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Research Article

Genetic analysis of backcross derived lines of *Oryza rufipogon* in the background of Samba Mahsuri a for yield enhancing traits in rice

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Abstract

Wild species of rice *Oryza rufipogon* is a potential source of genetic variation for yield-enhancing traits. With the objective of genetic enhancement of elite rice cultivar, Samba Mahsuri, a set of 120 lines of BC₂F₁ developed from *O. rufipogon* and was evaluated for yield-enhancing traits. The study revealed, the presence of significant genetic variability and transgressive segregations for productive tillers and grain yield/plant. Characters such as productive tillers per plant (38.37 and 35.48) and yield per plant (44.76 and 44.04) exhibited high PCV and GCV estimates. All the traits except days to 50% flowering displayed high heritability coupled with high genetic advance. Grain yield per plant exhibited a positive correlation with plant height (0.08), productive tillers per plant (0.05) and panicle length (0.20) these traits should be given due importance while practising selection. The identified transgressive segregants from this pre breeding study serve as valuable genetic resources for improvement of rice for yield and its attributing traits.

Key Words

Rice, backcross, yield, genetic variability, heritability, *O. rufipogon*, Samba Mahsuri

INTRODUCTION

Rice is a principal food crop of the world cultivated in all the continents, except Antarctica. It is a major player in the food and nutritional security. It provides 60-70% of caloric intake for more than 2 billion peoples of Asia and Africa. (Tripathi *et al.* 2020, Basavaraj 2020). Hence, rice crop is on the forefront in the fight against food insecurity and poverty. It is also a mark of social uniqueness and global unity. Hence, it is aptly called "Rice is Life" (Tejaswini *et al.* 2018). Increasing population growth combined with the effect of climate change threatening global food security leading to increase in the demand for rice at an alarming state. Thus, to meet the future needs of rice in food security, there is urgency in breeding new varieties which can break the barrier of yield plateau. In general the modern-day bred varieties are having a narrow genetic base and current practice of crossing

Elite x Elite further reduced genetic base. The genetic variation has wiped out during the process of domestication and selection but the valuable allele for yield enhancing traits is preserved in the form of wild relatives and landraces etc. This virtually hidden genetic variability in the wild *Oryza* can be utilized to improve the yield of cultivated rice varieties.

It is evident from the molecular mapping studies, two yield QTLs, *yld1.1* and *yld2.1*, were mapped from *O. rufipogon* each of these QTLs could able to increase the yield by 17% and 18% respectively (Xiao *et al.* 1996, 1998). This paved the way identification and introgression of several yield-enhancing QTLs (Xiao *et al.* 1996; 1998, Moncada *et al.* 2001; Brondani *et al.* 2002; Marri *et al.* 2005).

Samba Mahsuri (BPT-5204) a popular mega variety of rice, widely grown in the southern part of India having medium slender grain with excellent cooking quality. However yield levels of Samba Mahsuri reached a plateau. To break this yield plateau utilization of wild rice species through pre breeding is an advocated approach. Hence the present study aimed to develop an advance backcross population from *O. rufipogon* (Acc. TRP 3) in the background of popular cultivar Samba Mahsuri and evaluation of these population for yield-enhancing traits. These pre breeding materials serves as valuable sources of further yield improvement in rice.

MATERIALS AND METHOD

The population BC₂F₁ was developed by following advanced backcross strategy (Tanksley and Nelson, 1996) by crossing Samba Mahsuri as a female with *O. rufipogon* (Acc. TR63) as male.

The experiment was carried out at ICAR-Indian Institute of Rice Research, Hyderabad. The BC₂F₁ population consisting of 120 lines was evaluated in an augmented block design during the *Kharif* 2018 along with 4 checks namely Samba Mahsuri, RNR15048, IR64 and Swarna. The experimental materials were grown in two rows of 5.0 m length in an augmented block design with the spacing of 20 x 15 cm following standard agronomic practices to raise a good crop in good condition. Observations were recorded on randomly selected uniform five plants in each line for six quantitative traits viz., days to 50% flowering (DFF), plant height (PH), Number of tillers per plant (NT), productive tillers/plant (PT), panicle length (PL) (cm) and grain yield per plant (YPP) (g).

The averages were computed and utilised for further analysis of Analysis of Variance(ANOVA) using R v.4.0.0 software using a method of Panse and Sukhatme (1985). PCV and GCV were calculated following the method suggested by Burton and Dewane (1953). The heritability was estimated according to the method of Falconer (1981) and the genetic advance was computed

following the formula suggested by Johnson *et al.* (1955). Correlation coefficients and principal component analysis were estimated using Past (v4.0).

RESULTS AND DISCUSSION

Rice is a major staple food for more than half of the world's population. Decreasing cultivated land simultaneous with increasing food demand has forced harvesting more yields per unit area (Mueller *et al.* 2012). Enhancing the crop yield is a major focused area of the plant breeding programme. The narrow genetic base of present-day cultivars raised serious concern about genetic uniformity which may lead to yield plateau and become susceptible to many of the diseases and pests. Landraces and wild species are an important component of gene pool used in the broadening the genetic base of cultivated crops(Harlan, 1976; Hawkes, 1977). Molecular mapping studies demonstrated that phenotypically inferior wild relatives canable to contribute genes/QTL for yield-enhancing traits (Xiao *et al.* 1996; Tanksley and McCouch, 1997).

The Analysis Variance (ANOVA) revealed that the mean sum of square due to genotypes were significant for all the characters studied (**Table 1**), designating the existence of substantial genetic variability among the backcross derived lines. The achievement of any plant breeding programme relies on the extent of genetic variability and amount of heritability of the trait under consideration. Results of the genetic parameters in the present study are discussed below (**Table 2, Fig1a, 1b**)

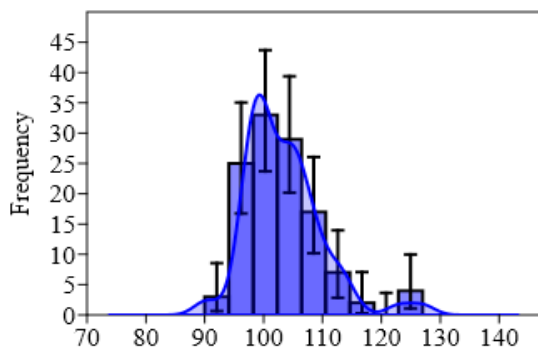
Days to 50 per cent flowering recorded an average of 103.5 days ranging from 90 (BL73 and BL74) to 127 (BL-50 and BL102) days. PCV (4.94) and GCV (4.73) estimates were low. High heritability (92.73) coupled with moderate genetic advance (12.03) was recorded for the trait DFF. High heritability attributed to positive environmental effect, signifying that trait is under non-additive gene action, selection for this character in a later generation might be useful. Comparable results were recorded by Marri *et al.* (2005) and Balakrishnan *et al.* (2016).

Table 1. Analysis of variance for yield and yield attributing traits in backcross derived lines

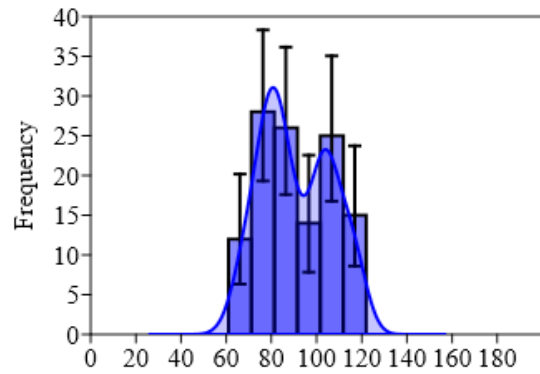
Source of variation	d.f	Mean sum of squares					
		DFF	PH	NT	PT	PL	YPP
Blocks (Eliminating check+Gen.)	3	0.56	0.01	0.01	0.01	0.022	0.02
Entries (Ignoring blocks)	123	72.17**	248.87**	31.36**	31.07**	6.37**	38.50**
Checks	3	221.63**	550.33***	3.66***	3.67***	7.15***	19.67**
Genotypes	119	42.38**	236.34**	30.25**	29.94**	6.00**	34.40**
Checks vs. Genotypes	1	3171.17**	835.76**	246.07**	249.03**	48.12**	584.05**
Error	9	1.22	0.01	0.02	0.01	0.01	0.02

**significant @ 1%

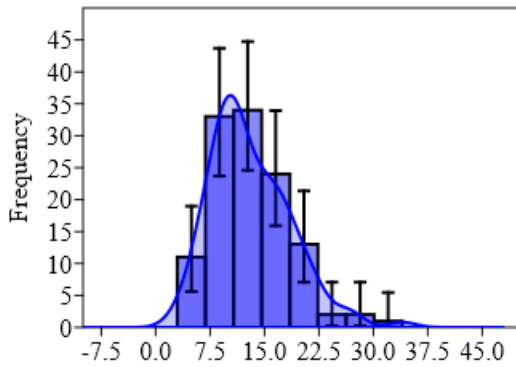
Note: DFF-Days to 50% flowering, PH-Plant height (cm), NT-Number of tillers/plant, PT-Productive tillers per plant, PL-Panicle length (cm), YPP-Yield per plant (g)



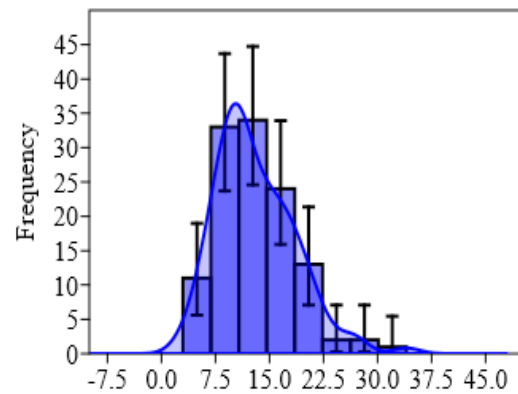
DFF



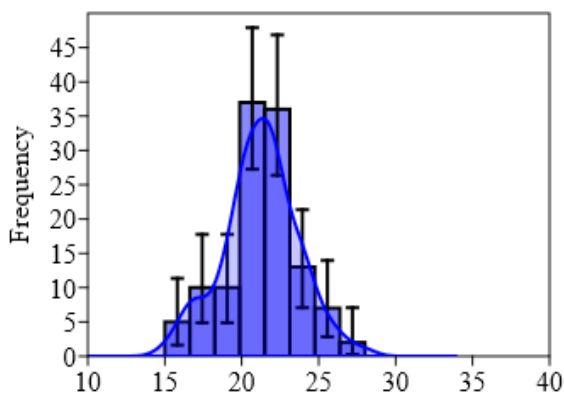
PH



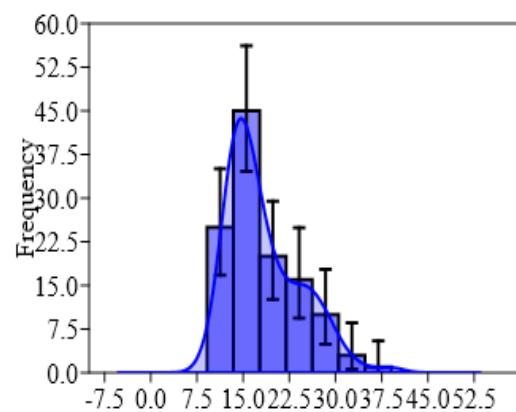
NT



NP



PL



YPP

Fig. 1a. Frequency distribution for yield traits in Samba mahsuri/ *O. rufipogon* Backcross derived lines (DFF- days to 50% flowering, PH- Plant height, NT-Number of Tillers, NP-Productive tillers per plant, PL-Panicle length, YPP-Grain Yield Per plant)

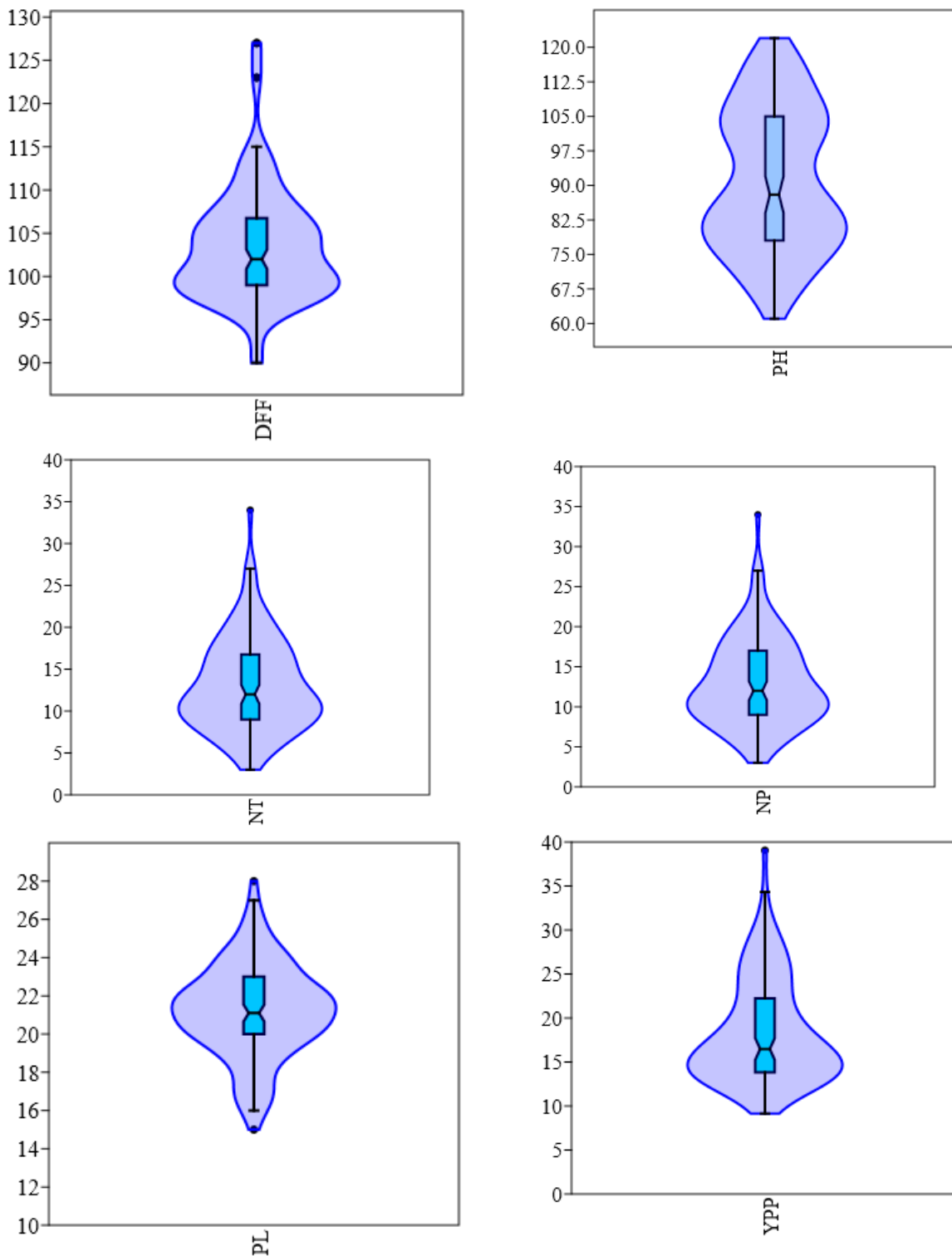


Fig. 1b. Violin and Box Plots depicting genetic variability for yield traits in Samba mahsuri/ *O. rufipogon* backcross derived lines. (DFF-days to 50% flowering, PH- Plant height, NT-Number of Tillers, NP-Productive tillers per plant, PL-Panicle length, YPP-Grain Yield Per plant)

Table 2. Estimates of genetic variability parameters in backcross derived lines of rice for yield enhancing traits

Sl. No.	Characters	Mean	Range		Coefficient of Variation (%)		Heritability (h^2_{bs} %)	Gen. Adv as per cent of Mean (at 5%)	SD	CV
			Min	Max	Phenotypic	Genotypic				
1	Days to 50% Flowering	103.5	90.0	127.0	4.94	4.73	92.73	12.03	6.51	6.29
2	Plant height (cm)	91.06	61.0	122.5	13.75	13.69	95.8	34.50	15.37	16.88
3	No. of tillers/ plant	13.08	4.0	34.0	38.37	35.48	85.4	67.58	5.5	42.02
4	No. of productive tillers/ plant	13.05	3.0	32.0	38.37	35.48	85.4	67.58	5.47	42.10
5	Panicle length(cm)	21.32	15.0	28.0	12.45	12.35	98.5	32.56	2.4	11.5
6	Grain yield/ plant (g)	19.32	9.15	39.06	44.76	44.04	96.81	89.27	5.87	32.2

Plant height is an important component character contributing to the grain yield (Piao *et al.* 2014). Most of the dwarf rice varieties are high yielding, non-lodging and harbour the *sd1* semi-dwarfing gene from Dee-geo-woogen (Poehlman and John, 1987). In the present study, plant height varied from 61 cm (BL6) to 122 cm (BL100) with an average height of lines was 91.6 cm. moderate estimates of PCV (13.75) and GCV (13.69) registered for the trait. High heritability combination with high genetic advance as was noted for the trait, suggesting trait is under the control of additive gene action. Simple selection practice would bring further improvement. The present results were in line with results of Marri *et al.* (2005) and Balakrishnan *et al.* (2016).

Rice tillering is a crucial stage for panicle formation, which in turn contribute to grain yield (Eixarch *et al.* 2015). The number of productive tillers is highly related to biomass and grain yield (Tanaka *et al.*, 1966). In the present investigation, the average number of tillers per plant were 13.8. Minimum tillers were 4 (BL62) and maximum tillers per plant were 34 (BL14). PCV (38.3) and GCV (35.48) values were high indicating that there is a wider range of variability existing for this character. High heritability (85.4) combined with high genetic advance (67.58) were also recorded, suggesting improvement through direct selection would be rewarding which is in line with conclusions of Abebe *et al.* (2017), Edukondalu *et al.* (2017).

Productive tillers ranged from 3 to 34 with an average number of productive tillers was 13.05. High PVC and GCV values were observed for the traits indicating the presence of high genetic variation for this trait. High heritability, high genetic advance together suggesting, trait could be further improved by simple selection, present results are similar to results of Abebe *et al.* (2017), Edukondalu *et al.* (2017) and Shaikh *et al.* (2017).

Panicle length is a key character for refining panicle architecture and grain yield in rice (Liu and Hong, 2016). The panicle length is a key indicator of rice yield. With respect to the panicle length, the longest panicle was of line BL62 (28 cm) while the shortest one was of BL102 (15 cm). The PCV and GCV for this trait were moderate 12.45 and 12.35 respectively, indicating the presence of a moderate range of genetic variability. The heritability (98.50 %) and genetic advance (32.56) were high for this trait, which indicated that the selection for improvement would be rewarding.

Grain yield is a complex quantitative trait governed by multiple genes. Breeding for high-grain yield is critical for ensuring food security of the ever-growing population, thus making it as necessary for any crop improvement programme. In the present study, the values for grain yield per plant ranged from 9.15 g (BL33) to 39.06g (BL62) with an average yield of 19.32 g. High GCV (44.04 %) and PCV (44.76 %) were noticed for this trait suggesting a

Table 3. Estimates of correlation coefficient for yield contributing traits in backcross derived lines of rice

Characters	DFF	PH	NT	NP	PL	YPP
DFF	1.0					
PH	0.10	1.0				
NT	0.04	-0.04	1.0			
NP	0.05	-0.04	1.00	1.0		
PL	-0.17	0.45	0.02	0.02	1.0	0.20

Note: DFF-Days to 50% flowering, PH-Plant height (cm), NT-Number of tillers/plant, PT-Productive tillers per plant, PL-Panicle length (cm), YPP-Yield per plant (g)

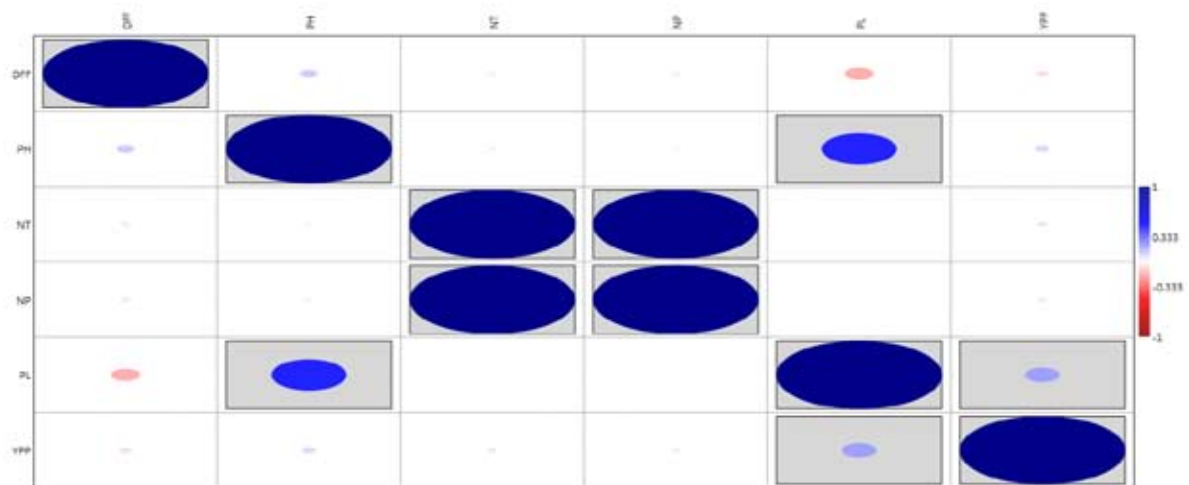


Fig. 2. Correlogram depicting association of yield with other traits in backcross derived lines.

(DFF-days to 50% flowering, PH- Plant height, NT-Number of Tillers, NP-Productive tillers per plant, PL-Panicle length, YPP-Grain Yield Per plant).

high range of genetic variability present among backcross derived lines. High heritability estimate (96.81%) coupled with high genetic advance (89.27%) were also recorded; results revealed that the selection would be very effective through direct selection for this trait. Similar results were recorded by Abebe *et al.* (2017); Shaikh *et al.* (2017).

Grain yield being a complex trait controlled by many genes, direct selection for yield may not profitable for any productive results, without giving much attention to their genetic background and component traits. The character association of yield and its constituent traits reveals the nature and degree of correlation between them. The association studies assist in determining the possibility of improving yield through an indirect selection of its constituent traits which are strongly associated (Ishwarya Lakshmi *et al.* 2020). Results of association studies are presented in **table 3 and fig. 2.**

Grain yield per plant significantly positively associated with panicle length (0.20). Non-significant Positive Correlation was observed with the number of tillers per plant (0.05) and the number of productive tillers per plant (0.05). Days to fifty per cent flowering (-0.07) negatively associated with grain yield per plant. The results suggest that panicle length, the number of productive tiller/plant, the number of tillers per plant could be considered as a criterion for selection of higher yield as they were interrelated among themselves showing the positive correlation. The present results were in line with the findings of Thippeswamy *et al.* (2016) and Priya *et al.* (2017).

The Eigen-values and per cent variability of different variables are presented in (**Table 4 and Fig 3**). In the present study, the first six principal components explained 99.99% of the total variability. The component with the

Table 4. PCA estimates of different characters in backcross derived lines of rice

	PC1	PC2	PC3	PC4	PC5	PC6
Eigen values	238.458	60.56	43.29	32.69	4.25	0.019
% variance explained	62.87	15.97	11.41	8.62	1.12	0.01
DFF	0.05	0.12	0.92	0.36	0.09	-0.001
PH	1.00	0.01	-0.03	-0.06	-0.07	0.000
NT	-0.02	0.70	-0.06	-0.08	-0.01	-0.705
NP	-0.02	0.70	-0.05	-0.08	-0.01	0.709
PL	0.07	0.01	-0.11	0.03	0.99	-0.003
YPP	0.04	0.08	-0.36	0.92	-0.07	0.005

(DFF-days to 50% flowering, PH- Plant height, NT-Number of Tillers, NP-Productive tillers per plant, PL-Panicle length, YPP-Grain Yield Per plant)

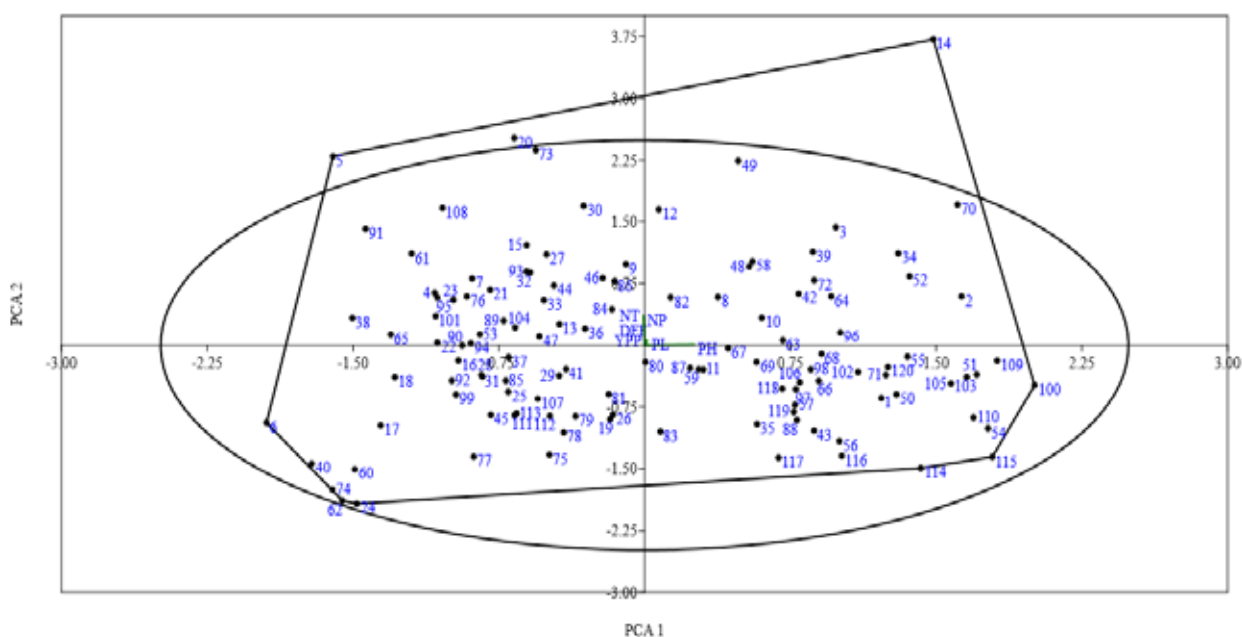


Fig. 3. PCA biplot based on the PC1 and PC2 using the grain yield and yield related traits in backcross derived lines

Eigen-values less than one were ignored as they are improbable to have any practical importance. Hence, significant features of the data set had been represented in the first two principal components PC1 (62.87) and PC2 (15.97) together contributed 78.84 % towards total variability.

The first principal component (PC1) explained maximum variability (62.87%). Characters such as days to 50% flowering (0.05), plant height (1.00), panicle length (0.07) and grain yield per plant (0.04) were positively loaded, whereas, characters number of tillers (-0.02) and the number of productive tillers per plant (-0.02) were negatively loaded. The second principal component PC2 contributed 15.97 per cent of the total variance. All the traits such as days to 50% flowering (0.12), plant height (0.01), the number of tillers per plant (0.70), the number of productive tiller per plant (0.70), panicle length (0.01) and grain yield per plant (0.08) contributed positively to the variation. Characters namely days to 50% flowering, plant height, the number of tillers/plant, the number of productive tillers/plant and grain yield per plant contributed significantly to the total variation.

To sum up, our study revealed that *Oryza rufipogon* is a prospective source for genetic enhancement of elite rice cultivars for yield-enhancing traits. Our study reported the transgressive segregants for yield attributing traits like the number of productive tillers per plant, and grain yield per plant. The presently identified transgressive segregants

from this pre-breeding study serve as valuable source genetic improvement of rice for yield and its attributing traits.

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