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Short Communication

Pattern of genetic variation in rice (*Oryza sativa* L.) population for sheath blight resistance over the seasons

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Abstract

A set of 192 *indica* rice accessions were evaluated in two seasons to generate information on the extent of genetic variability, broad-sense heritability and genetic advance for yield and sheath blight related traits. The estimated genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) varied over the season. Largely, PCV values were relatively higher than GCV with reference to the studied parameters. However, GCV was found to be medium for per cent disease index (PDI) of 14th day, 28th day, area under the disease progress curve (AUDPC), and tiller number over the seasons. Interestingly, grain yield was found to be high. The trait plant height and panicle length had moderate heritability coupled with moderate genetic advance, whereas AUDPC was moderately heritable coupled with high genetic advance. The findings may be useful in breeding improved rice genotypes.

Key words: Rice, sheath blight, GCV, PCV, heritability, genetic advance

Sheath blight disease caused by *Rhizoctonia solani* is an important disease next to blast and responsible for yield loss of up to 45% (Margani and Widadi 2018). The fungus causes lesions on the sheaths above the water surface, leaves, and entire stem that lead to stem lodging. To date, breeding resistant rice genotypes for sheath blight disease are unsuccessful due to the inability to identify the resistant sources from the available germplasm (Yadav et al. 2015). However, the rice germplasm has a high pool of useful genes that rice breeders can exploit for yield improvement programs. Therefore, gaining knowledge of the genetic variability of the trait is required to build an efficient breeding program. The genetic variability studies of sheath blight disease in rice was not reported earlier. Therefore, the present study was undertaken to estimate the genetic variability, broad-sense heritability and genetic advance for sheath blight disease and yield-related traits in diverse germplasm and strategies to have a credible breeding program to enhance the sheath blight resistance in rice.

The experimental material comprised of 192 diverse rice genotypes sown during the dry and wet seasons of 2019 at ICAR-NRRI, Cuttack, Odisha and evaluated for genetic variability, heritability and expected genetic advance of sheath blight disease related and other morphological traits. The materials were laid out in a 175 m^2 area with a RBD in three replicates with sheath blight resistant (Tetep, Jasmine 85 and Teqing) and susceptible (Pusa Basmati-1 and Tapaswini) checks. Agronomic traits such as plant height (cm), tiller numbers per plant, panicle length (cm), and grain yield/plant were recorded during the physiological maturity stage. At the time of the booting stage (six weeks after transplanting) of the crop, immature sclerotia of the *R. solani* (AG1-IA) (Gene bank accession no: MK478903) was inoculated in the plants. The disease scoring was performed using the 0-9 scale of the standard evaluation system (SES) given by IRRI (2013) and disease severity was recorded at seven days' interval from 7th day to 28th day of post

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inoculation (Goswami et al. 2019). During the dry season, 2019 disease severity was recorded up to the 21st day. The relative lesion height (RLH), percent disease index (PDI), and area under the disease progress curve (AUDPC) were calculated. Statistical analysis was performed for the pooled over the season data. Analysis of variance (ANOVA), phenotypic and genotypic variances, genotypic, phenotypic, and environmental coefficients of variation, broad-sense heritability (H^2), and genetic advance were calculated using Windostat computer software version 7.5.

Genetic parameters and sheath blight resistance

Understanding the genetic variation of the genotypes is crucial for a successful breeding program and the magnitude of variability imparts the foundation for selection. The result of analysis of variance showed significant variation was observed for G x S interaction and all the parameters among the genotypes (G) and seasons (S) for all the traits studied except grain yield (Table 2). This result has confirmed the existence of a considerable amount of variability among the accessions and seasons for the studied morphological and sheath blight disease related traits. The phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) of the nine traits pooled over the seasons is presented in Table 2. GCV ranged from 3.79% (PDI of 7th day) to 23.99% (grain yield), while PCV differed from 11.30% (panicle length) to 44.86% (grain yield). Among the variation analyses, the relative magnitude of differences of PCV was higher than GCV for all the studied traits indicating that wide variation is not only due to the genotype but might be due to the impact of the season and their interactions with the genotype as also reported by Singh et al. (2015).

The broad-sense heritability is the relative magnitude of both phenotypic and genotypic variations for the parameters studied and it plays a major role in the selection procedure (Bisen et al. 2019). The estimated heritability ranged from 4.42 % (PDI of 7th

Table 1. Analysis of variance (ANOVA) for various traits of rice genotypes over the seasons (Dry and wet season 2019)

Source of Variation	DF	7th day PDI	14th day PDI	21st Day PDI	28th day PDI#	Mean PDI	AUDPC	Plant height	Panicle length	No of tillers/ plant	Grain yield/ plant
Genotypes (G)	191	13.93**	115.86**	175.24**	374.27**	86.88**	72856.70**	1073.52**	34.55**	26.77**	99.21**
Season (S)	1	65.55**	1619.88**	3027.88**	783.78*	892.89**	14507545.25**	2679.89**	193.60**	95.89*	132.73*
G x S	191	14.19**	85.40**	124.60**	-	66.00**	61918.95**	723.21**	22.66**	14.54*	19.85ns
Error	384	9.61	53.30	67.76	135.45	32.03	24346.61	224.81	7.14	11.33	34.15

*** significant at 0.001%, ** significant at 0.01%, * significant at 0.05%, ns non significance, # measured during dry season

Table 2. Range, genetic variability, heritability, and genetic advance for agronomic and sheath blight related traits of 192 rice genotypes

S.No.	Parameter	Mean	Range		GCV	ECV	PCV	H^2	GA
			Min	Min					
1	7th day PDI	12.09	9.44	20.79	3.79	17.63	18.03	4.42	0.20
2	14th day PDI	20.93	11.11	35.56	13.70	24.61	28.16	23.67	2.80
3	21st Day PDI	31.51	11.11	50.00	9.77	18.83	21.22	21.20	2.85
4	28th day PDI#	40.19	11.11	77.78	15.33	25.00	29.32	27.33	6.64
5	Mean PDI	26.18	11.11	39.51	9.15	17.89	20.09	20.73	2.00
6	AUDPC	775.87	350.00	1202.64	13.39	20.37	24.38	30.18	85.96
7	Plant Height	110.18	68.87	148.18	7.69	9.68	12.37	38.70	10.82
8	Panicle Length	21.57	15.22	29.12	7.25	8.67	11.30	41.14	2.09
9	No. of tillers/plant	10.68	4.50	20.33	11.91	22.54	25.49	21.82	1.20
10	Grain yield/plant	10.55	1.98	19.27	23.99	37.90	44.86	28.61	2.91

measured during dry season

day) to 41.14 % (panicle length) which is in agreement with the earlier reports of Loitongbam et al. (2019) and Bisen et al. (2019). The expected genetic advance varied among the parameters from 0.20% (PDI of 7th day) to 85.96% (AUDPC) over the seasons.

Plant height is the major trait that influences the grain yield of rice and is expected to have a role in sheath blight tolerance. In present study, plant height ranged from 68.87 cm to 148.18 cm with the mean of 110.18 cm. The estimated GCV and PCV were low and moderate, respectively indicating that variation was influenced by the environment. The moderate heritability coupled with moderate genetic advance was observed indicating the possibility of further improvements through direct selection as also proposed by Rathod et al. (2020). Similarly, panicle length exhibited low and moderate GCV and PCV respectively with moderate and low heritability and the genetic advance. The grain yield/plant ranged from 1.98 gm to 19.27 gm with a mean of 10.55 gm. The estimates of GCV and PCV of the trait grain yield were found to be high, wherein the heritability and the genetic advance were low. This showed that the environment affects the selection of phenotypic expressions of this trait (Bisen et al. 2019).

The development of rice cultivars resistant to sheath blight needs knowledge of genetic variability on the concerned trait for the selection of reliable rice genotypes. In the present study, among the various sheath blight-related traits (PDI of 7th day, 14th day, 21st day, 28th day, Mean PDI, and AUDPC), the low to moderate magnitude of GCV and moderate to high PCV was noticed. The estimated heritability and genetic advance were found to have low heritability (20 to 27%) coupled with the genetic advance except for the trait AUDPC (30%) indicated that the environment has a significant effect on the establishment and tolerance against sheath blight disease in rice. Hence, direct selection of sheath blight-related traits could be least effective. To our knowledge, this might be the first report for variability studies on sheath blight resistance in rice and could help breeders for the selection of tolerant lines in the breeding program.

Author's contribution

Conceptualization of research (AA, NR); Designing of experiments (NR, AA); Contribution of experimental materials (AA, VS, PK); Execution of field experiments and data collection (NR, AA); Analysis of data and interpretation (NR, AA); Preparation of the manuscript (NR, AA, VS).

Declaration

The authors declare no conflict of interest.

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