Genetic Analysis of Key Traits for Sheath Blight Resistance and Yield Improvement in Rice (*Oryza sativa*)

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Authors' contributions

This work was carried out in collaboration among all authors All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

Rice (*Oryza sativa*) is a staple crop for more than half of the global population, with significant production in India. However, rice production suffers yield losses of 25-30% due to diseases, particularly sheath blight (ShB), caused by *Rhizoctonia solani*. This study evaluated genetic variability, heritability, and genetic advance in ShB resistance and yield-related traits in 360 recombinant inbred lines (RILs) across two seasons (dry season of 2022-23 and wet season of 2023) at ICAR-IIRR, Hyderabad. Traits such as plant height, lesion height, relative lesion height,

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and panicle number showed high heritability (>80%) and genetic advance (>30%), indicating their strong genetic influence and responsiveness to selection. These traits, especially relative lesion height, were identified as key indicators for breeding ShB resistance. In contrast, grain yield under inoculated conditions showed lower heritability, reflecting environmental effects and suggesting that indirect selection through stable, heritable traits may be more effective. This research offers a foundation for breeding high-yielding, disease-resistant rice cultivars, advancing sustainability in ShB-prone regions by maintaining stable yields even under pathogen pressure.

1. INTRODUCTION

Rice (*Oryza sativa*) is a staple food for over half of the world's population and a key component of the Indian diet (Srihari et al., 2019). Cultivated rice belongs to the family Poaceae and about 20 species of the genus *Oryza* are recognized. Due to its adaptability and high demand, rice cultivation has expanded across various regions worldwide. In India, rice is primarily cultivated in the eastern and southern regions, covering approximately 45.15 million hectares, with an estimated annual production of 123.81 million tonnes (Indiastat, 2023-24). To meet the demands of a growing population, it is projected that rice production must increase by at least 40% by 2030 (Ashkani et al., 2015).

In India, rice production faces significant challenges due to diseases, resulting in an annual yield loss of approximately 25-30% (Jha et al., 2012). Among these diseases, sheath blight (ShB), caused by the necrotrophic pathogen *Rhizoctonia solani* (Teleomorph: *Thanatephorus cucumeris*), is one of the most destructive threats to paddy (Bhaktavatsalam et al., 1978). This disease, also known as "Oriental sheath and leaf blight," occurs widely across India, with the severity of yield loss depending on the extent and progression of the infection. The *R. solani* anastomosis group AG1 IA is a primary causal agent of rice sheath blight (Khan et al., 2023). In severe cases, particularly when the infection reaches the plant's upper portions and panicles, yield losses from sheath blight can range from 30 to 40% (Burton, 1952). Given the economic impact of this disease and the need for comprehensive studies on genetic variability in rice to support the development of an effective resistance breeding program, the present study was undertaken.

Understanding genetic variability in rice is essential for designing effective breeding programs aimed at enhancing resistance to sheath blight and other traits. The variability among genotypes, often evaluated through coefficients of variation, reveals the potential range of improvement within specific traits (Dey et al., 2016). In addition to variability, insights into heritability and genetic advance provide a clearer picture of how consistently a trait can be passed on to progeny. Heritability, especially when paired with genetic advance, offers more reliable predictions of selection gains than heritability alone. Estimates of genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance are invaluable tools for guiding future research on rice improvement (IRRI, 2002). Heritability is particularly critical for breeders, as it indicates how well a genotype's phenotype reflects its genetic potential, while genetic advance helps in applying effective selection pressure to achieve desired improvements (Srinivas et al., 2013).

Over the decades, research has focused on breeding rice for ShB resistance, but challenges remain. Traditional breeding methods using phenotypic selection have been limited due to the complex and environmental nature of ShB resistance (Patel et al., 2021). Early research identified several key genes linked to resistance, but their effectiveness has varied across different conditions. To overcome these challenges, modern approaches like marker-assisted selection (MAS) and genomic technologies, including genotyping and genome-wide studies, have improved the mapping of resistance traits. While these methods show promise, a fully ShB-resistant rice variety has yet to be developed, emphasizing the need for further research on genetic variability and inheritance of resistance traits.

2. MATERIALS AND METHODS

A total of 360 recombinant inbred lines (RILs) and five checks were evaluated during the dry

season (DS) of 2022-23 and the wet season (WS) of 2023 at ICAR-IIRR, Hyderabad. The RILs were sown on raised beds and transplanted to the main field 27 days after sowing, with a spacing of 20 x 15 cm, using an augmented randomized complete block design (ARCBD). This is an experimental design which is used to test a large number of germplasm lines in a limited area (Federer, 1956). RILs were planted only once while the checks were replicated in all five blocks. All recommended package of practices were followed to ensure optimal crop establishment. RILs were evaluated and observations were recorded on random three plants in each line for sheath blight disease and yield traits viz., days to 50% flowering (DFF), plant height (PH) (cm), lesion height (LH), relative lesion height (RLH), standard evaluation score (SES), tiller number (TN), panicle number (PN), panicle length (PL), grain yield un-inoculated(GY_u), grain yield inoculated (GY_i) and relative yield loss (RYL). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to the method elucidated by Burton, 1952 and the estimates for variability were treated as per the categorization proposed by Sivasubramanian and Madhavamenon, (1973). Broad sense heritability (h^2) and genetic advance mean (GAM) were calculated based on the approaches of Lush, (1940), Burton, 1952, Johnson et al., (1955) and Allard, (1960).

The RILs were evaluated for sheath blight resistance using the standard Typha inoculation method, as described by Baktavatsalam et al., 1978. Inoculation was carried out at the maximum tillering stage (40 days after transplanting). Disease severity was scored based on the relative lesion height (RLH) metric, following the International Rice Research Institute (IRRI) Standard Evaluation System (SES) for rice (2002). The RLH was calculated using the following formula:

$$RLH\ (\%) = \frac{Lesion\,height}{Plant\,height} \times 100$$

A standardized rice sheath blight grading chart, ranging from 0 to 9, was used to record the severity of symptoms based on lesion height and overall disease reaction: 0 indicates no symptoms (immune), 1 indicates 20% symptoms (resistant), 3 indicates 21-30% symptoms (moderately resistant), 5 indicates 31-45%

symptoms (moderately susceptible), 7 indicates 46-65% symptoms (susceptible)and 9 indicates 66-100% symptomatic area or collapsed plants (highly susceptible).

3. RESULTS AND DISCUSSION

In the pursuit of enhancing rice productivity and disease resistance, particularly against sheath blight, understanding genetic variability is crucial for informed breeding strategies. Key genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) measure the extent of genetic and environmental influence on trait expression, respectively. High heritability combined with substantial genetic advance as a percentage of the mean (GAM) further highlights traits that are predominantly controlled by genetic factors and are responsive to selection (Prasad et al., 2017). These parameters collectively aid breeders in identifying traits that can reliably contribute to yield improvement and disease resilience, establishing a strong foundation for effective breeding programs focused on sustainable rice production.

In the present study, traits evaluated during the dry season demonstrated varying degrees of heritability and genetic advance, providing insights into their potential for selection. For instance, days to 50% flowering had high heritability (100%) with a moderate genetic advance (11.64%), suggesting that while this trait is highly heritable, gains through selection might be more modest, aligning with the findings of Paikomba et al., (2014). Traits such as lesion height and plant height exhibited high heritability (86.43% and 92.74%, respectively) (Fig. 1) with substantial genetic advance (34.51% and 35.13%), indicating that these traits are influenced by genetic factors and can be effectively improved through selection. This observation is consistent with the results reported by Prasad et al., (2017) for plant height. Relative lesion height, a critical indicator of sheath blight severity, also showed high heritability (90.57%) and high genetic advance (39.67%), suggesting that genetic improvements in resistance to sheath blight could be achieved. Traits with moderate heritability, such as the standard evaluation score, reflected some environmental influence, which could make direct selection for these traits slightly more challenging.

In the wet season, high heritability was observed for traits such as plant height (96.5%) and panicle length (97.01%). The genetic advance for these traits was also substantial, suggesting these are stable traits less influenced by environmental variability. These findings are in agreement with Tushara et al., (2013) and Srihari et al., (2023). Relative lesion height demonstrated high GCV, PCV, heritability (84.21%), and genetic advance (42.16%), supporting its suitability as a selection criterion in breeding programs targeting sheath blight resistance. In contrast, grain yield un-inoculated and grain yield inoculated had lower heritability values, indicating a significant environmental influence. This lower heritability suggests that while yield is an important trait, direct selection based on observed yield alone may be less effective unless environmental conditions are controlled or optimized. The lower heritability of grain yield suggests that direct selection based on yield alone may not be effective unless environmental factors such as temperature, humidity, and gene-by-environment interactions are controlled. These interactions often overshadow the genetic contributions to yield under disease-infected conditions. The mean values and genetic parameters are presented in Table 1.

High heritability coupled with high genetic advance in traits like plant height, lesion height, relative lesion height, and panicle number across both seasons suggests that these traits could be prioritized in breeding programs aimed at improving resistance to sheath blight while also potentially enhancing yield. High genetic advance in these traits implies that gains through selection are feasible, which is especially relevant for disease resistance traits. The extremely high variability observed in relative yield loss, suggests substantial environmental and genetic interaction effects on yield loss due to sheath blight, underlining the complexity of this trait. Thus, indirect selection using more stable, high-heritability traits related to sheath blight resistance, such as relative lesion height and lesion height, may prove to be a more effective approach for managing yield stability under disease pressure.

Table 1. Mean, variability, heritability and genetic advance as per cent of mean for yield and sheath blight disease traits in 360 RILs developed from ISM/Phougak

S. No.	Character	Mean	GCV%	PCV%	ECV%	Heritability (Broad Sense)	Genetic Advance as % of Mean at 5% level
1	DFFd	121.54	5.64	5.64	0.00	100.00	11.64
2	LHd	55.41	17.99	19.36	7.13	86.43	34.51
3	PHd	86.75	17.68	18.36	4.95	92.74	35.13
4	RLHd	72.51	20.20	21.23	6.52	90.57	39.67
5	SESd	8.18	9.69	12.98	8.64	55.71	14.92
6	TNd	13.18	19.02	22.81	12.60	69.49	32.70
7	PNd	11.63	21.98	23.23	7.52	89.52	42.90
8	PLd	20.50	11.94	12.70	4.32	88.41	23.16
9	Gyd	16.37	16.21	33.39	29.19	23.58	16.24
10	DFFw	97.41	6.78	6.78	0.00	100.00	13.98
11	LHw	62.94	15.75	16.96	6.28	86.31	30.19
12	PHw	146.73	15.37	15.65	2.93	96.50	31.15
13	RLHw	49.03	22.27	24.27	9.64	84.21	42.16
14	SESw	6.25	19.75	22.76	11.31	75.29	35.35
15	TNw	9.64	18.79	22.84	12.97	67.72	31.90
16	PNw	8.60	15.31	21.15	14.59	52.39	22.86
17	PLw	22.42	13.56	13.76	2.38	97.01	27.54
18	Gyuw	10.05	32.07	54.04	43.49	35.22	39.26
19	GYiw	4.59		76.22	79.80		
20	RYLw	0.26	6428.26	8602.37	5716.48	55.84	9909.87

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environment coefficient of variation, DFF-Days to 50% flowering, LH-Lesion height (cm), PH-Plant height (cm), RLH-Relative Lesion Height (%), SES-Standard Evaluation Score, TN- Tiller number, PN- Panicle number, PL- Panicle length (cm), GYu- Grain yield under un-inoculated conditions (g), GYi- Grain yield under inoculated conditions (g), RYL- Relative Yield Loss (%), d-dry season and w-wet season
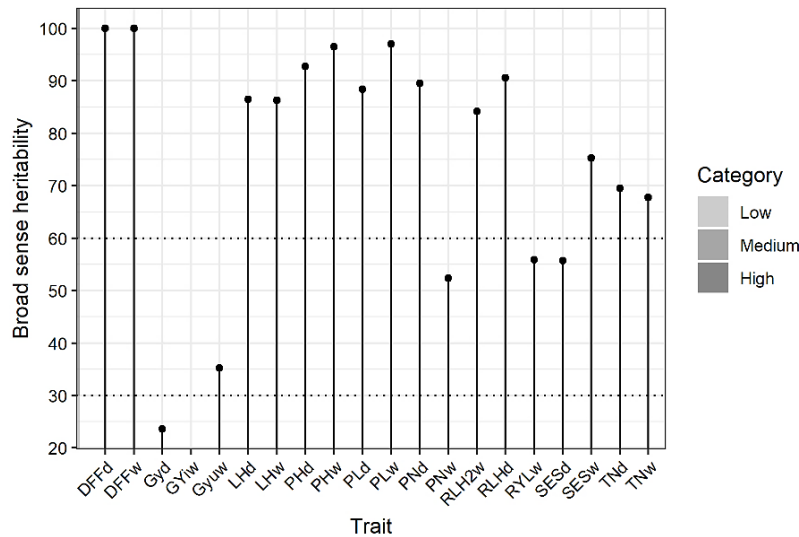
Fig. 1. Broad-sense heritability estimates of ShB disease and yield related traits in RILs
DFF-Days to 50% flowering, LH-Lesion height (cm), PH-Plant height (cm), RLH-Relative Lesion Height (%), SES-Standard Evaluation Score, TN- Tiller number, PN- Panicle number, PL- Panicle length (cm), GYu- Grain yield under un-inoculated conditions (g), GYi- Grain yield under inoculated conditions (g), RYL-Relative Yield Loss (%), d-dry season and w-wet season

4. CONCLUSION

This study underscores the potential of genetic variability as a foundation for enhancing sheath blight resistance and yield-related traits in rice. The observed high heritability and genetic advance in key traits such as lesion height, relative lesion height, plant height, and panicle number across both dry and wet seasons highlight their genetic stability and responsiveness to selection, making them prime candidates for breeding programs. Traits with moderate to low heritability, such as grain yield under inoculated conditions, suggest that yield improvement may benefit from indirect selection through associated stable traits with higher heritability. The substantial genetic advance in sheath blight-related traits, particularly lesion and relative lesion height, affirms the feasibility of improving disease resistance, which is crucial for sustaining productivity. Ultimately, this research provides a pathway for developing rice cultivars with enhanced disease resilience and stable yields, contributing to long-term sustainability in rice production systems, especially in disease-prone areas.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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