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RESEARCH ARTICLE

Genetic variability, association and path analysis in the F_2 population of rice (*Oryza sativa* L.)

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Abstract

The present study focused on estimating variability attributes, heritability, genetic advance, trait relationship and path coefficient analysis for ten traits in an F_2 individuals resulting from the cross between CO 52 and FR13A. Notably high values for genotypic and phenotypic coefficients of variation (GCV and PCV), along with high heritability and substantial genetic advance as a percentage of the mean, were observed for traits such as single plant yield, number of filled grains and number of productive tillers. These results suggest the influence of additive gene action and implied that simple selection methods would be effective for improving these attributes. Traits including the number of tillers, productive tillers, filled grains and spikelet fertility showed significant positive correlations and a significant absolute effect on single plant yield, indicating their potential value in enhancing yield. From the total of 190 F2 plants, 57 individuals carrying the favorable SUB1 QTL allele were identified for further submergence tolerance screening. The findings from this research offered valuable insights for selecting promising traits and can contribute to future rice breeding efforts aimed at improving yield.

Keywords: F_2 population; genetic parameters; rice; *SUB1* QTL

Introduction

Rice (*Oryza sativa L.*) is a fundamental staple crop, nourishing over half of the global population. Across Asia, Africa and Latin America, rice was cultivated in a range of ecosystems, including irrigated fields, rainfed lowlands and uplands. In 2023, global rice production reached approximately 520 million metric tons, with Asia contributing about 90 % of this yield. However, rice cultivation faced significant challenges from abiotic stresses, particularly submergence due to flooding. Annually, around 150 lakh hectares of paddy fields in South and Southeast Asia were prone to flash floods, leading to substantial yield losses (1). In Tamil Nadu 1.7 million hectares were occupied by rice and 75 % of the area was cultivated during samba season (Sep-Jan). This season was favourable for rice cultivation, especially for medium and long-duration varieties, which dominated the planted area. However, during the northeast monsoon, 2 to 3 lakh hectares became vulnerable to flooding. The excess rainfall, combined with inadequate drainage of canal water, led to submergence in several regions. The tail-end areas of the delta districts *viz.,* Thiruvarur, Nagapattinam and Cuddalore were particularly prone to flooding, often resulting in reduced crop productivity (2). CO 52 rice variety was medium duration with good cooking quality and was cultivated during the samba season but was susceptible to submergence (3). To address this issue, developing submergence tolerant rice varieties became a critical focus. Modern rice varieties typically could not survive more than a week of complete submergence in flooded water, resulting in crop failures and threatening food security in vulnerable regions. To address this issue, developing submergence-tolerant rice varieties has become a critical focus. FR13A was submergence tolerant rice landrace derived through pureline selection from Dhalputtia rice landrace from Orissa. A major breakthrough was the discovery of the *SUB1* quantitative trait locus (QTL) from the FR13A in rice chromosome 9 (4). The *SUB1* locus included genes encoding ethylene response factor (ERF) transcriptional regulators, notably SUB1A, which enhanced survival under prolonged submergence by limiting excessive elongation and conserving energy (1). Marker-assisted early generation selection (MAS) was involved in incorporating the SUB1 QTL into popular high-yielding rice varieties. This approach enabled precise and efficient transfer of submergence tolerance traits without altering other desirable agronomic characteristics. For instance, the CR 1009-*Sub1*(CR 1009/FR13A), Swarna-*Sub1* (Swarna/ IR 49830-7-1-2-2) and CO 43 *Sub-1* (CO 43/FR13A), developed through MAS, could withstand up to two weeks of complete submergence, significantly reducing yield losses in flood-prone areas (2, 5, 6). The success of MAS in developing submergence-tolerant rice underscored its importance in modern plant breeding (4, 6). By facilitating the rapid and accurate integration of stress-tolerance traits, MAS contributed to the resilience and sustainability of rice production systems, ensuring food security for millions dependent on this vital crop. The genotypic coefficient of variation (GCV) indicated the degree of genetic diversity within a trait, representing the proportion of overall variation that was attributed to genetic parameters. Heritability was a considered a dependable measure of the extent to which traits could be transmitted from parents to offspring (4). In light of these considerations, CO 52 a fine grain, elite variety was found to be cultivated during samba season which was mainly prone to flooding in flood prone areas of Tamil Nadu (3). To overcome this issue the present study emphasized on evaluating several genetic parameters and identifying marker associations in the segregating F_2 population derived from the cross CO 52 × FR13A. The success of all yield improvement programs was fundamentally based on genetic variability, coupled with the application of appropriate selection strategies (7).

Another important parameter-genetic advance provided insight into improvement of potentially specific traits within a population under selection pressure.

Furthermore, integrating correlation and path coefficient analyses offered a deeper insight into the interrelationships among various traits, helping to identify key factors that influenced overall performance. This combined approach supported the development of more effective breeding strategies aimed at producing improved plant varieties. Genetic variability coupled with advanced breeding techniques like marker-assisted selection, enabled the development of submergence-tolerant varieties. These innovations were vital for sustaining rice production in flood-prone regions, ensuring stable yields and supporting the livelihoods of farmers worldwide.

Materials and Methods

Genetically pure seeds of CO 52 (susceptible to submergence) and FR13A (tolerant to submergence) were used as parents in the crossing programme. The study was carried out at the Paddy Breeding Station (PBS), Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University, Coimbatore and seeds were sown and crosses were performed between CO 52 and FR13A to produce hybrid seeds. These crossed seeds were used to establish the F_1 generation and individual F_1 plants were selfed; seeds were bulked harvested to grow the F_2 generation. A total of 190 F_2 individual segregants were cultivated with a spacing of 25 × 25 cm, following recommended crop management practices. Ten attributing parameters were evaluated in each F_2 plant SF: Spikelet fertility (%), PH: Plant height (cm), NT: Number of tillers, NPT: Number of productive tillers, PL: panicle length (cm), NFG: Number of filled grains, NUFG: Number of unfilled grains, TG: Total number of grains, 100 GW: Hundred grain weight (g) and SPY: Single plant yield (g).

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following the method recommended (9). Variations were categorized into three levels: low for less than 10 %, moderate of 10 to 20 % and high for more than 20 % as suggested by Sivasubramanian and Madhava Menon (10). Since replicated trials were not possible for segregants, environmental variance was estimated from replicated experiment of parental lines. Broad-sense heritability was determined using (11) formula and was classified into high for more than 60 %, moderate as 30 to 60 % and low for lesser than 30 %. Genetic advance as a percentage of the mean was computed based on the method described by Johnson (12), with classifications as lower than 10 %, moderate of 10 to 20 % and higher than 20 %.

$$Heritability = \frac{Vg}{Vp} = \frac{Vg}{Vg + Vp}$$

Vg, Vp and Ve are genotypic, phenotypic and environmental components respectively

Genetic advance percent of mean =

Genetic advance / mean x 100

$$Genetic\ advance = \frac{\sigma_g^2}{\sigma_p^2} \times K$$

$\sigma^2{}_g$ = Genotypic variance, $\sigma^2{}_p$ =

Phenotypic variance and K is selection differential

The association among yield attributing traits was analysed using formula (13). Path was analysis was performed following the approach described (14). Data analysis was conducted using TNAUSTAT software (15). The classification of values obtained in path analysis was carried out based on the Lenka and Mishra (1973) and was classified into five categories: negligible for 0.00-0.09, low of 0.10-0.19, moderate of 0.20 to 0.29, high for 0.30 to 1.00 and very high of more than 1.00 (16). Hybridization was performed between the CO 52 X FR13A *Rabi* 2022, to develop F_1 and plants were selfed to generate to F_2 generation. DNA extraction of 190 F_2 plants along with parents was carried out using the method suggested by Murray and Thompson (17). InDel marker ART5 which was linked with *Sub1* QTL of chromosome 9 in rice was used for genotyping and exhibited polymorphism between both the parents (Fig. 2) (18). Polymerase Chain Reaction (PCR) was performed in a final reaction volume of 10 µL. The reaction mixture contained 2 µL of template DNA (20 ng/µL), 0.5 µL each of forward and reverse primers (10 µM), 4 µL of 2X master mix and 3 µL of sterile distilled water. The thermal cycling program performed using thermal cycler (Bio-Rad T 100) began with an initial denaturation at 95 °C for 5 min, followed by 35 cycles consisting of denaturation at 94 °C for 1 min, annealing at 58.5 °C for 45 sec and extension at 72 °C for 30 sec. A final extension was carried out at 72 °C for 10 min, after which the reaction was held at 4 °C. PCR products were separated on a 3 % agarose gel. A 100 bp DNA ladder (Bio-Helix) was used to distinguish the size of band. DNA bands were visualized under UV light using a Bio-Rad gel XR⁺ documentation system at 320 nm. The plants were selected based on the homozygous band products like of donor parent (FR13A).

ART5-Forward sequence	ART5-Reverse sequence	Annealing temperature
5'CAGGGAAAGAGATGGT GGA 3'	**5' TTGGCCCTAGGTTGTTTC AG 3'**	**58.5 °C**

Results and Discussion

Coefficient of variation

As the study began with analysis of F_2 generation therefore the variability among the 190 individuals was highly segregated. Statistically it was observed that the Phenotypic Coefficient of Variation (PCV) was higher than the Genotypic Coefficient of Variation (GCV) for all traits studied. The phenotype of the plants depended on both genotype and environmental factors (19). In this study the influence of environmental effect was higher in expression of the studied traits (Table 1) (20). Transgressive segregants were also observed in all the traits. Although environmental factors contributed to phenotypic variability, the presence of transgressive segregants and unexpected trait combinations among F_2 individuals provided strong evidence for the role of epistasis in trait inheritance (21). Such interactions might have either enhanced or suppressed the expression of certain traits, thereby complicating the selection process in early generations.

The High PCV and GCV were observed for traits such as the number of tillers per plant (33.07 and 29.04), number of productive tillers per plant (28.82 and 25.68), number of unfilled grains per panicle (39.87 and 33.98) and single plant yield (26.49 and 24.07). This observation aligns with the findings of earlier researchers, who reported similar findings for these traits (22-27).

Moderate PCV and GCV were noted for traits such as total number of grains (19.14 and 18.57) and hundred grain weight (11.63 and 11.22). Moderate PCV and low GCV were recorded for Plant height (11.80 and 9.40), spikelet fertility (12.86 and 8.96). These findings were consistent with the earlier reports, where similar results were documented for height and panicle length in rice (28, 29). Low PCV and GCV were observed for panicle length (9.36 and 6.65). Low PCV and GCV were noted for traits with relatively narrow genetic variability, which agreed with reported findings (25). High environmental coefficient of variation was observed for number of unfilled grains (5.89) followed by spikelet fertility (3.9) and number of tillers (3.63) indicating the high influence of environmental factors. Least environmental coefficient variation was found in hundred grain weight (0.41) followed by total number of grains (0.57) and number of filled grains (1.97) and these traits were least influenced by environmental factors.

Heritability and GAM

Heritability represented the proportion of phenotypic variation that was attributable to genetic factors and served as a reliable indicator of the extent to which traits were passed from parents to their offspring (11). The heritability (H^2) estimation showed high values for all traits, suggesting a strong genetic influence and concurrent findings was observed by previous researchers (22, 24). Traits such as the number of tillers per plant (79.24 and 53.99), number of productive tillers per plant (79.39 and 47.14), number of grains per panicle (94.16 and 37.14), number of filled grains per panicle (82.81 and 37.24), number of filled grains per panicle (82.81 and 37.24), number of unfilled grains per panicle (72.62 and 59.66), hundred grain weight (93.00 and 22.29) and single plant yield (82.59 and 66.95) exhibited high heritability and Genetic Advances as a percentage of the Mean (GAM). This indicated the predominance of additive gene action, which implied that selection for these traits would have been effective and more rewarding. These results aligned with the observations of earlier researchers for plant height, total number of grains and number of filled grains per panicle and single plant yield, panicle length, single plant yield and hundred grain weight (22, 24, 30, 16).

Traits with high heritability and high GAM, such as single plant yield (82.59 and 66.95), number of filled grains (82.81 and 37.24) and number of productive tillers (79.39 and 53.99), indicated potential for noteworthy genetic gain through selection, suggesting the presence of additive gene effects. Therefore selection based on these traits could be effectively carried out (22, 24, 31). High heritability coupled with moderate GAM was observed for plant height (63.09 and 15.39). Panicle length (50.57 and 9.75) exhibited high heritability with low GAM, suggesting the influence of non-additive genetic action,

Table 1. Genetic variability parameters of various biometrical observation for F_2 population of CO 52 x FR13A

Traits	Mean	Min	Max	PCV	GCV	H2	GAM	SK	Kurt
PH	115.31	90.00	138.00	11.84	9.40	63.09	15.39	-0.21	-1.16
NT	14.31	7.00	22.00	33.07	29.44	79.24	53.99	0.027	-1.20
NPT	10.81	4.00	19.00	28.82	25.68	79.39	47.14	0.11	-0.67
PL	27.96	22.90	32.40	9.36	6.65	50.57	9.75	-0.19	-1.14
NFG	155.06	78.00	243.00	21.83	19.86	82.81	37.24	0.30	-0.28
NUFG	58.53	20.00	96.00	39.87	33.98	72.62	59.66	-0.02	-1.27
TG	213.59	119.00	330.00	19.14	18.57	94.16	37.14	0.30	-0.06
SF	72.80	45.90	91.30	12.86	8.96	48.52	12.86	-0.05	-0.53
100 gw	2.30	1.80	2.90	11.63	11.22	93.00	22.29	0.60	-0.19
SPY	29.94	8.50	48.80	26.49	24.07	82.59	66.95	-0.49	-0.14

PH: Plant height, NT: Number of tillers, NPT: Number of productive tillers, PL: panicle length, NFG: Number of filled grains, NUFG: Number of unfilled grains, TG: Total number of grains, SF: Spikelet fertility, 100 GW: Hundred grain weight and SPY: Single plant yield.

indicating selection would be ineffective (32).

Correlation

Correlation indicated the strength and direction of the relationship between two variables. In the context of plant breeding and genetics, correlation coefficient analysis was used to assess the interrelationship among different plant traits and to identify key traits that could be targeted for selection to enhance yield through genetic improvement (13). Yield was a complex quantitative trait influenced by the several interactions of traits. Hence, yield improvement programs in rice should have emphasized indirect selection of traits strongly associated with yield. In present study, correlation analysis was conducted to examine the association between single plant yield and numerous agronomic traits, providing insights into their direct and indirect contributions to yield enhancement.

The analysis showed single plant yield had a significant positive correlation with number of tillers per plant ($r = 0.59$, $P \leq 0.001$) , spikelet fertility ($r = 0.32$, $P \leq 0.001$) , number of productive tillers per plant ($r = 0.66$, $P \leq 0.001$) , number of filled grains ($r = 0.45$, $P \leq 0.001$) and number of total grains ($r = 0.31$, $P \leq 0.001$) (Fig 1). These results suggested that these traits were important determinants of yield and could be targeted for genetic improvement. Similar findings were reported by earlier researchers, who emphasized the role of number of filled grains and number of productive tillers in enhancing yield in rice (25, 33-37).

The number of tillers per plant also revealed a positive association with spikelet fertility (SF) and number of productive tillers per plant

$r = 0.89$, $P \leq 0.001$) and significant negative association with hundred grain weight ($r = -0.36$, $P = 0.001$) and total number of grains ($r = -0.15$, $P \leq 0.01$). These associations were consistent with the findings from earlier experiment demonstrated the significance of number of productive tillers in rice yield improvement (25).

A significant negative correlation was observed between number of productive tillers per plant with total number of grains ($r = -0.16$, $P \leq 0.1$) and hundred grain weight ($r = -0.32$, $P \leq 0.001$). This aligned with reports suggested that these traits collectively enhanced the grain-filling process, ultimately contributing to higher yield (24, 38).

Spikelet fertility was positively correlated with number of filled grains ($r = 0.46$, $P \leq 0.001$) showed a significantly negative correlation with number of unfilled grains ($r = -0.87$, $P \leq 0.001$), which indicated that increased spikelet fertility minimized grain losses, improving yield potential (36, 39).

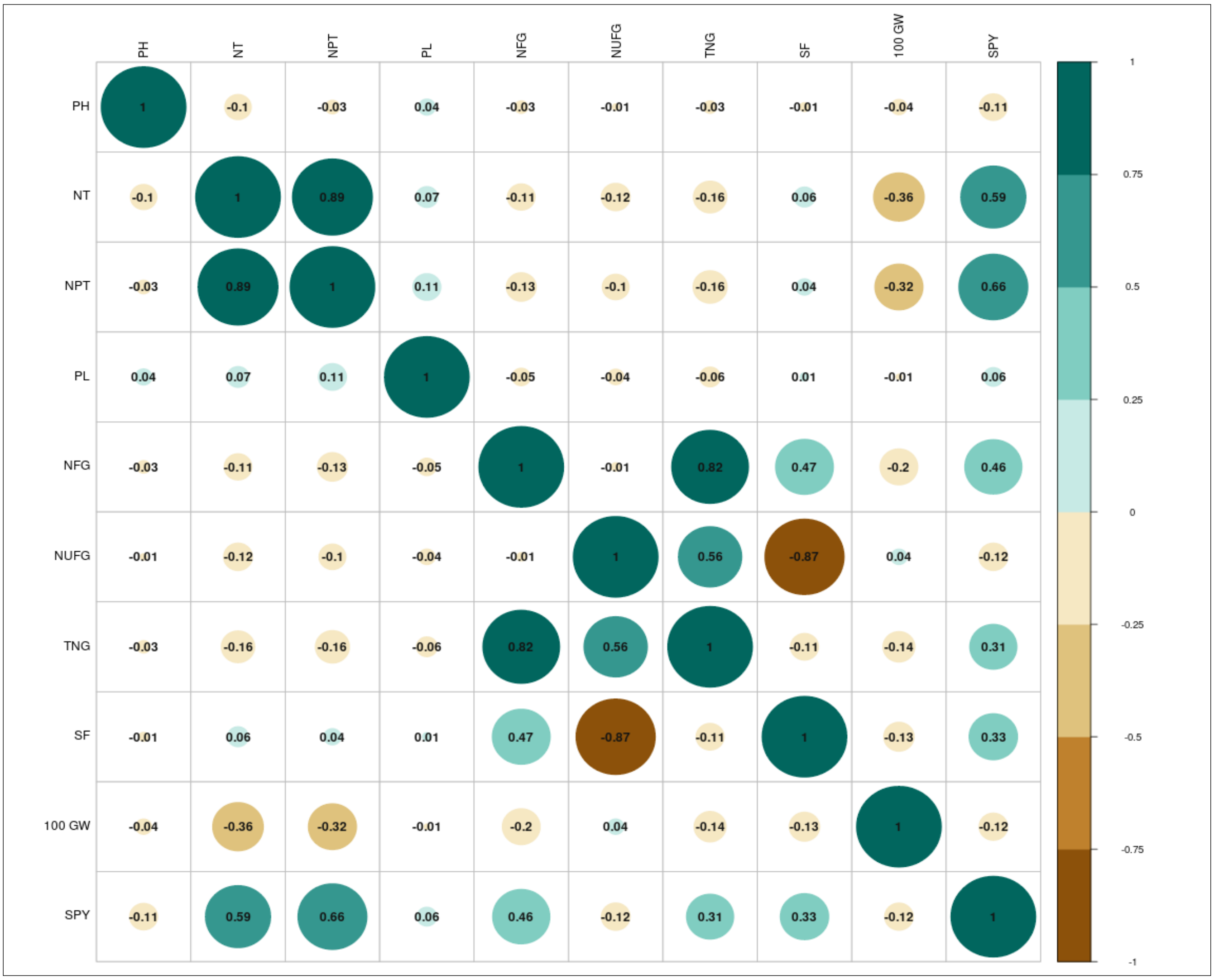

Fig. 1. Heat map depicting phenotypic correlation among the biometrical traits in F_2 generation of CO 52 X FR13A cross.

PH: Plant height, NT: Number of tillers, NPT: Number of productive tillers, PL: panicle length, NFG: Number of filled grains, NUFG: Number of unfilled grains, TG: Total number of grains, SF: Spikelet fertility, 100 GW: Hundred grain weight and SPY: Single plant yield.

Path analysis

Path analysis was a statistical method that partitioned the correlation coefficient into direct and indirect effects, allowing for the assessment of how each independent variable contributed to a dependent variable. Originally introduced by Wright in 1921, this technique was first applied to plant selection by Dewey and Lu (1959) in crested wheatgrass (14, 40). In plant breeding, path analysis helped determine whether the relationship between yield and its contributing traits was a result of direct influence or mediated through indirect effects via other associated traits. The path coefficient analysis of various traits related to rice yield provided insights into the direct and indirect contributions of each trait (Table 2). Number of filled grains (1.40) exhibited a very high positive direct effect on single plant high direct effect on single plant yield was also observed for number of productive tillers (0.77), spikelet fertility (0.34) and a moderate positive direct effect for hundred grain weight (0.28) and total number of grains (0.27) indicating their critical roles in yield improvement. This suggested that selection for genotypes with a higher number of filled grains will directly enhance yield. Similar findings were reported by previous studies (25). Emphasizing the importance of filled grains in yield enhancement. Spikelet fertility (0.34) displayed a moderate positive direct effect, demonstrating its importance as a key determinant of yield. This trait directly influenced grain filling which was also observed. A significant positive direct effect highlighted its role as a yield -contributing factor. Number of productive tillers were shown to be critical for increasing the total grain yield, aligning with the studies (36). Number of filled grains (1.18) exhibited a very high indirect effect on yield through its positive influence and traits total number of grains (0.85), spikelet fertility (0.74), number of productive tillers (0.58) and number of tillers (0.52). These traits exhibited high indirect effects on yield. The results suggested that number of filled grains, total number of grains, spikelet fertility, number of productive tillers and number of tillers improved yield through indirect effect. This indicated its importance traits in breeding programs focused on improving yield potential. This finding was consistent with earlier studies that reported similar relationships (37). The results emphasized the importance of prioritizing traits with strong direct effects on yield, such as number of filled grains, number of productive tillers, spikelet fertility and number of unfilled grains, in breeding programs. These traits were identified as key to improving the genetic potential for rice yield. Indirect contributions from traits like number of filled grains, total number of grains, spikelet fertility, number of productive tillers and number of tillers indicated the need for comprehensive selection strategies that accounted for their interactions with other yield determining factors.

The yield parameters number of filled grains ($r = 0.45$ and $p = 0.001$) which was positively and significantly correlated with single plant yield also marked very high direct effect (1.40) and very high indirect effect (1.18) (41).

Marker assisted selection for submergence tolerance F_2 segregating populations

A total of 190 plants in F_2 generation, evaluated in non-replicated trial were assessed genotypically using the submergence-specific InDel marker ART5 from chromosome 9 of rice. Parental polymorphism analysis was conducted and both parents exhibited polymorphism for the marker. F_1confirmation was done using this marker to identify heterozygous plants (true F_1). Out of 38 plants 13 plants were confirmed as true F_1. These true F_1 were selfed and 190 F_2 plants was developed. Marker exhibited polymorphism between both the parents at annealing temperature of 58.5 °C was used to identify the *SUB1* QTL positive plants (Fig. 2). Out of 190 segregants 71 plants were heterozygous and 62 plants having CO 52 allele and another 57 plants exhibited FR13A allele for ART 5 marker. Based on Chi-square analysis, it was observed that 50 percent probability of F_2 population genotyped using ART5 marker found to be fit in expected mendelian ratio of 1:2:1. Submergence screening was phenotypically destructive method hence these F_2 population was genotyped using submergence specific marker ART5 marker and plants were genotypically selected based on the banding pattern produced by FR13A. Out of 57 plants, line 173 (48.8 g), line 178 (43 g), 182 (42.7 g) and 110 (41.9 g) were observed to have high yield than CO 52 (41.26 g) indicating the nature of transgressive segregation (Table 3). Plants with the allele pattern resembling the allele size of FR13A allele were advanced to next generation. The preliminary findings of this study suggest that integrating marker-assisted selection (MAS) offered greater potential for enhancing submergence tolerance in early-generation breeding populations derived from elite crosses, compared to using conventional approach alone (42).

Table 2. Direct and indirect effects of different biometrical traits as partitioned by path analysis for the cross CO 54 X FR13A

Traits	PH	NT	NPT	PL	NFG	NUFG	TNG	SF	100 GW	SPY
PH	-0.05	-0.01	-0.02	0.01	-0.04	0.00	0.01	0.00	-0.01	-0.13
NT	0.01	0.07	0.68	0.01	-0.15	-0.04	0.04	0.02	-0.10	0.53
NPT	0.01	0.06	0.77	0.01	-0.18	-0.03	0.04	0.01	-0.09	0.58
PL	0.01	0.01	0.09	0.01	-0.07	-0.01	0.02	0.01	0.01	0.02
NFG	0.01	-0.01	-0.10	0.01	1.40	0.01	-0.22	0.16	-0.06	1.18
NUFG	0.01	-0.01	-0.08	0.01	-0.02	0.33	-0.15	-0.30	0.01	-0.21
TNG	0.01	-0.01	-0.13	0.01	1.15	0.19	-0.27	-0.04	-0.04	0.85
SF	0.01	0.01	0.03	0.01	0.66	-0.29	0.03	0.34	-0.04	0.74
100 GW	0.01	-0.02	-0.25	0.01	-0.28	0.01	0.04	-0.05	0.28	-0.26

PH: Plant height, NT: Number of tillers, NPT: Number of productive tillers, PL: panicle length, NFG: Number of filled grains, NUFG: Number of unfilled grains, TG: Total number of grains, SF: Spikelet fertility, 100 GW: Hundred grain weight and SPY: Single plant yield.

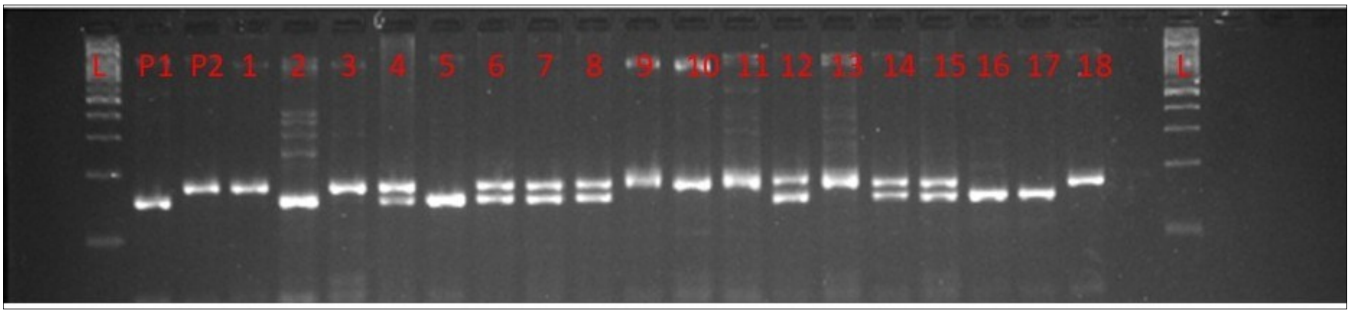

Fig. 2. Representative gel image showing amplification pattern of the cross CO52 X FR13A using Indel marker ART5.

Table 3. Data of single plant yield and the genotypic score of 190 F_2 individuals

S.No	SPY	GS	S.No	SPY	GS	S.No	SPY	GS	S.No	SPY	GS	S.No	SPY	GS
1	38.5	B	39	26.5	B	77	19.7	B	115	39.5	H	153	34.8	H
2	8.5	A	40	13.4	B	78	36.2	H	116	30.7	H	154	24.9	H
3	32.4	B	41	29	B	79	34.2	A	117	24.9	H	155	22.4	A
4	37.7	H	42	20.8	B	80	26.5	H	118	25	A	156	27	A
5	35.4	A	43	37.3	B	81	23	H	119	43.6	A	157	30.6	H
6	33.2	H	44	30.7	A	82	35.7	H	120	19.7	A	158	36.7	H
7	20.5	H	45	25.2	H	83	15.7	A	121	38	A	159	32.8	A
8	10.7	H	46	20.8	A	84	26.5	H	122	22.8	A	160	36.3	A
9	33	B	47	31.8	H	85	35.5	H	123	38.8	A	161	39.5	A
10	16.9	B	48	29.7	B	86	27.6	H	124	36.4	A	162	18.8	A
11	31.7	B	49	27.7	B	87	15.8	A	125	40.4	H	163	23.6	H
12	17.5	H	50	11.6	H	88	32.8	H	126	35	B	164	29.4	A
13	30.4	B	51	18.8	A	89	28.7	H	127	30.8	A	165	32.3	H
14	25.6	H	52	28.8	B	90	22.7	H	128	34.8	H	166	38.7	A
15	22	H	53	31.7	H	91	24.8	H	129	30.3	H	167	25.9	A
16	28.8	A	54	24.8	B	92	29.7	A	130	22.9	H	168	34	B
17	28.6	A	55	20.7	B	93	32.7	A	131	23.8	A	169	43.5	A
18	26.1	B	56	32.9	B	94	26.5	A	132	12.7	H	170	41	A
19	37.6	H	57	17.7	H	95	36.8	B	133	43.7	H	171	32.8	H
20	18.4	B	58	25.5	A	96	35.6	B	134	31.8	H	172	38.7	A
21	15.5	B	59	24.9	A	97	35.7	B	135	37.9	A	173	48.8	B
22	27.5	B	60	19.7	A	98	36.6	H	136	33.7	A	174	31.9	A
23	33.9	B	61	31.7	B	99	39.4	B	137	28.6	A	175	8.5	H
24	30.4	B	62	31.9	B	100	35.9	A	138	33	H	176	37.7	H
25	32.8	H	63	22.6	B	101	33.9	H	139	23	H	177	38.8	A
26	33.7	H	64	27.5	B	102	39.7	A	140	31.7	H	178	43	B
27	27.6	H	65	19.7	B	103	37.7	A	141	26.8	A	179	38.7	A
28	30.8	H	66	24.4	B	104	32.5	A	142	38.7	H	180	28.6	A
29	27.8	A	67	28.8	B	105	35.9	B	143	31.7	H	181	37.7	H
30	19.8	B	68	27.7	H	106	28.7	A	144	24.8	A	182	42.7	B
31	22.8	H	69	34.7	B	107	37.9	H	145	29.7	A	183	37.5	B
32	26.1	B	70	30.7	H	108	38.6	A	146	35.6	A	184	37.7	H
33	32.7	B	71	38.7	A	109	30.7	H	147	18.8	A	185	40.7	B
34	25	A	72	16.5	B	110	41.9	B	148	32.7	A	186	32.9	B
35	17.5	H	73	28.5	H	111	43.7	H	149	32.9	A	187	39.8	H
36	29.7	H	74	32.7	A	112	36.8	H	150	37.6	B	188	37.3	B
37	28	B	75	31.7	A	113	41.7	H	151	11.8	B	189	13.3	B
38	12.8	B	76	34.8	H	114	39.7	H	152	31.7	B	190	29	H

SPY: Single plant yield and GS: Genotyping score

Conclusion

In conclusion, traits with high heritability and high GAM, such as single plant yield, number of filled grains and number of productive tillers, indicated potential for significant genetic improvement through selection strategies. The findings from this correlation highlighted the significance of characters such as the number of tillers, number of productive tillers, number of filled grains and spikelet fertility which were significantly correlated with single plant yield. These traits should be ranked in rice breeding programs to achieve genetic gains in yield. The path coefficient identified the number of filled grains, number of productive tillers and spikelet fertility as the most critical traits for yield improvement. From the molecular analysis it was concluded that four segregants -line 110, 173, 178 and182 - outyielded the susceptible parent CO 52. Hence, early-generation marker-assisted selection at F_2 generation provided an opportunity to identify promising genotypes efficiently, saving both time and resources by focusing on selected line

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Authors' contributions

SV, MS, MRS conducted the field work and post-harvest data collection. RS, RK, SM, RP, RPA, MR, AJ, NS and KSB contributed to the formulation of the work and provided the field and laboratory facilities to carry out the research.

Compliance with ethical standards

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