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GENETIC DIVERSITY OF SELECTED MALAYSIAN MEGA RICE VARIETIES BASED ON AGRO-MORPHOLOGICAL TRAITS

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Abstract

The key to a successful crop improvement program lies in the great discovery of genetic diversity, which uncovers the roles of genes and traits in developing optimally while facing multiple biotic or abiotic factors. The objective of the present study was to investigate the genetic variation of six local mega rice varieties in Malaysia for twelve agro-morphological traits by using multivariate analysis viz., genetic parameters, correlation analysis and cluster analysis. The results showed that the Phenotypic coefficient of variance (PCV) was higher than the Genotypic coefficient of variance (GCV) in all traits among the rice varieties. All the traits recorded high heritability value with the highest value was found for the length of seed at 100% followed by length of panicle at 99.67%, which could be successfully inherited to the next generations. Traits such as number of tillers, number of panicles, number of filled grain per panicle, number of unfilled grain per panicle, and number of total grain per panicle showed high heritability and high genetic advance could be used as a selection criterion for hybridization programs in the future. Among the studied characters, panicle length and 1000-grain weight are the only characters with positive values for correlation coefficient and direct effect on yield rate per plant. According to UPGMA cluster analysis, the varieties were clustered into four groups. As for the principal cluster analysis, three out of twelve principal components explained 86.24% of total variation among the variety. Rice variety in Cluster II (MR219) and IV (MR297, MR303 and MR307) could be considered for further hybridization to attain a wide spectrum of variation as well as the greatest performances in agro-morphological traits.

INTRODUCTION

Rice (*Oryza sativa* L.) is a leading food crop that supplies more than 20% of all calories consumed by the entire human population. Globally, rice is produced in a large number of 728.066 million tons in 2018 [1]. In Malaysia, a total of 1.8 million tons of rice were produced with 695,000 hectares of paddy field in 2018 and the production remained constant for the next three years [1]. Local consumption of rice has seen a slight increase over the last several years. With a surging population, Malaysia needs to increase rice production to meet the growing population's demand.

Rice production is affected by several factors such as climate change (drought, submergence & salinity), pest attacks, disease transmissions, and nutrient deficiencies [2]. The broad spectrum of problems requires a comprehensive solution in which the development of new rice varieties is often prioritized in Malaysia [3]. A further assessment on agronomic traits possessed by rice needed to be done for better rice production. The primary focus to improve grain quality must be preceded by interrelationship analyses of different agronomic traits with yield rates. [4] reported that yield is a complex character in inheritance and may involve several related components. This stipulated the significance of selecting certain agronomic characters at different development stages for producing the optimum amount of rice.

There are three main stages of rice development: vegetative stage, reproductive stage and maturation stage [5]. Different agronomic traits are observed at each stage as they play an important role in determining rice production rate. The studies on relationships between rice agronomic characters had been carried out widely on the phenotypic and genotypic levels. These characters are analyzed through several genetic parameters, such as genotypic variance (σ^2g), phenotypic variance (σ^2p), heritability of broad sense (h_2b), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance (GA) and genetic advance as percentage of mean (GA%). These genetic parameters should be analyzed accurately when making the selection for breeding programs [6]. Heritability indicates the magnitude of a character's transmissibility from parental plants to future generations. A broad range of heritability linked to higher genetic advance (GA) is also helpful in genetic gain forecast [7]. However, these genetic parameters alone are insufficient to determine the association of characters with rice production rate and must be followed by correlation coefficient analysis [6].

Correlation analysis is necessary to disclose the positive association between agronomic characters and yield rate as they contribute significantly to the increment of productions [3]. A further path coefficient analysis is done next to illustrate the direct or indirect effects of each agronomic character to the yield performances [8,9]. Both tools are important for the formulation of selection criteria to produce optimal rice quantity in the upcoming breeding programs. The genetic diversity among rice variety can also be statistically measured through cluster analysis and principal component analysis (PCA). Cluster analysis is a tool used to classify and group various genotypes of a similar crop based on trait similarities [10]. Meanwhile, PCA reduces a large series of data by dividing the strength of interrelationship into specific groups based on their contributions toward the total variance [11].

In Malaysia, the local rice varieties were planted across the countries with most granary areas identified in the north of Peninsular Malaysia [12]. Malaysian local rice varieties were solely great in combating multiple diseases, producing high yield and containing good agronomic characters [12]. Malaysian Agricultural Research and Development Institute (MARDI) is the main authority responsible for producing new high yield varieties for farmers thus increasing the income for the individuals and country as a whole [12]. However, the yield rate and resistance rate of these varieties were decreasing as time marched on. Thus, in this study, six Malaysian rice varieties (MR84, MR219, MR284, MR297, MR303 and MR307) were selected for diversity evaluation with major focus on the rice yield rate and its agronomic characters. MR84 was the first modern local rice variety developed by MARDI back in 1986 [12]. This variety covered more than 80% of the Peninsular's rice granary area and slowly diminished due to bacterial leaf blight (BLB) disease towards the end of the year 2000 [13]. In 2001, MR219 was developed with a higher yield and greater resistance rate against BLB disease [12]. However, the demand for this variety was also decreasing as high yield losses were faced by farmers due to blast disease [13]. As a progressive solution, MARDI developed another two high-yielding varieties, MR284 and MR297, in 2015 and 2018 respectively [14,15]. MR284 has 7.2% more yield than MR219, meanwhile, MR297 has a high yield rate between 77.1% - 86.2% [15,16]. Moreover, MR297 is also the most demanded variety by current local farmers due to its great resistance against blast disease [15,16,17]. MR303 and MR307 were the latest high yield varieties developed by MARDI in 2018 [18]. They also have a great resistance rate against blast disease and brown planthopper [18]. Besides the easy access of getting these varieties from MARDI, all six varieties were chosen due to their wide spectrum of yield rate and resistance rate against multiple diseases. Thus, the present study was conducted with an objective to investigate the relationships between selected agronomic characters and yield rate of high-yielding Malaysian rice varieties through multivariate analysis viz., genetic parameters, correlation analysis and cluster analysis.

MATERIALS AND METHODS

The present study was conducted at the greenhouse and rice laboratory of Agrotechnology and Bioscience Division, Malaysia Nuclear Agency, Selangor, Malaysia. A total of sixty healthy seeds (10 seeds x 6 genotypes) were obtained from the Malaysian Agricultural and Research Development Institute (MARDI) Rice Genebank (as listed in Table 1).

Table 1. List of rice genotypes used in this experiment

No.	Rice genotypes	Released year	DOI*
1	MR 84	1986	10.18730/KAKYY
2	MR 219	2001	10.18730/KAM94
3	MR 284	2015	10.18730/KAMMF
4	MARDI Siraj 297	2018	10.18730/KAMNG
5	Sempadan 303	2018	10.18730/SEXCF
6	Sempadan 307	2018	10.18730/SEXDG

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

Plant Materials and Experimental Design

A total of sixty healthy seeds (ten seeds x six genotypes) were obtained from the Malaysian Agricultural and Research Development Institute (MARDI) Rice Genebank (Table 1). The seeds were sown on 20th August 2019 and transplanted into pots at the greenhouse on 06th September 2019 with one seedling per pot. The experiment was laid out in a Randomized Complete Block Design (RCBD) with 3 replications. Seedlings were grown in a 5-meter x 3-meter plot with a 20 cm x 15 cm distance. Urea fertilizers and NPK fertilizers were applied at a ratio of 200N, 100P, and 50K kg/ha following the standard rice cultivation management [19]. Watering was done once every two days while pesticide was applied once a month.

Agronomic Data Collection

The data were collected at different stages of rice development for twelve characters which were: 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), the weight of 1000 grains (1000GW, g), length of seed (LS, cm), 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, %). Standard Evaluation System (SES) for Rice [19] was used as the main reference to ensure every character was measured according to high international standards. Statistical analysis was implemented to evaluate the rice yield and its attributing character from the data recorded.

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. The genetic parameters including genotypic variance (σ^2g), phenotypic variance (σ^2p), heritability of broad sense (h^2b), 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:

Evaluation of Genotypic and Phenotypic Variances (σ^2g, σ^2p)

As provided by [7], both variances are estimated as follows:

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

Phenotypic variance, $\sigma^2p = \sigma^2g + EMS$

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

Evaluation of Heritability in Broad Sense (h^2b)

As formulated by [7], the h^2b can be estimated by:

$$Heritability, h^2 b = \frac{\sigma^2 g}{\sigma^2 p}\ x\ 100\%$$

h^2b was distinguished into different levels based on the percentages produced which were low (<30%), medium (30 – 60%) and high (>60%).

Evaluation of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV)

Both values were evaluated using the formula provided by [20] & [21].

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}}\ x\ 100$$

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}}\ x\ 100$$

Where, $\bar{X}$ = population mean

According to [22] , GCV and PCV can be categorized as low (<10%), moderate (10-20%), and high (>20%).

Evaluation of Genetic Advance (GA) and Genetic Advance as Percentage of Mean (GA%)

As stated by [7], the GA was calculated as follows:

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

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

As provided by [23], the GA% was calculated as follows:

$$GA\% = \frac{GA}{\bar{X}} x\, 100$$

According to [7] & [24], GA% can be classified as low (0-10%), moderate (10-20%), and high (>20%).

Cluster Analysis and Principal Cluster Analysis (PCA)

Cluster analysis and PCA were performed using NTSYS-PC software (version 2.1) based on the Euclidian distance method, which consisted of Dice's and Jaccard's similarity coefficient [25]. Unweighted pair group method with arithmetic means (UPGMA) algorithm and SAHN clustering was constructed to analyze genetic relationships among the rice lines. EIGEN and PROJ modules of NTSYS-pc and SAS version 9.2 were used to calculate the PCA of the six rice varieties.

RESULTS AND DISCUSSION

Evaluation of Genetic Parameters

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

Table 2. Evaluation of genetic parameters for yield attributing characters

Agronomic characters	σ^2g	σ^2p	h^2b	GCV	PCV	GA (%)
DF	69.751	74.168	94.04%	9.82%	10.12%	19.59%
DM	75.029	77.296	97.07%	7.66%	7.77%	15.54%
PH	64.003	70.687	90.54%	6.73%	7.08%	19.32%
NT	27.371	33.671	81.29%	26.20%	29.06%	48.62%
NP	27.211	56.978	47.76%	21.29%	30.81%	30.33%
LP	6.069	6.089	99.67%	9.57%	9.58%	19.61%
1000GW	1.906	1.947	97.89%	4.94%	5.00%	10.10%
LS	0.003	0.003	100%	6.09%	6.09%	12.54%
FGPP	675.460	769.339	87.80%	20.69%	22.08%	39.94%
UFGPP	137.301	148.796	92.27%	29.21%	30.40%	57.80%
TGPP	822.372	951.131	86.46%	17.30%	18.61%	33.14%
YPP	38.886	40.642	95.68%	8.25%	8.43%	16.64%

Note: σ^2g, genotypic variance; σ^2p, phenotypic variance; h^2b, heritability in broad sense; GCV, genotypic coefficient of variance; PCV, phenotypic coefficient of variance; 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; 1000GW, weight of 1000 grains; LS, length of seed; FGPP, number of filled grain per panicle; UFGPP, number of unfilled grain per panicle; TGPP, number of total grain per panicle; YPP, yield rate per plant

All characters showed a higher amount of PCV than their corresponding GCV. These findings denote that there was an influence of environment towards the analyzed characters. They are supported through similar findings on local rice analysis by [6] & [26]. The highest GCV value was represented by the number of unfilled grains per panicle (29.21%), followed by the number of tiller (26.20%), the number of panicle (21.29%) and the number of filled grain per panicle (20.69%). Previous studies by [6], [27] & [28] also recorded the number of unfilled grain per panicle as the character with the highest GCV. As for PCV, the number of panicle (30.81%) constituted the highest value, followed by the number of unfilled grains per panicle (30.40%), number of tiller (29.06%) and filled grain per panicle (22.08%). Similarly, [29] also reported the high value of number of unfilled grain per panicle in both GCV and PCV. Meanwhile, weight of 1000 grains are recorded as the lowest-valued characters for both GCV and PCV, at 4.94% and 5.00% respectively.

High heritability was found for all the characters studied except for the number of panicle (47.76%). Length of seed represented the highest heritability value with a maximum of 100%, followed by the length of panicle (99.67%), the weight of 1000 grains (97.89%) and days to maturity

(97.07%). The findings were in accordance with the study reported by [6] & [30], using the same characters with the weight of 1000 grains recorded the highest heritability.

Genetic advances are important selection parameters, while selection is made based on yield contributing traits. Heritability estimates along with genetic advances are normally more helpful in predicting the gain under selection than heritability estimates alone [25]. Based on the results, the number of unfilled grain per panicle has the highest GA (%) value with 57.80%, followed by the number of tiller (48.62%), the number of filled grain per panicle (39.94%) and the number of total grain per panicle (33.14%). These data indicated that the number of grains (unfilled, filled or total) plays a huge role in determining the expected actual gain or yield rate in the Malaysian local rice variety. [31] also found a high GA (%) for the number of tiller, together with [28]. A relationship between GA (%) and heritability is salient to determine the effect of additive genes on each character [32]. The high value of both parameters (Table 2) can be observed in the number of total grains per panicle, number of filled grain per panicle, number of unfilled grains per panicle, and number of tillers. As stated by [6], the characters with high values for both parameters can be selected directly and have a high possibility of attributing better development due to the accumulation of more additive genes. In addition, [33] also remarked the high value of both parameters in the number of tiller and number of filled grain per panicle.

Evaluation of Correlation Coefficient among Yield Attributing Characters

According to [34], correlation coefficient analysis is defined as relationships among independent characters and the degree of a linear relation between them. This analysis provides prominent data on the direction and magnitude of the selection process, although it is not enough to ensure selection success. The phenotypic correlation coefficient among the observed characters of six rice varieties is tabulated in Table 3. Significant positive correlations can be identified between the main characters, yield rate per plant with the number of filled grain per panicle (0.591 at p<0.01), the weight of 1000 grains (0.573 at p<0.01), and length of panicle (0.462 at p<0.05). [3] also discovered the significant positive correlation between the grain yield per plant with the same characters. In another study, [6] and [34] recorded a significant positive correlation of yield rate per plant with the number of filled grain per panicle and the length of panicle. Based on Table 3, the highest significant positive correlation can be recognized between days to flowering and days to maturity (0.939 at p<0.01); followed by number of filled grain per panicle with total number of

Table 3. The phenotypic correlation coefficient among different agronomic characters

Characters	DF	DM	PH	NT	NP	LP	1000GW	LS	FGPP	UFGPP	TGPP	GYP
DF	1	0.939 **	0.428 *	-0.737 **	-0.703 **	-0.552 **	-0.61 **	-0.473 **	-0.69 **	-0.107 NS	-0.662 **	-0.448 *
DM		1	0.339 NS	-0.742 **	-0.634 **	-0.589 **	-0.63 **	-0.521 **	-0.699 **	-0.097 NS	-0.667 **	-0.465 **
PH			1	-0.345 NS	-0.305 NS	0.214 NS	0.075 NS	0.128 NS	-0.531 **	-0.138 NS	-0.531 **	-0.224 NS
NT				1	0.679 **	0.187 NS	0.213 NS	0.121 NS	0.683 **	0.372 *	0.76 **	0.172 NS
NP					1	0.107 NS	0.147 NS	0.162 NS	0.502 **	0.359 NS	0.592 **	0.097 NS
LP						1	0.875 **	0.843 **	0.072 NS	-0.372 *	-0.081 NS	0.462 *
1000GW							1	0.685 **	0.242 NS	-0.396 *	0.062 NS	0.573 **
LS								1	-0.124 NS	-0.023 NS	-0.12 NS	0.07 NS
FGPP									1	0.053 NS	0.919 **	0.591 **
UFGPP										1	0.442 *	-0.759 **
TGPP											1	0.232 NS
GYP												1

Note : DF, days to flowering; DM, days to maturity; PH, plant height; NT, number of tiller; NP, number of panicle; LP, length of panicle; 1000GW, weight of 1000 grains; LS, length of seed; FGPP, number of filled grain per panicle; UFGPP, number of unfilled grain per panicle; TGPP, number of total grain per panicle; YPP, yield rate per plant

* and ** indicate significant level at 5% and 1% , respectively

grain per panicle (0.919 at $p<0.01$); and length of panicle with weight of 1000 grains (0.895 at $p<0.01$). It indicates that increasing days to flowering will increase days to maturity, while the total number of grains per panicle increases as number of filled grain per panicle increases. The previous studies conducted by [6] and [35] also recorded the same results in their findings. In contrast, [27] and [33] found a significant positive correlation between the number of tiller and yield rate per plant. This may be due to nutrient deficiencies or environmental influences during the active tillering phase in the vegetative stage, causing the tillers to have a great spectrum of varying lengths. Yield rate per plant also had a significant negative correlation with days to flowering (-0.448 at $p<0.05$), days to maturity (-0.465 at $p>0.01$) and number of unfilled grains per plant (-0.759 at $p<0.01$). The result was aligned with the study made by [30] and [36], who discovered the significant negative association between grain yield per plant with days to flowering and days to maturity. Negative associations indicated the declining value of yield rate per plant with the increasing values of related characters (inversely proportional).

Evaluation of Path Coefficient among Yield Attributing Characters

Table 4 indicates the direct effects of all ten characters on the yield rate of the plant. The other remaining characters are denoted as the indirect effects of one character via another character towards the yield rate of the plant.

Table 4. Direct and indirect effects of agronomic characters on the yield rate

Characters	DF	DM	PH	NT	NP	LP	1000GW	LS	UFGPP	TGPP	YPP
DF	**0.042**	-0.130	-0.017	0.049	-0.044	-0.074	-0.007	0.024	0.105	-0.396	-0.448*
DM	0.039	**-0.138**	-0.014	0.049	-0.040	-0.079	-0.007	0.026	0.095	-0.399	-0.465**
PH	0.018	-0.047	**-0.040**	0.023	-0.019	0.029	0.000	-0.006	0.136	-0.318	-0.224^{NS}
NT	-0.031	0.102	0.014	**-0.066**	0.043	0.025	0.002	-0.006	-0.365	0.454	0.172^{NS}
NP	-0.030	0.087	0.012	-0.045	**0.063**	0.014	0.002	-0.008	-0.353	0.354	0.097^{NS}
LP	-0.023	0.081	-0.009	-0.012	0.007	**0.134**	0.010	-0.042	0.365	-0.048	0.462*
1000GW	-0.026	0.087	-0.003	-0.014	0.009	0.117	**0.011**	-0.034	0.389	0.037	0.573**
LS	-0.020	0.072	-0.005	-0.008	0.010	0.113	0.008	**-0.050**	0.023	-0.072	0.07^{NS}
UFGPP	-0.004	0.013	0.006	-0.025	0.023	-0.050	-0.004	0.001	**-0.982**	0.264	-0.759**
TGPP	-0.028	0.092	0.021	-0.050	0.037	-0.011	0.001	0.006	-0.434	**0.598**	0.232^{NS}

Note : DF, days to flowering; DM, days to maturity; PH, plant height; NT, number of tiller; NP, number of panicle; LP, length of panicle; 1000GW, weight of 1000 grains; LS, length of seed; FGPP, number of filled grain per panicle; UFGPP, number of unfilled grain per panicle; TGPP, number of total grain per panicle; YPP, yield rate per plant

* and ** indicate significant level at 5% and 1% , respectively

At the phenotypic level, the highest direct positive effect on yield rate per plant was shown by the number of total grains per panicle, followed by the number of panicles, days to flowering, length of panicle, and weight of 1000 grains. Direct positive effects indicated that the characters are reliable and can be selected directly to improve the yield rate. A similar finding was recorded by [6,37,38] for panicle length. [39, 40] reported a greater yield rate by increasing the number of panicle and tillers. A direct positive effect was also found for the number of total grain per panicle, days to flowering and weight of 1000 grains [40, 41], which could be selected to improve yield in the *Indica* species. In contrast, [30] and [37] reported a direct negative effect for total grain per panicle and days to flowering. This was due to the planting of younger seedlings, timid spacing, and conventional methods of weeding and irrigation [42,43]. The present study recorded a direct negative effect for days to maturity, number of unfilled grains per panicle, number of tillers, length of seed, and plant height. The result was aligned with [31], [37], and [44] for plant height. In other findings, [28, 35] stated similar results for the number of unfilled grain per panicle and the number of tiller, respectively. Length of panicle and weight of 1000 grains showed a positive value for both correlation coefficients and direct effects on the yield rate per plant as found in [44]. It indicated that both characters could be considered for selection in the rice improvement project by fully revoking the unwanted indirect effects and optimizing the direct effects [45].

Cluster Analysis

The dendrogram formed through cluster analysis divided all six rice varieties into four main clusters at 18.5 dissimilarity coefficients (Figure 1). All clusters in this study consist of one variety each, except Cluster IV that contains three rice varieties. MR84, MR219, and MR284 rice varieties were grouped in Cluster I, II and III, respectively. Meanwhile, MR297, MR303 and MR307 were clustered together in Cluster IV due to the similarities in yield and agro-morphological traits. A higher Euclidian distance between rice variety concluded greater differences in performance of traits. In this case, MR84 had higher differences than MR303 or MR307 and the shortest distances of variability between them. According to [18], all three varieties in Cluster IV were the latest varieties developed by MARDI in 2018, which were slightly similar in yield and trait performances.

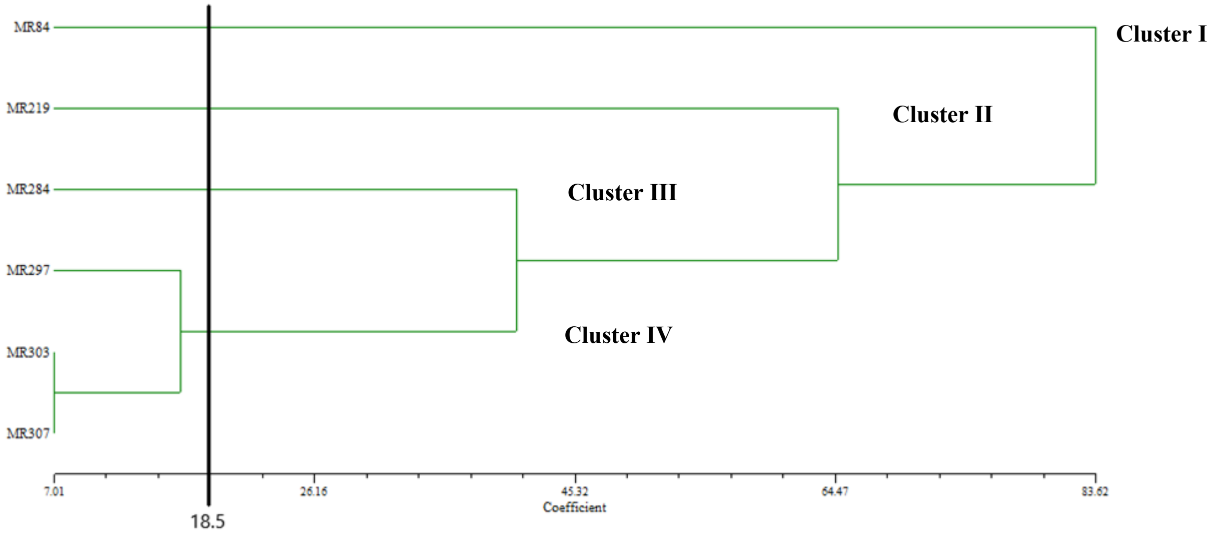

Figure 1. Dendrogram of six local rice varieties based on twelve agro-morphological traits

The variety in Cluster IV showed high performances in seven out of twelve traits viz; early days to flowering, early days to maturity, the maximum length of panicle, the maximum weight of 1000 grains, the maximum length of seed, the minimum number of unfilled grain per panicle, and the maximum yield rate per plant. In the future breeding program, the rice variety in Cluster IV could be highly considered as they had a greater number of highly performed traits compared to other clusters. Cluster II was ranked second after Cluster IV in terms of trait performance due to five highly performed traits, early days to flowering, minimum plant height, the maximum number of filled grain per panicle, the maximum number of total grain per panicle, and the maximum yield rate per plant. This was followed by Cluster III with two highly performed traits (maximum number of panicle & length of seed) and Cluster I with only one highly performed trait (minimum number of tiller). Similarly, [46] and [47] clustered 31 and 15 rice varieties into four main clusters at high dissimilarity coefficients. Based on different quantitative traits, they found no correlations of the clusters' characteristics with geographical factors. This indicated high variability among the rice variety based on specifically performed traits and not the origin. As suggested by [48], greater heterotic responses could be fulfilled by hybridizing genotypes from other distant clusters. A crossbreeding program could consider the combination between Cluster II and IV varieties as they had a large gap in distances and better performances in traits and yield rate, among others.

Principal Component Analysis (PCA)

Principal component analysis showed the six-rice varieties scattered in four different groups, which confirmed the cluster analysis result. [48] and [49] also found similar patterns in their PCA analysis of different rice varieties. The result in this study was made following the theory suggested by [50], which used an eigenvalue above 1.0 and owned proportions of more than 80% in the total variance. According to PCA, three out of twelve principal components had eigenvalues above 1.0 and contributed 86.24% of the total variance. PC1 contributed 45.61% of the total variance, followed by PC2 (26.11%) and PC3 (14.52%). [51] computed 64.56% of total variation among thirty nine rice varieties, with proportions of 27.60%, 24.93% and 12.02% in PC1, PC2, and PC3, respectively. [47] also revealed three principal components among fifteen rice varieties with total variability proportions of 82.9% (PC1 = 31.13%, PC2 = 14.95%, and PC3 = 6.49%). This suggested a strong correlation between morphological traits in determining high variability among rice varieties.

CONCLUSION

High heritability index (h_2b) and genetic advance (GA) were found for number of tillers, number of panicles, number of filled grain per panicle, number of unfilled grains per panicle and number of total grains per panicle. Pearson's correlation and path coefficient showed that the length of panicle and weight of 1000 grains have a strong correlation and direct positive effect with yield rate per plant. Thus, these two characters were suggested to be selected in future breeding programs for yield improvement, especially for the Malaysian rice genotypes. Rice varieties in Cluster II (MR219) and IV (MR297, MR303 and MR307) could be considered for further hybridization to attain a wide spectrum of variation and greatest performances in agro-morphological traits.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest regarding the publication of this manuscript.

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