Variability and correlation of yield traits in BIL x BIL populations derived from Swarna x *O. nivara*

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Abstract

Wild introgression lines have wider genetic diversity than normal cultivars and contribute for crop improvement. Segregating populations consisting of 161 families at F_3 and F_4 generations derived from BIL (back cross introgression line) parents were used in the present study. Field evaluation for yield traits were carried out during two seasons of *rabi* and *kharif* in 2017. Correlation analysis was performed to determine associations among yield traits and highly significant association was observed for SPY with TDM and HI in F_3 and F_4 generations. Significant positive association of TN, PTN with SPY and also highly significant negative association between SPY and TGW were observed in F_4. All the traits in F_3 and F_4 showed positively skewed distribution except for the traits, PH and TGW. Significant lines were identified through pair wise mean comparisons with parents 166S, 148S and Swarna. Four lines C_3-53, C_3-38, C_3-70, and C3-96 exhibited positively significant values for TGW compared with parents. These lines can be used further for yield improvement and genetic dissection of target traits

Key words: Correlation, yield, *Oryza nivara*, back cross introgression lines

Introduction

Increase in yield potential of crop varieties is a challenging task in modern plant breeding. It is estimated that 60% increase in agricultural production needs to be achieved by 2050 to feed the increasing population (Alexandratos and Bruinsma., 2012). Yield is a complex trait which is influenced by different contributing traits and their polygenic inheritance and environment interaction effects (Usman *et al*., 2017). So, we need to evaluate all yield component traits and their contribution in a holistic manner (Oladosu *et al*., 2018). The correlation analysis showing interrelationship among yield and its components, is also very helpful to carry out efficient selection process (Rasel *et al*., 2018). The present study was conducted with following objectives i) to study the variability in the population for all the yield traits ii) to study interrelationships among yield component traits and iii) to identify significantly different lines for each trait by comparing with control/ parents. The study will be useful for identifying traits and genotypes for yield improvement in advanced generations.

Materials and methods

The parents 166S and 148S (BC_2F_8 BILs) derived from Swarna x *O. nivara* (Swamy *et al*., 2014) were crossed for generating F_1. Both F_3 and F_4 population with 161 plants were forwarded by single panicle selection from F_2 generation (Kavitha *et al*., unpublished). The parental BILs, 166S and 148S were detected as stable lines using multi environment data (Divya *et al*., 2016). 166S is a potential donor for improving yield traits like single plant yield, grain number, productive tiller number, panicle weight and germination percentage (Kavitha *et al*., 2019), while it is also reported to be drought and salinity tolerant (Kota *et al*., 2012). Field experiment was carried out during *kharif* 2017 and

rabi 2017 at Indian Institute of Rice Research (IIRR) farm, Rajendranagar, Hyderabad, India at latitude of 17° 19′ N and longitude of 78° 29′ E. The experiment was conducted in randomized complete block design with two replications. Seedlings from the nursery bed were transplanted in field at one to two seedlings per hill with a spacing of 20 x 15 cm (plant x row) and followed with recommended agronomic practices for good crop growth.

Observations were recorded from five middle row plants from each line in two replications. Data were recorded for yield traits of plant height (PH), tiller number (TN), productive tiller number (PTN), single plant yield (SPY), biomass (BM), total dry matter (TDM), harvest index (HI) and thousand grain weight (TGW) using standard evaluation system of IRRI (SES, IRRI,2013). Statistical analysis was performed for descriptive statistics, frequency distribution and correlation using Pearson's product-moment correlation method at the significant levels of *P = 0.05-0.001 and **P ≥ 0.001 with PB tools (Version 1.4, http://bbi.irri.org/products) software and significant pair wise comparisons with controls were carried out using STAR v2.0.1 software.

Results and discussion

The range, variance and standard deviation values wesre lower for each trait (except for PH) in F_4 generation than in F_3 and the critical value (CV) for each trait were lower in F_4 than in F_3 except for the traits BM and TDM (**Table 1**). TGW was observed with almost equal values of range, variance, standard deviation and critical values in F_3 and F_4. All the traits in F_3 and F_4 showed positively skewed distribution except for the traits PH (Vijaya and Shailaja., 2016) and TGW which showed negatively skewed distribution. Except the traits of TN, PTN and SPY all other traits showed leptokurtic distribution (Raghavendra and Hittalmani., 2015) with more than three values. Remaining yield

Table 1. Descriptive statistics for the yield traits in F_3 and F_4 population of 166S x 148S

Trait	Generation	Min	Max	Mean	Range	Variance	Standard deviation	Critical value	Skewness	Kurtosis
PH	F_3	59.67	153.67	111.57	94	339.65	18.43	16.52	-0.75	0.29
	F_4	71.5	155.33	119.34	83.83	344.19	18.55	15.55	-0.59	-0.29
TN	F_3	4.67	28	11.76	23.33	11.04	3.32	28.26	1.1	3.27
	F_4	4.67	16.4	7.15	11.73	2.47	1.57	21.98	2.18	8.94
PTN	F_3	4.67	28	11.72	23.33	11.13	3.34	28.47	1.07	3.23
	F_4	4.67	15.4	7.13	10.73	2.29	1.51	21.21	1.85	6.54
SPY	F_3	1.65	25.57	9.49	23.92	22.38	4.73	49.84	0.85	0.71
	F_4	3.93	32.47	11.11	28.54	13.12	3.62	32.6	1.56	7.01
BM	F_3	9.37	62.9	26.44	53.53	83.57	9.14	34.57	0.68	0.8
	F_4	5.13	31.6	13.55	26.47	27.09	5.21	38.41	1.29	2.18
TDM	F_3	15.97	67.47	35.88	51.5	101.65	10.08	28.1	0.32	0.24
	F_4	11.08	53.26	24.62	42.18	59.04	7.68	31.21	0.96	1.36
HI	F_3	4.23	57.32	26.77	53.09	130.28	11.41	42.64	0.27	-0.47
	F_4	23.77	70.05	45.5	46.28	60.55	7.78	17.1	0.4	0.6
TGW	F_3	12.16	30.44	22.48	18.28	8.22	2.87	12.76	-0.33	1.28
	F_4	12.16	30.44	22.49	18.28	8.05	2.84	12.62	-0.26	1.14

PH- plant height, TN- Tiller number, PTN- Productive tiller number, SPY- Single plant yield, BM- Biomass, TDM- Total dry matter, HI- Harvest index, TGW-Thousand grain weight.

traits exhibited platykurtic distribution with less than three and frequency distribution of each trait in F_3 and F_4 (**Figure 1**).

Correlation coefficient analysis showed highly significant association among yield traits in F_3 and F_4 (**Table 2**). In F_3, SPY showed highly positive significant association with BM, TDM and HI. Earlier workers reported Similar associations for SPY with HI (Kishore *et al*., 2018 and Archana *et al*., 2018), and SPY with BM (Bitew *et al*., 2018). In the present study, positive association was also significant among PH with BM and TDM, TN and PTN as well as BM and TDM. Highly negative significant association was observed for HI with PH, TN, PTN and BM as well as PH with TN and PTN. Similar results were reported by Sadimantara *et al*., (2018) in case of PH

with TN and PTN. Archana *et al*., (2018) reported negative association between HI and PH.

The traits TN and PTN showed significant positive association with BM and significant negative association between HI and TDM; SPY and PH, TGW with TN and PTN. Sreedhar and Uma Reddy., (2019) reported similar association between SPY and PH. In F_4, highly significant association was shown by SPY with PH, BM, TDM and HI; TDM with PH and BM; PH with BM and TDM and in between TN and PTN. Highly significant negative association of PH with TN, PTN and HI; TGW with SPY, BM and TDM; HI with PH, BM and TDM was also observed. Significant positive correlation of SPY with TN and PTN and significant negative association for TGW with TN and PTN were observed. Consistent correlation among

Table 2. Correlation among yield traits in F_3 and F_4 population of 166S x 148S

Trait	Generation	PH	TN	PTN	SPY	BM	TDM	HI	TGW
PH	F_3	1.00							
	F_4	1.00							
TN	F_3	-0.25**							
	F_4	-0.26**							
PTN	F_3	-0.23**	0.99**						
	F_4	-0.26**	1.00**						
SPY	F_3	-0.15*	-0.06	-0.07					
	F_4	0.28**	0.12*	0.11*					
BM	F_3	0.43**	0.12*	0.13*	-0.08				
	F_4	0.50**	0.09	0.08	0.46**				
TDM	F_3	0.33**	0.08	0.09	0.39**	0.88**			
	F_4	0.48**	0.09	0.08	0.77**	0.91**			
HI	F_3	-0.35**	-0.17**	-0.19**	0.81**	-0.57**	-0.14*		
	F_4	-0.28**	-0.05	-0.05	0.35**	-0.58**	-0.23**		
TGW	F_3	-0.01	-0.12*	-0.12*	-0.07	0.02	-0.01	-0.06	1.00
	F_4	0.01	-0.14*	-0.13*	-0.31**	-0.17**	-0.25**	-0.08	1.00

[*]P = 0.05-0.001, significant lines, [**]P ≥ 0.001, highly significant lines

Highly significant positive values in italics, highly significant negative values in bold

PH- plant height, TN- Tiller number, PTN- Productive tiller number, SPY- Single plant yield, BM- Biomass, TDM- Total dry matter,

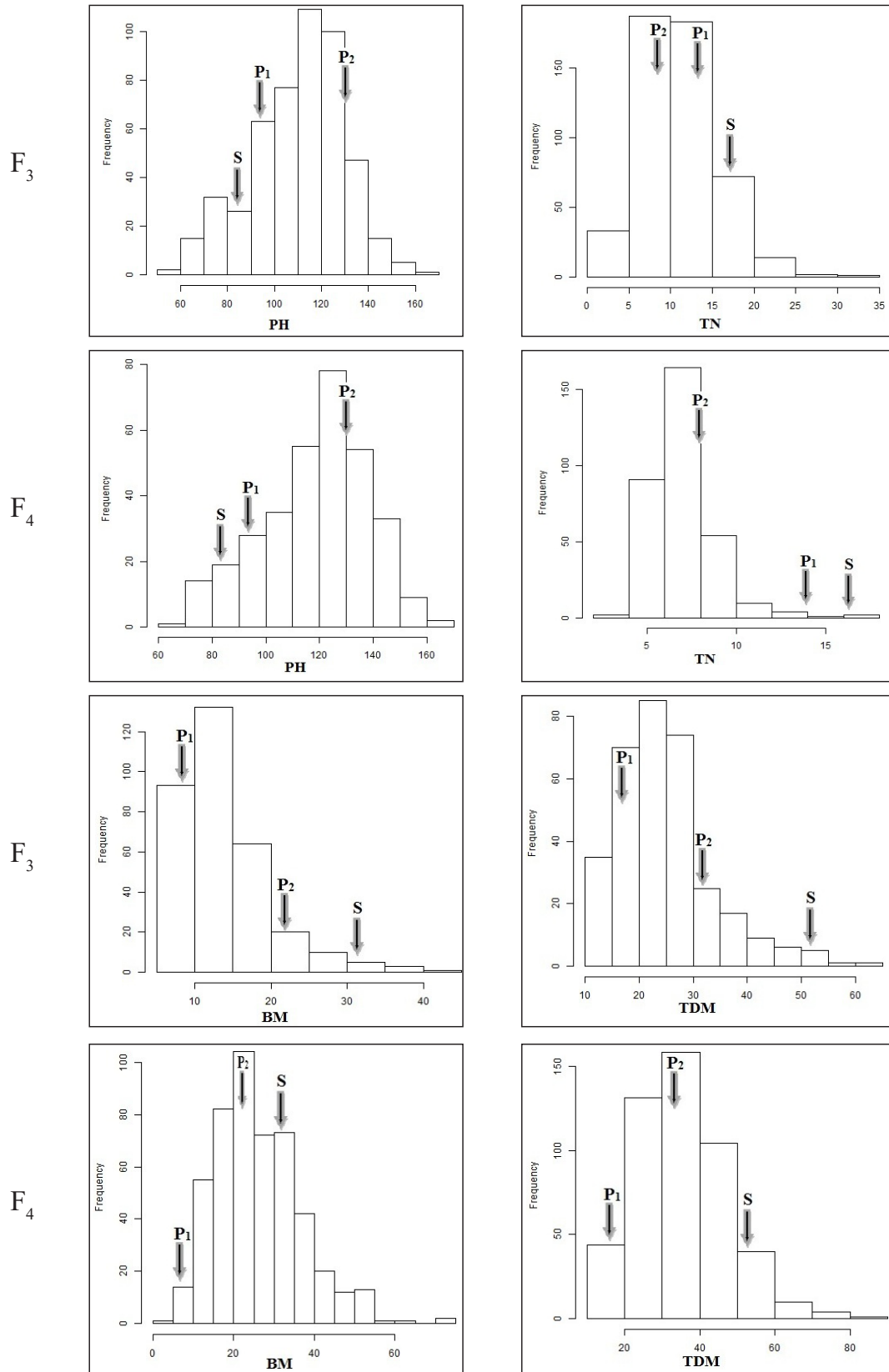HI- Harvest index, TGW-Thousand grain weight. F_3 and F_4- Generation.
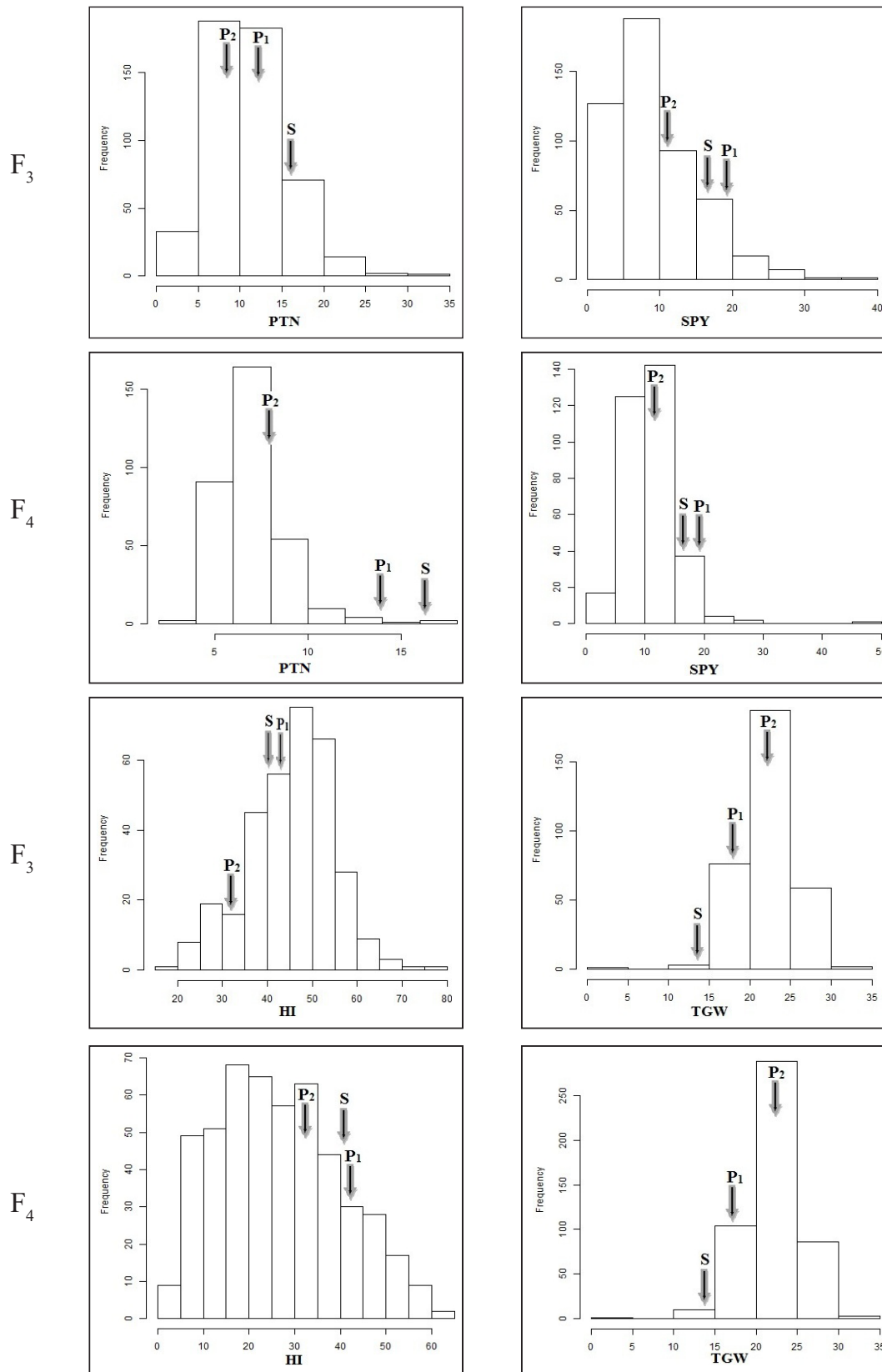
Figure1. Frequency distribution of yield traits in F3 and F4 populations of 166S x 148S

PH- plant height, TN- Tiller number, PTN- Productive tiller number, SPY- Single plant yield, BM- Biomass, TDM- Total dry matter, HI- Harvest index, TGW-Thousand grain weight.

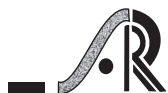F_3 and F_4- Generation. P1- 166S, P_2- 148S, S- Swarna

Figure1. Frequency distribution of yield traits in F3 and F4 populations of 166S x 148S

PH- plant height, TN- Tiller number, PTN- Productive tiller number, SPY- Single plant yield, BM- Biomass, TDM-
Total dry matter, HI- Harvest index, TGW-Thousand grain weight.

F_3 and F_4- Generation. P1- 166S, P_2- 148S, S- Swarna

traits in both the generations included SPY with TDM and HI; PH with BM and TDM and between TN and PTN with highly significant positive association and other traits PH with TN, PTN and HI; HI with BM and PH showing highly significant negative association. TGW showed significantly negative association consistently with TN and PTN. Similar associations between PH and PTN; TGW and PTN were reported by Lakshmi *et al*., (2014), while Zahid *et al*., (2006) observed the same result of TN with PH and TGW.

Significant lines for each trait from two populations were identified through pair wise comparisons by comparing with parents 166S and 148S along with Swarna (**Table 3**). Positive significant lines compared with 166S were identified for PH (93L in F_3 and F_4), TN (3L in F_3), PTN (3L in F_3), BM (14L in F_3, 1L in F_4), TDM (3L in F_3, 1L in F_4) and for TGW (116L in F_3, 44L in F_4). In case of 148S, positive significant lines compared were identified for TN (6L in F_3), PTN (5L in F_3), SPY (1L in F_3, 2L in F_4), for BM and TDM 6L and 3L respectively in F_3, for HI (2L in F_3, 14L in F_4) and for TGW (10L in F_3, 2L in F_4) traits. Positive significant lines compared with Swarna were identified for PH (110 in F_3, 109 in F_4), for TN and PTN 1L each in F_3, SPY (1L in F_4), BM (1L in F_3) and for TGW (155L in F_3, 117L in F_4). From the results it was observed that C_3 53, C_3 38, C_3 70 and C_3 96 lines showed positive significant values over 166S, 148S and Swarna for TGW. For SPY, the line C_3 36 showed positive significance with 148S and Swarna while the lines C_3 145 and C_3 3 showed positive significance with 148S. These significant lines for TGW and SPY can be further used for yield improvement.

Table 3. 166S x 148S significant lines for 166S, 148S and Swarna

Significant lines *	PH		TN		PTN		SPY		BM		TDM		HI		TGW	
	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4
166S (+ve)	93	93	3	-	3	-	-	-	14	1	3	1	-	-	116	44
148S (+ve)	-	-	6	-	5	-	1	2	6	-	3	-	2	14	10	2
Swarna (+ve)	110	109	1	-	1	-	-	1	1	-	-	-	-	-	155	117
Total	203	202	10	-	9	-	1	3	21	1	6	1	2	14	276	163
166S (-ve)	-	-	-	-	-	-	41	15	-	-	-	-	40	-	-	-
148S (-ve)	56	24	-	-	-	-	-	-	-	27	-	-	2	-	7	3
Swarna (-ve)	-	-	6	160	5	160	20	3	7	147	47	146	25	-	-	-
Total	56	24	6	160	5	160	61	18	7	174	47	146	67	-	7	3

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