

Genetic diversity of selected Malaysian aromatic rice varieties based on agro-morphological traits

¹Shukri, A.I.A., ^{2,*}Abdullah, S., ³Hussein, S., ²Abdullah, N.S., ⁴Aziz, N.A., ⁵Razak, M.S.F.A., ³Ahmad, F. and ⁶Hasan, N.A.

¹Faculty of Plantation and Agrotechnology, Universiti Teknologi MARA Cawangan Melaka, Kampus Jasin, 77300, Merlimau, Melaka, Malaysia

²Agricultural Biotechnology Research Group, Faculty of Plantation and Agrotechnology, Universiti Teknologi MARA Cawangan Melaka, Kampus Jasin, 77300, Merlimau, Melaka, Malaysia

³Agrotechnology and Bioscience Division, Malaysia Nuclear Agency, 43600, Kajang, Selangor, Malaysia

⁴Faculty of Plantation and Agrotechnology, Universiti Teknologi MARA Cawangan Pahang, Kampus Jengka, 26400, Bandar Tun Abdul Razak Jengka, Pahang, Malaysia

⁵Agri-Omic and Bionformatic Programme, Biotechnology and Nanotechnology Research Centre, MARDI Headquarters, 43400, Serdang, Selangor, Malaysia

⁶Biotechnology, Microbiology and Environmental Collaboration Sciences (BIOMECS) Special Interest Group, Faculty of Applied Sciences, Universiti Teknologi MARA Cawangan Negeri Sembilan, Kampus Kuala Pilah, 72000, Kuala Pilah, Negeri Sembilan, Malaysia

Article history:

Received: 3 May 2024

Received in revised form: 22 May 2024

Accepted: 23 September 2025

Available Online: 3 November 2025

Keywords:

Aromatic rice,
Cluster analysis,
Correlation coefficient
analysis,
Genetic parameters,
Path coefficient analysis

DOI:

[https://doi.org/10.26656/fr.2017.9\(S3\).5](https://doi.org/10.26656/fr.2017.9(S3).5)

Abstract

Genetic diversity has been pivotal in unleashing the roles of genes and traits in crop productivity and resistance ability against multiple stresses. In this study, the main objective was to investigate the genetic variation of six local aromatic rice varieties in Malaysia for twelve agronomic characters by using multivariate analysis, *viz.*, genetic parameters, correlation analysis, path coefficient analysis and cluster analysis. The results illustrated that the phenotypic coefficient of variance (PCV) was higher than the genotypic coefficient of variance (GCV) for all characters, despite small differences in values among them. All the characters also revealed a high heritability index (h^2b) except for the length of the panicle. Five characters, namely plant height, number of tillers, number of panicles, weight of 1000 grains and number of unfilled grains per panicle, possessed both a high heritability index and genetic advance as percentage of mean (GA%). These five characters could be used as primary selection criteria for future rice hybridisation or improvisation of the sole aromatic variety. As for the correlation analysis, the number of filled grains per panicle and the length of the seed illustrated a strong correlation and a positive direct effect on the yield rate per plant. According to UPGMA cluster analysis, the varieties were clustered into three groups. Rice variety in Cluster III (MRQ 76 and MRQ 104) and II (MRQ74, MRQ88 and MRQ103) could be considered for further hybridisation to attain a wide spectrum of variation as well as the greatest performance in agronomic performance.

1. Introduction

Rice (*Oryza sativa* L) is the third most produced crop in the world at an estimated value of 800 million tonnes annually (Food and Agriculture Organization, 2022). Globally, rice provides 60% of the total calories needed by the human population (FAO, 2022) and over 75% of the protein for developing nations (Samal *et al.*, 2022). However, the consumption of rice is continuously tough in most African and Asian countries due to the emerging population density and economic growth

(Samal *et al.*, 2022). As in Malaysia, we only achieved 73.4% of the self-sufficiency level (SSL), thus urging us to import around 26.6% of rice to fulfil the local demands (Ministry of Agriculture and Food Industry, 2021).

The economic value of rice is greatly determined by two main classes: non-aromatic rice and aromatic rice. Aromatic rice is more premium and unique due to its subtle aroma, flavour and texture (Singh *et al.*, 2000; Roy *et al.*, 2020; Dwiningsih and Alkahtani, 2022). The

*Corresponding author.

Email: shamsiah3938@uitm.edu.my

most notable aromatic rice varieties include Basmati (India), Pusa Basmati (Pakistan) and Khao Dawk Mali 105 / Jasmine (Thailand) (Chauhan *et al.*, 2017). Despite their premium quality, most nations do not emphasise the improvement of aroma and grain quality as they are more worried about the local demand-production clash rather than complex issues such as aroma and taste (Verma *et al.*, 2018; Sharma and Khanna, 2019). Moreover, aromatic rice varieties require extra efforts during cultivation as they are highly susceptible to diseases, environmental shifts and climate changes (Fahad *et al.*, 2019). Accurate analyses of the agronomic traits and proper selection of the variety are important to produce the best aromatic variety with good plant characters and yield.

The wide gamut of problems requires an extensive solution prior to the development of new aromatic rice varieties in Malaysia. The analysis of various agronomic traits must be practised for a broad collection of aromatic rice before selecting cultivars with the best overall performance (International Rice Research Institute, 2013). The primary focus to improve the yield and grain quality of aromatic rice must be preceded by interrelationship analyses of different agronomic traits with yield rates (Augustina *et al.*, 2013). Common analyses on the agronomic characters of aromatic rice include partitioning of genetic parameters, correlation coefficient, path coefficient and cluster (Borah *et al.*, 2023; Shrivastav *et al.*, 2023).

The genetic parameters allowed the measurement of agronomic performances through genotypic variance (σ^2_g), phenotypic variance (σ^2_p), heritability of broad sense (h^2_b), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance (GA) and genetic advance as percentage of mean (GA%). Among all, heritability (h^2_b) is the principal data that indicates the magnitude of a character's transmissibility from parental plants to future generations (Shukri *et al.*, 2021). In addition, a broad range of heritability linked to higher genetic advance (GA) will be helpful in genetic gain forecast (Johnson *et al.*, 1955; Akter *et al.*, 2018). However, these genetic parameters alone are insufficient and must be followed by correlation coefficient analysis to determine the association of characters with yield rate (Saha *et al.*, 2019). Correlation analysis is compulsory to identify the significant positive associations between agronomic characters and their contributions toward production. Apart from correlation analysis, path coefficient analysis (multiple linear regression) is also important to illustrate the direct or indirect effects of each agronomic character on the yield performances (Jan and Kashyap, 2019). As for the genetic diversity among rice varieties, cluster

analysis is a way to measure the genetic distance among rice varieties with similarities of agronomic performances (Iqbal *et al.*, 2018).

In Malaysia, the Malaysia Agriculture Research and Development Institute (MARDI) is the main research institution responsible for the development of aromatic rice varieties (Zainuddin *et al.*, 2012; Ramli, 2019). The development of aromatic rice started in 1990 with a prime objective of producing local aromatic varieties with Basmati or Jasmine-like traits, including good grain elongation ratio, strong aroma and soft texture upon cooking (Rahman *et al.*, 2020). The released Malaysian aromatic varieties include MRQ 50, MRQ 74, MRQ 76, MRQ 88 (MARDI Wangi 88), MRQ 103 (MARIA) and MRQ 104 (Kembanghari) (Rahman *et al.*, 2020; Ramli *et al.*, 2021). However, production is not as expected, either for local consumption or export purposes. The production is largely influenced by environmental factors in Malaysia including climate change (warmer than most aromatic rice cultivation area in Pakistan, India and Thailand), outbreak of major diseases (bacterial leaf blight and tungro disease) as well as frequent alternate environmental constraints (irrigation, drought and flood) (Rajamoorthy and Munusamy, 2015; Firdaus *et al.*, 2020).

In this study, six Malaysian aromatic rice varieties (MRQ50, MRQ74, MRQ76, MRQ88, MRQ103 and MRQ104) were selected for diversity appraisal on the rice yield rate and their agronomic characters. Besides the easy access to getting these varieties from MARDI, all six varieties were chosen due to their insignificantly low yield and resistance rate against multiple abiotic and biotic stresses. In 1999, MRQ50 was the first Malaysian modern aromatic variety developed with Jasmine-like properties, including good aroma and fluffy rice appearance (Razak *et al.*, 2020). After MRQ50, MRQ74 was later released as a progeny between Q34 and the Kasturi line (Basmati derivatives line) (Razak *et al.*, 2020). Previous findings illustrated MRQ74 as a variety with 80% similar attributes to Basmati, including moderate aroma intensity and long grain (Jamal *et al.*, 2014). Over five years, MARDI developed MRQ76 and MRQ88 in 2011 and 2016, respectively (Ramli *et al.*, 2021; Elixon *et al.*, 2022). MRQ76 was developed for its low amylose content (17.0 %) and higher yield potential per hectare (3.4 – 6.2 t/ha) (Ramli *et al.*, 2021; Elixon *et al.*, 2022). On the other hand, MRQ88 has a slightly lower yield than MRQ76 (5.0 t/ha) but was developed for its moderate amylose content and strong aroma (Ariff *et al.*, 2019; Elixon *et al.*, 2022). As for MRQ103 and MRQ104, both varieties were developed in 2022 for their moderate aroma and low glycemic index (Ramli *et al.*, 2021; Ramli *et al.*, 2023). Low glycemic index in

aromatic rice is preferred as it allows carbohydrates to break down slowly, hence releasing glucose gradually into the bloodstream, causing a stable blood glucose level (NDSS, 2023). All selected varieties have their benefits and 1 common disadvantage: decreasing yield rate and tolerance towards multiple biotic and abiotic stresses. Thus, the present study was conducted to investigate the relationships between selected agronomic characters and the yield rate of Malaysian aromatic rice varieties through multivariate analysis, *viz.*, genetic parameters, correlation analysis and cluster analysis.

2. Materials and methods

2.1 Materials

The present study was conducted at the greenhouse and plant physiology laboratory of Agrotechnology and Bioscience Division, Malaysia Nuclear Agency, Selangor, Malaysia. A total of 180 healthy seeds (6 genotypes \times 30 seeds) were obtained from the Malaysian Agricultural and Research Development Institute (MARDI) Rice Genebank (Table 1).

2.2 Plant cultivation and maintenance

The seeds were germinated on 3rd May 2023 and transplanted into individual pots at the greenhouse on 18th May 2023. The experiment was laid out in a Randomised Complete Block Design (RCBD) with 10 plants \times 3 replications for each variety. Four types of fertilisers were used: NPK Green, Triple Superphosphate (TSP), Muriate of Potash (MOP) and urea fertilisers as suggested in the standard rice cultivation management provided by Malaysian Agricultural Research and Development Institute, MARDI (Omar *et al.*, 2008). As for the plant maintenance, water and pesticide application (Malathion-57, pest: *Leptocorisa* sp.) were done daily and monthly, respectively.

2.3 Agro-morphological data collection

The data was collected at different phases of rice development for twelve agronomic characters: days to flowering (DF), days to maturity (DM), plant height (PH, cm), number of tiller (NT), number of panicle (NP), length of panicle (LP, cm), weight of 1000 grains

(1000GW, g), length of seed (LS, mm), number of filled grain per panicle (FGPP), number of unfilled grain per panicle (UFGPP), number of total grain per panicle (TGPP), and yield rate per plant (YPP, %). Each character was measured accordingly to the international standard procedure listed in the Standard Evaluation System (SES) for Rice (IRRI, 2013).

2.4 Statistical analysis

Statistical Package for Social Scientists software version 25 (SPSS 25) was used to perform descriptive statistics analysis (Analysis of Variances, ANOVA), correlation coefficient analysis and path coefficient analysis (multiple linear regression). The genetic parameters, including genotypic variance (σ^2_g), phenotypic variance (σ^2_p), heritability of broad sense (h^2_b), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance (GA) and genetic advance as percentage of mean (GA%), were measured using the following formula:

2.3.1 Evaluation of genotypic and phenotypic variances

According to Johnson *et al.* (1955), both variances are evaluated as follows:

$$\text{Genotypic variance, } \sigma^2_g = \frac{GMS - EMS}{r}$$

$$\text{Phenotypic variance, } \sigma^2_p = \sigma^2_g + EMS$$

Where GMS = Genotypic Mean Square, EMS = Error Mean Square, and r = replication number.

2.3.2 Evaluation of heritability in the broad sense

As provided by Johnson *et al.* (1955), the h^2_b can be calculated through:

$$\text{Heritability, } h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Based on the percentages achieved, h^2_b can be classified into distinguished levels *viz.*, low (<30%), medium (30 – 60%) and high (>60%).

Table 1. Malaysian aromatic rice genotypes used in this study.

No.	Name of rice genotypes	Released year	Digital Object Identifier (DOI)
1	MRQ50	1999	https://doi.org/10.18730/KAM72
2	MRQ74	2005	https://doi.org/10.18730/KAMB6
3	MRQ76	2011	https://doi.org/10.18730/KAME9
4	MRQ88	2016	https://doi.org/10.18730/KAMPH
5	MRQ103	2022	NONE
6	MRQ104	2022	https://doi.org/10.18730/ZR8H

*Digital Object Identifier is a Global Identification registered in the Global Information System (GLIS) under the Food and Agriculture Organization of the United Nations (FAO)

2.3.3 Assessment of genotypic coefficient of variation and phenotypic coefficient of variation

Both variations were calculated by using the following formula (Burton and De Vane, 1953; Singh and Chaudhary, 1977):

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where \bar{X} = population mean

As illustrated by Sivasubramanian and Madhavanon (1973), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) can be categorised as low (<10%), moderate (10-20%), and high (>20%).

2.3.4 Assessment of genetic advance and genetic advance as percentage of mean

The genetic advance (GA) and genetic advance as percentage of mean (GA%) were calculated according to the formula provided by Johnson *et al.* (1955) and Comstock and Robinson (1952), respectively.

$$GA = h^2b.K.\sigma_p$$

Where h^2b = heritability in the broad sense; K = selection differential, which is 2.06 at 5% selection intensity, σ_p = phenotypic standard deviation

$$GA\% = \frac{GA}{\bar{X}} \times 100$$

The GA% can be classified as low (0-10%), moderate (10-20%), and high (>20%) (Johnson *et al.*, 1955; Falconer, 1966).

2.4 Cluster analysis

Cluster analysis was performed in NTSYS-PC software (version 2.1) based on the Euclidean distance method that contained Dice's and Jaccard's similarity coefficient (Oladosu *et al.*, 2020). SAHN clustering and the unweighted pair group method with arithmetic means (UPGMA) algorithm were combined to analyse genetic relationships among rice lines based on agronomic performances.

3. Results and discussion

3.1 Evaluation of genetic parameters

The assessment of genetic parameters for all characters was presented in Table 2. The parameters include genotypic variances (σ^2g), phenotypic variances (σ^2p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability of broad sense (h^2b), and genetic advance as percentage of mean (GA%).

All characters have higher values of PCV than their corresponding GCV. As observed by Debsharma *et al.* (2023), PCV values are always higher than GCV due to additional environmental influences on the characters. However, the differential values between PCV and GCV are very small in this study, indicating that genetic factors primarily regulate the characters' expression rather than the environment (Debsharma *et al.*, 2023). Multiple studies, including Akhtar *et al.* (2022), also revealed the higher value of PCV than GCV in all characters of 58 Indian aromatic rice varieties. Individually, the highest GCV and PCV were illustrated by the number of unfilled grain per panicle (GCV

Table 2. Evaluation of genetic parameters for twelve agronomic characters.

Agronomic Characters	σ^2g	σ^2p	GCV	PCV	h^2b	GA (%)
DF	70.78	71.27	9.19	9.22	99.32	18.86
DM	35.93	36.22	4.92	4.94	99.19	10.08
PH	180.95	181.82	13.14	13.17	99.52	26.99
NT	4.16	5.37	16.88	19.16	77.60	30.63
NP	5.36	6.40	15.52	16.96	83.80	29.27
LP	0.15	0.39	1.54	2.50	38.01	1.96
1000GW	9.83	9.89	14.89	14.94	99.37	30.58
LS	0.16	0.18	6.19	6.58	88.54	11.99
FGPP	35.70	52.37	6.90	8.35	68.16	11.73
UFGPP	107.29	125.44	18.83	20.36	85.53	35.87
TGPP	93.48	116.85	6.83	7.63	80.00	12.58
YPP	26.80	33.03	8.44	9.37	81.14	15.66

σ^2g : genotypic variances, σ^2p : phenotypic variances, h^2b : heritability of broad sense, PCV: phenotypic coefficient of variation, GCV: genotypic coefficient of variation, GA: genetic advance, GA%: genetic advance as percentage of mean; DF: days to flowering, DM: days to maturity, PH: plant height, NT: number of tiller, NP: number of panicle, LP: length of panicle, LS: length of seed, 1000GW – weight of 1000 grains, FGPP: filled grain per panicle, UFGPP: unfilled grain per panicle, TGPP: total grain per panicle, YPP: yield rate per plant.

=18.83%, PCV= 20.36%), followed by the number of tillers (GCV=16.88%, PCV=19.16%) and the number of panicles (GCV=15.52%, PCV=16.96%). Previous findings by Bitew (2016) and Borah *et al.* (2023) also recorded high values of both GCV and PCV for the number of unfilled grains per panicle. As observed, all characters have low to medium percentage of GCV and PCV, except for the number of unfilled grains per panicle, UFGPP (GCV = high, 20.36%). The results denoted that UFGPP has a higher percentage of expression at the phenotypic level based on the genetic constitution. As stated by Saha *et al.* (2019), the possibility of yield improvement will increase through the improvement of characters with high percentages in GCV and PCV.

A high heritability index was observed in all characters except for the length of the panicle (38.01%). Four characters had a 99% heritability index, *viz.*, plant height (99.52%), weight of 1000 grains (99.37%), days to flowering (99.32%) and days to maturity (99.19%). Akter *et al.* (2018) also reported the highest heritability index for plant height in 26 genotypes of Bangladesh aromatic cultivars. As a comparison, the results indicated that the plant height could be inherited with almost 100% similarity into future progenies. A higher h^2b provides a wider extent of transmissibility of a character into future generations (Sabesan *et al.*, 2009 in Akter *et al.*, 2018). In addition, it is also an indicator of small influences by environmental conditions on the phenotypic expression of the characters.

Based on the results, the number of unfilled grains per panicle has the highest GA (%) value with 35.87%, followed by the number of tillers (30.63%), and the weight of 1000 grains (30.58%). These findings revealed that the number of unfilled grains plays a bigger role in

determining the expected output or yield rate. According to Oladosu *et al.* (2018), the combination of heritability appraisal and genetic advance is normally more helpful in predicting the output under selection than heritability estimation alone (Oladosu *et al.*, 2018). High heritability and genetic advance also indicated the dominant influence of additive gene(s) that could produce an effective selection program (Borah *et al.*, 2023). As observed in Table 2, five characters have high percentages in both h^2b and GA (%), including plant height, number of tillers, number of panicles, weight of 1000 grains and number of unfilled grains per panicle. Kuma *et al.* (2020) and Basu *et al.* (2022) also observed a high GA (%) for the number of tillers in aromatic rice cultivars. In this study, the diversified group of characters with high h^2b + GA (%) will provide a broader spectrum of choices for the future Malaysian aromatic rice development program.

3.2 Evaluation of the correlation coefficient among agronomic characters

Correlation coefficient analysis is the elucidation of relationships among characters and the degree (strength) of linear relation between them (Shrivastav and Verma, 2023). Besides the correlation among agronomic characters, the degree of correlation between those characters with yield rate is much important and is often applied in multiple breeding programs.

As observed in Table 3, the yield rate per plant (YPP) had multiple significant positive correlations with the number of filled grain per panicle (0.650 at $p<0.01$), length of seed (0.548 at $p<0.01$), plant height (0.540 at $p<0.01$), weight of 1000 grains (0.535 at $p<0.01$) and number of panicle (0.332 at $p<0.01$). A study on eighteen advanced lines of Malaysian varieties also

Table 3. Phenotypic correlation coefficients among twelve agronomic characters.

Characteristics	DF	DM	PH	NT	NP	LP	1000GW	LS	FGPP	UFGPP	TGPP	YPP
DF	1	0.928**	-0.853**	-0.473**	-0.238*	0.048	-0.397**	0.095	-0.2	0.373**	0.248*	-0.364**
DM		1	-0.660**	-0.479**	-0.341**	-0.065	-0.103	0.19	-0.377**	0.214*	-0.035	-0.294**
PH			1	0.556**	0.295**	0.013	0.803**	0.231*	0.077	-0.646**	-0.614**	0.540**
NT				1	0.528**	0.250*	0.371**	0.218*	0.079	-0.175	-0.127	0.155
NP					1	0.351**	0.134	-0.028	0.422**	-0.258*	0.02	0.332**
LP						1	0.032	0.264*	0.284**	-0.122	0.067	0.195
1000GW							1	0.538**	-0.144	-0.728**	-0.848**	0.535**
LS								1	0.171	-0.591**	-0.493**	0.548**
FGPP									1	-0.373**	0.292**	0.650**
UFGPP										1	0.778**	-0.946**
TGPP											1	-0.535**
YPP												1

*significant at ($p<0.05$), **significant at ($p<0.01$), NS: not significant, DF: days to flowering, DM: days to maturity, PH: plant height, NT: number of tiller, NP: number of panicle, LP: length of panicle, LS: length of seed, 1000GW – weight of 1000 grains, FGPP: filled grain per panicle, UFGPP: unfilled grain per panicle, TGPP: total grain per panicle, YPP: yield rate per plant.

revealed significant positive correlations between yield rate and all aforementioned characters except plant height (Sabri *et al.*, 2020). Okasa *et al.* (2022) also discovered the highest significant positive correlation between the yield rate per plant with the number of filled grains per panicle. In contrast, grain yield per plant had significant negative correlations with days to flowering, days to maturity, number of unfilled grain per panicle, and total grain per panicle. These findings were also observed by Sabri *et al.* (2020), who discovered the significant negative association between grain yield per plant with days to flowering and days to maturity. Generally, the negative relationship indicated weak and inverse proportionality between characters. The consideration of both characters is not advisable for the mutual character development of aromatic rice.

Among other agronomic characters, the highest significant positive correlation occurred between days to maturity with days to flowering (0.928 at $p < 0.01$), followed by plant height with weight of 1000 grains (0.803 at $p < 0.01$) and number of unfilled grains per panicle with total grain per panicle (0.778 at $p < 0.01$). The strong relationships at a 0.01 significance level illustrated a direct proportionality, which indicates a big change in one character's value over the change of another (Shukri *et al.*, 2021). As observed by Saha *et al.* (2019), days to flowering have the strongest relationship with days to maturity. This is true because days to flowering initiate the reproduction to begin faster and mature earlier, before encountering unfavourable climate cum weather change that could affect the rice growth (Matsubara and Yano, 2018). In contrast, Lakshmi *et al.* (2017) discovered an insignificant correlation between plant height and the weight of 1000 grains.

3.3 Evaluation of path correlation coefficients toward yield rate

Path correlation coefficient involves a multiple

regression analysis that measures the direct and indirect effects of agronomic characters on yield rate. As illustrated in Table 4, the bold values indicate the direct effects of all characters on the yield rate of the plant. Meanwhile, the other unhighlighted values are denoted as the indirect effects of one character via another character towards the yield rate of the plant.

The highest direct positive effect on yield rate was shown by the number of filled grain per panicle (0.903), followed by days to maturity (0.063), number of tillers (0.015), length of panicle (0.008) and length of seed (0.004). Direct positive effects implied that the characters are highly reliable and can be selected directly for the characters and yield improvement program. Several scholars also recorded the strong direct effects of filled grain per panicle towards yield rate, including 63 hybrid Indian aromatic and non-aromatic varieties (Shrivasta and Verma, 2023) and 55 Indian aromatic varieties (Lakshmi *et al.*, 2017). As for the highest positive indirect effect towards yield rate weight of 1000 grains (0.700) ranked in first place, followed by plant height (0.507) and length of seed (0.407), all via the total grain per panicle pathways. The improvement of these characters will eventually improve the direct effect of total grain per panicle towards the yield rate.

On the flip side, five characters expressed negative direct effects on yield rate lead including days to flowering, plant height, number of panicles, weight of 1000 grains, and total grain per panicle. The negative values, especially for plant height, were also recorded in various studies such as Kumar and Pandey (2021) as well as Dinkar *et al.* (2023). More often than not, the negative direct effects also resulted from the broad continuum of aforementioned characters between varieties. In addition, the stacking factors of individual characters in one particular variety could also determine the resultant yield rate. For example, the differences in days to flowering among varieties were affected by

Table 4. Direct and indirect effect (path coefficient) of different agronomic characters toward yield rate.

	DF	DM	PH	NT	NP	LP	1000GW	LS	FGPP	TGPP	YPP*
DF	-0.090	0.058	0.044	-0.007	0.006	0.004	0.011	0.000	-0.181	-0.205	-0.364
DM	-0.084	0.063	0.034	-0.007	0.008	0.001	0.003	0.001	-0.340	0.029	-0.294
PH	0.077	-0.042	-0.051	0.008	-0.007	0.000	-0.022	0.001	0.070	0.507	0.540
NT	0.043	0.030	-0.028	0.015	-0.013	0.002	-0.010	0.001	0.071	0.105	0.155
NP	0.021	-0.021	-0.015	0.008	-0.024	0.003	-0.004	0.000	0.381	-0.017	0.332
LP	-0.004	-0.004	-0.001	0.004	-0.008	0.008	-0.001	0.001	0.256	-0.055	0.195
1000GW	0.036	-0.006	-0.041	0.006	-0.003	0.000	-0.028	0.002	-0.130	0.700	0.535
LS	-0.009	0.012	-0.012	0.003	0.001	0.002	-0.015	0.004	0.154	0.407	0.548
FGPP	0.018	-0.024	-0.004	0.001	-0.010	0.002	0.004	0.001	0.903	-0.241	0.650
TGPP	-0.022	-0.002	0.031	-0.002	-0.001	0.001	0.024	-0.002	0.264	-0.825	-0.535

*The values in this column are the correlation coefficients of each agronomic character towards yield rate. Bold values: direct effect, unbold values: indirect effect

transplantation of seedlings, tight spacing, and the conventional method of irrigation (Ranawake *et al.*, 2014). These factors could possibly reduce the direct effects of days to flowering towards the yield rate. On another note, the negative direct effects of plant height on yield rate are determined by the higher accumulation of photosynthates in vegetative parts rather than the reproductive parts of plants (Saha *et al.*, 2019). A study made by Islam *et al.* (2019) also revealed identical illustrations on the direct negative effects of plant height. According to Saha *et al.* (2019), the negative direct effect of one character was also affected by its considerably larger values of negative indirect effect, despite the presence of multiple characters that provided positive values. The negative values could be simultaneously increased in future programs to bring more positive direct effects toward the yield rate. One model that could be practised is the restricted simultaneous selection model as proposed by Pradhan *et al.* (2015). Rashid *et al.* (2010) and Shukri *et al.* (2021) explained that this restriction happened through the optimisation of direct effect via full elimination/upgrade of indirect effects.

Additionally, the combination of a positive correlation coefficient and a path coefficient could provide high positive effects and a greater success rate when selected for a breeding program (Gour *et al.*, 2017). In this study, two characters showed high positive values at both correlation and direct effects, which are the number of filled grains per panicle and the length of the seed. In a study by Saha *et al.* (2019), both characters also demonstrated strong and positive results for both analyses. On another note, various studies have mutually suggested the improvement of characters with aforementioned quality for a much systematic selection prior to a mega aromatic development program (Pradhan *et al.*, 2015; Debsharma *et al.*, 2023; Dinkar *et al.*, 2023).

3.4 Cluster analysis

The cluster analysis divided all six aromatic rice varieties into three main clusters at 7.93 dissimilarity coefficients. Each cluster has a different number of varieties, with one for Cluster I (MRQ50), three for Cluster II (MRQ74, MRQ88, and MRQ103) and two for Cluster III (MRQ76 and MRQ104). All varieties were separated by Euclidean dissimilarity coefficients based on the combined performances of twelve agronomic characters (Figure 1). At 7.93, the distance revealed greater differences in the performance of characters between clusters. A report by Bairwa *et al.* (2022) also illustrated the partitioning of 96 aromatic cultivars into three clusters at high Euclidean distances. As compared to the analysis of six Malaysian white rice varieties by

Shukri *et al.* (2021), the distance in this study is higher at 18.5 dissimilarity coefficient. The comparison indicated that Malaysian aromatic rice varieties have large differences between them, but not as large as the differences among Malaysian white rice varieties.

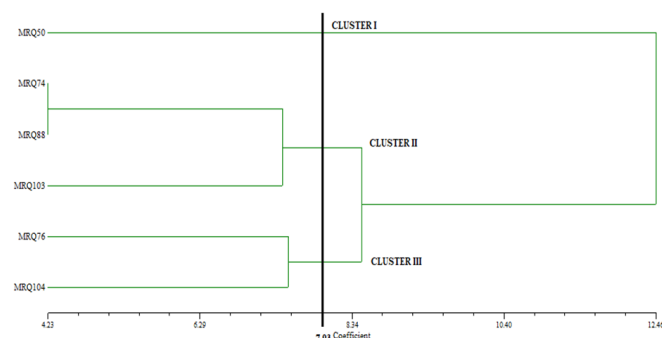


Figure 1. Clusters of six Malaysian aromatic rice varieties based on the performances of twelve agronomic characters.

In between clusters, MRQ50 had the highest differences with MRQ76 and MRQ104. Meanwhile, both latter accessions had the shortest distances of variability between them. According to Ramli *et al.* (2021), both accessions in Cluster III had the highest yield rate and were slightly identical in characters' performances. According to the timeline, all selected varieties were cultivated in Malaysia over different eras between 1999-2022 (Rahman *et al.*, 2020). As seen in every cluster, the genotypes from similar eras are not in the same cluster, indicating that the genotypes' genetic divergence is continuously evolving and influenced by the environment. For example, MRQ76 and MRQ104 were released back in 2011 and 2022, respectively (Ramli *et al.*, 2021). MRQ104 was released with better agronomic performances and yield rate than MRQ76 during the initial year (Ramli *et al.*, 2021). However, this study revealed that both varieties have similar agronomic performances, which led them to be clustered in Cluster III. Based on different quantitative traits, we also found no correlations of the clusters' characteristics with geographical factors. This indicated high variability among rice accessions based on specifically performed traits and not the origin.

The accessions in Cluster III showed high performances in eight out of twelve traits, viz, days to flowering, days to maturity, number of tillers, number of panicles, number of filled grain per panicle, number of unfilled grain per panicle, total grain per panicle and yield rate per plant. As for future development programs, the rice accessions in Cluster III could be highly considered as they had a greater number of highly performing traits compared to other clusters. Cluster II came in second rank with three highly performing characters, namely length of panicle, weight of 1000 grains and length of seed. Meanwhile, for Cluster I,

MRQ50 only dominated the best performance for one character, the plant height. As suggested by and Krishna *et al.* (2022) and Dinkar *et al.* (2023), greater heterotic responses could be fulfilled through hybridisation of varieties from different clusters. A further cross-breeding program could consider the combination between accessions in Cluster II and III, as they had large gaps in distances, as well as better performances in traits and yield rate, among others.

4. Conclusion

Five characters have high percentages in both h^2b and GA (%), including plant height, number of tillers, number of panicles, weight of 1000 grains and number of unfilled grains per panicle. As for correlation coefficient and path coefficient analysis, the number of filled grains per panicle and the length of the seed illustrated a strong correlation and a positive direct effect on the yield rate per plant. Based on characters quality, all aforementioned characters could be selected for the aromatic rice yield improvisation program. According to cluster analysis, rice varieties in Cluster III performed well in eight out of twelve agronomic characters and should be considered as the primary choice for further cultivation. On another note, the varieties in Cluster III and II could also be deliberated for hybridisation as it will bring greater heterotic response and better agronomic characters in future aromatic progenies.

Conflict of interest

The authors declare no conflict of interest.

Acknowledgements

The authors would love to acknowledge the Malaysian Ministry of Higher Education for providing financial assistance through the Fundamental Research Grant Scheme (FRGS/1/2022/WAB04/UITM/02/3). Our deepest gratitude also goes to every related personnel at the Agrotechnology and Biosciences Division of Malaysia Nuclear Agency, and the Faculty of Plantation and Agrotechnology of Universiti Teknologi MARA Cawangan Melaka Kampus Jasin for their help in providing guidance and facilities throughout the project.

References

- Akter, N., Khalequzzaman, M., Islam, M., Mamun, M. and Chowdhury, M. (2018). Genetic variability and character association of quantitative traits in Jhum rice genotypes. *SAARC Journal of Agriculture*, 16(1), 193-203. <https://doi.org/10.3329/sja.v16i1.37434>
- Ariff, E.E.E., Rahim, H., Harun, R. and Sobri, A.A. (2019). Fragrant rice overview: benefits and

implications of local production. *Economic and Technology Management Review*, 14, 1-11.

- Augustina, U.A., Iwunor, O.P. and Ijeoma, O.R. (2013). Heritability and character correlation among some rice genotypes for yield and yield components. *Journal of Plant Breeding and Genetics*, 1(2), 73-84.
- Bairwa, R.K., Yadav, M.C., Gopalakrishnan, S., Kushwaha, A. and Joshi, M.A. (2023). Morphological and molecular analyses of grain traits in aromatic rice landrace accessions from indo-gangetic plain region of India. *Indian Journal of Plant Genetic Resources*, 36(2), 290-300. <https://doi.org/10.5958/0976-1926.2023.00036.2.11>
- Basu, S.R., Baskheti, D., Deo, I., Nautiyal, M., Singh, S. and Sharma, N. (2022). Studies on genetic variability parameters for yield, quality and nutritional traits in basmati and aromatic rice (*Oryza sativa* L.). *Biological Forum—An International Journal*, 14(4a), 379-384.
- Bitew, J.M. (2016). Estimation of genetic parameters, heritability and genetic advance for yield related traits in upland rice (*Oryza sativa* L. and *Oryza glaberrima* Steud) genotypes in northwestern Ethiopia. *World Scientific News*, 47(2), 340-350.
- Borah, N., Behera, P., Borah, V. and Sarma, R. (2023). Genetic variability, heritability and genetic advance of aromatic rice for yield and its components. *Biological Forum—An International Journal*, 15(5), 1516-1522.
- Burton, G. and De Vane, E. (1953). Estimating heritability in tall fescusce from replicated clone natural materials. *Agronomy Journal*, 45(10), 171-181. <https://doi.org/10.2134/agronj1953.00021962004500100005x>
- Chauhan, B.S., Jabran, K. and Mahajan, G. (2017). Rice production worldwide. Cham, Switzerland: Springer International Publishing. <https://doi.org/10.1007/978-3-319-47516-5>
- Comstock, R. and Robinson, H. (1952) Genetic parameters, their estimation and significance, presented at the 6th International Grassland Congress, Pennsylvania, 1952. Pennsylvania, USA: Pennsylvania State College.
- Debsharma, S.K., Syed, M.A., Ali, M.H., Maniruzzaman, S., Roy, P.R., Brestic, M., Gaber, A. and Hossain, A. (2022). Harnessing on genetic variability and diversity of rice (*Oryza sativa* L.) genotypes based on quantitative and qualitative traits for desirable crossing materials. *Genes*, 14(1), 10. <https://doi.org/10.3390/genes14010010>
- Dinkar, A.K., Kumar, R.R., Kumar, M. and Singh, S. (2023). Genetic variability, correlation and path analysis for selection in elite breeding materials of

- aromatic rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, 12(3), 5733-5740.
- Dwiningsih, Y. and Alkahtani, J. (2022). Rojolele: a premium aromatic rice variety in Indonesia. *International Journal of Agricultural Sciences and Technology*, 2(2), 42-53. <https://doi.org/10.51483/IJAGST.2.2.2022.42-53>
- Fahad, S., Adnan, M., Noor, M., Arif, M., Alam, M., Khan, I.A., Ullah, H., Wahid, F., Mian, I.A. and Jamal, Y. (2019). Major constraints for global rice production. In Hasanuzzaman, M., Fujita, M., Nahar, K. and Biswas, J.K. (Eds.). *Advances in Rice Research for Abiotic Stress Tolerance*, p. 1-22. Amsterdam, Netherlands: Elsevier. <https://doi.org/10.1016/B978-0-12-814332-2.00001-0>
- Falconer, D.S. (1996) *Introduction to Quantitative Genetics*. Chennai, India: Pearson Education India.
- Firdaus, R.B.R., Leong, M.T., Rahmat, S.R. and Senevi Gunaratne, M. (2020). Paddy, rice and food security in Malaysia: a review of climate change impacts. *Cogent Social Sciences*, 6(1), 1818373. <https://doi.org/10.1080/23311886.2020.1818373>
- Food and Agriculture Organization (FAO). (2022). *World food and agriculture - statistical yearbook 2022*. Rome, Italy: Food and Agriculture Organization.
- International Rice Research Institute (IRRI). (2013). *IRRI - Standard Evaluation System of Rice*. 5th ed. Los Banos, Philippines: International Rice Research Institute.
- Iqbal, T., Hussain, I., Ahmad, N., Nauman, M., Ali, M., Saeed, S., Zia, M. and Ali, F. (2018). Genetic variability, correlation and cluster analysis in elite lines of rice. *Journal of Scientific Agriculture*, 2, 85-91. <https://doi.org/10.25081/jsa.2018.v2.900>
- Islam, M., Mian, M., Ivy, N., Akter, N. and Rahman, M. (2019). Genetic variability, correlation and path analysis for yield and its component traits in restorer lines of rice. *Bangladesh Journal of Agricultural Research*, 44(2), 291-301. <https://doi.org/10.3329/bjar.v44i2.41819>
- Jamal, K., Kamarulzaman, N., Abdullah, A., Ismail, M. and Hashim, M. (2014). Adoption of fragrant rice farming: the case of paddy farmers in the east coast Malaysia. *UMK Procedia*, 1, 8-17. <https://doi.org/10.1016/j.umkpro.2014.07.002>
- Jan, N. and Kashyap, C. (2019). Correlation and path analysis in rice (*Oryza sativa* L.) for seed and seed vigour traits. *Journal of Pharmacognosy and Phytochemistry*, 8(1), 222-226.
- Johnson, H.W., Robinson, H. and Comstock, R. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy Journal*, 47(7), 314-318. <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Krishna, K., Mohan, Y.C., Krishna, L., Parimala, G. and Jagadeeshwar, R. (2022). Multivariate analysis based prediction of phenotypic diversity associated with yield and yield component traits in germplasm lines of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 13(3), 764-771. <https://doi.org/10.37992/2022.1303.129>
- Kuma, A., Prasad, J., Kumar, S., Singh, S., Jeena, A.S. and Upreti, M.C. (2020). Estimation of genetic parameter for yield components and quality traits in rice (*Oryza sativa* L.). *International Journal of Chemical Studies*, 8, 1369-1372. <https://doi.org/10.22271/chemi.2020.v8.i4l.9792>
- Kumar, S. and Pandey, I.D. (2021). Genetic diversity, character association and path coefficient analysis in Kalanamak advanced lines of rice (*Oryza sativa* L.). *Indian Journal of Plant Genetic Resources*, 34(3), 483-489. <https://doi.org/10.5958/0976-1926.2021.00043.7>
- Lakshmi, L., Rao, M.B., Raju, C.S. and Reddy, S.N. (2017). Variability, correlation and path analysis in advanced generation of aromatic rice. *International Journal of Current Microbiology and Applied Sciences*, 6(7), 1798-1806. <https://doi.org/10.20546/ijemas.2017.607.217>
- Matsubara, K. and Yano, M. (2018). Genetic and molecular dissection of flowering time control in rice. In Sasaki, T. (Ed.). *Rice Genomics, Genetics and Breeding*, p. 177-190. Singapore: Springer Nature. https://doi.org/10.1007/978-981-10-7461-5_10
- Ministry of Agriculture and Food Industry (MAFI). (2021). *Dasar Agromakanan Negara 2021-2030*. Kuala Lumpur, Malaysia: Ministry of Agriculture and Food Industry.
- Okasa, A.M., Sjahril, R., Riadi, M., Mahendradatta, M., Sato, T., Toriyama, K., Ishii, K., Hayashi, Y. and Abe, T. (2021). Correlation and path coefficient analysis of grain yield and its components in Toraja land-race aromatic rice mutants induced by heavy ion beam. *Asian Journal of Plant Sciences*, 20(3), 406-413. <https://doi.org/10.3923/ajps.2021.406.413>
- Oladosu, Y., Rafii, M.Y., Arolu, F., Chukwu, S.C., Muhammad, I., Kareem, I., Salisu, M.A. and Arolu, I.W. (2020). Submergence tolerance in rice: review of mechanism, breeding and, future prospects. *Sustainability*, 12(4), 1632. <https://doi.org/10.3390/su12041632>
- Oladosu, Y., Rafii, M.Y., Magaji, U., Abdullah, N., Miah, G., Chukwu, S.C. and Kareem, I. (2018). Genotypic and phenotypic relationship among yield components in rice under tropical conditions. *BioMed Research International*, 2018(1), 8936767. [https://doi.org/10.26656/fr.2017.9\(S3\).5](https://doi.org/10.26656/fr.2017.9(S3).5)

- doi.org/10.1155/2018/8936767
- Omar, O., Daud, A.H., Ismail, A., Hamid, A.A., Razak, A.A., Man, A., Amzah, B., Saad, M.M., Harun, M., Abdullah, S., Othman, S., Misman, S.N., Suhaimi, S. and Hussain, Y. (2008). Manual Teknologi Penanaman Padi Lestari. Selangor, Malaysia: Malaysian Agricultural Research and Development Institute (MARDI) Publication.
- Pradhan, B., Mishra, T. and Das, S. (2015). Genetic basis of yield variations in lowland rice. *International Journal of Sciences: Basic and Applied Research*, 19 (2), 306-318.
- Rahman, S.N.A., Kamaruzaman, R., Rahim, N.I.A., Othman, M.R. and Sebaweh, N.S. (2020). Varieti padi berpotensi bagi pembangunan varieti padi spesialti. *Buletin Teknologi MARDI*, 21, 9-18. [In Bahasa Malaysia].
- Rajamoorthy, Y. and Munusamy, S. (2015). Rice industry in Malaysia: Challenges, policies and implications. *Procedia Economics and Finance*, 31, 861-867. [https://doi.org/10.1016/S2212-5671\(15\)01183-1](https://doi.org/10.1016/S2212-5671(15)01183-1)
- Ramli, A. (2019). Report on rice R&D at MARDI. Selangor, Malaysia: Malaysian Agricultural Research and Development Institute (MARDI) Publication.
- Ramli, A., Saidon, S.A., Kamaruzaman, R., Sunian, E., Jamal, M.S., Ramachandran, K., Misman, S.N., Masarudin, M.F., Hashim, S., Hosni, H., Rahim, H., Zuki, Z.M. and Sarif, H.M. (2021). Varieti padi MRQ 104 – Padi wangi tempatan baharu. *Buletin Teknologi MARDI*, 24, 29-39. [In Bahasa Malaysia].
- Ranawake, A., Amarasinghe, U., Hewage, M. and Pradeepika, N. (2014). Effect of days to flowering on plant height and yield of rice (*Oryza sativa* L.). *International Journal of Plant and Soil Science*, 3(9), 1143-1152. <https://doi.org/10.9734/IJPSS/2014/11421>
- Rashid, M., Parveen, S. and Bhuiyan, M. (2010). Genetic variability, correlation and path coefficient analysis in nineteen *Brassica rapa* germplasm. *Journal of Sher-e-Bangla Agricultural University*, 4(1), 84-89.
- Razak, S.A., Azman, N.H.E.N., Kamaruzaman, R., Saidon, S.A., Yusof, M.F.M., Ismail, S.N., Abdullah, N. (2020). Genetic diversity of released Malaysian rice varieties based on single nucleotide polymorphism markers. *Czech Journal of Genetics and Plant Breeding*, 56(2), 62-70. <https://doi.org/10.17221/58/2019-CJGPB>
- Roy, S., Banerjee, A., Basak, N., Kumar, J. and Mandal, N.P. (2020). Aromatic Rice. In de Oliveira, A.C., Pegoraro, C. and Viana, V.E. (Eds.). *The Future of Rice Demand: Quality Beyond Productivity*, p. 251-282. Cham, Switzerland: Springer International Publishing. https://doi.org/10.1007/978-3-030-37510-2_11
- Sabri, R.S., Rafii, M.Y., Ismail, M.R., Yusuff, O., Chukwu, S.C. and Hasan, N.A. (2020). Assessment of agro-morphologic performance, genetic parameters and clustering pattern of newly developed blast resistant rice lines tested in four environments. *Agronomy*, 10(8), 1098. <https://doi.org/10.3390/agronomy10081098>
- Saha, S.R., Hassan, L., Haque, M.A., Islam, M.M. and Rasel, M. (2019). Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. *Journal of the Bangladesh Agricultural University*, 17(1), 26-32. <https://doi.org/10.3329/jbau.v17i1.40659>
- Samal, P., Babu, S.C., Mondal, B. and Mishra, S.N. (2022). The global rice agriculture towards 2050: An inter-continental perspective. *Outlook on Agriculture*, 51(2), 164-172. <https://doi.org/10.1177/00307270221088338>
- Sharma, N. and Khanna, R. (2019). Rice Grain Quality: Current Developments and Future Prospects. In Shah, F., Khan, Z., Iqbal, A., Turan, M. and Olgun, M. (Eds.). *Recent Advances in Grain Crops Research*. London, UK: IntechOpen Publication. <https://doi.org/10.5772/intechopen.89367>
- Shrivastav, S.P. and Verma, O. (2023). Correlation and path coefficients analysis for yield and its contributing traits in rice (*Oryza sativa* L.) under sodic soil. *Journal of Rice Research*, 16(1), 32-40. <https://doi.org/10.58297/GQOK7001>
- Shukri, A.I.A., Hasan, N.A., Ahmad, F., Ramachandran, K., Rafii, M.Y., Harun, A.R. and Manaf, M.N.A. (2021). Genetic diversity of selected Malaysian mega rice varieties based on agro-morphological traits. *Malaysian Journal of Biochemistry and Molecular Biology*, 2, 1-9.
- Singh, R., Singh, U. and Khush, G. (2000). *Aromatic rices*. 1st ed. New Delhi, India: Oxford and IBH Publishing Co. Pvt. Ltd.
- Singh, R.K. and Chaudhary, B.D. (1977). *Biometrical methods in quantitative genetic analysis*. New Delhi, India: Kalyani Publishers.
- Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agriculture Journal*, 60, 9-13.
- Verma, D.K., Srivastav, P.P. and Nadaf, A.B. (2018). *Rice Science: Biotechnological and Molecular Advancements*. Florida, USA: CRC Press. <https://doi.org/10.1201/9781351136587>
- Zainuddin, H., Mokhtar, A., Amzah, B., Hashim, M. and Abd Ghafar, M. (2012). Enam varieti padi popular MARDI. *Buletin Teknologi MARDI*, 1, 1-10. [In Bahasa Malaysia].