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Variability and association analysis for yield and yield contributing traits in early segregating backcross population in Rice (*Oryza sativa* L.)

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Abstract

Rice production was hampered by increased prevalence of abiotic stresses due to ever changing climates. Drought being major abiotic stress, negatively impacts yield mainly during reproductive stage. Determining the major contributing traits, their association with yield as well as inter-relationship between the traits will be helpful in selecting best progenies. In the present study early segregating backcrossed population (BC₂F₂) of ADT(R) 45/Way Rarem was evaluated to assess the genetic variability parameters, trait association and direct and indirect effects among yield and yield components. The results revealed that high estimates of PCV, GCV, broad sense heritability coupled with high genetic advance for three traits *viz.*, single plant yield, number of productive tillers per plant and total number of tillers per plant, which infers prevalence of additive gene action and these three traits majorly contributed for variation in the population. Correlation analysis showed single plant yield had highly significant positive association with number of productive tillers per plant, total number of tillers per plant, spikelet fertility and hundred grain weight. Path coefficient analysis revealed that number of productive tillers per plant exhibit high positive direct effect on single plant yield followed by hundred grain weight. Based on correlation, direct and indirect effects of correlation coefficients, selection for four traits *viz.*, number of productive tillers per plant, total number of tillers per plant, spikelet fertility and hundred grain weight would be rewarding.

Keywords: Rice, segregating backcross population, Genetic variability, Heritability, Correlation and Path coefficient

1. Introduction

Rice is the primary source of nutrition for about 3 billion people in the world. By 2050, it is predicted that 160 million tons of rice needed to feed ever increasing Indian population (Muthu *et al.*, 2020) [1]. Due to climate change, abiotic stresses became serious hinderance in rice production areas. Drought being major abiotic stress, is anticipated to have a greater influence on rice productivity due to global warming scenarios and declining water supply. While all phases of the rice crop are impacted by drought, the reproductive stage is particularly sensitive and has a significant impact on yield (Priyadharsini *et al.* 2018). Development of varieties with inherent tolerance will be the best strategy to ensure rice production under reproductive stage drought. Due to the slow progress made in creating superior rice cultivars that are drought tolerant through conventional breeding, contemporary methods like marker assisted breeding can be very helpful.

Marker assisted backcross breeding using high yielding varieties and well-defined QTLs will allow combining of high yield and stress tolerance. To develop ideal plant type of rice, knowledge of genetic variability, gene action, and heritability of yield-contributing characteristics is a prerequisite (Nithya *et al.* 2020) [7]. In addition to the biometrical traits, estimating the genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), heritability and genetic advance for morphological traits would be critical in rice breeding programmes. The heritability estimations would be rewarding and useful to the plant breeder in selecting which traits to consider for selection and is to provide information on transmission of traits from one generation to the next. Correlation analysis assists in figuring out whether a trait's association to yield is positive or negative so that it can be considered while breeding towards the ideal plant type. Path analysis combined with correlation would provide a clearer understanding of the cause and effect between different morphological traits.

Hence, assessing correlation and path analysis will help in the identification of appropriate selection criteria for enhancing yield. Considering the above points, the current research was conducted to evaluate genetic variability, heritability, and genetic advances among yield and yield-contributing characteristics in rice. This study offers knowledge that can help future breeding programmes to develop desirable rice genotypes and traits to target to achieve yield enhancement.

2. Materials and Methods

ADT(R) 45, a short duration popular rice cultivar of Tamil Nadu as well as south Indian states was selected as recipient parent which was drought susceptible in nature. Way rarem an Indonesian upland rice cultivar was utilized as drought tolerant donor parent which possess mega drought yield QTL *qDTY12.1*. The QTL was flanked between microsatellite markers RM28048 and RM511 on chromosome 12, increases 38.8% to 47% mean yield under drought. ADT(R) 45 hybridized with Way rarem at Tamil Nadu Rice Research Institute, Aduthurai during *Kharij*, 2019. The resulted F₁s were genotyped with RM511 peak marker for the drought yield QTL *qDTY12.1*. The identified true F₁s were back crossed with recurrent parent ADT(R) 45 and resulted BC₁F₁s were genotyped with RM511. The cycle is repeated for one more season and true BC₂F₁s were identified. The BC₂F₁ was selfed to produce segregating early back cross population BC₂F₂. Eight morphological traits *viz.*, days to flowering, plant height(cm), panicle length(cm), number of productive tillers per plant, total number of tillers per plant, spikelet fertility percentage, hundred grain weight(g) and single plant yield(g) were recorded for 258 number of BC₂F₂ plants. The data was analysed using progeny analysis: non replicated data and correlation and path analysis in TNAU stat. The variability parameters genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), heritability and genetic advance were calculated manually.

3. Results and Discussion

3.1. Variability parameters

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as percentage of mean were estimated for yield and yield related traits in BC₂F₂ generation as presented in Table 1. Phenotypic coefficient of variation was higher than that of genotypic coefficient of variation for all the eight traits studied. Environment plays a role in the difference between PCV and GCV. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified by as low (<10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanian and Menon (1973) [5]. PCV and GCV were found to be high in single plant yield (30.20% & 27.39%), number of productive tillers per plant (25.61% & 23.24%) and total number of tillers per plant (23.92% & 20.46%). Moderate level of PCV and GCV were observed in panicle length and hundred grain weight. While, both were found to be low in case of days to flowering (5.36% &

5.23%), plant height (9.14% & 8.80%) and spikelet fertility (6.77% & 4.52%). Similar results were reported by Manivelan *et al.* (2022) [4], Devi *et al.* (2022) [10], Srinivas *et al.* (2021) [17], Yadav and Gabriyal (2021) [19], Bhargava *et al.* (2021) [9], Sudeepthi *et al.* (2020) [18], Hema *et al.* (2019) [12], Archana *et al.* (2018) [8], Rani *et al.* (2016) [14], Haque *et al.* (2014) [24], Manjappa *et al.*, (2014) [22], Singh *et al.*, (2014), Mural *et al.*, (2012) [31], Shet *et al.*, (2012) [29], Sohrabi (2012) [28], Sravan *et al.*, (2012) [27] and Fiyaz *et al.*, (2011) [32].

Heritability is a reliable indicator of how traits are passed from parents to their offspring. Broad sense heritability is classified as low (below 30%), medium (30% to 60%) and high (above 60%) as suggested by Johnson *et al.* (1955) [6]. Heritability was found to be high for all the traits except spikelet fertility which recorded at medium level. These results were in line with earlier findings of Devi *et al.* (2022) [10], Singh *et al.* (2021), Yadav and Gabriyal (2021) [19], Prasannakumari *et al.* (2020) [13], Sudeepthi *et al.* (2020) [18], Hema *et al.* (2019) [12], Archana *et al.* (2018) [8], Kahani and Hittalmani (2015) [20], Arvind *et al.*, (2015), Mani *et al.*, (2014), Singh *et al.*, (2014), Seyoum *et al.*, (2012) [30], Shet *et al.*, (2012) [29], Sohrabi (2012) [28], Sravan *et al.*, (2012) [27] and Fiyaz *et al.*, (2011) [32]. The genetic advance serves as an effective and efficient indicator of the selection progress that may be anticipated as a result of performing selection on the base population. Genetic advance as percent of mean classified as low (<10%), moderate (10-20%) and high (>20%) as per Johnson *et al.* (1955) [6]. Based on this classification, low to high level genetic advance as percentage of mean (GAM) was manifested in the present study. Four traits *viz.*, number of productive tillers per plant (43.4%), total number of tillers per plant (36.0%), hundred grain weight (21.0%) and single plant yield (51.1%) recorded high estimates of GAM. Moderate level of GAM was recorded in days to flowering (10.5%), plant height (17.5%) and panicle length (19.0%), While, spikelet fertility percentage (6.21%) recorded as low.

GCV, heritability at broad sense and genetic advance as percent of mean were high for three traits *viz.*, number of productive tillers per plant, total number of tillers per plant and single plant yield, which indicates predominance of additive gene action for these characters. Hence, these characters could be effective indicators of rice grain yield. Similar findings were reported by Manivelan *et al.* (2022) [4], Devi *et al.* (2022) [10], Ramasamy *et al.*, (2021) [3], Srinivas *et al.* (2021) [17], Singh *et al.* (2021), Yadav and Gabriyal (2021) [19], Bhargava *et al.* (2021) [9], Prasannakumari *et al.* (2020) [13], Sudeepthi *et al.* (2020) [18], Hema *et al.* (2019) [12], Archana *et al.* (2018) [8], Rani *et al.* (2016) [14], Singh *et al.*, (2015), Sahu and Verulkar (2015) [25], Kahani and Hittalmani (2015) [21], Arvind *et al.*, (2015), Mani *et al.*, (2014), Singh *et al.*, (2014), Haque *et al.* (2014) [24], Manjappa *et al.*, (2014) [22], Sathya and Jebaraj (2013) [26], Seyoum *et al.*, (2012) [30], Shet *et al.*, (2012) [29], Sohrabi (2012) [28] and Sravan *et al.*, (2012) [27].

Table 1: Estimates of Mean, PCV, GCV, heritability (broad sense) GA and GA as percentage of Mean in BC₂F₂ population

Character	Mean	PCV (%)	GCV (%)	H ² b (%)	GA	GAM (%)
Days to flowering	88.03±0.29	5.355	5.233	95.500	9.273	10.534
Plant height	86.33±0.49	9.138	8.798	92.686	15.063	17.448
Panicle length	23.64±0.18	11.994	10.512	76.803	4.486	18.977
Number of productive tillers per plant	25.03±0.40	25.607	23.238	82.352	10.873	43.440

Total number of tillers/plants	28.33±0.42	23.922	20.455	73.111	10.207	36.029
Spikelet fertility percentage	83.17±0.35	6.770	4.517	44.517	5.163	6.208
Hundred grain weight	2.39±0.02	11.070	10.621	92.047	0.502	20.991
Single plant yield	39.48±0.74	30.202	27.385	82.215	20.195	51.152

DF- Days to flowering, PH- Plant height, PL- Panicle length, NPT- Number of productive tillers per plant, TNT- Total number of tillers per plant, SF- Spikelet fertility percentage, HGW- Hundred grain weight and SPY- Single plant yield.

3.2. Association analysis

Correlation coefficients of yield and other seven biometrical traits were tabulated in Table 2. Correlation studies revealed that single plant yield positively highly significant association with number of productive tillers per plant (0.7742**), total number of tillers per plant (0.7277**), spikelet fertility percentage (0.3513**) and hundred grain weight (0.1620**). The trait panicle length (0.1401*) exhibit positive significant correlation with yield.

The remaining traits days to flowering (0.0105) and plant height (0.0799) had positive non-significant correlation with single plant yield. Total number of tillers per plant was

positively highly significant correlation with number of productive tillers per plant (0.9795**). Spikelet fertility percentage was positively highly significant correlation with number of productive tillers per plant (0.3579**) and total number of tillers per plant (0.3473**). Similar results were obtained by Manivelan *et al.* (2022)^[4], Devi *et al.* (2022)^[10], Ramasamy *et al.*, (2021)^[3], Srinivas *et al.* (2021)^[17], Singh *et al.* (2021), Yadav and Gabriyal (2021)^[19], Bhargava *et al.* (2021)^[9], Prasannakumari *et al.* (2020)^[13], Sudeepthi *et al.* (2020)^[18], Archana *et al.* (2018)^[8], Hema *et al.* (2019)^[12] and Rani *et al.* (2016)^[14].

Table 2: Correlation coefficients of yield and other yield contributing traits

Character	DF	PH	PL	NPT	TNT	SF	HGW	SPY
DF	1.0000							
PH	-0.0793	1.0000						
PL	-0.0234	-0.0250	1.0000					
NPT	0.0016	0.1168	0.0640	1.0000				
TNT	0.0134	0.0989	0.0752	0.9795**	1.0000			
SF	-0.0581	-0.0350	0.1191	0.3579**	0.3473**	1.0000		
HGW	-0.0614	-0.0237	0.0166	-0.1048	-0.1183	0.0628	1.0000	
SPY	0.0105	0.0799	0.1401*	0.7442**	0.7277**	0.3513**	0.1620**	1.0000

DF- Days to flowering, PH- Plant height, PL- Panicle length, NPT- Number of productive tillers per plant, TNT- Total number of tillers per plant, SF- Spikelet fertility percentage, HGW- Hundred grain weight and SPY- Single plant yield.

Path coefficient analysis enables the partition of correlation coefficients into direct and indirect effects, provides a more accurate portrayal of the character relationships, and aids in the detection of the key attributes to grain yield. By improving those key traits yield can be enhanced. Direct and indirect effects of different quantitative traits of the present study results were presented in Table 3. Path coefficient analysis of yield and its component traits showed that number of productive tillers per plant (0.7073) had the highest positive direct effect on single plant yield followed by hundred grain weight (0.2367). Indirect effect of total number of tillers per plant (0.6929) through number of productive tillers per plant to single plant yield was high and positive. Spikelet fertility percentage (0.2531) exhibit moderate and positive indirect effect through number of productive tillers per plant to single plant yield. Similar results were reported

by Manivelan *et al.* (2022)^[4], Devi *et al.* (2022)^[10], Ramasamy *et al.*, (2021)^[3], Srinivas *et al.* (2021)^[17], Singh *et al.* (2021), Yadav and Gabriyal (2021)^[19], Bhargava *et al.* (2021)^[9], Prasannakumari *et al.* (2020)^[13], Sudeepthi *et al.* (2020)^[18], Archana *et al.* (2018)^[8], Hema *et al.* (2019)^[12] and Rani *et al.* (2016)^[14].

4. Conclusion

Path coefficient analysis results were in line with correlation and inter trait association results. From combing path and correlation analysis results, we can inferred that total number of tillers per plant, number of productive tillers per plant and spikelet fertility percentage contributed more to the yield in the given environment. Therefore, these three traits should be given more importance in selection for enhancing grain yield.

Table 3: Direct (diagonal) and indirect effects of different quantitative traits in BC₂F₂ generation

Character	DF	PH	PL	NPT	TNT	SF	HGW	r
DF	0.0295	-0.0005	-0.0019	0.0012	0.0004	-0.0037	-0.0145	0.0105
PH	-0.0023	0.0062	-0.0020	0.0826	0.0033	-0.0022	-0.0056	0.0799
PL	-0.0007	-0.0002	0.0816	0.0453	0.0025	0.0076	0.0039	0.1401*
NPT	0.0000	0.0007	0.0052	0.7073	0.0328	0.0229	-0.0248	0.7442**
TNT	0.0004	0.0006	0.0061	0.6929	0.0335	0.0222	-0.0280	0.7277**
SF	-0.0017	-0.0002	0.0097	0.2531	0.0116	0.0639	0.0149	0.3513**
HGW	-0.0018	-0.0001	0.0014	-0.0742	-0.0040	0.0040	0.2367	0.1620**

DF- Days to flowering, PH- Plant height, PL- Panicle length, NPT- Number of productive tillers per plant, TNT- Total number of tillers per plant, SF- Spikelet fertility percentage, HGW- Hundred grain weight and SPY- Single plant yield.

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