19.53	24.71	27.86	7.65	8.67	10.66	11.27	12.35	13.33	14.23	14.35	14.54
MTU 5204	63.14	129.13	24.07	16.14	562.99	1.96	7.14	10.38	13.06	16.72	19.41	22.34	25.55	30.72	33.88	5.89	6.88	8.87	9.37	10.45	14.24	14.74	14.86	15.33
RGL 1880	73.29	157.80	36.37	32.30	1178.99	2.55	0.00	3.23	5.91	9.66	12.26	15.26	18.40	23.54	26.72	6.22	9.21	10.77	11.32	12.40	13.38	14.28	14.40	14.59
MTU 1121	67.46	137.80	29.33	32.63	771.99	2.22	4.63	7.91	10.59	14.21	16.94	19.91	23.08	28.28	31.41	0.00	2.95	4.94	6.92	8.00	8.99	9.88	10.01	10.29
GRGL 11226	70.15	146.13	30.03	25.63	1178.04	2.57	0.00	3.28	5.96	9.72	12.31	15.31	18.45	23.61	26.78	7.08	7.98	7.46	8.56	9.94	10.93	11.67	11.79	12.16
RGL 2538	82.41	154.13	34.20	28.43	771.04	2.43	1.31	4.59	6.79	10.50	13.17	16.16	19.31	24.52	27.64	7.42	8.13	8.79	9.26	10.28	10.57	11.32	11.79	12.12
NLR 34449	67.73	95.13	29.83	23.50	516.04	2.05	2.29	5.57	7.77	11.48	14.15	17.15	20.30	25.47	28.63	7.16	7.74	8.06	8.64	9.23	11.65	12.13	12.25	12.54
MTU 1156	72.72	269.80	33.30	24.30	840.04	2.17	5.57	8.85	11.05	14.80	17.43	20.32	23.58	28.72	31.87	10.89	13.91	15.07	16.17	17.25	17.94	18.83	18.96	19.34
IR 64	72.86	299.47	52.37	26.80	711.04	2.36	2.48	5.76	7.96	11.61	14.34	17.32	20.63	25.80	28.96	17.88	20.90	22.06	23.16	24.24	24.93	25.82	25.95	26.41
BPT 2782	62.99	332.47	31.17	30.50	662.04	2.24	4.39	7.67	9.87	13.57	16.25	19.22	22.54	27.64	31.73	6.51	7.53	8.54	9.64	10.71	11.40	12.30	12.42	12.65
MTU 1224	63.32	136.47	33.83	26.76	626.04	2.15	5.68	8.96	11.16	14.81	17.54	20.51	23.83	29.05	33.02	15.93	18.95	20.11	21.21	22.28	22.97	23.87	23.99	24.36

BPT 3082	63.62	247.47	39.27	25.93	775.04	2.06	6.19	9.47	11.67	15.42	18.05	21.07	24.34	29.43	33.53	7.89	10.91	11.32	12.08	12.56	13.25	13.79	13.92	14.12
MTU 1210	68.30	206.47	35.75	30.63	648.04	2.14	5.94	9.22	11.42	15.15	17.80	20.69	24.09	29.16	33.28	15.62	18.64	19.80	20.90	21.97	22.66	23.20	23.33	23.45
RNR 15048	79.06	222.13	26.82	28.90	741.04	1.87	8.28	11.56	13.76	17.50	20.14	23.13	26.43	31.63	35.62	17.89	20.91	22.07	23.17	24.24	24.93	25.47	25.60	26.06
NLR 3354	70.86	184.47	23.88	36.73	719.04	2.05	6.24	9.52	11.72	15.45	18.10	11.05	24.39	29.55	33.58	15.38	18.40	19.56	20.66	21.74	22.43	22.97	23.09	23.26
CR	78.57	209.80	29.62	29.30	915.04	1.92	7.16	10.44	12.64	16.39	19.02	22.01	25.31	30.43	34.50	13.05	16.07	17.23	18.32	19.40	20.09	20.63	20.76	21.04
Mar-vel 1011	69.89	304.13	29.38	25.83	556.04	1.90	7.76	11.04	13.24	16.97	19.62	22.59	25.91	31.13	35.10	9.54	10.64	11.80	12.13	12.94	13.26	13.68	13.80	14.09
CR 315	71.55	113.47	31.88	52.60	529.04	2.29	4.11	7.39	9.59	13.32	15.97	18.68	22.26	27.43	31.45	12.11	15.13	16.29	17.38	18.46	19.15	19.69	19.82	20.12
RNR Mar-vel	73.86	184.80	24.28	24.76	572.04	2.21	4.79	8.07	10.27	10.05	16.65	19.54	22.94	28.11	32.13	12.70	15.72	16.88	17.98	19.05	19.74	20.29	20.41	20.72
MTU 101	76.18	153.13	16.65	22.90	518.04	2.19	5.31	8.59	10.79	14.51	17.17	20.16	23.46	28.61	32.65	16.98	19.99	21.15	22.25	23.33	24.02	24.56	24.69	25.03
Soubhagya	78.48	169.04	39.35	33.60	586.04	1.98	6.98	10.26	12.46	16.19	18.84	21.73	25.13	30.29	34.32	13.93	16.95	18.11	19.21	20.29	20.98	21.52	21.64	21.91
CR Dhan 308	74.95	298.04	30.62	25.33	695.04	1.99	6.91	10.19	12.39	16.14	18.77	21.75	25.06	30.19	34.25	16.31	19.33	20.49	21.59	22.67	23.36	23.90	24.02	24.15
Mo-hani	94.47	90.71	27.82	34.99	624.04	2.35	2.69	5.97	8.17	11.86	14.55	17.55	20.84	26.08	30.03	11.88	14.89	16.05	17.15	18.23	18.92	19.46	19.59	19.93
CR Dhan 319	93.61	184.71	22.58	24.56	565.04	2.28	4.09	7.37	9.57	13.31	15.95	18.95	22.24	27.46	31.43	14.24	17.26	18.41	19.51	20.59	21.28	21.82	21.95	22.31
MTU 1010	72.	144	20.52	24.	640.04	1.	8.	11.91	14.11	17.81	20.49	23.43	26.78	31.94	35.97	13.29	16.31	17.47	18.57	19.65	20.34	20.88	21.01	21.29

	69	.71		39		85	63																	
RGL 2624	78.72	159.04	25.55	30.53	794.04	2.23	4.42	7.70	9.90	12.65	16.28	19.18	22.57	27.73	31.76	19.18	22.20	23.36	24.46	25.54	26.23	26.77	26.89	27.16
Mani-puri local	92.17	236.38	28.07	25.96	552.04	1.91	7.34	10.62	12.82	16.47	19.20	22.21	25.49	30.61	34.68	13.84	16.86	18.02	19.12	20.20	20.89	21.43	21.56	21.94
RNR 15048	79.08	133.04	41.50	39.39	821.04	2.25	4.38	7.66	9.86	13.59	16.24	19.23	22.53	27.27	31.72	18.01	21.03	22.19	23.29	24.37	25.05	25.60	25.72	26.15
Juvraj Dhano	100.38	157.71	34.60	32.49	906.04	1.84	8.49	11.77	13.97	17.64	20.35	23.31	26.64	31.81	35.83	13.33	16.35	17.51	18.61	19.68	20.37	20.92	21.04	21.28
Puja	77.63	179.38	42.50	40.39	796.04	2.00	6.84	10.12	12.32	16.07	18.70	21.66	24.99	30.17	34.18	18.51	21.53	22.69	23.79	24.87	25.56	26.10	26.22	26.55
Lal Bas-mati	89.21	178.04	26.17	24.06	849.04	2.19	5.27	8.55	10.75	14.48	17.13	20.12	23.39	28.21	32.61	14.26	12.03	13.75	14.28	15.10	16.41	16.95	17.08	17.20
SEm	0.27	0.27	0.09	0.09	0.76	0.01	0.10	0.09	0.09	0.26	0.25	0.27	0.27	0.27	0.28	0.12	0.11	0.11	0.11	0.12	0.12	0.12	0.12	0.09
SEd	0.38	0.38	0.13	0.13	1.08	0.01	0.14	0.13	0.13	0.37	0.36	0.38	0.38	0.38	0.40	0.17	0.16	0.16	0.16	0.17	0.17	0.17	0.16	0.13
CD 5%	0.75	0.75	0.25	0.25	2.14	0.02	0.27	0.25	0.25	0.74	0.72	0.76	0.75	0.75	0.79	0.34	0.31	0.31	0.31	0.35	0.35	0.35	0.33	0.25
CD 1%	1.00	1.00	0.33	0.33	2.84	0.03	0.36	0.33	0.33	0.99	0.95	1.01	0.99	0.99	1.05	0.45	0.41	0.41	0.41	0.46	0.46	0.46	0.43	0.33
Mean	49.86	133.33	22.95	20.48	563.78	1.59	2.44	4.71	6.44	9.03	10.88	12.69	15.20	18.79	21.19	5.54	7.05	7.87	8.56	9.23	9.93	10.42	10.57	10.69
SD	9.66	63.43	6.74	6.43	190.12	0.25	2.81	2.82	2.69	2.74	2.70	3.63	2.74	2.73	3.04	5.96	6.35	6.38	6.52	6.61	6.51	6.52	6.49	6.45
CV	19.37	47.57	29.39	31.41	33.72	15.84	115.44	59.83	41.72	30.32	24.79	28.58	18.03	14.53	14.33	107.64	90.07	81.06	76.24	71.58	65.59	62.55	61.46	60.35

3.6. Disease progression modeling in rice genotypes by Gompertz model

The Gompertz model aptly explained the disease development of five genetic types of rice germplasm: Highly Susceptible (HS), Moderately Resistant (MR), Moderately Susceptible (MS), Resistant (R) and Susceptible (S) of course across the Kharif of 2022, 2023 and 2024 as per (Table 10) Estimate of the parameters of Gompertz model (A, B, C) standard error, test statistic, p-value and R^2 of highly susceptible (Results that represented excellent fit of the model were achieved in all the cases with the ranges containing R^2 values of 0.9747 to 0.9963.

Regarding parameter A, which represents the asymptotic maximum, in HS genotype, the parameter increased by more than 40% between 2022 and 2024, 61.64 and 100.71 respectively, whereas in R genotypes, lower results were observed. Both parameters B, which denotes rate of disease increase, and parameter C which indicates inflection point were statistically significant ($p < 0.05$) in all genotypes and years. The results justify the applicability of Gompertz model in modeling the disease dynamics in rice (Figure 17,18,19).

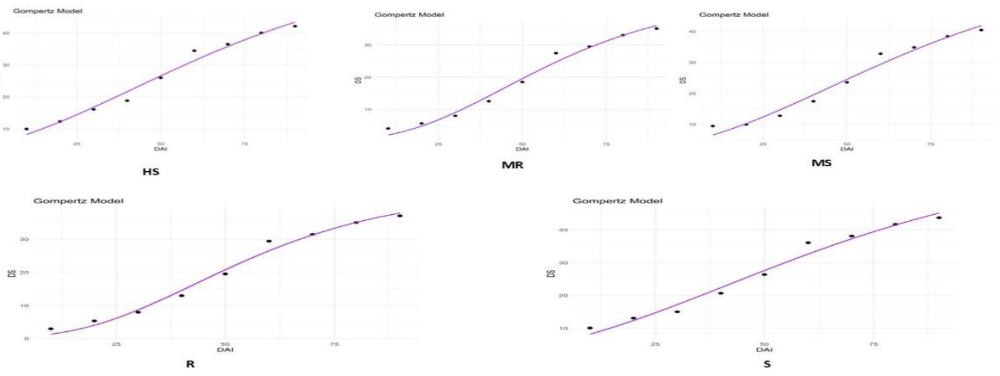

Fig. 17: Gompertz Model Kharif-2022.

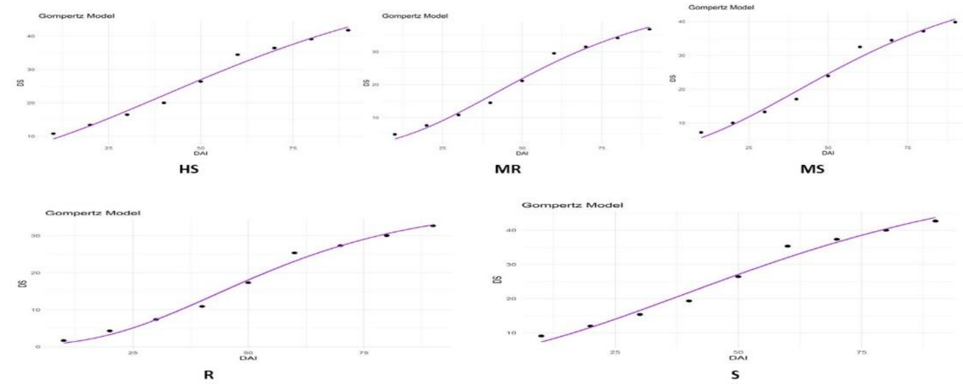

Fig. 18: Gompertz Model Kharif-2023.

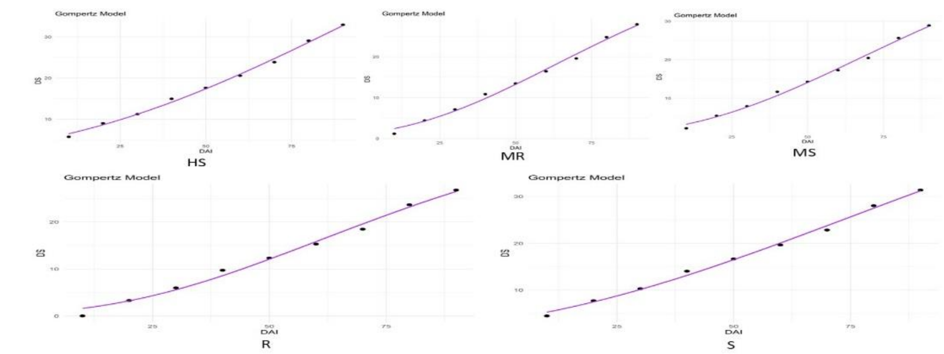

Fig. 19: Gompertz Model Kharif- 2024.

Table 10: Estimate of the Parameters of Gompertz Model (A, B, C), Standard Error, Test Statistic, P-Value and R 2 of Highly Susceptible (HS, MR, MS, R, S) Rice Genotypes of Kharif Season 2022, 2023 And 2024

2022 HS							2023 HS							2024 HS						
Model	term	estimate	std.error	statistic	p.value	R^2	Model	term	estimate	std.error	statistic	p.value	R^2	Model	term	estimate	std.error	statistic	p.value	R^2
	A	61.6429	12.7632	4.82973	0.00291	0.98081		A	60.3107	11.8648	5.08315	0.002259	0.98204		A	100.707	36.1040	2.78937	0.03160	0.99633
Gompertz	B	2.50292	0.19529	12.8164	1.39E-05	0.98081	Gompertz	B	2.32807	0.16516	14.09527	7.96E-06	0.98204	Gompertz	B	3.07240	0.27697	11.0928	3.2E-05	0.99633
	C	0.02181	0.00595	3.66675	0.01049	0.98081		C	0.02122	0.00565	3.753521	0.00947	0.98204		C	0.01118	0.00248	4.50320	0.00409	0.99633
MR							MR							MR						
Gompertz	A	45.1731	5.91266	7.53983	0.00028	0.98494	Gompertz	A	47.0611	5.78626	8.133255	0.00018	0.98626	Gompertz	A	48.7301	10.1028	4.82342	0.00293	0.99302

	B	4.28158	0.73006	5.86464	0.00108	0.98494		B	3.54145	0.46025	7.694596	0.00025	0.98626		B	3.69113	0.22066	16.7272	2.91E-06	0.99302
	C	0.03264	0.00669	4.87922	0.00276	0.98494		C	0.03053	0.00588	5.190688	0.00203	0.98626		C	0.02084	0.00405	5.14597	0.00212	0.99302
MS							MS							MS						
	A	60.3804	14.9671	4.03420	0.00684	0.97466		A	53.0109	7.86338	6.74149	0.00051	0.98364		A	55.7882	12.2977	4.53644	0.00394	0.99440
Gompertz	B	2.77508	0.27621	10.0466	5.64E-05	0.97466	Gompertz	B	2.92853	0.30679	9.545457	7.55E-05	0.98364	Gompertz	B	3.41853	0.14521	23.5406	3.86E-07	0.99440
	C	0.02250	0.00702	3.20245	0.01854	0.97466		C	0.02673	0.00589	4.531843	0.00396	0.98364		C	0.01819	0.00342	5.30545	0.00182	0.99440
R							R							R						
	A	44.8756	4.58083	9.79639	6.51E-05	0.98726		A	38.5929	3.23306	11.93695	2.09E-05	0.99100		A	43.8681	9.36855	4.68248	0.00338	0.99098
Gompertz	B	5.12432	1.02756	4.98685	0.00248	0.98726	Gompertz	B	5.38880	0.96739	5.570402	0.00141	0.99100	Gompertz	B	4.17180	0.39490	10.5641	4.23E-05	0.99098
	C	0.03793	0.00686	5.52618	0.00147	0.98726		C	0.03916	0.00597	6.554045	0.00060	0.99100		C	0.02348	0.00499	4.70093	0.00332	0.99098
S							S							S						
	A	63.0117	12.8403	4.90732	0.00269	0.97950		A	57.7711	9.39151	6.151416	0.00084	0.98178		A	70.2583	17.5290	4.00811	0.00705	0.99566
Gompertz	B	2.55799	0.21826	11.7197	2.33E-05	0.97950	Gompertz	B	2.64610	0.24855	10.64601	4.05E-05	0.98178	Gompertz	B	2.99237	0.15715	19.0409	1.36E-06	0.99566
	C	0.022624	0.006214	3.640897	0.010823	0.979501		C	0.025022	0.006001	4.169768	0.00588	0.981788		C	0.014506	0.002788	5.203754	0.002008	0.995665

3.7. Virulence detection through seed mortality test

Pathogen virulence was determined through seed mortality test of six rice germplasms including V1 (CR411), V2 (CR315), V3 (Go-vindbhog), V4 (CR Dhan 308), V5 (Soubhagya) and V6 (IR 64) as shown in (Table- 11) and in (Figure 20). In all the genotypes seed mortality percentage rose with sequential iterations. V6 (IR 64) had the highest mortality rate which was 100 percent in the final count followed by V5 (Soubhagya) whereby the mortality rate was 96.67 percent and higher, and V4 (CR Dhan 308) whose mortality rate was higher than 96.67 percent. V1 (CR411) on the other hand exhibited the least seed mortality hence reduced susceptibility. The statistical analysis indicated that there was a significant difference among genotypes, the coefficient of variation (CV) scored 18.21% in V2 and 38.58% in V6, which implies that there is a broad extent in the reaction of high-susceptible lines. The findings affirm that IR 64 (V6) is extremely sensitive to the pathogen but in comparison, CR411 (V1) exudes a resistant reaction when subjected to seed death conditions.

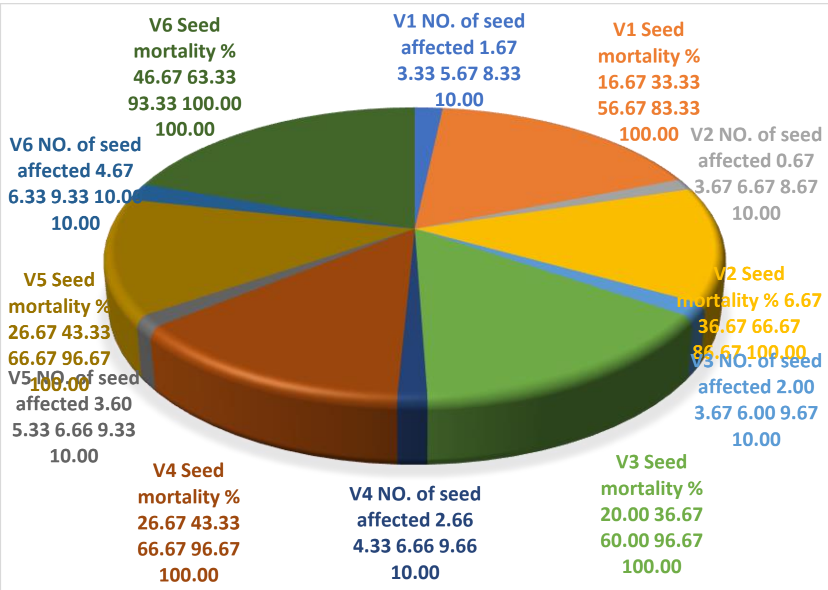

Fig. 20: Virulence Detection by Seed Mortality Test: Comparative Virulence of the *R. Solani* Isolates on Rice Seed, Where the Mortality Rate Varies Among Test Samples.

Table 11: Virulence Detection Through Seed Mortality Test by Using 6 Different Germplasm

	V1(CR411)		V2(CR315)		V3(Govindbhog)		V4(CR Dhan 308)		V5(Soubhagya)		V6(IR 64)	
	NO. of seed affected	Seed mortality %	NO. of seed affected	Seed mortality %	NO. of seed affected	Seed mortality %	NO. of seed affected	Seed mortality %	NO. of seed affected	Seed mortality %	NO. of seed affected	Seed mortality %
	1.67	16.67	0.67	6.67	2.00	20.00	2.66	26.67	3.60	26.67	4.67	46.67
	3.33	33.33	3.67	36.67	3.67	36.67	4.33	43.33	5.33	43.33	6.33	63.33
	5.67	56.67	6.67	66.67	6.00	60.00	6.66	66.67	6.66	66.67	9.33	93.33
	8.33	83.33	8.67	86.67	9.67	96.67	9.66	96.67	9.33	96.67	10.00	100.00
	10.00	100.00	10.00	100.00	10.00	100.00	10.00	100.00	10.00	100.00	10.00	100.00
SEm	0.13	1.31	0.10	0.98	0.11	1.13	0.10	1.02	0.10	0.99	0.15	1.49
SEd	0.19	1.86	0.14	1.39	0.16	1.60	0.14	1.44	0.14	1.40	0.21	2.11
CD 5%	0.37	3.69	0.28	2.76	0.32	3.18	0.29	2.86	0.28	2.79	0.42	4.20
CD 1%	0.49	4.89	0.37	3.65	0.42	4.22	0.38	3.79	0.37	3.70	0.56	5.56
Mean	0.67	6.74	0.69	6.90	0.73	7.29	0.78	7.75	0.81	8.14	0.94	9.38
SD	3.44	34.37	3.79	37.89	3.55	35.54	3.22	32.23	2.69	32.23	2.43	24.31
CV	19.62	19.62	18.21	18.21	20.50	20.50	24.04	24.05	30.29	25.25	38.58	38.58

3.8. Pathogenicity test through detach leaf assay

The evaluation of the pathogenicity of the test isolate on a detached leaf was carried out with the observations recorded after every 2 days until 10 days after inoculation (DAI) in the following (Table 12). The disease severity percentage (DS%) recorded a monotonic upward trend with having an initial value of 16.66 at 2 DAI ascending up to 100% at 10 DAI. Accordingly, the length of symptoms (SL) increased as well, starting at 1.00 cm and growing to 6.00 cm which means the extension of a lesion along the infected surface of a leaf. Statistical evaluation showed that there was a significant rise in disease severity with time with the corresponding critical difference (CD) at 5 and 1 percent levels being 1.37 and 1.82 respectively. Standard error of difference (SEd) and standard error of the mean (SEm) were quite low (0.49 and 0.69, respectively), which proves the reliability of the obtained results. The results reveal a quick and violent progression of the disease in controlled conditions with the optimal spread of the lesions by 10 DAI.

Table 12: Pathogenicity Test Through Detach Leaf Assay

	DAI	L.L(C.M)	S.L(C.M)	DS %es
	2	6	1.00	16.66
	4	6	2.77	46.11
	6	6	4.53	75.55
	8	6	5.80	96.66
	10	6	6.00	100.00
SEm	_	_	0.03	0.49
SEd	_	_	0.04	0.69
CD 5%	_	_	0.08	1.37
CD 1%	_	_	0.11	1.82
MEAN	_	_	0.47	7.79

3.9. Model evaluation using data splitting

In order to evaluate the performance of the Random Forest classifier or the artificial neural network the data was divided into training and testing sets. To ensure the use of both of the subsets had the same level of distribution of classes, the data was stratified by the target variable. In particular, 20 percent of the data was put aside in the form of testing and 80 percent of the data were used as training. Stratification makes sure classes are represented in a balanced manner which is crucial in case of imbalanced classification problems.

3.10. Random forest model development

A Random Forest was created based on the Random Forest Classifier instance of the sklearn ensemble package. In order to maximize the predictive abilities of the model, hyperparameter optimization was performed on Grid Search, intertwined with 10-fold cross-validation. It was an exhaustive search over a prespecified hyperparameter space finding the combination with maximum cross-validated accuracy (Figure 21). The best parameters arrived at are:

- n_estimators: 255 (trees in the forest)
- max_depth: None (no restriction on max depth of a tree)
- min_samples_split: 5 (minimal quantity of samples needed to divide a inside node)
- random_state: 42 (to get reproducibility)

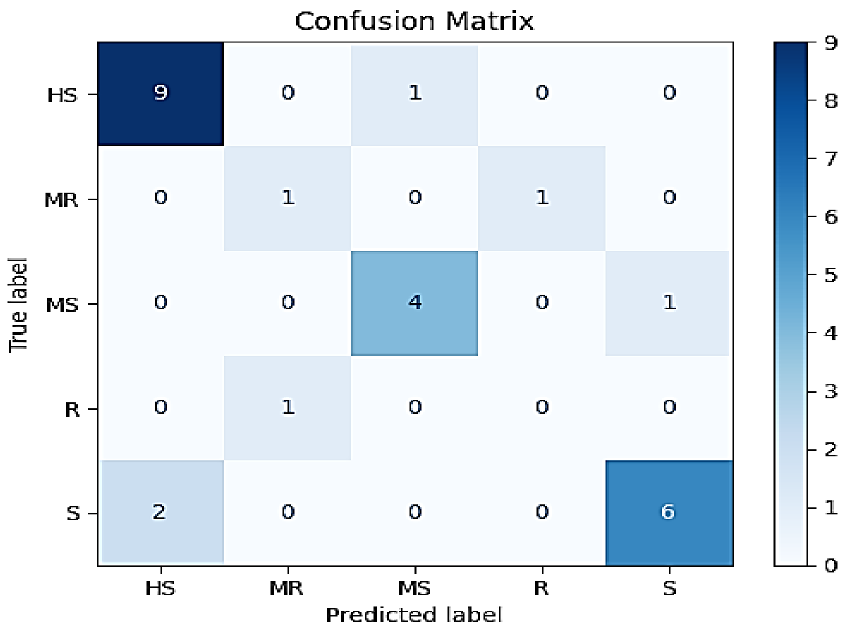

Fig. 21: Random Forest Classification Confusion Matrix: Model Testing in the form of a Confusion Matrix Showing the Degree of Accuracy with which the Random Forest Algorithm Can Distinguish Between Resistant and Susceptible Genotypes.

3.11. Analysis and evaluation of models and accuracy

On the testing set, the predictions were done after training. The model accuracy was then computed. Random Forest model had a testing accuracy of 76.92 which shows a nearly satisfactory level of performance in unseen data. (Figure 21)

3.12. Development of artificial neural network (ANN) model

An Artificial Neural Network (ANN) model was built using a feedforward structure to do a multi-class classification on the data, The ANN was structured with an input layer of 6 neurons to represent the input features, The ANN structure had an input layer, 3 hidden neurons and an output layer of 3 which was the number of classes to be predicted. This layer had the Rectified Linear Unit (ReLU) as an activation layer. A dropout layer of 0.3 was applied before the first hidden layer where 0.3 dropout was used in order to minimize the overfitting problem and improve generalization of the model. It was then followed by two hidden dense with 65 and 17 neurons respectively. Both ReLU layers were also used and another dropout layer with the same dropout probability (0.3) was added as well. The last layer was also a dense layer and had the same number of classes as the target classes and utilized SoftMax activation function to facilitate multi-class predictions. Adam optimizer with a learning rate of 0.01 was used to compile the model. We considered categorical cross entropy as loss function because it is a multi-class classification problem and the model accuracy was set as the main evaluation measure. Early stopping was used to avoid overfitting and to achieve the best performance of this model, so the patience of 10 epochs was used.
The training was done at a maximum of 200 epochs in a batch size of 4. In testing on the set, the ANN model showed that it was able to classify unseen data with an accuracy of 81% indicating that it was well generalized and could still classify data effectively. (Figure 22,23)

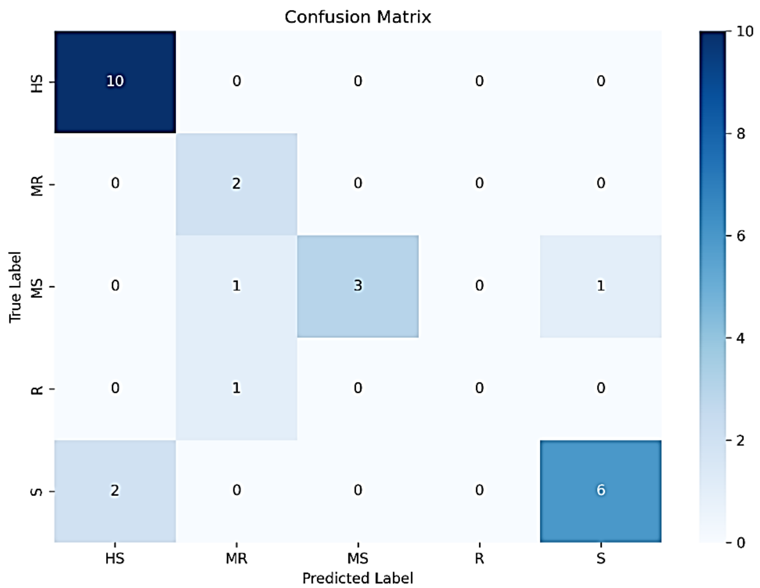

Fig.22: ANN Classification Confusion Matrix: A Genotype Classification ANN Performance is Represented in Confusion Matrix, Most Often with Sensitivity and Specificity of Prediction in the Center.

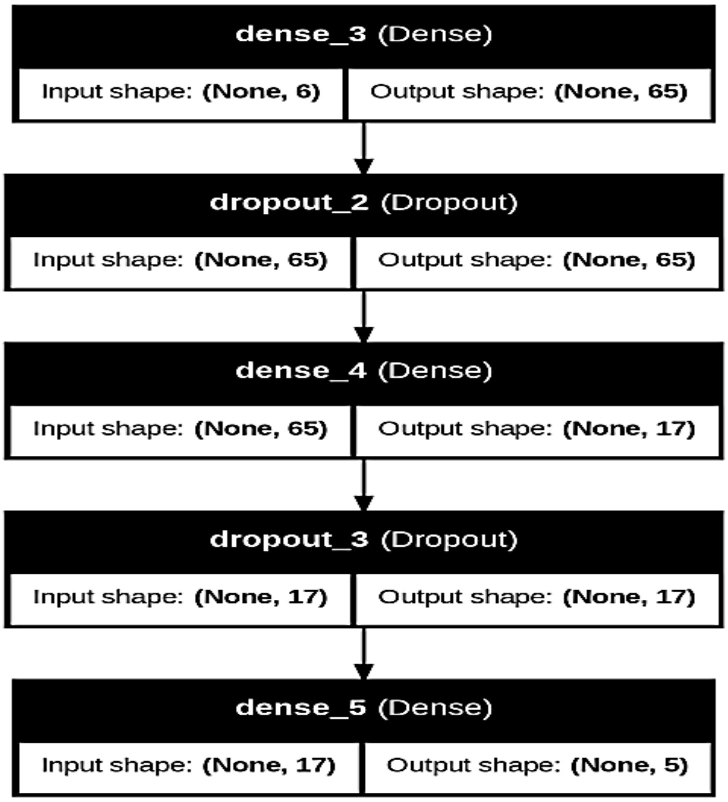

Fig. 23: Architecture of Fitted ANN Model: The Structural Model of the Trained ANN Model, I.E., the Input Layers (Phenotypic/Env. Variables), Hidden Layers and Output Layers (Phenotypic Resistance Disease Classes).

4. Discussion

The current study outlines the convoluted relationship between *Rhizoctonia solani*, which causes sheath blight and the rice genotypes in the context of different environment and experiments. As revealed in a field-based survey, the severity of sheath blight is significantly different across geographical locations which was largely due to environmental factors. In Gania (80–90% infestation) high humidity, frequent rainfall and a dense canopy created a favorable microclimate for *Rhizoctonia solani*. In contrast, Ranadevi (50–60% infestation) had relatively lower humidity, better aeration and less favorable conditions for pathogen spread, resulting in reduced disease stress. This finding suggests a role for local environment and agronomy in the movement and virulence of the disease. The differing genotype performance was identified as a result of performing resistance screening in multi-season field tests. Some of the genotypes like those of Swarna Subhagya, CR 1017, and NLR 33892 showed consistently resistant to moderately resistant reaction in all three years of Kharif seasons and AUDPC value and GC scores were also low (1-2). Instead, over 15 genotypes, some of which were widely cultivated varieties, such as the IR 64, MTU 1010, and CR Dhan 308, were highly susceptible (GC score 5) ranging in AUDPC as high as above 1500 and in most cases as high as 2024, when disease pressure is high. This shows why there should be incorporation of lower-resistant sources in breeding activities especially with the current worsening condition of diseases as noted with the passage of years. The high virulence of isolates on susceptible lines such as IR 64 and CR Dhan 308 was obtained by pathogenicity testing using detached leaf method and seed mortality tests. The seed mortality response confirmed the hypersensitivity of IR 64 because it registered 100 percent and the maximum coefficient of variation (CV = 38.58). In the meantime, CR411 has regularly shown low percentages of mortality and can be one of the possible sources of resistance. The assays were known to be quick and consistent screening tools that were an effective way of differentiating virulence levels in the germplasm. Results of the correlation analysis between three seasons confirmed significant and always positive relationship between Percent Disease Index (PDI), AUDPC, and GC scores. AUDPC and PDI were reliable indicators of genotypic resistance levels in the field since they obtained high positive relationship. This trend was also confirmed by the pooled analysis indicating that the resistance reactions could be described as stable and replicable. The analysis of the disease progression with Gompertz model also confirmed the biological trends of sheath blight development in various genotype sides. The model was very reliable (R^2 ranged between 0.9747 to 0.9963) and significant between all genotypes and years and it was clear that the genotypes differed with respect to asymptotic severity (parameter A), rate of infection (parameter B) and the point of infliction (parameter C). This is one further testament to the usefulness of the Gompertz model to explain time dynamics of diseases in the rice-pathogen unit. Lastly, the classification method, which involved different modeling, showed the possibility of using computational models to predict susceptibility to a disease. Random Forest classifier displayed 76.92 per cent accuracy, compared to the ANN model configuration that displayed an accuracy of 81 per cent. The high capacity to generalize and classify has given the ANN a higher capability in manipulating the complexity and non-linearity of biological data. The next step in research is to identify the genetic markers linked with resistance in promising lines like CR 1017 that can help in the acceleration of marker-assisted breeding of sheath blight resistance. In addition, the Artificial Neural Networks (ANN) and the random forest (RF) classifier and the real-time disease surveillance system may potentially improve the performances of the forecasting even further and provide the response in the dimension of the farmer in the moment. The use of resistant and moderately resistant cultivars, especially in high-risk areas such as Gania and Daspalla should be given priority in practice, where disease pressure is high year-round. Integrating genetic resistance with digital disease forecasting applications will help offer a sustainable and scalable solution to sheath blight management in evolving climatic conditions.

5. Conclusion

The present work is an intensive assessment of the sheath blight disease infection and resistance in rice using multitiered methodologies integrating phenotyping in the field, pathogenicity tests, statistical models, and machine learning-based mechanisms. Large-scale surveys in five geographical sites showed a difference in the disease incidence level with the maximum virulence shown in Gania and Daspalla (80-90 percent infestation) as highlighted in the spatial variability in effect of *Rhizoctonia solani* on rice cultivation. It was possible to contain and assess the resistance of 43 rice genotypes across three consecutive Kharif seasons (2022, 2023, and 2024) to evaluate the accurate and standardized levels of resistance based on the parameters of disease severity, viz., Percent Disease Index (PDI), Area Under Disease Progress Curve (AUDPC), and Genotypic Category (GC). Out of the genotypes screened, few, such as Swarna Subhagya, CR 1017, and NLR 33892 showed consistent resistant or moderate resistant throughout all seasons, lower AUDPC scores and good GC ratings, and these genotypes can be used as stable resistance donors in further breeding programs. Conversely, a portion of the genotypes especially the most common cultivar which include IR 64, CR Dhan 308, MTU 1010, Juvraj Dhano were highly susceptible with AUDPC exceeding 1500 and GC from 5, which demonstrates the fact that "these genotypes are susceptible to sheath blight and that such genotypes must be genetically improved by incorporating resistant parents" as a way of providing a resistant solution. Seed mortality and detached leaf tests were also performed to confirm the opinion in relation to the different virulence of isolates and the genetic sensitivity of tested genotypes. The high susceptibility of IR 64 and CR Dhan 308 was confirmed because they exhibited total seed mortality and high rates of lesion expansion. In the meantime, the seed mortality rates were substantially smaller when it came to CR411, which demonstrates natural resistance. Parameters such as coefficient of variation (CV) were used as well as other parameters to confirm the reliability and significance of the experimental results. It was shown that the application of the correlation analysis is very strong and consistent positive relationships were achieved correspondingly PDI, AUDPC and GC values of all the three years to be reflected indicating stable levels of disease expression and appropriateness of the phenotyping methods applied in a natural field environment. The degree of the disease progression in various resistance classes of rice with the Gompertz model also reinforced the results. The model fitted really well (R^2 = 0.9747-0.9963) in all categories of genotypes and seasons, with significantly estimated values of progression parameters of the disease, asymptotic severity (A), infection rate (B) and inflection point (C). These parameters served to well characterize the dynamics of the disease development with time. Furthermore, the use of the machine learning techniques has shown the practical value of computer tools in the classification of the diseases. Random Forest classifier demonstrated good generalization and making predictions in the processing of complicated, multi-class biological data as it had a sufficient testing accuracy of 76.92% with an Artificial Neural Network (ANN) model surpassing it 81% testing accuracy considering predictive abilities.

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