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Mutation-driven Improvement of Yield Components in Advanced Aromatic Rice Mutants

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ABSTRACT

The study was conducted during *kharif* season (June–December) 2019 at Agriculture Farm, Visva-Bharati, Sriniketan. The present investigation evaluated the yield-contributing traits of forty-six advanced-generation (M_4) mutant families along with their mother genotype, with the aim of identifying promising lines for future improvement of this valuable aromatic rice cultivar. A yield assessment by applying RCBD was carried out on a population of forty-six advanced generation (M_4) morphologically distinct induced mutants derived from the popular short-grain aromatic non-basmati cultivar '*Badshabhog*' of eastern India. Replicated mean data of twelve quantitative characters of forty-six mutants along with parent were applied for statistical analysis by Windostat Version 9.2. The results revealed that high (>20%) GCV and PCV were observed for panicle exertion, number of productive tillers hill^{-1}, spikelets panicle^{-1}, and seed weight indicated low sensitivity in fluctuating environments. High estimates of broad-sense heritability accompanied with genetic advance as percentage of mean were observed for days to 50% flowering, culm length, panicle exertion, number of productive tillers hill^{-1}, panicle length, number of spikelets panicle^{-1}, seed weight and grain yield hill^{-1}. These results suggested that selection for culm length, panicle exertion, productive tillers hill^{-1}, spikelets panicle^{-1}, and seed weight could effectively enhance grain yield. Grain yield hill^{-1} showed a significant positive association with productive tillers hill^{-1} and spikelet fertility (%) at both genotypic and phenotypic levels. Overall, the findings indicated that high-yielding, short-stature, and early-duration mutants could be developed through simultaneous selection for more productive tillers, enhanced spikelet fertility, and balanced panicle- and leaf-related traits.

KEYWORDS: Induced mutant, variability, character association, aromatic rice

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1. INTRODUCTION

Aromatic rice, including both basmati and non-basmati types, enjoys high global demand because of its characteristic fragrance and superior cooking quality (Burman et al., 2021; Sahoo et al., 2025). India is a major contributor to the international aromatic rice market, exporting substantial quantities of both categories (Anonymous, 2025). West Bengal is one of the most important rice-producing states in India; however, farmers are often reluctant to cultivate long-grain Basmati rice as its aroma and grain quality deteriorate under the region's humid climatic conditions. In addition, Basmati rice is characterized by low head rice recovery during milling and high susceptibility to diseases and insect pests (Chakraborty and Kole, 2014). In contrast, *Badshabhog*, a non-basmati aromatic short-grain rice cultivar, is widely preferred in West Bengal for its pleasant aroma, superior grain quality, and excellent cooking attributes. Despite its popularity, the cultivation area of Badshabhog has declined due to the increasing dominance of high-yielding, non-aromatic varieties. Moreover, this cultivar suffers from several agronomic limitations, including tall plant height (>155 cm) with weak culms leading to lodging, long growth duration (>160 days), photoperiod sensitivity, and susceptibility to blast disease under fluctuating weather conditions. These constraints collectively contribute to its relatively low yield potential (Kant et al., 2020). Therefore, improving the yield performance of Badshabhog while preserving its unique grain and cooking qualities has become an urgent breeding objective. Induced mutagenesis, particularly using gamma (γ) irradiation, has proven to be an effective approach for generating genetic variability in a wide range of crops, including cereals, pulses, and oilseeds, for the improvement of economically important traits (Chaudhary et al., 2019). Numerous mutant varieties developed through this approach have been successfully integrated into breeding programs of seed-propagated crops to address challenges related to food and nutritional security (Celik and Atak, 2017; Kant and Chakraborty, 2021a). In rice, mutation breeding has been widely adopted and has contributed significantly to varietal improvement worldwide (Roy et al., 2018; Kant and Chakraborty, 2021b). In Badshabhog, induced mutagenesis has led to the development of several morphologically distinct mutant lines that retain the characteristic aroma of the parent genotype (Kant and Chakraborty, 2021b). The present investigation evaluates the yield-contributing traits of forty-six advanced-generation (M_4) mutant families along with their mother genotype, with the objective of identifying promising lines for future genetic improvement of this valuable aromatic rice cultivar.

Genetic variability within a plant population is a prerequisite for effective selection and crop improvement. The magnitude and nature of variability are commonly assessed using genotypic and phenotypic coefficients of variation (GCV and PCV), along with estimates of heritability and genetic advance. Partitioning total phenotypic variance into its genetic and environmental components is essential for understanding the true breeding potential of a trait, as phenotypic expression is influenced by genotype–environment interactions. Heritability estimates, when considered together with expected genetic advance, provide reliable information on the extent of exploitable genetic variability and the likely response to selection (Johnson et al., 1955a).

Grain yield is a complex trait governed by multiple component characters that are interrelated either directly or indirectly. Therefore, understanding the nature and extent of character associations is crucial for effective selection. Genetic correlation coefficients offer a more dependable guide than phenotypic correlations, as they reflect inherent genetic relationships among traits (Falconer, 1981). Furthermore, path coefficient analysis partitions correlation coefficients into direct and indirect effects, thereby clarifying the relative importance of individual traits in yield determination. Originally developed by Wright, path analysis remains a valuable tool for identifying key yield-contributing characters in crop improvement programs (Niles, 1922).

2. MATERIALS AND METHODS

2.1. Experimental location

The present study was conducted during *kharif* seasons, from June to December 2019 at the Agriculture Farm, P.S.B. (Institute of Agriculture), Visva-Bharati, Sriniketan. The experimental site is situated at 23° 19' N latitude and 87° 42' E longitude and at an altitude of 58.9 m above sea level.

2.2. Experimental material

The seeds of the *Badshabhog* cultivar were exposed to five different doses of gamma rays, including 200 Gy, 250 Gy, 300 Gy, 350 Gy, and 400 Gy, from the $Cobalt^{60}$ gamma rays source at BARC, Trombay, Mumbai, India, for as long as was needed for each dose based on the half-life of the source. The dose rate was of the order of 17 Gy min^{-1} in a radiation chamber. Individual plants from the M_1, M_2, M_3, and M_4 generations were cultivated and selected using the pedigree approach. Each generation used standard agronomic packages and methods to optimize crop growth. The mutant plants were designated as follows: 'Mut', followed by a number representing the dose in Gray 100^{-1}, a number in parenthesis representing the M_2 family, a number indicating the selected plant, or a symbol (B) indicating the selected bulk family plant in the M_2 generation, and a number in parentheses indicating the selected plant in the

M_3 generation. The M_4 generation was produced using seeds obtained from selected M_3 plants.

Seeds from the promising 46 mutants selected from 22 mutant families and 9 bulk families in M_3 generation were used for raising M_4 generation. Selected 46 mutant plants and their mother genotype are presented in Table 1 with their pedigree records.

2.3. Experimental methodology and field techniques

A total of 46 M_4 families along with control were grown in well fertile nursery bed during *kharif*, June-December 2019. Twenty-five to thirty days old seedlings of each progeny along with control were transplanted to the main field with single seedling hill^{-1} following plant to row progeny method in a randomized complete block design (RCBD) with three

Table 1: Selected 46 mutant plants and its original parent for raising M_4 generation

Mut2(8)1(4)	Mut2(950)3(2)	Mut3(615)B(1)	Mut4(48)2(9)
Mut2(207)2(2)	Mut3(9)2(10)	Mut3(615)B(2)	Mut4(100)1(5)
Mut2(267)B(1)	Mut3(30)1(5)	Mut3(615)B(3)	Mut4(136)1(2)
Mut2(267)B(2)	Mut3(40)1(3)	Mut3(615)B(4)	Mut4(141)1(3)
Mut2(381)B(1)	Mut3(40)B(1)	Mut3(615)B(5)	Mut4(211)1(5)
Mut2(381)B(2)	Mut3(40)B(2)	Mut3(615)B(6)	Mut4(211)2(3)
Mut2(424)1(5)	Mut3(98)1(3)	Mut3(615)B(7)	Mut4(211)B(1)
Mut2(424)B(1)	Mut3(615)1(1)	Mut3(615)B(8)	Mut4(211)B(2)
Mut2(637)1(6)	Mut3(615)2(5)	Mut3(615)B(9)	Mut4(211)B(3)
Mut2(637)B(1)	Mut3(615)3(8)	Mut3(615)B(10)	Mut4(211)B(4)
Mut2(786)B(1)	Mut3(615)4(10)	Mut4(15)1(6)	Badshabhog
Mut2(826)B(1)	Mut3(615)5(5)	Mut4(48)1(4)	

replications. Each plot consisted of five rows of twenty plants each with a spacing of 15×20 cm^2.

2.4. Data collections and statistical analysis

Data on twelve quantitative characters viz., Days to 50% flowering, Culm length (cm.), Panicle exsertion (cm.), Flag leaf length (cm.), Flag leaf width (cm.), Number of productive tillers hill^{-1}, Days to maturity from flowering (Ripening phase), Panicle length (cm), Number of spikelets panicle^{-1}, Spikelet fertility %, 250 seed weight (g), Grain yield hill^{-1} (g) were recorded from five random plants of the middle three rows from each replication. Single plant harvesting was performed at maturity. The mean data were subjected to Statistical analysis of phenotypic and genotypic co-efficients of variability (Burton, 1952), heritability and genetic advance (Johnson et al., 1955a) and genotypic and phenotypic correlation (Johnson et al., 1955b) and path coefficients (Dewey and Lu, 1959). Windostat Version 9.2 statistical software was applied for statistical analysis.

3. RESULTS AND DISCUSSION

The analysis of variance for 46 mutant families and their mother genotype across 12 quantitative traits revealed highly significant mean sum of squares for all characters, indicating the presence of substantial genetic variability among the experimental materials. The success of any plant breeding program largely depends on the availability of adequate genetic variability within the germplasm. In the present study, estimates of the genotypic coefficient of variation (GCV) ranged from 5.34% for days to maturity from flowering to 36.61% for panicle exsertion (Table 2). The phenotypic coefficient of variation (PCV) ranged from 9.71% for days to maturity from flowering to 37.90% for the number of productive tillers hill^{-1}.

High (>20%) GCV and PCV values were recorded for panicle exsertion, number of productive tillers hill^{-1}, number of spikelets panicle^{-1}, and 250-seed weight. Culm length exhibited moderate GCV (10–20 %) along with high PCV (>20%). Intermediate GCV and PCV (10–20%) were observed for grain yield hill^{-1}, flag leaf length, days to 50% flowering, panicle length, and flag leaf width. Low (<10%) values of both GCV and PCV were recorded for spikelet fertility (%) and days to maturity from flowering.

These findings corroborated earlier reports of high GCV and PCV for panicle exsertion (Sahoo et al., 2025), number of productive tillers hill^{-1} (Kole and Chakraborty, 2012; Islam et al., 2019; Sharifi, 2019), number of spikelets panicle^{-1} (Thakur and Pandey, 2020), and seed weight (Devi et al., 2020). Moderate GCV and PCV for culm length (Sharma et al., 2014), flag leaf dimensions (Kole and Chakraborty, 2012; Roy and Shil, 2020), days to 50% flowering (Sahoo et al., 2025), panicle length (Guo et al., 2020; Thakur and Pandey, 2020), and grain yield hill^{-1} (Kole

Table 2: Genetic parameters of mutant lines for twelve quantitative characters in M_4 generation

Characters	Grand mean	Range		Coefficient of variation (%)		h^2bs (%)	GA	GA (%)
		Min.	Max.	GCV	PCV			
Days to 50% flowering	110.12	90.00	130.00	12.698	12.774	98.80	28.637	26.003
Culm length (cm)	108.73	67.06	140.75	19.960	20.367	96.00	43.817	40.296
Panicle exertion (cm)	12.62	3.93	19.29	36.615	37.471	95.50	9.306	73.706
Flag leaf length (cm.)	26.49	21.02	34.63	12.710	15.090	70.90	5.843	22.053
Flag leaf width (cm)	1.02	0.80	1.30	10.637	11.768	81.70	0.203	19.805
Number of productive tillers $hill^{-1}$	17.41	9.06	39.93	35.886	37.904	89.60	12.191	69.989
Days to maturity from flowering (Ripening phase)	26.22	21.66	30.00	5.344	9.711	30.30	1.588	6.058
Panicle length (cm)	24.14	18.34	28.56	11.510	12.443	85.60	5.296	21.931
Number of spikelets $panicle^{-1}$	145.95	64.18	230.89	30.329	31.953	90.10	86.557	59.303
Spikelet fertility %	79.68	64.47	94.62	9.036	9.997	81.70	13.406	16.823
250 seed weight (g)	2.77	2.18	4.74	21.475	21.972	95.50	1.201	43.236
Grain yield $hill^{-1}$ (g)	19.89	14.05	31.21	15.026	19.130	61.70	4.837	24.313

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h^2bs: Broad sense heritability; GA: Genetic advance; GA (%): Genetic advance as % of mean

and Chakraborty, 2012; Islam et al., 2019; Sharifi, 2019; Thakur and Pandey, 2020; Andrew-Peter-Leon et al., 2021) have also been documented. Low GCV and PCV values for days to maturity (Islam et al., 2019) and spikelet fertility (%) (Kole and Chakraborty, 2012; Thakur and Pandey, 2020) have been similarly consistent with previous studies.

The differences between PCV and GCV were minimal for most traits, suggesting low environmental influence and a predominant role of genetic factors in their expression. However, comparatively larger differences observed for days to maturity from flowering, followed by grain yield $hill^{-1}$ and flag leaf length, indicate that these traits are more strongly influenced by environmental factors.

3.1. Heritability and genetic advance as percentage of mean

Very high broad-sense heritability was recorded for days to 50% flowering (98.80%), culm length (96.0%), panicle exsertion (95.5%), 250-seed weight (95.5%), number of spikelets $panicle^{-1}$ (90.10%), number of productive tillers $hill^{-1}$ (89.6%), panicle length (85.6%), flag leaf width (81.7%), and spikelet fertility percentage (81.7%). Flag leaf length (70.9%) and grain yield $hill^{-1}$ (61.7%) exhibited moderately high heritability. Comparable levels of heritability for these traits have been documented by Islam et al. (2019), Sharifi (2019), Roy and Shil (2020), and Andrew-Peter-Leon et al. (2021), although differences were noted for culm length (Khan et al., 2019) and panicle exsertion (Satturu et al., 2023). Days to maturity from flowering showed low heritability (30.3%), which was in line with the findings of Thakur and Pandey (2020).

Genetic advance expressed as a percentage of the mean (GAM) was also high (>20%) for several traits panicle exsertion (73.70%), number of productive tillers $hill^{-1}$ (69.98%), number of spikelets $panicle^{-1}$ (59.30%), 250-seed weight (43.23%), culm length (40.29%), days to 50% flowering (26.01%), grain yield $hill^{-1}$ (24.31%), flag leaf length (22.05%), and panicle length (21.93%). These findings corresponded closely with earlier reports by Islam et al. (2019), Sharifi (2019), and Andrew-Peter-Leon et al. (2021), with some variation observed for culm length (Sharma et al., 2014) and panicle exsertion (Satturu et al., 2023). Moderate GAM values (10–20%) were recorded for flag leaf width (19.80%) and spikelet fertility percentage (16.82%), while days to maturity from flowering exhibited low GAM (<10%), consistent with the observations of Thakur and Pandey (2020).

The combined interpretation of heritability and genetic advance offered insights into the underlying gene action. Traits such as days to 50% flowering, culm length, panicle exsertion, flag leaf length, number of productive tillers $hill^{-1}$, panicle length, number of spikelets $panicle^{-1}$, 250-seed weight, and grain yield $hill^{-1}$ demonstrated both high heritability and high GAM, indicating that additive genetic effects played a major role in their expression (Johnson et al., 1955a). Consequently, these traits were particularly responsive to improvement through direct selection. Flag leaf width and spikelet fertility (%) also showed

high heritability along with moderate GAM, suggesting predominantly additive gene action and suitability for enhancement via simple or progeny selection methods (Panse and Sukhatme, 1957).

Overall, the combined evaluation of genotypic and phenotypic variability, heritability, and genetic advance underscored that selection for culm length, panicle exsertion, number of productive tillers hill^{-1}, number of spikelets panicle^{-1}, and 250-seed weight would be highly effective for improving grain yield in this mutant population.

3.2. Character association

Genotypic and phenotypic correlation coefficients were assessed among twelve traits to understand their collective influence on grain yield. The correlation estimates (Table 3) revealed that grain yield hill^{-1} showed a highly significant (p=0.01) and positive association with the number of productive tillers hill^{-1} and spikelet fertility (%). Days to 50% flowering and 250-seed weight also displayed positive correlations with grain yield at both genotypic and phenotypic levels, indicating that improvements in these traits were likely to enhance grain yield. Similar trends have been reported for productive tillers (Akter et al., 2019; Hema et al., 2019; Islam et al., 2019; Mishra et al., 2019; Sabri et al., 2020; Singh et al., 2020), spikelet fertility (Akter et al., 2019; Dey et al., 2019; Mishra et al., 2019; Nithya et al., 2020; Sabri et al., 2020; Sahoo et al., 2025), days to 50% flowering (Islam et al., 2019; Mishra et al., 2019; Sahoo et al., 2025), and seed weight (Dey et al., 2019; Hema et al., 2019; Lalitha et al., 2019b; Sabri et al., 2020).

Table 3: Genotypic (G) and phenotypic (P) correlation of mutant lines for eleven quantitative characters associated with grain yield in M_4 generation

Characters		CL	PEx	FLL	FLW`	NPTH^{-1}	DMF	PL	NSP^{-1}	Fertility %	250 SW	GYH^{-1}
DFF	G	-0.739**	-0.823**	-0.547**	0.105	0.137	-0.189	-0.764**	-0.292**	0.609**	0.322**	0.069
	P	-0.721**	-0.802**	-0.461**	0.092	0.125	-0.158	-0.704**	-0.277**	0.546**	0.314**	0.041
CL	G		0.637**	0.643**	0.033	-0.268**	0.234**	0.592**	0.551**	-0.577**	-0.539**	-0.006
	P		0.614**	0.551**	0.031	-0.245**	0.119	0.518**	0.502**	-0.505**	-0.517**	-0.020
PEx	G			0.383**	-0.247**	0.149	0.378**	0.551**	0.015	-0.433**	-0.255**	-0.114
	P			0.308**	-0.209*	0.129	0.216**	0.490**	0.009	-0.374**	-0.234**	-0.088
FLL	G				-0.182*	-0.223**	-0.071	0.619**	0.163	-0.461**	-0.090	-0.012
	P				-0.084	-0.197*	-0.060	0.508**	0.179*	-0.367**	-0.075	0.009
FLW	G					-0.753**	0.201	0.096	0.515**	-0.129	0.008	-0.537**
	P					-0.666**	0.113	0.109	0.473**	-0.086	0.007	-0.361**
NPTH^{-1}	G						-0.123	-0.513**	-0.706**	0.207*	0.059	0.377**
	P						-0.042	-0.462**	-0.662**	0.154	0.054	0.382**
DMF	G							-0.046	0.152	-0.324**	-0.197*	-0.462**
	P							0.006	0.096	-0.163	-0.092	-0.121
PL	G								0.416**	-0.523**	-0.138	-0.195*
	P								0.432**	-0.456**	-0.123	-0.051
NSP^{-1}	G									-0.369**	-0.674**	-0.089
	P									-0.334**	-0.622**	0.021
Fertility %	G										0.465**	0.489**
	P										0.407**	0.357**
250 SW	G											0.048
	P											0.085

*, ** Significant at p=0.05, 0.01 respectively; DFF: Days to 50% flowering; CL: Culm length (cm); PEx: Panicle exsertion (cm); FLL: Flag leaf length (cm.); FLW: Flag leaf width (cm); NPTH^{-1}: Number of productive tillers hill^{-1}; DMF: Days to maturity from flowering; PL: Panicle length (cm); NSP^{-1}: Number of spikelets panicle^{-1}; Fertility %: Spikelet fertility %; 250 SW: 250 seed weight (g); GYH^{-1}: Grain yield hill^{-1} (g)

Conversely, flag leaf width exhibited a significant negative correlation with grain yield at both levels and was also negatively associated with flag leaf length. The reduction in net flag leaf area likely diminishes the photosynthetic supply to developing grains, thereby reducing yield. Ripening duration (days to maturity from flowering) and panicle length were negatively correlated with grain yield at the genotypic level, suggesting that prolonged ripening did not inherently support higher yield. Instead, the accumulation of photosynthates during the early ripening stages (approximately 25–26 days after flowering) appeared more critical for grain development. Mutants with long panicles tended to produce fewer tillers and exhibited poorer grain filling, likely due to the negative association between panicle length and spikelet fertility. Overall, grain yield displayed inverse relationships with flag leaf width, panicle length, and days to maturity from flowering, supporting earlier findings in rice (Dey et al., 2019; Islam et al., 2019). Culm length and panicle exsertion showed very low and non-significant negative correlations with grain yield at both levels. Flag leaf length and number of spikelets panicle^{-1} also showed weak and non-significant negative correlations at the genotypic level, implying limited influence on grain yield. Similar observations were reported for plant height (Dey et al., 2019; Islam et al., 2019; Mishra et al., 2019) and spikelets panicle^{-1} (Mishra et al., 2019).

Several positive and significant trait associations were observed, which hold practical importance for indirect selection. Days to 50% flowering was positively associated with spikelet fertility (%) and 250-seed weight; culm length with panicle exsertion, flag leaf length, panicle length, and spikelets panicle^{-1}; panicle exsertion with flag leaf length, ripening duration, and panicle length; flag leaf length with panicle length; flag leaf width with spikelets panicle^{-1}; panicle length with spikelets panicle^{-1}; and spikelet fertility (%) with 250-seed weight. Many of these associations concur with earlier research (Nayak et al., 2016; Nuruzzaman et al., 2017; Jan et al., 2017; Oladosu et al., 2018).

Negative correlations were also prominent. Days to 50% flowering showed significant negative associations with culm length, panicle exsertion, flag leaf length, panicle length, and spikelets panicle^{-1}. Previously, a negative relationship between days to 50% flowering and total spikelet number (Nayak et al., 2016), panicle length (Jan et al., 2017), and plant height (Oladosu et al., 2018) was observed. Culm length was negatively associated with productive tillers hill^{-1} (Jan et al., 2017), spikelet fertility (Nayak et al., 2016), and seed weight (Oladosu et al., 2018). Productive tillers were also associated negatively with spikelets panicle^{-1} (Nayak et al., 2016).

The negative association between spikelet number and productive tillers reflects the well-known phenomenon of "yield component compensation," wherein developmental trade-offs arise due to competition for assimilates during spikelet differentiation (Grafius and Thomas, 1971; Grafius et al., 1976). This compensation mechanism often limits progress in yield improvement through indirect selection of component traits. In the present study, late-flowering mutants generally exhibited reduced culm length, exsertion, panicle size, and spikelet number but compensated with higher spikelet fertility and 250-seed weight. In contrast, early-flowering mutants displayed larger structures but lower fertility-a likely result of competition among developing organs for limited resources.

Pleiotropy or linkage might also underlie some of these negative associations. When two traits were unfavourably correlated at both genotypic and phenotypic levels, their simultaneous improvement becomes challenging (Newell and Eberhart, 1961). Nevertheless, balanced and strategic selection schemes could help achieve optimal combinations of key yield components.

The strong positive association of grain yield with productive tillers hill^{-1} and spikelet fertility (%) suggests that selecting for these traits would be most effective for yield improvement in the aromatic non-basmati rice mutant population under study. Breeding genotypes with improved tillering ability and superior grain filling could therefore enhanced the yield potential of this material.

3.3. Path coefficient analysis

Path coefficient analysis revealed substantial variation in the direct and indirect contributions of different traits toward grain yield hill^{-1} (Table 4 and Figure 1). The number of spikelets panicle^{-1} exerted the highest positive direct effect on grain yield (1.733), followed by 250-seed weight (1.152), panicle exsertion (0.383), number of productive tillers hill^{-1} (0.290), spikelet fertility (%) (0.130), and culm length (0.115). These traits therefore represented the most influential yield components in the present mutant population.

The number of spikelets panicle^{-1} exhibited the strongest direct contribution to yield; however, its overall correlation with grain yield was slightly negative and non-significant due to suppressive indirect effects. Although its indirect paths through days to 50% flowering, culm length, and panicle exsertion were positive, negative indirect effects via flag leaf length, flag leaf width, number of productive tillers hill^{-1}, days to maturity, panicle length, spikelet fertility, and 250-seed weight outweighed the positive influence. This suggested that grain yield might have been limited by constraints on the supply of photosynthates and/or reduced grain filling. As reported by Yoshida (1972), grain filling in rice depends on assimilates produced after heading and on pre-heading carbohydrate reserves in culm and leaf sheaths.

Table 4: Genotypic path coefficient analysis of mutant lines for eleven characters associated with grain yield in M_4 generation

Characters	DFF	CL	PEx	FLL	FLW	NPTH^{-1}	DMF	PL	NSP^{-1}	Fertility %	250 SW	GYH^{-1}
DFF	*-0.222*	-0.085	-0.315	0.035	-0.096	0.039	0.093	0.675	-0.506	0.079	0.371	0.069
CL	0.164	*0.115*	0.244	-0.041	-0.030	-0.078	-0.115	-0.523	0.956	-0.075	-0.621	-0.006
PEx	0.182	0.073	*0.383*	-0.024	0.226	0.043	-0.187	-0.487	0.026	-0.056	-0.293	-0.114
FLL	0.121	0.074	0.147	*-0.063*	0.167	-0.065	0.035	-0.547	0.283	-0.060	-0.104	-0.012
FLW	-0.023	0.003	-0.094	0.011	*-0.916*	-0.219	-0.099	-0.085	0.893	-0.016	0.009	-0.537**
NPTH^{-1}	-0.030	-0.030	0.057	0.014	0.690	*0.290*	0.061	0.454	-1.224	0.027	0.068	0.377**
DMF	0.042	0.026	0.144	0.004	-0.184	-0.035	*-0.495*	0.041	0.263	-0.042	-0.226	-0.462**
PL	0.169	0.068	0.211	-0.039	-0.088	-0.149	0.023	*-0.883*	0.721	-0.068	-0.159	-0.195*
NSP^{-1}	0.064	0.063	0.005	-0.010	-0.472	-0.205	-0.075	-0.368	*1.733*	-0.048	-0.777	-0.089
Fertility %	-0.135	-0.066	-0.166	0.029	0.118	0.060	0.160	0.462	-0.640	*0.130*	0.535	0.489**
250 SW	-0.071	-0.062	-0.097	0.005	-0.007	0.017	0.097	0.122	-1.169	0.060	*1.152*	0.048

Residual effect=0.303; Italic figures indicate direct effects; *, ** Significant at p=0.05, 0.01 respectively; DFF: Days to 50% flowering; CL: Culm length (cm.); PEx: Panicle exsertion (cm.); FLL: Flag leaf length (cm.); FLW: Flag leaf width (cm.); NPTH^{-1}: Number of productive tillers hill^{-1}; DMF: Days to maturity from flowering; PL: Panicle length (cm); NSP^{-1}: Number of spikelets panicle^{-1}; Fertility %: Spikelet fertility %; 250 SW: 250 seed weight (g); GYH^{-1}: Grain yield hill^{-1} (g)

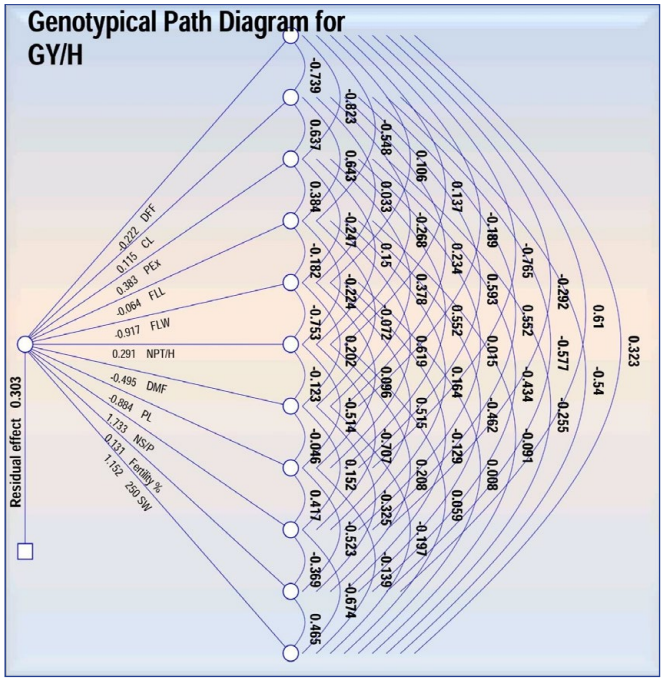

Figure 1: Genotypic path coefficient analysis of mutant lines for eleven characters associated with grain yield in M_4 generation

Similar positive direct effects of spikelet number on yield were earlier reported by Dudhane and Kole (2017).

Seed weight (250-seed weight) showed a strong positive direct effect (1.152) and positive indirect effects via flag leaf length, productive tillers, ripening duration, panicle length, and spikelet fertility. However, negative indirect effects through spikelet number, days to flowering, culm length, panicle exsertion, and flag leaf width reduced its overall correlation with grain yield to a non-significant level. Earlier studies also demonstrated the positive direct contribution of seed weight to yield (Akter et al., 2019).

Panicle exsertion (0.383) and the number of productive tillers hill^{-1} (0.290) also exerted positive direct effects. Panicle exsertion showed positive indirect effects via days to flowering, culm length, flag leaf width, productive tillers, and spikelet number, but negative paths through other traits diminished its overall influence, resulting in a non-significant negative correlation with yield. Earlier findings by Sahoo et al., 2025 also highlighted its direct positive contribution.The number of productive tillers hill^{-1} exhibited positive indirect effects through panicle exsertion, flag leaf attributes, days to maturity, panicle length, spikelet fertility, and seed weight, which outweighed its negative indirect effects through days to flowering, culm length, and spikelet number, leading to a significant positive correlation with yield. This was consistent with the findings of Akter et al. (2019), Singh et al. (2020).

Spikelet fertility (%) showed a moderate positive direct effect (0.130) along with positive indirect effects through flag leaf traits, productive tillers, ripening duration, panicle length, and seed weight. Negative indirect paths occurred through days to flowering, culm length, panicle exsertion, and spikelet number. Its overall correlation with grain yield was significant and positive, in agreement with earlier reports (Akter et al., 2019; Dey et al., 2019).

Culm length had a small positive direct effect (0.115), but its negative indirect contributions through most other traits

resulted in a non-significant negative association with grain yield. Reports by Akter et al. (2019) and Singh et al. (2020) also show such positive direct effects of plant height.

In contrast, flag leaf width (–0.916), panicle length (–0.883), and days to maturity (–0.495) recorded the highest negative direct effects on grain yield. Their indirect effects through spikelet number were also negative, reinforcing strong and significant negative correlations with grain yield. This result underscored that a positive correlation with yield does not necessarily imply a positive causal effect-a distinction that path analysis clarifies.

Overall, the traits with the strongest positive direct effects-number of spikelets panicle^{-1} and 250-seed weight-emerged as the key contributors to grain yield. Although several traits exhibited positive indirect contributions, their magnitudes were smaller and often offset by negative paths.

Among the short-stature mutant families, genotypes such as Mut2(267)B(1), Mut2(267)B(2), Mut2(826)B(1), Mut2(950)3(2), Mut4(141)1(3), Mut4(211)B(1), and Mut4(211)B(3) achieved higher grain yield hill^{-1} than the mother genotype. Their superior performance resulted primarily from a higher number of productive tillers and enhanced spikelet fertility, even though negative mutational effects were reflected through flag leaf width, days to maturity, and panicle length. Similar negative direct effects of panicle length have been reported by Dudhane and Kole (2017) and Dey et al. (2019).

The residual effect (0.30) for genotypic path coefficients (Figure 1) indicated that approximately 70% of the variation in grain yield hill^{-1} was explained by the eleven component traits included in the analysis, while the remaining 30% was accounted for by other unmeasured factors.

4. CONCLUSION

Wide genetic variability among advanced mutants of aromatic non-Basmati rice, enabling efficient selection for yield enhancement. Correlation and path analyses highlighted productive tillers hill^{-1} and spikelet fertility (%) as key determinants of grain yield, complemented by positive contributions from 250-seed weight, panicle exertion, and spikelets panicle^{-1}. Several early and short-stature mutants surpassed the parent genotype, confirming the effectiveness of induced mutation breeding.

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