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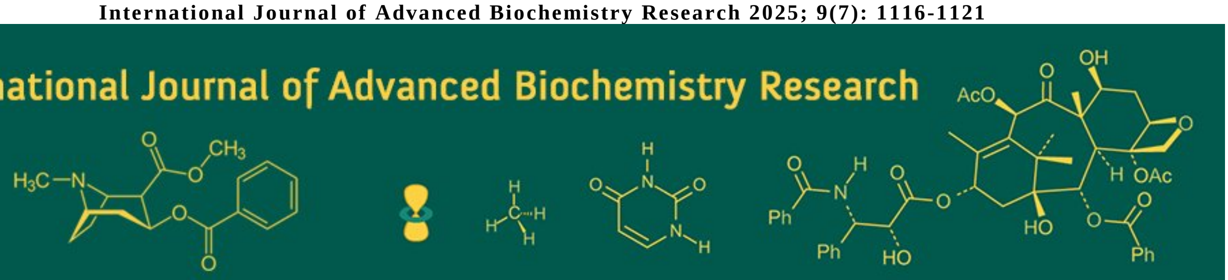

Genetic variability, correlation and path coefficient analysis in *Sub1* introgressed restorer lines of Rice (*Oryza sativa* L.)

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Abstract

The present study was conducted to assess the genetic variability parameters, correlation and path coefficient analysis for seven yield related traits in BILs (BC_2F_5) of an elite restorer KMR-3R and Swarna-Sub1 at ICAR-IIRR, Hyderabad during *Kharif*, 2020 and *Rabi*, 2021. The results indicated that, estimates of Phenotypic coefficient of variation (PCV) were higher than Genotypic coefficient of variation (GCV) for all the traits studied, suggesting that these traits were influenced by the environment. Single plant yield (SPY) and plant height (PH) showed moderate PCV, and GCV, high heritability [h^2 (%)] and genetic advance as percent of mean (GAPM). Correlation and path coefficient studies showed that SPY was associated significantly positive with days to 50% flowering (DFF) and number of productive tillers (PT), high positive direct effect on single plant yield was recorded by number of productive tillers, days to 50% flowering and spikelet fertility [SF (%)]. These traits should be prioritized for the selection of the potential BILs of restorer for developing high yielding submergence-tolerant rice hybrids suitable for flood-prone areas.

Keywords: Submergence, rice, variability, correlation

Introduction

Rice (*Oryza sativa* L.) is a staple food crop and a vital source of sustenance for over half of the global population, particularly in Asia, where more than 90% of the global rice is cultivated (Bandumula, 2018) [4]. As demands for food security increase beside climate change, resource constraints, and evolving agroecosystems, developing high-yielding and climate-resilient rice varieties has become a major goal of modern plant breeding programs (Sandhu *et al*., 2021) [35].

Among the strategies to enhance rice productivity, hybrid rice produces 15-20% yield advantage over high-yielding varieties, making it one of the most cost-effective approaches for enhancing rice productivity and food security (Ravindra Babu *et al*., 2012) [32]. However, the rice production is increasingly threatened by abiotic stresses like submergence, especially in rainfed lowland areas. Submergence stress occurs when rice plants are fully submerged during flash floods at the seedling or vegetative stage, that can persist for up to two weeks (Hussain *et al*., 2024) [14]. The causes of submergence include heavy rainfall, river overflow, cyclonic storms, tides, poor drainage, low-lying topography and climate changes (Oladosu *et al*., 2020) [25]. Flooding annually affects over 20 million hectares of rice-growing land across Asia, causing economic losses between $650 million and $1 billion, whereas in India, about 4.4 M ha are flood-prone, leading to yield loss depending on flood intensity, duration and crop stage (Singh *et al*., 2022) [37]. Submergence stress reduces oxygen availability, inhibits root growth, and disrupts water and nutrient uptake resulting in reduced plant vigour, impairs leaf nitrogen content, water potential, and photosynthesis, while accelerating chlorosis and leaf senescence (Zheng *et al*., 2009) [43]. Increased ROS production under waterlogging causes oxidative damage, lipid peroxidation, and cell death (Sharma *et al*., 2012) [38]. Submergence limits photosynthesis and accelerates sugar consumption via fermentation, depleting carbohydrates and potentially leading to plant death (Bailey-Serres and Voesenek, 2008; Colmer and Voesenek, 2009) [3, 10].

Understanding the extent of genetic variation in yield- and its related traits is important for efficient selection in breeding programs. Parameters such as genetic variability and heritability along with genetic advance, helps in efficient selection (Parimala and Devi, 2019) [38]. Correlation evaluates the relative effect of various traits on grain yield whereas path coefficient analysis assesses the direct and indirect effects through traits (Dewey and Lu, 1959) [11]. To overcome this, marker assisted backcross breeding for developing submergence tolerant rice varieties has been widely adopted (Mackill *et al*., 2012) [22]. In this context, the present study was conducted to evaluate 19 BILs developed by introgression of *Sub1* into the elite restorer KMR-3R using Swarna-Sub1 as the donor. The BILs were evaluated along with parents during wet and dry seasons to assess the variability, and the interactions among yield-related traits.

Materials and methods

The present study was carried out using 21 genotypes (19 BILs and 2 parents) in RCBD design with three replications during *Kharif*, 2020 and *Rabi*, 2021 at ICAR-IIRR farm, Rajendranagar, Hyderabad. The experimental material consists of nineteen BILs (BC_2F_5) derived from KMR-3R (recurrent parent) and Swarna-Sub1 (donor parent). The BILs were coded as TCP lines for readability and their details were given in the Table-1. The phenotypic data of genotypes in both wet and dry seasons were recorded for all the BILs along with parents for yield and its related traits. The traits are days to 50% flowering (DFF), plant height (PH, cm), number of productive tillers (PT), panicle length (PL, cm), spikelet fertility (SF, %), thousand grains weight (TGW, g) and Single plant yield (SPY, g).

Statistical analysis

Analysis of variance (ANOVA) was conducted across two seasons (*Kharif*, 2020 and *Rabi*, 2021) to evaluate the significance of variation for various agronomic traits among the genotypes. ANOVA, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (GAPM), Correlation and path coefficient analysis were estimated for yield and its attributing characters in 21 rice genotypes using Window Stat version 9.1 software.

ANOVA was done by using Panse and Sukhatme, 1985. GCV and PCV were calculated by using the formula given by Falconer, (1981) [13]. Range of variation was classified as high (>20%), moderate (10-20%) and low (<10%) as proposed by Sivasubramanian and Madhavamenon (1973) [39]. Broad sense heritability was estimated by Allard, (1960). According to Johnson *et al*. (1955) [18], the estimates of heritability were categorised as high (>60%), moderate (30-60%) and low (0-30%). Genetic advance as percent of mean was calculated and classified as high (>20%), moderate (10-20%) and low (<10%) as given by Johnson *et al*., 1955 [18]. Correlation coefficients were calculated at the genotypic and phenotypic levels using the formulae given by Falconer (1981) [13]. Path coefficient analysis was carried out using the formula given by Wright (1921) [42] and Dewey and Lu (1959) [11].

Results and discussion

Genetic parameters

Analysis of variance (ANOVA) revealed highly significant differences (*p*<0.001) among genotypes for all the studied traits (Table 2). The estimates of mean, range and genetic parameters obtained in the study are presented in Table 3. For the trait days to 50% flowering (DFF) it ranged from 96 to 110.5 days with a mean of 105.12 days, whereas for plant height (PH) it ranged from 79 to 123 cm with a mean of 106.37 cm. Panicle length (PL) had a mean of 23.16 while it ranged from 20 to 26 cm. Productive tillers (NPT) showed a great variation from 7.5 to 13.5 tiller per plant while the mean was 10.83. The trait spikelet fertility (SF%) ranged from 73.11 to 96.74 with a mean of 87.27. Thousand grain weight (TGW) had a mean of 19.34, while it ranged from 14.9 to 22.5 gm. The trait Single plant yield (SPY) had a mean of 26.43 gm while it ranged from 36.09 to being the maximum while 20.43 was the minimum.

In all the traits evaluated, GCV was lower than their corresponding PCV, indicating that both genetic and environmental influences contributed to trait expression, though genetic factors are the primary components (Choudhary *et al*., 2024: Chandramohan *et al*., 2016) [9, 8]. Moderate PCV and GCV was seen in plant height and Single plant yield. These results were in accordance with the findings of Paramanik *et al*., 2023 [27], Ravikanth *et al*., 2018 [31] for plant height (11.22% and 10.89%), and Sudeepthi *et al*., 2020 [40] for SPY (13.09% and 12%). Low variability was recorded for TGW (PCV: 9.78%, GCV: 8.9%), SF (6.81% and 6.27%), panicle length (5.86% and 4.56%), and DFF (4.01% and 3.93%), indicating a lack of inherent variability and limited scope for improvement through selection for these traits among the genotypes. Similar findings were reported by Kylash *et al*., 2023 [19], Sudeepthi *et al*., 2020 [40] for DFF, Kylash *et al*., 2023 [19]; Reddy *et al*., 2021 [33] for panicle length, Nithya *et al*., 2020 [24] for SF (%) and Bhargava *et al*., 2021 [5] for TGW.

All traits showed a high heritability viz., DFF (96.08%), plant height (94.34%), and spikelet fertility (84.73%), TGW (82.70%), PL (60.56%) and PT (60.28%), suggesting these traits are governed by genetic factors. The results of DFF, PH, PL and TGW were similar to the findings of Chacko *et al*., 2023. Correspondingly, high genetic advance as percent of mean was observed for SPY (22.65%) and PH (21.8%). This aligns with Sudeepthi *et al*., 2020 [40] K; Lakshmi *et al*., 2021 [21]. High heritability alone is not enough to make sufficient improvement through selection in advanced generations unless accompanied by a substantial amount of genetic advance. The efficacy of heritability is increased with the estimation of genetic advance, which indicates the degree of gain in a trait obtained under particular selection pressure. Plant height and SPY recorded high heritability and high genetic advance as percent of mean, which favours additive gene action. This is similar to the earlier reports of Lakshmi *et al*., 2021 [21], Bhargava *et al*., 2021 [5], Javid *et al*., 2025 [16], Paramanik *et al*., 2023. High heritability with low GAPM was recorded for DFF, which aligns with Kumar *et al*., 2018 [41], Choudhary *et al*., 2024 [9]. High heritability with moderate GAPM was recorded for SF and TGW, similar findings were reported by Bhargava *et al*., 2021 [5].

Correlation and Path coefficient analysis

Analysis of correlation coefficients revealed significant associations among key agronomic traits (Fig 1). Days to 50% flowering (DFF) exhibited a significant positive correlation with productive tillers (PT) as, reported by Tejaswini *et al*., 2018 [41] and for SPY by Saketh *et al*., 2023 [24]. Conversely DFF was negatively associated with PH

(Saran and Gauraha, 2023) [36] and TGW (Saketh *et al*., 2023) [24]. PH showed a positive correlation with PL and TGW, consistent with findings from Jeke *et al*., 2021 [17] and Parimala *et al*., 2020 [29]. However, PH was negatively associated with DFF, as reported by Choudhary *et al*., 2024 [9] and for SF by Mahalakshmi *et al*., 2024 [23]. Panicle length showed a positive correlation with PH consistent with reports by Choudhary *et al*., 2024 [9] and Elayaraj *et al*., 2022 [12]. PT was positively correlated with DFF (Mahalakshmi *et al*., 2024) [23] and SPY which aligned with findings of Elayaraj *et al*., 2022 [12], Ratna *et al*., 2015 [30], Ravindra Babu *et al*., 2012 [32], and Saketh *et al*., 2023 [24]. Spikelet fertility (%) exhibited negative correlations with PH and PL, corroborated by Choudhary *et al*., 2024 [9]. SPY was positively correlated with both DFF and PT, which is consistent with the findings of Lakshmi *et al*., 2021 [21], Sudeepthi *et al*., 2020 [40], and Chandra *et al*., 2009 [7].

Path coefficient analysis revealed that PT had the highest positive direct effect on single plant yield (0.34936), indicating it as the most important yield contributing trait while DFF and SF (Chandra *et al*., 2009) [7] also showed positive direct effects (0.11064 and 0.07046, respectively) (Table 3). These results were similar to the findings of Jangala *et al*., 2022 [15]. In contrast, PH exhibited a strong negative direct effect (-0.1266), while TGW and PL showed minimal direct effects but overall negative contributions to SPY. The results of PH and PL was consistent with Jangala *et al*., 2022 and TGW (Ravindra Babu *et al*., 2012) [15].

Tables and figure

Table 1: Details of BILs used in the study

S. No	BIL ID	Code
1.	RP-6342-VTCP2	TCP2
2.	RP-6342-VTCP6	TCP6
3.	RP-6342-VTCP7	TCP7
4.	RP-6342-VTCP8	TCP8
5.	RP-6342-VTCP9	TCP9
6.	RP-6342-VTCP10	TCP10
7.	RP-6342-VTCP11	TCP11
8.	RP-6342-VTCP12	TCP12
9.	RP-6342-VTCP14	TCP14
10.	RP-6342-VTCP15	TCP15
11.	RP-6342-VTCP18	TCP18
12.	RP-6342-VTCP23	TCP23
13.	RP-6342-VTCP25	TCP25
14.	RP-6342-VTCP26	TCP26
15.	RP-6342-VTCP28	TCP28
16.	RP-6342-VTCP30	TCP30
17.	RP-6342-VTCP31	TCP31
18.	RP-6342-VTCP32	TCP32
19.	RP-6342-VTCPMB44	MB44

Table 2: ANOVA for yield and its related traits during *Kharif* 2020 and *Rabi* 2021

Source of variation	D.F	Mean sum of squares						
		DFF	PH	PL	PT	SF	TGW	SPY (g)
Genotypes	20	103.8^{***}	822^{***}	8.15^{***}	8.46^{***}	190.4^{***}	19^{***}	64.12^{***}
Replication	1	4.3	72^{*}	3.24	0.58	2.8	0.606	4.42
Season	1	672.1^{***}	4411^{***}	48.29^{***}	304.89^{***}	1344.7^{***}	$5.586^{\cdot}$	206.44^{***}
Genotypesx Season	20	53.2^{***}	129^{***}	11.84^{***}	6.04^{***}	81.1^{***}	2.691^{*}	32.93^{***}
Residuals	83	1.6	17	2.25	2.06	12	1.51	4.03

*: Indicates significance at 5 percent probability level; ***: Indicates significance at 1 percent probability level; D.F: degrees of freedom

Table 3: Estimation of genetic variability parameters for yield and its components

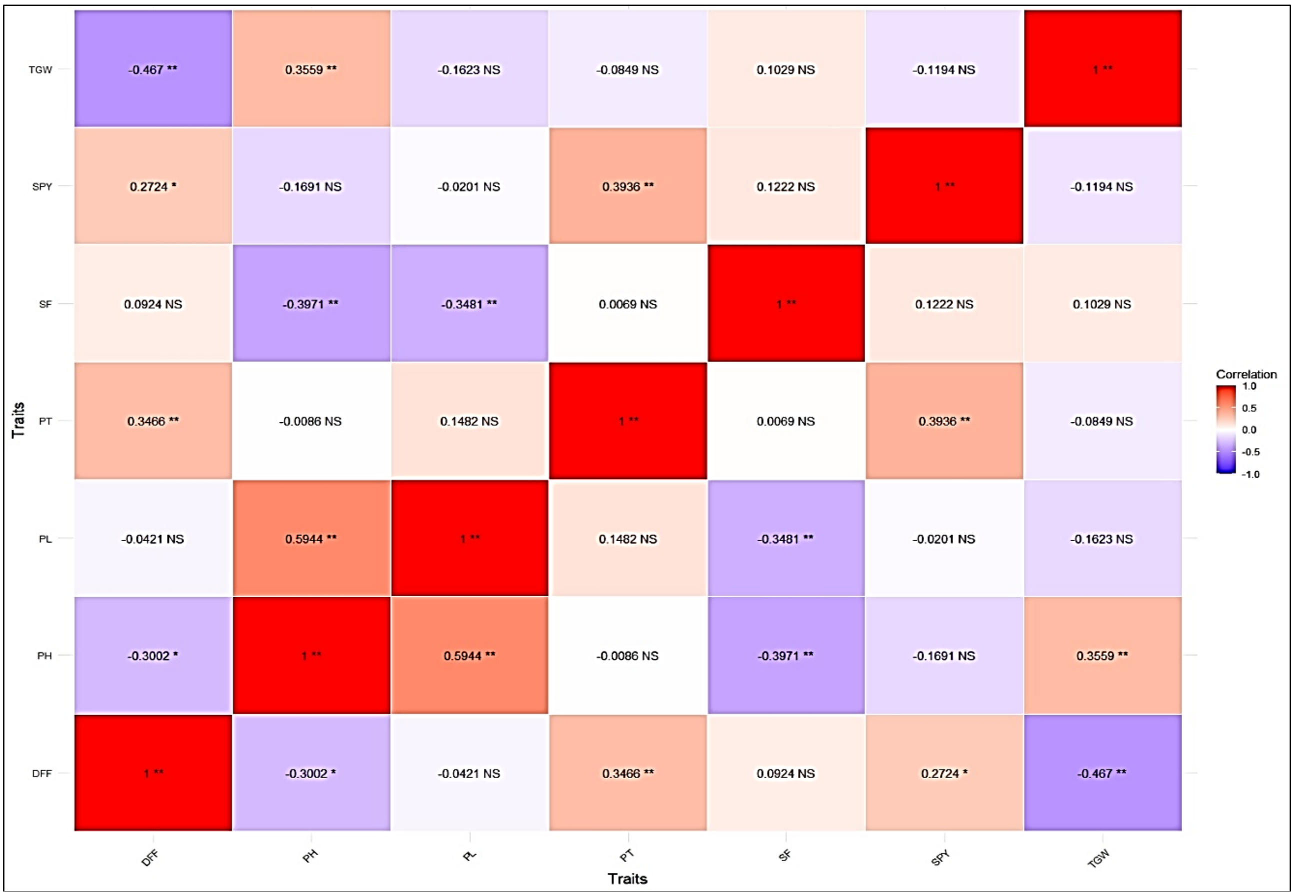
Sl. No.	Traits	Grand Mean	Range	GCV (%)	PCV (%)	h^2 (%)	GAPM
1.	DFF	105.12	96-110.5	3.93	4.01	96.08	7.94
2.	PH	106.37	79-123	10.89	11.22	94.34	21.80
3.	PL	23.16	20-26	4.56	5.86	60.56	7.31
4.	PT	10.83	7.5-13.5	9.93	12.79	60.28	15.88
5.	SF	87.27	73.11-96.74	6.27	6.81	84.73	11.89
6.	TGW	19.34	14.9-22.57	8.90	9.78	82.70	16.67
7.	SPY (g)	26.43	20.43-36.09	12.00	13.09	84.00	22.65

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h2: heritability; GAPM: Genetic advance as percent of mean (at 5%)

Table 4: Phenotypic path coefficient analysis for yield and its components in genotypes

Traits	DFF	PH	PL	PT	SF	TGW	SPY
DFF	0.11064	0.03801	-0.00141	0.12105	0.0065	-0.00239	0.2724
PH	-0.03321	-0.1266	0.01987	-0.003	-0.02798	0.00182	-0.1691
PL	-0.00466	-0.07525	0.03344	0.05183	-0.02453	-0.00083	-0.0201
PT	0.03835	0.00109	0.00496	0.34936	0.00048	-0.00044	0.3936
SF	0.01021	0.05027	-0.01164	0.00237	0.07046	0.00053	0.1222
TGW	-0.05167	-0.04506	-0.00543	-0.02972	0.00726	0.00512	-0.1194

DFF-Days to 50% flowering; PH-Plant height; PL-Panicle length; PT- Productive tillers; SF-Spikelet fertility; TGW-Thousand grain weight; and SPY- Single plant yield



*p=0.05; **p=0.01; DFF: Days to 50% flowering; PH: Plant height; PL: Panicle length; PT: Productive tillers; SF: Spikelet fertility; TGW: Thousand grain weight; and SPY: Single plant yield

Fig 1: Correlation heatmap of traits

Conclusion

The present study revealed the effectiveness of MABB for developing *Sub1* introgressed restorer lines with enhanced agronomic performance. Significant variation among the BILs across seasons highlighted their genetic potential and adaptability under different environmental conditions. The consistent higher PCV over GCV indicated environmental influences, while traits such as SPY, PH and DFF exhibited considerable genetic variability and high heritability, these can be used for selection in rice improvement. PT showed higher direct impact on rice yield, highlighting it as a key trait for selection. DFF and Spikelet fertility (%) also positively influenced yield. The evaluated BILs of KMR-3R demonstrate a promising genetic base for developing high-yielding, submergence tolerant rice hybrids in flood affected areas.

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