



Assessment of Chemical and Biological Measures of Controlling Rice Sheath Blight: Field Trials and ML-based Yield Prediction

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ABSTRACT

Background: *Rhizoctonia solani* is the cause of sheath blight of rice that is a significant limitation to *Kharif* productivity, requiring effective and unstable management approaches.

Methods: A field test, using eight treatments, was carried out: T1- Control, T2- Validamycin 3% L, T3- Azotrix (Azoxystrobin 16.7% + Tricyclazole 33.3%), T4- Nativio (Tebuconazole 50% + Trifloxystrobin 25% WG), T5- Tilt, T6- Contaf Plus, T7-*Trichoderma* and T8-*Pseudomonas*. The severity of the disease (DS%), PDI, yield, number of grains per panicle and weight of 1000 grains were noted. ANOVA was used to analyze data (Tukey, DMRT) and prediction of yields was carried out using machine-learning models (Random forest, LightGBM, CatBoost, XGBoost).

Result: The effects of treatment were very substantial ($p < 0.001$) and the effect of year and the interaction of year $\times$ treatment were not significant ($p = 0.608$). Nativio (T4) performed better, with maximum yield (11.62 kg plot⁻¹), grains per panicle (131.22) and 1000 gm seed weight (23.94 g) and minimum DS (18.47-20.25%) and PDI (16.50-19.06%). Azotrix and Validamycin followed. The maximum DS (40.57%) and PDI (52.38) were observed with minimum yield (7.49 kg plot⁻¹). Random Forest got the best accuracy ($R^2 = 0.848$; RMSE = 0.566), which validated nativo, azotric and validamycin as the most suitable management choices.

Key words: Disease severity, Machine-learning, Management, *Rhizoctonia solani*.

INTRODUCTION

Rhizoctonia solani AG1-1A (Kuhn) is a soil-borne fungus causing sheath blight, whose teleomorph is *Thanatephorus cucumeris* (Uppala and Zhou, 2018; Hussein *et al.*, 2025). Disease yield loss about 10-30% and up to 50% given good conditions in the environment (Uppala and Zhou, 2018; Biswal and Das, 2024). It is tightly linked with the rise of semi-dwarf and nitrogen-sensitive varieties of rice in the world (Liu *et al.*, 2025). The pathogen has right-angle branching hyphae and generates white mycelium and brown sclerotia (1-3 mm) on the infected tissues (Uppala and Zhou, 2018). The onset of disease is at late tillering stage of rice, early internode elongation showing water-soaked lesions and greenish-grey color center in the sheath. resulting in senescence, tiller lodging (Uppala and Zhou, 2018; IRRI Rice Knowledge Bank, 2019). The mode of action used by *Trichoderma spp.* is the release of antifungal enzymes such as chitinase and glucanase causing the degradation of hypha and sclerotia, whereas *Aspergillus* has also been reported to exert mycoparasitic relationships with *R. solani* (Abbas *et al.*, 2022).

The recent progress of deep learning has greatly enhanced the system of sheath blight detection, severity and decision support system in managing rice disease (Rezaei *et al.*, 2025). The models are quite effective in reflecting the intricate non-linear integration between the severity of the disease, environmental conditions, crop developmental phases and farming practices (El Amraoui *et al.*, 2024). There are recurrent architectures like LSTM and BiLSTM, which obtain temporal patterns of disease

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progression depending on the weather conditions, nitrogen content, canopy density and pathogen dynamics (Jeong

et al., 2023; Li *et al.*, 2025). Deep learning in combination with biological knowledge can be used to detect the disease in its early stages and can provide optimal and sustainable strategies of sheath blight management (Paquet *et al.*, 2022; Sushmit *et al.*, 2023; Singh *et al.*, 2019).

MATERIALS AND METHODS

Experimental site and experimental design

The experiment was conducted *rabi* season of 2022-2024 at Ranadevi farm of Centurion University of Technology and Management, Parlakhemundi, Odisha. The experiment was conducted in Swarna (MTU 7029) variety of rice. The land was ploughed twice crosswise by tractor drawn harrow and weeds were removed thoroughly from the field. Nursery bed was raised and sowing was done (Fig 1). Main field was prepared in an area of (13.6 × 21.7) m², along with 0.5 m irrigation channel. Thirty days aged seedlings were transplanted into the main field in three replications with a spacing (4.2 × 3.2) m². Plant to plant and the row-to-row distance were 10 × 20 cm. 30 days old seedlings were transferred from the nursery to the main field.

Symptomatic characterization

The symptoms of sheath blight were studied and systematically monitored in the field as well as microscopic study and photographed. The symptoms first appeared: small, water soaked, oval-irregular spots on the waterline on the leaf sheath which gradually increased in size with greyish centers and brown margins, ascending and descending the sheath and the leaf blades. Lesions formed large necrotic spots as the disease progressed and in extreme cases sheaths and leaves were heavily affected resulting in wilting and lodging (Fig 2). Microscopic studies were also able to confirm the morphological character of *Rhizoctonia solani* (Fig 3).

Experimental design and treatments

The experiment was laid out in a randomized complete block design (RCBD) with eight treatments and three replications per year. The field was artificially inoculated with *R. solani* (Fig 4,5). The treatments comprised, T1- Control, T2- Validamycin 3% L, T3- Azotrix (Azoxystrobin 16.7% + Tricyclazole 33.3%), T4- Natio (Tebuconazole 50% + Trifloxystrobin 25% WG), T5- Tilt (Propiconazole 25% EC), T6- Contaf plus (Hexaconazole 5% SC), T7- *Trichoderma harzianum*, T8- *Pseudomonas fluorescens*. Foliar application was done at maximum tillering and panicle initiation stage of crop.

Data sources

DS and PDI were recorded at Ranadevi farm of Centurion University, data is taken in 10 days interval after inoculation up to 9 observations. The disease was scored by using 0-9 scale based on lesion character and lesion area, where 0 represented no lesion characteristics and 9 represented

lesions in more than 75% leaf area. DS and PDI was calculated by formula given by Shrestha and Mishra (1994).

$$DS = \frac{\text{Total lesion length}}{\text{Total length of sheath}} \times 100$$

PDI =

$$\frac{\text{Sum of all individual disease ratings}}{\text{Total no. of plant assessed} \times \text{Maximum ratings}} \times 100$$

Measurement of yield and yield attribute

Plant height was assessed at maturity from ground level to the tip of the tallest panicle on 10 randomly selected plants per plot using a measuring tape. Ten representative panicles were selected randomly in each plot and manual counting of grains was done. Weighed clean and sun-dried seeds with 1000-grain weight (g) of the adjustment to 14% of moisture. The harvested net plot yield was dried and adjusted to 14% moisture content and recorded as grain yield (Kg plot⁻¹).

Statistical analysis

Over the course of three years, a mixed analysis of variance (ANOVA) was performed based on the described linear model. The means of treatment were isolated with the help of the Tukey's honest significant difference (HSD) test and the Duncan's multiple range test (DMRT) at $p < 0.05$. Statistical analysis was done in R software with the help of agricolae package (Das *et al.*, 2019).

Machine learning analysis

The regression analysis was conducted using the pooled data of 2022-2024 cropping seasons ($n = 72$) to forecast the rice grain yield under sheath blight pressure. Before developing the model, the numerical variables had been normalized *via* Z-score transformation and the categorical ones transformed into codes and the dataset was splitting into training (80) and testing (20) sets. The analysis used a constant random state (42) so that it can be reproducible and comparable across models.

Four machine-learning models were tested on predicting the grain yield under different sheath blight pressure with the use of four regression-based models, i.e., RF regressor, light gradient boosting machine (LightGBM), extreme gradient boosting (XGBoost) and CatBoost regressor. The random forest model was configured with 500 trees, a maximum depth of 12, bootstrap sampling enabled and a fixed random state of 42, using RMSE as the evaluation criterion. LightGBM was implemented with a GBDT boosting type, 1,500 estimators, a learning rate of 0.02, 45 leaves, subsample frequency of 1, column subsampling of 0.8, minimum child samples of 15, regularization parameters (α and λ) set to 0.5 and a random state of 42. The XGBoost regressor utilized 900 estimators, a learning rate of 0.03, maximum depth of 6, subsampling and column subsampling rates of 0.85, with regularization parameters $\lambda = 1$ and $\alpha = 0.3$. The CatBoost regressor was trained with 3,000 iterations, a learning rate

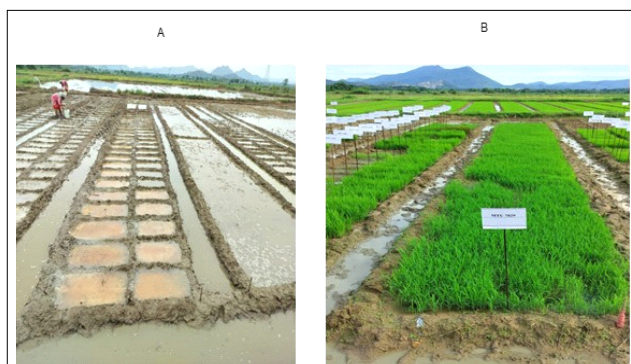


Fig 1: Raising of seedlings in nursery bed of rice preparation under field conditions (A) and experiment to manage sheath blight (*Rhizoctonia solani*) using rice nursery of variety MTU 7029 (B).

of 0.015, maximum depth of 8, subsample rate of 0.75, RSME of 0.85 and RMSE as the loss function. All models were trained using a constant random seed (42) to ensure reproducibility. Model performance was evaluated using R^2 and RMSE on training and testing datasets, respectively. The model showing the most consistent performance was re-fitted using the complete dataset ($n = 72$) for final treatment-wise yield prediction.

RESULTS AND DISCUSSION

Fungicidal and biological treatments on the sheath blight, yield and yield attributes

The relative analysis of fungicidal and biological management of rice sheath blight in three seasons showed that there were vast variations in DS, PDI, grain yield and

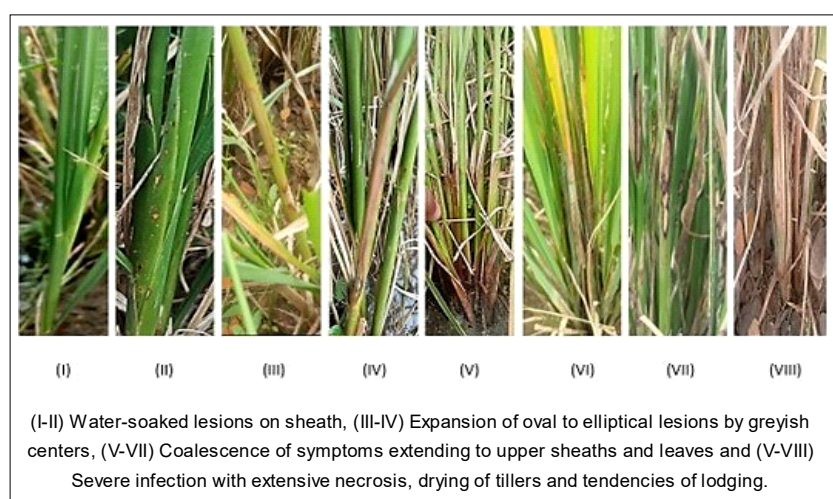


Fig 2: Development of symptoms of rice sheath blight under field conditions.

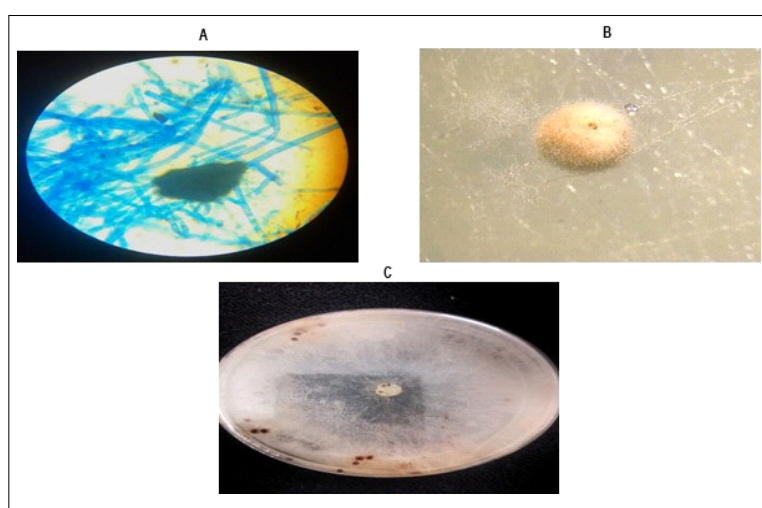


Fig 3: Microscopic image of *Rhizoctonia solani* distinct right-angle branching and septation of hyphae (A), Sclerotium of *R. solani* in stereoscopic microscope (B) and *Rhizoctonia solani* on potato dextrose agar (PDA) (C).



Fig 4: Field experiments Intercultural operations in transplanted rice under field conditions (A), Fungicidal and biological treatment of rice field made in knapsack sprayer (B) and Field observation of the experimental plots of rice at the time of maturity with treatment-wise crop response (C).

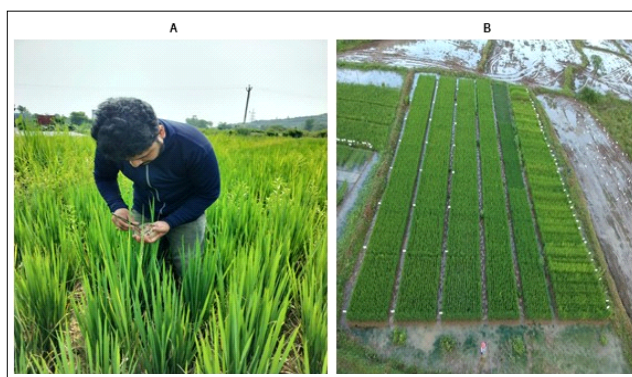


Fig 5: Inoculation of rice plants by artificial inoculation of *Rhizoctonia solani* (A) and Oblique view of reproduced irrigated rice plots using drones (B).

yield-attributing characters (Table 1-3). The highest incidence of the disease (38.65-41.56%), PDI (50.43-53.88%) and the lowest yield (6.81-8.07 kg plot⁻¹) were observed in the untreated control. Uncontrolled sheath blight has been reported to cause similar decreases and losses in yields has been reported by Chitti *et al.*, 2024).

The best was native (Tebuconazole + Trifloxystrobin @ 0.4 g l⁻¹) with minimum disease severity (17.67-19.85%) and PDI (15.87-17.15) and the highest grain yield (11.43-11.80 kg plot⁻¹), grains per panicle (128-135), 1000-grain weight (22.70- 24.95 g) and panicle length. This was to be followed by the applications of validamycin 3% I L @ 2.5 ml l⁻¹ and Azotrix (Azoxystrobin + Tricyclazole @ 1 ml l⁻¹), which revealed similar disease suppressing and improvement in yield, these treatments also contributed significantly to disease reduction, as similarly reported by Yadav *et al.* (2023). Tilt (Propiconazole) and contaf plus (Hexaconazole) had

moderate efficacies, whereas biological treatments (*Trichoderma* and *Pseudomonas*) offered moderate efficacies and gain yields, which implies their appropriateness to integrated disease management. Differences in treatment were found to be significant by statistical analysis (SOM, SEd, CD at 5% and 1%).

Correlation analysis

The correlation analysis showed that there was a negative correlation between yield and disease severity (DS; $r = -0.69$) and percent disease index (PDI; $r = -0.67$), which implied that with greater disease intensity, yield was reduced. The severity of the disease had a strong positive correlation with PDI ($r = 0.86$) and negative correlation with cluster number ($r = -0.76$). Cluster number had a negative association with PDI ($r = -0.81$) and a positive relationship with yield-related characteristics. On the contrary, there was a significant positive correlation between grain yield on the one hand and cluster number ($r = 0.71$), 1000-grain weight ($r = 0.60$) on the other hand and grains per panicle ($r = 0.53$) showing that they have a positive contribution to yield (Fig 6). In general, yield components had a positive impact, whereas disease parameters had a negative impact on yield.

The cluster analysis was able to group treatments into three different categories by disease and yield characteristics (Fig 7A). The high-yield, low-disease observations (Cluster 0), intermediate performers (Cluster 1) and poor performers (Cluster 2) were separated by k-means. Cluster 0 showed high grain yield, a greater number of grains per panicle and higher 1000-grain weight, along with low disease severity (DS %) and low PDI. This cluster included Native, Azotrix and Validamycin., Cluster 1 had moderate levels

Table 1: Yield and disease response fungicidal and biological control of rice sheath blight (2022).

Treatment	Dose (g/l or ml/l)	Yield (kg plot ⁻¹)	DS %	Grain per panicle	1000 grain weight (g)	Plant height (cm)	PDI %	% PDC
Control	-	6.81	38.65	96.00	19.07	55.76	50.43	0.00
Validamycin 3%L	2.5	10.32	18.77	122.00	19.47	64.16	18.80	51.45
Azotrix (Azoxistrobin 16.70%+tricyclazole 33.3%)	1	10.88	19.42	103.00	22.38	59.45	16.15	49.74
Native (Tebuconazole 50%+trifloxystrobin 25% WG)	0.4	11.43	19.85	135.00	24.95	55.91	17.15	48.58
Tilt (Propiconazole 25%EC)	1	7.88	26.38	107.00	22.30	56.71	25.84	31.66
Contaf plus (Hexaconazole 5% SC)	2	8.75	27.02	113.00	22.00	56.85	22.61	30.21
<i>Trichoderma harzianum</i>	10	8.09	27.45	97.00	18.32	57.27	38.30	28.80
<i>Pseudomonas fluorescens</i>	5	9.32	30.13	99.00	22.26	53.78	42.57	22.08
SEm	-	0.27	0.54	3.46	0.49	1.65	0.92	1.39
SEd	-	0.38	0.76	4.90	0.70	2.33	1.30	1.96
CD 5%	-	0.76	1.51	9.73	1.39	4.63	2.58	3.90
CD 1%	-	1.01	2.00	12.90	1.84	6.13	3.41	5.16

Table 2: Yield and disease response fungicidal and biological control of rice sheath blight (Season-2023).

Treatment	Dose (g/l or ml/l)	Yield (kg plot ⁻¹)	DS %	Grain per panicle	1000 grain weight (g)	Plant height (cm)	PDI %	% PDC
Control	-	7.58	41.56	90.00	18.91	53.85	52.85	41.87
Validamycin 3% L	2.5	10.05	20.49	117.00	22.71	60.49	19.13	34.11
Azotrix (Azoxistrobin 16.70%+Tricyclazole 33.3%)	1	9.53	20.69	124.00	24.35	62.52	17.24	34.70
Native (Tebuconazole 50%+Trifloxystrobin 25% WG)	0.4	11.80	17.67	131.00	24.14	64.63	16.53	35.10
Tilt (Propiconazole 25% EC)	1	9.19	30.95	112.00	19.36	52.84	29.03	33.74
Contaf Plus (Hexaconazole 5% SC)	2	8.60	25.95	112.00	19.71	60.49	22.43	34.21
<i>Trichoderma harzianum</i>	10	8.38	28.89	105.00	17.71	55.87	45.64	39.74
<i>Pseudomonas fluorescens</i>	5	8.74	27.74	94.00	20.00	52.03	35.72	35.92
SEm	-	0.21	0.78	2.87	0.41	0.97	0.67	2.44
SEd	-	0.30	1.10	4.06	0.58	1.38	0.95	3.45
CD 5%	-	0.60	2.19	8.07	1.16	2.74	1.88	6.86
CD 1%	-	0.79	2.90	10.69	1.53	3.63	2.49	9.09

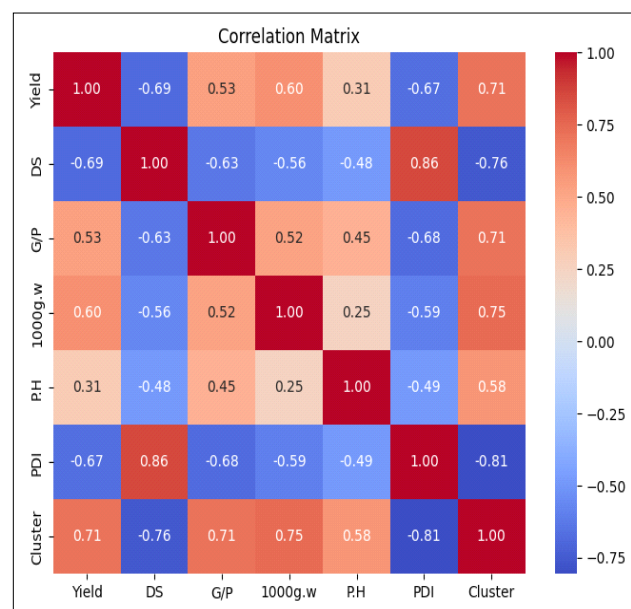
Table 3: Yield and disease response Fungicidal and biological control of rice sheath blight (Season-2024).

Treatment	Dose (g/l or ml/l)	Yield (kg plot ⁻¹)	DS %	Grain per panicle	1000 grain weight (g)	Plant height (cm)	PDI %	% PDC
Control	-	8.072	41.5	97	19.1	53.38	53.88	42.12
Validamycin 3% L	2.5	9.430	21.5	117	21.8	58.3	19.30	33.13
Azoxistrobin 16.70%+Tricyclazole 33.3%)	1	10.081	19.57	126	22.5	58.92	17.15	32.86
Native (Tebuconazole 50%+Trifloxystrobin 25% WG)	0.4	11.615	17.91	128	22.7	63	15.87	33.86
Tilt (Propiconazole 25% EC)	1	8.517	29.62	103	20.8	55.16	29.26	35.07
Contaf Plus (Hexaconazole 5% SC)	2	9.160	27.29	111	21.5	58.14	21.74	33.79
<i>Trichoderma harzianum</i>	10	8.376	30.2	101	19.5	53.6	43.58	38.89
<i>Pseudomonas fluorescens</i>	5	8.672	28.13	108	19.8	54.4	37.28	37.16
SEM	-	0.148	0.109	0.251	0.0558	0.046	0.042	0.446
SED	-	0.210	0.154	0.356	0.079	0.065	0.059	0.632
CD 5%	-	0.418	0.307	0.708	0.157	0.130	0.118	1.256
CD 1%	-	0.554	0.407	0.939	0.208	0.172	0.156	1.665

of disease and yield and included Contaf Plus, Tilt and biological treatments and Cluster 2 had a high level of disease pressure, low panicle length and grain weight along with low yield similar to the untreated plots. The pairplot visualization ensured that the separation of clusters was clear in the case of DS%, PDI and yield traits. Clustering was supported by the principal component analysis (PC1 = 63.90 and PC2 = 13.66) with 77.56% variance being explained in the two principal components: PC1 exhibited positive loadings on yield attributes and PC2 negative loadings on the disease parameters, indicating a negative disease-yield relationship. PCA biplot (Fig 7B) placed high-yield, low-disease treatments of the positive PC1 axis and highly infected plots of the negative axis, which confirms that successful disease-suppressive treatments have a unique multivariate performance space that is consistent with field, correlation and machine-learning findings.

Correlation between grain yield and disease severity

It was found that grain yield had a significant negative association with the level of disease severity (DS), which is reflected in the scatter-plot (Fig 8) where a decline in yield was recorded with increase in disease severity. The regression equation and confidence band fitted indicated a statistically significant downward trend as the higher yields in the lower DS ranges (15-25%) of 10-13 kg plot⁻¹ and that an increase in the value of the DS beyond 35% led to a sharp decrease in the yields to below 8 kg plot⁻¹. This downward trend has been maintained consistently since the increasing sheath blight severity is very sensitive to yield and thus effective management of the disease is necessary to maintain productivity.

**Fig 6:** Correlation analysis of yield, agronomic traits and disease parameters.

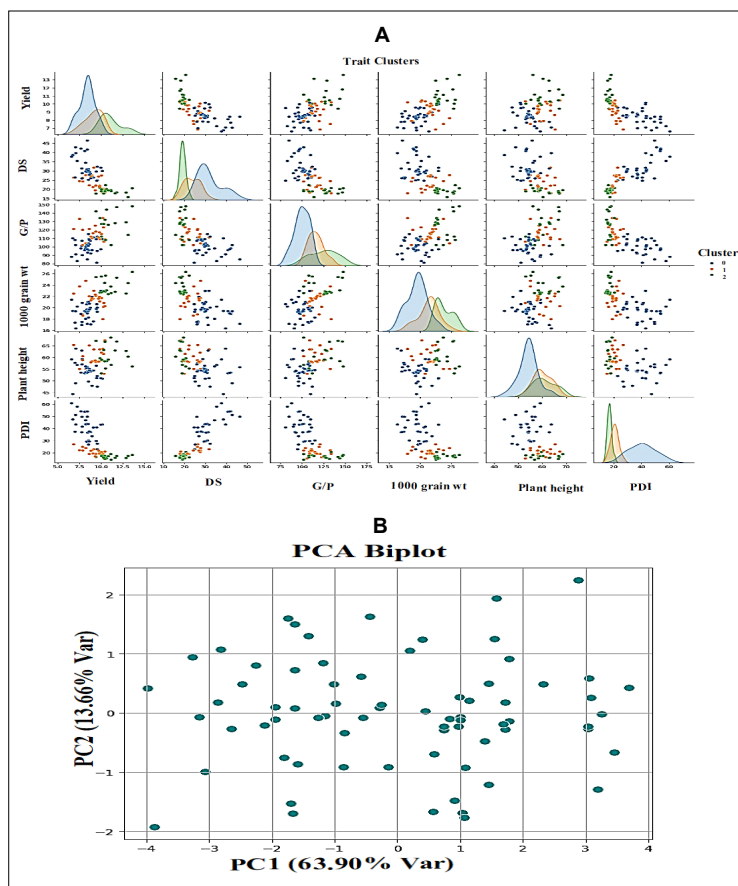


Fig 7: (A) Trait correlations and cluster analyses between the variables of yield and disease (B) PCA depicting significant factors of variation.

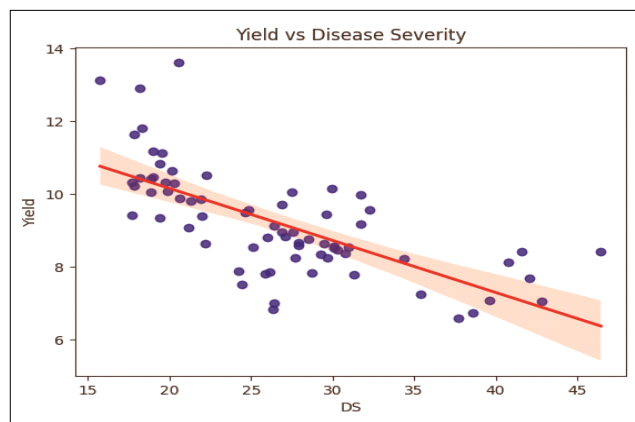


Fig 8: Negative correlate between yield and disease severity.

Table 4: Comparison of machine learning models in predicting the yield of rice in relation to R^2 and RMSE.

Model	R^2 (Overall)	RMSE (Overall)
Random forest	0.848	0.566
LightGBM	0.79136	0.6358
XGBoost	0.67901	0.78861
CatBoost	0.64564	0.82859

Machine-learning model performance

Among the implemented machine-learning models, RF was the most accurate in prediction ($R^2 = 0.848$; RMSE = 0.566), then LightGBM ($R^2 = 0.7914$; RMSE = 0.6358), XGBoost ($R^2 = 0.6790$; RMSE = 0.7886) and CatBoost ($R^2 = 0.6456$; RMSE = 0.8286) (Table 4, Fig 9).

The preferred treatment based on the Random Forest model was very similar to the results of the fields, with the highest ranking going to Nativio, then subsequently Azotrix and Validamycin followed by the control as the lowest. This contract confirms the strength of machine-learning models to predict yields in different sheath blight pressure. Which is also explain by Xin *et al.* (2024).

Analysis of variance for disease and yield traits: ANOVA on three years found a significant difference in treatment (DS%) to the point of being highly significant ($F = 88.528$, $p < 2 \times 10^{-16}$), year and year $\times$ treatment interaction were not significant.

The highest DS% (40.57) was observed in the untreated control, which formed a separate Tukey group (a). The lowest DS% was reported with nativo (18.47%), azotrix (19.89%) and validamycin (20.25%) and they were combined into a single group (Tukey group c) due to the lack of seasonal differences regarding the suppression of

the disease (Fig 10A). The effect of treatment on PDI was very significant ($F = 225.009$, $p < 2 \times 10^{-16}$). Control had the highest PDI (52.38%) whereas nativo (16.50%), azotrix (16.85%) and validamycin (19.07%) constituted the lowest DMRT group (e). Tilt, contaf plus, *Trichoderma* and *Pseudomonas* showed intermediate values of PDI (Fig 10B). A significant treatment was also found in grains per panicle ($F = 12.798$, $p = 1.151 \times 10^{-8}$). Nativo recorded the highest grains per panicle (131.22) followed by Validamycin (118.67) and Azotrix (117.67), while the lowest value was observed in control (94.44) (Fig 10C).

Treatment had a considerable effect on 1000 grain weight ($F = 14.472$, $p = 2.094 \times 10^{-9}$). Nativo recorded

highest grain weight (23.94 g), then azotrix (23.07 g). The lowest grains weights were observed in the control and *Trichoderma* treatments (Fig 10D). A significant difference among treatments was also observed for plant height ($F = 4.5927$, $p = 0.0006983$). Nativo (61.18 cm), validamycin (60.97 cm) and azotrix (60.30 cm) produce the tallest plants. Contaf plus, *Trichoderma* and tilt showed moderate plant heights (54.90-58.49 cm). The lowest heights were recorded in the *Pseudomonas* (53.40 cm) and control (54.32 cm) (Fig 10E). There was also a considerable difference in grain yield between treatments ($F = 19.976$, $p = 1.719 \times 10^{-11}$). The highest yield was obtained with Nativo (11.62 kg plot⁻¹) followed by Azotrix (10.16 kg plot⁻¹) and Validamycin

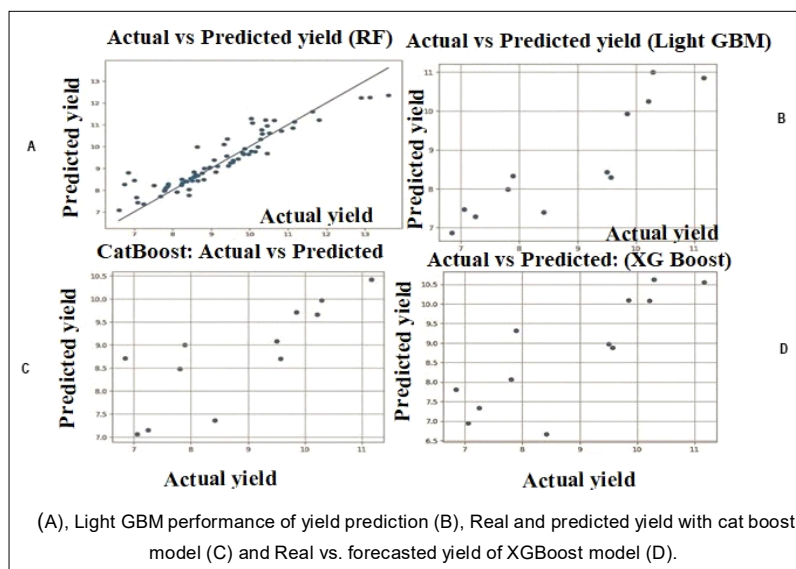


Fig 9: Random forest (RF) yield prediction results.

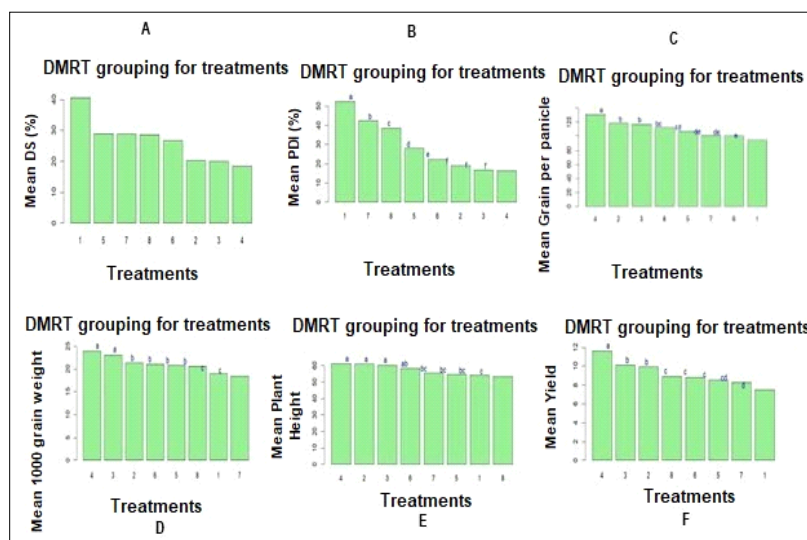


Fig 10: DMRT classification of treatments according to the average disease severity (DS%) (A), DMRT treatment grouping in terms of average percent disease index (PDI%) (B), DMRT treatment grouping in terms of average Grain per panicle (C), DMRT treatment grouping in terms of average 1000 Grain wt. (D), DMRT treatment grouping in terms of average plant height (E) and DMRT treatment grouping in terms of average yield (F).

(9.93 kg plot⁻¹). The fungicides based on hexaconazoles and the biological treatment gave intermediate values (8.28-8.91 kg plot⁻¹), whereas the control had the lowest yield (7.49 kg plot⁻¹) (Fig 10F).

CONCLUSION

The sheath blight is a serious challenge affecting the productivity of rice and proper fungicidal management averts these losses. Nativo was found to be better because of its dual systemic triazole-strobilurin effect, which was succeeded by validamycin and azotrix as statistically similar agents to rotate. Tilt and contaft plus gave moderate control and *Trichoderma* and *Pseudomonas* were to give an integrated management of the disease with moderate advantages of yield. Important correlations amid disease severity and yield components affirmed disease effect. The multivariate and machine-learn test confirmed the orders of treatments and proved the consistency of combined statistical methods to make predictions on yield with different degrees of sheath blight.

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Disclaimers

The views expressed in this article are solely those of the authors. The authors are responsible for the accuracy of the information presented.

Informed consent

This study did not include human participants, animal subjects, or any materials that would necessitate ethical approval.

Conflict of interest

In this investigation there is no any potential bias or conflict of interest in terms of financial or any other means.

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