PLANT SCIENCE TODAY
Vol XX(1): 1-XX
https://doi.org/10.14719/pst.16175

eISSN 2348-1900
OPEN ACCESS

Research Article | Agriculture
2026, Volume XX, Issue X, pp. 1-XX

Dissecting genetic architecture of quantitative traits using higher order statistics, variability studies and association analysis in rice MAGIC population

P Yogameenakshi[1], A Sheeba[2*], S Banumathy[1*], V A Vijayashanthi[3], C Tamilselvi[4] & S Sudhasha[5]

[1]Plant Breeding and Genetics, Rice Research Station, Tamil Nadu Agricultural University (TNAU), Tirur 602 025, Tamil Nadu, India
[2]Plant Breeding and Genetics, Krishi Vigyan Kendra, Tamil Nadu Agricultural University (TNAU), Tirur 602 025, Tamil Nadu, India
[3]Agricultural Entomology, Krishi Vigyan Kendra, Tamil Nadu Agricultural University (TNAU), Tirur 602 025, Tamil Nadu, India
[4]Crop Physiology, Rice Research Station, Tamil Nadu Agricultural University (TNAU), Tirur 602 025, Tamil Nadu, India
[5]Plant Pathology, Krishi Vigyan Kendra, Tamil Nadu Agricultural University (TNAU), Tirur 602 025, Tamil Nadu, India

***Correspondence:** A Sheeba, sheeba.a@tnau.ac.in; S Banumathy, banumathy.s@tnau.ac.in

Abstract

Rice is cultivated across diverse agro-climatic regions worldwide and its productivity is affected by many biotic and abiotic stresses. With the ever-increasing global population and changing climatic factors, the need to produce 25 % more rice by 2030 is becoming paramount. Improving the yielding ability of rice varieties vis-a-vis reducing the crop loss due to abiotic and biotic stresses is a promising approach. Breeding of varieties was mostly concentrated on developing single-, three-way-, or double-cross hybrids involving two, three or four parents to increase the genetic variation in breeding population. Multi-parental advanced inter-cross (MAGIC) populations provide a useful resource with diverse allelic combinations to be exploited by the rice community. The MAGIC population also presents opportunities for studying interactions of genome introgression and chromosomal recombination. Hence the present investigation was undertaken at Rice Research Station, Tirur during Samba (Aug–Dec), 2024 with two 8-parent MAGIC F_3 rice populations to study the nature of trait distribution, genetic variability, heritability (h^2), genetic advance as per cent of mean (GAM), genotypic correlation and path coefficient analysis for 15 agro-morphological, grain quality and physiological drought response (DR) traits. Phenotypic frequency distributions of traits indicated substantial phenotypic variation predominantly of quantitative nature as witnessed from the continuous normal curve in both the populations. Variability and h^2 studies indicated high genotypic coefficient of variation (GCV), high h^2 and high GAM were concurrently recorded for productive tillers per plant, number of grains per panicle, root length (RL) at 45 days after sowing and single plant yield (SPY) in Cross I and L/B ratio, RL, root : shoot ratio (RSR), drought recovery and SPY in Cross II. Correlation studies revealed significant positive genotypic correlations of SPY with productive tillers per plant, number of grains per panicle and spikelet fertility in Cross I and these yield-attributing traits are valuable for improving grain yield. Path coefficient analysis revealed that productive tillers per plant and number of grains per panicle were the primary direct contributors to SPY in Cross I. These findings provide a quantitative basis for trait-based selection and genotype advancement in MAGIC rice breeding programmes targeting drought-prone environments.

Keywords: association; breeding lines; genome introgression; MAGIC; rice; variability

Received: 18 June 2026. **Accepted:** 17 August 2026. **Published:** 12 November 2026.

Cite this article: Yogameenakshi P, Sheeba A, Banumathy S, Vijayashanthi VA, Tamilselvi C, Sudhasha S. Dissecting genetic architecture of quantitative traits using higher order statistics, variability studies and association analysis in rice MAGIC population. Plant Science Today. 2026;XX(X):1-XX. https://doi.org/10.14719/pst.16175

Introduction

Rice is the second most consumed cereal in the world after wheat and forms the primary staple food for more than 3.5 billion people, supplying over 20 % of global dietary energy intake (1). Its extensive genetic and geographic diversity facilitates cultivation in diverse agro ecological conditions ranging from rainfed uplands, lowlands, hilly and deep-water conditions making it an ideal candidate for climate change. Climate change has increased the frequency and intensity of droughts, storms, erratic rainfall and salinity adversely affecting rice production. Moreover, the traditional patterns of pest and disease severity have changed with minor pests shifting to take the place of predominance and widespread incoherency in expression across different weather elements. The concept of building up stronger genotypes to withstand the adversities has long been pursued by plant breeders globally. Addressing a single abiotic factor is no longer viable and genotypes with inherent capacity to mitigate multiple abiotic and biotic stress elements will prove to be more successful. For restructuring the prevailing genotypes, diverse plant types are of immense value as they form the base for the plant breeders to operate (2).

Biparental populations, conventionally employed in rice breeding capture allelic diversity from only two founder parents limiting the genetic space available for selection and trait dissection (3). Multi-parent advanced generation inter-cross (MAGIC), first proposed is a potential strategy that could overcome this constraint by converging alleles from multiple (typically 4–16) genetically diverse founders through successive rounds of intercrossing and selfing thereby pyramiding the characteristics needed in an ideal genotype like higher yield, good grain quality and biotic and abiotic stress tolerance (4). The resulting populations accumulate a rich mosaic of recombinant haplotypes, providing high mapping resolution, broad allelic coverage and can be exploited as a breeding resource either for development of varieties from descendants or as pre-breeding genetic stocks for further advancements (4, 5). The MAGIC populations have been developed and characterised in *Arabidopsis* (5), wheat (6), maize (7) and rice (8, 9). Hence an attempt was made at Rice research Station, Tirur from 2020–24 to develop MAGIC population in rice with multiple genetic parameters that could meet the growing demands and vulnerabilities posed by climate change.

However, the successful exploitation of a MAGIC population rests nonetheless on a thorough characterisation of its phenotypic variability, heritability (h^2) structure and inter-trait dependencies. The genetic parameters of variability present a clear picture of the genetic and environmental factors of variation, the heritable nature of the characters in study and also the nature of gene action based on the genetic advance (GA) gained over selection and helps breeders to decide upon the correct breeding methodology to adopt in order to gain advantage over the character under improvement and to decide upon which traits are amenable for phenotypic selection and which require indirect or marker-assisted strategies (10). Trait correlations and path coefficient analyses, in turn, identify components that can serve as surrogate selection criteria for grain yield, a trait that is polygenic and strongly influenced by G × E interaction (11, 12). Moreover, the third order statistics like skewness and kurtosis assessed in third or fourth generation of a cross would elucidate the population behaviour for the characters, the polygenic nature and epistatis that might possibly control the expression of a character (13, 14).

Hence the present study undertaken at Rice Research Station, Tirur aims to converge the high yield and grain quality parameters with biotic and abiotic stress tolerance factors through development of two 8-parent MAGIC populations. The parameters of genetic variability, character association, path coefficients and descriptive statistics viz., skewness and kurtosis in F_3 generation of the MAGIC population were assessed for 15 agronomic, grain quality, root and DR parameters in order to decipher the genetic nature of the characters under study and to decide upon the breeding strategy to be adopted with the MAGIC population.

Materials and Methods

a. Plant material and experimental design

The present investigation was conducted at Tamil Nadu Agricultural University Rice Research Station, Tirur, Tiruvallur district which lies in the latitudinal and longitudinal position of 13°7' N and 79°58' E respectively. In order to undertake the study, the two 8-parent MAGIC populations were synthesised at first as step by step crossing and inter crossing in subsequent generations from 2020–24 in order that the resultant population is a highly recombinant mosaic of quality, yield and tolerance attributes. The F_3 population of the two 8-parent MAGIC population viz., TKM 13/CR 1009//ADT 52/Mappilai Samba///IW Ponni/RNR 15048//Eramalli/IR 64 (Drt) and AD 18573/WRM 23-25//RNR 15048/WRM 23-25///CB 14154/VGD 1//ADT 37/Poongar was advanced through single seed descent of precedent F_2 generation.

Phenotyping of the two MAGIC populations was done by raising F_3 populations in unreplicated blocks having minimum 500 plants each during Samba (Aug–Dec), 2024 under wet direct sown condition. Their respective two-way cross parents were also raised adjacently with minimum of 50 plants.

b. Imposition of drought stress

Drought stress was imposed by withholding irrigation at 45 days after sowing (DAS), coinciding with the vegetative–reproductive transition and maintained for 15 consecutive days. The soil moisture was at field capacity at the time of imposition of drought and the time of sowing was adjusted so as ensure absence of rainfall during the drought imposition period. Irrigation was subsequently resumed to allow plant recovery. Leaf drying (LD) was scored at the end of the stress period and drought recovery was assessed 10 days after re-watering, both on a standard 1–9 scale (15).

c. Traits recorded

Fifteen yield contributing agronomic traits viz., days to 50 % flowering, plant height (cm), productive tillers/plant (no.), panicle length (cm), number of grains/panicle, spikelet fertility (%), grain quality traits viz., grain length (cm), L/B ratio, 100 grain weight (g) were recorded at maturity and drought parameters viz., LD, shoot length (SL) and root length (RL) at 45 DAS (cm), root: shoot ratio (RSR) and drought recovery were recorded at and after imposing 15 days of drought at 45 DAS.

d. Observations of drought parameters

Leaf drying

Leaf drying was scored according to Standard Evaluation System for Rice, IRRI, (15) in the afternoon on a 0 to 9 scale (ranging from no symptom to all leaves apparently dead) at the end of stress period.

Root length (cm)

The maximum RL of the longest root was recorded in cm at 45 DAS in the selected plants.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

Shoot length (cm)

The length of the shoot from the base to the tip at 45 DAS was recorded in cm in the selected plants.

Root/shoot ratio

Root/shoot ratio was worked out by dividing the RL by shoot length (SL).

Drought recovery

Drought recovery was recorded 10 days after restoring irrigation and was scored on a 1–9 scale (ranging from 90–100 % recovery to 0–19 % recovery) according to Standard Evaluation System for Rice, International Rice Research Institute (IRRI) (15).

e. Statistical analysis

Statistical analysis was done using the data recorded on 50 randomly selected F_3 individual plants in both the MAGIC populations along with five plants in the two-way cross parents of both the crosses.

i. Variability and heritability parameters

Analysis on variability, h^2, GA as per cent of mean was done following the standard procedure (16, 17). Phenotypic variance (σ^2p) was computed from the variance of the 50 F_3 lines.

Environmental variance (σ^2e) was estimated as the mean of the parental variances (V^{P1} and V^{P2}) as follows

$$\sigma^2e = \frac{(V^{P1} + V^{P2})}{2}$$

Genotypic variance (σ^2g) was derived as difference between phenotypic and environmental variance with a floor of zero applied where σ^2e exceeded σ^2p

$$\sigma^2g = \sigma^2p - \sigma^2e$$

The phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated as:

$$PCV\ (\%) = (\sqrt{\sigma^2p} / \mu) \times 100 \text{ and}$$

$$GCV\ (\%) = (\sqrt{\sigma^2g} / \mu) \times 100,$$

where μ is the population mean.

Variability scores were categorised into low, medium and high; with PCV / GCV values <10 % as low; 10–20 % as moderate and >20 % as high (10). Likewise, Heritability is categorised into low (<30 %), moderate (30–60 %) or high (>60 %) and GA as per cent of mean to low (<10 %), moderate (10–20 %) or high (>20 %) (18).

ii. Estimation of higher order statistics

The analysis on higher order statistics viz., skewness and kurtosis (excess) were done and based on the values obtained were classified to positive or negatively skewed and leptokurtic (kurtosis >0), platykurtic (kurtosis <0) and mesokurtic (kurtosis ~ 0) (19).

iii. Association studies

Correlation (20) and path coefficient analyses (12) were carried out and the inter-trait relationships were quantified by Pearson product–moment correlation coefficients, with significance assessed via the standard t-transformation ($t = r \cdot \sqrt{((n-2) / (1-r^2))}$; df = n-2 = 48). Significance is reported at the $p < 0.05$, $p < 0.01$ and $p < 0.001$ thresholds.

All analyses were performed in Python 3 using the pandas (v2.x) and NumPy (v1.26) libraries; figures were generated with matplotlib (v3.9).

Results and Discussion

Phenotypic distributions and descriptive statistics

Descriptive statistics including mean, standard deviation, range, skewness and kurtosis for all 15 traits in both MAGIC F_3 populations (Cross I and II) are presented in Table 1. Frequency distributions for all traits in both crosses are illustrated in Fig. 1 and 2. The results indicated that there was wide variation among the F_3 populations for the characters under study. This is evident from the wide range observed for each character (Tables 1 and 2) exhibited by the F_3 population. Wide range was noticed for most of the characters in both the crosses, while the median values almost correspond to the mean value for all the characters indicating a near normal or symmetric distribution and specifies the central tendency of the population consistent with polygenic (quantitative) inheritance and the extensive recombination characteristic of MAGIC populations derived from eight diverse founders (5, 9).

Distribution properties viz., coefficient of skewness and kurtosis are more powerful than first and second order statistics in deciphering the genetic nature of the traits (13, 14). Asymmetry in trait distribution is visualised by skewness whereas kurtosis is suggestive of peakedness or flatness of distribution in comparison to normal. A skewed distribution is suggestive of the trait being influenced by epistasis and environmental variables. More intensive selection from the existing variability is warranted for maximising the genetic gain in respect of skewed biometrical traits.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

Table 1. Descriptive statistics (mean, standard deviation, minimum, maximum, skewness and excess kurtosis) for 15 agro-morphological and physiological traits in both MAGIC F_3 rice populations (n = 50 per cross)

Trait	Mean	SD	Min	Max	Skew.	Kurt.	Mean	SD	Min	Max	Skew.	Kurt.
	Cross I (n = 50)						Cross II (n = 50)					
Days to 50 % flowering	95.12	8.16	73.0	118.0	0.035	0.844	85.74	7.12	72.0	100.0	-0.162	-0.808
Plant height (cm)	103.96	11.48	72.6	126.3	-0.521	0.241	99.52	6.70	85.6	112.8	-0.010	-0.715
Productive tillers/plant (no.)	15.28	5.36	8.0	31.0	1.130	1.054	11.90	2.55	8.0	17.0	0.113	-1.048
Panicle length (cm)	26.54	2.68	20.6	31.4	-0.181	-0.929	25.57	2.98	19.6	31.4	-0.084	-0.994
No. of grains/panicle (no.)	221.52	49.72	113.0	342.0	0.273	-0.375	219.50	40.73	123.0	312.0	0.000	-0.056
Spikelet fertility (%)	82.86	9.35	46.1	96.3	-1.519	3.354	85.12	5.94	69.5	96.2	-0.504	-0.125
Kernel length (mm)	6.08	0.48	5.12	7.40	0.534	0.696	5.46	0.31	5.00	6.20	0.561	-0.617
L/B ratio	3.03	0.43	1.80	3.60	-1.489	1.989	2.29	0.54	1.45	3.20	0.158	-1.482
100 grain wt (g)	1.73	0.31	1.32	2.56	0.975	0.469	2.14	0.22	1.64	2.65	-0.121	-0.331
Shoot length at 45 DAS (cm)	46.55	5.99	34.6	56.4	-0.074	-1.146	35.62	6.68	20.6	50.1	-0.239	-0.456
Root length at 45 DAS (cm)	14.77	3.61	8.20	22.1	0.160	-0.859	9.85	3.42	4.20	18.1	0.344	-0.435
Root: shoot ratio	0.314	0.049	0.215	0.405	-0.004	-0.892	0.277	0.088	0.149	0.580	1.155	1.704
Leaf drying	3.68	1.44	1.0	7.0	0.073	-0.244	4.32	1.38	1.0	7.0	-0.212	-0.063
Drought recovery	2.64	1.44	1.0	5.0	0.276	-1.012	4.32	2.16	1.0	7.0	-0.272	-1.168
Single plant yield (g)	26.81	8.36	16.7	51.6	1.041	0.595	25.14	5.99	15.6	41.2	0.690	0.071

DAS: days after sowing; L/B: length-to-breadth.

Table 2. Variability parameters and estimates of heritability and genetic advance as per cent of mean (GAM)

Characters	PV	GV	PCV	GCV	H2	GAM	PV	GV	PCV	GCV	H^2	GAM
	Cross I						Cross II					
Days to 50 % flowering	66.52	63.62	8.57	8.39	95.64	16.89	50.73	49.43	8.31	8.2	97.44	16.67
Plant height	131.68	121.39	11.04	10.6	92.18	20.96	44.82	40.79	6.73	6.42	91	12.61
No. of productive tillers/plant	28.74	26.24	35.08	33.52	91.3	65.98	6.5	2.4	21.42	13.02	36.92	16.3
Panicle length	7.19	5.54	10.11	8.87	77	16.03	8.85	6.55	11.64	10.01	73.97	17.73
No.õf grains/panicle	2471.93	2240.78	22.44	21.37	90.65	41.91	1658.58	1443.08	18.55	17.31	87.01	33.25
Spikelet fertility	87.5	72.71	11.29	10.29	83.1	19.33	35.23	18.65	6.97	5.07	52.95	7.61
Kernel length	0.23	0.21	7.93	7.55	90.58	14.8	0.1	0.09	5.68	5.4	90.27	10.56
L/B ratio	0.19	0.18	14.26	13.94	95.5	28.06	0.29	0.29	23.56	23.35	98.24	47.68
100-grain weight	0.1	0.09	17.83	17.11	92.13	33.83	0.05	0.05	10.39	10.03	93.21	19.95
Shoot length at 45 DAS	35.91	27.07	12.87	11.18	75.38	19.99	44.63	37.93	18.75	17.29	84.97	32.83
Root length at 45 DAS	13.04	10.54	24.45	21.97	80.78	40.68	11.68	10.89	34.69	33.5	93.26	66.65
Root: shoot ratio	0.0024	0.0019	15.64	13.9	79.03	25.46	0.01	0.01	31.9	30.91	93.92	61.71
Leaf drying	2.06	0.86	38.99	25.18	41.71	33.5	1.9	0.7	31.87	19.3	36.69	24.09
Drought recovery	2.07	0.87	54.52	35.37	42.08	47.26	4.67	3.67	50.03	44.35	78.59	81
Single plant yield	69.82	63.01	31.16	29.6	90.25	57.94	35.89	33.83	23.82	23.13	94.28	46.27

PV: phenotypic variance; GV: genotypic variance; PCV: phenotypic coefficient of variation; GCV: genotypic coefficient of variation; H^2: heritability in the broad sense; GAM: genetic advance as percentage of mean.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

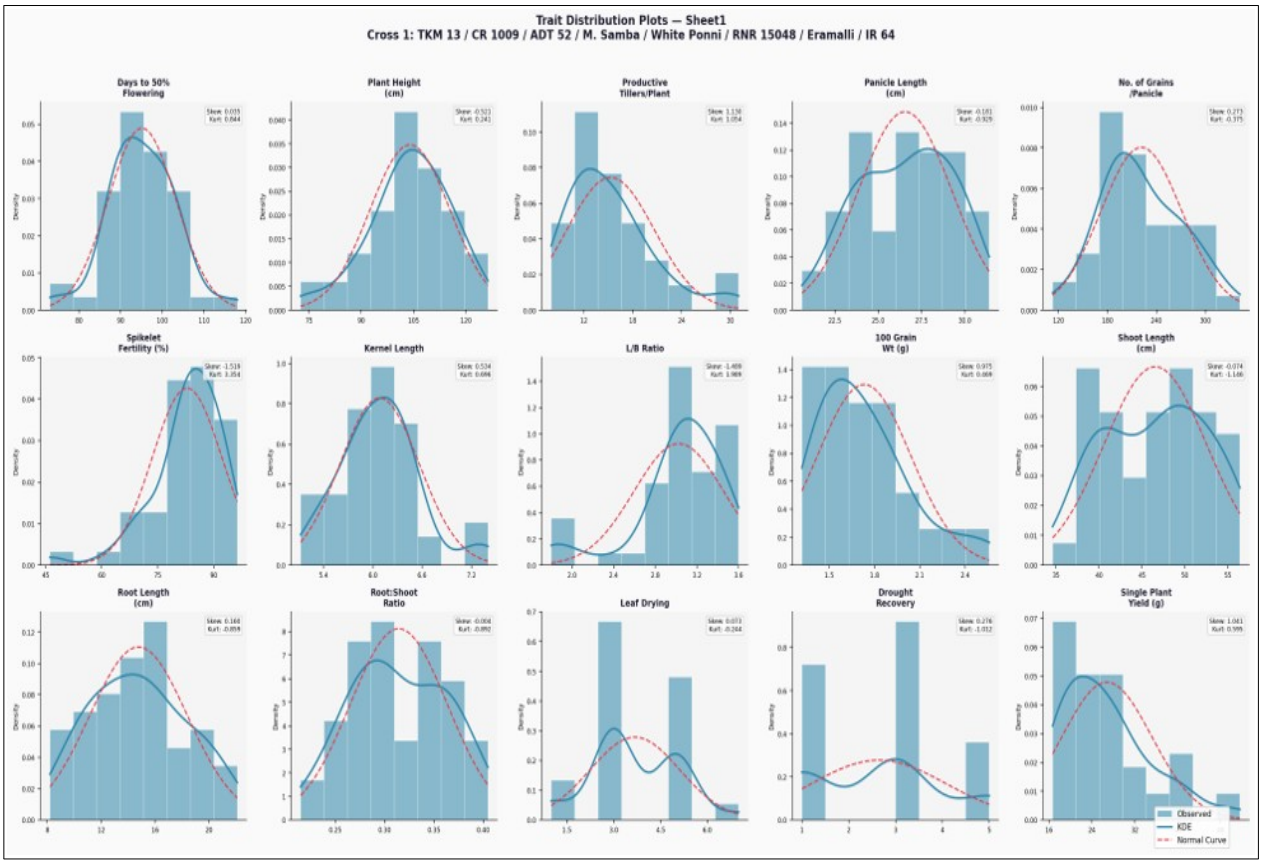


Fig. 1. Frequency distributions of 15 agro-morphological and physiological traits in Cross I (Population 1) of the 8-parent MAGIC F_3 rice population (n = 50).

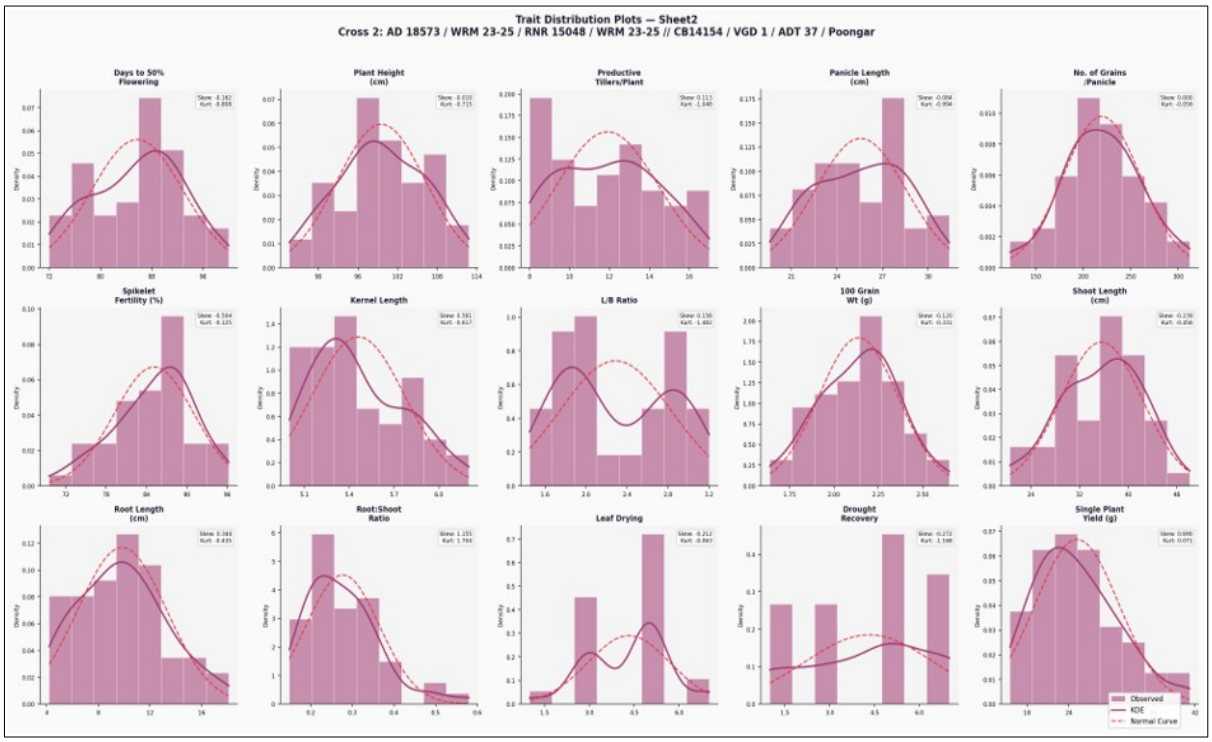


Fig. 2. Frequency distributions of 15 traits in Cross II (Population 2) of the 8-parent MAGIC F_3 rice population (n = 50).

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

In Cross I, single plant yield (SPY) ranged from 16.7–51.6 g (mean = 26.81 g; SD = 8.36 g) with a positive skewness of 1.041 indicating that a proportion of F_3 lines exceeded the mean, suggestive of possible transgressive segregation favouring yield (Fig. 1). Productive tillers per plant similarly showed positive skewness (1.130), with a range of 8–31 tillers per plant. Other traits with positive skewness in Cross I are 100 grain weight (0.975) and kernel length (KL) (0.534). Days to 50 % flowering and number of grains/panicle were near-normally distributed with skewness (0.035 and 0.23 respectively) with a broad range of 45 days (73–118 days) and 229 grains /panicle (113–342), reflecting substantial diversity in maturity and grain number among F_3 lines. Spikelet fertility was negatively skewed (−1.519; kurtosis = 3.354), indicating a concentration of lines with high spikelet fertility and a tail of less fertile lines. Similarly, L/B ratio also exhibited negative skewness (-1.489; kurtosis = 1.989) indicative of concentration of slender grain types (Fig. 1, Table 1).

In Cross II, distributions were more symmetric, with most traits exhibiting skewness values between −0.5 and +0.7 (Fig. 2). Days to 50 % flowering in Cross II (mean = 85.74 days) was approximately 10 days earlier than Cross I, reflecting differences in maturity between the populations and the corresponding founder parents. The RSR showed positive skewness (1.155) and leptokurtic distribution (kurtosis = 1.704) in Cross II, indicating a few lines with exceptionally high RSR, likely associated with deeper root development under drought stress. Similarly, the traits SPY (0.690) and KL (0.561) were also positively skewed.

Complementary epistasis may be attributed to traits with positive skewness, while the duplicate epistasis is associated with negatively skewed characters. In general, mild selection intensity for positively skewed characters may bring about faster genetic gains intended towards the improvement of the character while negatively skewed characters may require higher selection intensity (21–24). However, the confounding nature of the environment in single environment trial may not be ignored and a smaller subset of selected progenies may further be probed for expected gain in selection.

Kurtosis values indicate platykurtic curve for the characters panicle length, number of grains/panicle, SL at 45 DAS, RL at 45 DAS, RSR, LD and drought recovery in cross I and for all the characters except root: shoot ratio in cross II. Leptokurtic curve is witnessed for number of productive tillers/plant, spikelet fertility, L/B ratio in Cross I and RSR in Cross II. The character spikelet fertility in Cross I also represent heavy peakedness since the Kurtosis value is more than 3.

High positive skewness and leptokurtic distribution for SPY and productive tillers per plant in Cross I and RSR in Cross II indicate that a subset of F_3 lines exceeded both parental values through complementary allele combinations, providing direct evidence of transgressive segregation. Such transgressive segregation is more frequent and of greater magnitude in MAGIC than in biparental populations, providing a richer reservoir of superior genotypes for selection and exploitation as pre-breeding genetic stocks (9, 25).

Genetic variability and heritability

The parameters of genetic variability and h^2 estimates are presented in Table 2. The phenotypic variance was computed from the variance of F_3 lines. Since this is an unreplicated trial comprising segregating population, the environmental variance was arrived from the parental variance. The variability parameters studied in Cross I indicated that the trait drought recovery recorded maximum PCV (54.52 %) and GCV (35.37 %) and followed by number of productive tillers/plant (35.08 and 33.52 %), SPY (31.16 % and 29. 6 %) and LD (38.99 and 25.18 %) respectively. Number of grains per panicle and RL at 45 DAS also manifested high GCV and PCV of more than 20 %. While in Cross II, the characters contributing to drought tolerance viz., drought recovery (50.03 and 44.35) followed by RL at 45 DAS (34.69 and 33.5) and RSR (31.9 and 30.91) recorded the highest PCV and GCV in comparison to yield contributing characters viz., SPY (23.82 and 23.13), L/B ratio (23.56 and 23.35) and number of productive tillers/plant (21.42 and 13.02). Productive tillers per plant showed moderate GCV (13.02 %) in Cross II compared to high GCV (33.52 %) in Cross I, indicating reduced genetic diversity for this key yield component in the Cross II background. Days to 50 % flowering, panicle length and KL in both the crosses and plant height and spikelet fertility in cross II had low GCV, suggesting that these adaptive traits are more conserved across the founder parent genotypes.

Close proximity between GCV and PCV for most of the traits studied implies high degree of genetic variability and limited environmental influence and indicate that phenotypic variation is predominantly of genetic origin lending confidence to phenotypic selection in single environment (10, 25, 26). However, in unreplicated trials, where error variance is computed using parental variance, it is impossible to separate micro-environmental variation (e.g., soil gradients, moisture differences) from the phenotypic variance of the parental lines. The scope for predictability is also limited due to the study being conducted in a single season and environment.

Heritability measures the proportion of phenotypic variance that could be attributable to genotypic variance and categorised as low (<30 %), moderate (30–60 %) and high (>60 %), while GAM indicates expected gain from selection which is scored as low (<10 %), moderate (10–20 %) and high (>20 %). In Cross I, all the traits studied registered high h^2 of more than 60 % except LD and drought recovery which recorded moderate h^2. The traits number of productive tillers/plant (65.98 %), followed by SPY (57.94 %), drought recovery (42.08 %), number of grains/panicle (41.91 %), RL at 45 DAS (40.68 %), LD (33.5 %), 100

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

grain weight (33.83 %), L/B ratio (28.06 %), RSR (25.46 %) and plant height (20.96 %) recorded high GAM, while days to 50 % flowering (16.89), panicle length (16.03), spikelet fertility (19.33), KL (14.8) and SL at 45 DAS (19.99) recorded moderate GAM in Cross I.

In cross II, high h^2 was noticed in all the characters except for No. of productive tillers/plant, spikelet fertility and LD which all registered moderate h^2. Whereas, high GAM was noticed in most of the drought tolerance contributing traits viz., SL at 45 DAS (32.83 %), RL at 45 DAS (66.65 %), RSR (61.71 %), drought recovery (81 %), LD (24.09 %) along with SPY (46.27 %), number of grains/panicle (33.25 %) and L/B ratio (47.68 %) and moderate GAM was recorded in all other characters except spikelet fertility.

High GAM and h^2 values for grain yield and its contributing characters viz., productive tillers/plant, number of grains/panicle, 100 grain weight and also root architectural and drought mechanism traits in Cross I align with previous reports of high h^2 and GA for productive tillers and grain number in segregating rice populations (26–28). Moreover, moderate h^2 for drought recovery and LD in Cross I with high GAM suggests that while some non-additive components are present, directional selection for lower drought sensitivity scores remains feasible and efficient in this population. High h^2 coupled with high GAM for drought tolerance traits in Cross II appear to contribute broadly divergent alleles for post-stress recovery from diverse founder genotypes, creating a wide genetic range that is exploitable through selection compared to those characters with moderate GAM with high h^2. However, the study was conducted in a single season and environment and the G × E interactions could not be separated adequately from the genetic components which warrants further validation across environments and seasons.

Genotypic correlation analysis

Significant genotypic correlations among traits in both crosses are presented in Table 3. Correlation heat maps for Cross I and Cross II are shown in Fig. 3 and 4 respectively. In Cross I (Fig. 3), SPY showed significant positive genotypic correlations with the productive tillers per plant (r = 0.732, p < 0.001), number of grains per panicle (r = 0.521, p < 0.001) and spikelet fertility (r =0.33, p < 0.05) and these yield attributing traits are to be considered for improving grain yield. Similar results were reported earlier for productive tillers per plant (29), for productive tillers per plant and spikelet fertility (30) and filled grains per panicle and spikelet fertility (31). Significant negative correlations were exhibited by SPY with drought recovery score (r = −0.476, p < 0.001) with LD (r = −0.336, p < 0.05), probable that lines with lower drought stress impact showed lesser reduction in yield. Inverse relationship of LD to yield performance may be attributed to possible source sink relationship in accordance with the earlier findings (32, 33). Among the inter-trait associations, the strongest correlations were recorded between RL and RSR (r = 0.875, p < 0.001), SL and RL (r = 0.852, p < 0.001), L/B ratio and 100-grain weight (r = −0.851, p < 0.001), KL and L/B ratio (r = 0.788, p < 0.001), number of grains per panicle and spikelet fertility (r = 0.755, p < 0.001) and LD and drought recovery (r = 0.753, p < 0.001). These clusters of correlated traits reflect three functional complexes of root architecture (RL–RSR–SL), grain morphology (KL–LBR–GW) and response to drought stress (LD–DR).

In Cross II, no trait showed a statistically significant direct correlation with SPY (all p > 0.05), consistent with the low coefficient of determination in path analysis (R^2 = 0.218) (Fig. 4). Nevertheless, strong inter-trait associations were maintained between RL and drought recovery (r = −0.884, p < 0.001), root : shoot ratio and drought recovery (r = −0.747, p < 0.001), LD and drought recovery (r = 0.802, p < 0.001), RL and root : shoot ratio (r = 0.851, p < 0.001) and KL and L/B ratio (r = 0.754, p < 0.001). The strong negative association between RL/RSR and drought recovery score indicates that deeper-rooted genotypes in Cross II recovered more quickly from drought stress, underscoring the role of root architecture in drought avoidance- a reasonable relationship consistent with earlier reports linking deeper rooting with improved water uptake under drought conditions in rice (34–36). Bivariate scatter plots of SPY against the four highest-magnitude genotypic correlates in Crosses I and II are presented in Fig. 5 and 6, visually demonstrating the diffuse yield relationships in these populations.

The genotypic correlation heat maps reveal conserved functional trait complexes across both populations. The grain morphology cluster (KL–LBR–GW) and root architecture cluster (RL–RSR–SL) were strongly conserved, reflecting the functional interdependencies among these traits that are independent of the specific founder (parent) combination. The drought response cluster (LD–DR) was also consistent across crosses, confirming that LD and drought recovery score capture the same underlying stress response mechanism. The contrasting relationship between these functional clusters and SPY -strong in Cross I, absent in Cross II-highlights the importance of genetic background in determining the yield relevance of component traits.

Path coefficient analysis

Results of the path coefficient analysis on SPY are presented in Table 4, with direct effects illustrated in Fig. 7 and 8 and the indirect effect matrices in Fig. 9 and 10. In Cross I, the 14 predictor traits collectively accounted for 94.46 % of the variation in SPY (R^2 = 0.9446; residual effect = 0.2353), indicating that the measured traits provide a highly adequate description of yield variation in this population. Productive tillers per plant exerted the largest positive direct effect (β = +0.837), followed by number of grains per panicle (β = +0.527) and 100-grain weight (β = +0.364). This represents the classic yield component system in rice, whereby sink size (tiller and grain number) and quality (grain weight) are the primary

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

drivers of yield (37, 38). Selection indices combining productive tillers, grain number per panicle and SPY would therefore be highly effective in Cross I. Root length also contributed positively (β = +0.266; Fig. 7), suggesting that root system development under drought indirectly sustains yield by maintaining water uptake (34, 39). Leaf drying recorded a positive direct effect (β = +0.155) that was offset by a large negative indirect effect through drought recovery (−0.236), resulting in a net negative total correlation with yield (r = −0.336). This reveals that the apparent negative effect of LD on yield is mediated partly through its coupling with drought recovery score. The indirect effect matrix for Cross I clearly shows the compensatory indirect pathways operating through the correlated root architecture and DR trait complexes (Fig. 9).

In Cross II, only 21.82 % of yield variation was explained by the 14 traits (R^2 = 0.2182; residual effect = 0.8842), implying that unmeasured factors or non-additive genetic effects dominate yield determination in this population. The study although suggested largest direct effects from L/B ratio (β = −0.492) and SL (β = +0.414), followed by 100-grain weight (β = −0.324) and KL (β = +0.291) as shown in Fig. 8, it explained roughly 22 % of total yield variation and could not be considered as such as the primary indicators of yield. Hence additional physiological and agronomic parameters need to be studied for predicting the yield variation in this population. However, the contrasting direct effects of KL and L/B ratio in Cross II-both with near-zero total correlations with yield-indicate opposing indirect effects that cancel each other, a pattern visible in the indirect effect matrix (Fig. 10). A similar trend was observed, where the positive indirect effects of both 100-grain weight and L/B ratio were offset by their negative direct effects, resulting in near-zero correlations with grain yield. The high residual effect (0.884) in Cross II suggests that traits not measured in this study (e.g., harvest index, panicle branching, canopy architecture) or non-additive genetic interactions account for the majority of yield variation in this population.

Table 3. Significant genotypic correlation coefficients (r) among traits in Cross I and Cross II MAGIC F3 rice populations

Trait 1	Trait 2	r	*p*-value	Sig.	Trait 1	Trait 2	r	*p*-value	Sig.
Cross I - Significant genotypic correlations					**Cross II- Significant genotypic correlations**				
Productive tillers/plant	Single plant yield	0.732	<0.001	***	No. of grains/panicle	Spikelet fertility	0.617	<0.001	***
No. of grains/panicle	Single plant yield	0.521	<0.001	***	Kernel length	L/B ratio	0.754	<0.001	***
No. of grains/panicle	Spikelet fertility	0.755	<0.001	***	L/B ratio	100 grain wt	-0.839	<0.001	***
Kernel length	L/B ratio	0.788	<0.001	***	Root length at 45 DAS	Root : shoot ratio	0.851	<0.001	***
L/B ratio	100 grain Wt	-0.851	<0.001	***	Root length at 45 DAS	Drought recovery	-0.884	<0.001	***
Root length at 45 DAS	Root : shoot ratio	0.875	<0.001	***	Root : shoot ratio	Drought recovery	-0.747	<0.001	***
Shoot length at 45 DAS	Root length at 45 DAS	0.852	<0.001	***	Root : shoot ratio	Leaf drying	-0.692	<0.001	***
Shoot length at 45 DAS	Root : shoot ratio	0.501	0.0002	***	Leaf drying	Drought recovery	0.802	<0.001	***
Leaf drying	Drought recovery	0.753	<0.001	***	Shoot length at 45 DAS	Root length at 45 DAS	0.492	0.0003	***
Drought recovery	Single plant yield	-0.476	0.0005	***	Shoot length at 45 DAS	Drought recovery	-0.456	0.0009	***
Plant height	Shoot length at 45 DAS	0.625	<0.001	***	Days to 50 % flowering	Drought recovery	-0.362	0.0098	**
Plant height	Root length at 45 DAS	0.563	<0.001	***	No. of grains/panicle	Leaf drying	-0.306	0.0306	*
No. of grains/panicle	Drought recovery	-0.338	0.0162	*	Plant height	Shoot length at 45 DAS	0.317	0.0249	*
Plant Height	Panicle length	-0.384	0.0058	**	No. of grains/panicle	Drought recovery	-0.293	0.0390	*
Leaf Drying	Single plant yield	-0.336	0.0169	*	Shoot length at 45 DAS	Leaf drying	-0.332	0.0184	*

* p < 0.05; ** p < 0.01; *** p < 0.001; DAS: days after sowing; L/B: length-to-breadth.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

Table 4. Path coefficient analysis of direct and indirect effects of fourteen traits on single plant yield (SPY) in both MAGIC F3 populations

Trait	Direct effect	Sum indirect	Total *r* with SPY	Direct effect	Sum indirect	Total *r* with SPY
	Cross I (R^2 = 0.9446; Residual = 0.2353)			Cross II (R^2 = 0.2182; Residual = 0.8842)		
Days to 50 % flowering	-0.0087	-0.0472	0.047	+0.0318	+0.0393	0.082
Plant height	+0.0071	+0.0641	-0.084	-0.1958	+0.1802	-0.084
Productive tillers/plant	+0.8371	-0.1051	0.732	-0.1191	+0.0091	-0.231
Panicle length	+0.0474	+0.0338	0.081	-0.0647	+0.0014	-0.062
No. of grains/panicle	+0.5273	-0.0063	0.521	+0.0890	-0.0100	0.079
Spikelet fertility	-0.0148	+0.0498	0.335	-0.0293	+0.0647	-0.036
Kernel length	+0.0151	-0.0771	-0.062	+0.2912	+0.2848	0.007
L/B ratio	-0.0145	-0.0655	-0.080	-0.4920	+0.5562	-0.064
100 grain wt	+0.3644	-0.2304	0.134	-0.3242	+0.3322	0.015
Shoot length at 45 DAS	-0.1347	+0.1997	0.065	+0.4141	-0.1888	0.225
Root length at 45 DAS	+0.2658	-0.1688	0.097	-0.0309	-0.0171	-0.048
Root : shoot ratio	-0.0676	+0.2036	0.136	-0.1746	+0.1746	-0.202
Leaf drying	+0.1548	-0.4908	-0.336	+0.0140	+0.0020	0.016
Drought recovery	-0.1139	-0.3621	-0.476	+0.0611	-0.0531	0.008

DAS: days after sowing; L/B: length-to-breadth; SPY: single plant yield.

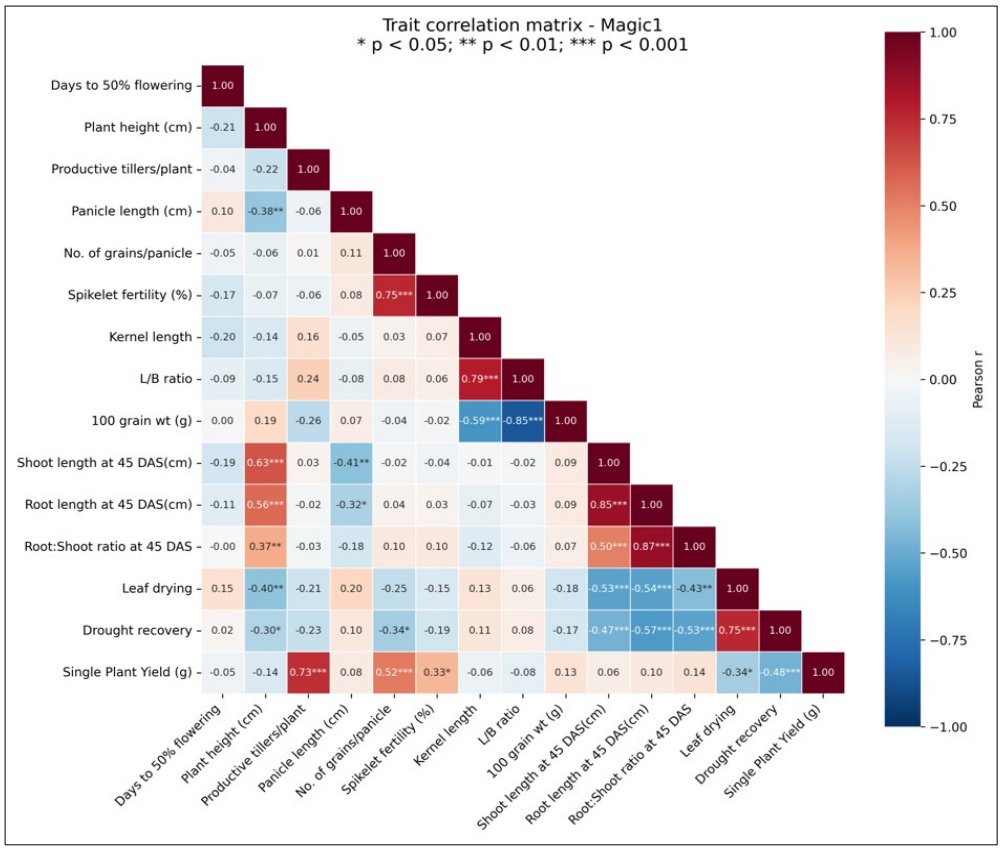


Fig. 3. Genotypic correlation matrix (lower triangle) for 15 traits in Cross I of the 8-parent MAGIC F_3 rice population. (Colour gradient: blue = positive correlation, red = negative correlation; intensity proportional to |r|. Asterisks indicate significance (*p < 0.05; **p < 0.01; ***p < 0.001). Three distinct correlation clusters are visible: root architecture traits (RL, RSR, SL), grain morphology traits (KL, LBR, GW) and drought response traits (LD, DR). Productive tillers per plant and number of grains per panicle show the strongest positive correlations with single plant yield.)

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

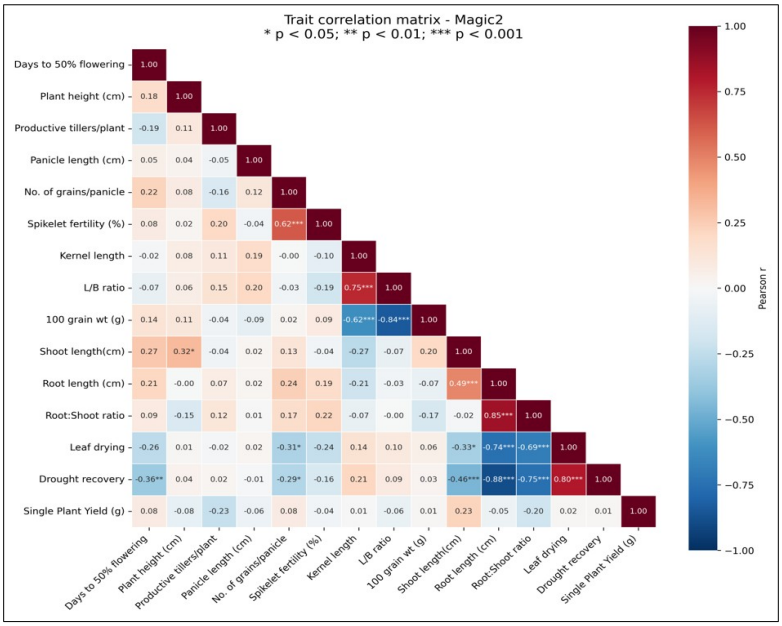


Fig. 4. Genotypic correlation matrix (lower triangle) for 15 traits in Cross II of the 8-parent MAGIC F_3 rice population. (The strong negative correlations between root length/root: shoot ratio and drought stress scores (LD and DR) indicate that deeper-rooted genotypes recover more rapidly from drought. The absence of significant correlations between any trait and single plant yield in Cross II (all $p > 0.05$) contrasts sharply with Cross I and reflects the more complex, multi-factorial yield determination in this genetic background.)

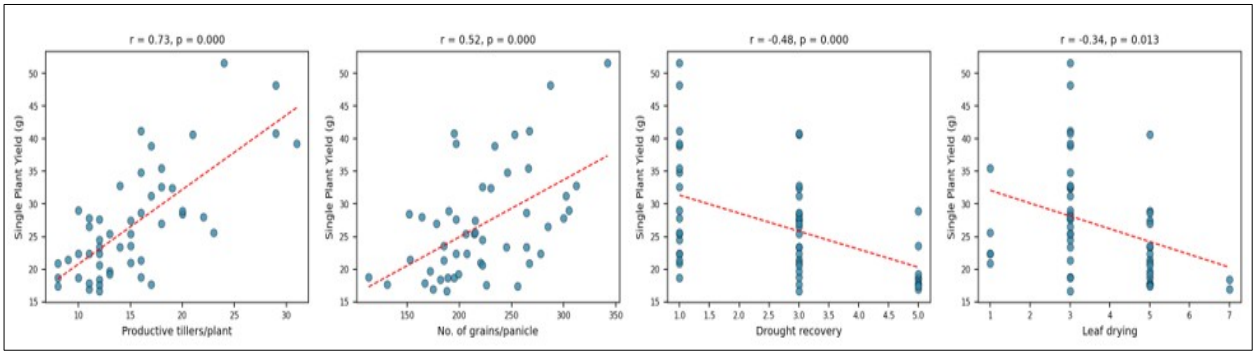


Fig. 5. Bivariate relationships between single-plant yield and the four highest-magnitude correlates in Cross I (Dashed line: least-squares regression fit).

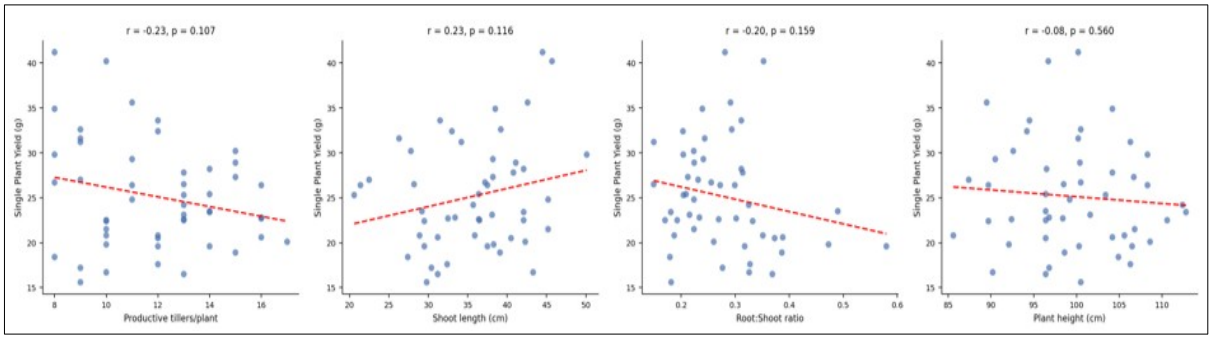


Fig. 6. Bivariate scatter plots of single plant yield (g) versus the four highest-magnitude genotypic correlates in Cross II (Population 2) of the 8-parent MAGIC F_3 rice population (n = 50). (Blue points = individual F_3 lines; red dashed line = ordinary least-squares regression fit. Correlation coefficient (*r*) and p-value are shown in each panel title. Despite the moderate inter-trait correlations, the wide scatter of points confirms the diffuse, multi-trait nature of yield determination in Cross II, consistent with the low R^2 (0.218) in path coefficient analysis).

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

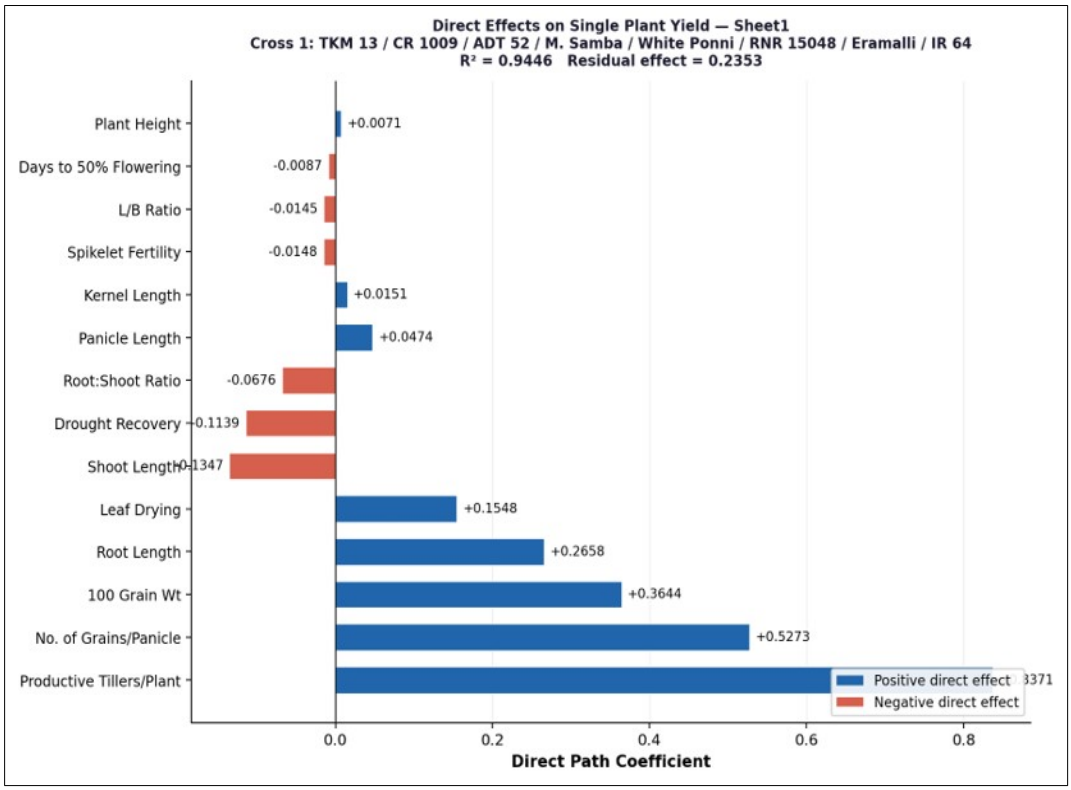


Fig. 7. Direct path coefficients (β) on single plant yield for 14 predictor traits in Cross I of the 8-parent MAGIC F_3 rice population. (Bars are colour-coded: blue = positive direct effect, red = negative direct effect. R^2 = 0.945; residual effect = 0.235).

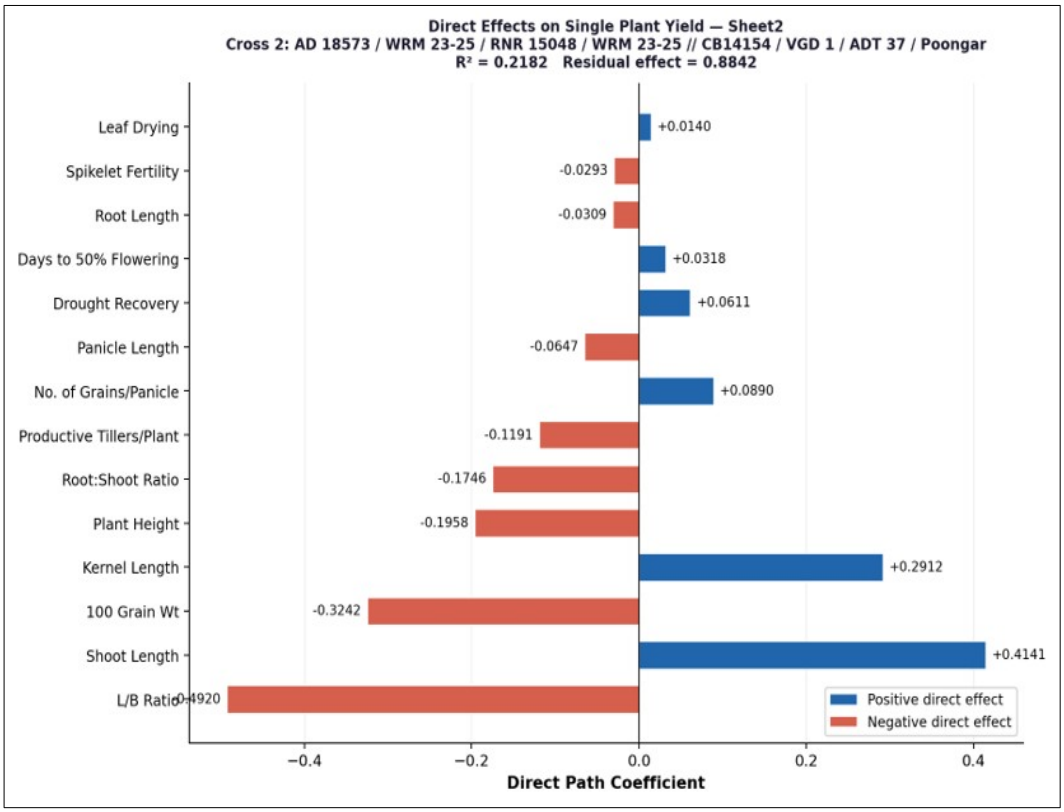


Fig. 8. Direct path coefficients on single plant yield (SPY) for 14 traits in Cross II (Residual effect – 0.884).

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

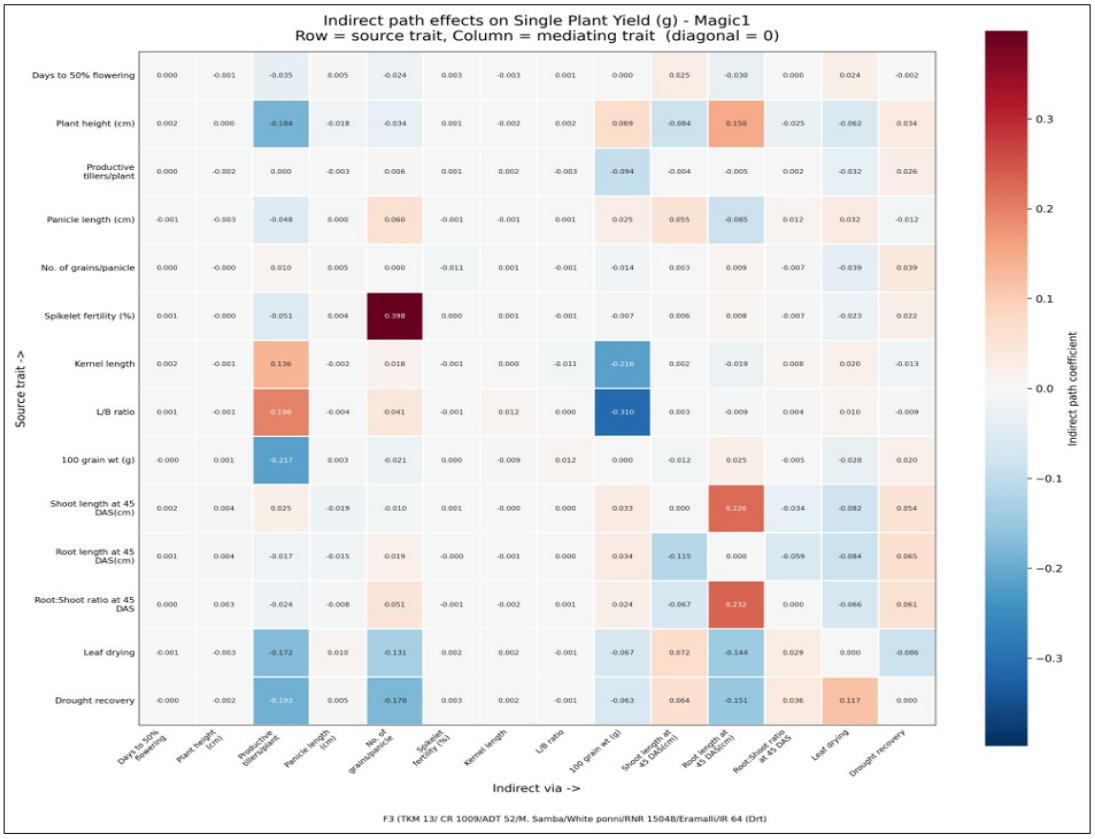


Fig. 9. Indirect effect matrix for Cross I showing influence of each trait (rows) on single plant yield (SPY) through every other mediating trait (columns). (Colour intensity indicates the magnitude of the indirect effect; blue = positive, red = negative indirect pathway).

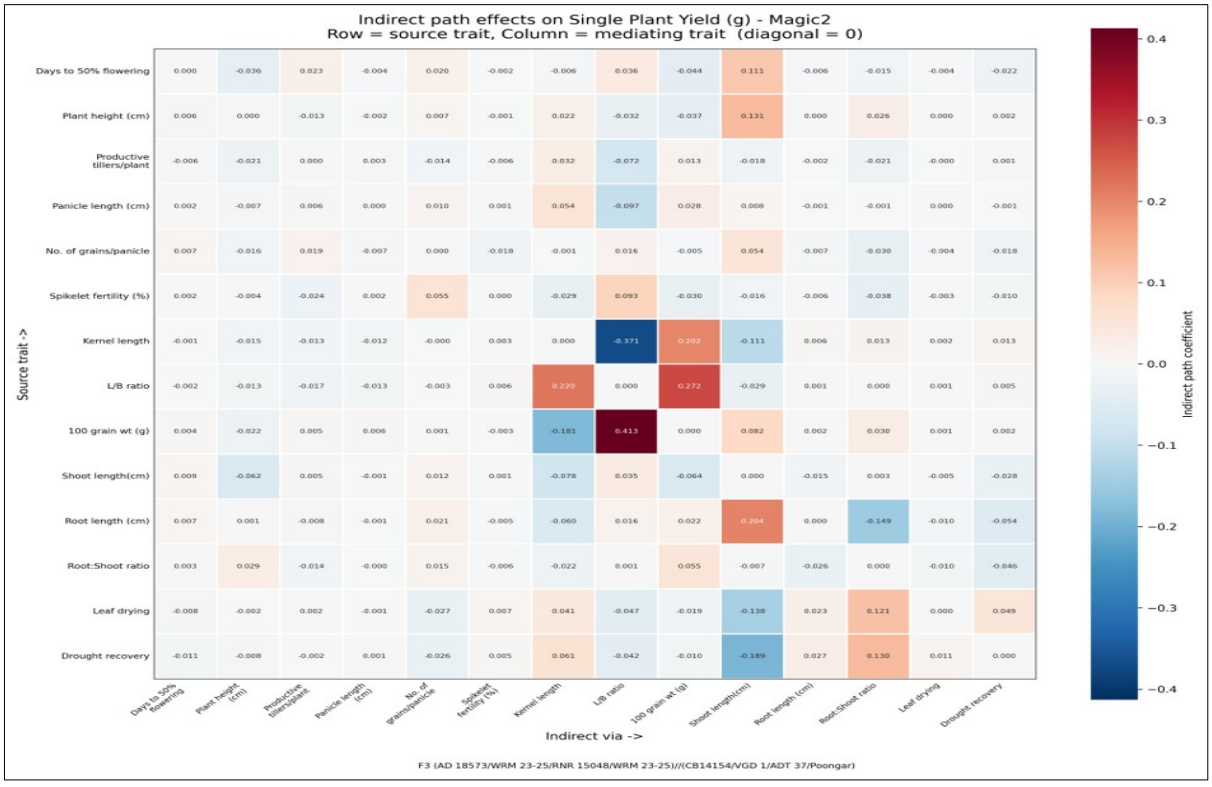


Fig. 10. Indirect effect matrix of path coefficients for Cross II.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

Conclusion

Both 8-parent multi-parent advanced generation inter-cross (MAGIC) F_3 rice populations evaluated in this study harboured substantial genetic variability for yield-related and drought-adaptive traits, as confirmed by continuous phenotypic distributions and broad range of all recorded traits. Cross I exhibited a tractable genetic architecture dominated by additive gene action, with productive tillers per plant, number of grains per panicle and 100-grain weight identified as the primary direct contributors to single plant yield (SPY) through correlation and path coefficient analysis (R^2 = 0.945). These traits, combined with high heritability (h^2) and high genetic advance (GA), constitute effective primary selection criteria in this population. Cross II demonstrated broader allelic diversity for drought-adaptive traits, particularly root length (RL) and drought recovery, but more complex and partially unexplained yield determination (R^2 = 0.218), suggesting the need for genomic or multi-trait index selection approaches in advanced generations. The genotypic correlation and path coefficient analyses identified three conserved functional trait complexes-root architecture, grain morphology and drought response (DR)-in both populations. The strong negative correlation between RL and drought recovery score in Cross II (r = −0.884) provides a mechanistic basis for indirect selection for drought tolerance through root morphology traits. The framework of genetic parameters and trait associations established here provides a quantitative basis for designing efficient selection strategies in 8-parent MAGIC rice populations targeting drought-tolerant, high-yielding genotypes.

Acknowledgements

The authors profoundly thank Tamil Nadu Agricultural University for successfully conducting the research experiment.

Authors' contributions

PY conducted the experiments, analysed the data and wrote the first draft of the research paper. AS performed statistical analysis and assisted in writing the research paper. SB participated in the design of the study, data analysis and editing the manuscript. CT coordinated in the field experiments, collection and compilation of data. VAV, SS arranged for the literary search and corrected the final draft. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest

Authors do not have any conflict of interests to declare.

Ethical issues

None

References

1. Khush GS. What it will take to feed 5.0 billion rice consumers in 2030. Plant Mol Biol. 2005;59:1–6.
2. Savitha P, Ushakumari. Genetic performance of medicinal landraces and improved cultivars for grain and nutritional quality traits in rice. Oryza. 2015;51(1):6–11.
3. Bernardo R. Molecular markers and selection for complex traits in plants: learning from the last 20 years. Crop Sci. 2008;48:1649–64.
4. Cavanagh C, Morell M, Mackay I, Powell W. From mutations to MAGIC: resources for gene discovery, validation and delivery in crop plants. Curr Opin Plant Biol. 2008;11:215–21.
5. Kover PX, Valdar W, Trakalo J, Scarcelli N, Ehrenreich IM, Puruggaban MD, et al. A multiparent advanced generation inter-cross to fine-map quantitative traits in *Arabidopsis thaliana*. PLoS Genet. 2009;5:e1000551
6. Huang BE, George AW, Forrest KL, Kilian A, Hayden MJ, Morell MK, et al. A multiparent advanced generation inter-cross population for genetic analysis in wheat. Plant Biotechnol J. 2012;10:826–39.
7. Dell'Acqua M, Gatti DM, Pea G, Cattonaro F, Coppens F, Magris G, et al. Genetic properties of the MAGIC maize population: a new platform for high definition QTL mapping in *Zea mays*. Genome Biol. 2015;16:167. http://doi.org/10.1186/s13059-015-0716-z
8. Bandillo N, Raghavan C, Muyco PA, Sevilla MA, Lobina IT, Dilla-Ermita CJ, et al. Multi-parent advanced generation inter-crosses (MAGIC) in rice: progress and potential for genetics research and breeding. Rice. 2013;6:11. http://doi.org/10.1186/1939-8433-6-11
9. Meng L, Li H, Zhang L, Wang J. QTL IciMapping: integrated software for genetic linkage map construction and quantitative trait locus mapping in biparental populations. Crop J. 2015;3:269–83. http://doi.org/10.1016/j.cj.2015.01.001
10. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. Madras Agric J. 1973;60:1093–96.
11. Wright S. Correlation and causation. J Agric Res. 1921;20:557–85.
12. Dewey DR, Lu KH. A correlation and path-coefficient analysis of crested wheatgrass seed production. Agron J. 1959;51:515–8.
13. Fisher RA, Immer FR, Tedin O. The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. Genetics. 1932;17(2):107–24.
14. Robson DS. Applications of the k4 statistic to genetic variance component analyses. Biometrics. 1956;12(4):433–44.
15. International Rice Research Institute. Standard Evaluation System (SES) for Rice. 5th ed. Los Baños, Philippines: IRRI; 2013.
16. Burton GW, DeVane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron J. 1953;45(10):478–81.
17. Allard RW. Principles of Plant Breeding. New York: John Wiley & Sons; 1960.
18. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47:314–8.
19. Pearson K. Mathematical contributions to the theory of evolution, XIX; second supplement to a memoir on skew variation. Phil Trans Roy Soc. 1896;216:429–57.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.16175

20. Al-Jibouri HR, Miller PA, Robinson HF. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. Agron J. 1958;50:633–6.
21. ShaiPrasanna GS, Joshi JL, Muraleedharan A. Utilizing genetic traits distributions to enhance rice breeding programs: a study of skewness and kurtosis in segregating generations. J Exp Agric Int. 2024;46(9):741–60. http://doi.org/10.9734/jeai/2024/v46i92871
22. Nikhitha TC, Pushpham R, Raveendran M, Manonmani S. Genetic variability and frequency distribution studies in F2 population involving traditional variety Mappillai Samba. EJPB.2020;11(3):933–8. http://doi.org/10.37992/2020.1103.151
23. Shamini K, Selvi B. Assessment of frequency distribution in F3 generation of sorghum (*Sorghum bicolor* L. Moench.) for grain yield and its attributed traits. Madras Agric J. 2023;109(4–6):24–8. http://doi.org/10.29321/MAJ.10.000623
24. Muthuramu S, Ragavan T. Genetic analysis for yield attributes in F3 populations involving traditional rice (*Oryza sativa* L.) cultivar Poongar. J Pharmacogn Phytochem. 2020;9(3):428–32.
25. Cavanagh CR, Chao S, Wang S, Huang BR, Stephen S, Kiani S, et al. Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. Proc Natl Acad Sci U S A. 2013;110:8057–62. http://doi.org/10.1073/pnas.1217133110
26. Suresh R, Satheesh Kumar P, Muthuramu S, Jebaraj S. Genetic variability studies for yield and yield attributes in rice (*Oryza sativa* L.). EJPB. 2014;5:828–31.
27. Venkatesan M, Prabhakaran N, Vinod KK, Sritharan N, Nair NV. Genetic variability and performance of rice genotypes. J Trop Agric. 2004;42:52–54.
28. Kumar B, Lal GM, Srivastava SBL. Genetic variability, correlation and path analysis among yield and yield contributing characters in rice. Agric Sci Digest. 2009;29:196–99.
29. Sheeba A, Mohan S. Genetic diversity studies in drought tolerant rice (*Oryza sativa* L.) genotypes. Agric Sci Digest. 2025;45(1):86–90. http://doi.org/10.18805/ag.D-5434
30. Subramanian S, Ramamoorthy P, Alagesan S, Amalraj JJ, Muthurajan R, Alagarsamy S, et al. Unraveling the genetic potential of Indian rice germplasm for reproductive stage drought tolerance. Front Plant Sci. 2025;16:1454299. http://doi.org/10.3389/fpls.2025.1454299
31. Prasad KR, Radha Krishna KV, Sudheer Kumar S, Subba Rao LV, Nagaraju P, Senguttuvel P. Studies on correlation and path coefficient analysis for yield and its components in hybrid rice. J Adv Biol Biotechnol. 2025;28(9):331–40. http://doi.org/10.9734/jabb/2025/v28i92885
32. Hassan MA, Dahu N, Hongning T, Qian Z, Yueming Y, Yiru L, et al. Drought stress in rice: morpho-physiological and molecular responses and marker-assisted breeding. Front Plant Sci. 2023;14:1151198. http://doi.org/10.3389/fpls.2023.1151198
33. Dharmaraj D, Selvaraj R, Kari B, Govindan S, Muthurajan R, Paramasivam J. Marker-assisted pseudo-backcrossing for developing climate-resilient rice. Sci Rep. 2024;14:30219. http://doi.org/10.1038/s41598-024-81598-2
34. Sandhu N, Raman KA, Torres RO. Rice root architectural traits and their interactions with seed size are associated with grain yield under drought stress. Sci Rep. 2016;6:35535. http://doi.org/10.1038/srep35535
35. Wasson AP, Richards RA, Chatrath R, Misra SC, Prasad SS, Rebetzke GJ, et al. Traits and selection strategies to improve root systems and water uptake in water-limited wheat growing environments. J Exp Bot. 2012;63:3485–98. http://doi.org/10.1093/jxb/ers111
36. Lucas K, Wissuwa M, Dinh LT. Heritable variation in root emergence during post-drought recovery reveals potential links to seedling drought recovery in rice. Curr Plant Biol. 2025. http://doi.org/10.1016/j.cpb.2025.100509
37. Ikeda M, Miura K, Aya K, Kitano H, Matsuoka M. Genes offering the potential for designing yield-related traits in rice. Curr Opin Plant Biol. 2013;16:213–20. http://doi.org/10.1016/j.pbi.2013.02.002
38. Kato T, Tamaki K. Relationship between spikelet number and other yield components in recent high-yielding rice varieties. Plant Prod Sci. 2002;5:66–70. http://doi.org/10.1626/pps.5.66
39. Price AH, Steele KA, Moore BJ, Barraclough PB, Clark LJ. A combined RFLP and AFLP linkage map of upland rice (*Oryza sativa* L.) used to identify QTLs for root-penetration ability. Theor Appl Genet. 2000;100:49–56. http://doi.org/10.1007/s001220050007

Additional information

Peer review: Publisher thanks the Sectional Editor and anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information: Available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy.

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting.

Copyright: © The Author(s). This is an open-access article distributed under the Creative Commons Attribution License CC BY 4.0.

Publisher information: Plant Science Today is published by Horizon e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.

https://doi.org/10.14719/pst.16175