Received: 23 Aug 2023 | Revised: 17 Sep 2023 | Accepted: 27 Sep 2023

Electronic Journal of Plant Breeding

Research Article

Performance of qDTY QTL introgressed lines of rice (*Oryza sativa* L.) under target production environment

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Abstract

Drought is an important factor limiting rice productivity in rainfed ecosystem. Development of high yielding drought tolerant rice varieties would increase rice production under such condition. In the present study, 116 qDTY QTL introgressed back crossed inbred lines (BILs) derived from the crosses *viz*., ADT (R) 45 * 3/Apo, ADT (R) 45 * 3/ Way Rarem and ADT (R) 45 * 2/Apo // ADT (R) 45 * 2/ Way Rarem along with parents were evaluated to assess their performance under target production environment. Estimates on genetic variability, trait association, direct and indirect effects of yield and yield components and principal component analysis were worked out. The results of genetic variability showed wide variation among the genotypes for different traits. High values of PCV than GCV showed the influence of environment on the traits. Genotypes could be selected based on total number of tillers per plant, number of productive tillers per plant, spikelet fertility, single plant yield, 1000 seed weight and grain yield per plot, which were found to have high heritability and genetic advance. Correlation analysis exhibited high and significant positive correlation of grain yield per plot with single plant yield and non significant positive association of all the traits except plant height that was negatively correlated. Path coefficient analysis of the genotypes showed that total number of tillers per plant had maximum direct effect on grain yield, while number of productive tillers per plant had high indirect effect on grain yield via total number of tillers. Based on genetic variability, correlation and path analysis, selection for six traits, *viz*., total number of tillers per plant, number of productive tillers per plant, single plant yield, spikelet fertility, 1000 seed weight and grain yield per plot, would be rewarding. The results of principal component analysis revealed that, four out of eleven principal components *viz*., PC1, PC2, PC3 and PC4 contributed 72.62% of the total variation with eigen values more than 1. PC1 accounted for the highest variability with 24.66% followed by PC2 (20.42%), PC3 (16.19%) and PC4 (11.35%). From this study, the traits contributing for variation were identified and the resulting genotypes would be beneficial for improving yield with drought tolerance.

Keywords: target production environment, variability, correlation, principal component analysis

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food crop of India, providing 43 per cent of caloric requirement for more than 70 per cent Indian population (Madakemohekar *et al.,* 2014). With an area, production, and productivity of 43.80 million ha, 118.88 million tonnes, and 2650 kg ha^{-1}, respectively, India is one of the world's top producers of rice. By 2050, it is predicted that 160 million tons of rice is needed to

https://doi.org/10.37992/2023.1403.135

feed ever increasing Indian population. 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).

Many morpho-physiological traits putatively contribute to drought tolerance (DT), and each of these traits is typically controlled by multiple genes or quantitative trait loci (QTLs), and is influenced by environment to a great extent (Zeng *et al.,* 2006). The discovery of such genes in rice is considered to be one of the most important and difficult challenges (Xu *et al.,* 2005). 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. Grain yield under drought is considered to be an effective criterion for drought tolerance breeding programme. Thus, detection of drought yield QTLs might be a useful tool for drought breeding. First drought QTL $qDTY_{12.1}$ with consistent and large effect, was detected by Bernier *et al.*(2007) from the population of Vandana/Way Rarem. Introgression of drought tolerant QTLs from non-elite backgrounds into elite genotypes revealed considerable drought tolerance in them.

The degree of variation and the influence of environment on traits can be investigated using genotypic (GCV) and phenotypic (PCV) coefficients of variation. Correlation shows the relationship of different traits with each other that help to determine the traits for selection. Partitioning of correlation coefficients can be done by path coefficient analysis. It is done to study the direct and indirect effects of different traits on yield. Principal Component Analysis is a powerful tool in modern data analysis used to identify the minimum number of components, which can explain maximum variability out of the total variability. In this context, the present study was conducted to assess the genetic variability, heritability, correlation, path analysis and principal component analysis for yield and component traits in 116 qDTY QTL introgressed lines of rice to assist the future breeding programmes for yield improvement under drought stress condition.

Table 1. List of 116 introgressed lines evaluated in the study

Code	Line	Code	Line	Code	Line	Code	Line	Code	Line
1	W11	25	W94	49	W177	73	A62	97	7-4-4
2	W16	26	W95	50	W179	74	A63	98	A83
3	W18	27	W96	51	W180	75	A91	99	A89
4	W24	28	W97	52	W187	76	A11	100	A99
5	W26	29	W99	53	W191	77	A41	101	I74
6	W27	30	W100	54	W192	78	A43	102	I76
7	W33	31	W103	55	W195	79	A59	103	I92
8	W34	32	W106	56	W197	80	A88	104	I5
9	W39	33	W115	57	W199	81	A16	105	I12
10	W43	34	W117	58	W214	82	A22	106	I33
11	W47	35	W121	59	W216	83	A35	107	I39
12	W51	36	W125	60	W220	84	A52	108	I40
13	W60	37	W129	61	W225	85	A67	109	I45
14	W61	38	W132	62	W231	86	A70	110	I69
15	W62	39	W135	63	W234	87	A75	111	I85
16	W63	40	W138	64	W235	88	A81	112	7-4-1
17	W64	41	W145	65	W237	89	A82	113	7-4-2
18	W69	42	W149	66	W242	90	A95	114	18-8-7
19	W84	43	W162	67	W248	91	A4	115	I127
20	W85	44	W164	68	W249	92	A14	116	I172
21	W86	45	W168	69	A24	93	A53	117	APO
22	W89	46	W170	70	A26	94	A58	118	WR
23	W90	47	W171	71	A29	95	A78	119	ADT 45
24	W92	48	W172	72	A39	96	A80		

MATERIALS AND METHODS

A total of 116 multiple qDTY QTL introgressed lines derived from three crosses: ADT (R) 45 *3/Apo, ADT (R) 45 *3/Way Rarem, and ADT (R) 45 *2/Apo // ADT (R) 45 *2/Way Rarem and the parents Apo, Way Rarem, and ADT (R) 45, were evaluated in augmented block design (**Table 1**). The experiment was carried out during *Rabi* 2022 at Agricultural Research Station, Paramakudi which is the target production environment (TPE), where the crop is grown under rainfed condition. Seeds of each genotype were directly sown in three rows of 3-meter length with spacing of 20 cm between rows and 15 cm within rows. The crop was completely raised under rainfed ecosystem. The details of site, soil and drought characteristics of the field are given in **Table 2**. Due to the occurrence of unexpected downpours during the crop period, drought was not observed. The observations were made on five plants that were chosen at random. Eleven traits, early shoot length (cm), early root length (cm), plant height (cm) at maturity, total number of tillers per plant (TNT), number of productive tillers per plant (PT), panicle length (cm), number of filled grains per panicle, spikelet fertility (%), single plant yield (g), 1000 seed weight (g), and grain yield per plot (g) were examined. Early shoot length and early root length were recorded 28 days after sowing. TNAUSTAT was used to carry out the analysis of variance and the path analysis (Manivannan, 2014). The breeding tool GRAPES 1.1.0 (Gopinath *et al.*, 2021) was used to conduct the correlation studies. The PCA and basic descriptive statistics were carried by using the statistical program STAR 2.0.1.

RESULTS AND DISCUSSION

The analysis of variance for grain yield and its contributing characteristics revealed significant variation for the genotypes examined among treatments, checks, test entries, and checks Vs test entries. However, no significant changes were found between test entries and treatments for plant height and panicle length. (**Table 3**). Mean performance of parents and introgressed lines: Trait wise mean values for the parents and the introgressed lines are listed in **Table 4.** On comparing the parental means with means of lines from different crosses, higher values are found among the lines than that of the parents for almost all the traits. The mean of lines from the inter cross of ADT (R) 45 *2/Apo // ADT (R) 45 *2/Way Rarem were found to be high for the traits such as early shoot length (36.28), early root length (16.92), plant height (99.33), panicle length (21.27), spikelet fertility (86.33), single plant yield (11.09), 1000 seed weight (19.80) and grain yield (698.63). However, the maximum mean value for number of productive tillers per plants (11.25) and number filled grains per panicle (126.87) were reported in the lines from the cross ADT (R) 45 * 3/Apo.

Table 2. Site, soil and drought characteristics of field trial

Particulars	
Elevation (meters above sea level)	40
Latitude and longitude	9°N, 70°E
Soil texture	Black clay
Soil pH	8.1
Number of rainy days during crop period	13
Rainfall during crop period (mm)	288.3
Mean temperature maximum/minimum (°C)	37.8/19.0
Average relative humidity (%)	86.5

Table 3. Analysis of Variance for Augmented Design I

Source	DF	Mean Sum of Squares										
		ESL	ERL	PH	TNT	PT	PL	FG	SF	SPY	TSW	GY
Treatment	118	32.111**	7.958*	226.451	32.284*	32.473*	8.238	1565.952	208.576**	8.803*	5.058**	35372.839**
Checks	2	163.986**	26.702**	2296.273**	1.267	1.267	38.253**	1769.867	751.770**	4.353	32.133**	17145.648*
Test entries	115	27.122**	7.454*	183.768	32.990*	33.193*	7.609	1575.596	200.473**	8.950*	4.284**	35516.942**
Checks Vs Test entries	1	342.144**	28.427**	995.266*	13.161	12.046	20.579**	49.029	54.128*	0.891	39.957**	55255.399**
Error	12	4.392	2.570	131.354	10.933	10.933	3.781	990.667	9.273	3.172	0.172	3328.623

*- Significant at 5% level; **- Significant at 1% level; DF – degrees of freedom
ESL – Early Shoot Length (cm); ERL – Early Root Length (cm); PH – Plant Height (cm); TNT – Total Number of tillers per plant; PT – Number of Productive tillers per plant; PL – Panicle Length (cm); FG – Number of filled grains per panicle; SF – Spikelet fertility (%); SPY – Single Plant Yield (g); TSW – 1000 seed weight (g); GY – Grain Yield per plot (g)

Table 4. Trait wise mean values of the introgressed lines from different crosses

Mean of the lines from different crosses	ESL	ERL	PHT	TNT	PT	PL	FG	SF	SPY	TSW	GY
ADT (R) 45 * 3/ Way Rarem	29.40	15.40	74.32	11.31	11.22	19.52	100.57	76.05	9.80	17.09	617.20
ADT (R) 45 * 3/Apo	34.54	16.32	82.60	11.25	11.25	20.30	126.87	79.74	10.34	18.44	651.71
Intercrossed lines	36.28	16.92	99.33	7.75	7.75	21.27	125.46	86.33	11.09	19.80	698.63
Overall Mean	31.56	15.84	79.34	10.86	10.82	20.01	110.39	78.19	10.09	17.76	635.55
Parental Mean											
Apo	40.50	16.52	112.70	9.80	9.80	24.30	124.60	86.54	10.78	22.07	625.34
Way Rarem	39.36	19.90	76.84	10.40	10.40	20.56	113.00	62.64	10.98	19.41	578.82
ADT (R) 45	30.06	15.48	74.44	9.40	9.40	18.90	87.80	79.33	9.28	17.00	509.00

The mean of grain yield ranges from 133.47 g (W33) to 1137.5 g (A4) per plot. On comparing the overall mean with the mean of lines from different crosses, the lines from intercross showed maximum mean of 698.63 g, greater than that of the parental means. The mean for 1000 seed weight ranges from 12.48 g (W26) to 23.38 g (I12), which is on par with the mean of lines from intercross with the highest value (19.80 g). Likewise, the mean for spikelet fertility ranges from 24.60% (A63) to 96.77% (I92). The average of the lines from intercross for spikelet fertility is found to be maximum (86.33%) over the parental means. The overall mean for number of productive tillers per plant ranges from 4.00 (W89) to 38.00 (A99), that is supported by the mean of lines from the cross ADT (R) 45 * 3/Apo with maximum mean value of 11.25. The overall mean value of the introgressed lines ranges from 19.90 cm (W64) to 43.30 cm (A67) for early shoot length, 6.00 cm (W64) to 22.20 cm (W237) for early root length, 47.00 cm (W92) to 125.00 cm (I76) for plant height, 11.50 cm (W69) to 28.50 cm (A89) for panicle length and 39.00 (W95) to 221.00 (A35) for number of filled grains per panicle, respectively.

The following 21 genotypes, *viz*., A4 (1137.50 g), W106 (1125.00 g), W69 (1090.38 g), A22 (1006.25 g), W18, W95 and W172 (945.00 g each), A70 (925.00 g), W85 (918.75 g), 7-4-1 (906.82 g), 7-4-4 (900.00 g), W117 (843.75 g), A82 (835.71 g), W92, W125 (828.95 g), W94 (816.67 g), W237 (814.66 g), W16 and I40 (807.69 g each), W132 (805.81 g) and I33 (803.57 g) were found to have high grain yield per plot.

Estimation of Variability parameters and heritability: **Table 5** shows the results of basic descriptive statistics for the introgressed lines in the study. Higher PCV values than GCV in this study show that the environment has an important influence in influencing the extent of variation existing among the lines. The values of GCV and PCV were classified as low (less than 10%), moderate (10 – 20%) and high (more than 20%), suggested by Sivasubramanian and Madhavamenon (1973). In this study, high GCV and PCV were observed for number of productive tillers per plant (43.73% and 53.40%), total number of tillers per plant (43.37% and 53.04%),grain yield per plot (28.30% and 29.73%), number of filled

Table 5. Characteristic means and variations of introgressed lines in the study

Traits studied	Mean	Minimum		Maximum		GCV	PCV	h^2 (%)	GA	GAM (%)
		Value	Line	Value	Line					
ESL	31.56	19.90	W64	43.30	A67	15.07	16.44	84.04	9.02	28.45
ERL	15.84	6.00	W64	22.20	W237	13.93	17.20	65.52	3.69	23.22
PH	79.34	47.00	W92	125.00	I76	9.10	17.04	28.52	7.96	10.01
TNT	10.86	4.00	W89	38.00	A99	43.37	53.04	66.86	7.91	73.05
PT	10.82	4.00	W89	38.00	A99	43.73	53.40	67.06	7.96	73.76
PL	20.01	11.50	W69	28.50	A89	9.76	13.77	50.31	2.86	14.27
FG	110.39	39.00	W95	221.00	A35	21.92	35.97	37.12	30.36	27.51
SF	78.19	24.60	A63	96.77	I92	17.70	18.12	95.37	27.82	35.60
SPY	10.09	2.12	W33	18.06	A4	23.27	28.96	64.56	3.98	38.52
TSW	17.76	12.48	W26	23.38	I12	11.54	11.78	95.98	4.09	23.29
GY	635.55	133.47	W33	1137.5	A4	28.30	29.73	90.63	351.84	55.50

GCV – Genotypic Coefficient of Variation; PCV – Phenotypic Coefficient of Variation; h^2 – Broad sense heritability; GA – Genetic Advance; GAM – Genetic Advance as percent of Mean grains per panicle (21.92% and 35.97%) and single plant yield (23.27% and 28.96%).Gayathri and Padmalatha (2023) found that the number of filled grains per panicle had a high PCV and GCV. Moderate GCV and PCV were observed for early shoot length (15.07% and 16.44%), early root length (13.93% and 17.20%), spikelet fertility (17.70% and 18.12%) and 1000 seed weight (11.54% and 11.78%). Low GCV and moderate PCV were observed for plant height (9.10% and 17.04%) and panicle length (9.76% and 13.77%). The findings of Zayed *et al.* (2023) showed that panicle length had a moderate GCV and PCV, plant height had a low GCV and PCV and 1000 seed weight had a moderate GCV and PCV. The studies of Pathak *et al.* (2022) showed high GCV and PCV for number of productive tillers per plant. Abarshahr *et al.* (2011) and Srihari *et al.* (2023) observed low PCV and GCV for panicle length.

Another estimate that is significant in the selection of lines for subsequent breeding is heritability. The values of heritability were classified as low (less than 30%), moderate (30 – 60%) and high (more than 60%) by Johnson *et al.* (1995). The extent of genetic variability, heritability, and selection intensity all influence genetic advancement as a percentage of the mean. The values of genetic advance as percent of mean were also classified as low (less than 10%), moderate (10 – 20%) and high (more than 20%) by Johnson *et al.* (1995). In this study, early shoot length (84.04% and 28.45%), early root length (65.52% and 23.22%), total number of tillers per plant (66.86% and 73.05%), number of productive tillers per plant (67.06% and 73.76%), spikelet fertility (95.37% and 35.60%), single plant yield (64.56% and 38.52%), 1000 seed weight (95.98% and 23.29%), and grain yield per plot (90.63% and 55.50%) all exhibit strong heritability and genetic advance respectively. This demonstrated that heritability was caused by additive gene effects and that selection might be successful. The results were in accordance with the findings of Pathak *et al.* (2022) and Gayathri and Padmalatha(2023), who reported high heritability and moderate genetic advance for yield and its related traits. Zayed *et al.* (2023) reported high heritability and high genetic advance for grain yield. Srihari *et al.* (2023) observed high heritability and high genetic advance for number of filled grains per panicle.

Plant height has low heritability and genetic advance, indicating that it is heavily impacted by the environment, therefore selection based on plant height would be futile. However, the findings of Abarshar *et al.* (2011), Zayed *et al.* (2023) and Srihari *et al.* (2023) were found to be in contrast, where plant height showed high heritability and high genetic advance. Selection based on number of filled grains per panicle also ineffective due to low heritability (37.12%). Though, panicle length showed moderate heritability (50.31%), it also had moderate genetic advance (14.27%) that showed non additive gene action and so, selection was ineffective. These results were supported by Gayathri and Padmalatha (2023).

Correlation studies: The correlation coefficients for yield and related traits are listed in **Table 6**.Grain yield per plot had a highly significant positive correlation (0.8672) with single plant yield. Early shoot length (0.1542), early root length (0.0309), number of filled grains per panicle (0.0587),total number of tillers per plant (0.1013), productive tillers per plant (0.1040), panicle length (0.0970), spikelet fertility (0.1379), and 1000 seed weight (0.0076)had a non-significant positive correlation with grain yield, whereas, plant height (-0.1048) had a negative correlation. These findings were similar to that of Farheen *et al.*(2023), who found that spikelet fertility and 1000 seed weight had a positive association with grain yield. Saikumar *et al.* (2014) discovered that number of filled grains per panicle and plant height was both positively associated to grain yield. The positive association between filled grains per panicle and grain yield was also described by Srihari *et al.*(2023).

Table 6. Correlation coefficients of yield and yield attributing traits

Traits	ESL	ERL	PH	TNT	PT	PL	FG	SF	SPY	TSW	GY
ESL	1.0000										
ERL	0.4751**	1.0000									
PH	0.4786**	0.2271*	1.0000								
TNT	0.0037	0.1231	-0.0443	1.0000							
PT	0.0057	0.1249	-0.0411	0.9991**	1.0000						
PL	0.3315**	0.2641**	0.3551**	0.1644	0.1654	1.0000					
FG	0.3920**	0.1238	0.2002*	0.2071*	0.2121*	0.2559**	1.0000				
SF	0.2661**	0.1080	0.0847	0.1003	0.1003	0.1568	0.6394**	1.0000			
SPY	0.2209*	0.0774	0.1545	0.1060	0.1078	-0.0426	0.0529	0.0456	1.0000		
TSW	0.1899*	0.1936*	0.2125*	-0.1292	-0.1262	0.1600	0.1000	0.2302*	-0.2491**	1.0000	
GY	0.1542	0.0390	-0.1048	0.1013	0.1040	0.0970	0.0587	0.1379	0.8672**	0.0076	1.0000

*- Significant at 5% level; **- Significant at 1% level

Total number of tillers per plant was shown to be strongly and positively correlated with number of productive tillers per plant (0.9991) similar to the studies by Renuprasath *et al.* (2023). Highly significant and positive correlation was found between number of filled grains per panicle with spikelet fertility (0.6394). Similar results were reported by Saikumar *et al.* (2014), Bhutta *et al.* (2019). Likewise, significant and positive correlation between plant height and panicle length (0.3551) was supported by Reshma *et al.* (2023).Early shoot length correlates favorably with all other variables, including total number of tillers per plant (0.0037), productive tillers per plant (0.0057), and grain yield (0.1542).Early root length (0.4751), plant height (0.4786), panicle length (0.3315), number of filled grains per panicle (0.3920), spikelet fertility (0.2661), 1000 seed weight (0.1899), and single plant yield (0.2209) are all significant.Similar to early shoot length, early root length also exhibited positive correlations with other traits. The significant and positive correlation between number of filled grains per panicle and panicle length (0.2559) were supported by Saikumar *et al.* (2014), Madhukar *et al.* (2017), Bhutta *et al.* (2019) and Gayathri and Padmalatha (2023).

Path coefficient analysis: The results of the path coefficient analysis for the yield and yield component traits are discussed in **Table 7**, suggested by Dewey and Lu, 1959.In the present study, total number of tillers per plant expressed high positive direct effect on grain yield (1.1121), followed by single plant yield (0.9530), 1000 seed weight (0.2904) and number of filled grains per panicle (0.0885). These results were in accordance with the studies by Saikumar *et al.* (2014), Farheen *et al.*(2023), Srihari *et al.*(2023), Renuprasath *et al.* (2023), and Gayathri and Padmalatha (2023). The other traits, number of productive tillers per plant (-1.0702), panicle length (-0.0714), spikelet fertility (-0.0916), early shoot length (-0.0539), plant height (-0.0486) and early root length (-0.0398) expressed negative direct effects. However, these traits influenced grain yield per plot through indirect effects.

The highest positive indirect effect of number of productive tillers per plant (1.1111) was reported on grain yield via total number of tillers per plant as explained by Renuprasath *et al.* (2023). The negative direct effect of plant height (-0.0486) and panicle length (-0.0714) were in accordance with the findings of Reshma *et al.* (2023) but, in contrast to that of Renuprasath *et al.* (2023). Early shoot length and early root length, respectively showed negligible indirect effects on grain yield via total number of tillers per plant (0.0041 and 0.1369), number of filled grains per panicle (0.0347 and 0.0110), single plant yield (0.2105 and 0.0737) and 1000 seed weight (0.0551 and 0.0562). Plant height showed positive indirect effect on grain yield via single plant yield (0.1472), 1000 seed weight (0.0617), number of productive tillers per plant (0.0440) and number of filled grains per panicle (0.0177). It showed negative indirect effect on grain yield via spikelet fertility (-0.0078) reported by Saikumar *et al.* (2014), early shoot length (-0.0258), early root length (-0.0090), total number of tillers per plant (-0.0492) and panicle length (-0.0253). Panicle length had negligible positive indirect effect on grain yield through total number of tillers per plant (0.1828), number of filled grains per panicle (0.0227), and 1000 seed weight (0.0465). It also had an indirect negative influence on early shoot length (-0.0179), early root length (-0.0105), plant height (-0.0173), productive tiller number per plant (-0.1770), spikelet fertility (-0.0144), and single plant yield (-0.0406). Reshma *et al.* (2023) found that panicle length had an indirect positive effect on 1000 seed weight, number of filled grains per panicle, and number of tillers per plant.

The traits, total number of tillers per plant (0.2303), single plant yield (0.0504), and 1000 seed weight (0.0290) all showed positive indirect effects. The number of productive tillers per plant (-0.2270), early root length

Table 7. Path coefficients of yield and yield attributing traits

Traits	ESL	ERL	PH	TNT	PT	PL	FG	SF	SPY	TSW	GY (r)
ESL	**-0.0539**	-0.0189	-0.0233	0.0041	-0.0061	-0.0237	0.0347	-0.0244	0.2105	0.0551	0.1542
ERL	-0.0256	**-0.0398**	-0.0110	0.1369	-0.1337	-0.0188	0.0110	-0.0099	0.0737	0.0562	0.0390
PH	-0.0258	-0.0090	**-0.0486**	-0.0492	0.0440	-0.0253	0.0177	-0.0078	0.1472	0.0617	0.1048
TNT	-0.0002	-0.0049	0.0022	**1.1121**	-1.0693	-0.0117	0.0183	-0.0092	-0.1011	-0.0375	-0.1013
PT	-0.0003	-0.0050	0.0020	1.1111	**-1.0702**	-0.0118	0.0188	-0.0092	-0.1027	-0.0366	-0.1040
PL	-0.0179	-0.0105	-0.0173	0.1828	-0.1770	**-0.0714**	0.0227	-0.0144	-0.0406	0.0465	-0.0970
FG	-0.0211	-0.0049	-0.0097	0.2303	-0.2270	-0.0183	**0.0885**	-0.0586	0.0504	0.0290	0.0587
SF	-0.0144	-0.0043	-0.0041	0.1115	-0.1074	-0.0112	0.0566	**-0.0916**	-0.0400	0.0668	-0.0379
SPY	-0.0119	-0.0031	-0.0075	-0.1179	0.1154	0.0030	0.0047	0.0038	**0.9530**	-0.0723	0.8672^{**}
TSW	-0.0102	-0.0077	-0.0103	-0.1437	0.1350	-0.0114	0.0089	-0.0211	-0.2374	**0.2904**	-0.0076

GY (r) – Phenotypic correlation coefficient for grain yield per plot; Diagonal bold values are direct effects and others are indirect effects

Residual effect = 0.4201

(-0.0049), plant height (-0.0097), early shoot length (-0.0211), panicle length (-0.0183), and spikelet fertility (-0.0586) were all affected negatively by this feature. This was consistent with the conclusions reached by Gayathri and Padmalatha(2023). Spikelet fertility had a favorable indirect effect on grain yield via total number of tillers per plant (0.1115), number of filled grains per panicle (0.0566), and 1000 seed weight (0.0668). Indirect negative impacts were observed in the number of productive tillers per plant (-0.1074), early root length (-0.0043), plant height (-0.0041), early shoot length (-0.0144), panicle length (-0.0112), and single plant yield (-0.0400). Saikumar *et al.* (2014) discovered a favorable indirect influence of spikelet fertility on grain yield via the number of filled grains per panicle.

Principal Component Analysis: Principal Component Analysis is done to reduce the dimensionality of the parameter dataset and to identify new underlying variables (Gour, Lokesh *et al.*, 2017). The results of principal component analysis are shown in **Table 8**. Eigen values of more than 1 were observed in the first four principal components (PC1 to PC4), *viz*., 2.7128, 2.2463, 1.781 and 1.2485 respectively, that contributed 72.62% to the total divergence in the study. The percentage of variance in relation with each principal component could be demonstrated by a scree plot, obtained by a graph between eigen values and principal component numbers. From the graph, it could be observed that the first principal component PC1 had eigenvalue 2.7128, with 24.66% contribution to variance. The graph gradually decreased with decreasing eigen value with increasing principal component numbers (**Fig. 1**). The maximum contribution to the variance was due to PC1 (24.66%) followed by PC2 (20.42%), PC3 (16.19%) and PC4 (11.35%). The studies of Pavithra and Vengadesan (2020) showed that, the first three components contributed 98.9% and 93.3% of total variation in normal and drought conditions. Also, the results of Zayed *et al.*(2023) conveyed that two principal components contributed 88.37% and 90.70% of total variation, having eigen values more than 1, in two growing seasons. Sanni *et al.* (2012) explained the contribution of 72.74% of the total variation by three principal components.

PC1 showed maximum variation (24.66%) with the traits, early shoot length (-0.4399), number of filled grains per panicle (-0.4207) and panicle length (-0.3585) loading significantly and negatively correlated. It could be explained that these characters contributed maximum to total variance (**Fig. 2**). However, these results were found to be in contrast to that of Pavithra and Vengadesan (2020), in which number of filled grains per panicle had significant loading and positively correlated to PC1. PC2 contributed 20.42% to total variance and negatively correlated with total number of tillers per plant (-0.4839), number of productive tillers per plant (-0.4842) single plant yield (-0.4562) and grain yield per plot (-0.4498). However, the traits, early shoot length (0.2336) and plant height (0.2266) showed positive correlation with PC2. Sanni *et al.* (2012) observed high loading of total number of tillers per plant and number of productive tillers per plant in PC2. Studies of Pavithra and Vengadesan (2020) reported contribution and positive correlation of plant height to PC2. Rahangdale *et al.* (2021) reported the dominance of grain yield per plant in PC2. Likewise, the traits, single plant yield (-0.5093), grain yield per plot (-0.4610) and 1000 seed weight (-0.4178) showed high negative correlation with PC3 that contributed 16.19% to total variance. PC4 contributed 11.35% to the total

Table 8. Principal Component Analysis of different traits of introgressed lines evaluated under TPE – Eigen vectors

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
ESL	-0.4399	0.2336	0.0612	0.1351	0.0280	0.2977	-0.2623	0.6792	0.3270	-0.0585	-0.0013
ERL	-0.3338	0.0746	0.0416	0.3838	-0.4582	0.5521	0.1367	-0.3945	-0.2090	-0.0338	0.0008
PH	-0.3284	0.2266	0.1168	0.2985	0.3594	-0.3341	-0.5559	-0.4291	-0.0393	-0.0508	0.0013
TNT	-0.2434	-0.4839	-0.3874	0.0983	-0.1109	-0.1456	-0.0920	0.0278	0.0659	0.0139	0.7068
PT	-0.2453	-0.4842	-0.3851	0.0982	-0.1105	-0.1459	-0.0951	0.0293	0.0547	0.0290	-0.7073
PL	-0.3585	-0.0366	0.1289	0.2801	0.4239	-0.2011	0.7404	0.0369	0.0605	-0.0423	-0.0017
FG	-0.4207	-0.0265	0.0006	-0.5097	0.1700	0.0815	-0.0320	0.1307	-0.7098	0.0708	0.0072
SF	-0.3460	-0.0392	0.1394	-0.6144	-0.0624	0.0781	0.0645	-0.3842	0.5606	-0.0765	-0.0051
SPY	-0.0693	0.4562	-0.5093	-0.0416	0.0126	-0.0293	0.1139	-0.0805	0.1034	0.7034	0.0055
TSW	-0.1850	0.0770	0.4178	0.0070	-0.6093	-0.5711	0.0434	0.1558	-0.0585	0.2413	0.0039
GY	-0.0587	0.4498	-0.4610	-0.0924	-0.2273	-0.2688	0.1333	0.0225	-0.0684	-0.6529	-0.0075
Pro. Var. (%)	24.66	20.42	16.19	11.35	7.74	6.98	5.55	3.52	2.83	0.75	0.01
Cu. Pro. (%)	24.66	45.08	61.27	72.62	80.37	87.34	92.90	96.42	99.25	99.99	100.00
Eigen values	2.7128	2.2463	1.7810	1.2485	0.8518	0.7673	0.6109	0.3876	0.3107	0.0822	0.0008

Pro. Var. – Proportion of Variance; Cu. Pro. – Cumulative Proportion

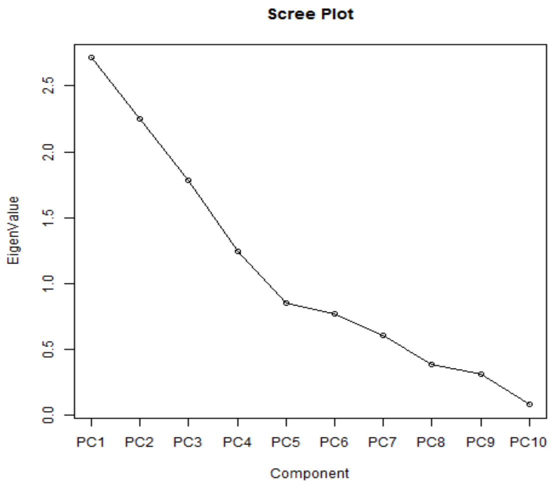

Fig. 1. Scree plot

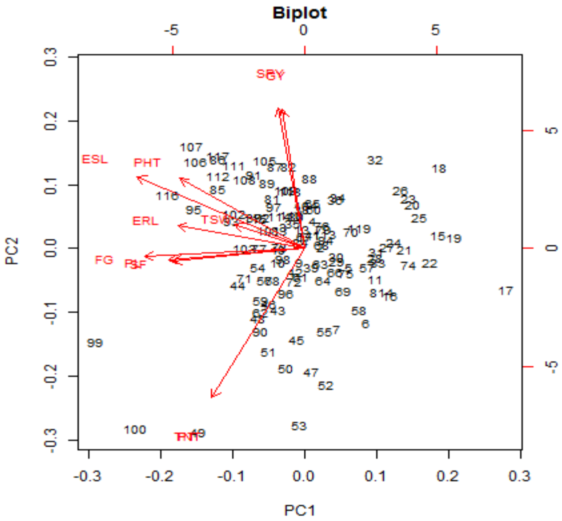

Fig. 2. Biplot of PC1 and PC2

Table 9. Genotypes selected on the basis of PC scores in each component having positive value & more than 1.0 in each PCs

PC1		PC2		PC3		PC4	
W64 (5.0392)	W61 (2.0410)	I39 (2.6118)	W95 (1.5097)	W33 (3.0286)	A41 (1.3541)	A63 (3.1611)	W125 (1.1782)
W84 (3.7454)	W115 (1.8197)	A70 (2.2957)	I45 (1.5062)	A24 (2.6407)	W242 (1.3519)	A75 (2.5542)	7-4-1 (1.1609)
W69 (3.3697)	W103 (1.7913)	W106 (2.2920)	W51 (1.5040)	I74 (2.3037)	A43 (1.3500)	W90 (2.2358)	W60 (1.1421)
W62 (3.3183)	W47 (1.7666)	I12 (2.2446)	I172 (1.3805)	W197 (2.2600)	W214 (1.2771)	W187 (2.0838)	A80 (1.1343)
W89 (3.1183)	W97 (1.7653)	I33 (2.2171)	W117 (1.3225)	W248 (2.1124)	W249 (1.2435)	A91 (1.9357)	W16 (1.1177)
W94 (2.8664)	W106 (1.7520)	I85 (2.1454)	W90 (1.2867)	W63 (1.9946)	W27 (1.2370)	W95 (1.8987)	W225 (1.1105)
W85 (2.6970)	W34 (1.7207)	A22 (2.1052)	A16 (1.2858)	A29 (1.9514)	I76 (1.2337)	W220 (1.8690)	W234 (1.0740)
W90 (2.5905)	W199 (1.5711)	A75 (2.1005)	W125 (1.2582)	W235 (1.6953)	W225 (1.2208)	W179 (1.8284)	W180 (1.0621)
A63 (2.5887)	W27 (1.5285)	W69 (2.0750)	W237 (1.1720)	I12 (1.6667)	W234 (1.1946)	W248 (1.6713)	A81 (1.0078)
W86 (2.5158)	W214 (1.3762)	A4 (1.8968)	W85 (1.1251)	W216 (1.5438)	W99 (1.1904)	A11 (1.4817)	W237 (1.0040)
W95 (2.4079)	A26 (1.1568)	7-4-1 (1.8591)	I5 (1.1111)	W199 (1.5073)	W61 (1.1501)	W177 (1.3633)	W121 (1.0009)
W92 (2.2436)	W26 (1.1077)	A81 (1.8108)	7-4-4 (1.0833)	I92 (1.4908)	A91 (1.0797)	W96 (1.1912)	
W63 (2.1385)	A91 (1.0193)	I40 (1.7721)	W132 (1.0243)	A80 (1.4645)	A53 (1.0441)		
W96 (2.0748)		A82 (1.6869)	A78 (1.0215)	A39 (1.3662)			
		A67 (1.5257)	W220 (1.0214)				

variance with the traits, spikelet fertility (-0.6144) and number of filled grains per panicle (-0.5097) showing negative association with PC4.. The findings of present study were in partial confirmation with Kumari *et al.* (2021), in which spikelet fertility and number of filled grains per panicle dominated PC3. Thus, early shoot length, number of filled grains per panicle and panicle length in PC1, number of productive tillers, plant height, single plant yield and grain yield per plot in PC2, 1000 seed weight in PC3 and spikelet fertility in PC4 could be studied owing to their to total variance. Selection of these traits would be rewarding.

The genotypes chosen for the study were displayed in **Table 9** based on PC scores. These scores can aid in the selection of genotypes whose variability is explained by each main component. A high PC score for a specific genotype in a specific component indicates high values for the variables in that specific genotype (Singh and Chaudhary, 1977). In each of the four principle components, the top PC scores with positive values greater than one were chosen. W90 and W95 had high PC scores in PC1, PC2, and PC4, while A91 had high PC scores in PC1, PC3, and PC4. As a result, these lines possessed excellent yield and other quantitative features. W90 (2.5905) received the highest positive value based on PC scores. Similar study has been done and supported by Gour, Lokesh *et al.* (2017), Rahangdale *et al.* (2021) in rice, and Singh *et al.* (2020) in capsicum. It is possible to conclude that principal component analysis highlights the characters with the greatest variability. As a result, intensive selection strategies can be devised to produce rapid improvements in yield and component attributes.

From the mean performance of the introgressed lines, it could be concluded that the lines of the intercrosses harbouring more than a qDTY QTL showed high mean values for yield. Studies on variability and heritability revealed the traits such as early shoot length, early root length, total number of tillers per plant, number of productive tillers per plant, spikelet fertility, single plant yield, 1000 seed weight and grain yield per plot showed high heritability and genetic advance. Hence, the selection of genotypes based on these traits would be effective. The results of correlation and path analysis reveal that the genotypes with high number of productive tillers, increased number of filled grains and reduced plant height are expected to yield high. From the principal component analysis, the genotypes with high PC scores falling under each component contributing to particular trait would be chosen for further breeding programmes. Thus, the genotypes W16, W69, W85, W92,W94, W95, W106,W117, W125,W132, W237, 7-4-4, 7-4-1, A4,A22, A70,A82, I33 and I40 could be chosen on the basis of overall mean performance and analysis performed for selection under target production environment.

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