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Genetic variability in recombinant inbred population for yield-related traits in rice (*Oryza sativa* (L.)

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Abstract
The present study was carried out at Agricultural College and Research Institute, Madurai, under nitrogen-starved conditions. The experimental material comprised 245 recombinant inbred populations (RILs) of ASD 16 X Basmati 370 cross, which were laid out in randomized complete block design with two replications. Observations were recorded for eighteen quantitative characters, and the data were analyzed for biometric characters *viz*., phenotypic coefficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability (h^2), and genetic advance as percent of the mean (GAM). High GCV and PCV were observed for straw nitrogen uptake, total nitrogen uptake, grain nitrogen uptake, grain yield per plant, dry matter production, and grains per panicle, indicating the presence of high genetic variability among the rice genotypes of the RIL population. High heritability coupled with genetic advance as a percent of mean was observed for all the characters except nitrogen translocation efficiency, straw nitrogen content, 100-grain weight, and grain nitrogen content; it could be due to the presence of additive gene action and the selection for these traits effective. Hence the present study concluded that there was adequate genetic diversity present in the RIL population for most of the characters.

Keywords: Rice, recombinant inbred line, heritability, PCV, GCV, genetic advance

Introduction

Rice serves as a primary staple food for over half of the world's population and plays an important role as a cereal crop in ensuring global food security. Hence, enhancing food production is essential to meet the needs of the ever-growing population and ascertain food security for the future. Genetic variability serves as the fundamental asset for plant breeders seeding to enhance plant performance. The variability within a population arises from genetic diversity, environmental influences, and interaction between the genotype and environment.

The ideal generation for imposing selection is one that exhibits significant levels of segregation and recombination. there must be the existence of genetic variability in the population for effective selection of better progenies from segregating generations for further selection. The success of any crop improvement programme relies upon the nature and magnitude of genetic variability in the population. The level of genetic variability within the plant population determines the efficiency of the selection process. Due to the polygenic nature of yield and yield-related traits, the knowledge of the variation of characters is key for the breeders to identify desirable genotypes from the mixed population. Hence, the present study was conducted to assess the variability of yield and yield component traits to identify superior lines in the recombinant inbred population of ASD 16 X Basmati 370 cross.

Materials and methods

The present investigation was conducted at Agricultural College and Research Institute, Madurai, under nitrogen-starved conditions with 245 recombinant inbred lines of ASD 16 X Basmati 370 cross. The experiment was laid out in a randomized block design with two replications. The observations were recorded from five randomly selected plants in each genotype for eighteen characters *viz*., days to 50 % flowering, plant height, pollen fertility, tillers per plant, productive tillers per plant, panicle length, grains per panicle, spikelet fertility, 100 grain weight, dry matter production, grain yield per plant, straw nitrogen content, grain nitrogen content, grain nitrogen uptake, straw nitrogen uptake, total nitrogen uptake, nitrogen use efficiency and nitrogen translocation efficiency. The data were subjected to analysis of variance according to the method recommended by Panse and Sukhatme (1985) [20]. Phenotypic and genotypic co-efficient of variation were computed according to the method suggested by Burton (1952) [4]. Heritability on broad sense was calculated as per formula given by Allard (1960) [2]. Genetic advance was expressed by using the formula suggested by Johnson *et al.* (1955) [12].

Result and discussion

The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability (h^2), and genetic advance as percent of the mean (GAM) were presented in Table 1. The average performance and maximum and minimum values of the characters studied indicated the presence of sufficient genetic variation among the rice genotypes of the RIL population, and these genotypes could be used for genetic mapping and as donors for further breeding programs.

The higher GCV and PCV values and minimum variation between them were observed for straw nitrogen uptake (43.97% and 44.17%) followed by total nitrogen uptake (39.75% and 39.83%), grain nitrogen uptake (35.85% and 53.91%), grain yield per plant (34.17% and 34.35%), dry matter production (34.07% and 34.09%) and grains per panicle (29.26% and 29.63%) indicating lesser influence of environment resulting in high heritability values. Similar findings were reported by Nayak *et al.* (2002) [17], Habib (2005) [10], Deepa Sankar *et al.* (2006) [6] and Faysal *et al.* (2022) [9]. The observations are in agreement with the inferences of Williams *et al.* (2021) [29] for the number of productive tillers per plant and grain yield per plant,) Nikhitha *et al.* (2020) [19], Fatima *et al.* (2021), Bhargava *et al.* (2021) [3] and Singh *et al.* (2021) [27] reported for plant height, number of productive tillers per plant, and number of grains per panicle while Lakshmi *et al.*(2021) [14] and Mounika *et al.*(2022) [16] reported for the trait number of grains per panicle and Harshita *et al.* (2024) and Prashanth *et al.* (2024) for number of tillers per plant, number of productive tillers per plant and grain yield per plant.

Moderate PCV and GCV were recorded for plant height (15.05% and 15.06%), spikelet fertility (14.82% and 14.83%), tillers per plant (12.61% and 13.09%), tillers per plant (12.61% and 13.09%), panicle length (11.67% and 11.79%), productive tillers per plant (11.44% and 13.06%), pollen fertility (11.36% and 11.36%) and nitrogen use efficiency (10.15% and 10.20%). The low PCV and GCV were observed for the grain nitrogen content (6.53% and 8.93%). The results were in accordance with Nayak *et al.* (2003) [18], Patil *et al.* (2003) [21], and Sarkar *et al.* (2007) [24]. Divya and Pandey (2020) [7], Sudeepthi *et al.* (2020) [28], Sadhana *et al.* (2022) [23] for grain yield per plant, and Manjunatha and Kumara (2019) [15] for the number of grains per panicle. The moderate and low values of PCV and GCV, restrict the scope for the selection of genotypes based on these characters.

The rice genotypes under study showed high heritability for all the characters except grain nitrogen content and grain nitrogen uptake. The highest heritability was recorded for plant height (99.93%) followed by pollen fertility (99.86%), spikelet fertility (99.86%), dry matter production (99.84%), total nitrogen uptake (99.58%), nitrogen translocation efficiency (99.20%), straw nitrogen uptake (99.09 and grain yield per plant (99.01%). Heritability estimates were more than 60% for these characters which indicates that these characters were less influenced by environmental conditions and phenotypic selection would be effective for these characters.

It is a difference between the mean genotypic value of selected lines and the mean genotypic value of the population before selection. The highest value of genetic advance was recorded for all the traits except nitrogen translocation efficiency, straw nitrogen content, 100-grain weight, and grain nitrogen content. Heritability and genetic advance are important selection parameters. The heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection (Johnson *et al.*, 1955) [12]. High heritability and high genetic advance were recorded for all the characters except nitrogen translocation efficiency, straw nitrogen content, 100-grain weight, and grain nitrogen content. Hence, direct selection for the improvement of these traits can be achieved and early generation selection may be effective in improving these traits due to the presence of additive gene action. Similar results of high heritability and high genetic advance were obtained by Nayak *et al.* (2002) [17], Chaudhary and Motiramani, (2003) [5], Deepa Sankar *et al.* (2006) [6], Akinwale *et al.* (2011) [1], Kavyashree *et al.* (2022) [13], Fatima *et al.* (2021), Bhargava *et al.* (2021) [3] and Sheena and Lavanya (2023) for plant height, number of productive tillers per plant, number of grains per panicle and grain yield per plant. Nikhitha *et al.* (2020) [19] and Singh *et al.* (2021) [27] reported for plant height. Lakshmi *et al.* (2021) [14] for spikelet fertility and grains per panicle, Shankar *et al.* (2016) [25] reported for grain yield per plant.

Conclusion

Higher values of PCV and GCV for the characters straw nitrogen uptake followed by total nitrogen uptake, grain nitrogen uptake, grain yield per plant, dry matter production, and grains per panicle indicate higher variability among these characters. The estimates of high heritability and high genetic advance were observed for all the characters except nitrogen translocation efficiency, straw nitrogen content, 100 grain weight, and grain nitrogen content, indicating the effectiveness of direct selection for the improvement of these traits. Hence the present study helpful for the breeders to utilize these genotypes for mapping experiments and donors for further breeding programme.

Table 1: Variability parameters for yield and other component traits in the rice RIL population

Character	Mean	Range	GCV (%)	PCV (%)	Heritability	GAM
Days to 50% flowering	81.32	72.76-87.31	3.62	3.66	97.98	7.4
Plant height	107.94	73.23-148.36	15.05	15.06	99.93	31.00
Pollen fertility	89.31	22.48-99.68	11.36	11.36	99.86	23.38
Tillers per plant	11.50	6.97-17.04	12.61	13.09	92.84	25.04
Productive tillers per plant	6.87	4.96-10.85	11.44	13.06	76.83	20.67
Panicle length	23.64	15.04-32.85	11.67	11.79	97.96	23.79
Grains per panicle	123.78	34.00-254.00	29.26	29.63	97.54	59.54
Spikelet fertility	78.53	26.57-98.00	14.82	14.83	99.86	30.51
100 grain weight	2.34	1.88-3.05	7.31	7.55	93.84	14.60
Drymatter production	28.87	9.74-77.13	34.07	34.09	99.84	70.13
Grain yield per plant	12.04	3.6-29.48	34.17	34.35	99.01	70.06
Straw nitrogen content	1.00	0.82-1.27	7.77	7.92	96.16	15.70
Grain nitrogen content	1.16	1.04-1.29	4.66	6.10	58.28	7.33
Grain nitrogen uptake	0.14	0.04-0.37	35.85	53.91	44.23	49.12
Straw nitrogen uptake	0.17	0.05-0.61	43.97	44.17	99.09	90.17
Total nitrogen uptake	0.31	0.09-0.97	39.75	39.83	99.58	81.72
Nitrogen use efficiency	39.33	29.61-49.96	10.15	10.20	98.95	20.80
Nitrogen translocation efficiency	45.51	33.97-54.91	9.45	9.49	99.20	19.39

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