

Studies on heritability and genetic variability for grain physical properties in Malaysian rice germplasm

S A Saidon¹, R Kamaruzaman^{1*}, M S F A Razak², A Ramli³, H M Sarif¹, Z M Zuki¹, S N A Rahman⁴, T Devarajan⁵ and E Sunian¹

¹ Rice Research Centre, Malaysian Agricultural Research and Development Institute (MARDI), Seberang Perai, Penang, Malaysia

² Gene Bank and Seed Centre, MARDI, Headquarters, Serdang, Selangor, Malaysia

³ Rice Research Centre, MARDI, Headquarters, Serdang, Selangor, Malaysia

⁴ Gene Bank and Seed Centre, MARDI, Seberang Perai, Penang, Malaysia

⁵ Crop and Soil Science Centre, MARDI, Bachok, Kelantan, Malaysia

*E-mail: rahiniza@mardi.gov.my

Abstract. Genetic based information of different traits plays important role in varietal improvement of rice. Twenty rice accessions (*Oryza sativa* L.) obtained from National Rice Gene Bank were evaluated during main season 2015/2016 to estimate heritability, genetic variability and genetic advance for seven grain physical properties. Among the traits, milled grain length/width ratio, milled grain length, milled grain length after cooking and grain length exhibited high estimates of phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV). Highest broad sense heritability and genetic advance was obtained for grain length (98.66% and 62.25%), milled grain length (98.95% and 67.31%), milled grain length/width ratio (98.50% and 80.41%) and milled grain length after cooking (98.93% and 65.44%) which suggest these traits are most probably controlled by additive gene action and hence they can be fixed by selection. However, kernel elongation ratio showed lowest value of broad sense heritability and genetic advance (11.76% and 1.38%, respectively) and may suggest non-additive gene action in their inheritance and selection of this trait may difficult due to high environmental influences. Therefore, improvement of high quality rice with kernel elongation ability may require molecular marker application as it is highly affected by environment for precise selection.

Keywords: germplasm, heritability, genetic advance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV).

1. Introduction

Grain quality assessment is one of major component in rice breeding program as it determines consumer acceptance for the particular rice variety. Plant breeders typically concentrated on development of high rice variety. However, good grain quality provides better prospects of high economic value for local consumption or for export. Grain physical properties such as uniform shape and general appearance are major factors defining market value [1,2]. Therefore, parental selection from germplasm collection should incorporate wide range of genetic variability for desirable traits. Other than that, it is important to understand the extent of variation that is due to heritable component



and can be used as guidance in planning effective breeding program, as certain quality related traits is influenced by environment.

Genetic parameters, such as genotypic coefficient of variation and phenotypic coefficient of variation are very useful in determining the magnitude of variability that exists in the germplasm. Furthermore, combination of broad-sense heritability and genetic advance estimation allow rice breeder to determine the influence of environment on the expression of genetic factors and repeatability of trait throughout selection process [3]. Kernel elongation trait of indica rice was found to be controlled by genotype, major gene effects and environment interaction using genetic models in two environments [4]. This study was conducted to determine the genetic variability, heritability and genetic advance of grain physical properties in Malaysian germplasm as an early investigation for high quality rice varietal development.

2. Materials and methods

Twenty accessions of rice were evaluated in a field trial in research plot of MARDI Seberang Perai during main season 2015/2016. The seeds were obtained from National Rice Gene Bank, MARDI Seberang Perai (Table 1) and were transplanted in 3 m × 1 m plots with 25 cm spacing in a randomized complete block design (RCBD) with three replications for each accession. Three plants from each accession were selected randomly from each replication for data collection of the following characters which are grain length (mm), grain width (mm), milled grain length (mm), milled grain width (mm), milled grain length/width ratio, milled grain length after cooking (mm) and kernel elongation ratio.

Table 1. List of rice germplasm used in this study.

Acc. number	Rice accession	Sub-species	Origin
MRGB06725	Fawng Nan	<i>Indica</i>	IRRI
MRGB00698	Khao Pra Guad 55-2-133	<i>Indica</i>	Thailand
MRGB00653	Kapuri	<i>Indica</i>	Suriname
MRGB01727	SML 242	<i>Indica</i>	Suriname
MRGB10778	Ceysvoni	<i>Indica</i>	Suriname
MRGB01846	Washabo	<i>Indica</i>	Suriname
MRGB01726	SML 81B-25	<i>Indica</i>	Suriname
MRGB01873	ARC7110	<i>Indica</i>	India
MRGB09874	Padi Mosilou	<i>Indica</i>	East Malaysia (Sabah)
MRGB03532	Rambai Kersik	<i>Indica</i>	East Malaysia (Sarawak)
MRGB03337	Karok	<i>Indica</i>	East Malaysia (Sarawak)
MRGB05031	Padi Lalang	<i>Indica</i>	Peninsular Malaysia
MRGB05022	Lembut Terong	<i>Indica</i>	Peninsular Malaysia
MRGB01154	Burong 1	<i>Indica</i>	Peninsular Malaysia
MRGB00694	Ketitir	<i>Indica</i>	Peninsular Malaysia
MRGB00174	Banyak Anak 192	<i>Indica</i>	Peninsular Malaysia
MRGB00490	H 8	<i>Indica</i>	Sri Lanka
MRGB00280	Ceylon 8	<i>Indica</i>	Sri Lanka
MRGB00533	Hsin Chu 56	<i>Japonica</i>	Taiwan
MRGB00348	Cho Ko To	<i>Japonica</i>	China

The milled grain length/width ratio was calculated by dividing average length by the average of width of rice kernel. Based on the value, rice grains were classified into short bold (SB), long bold (LB), short slender (SS), medium slender (MS) and long slender (LS) [5]. Furthermore, kernel elongation ratio was calculated by dividing the average length of cooked kernel by the average length of the raw rice [6].

The data was analyzed by analysis of variance (ANOVA) using SAS software version 9.1 (SAS Institute 1998). Moreover, genetic parameters, such as genotypic (σ^2g) and phenotypic (σ^2p) variances, genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad-sense heritability (h^2) and genetic advance (GA), were calculated using mean square values from individual and combined ANOVA tables [7] as the following formula:

$$\sigma^2p = \sigma^2g + \sigma^2e \quad \sigma^2g = \frac{(M2-M1)}{r}$$

where: r = number of replications, σ^2e = error mean squares, $M1$, $M2$ = error and genotype mean squares.

$$GCV = \frac{\sqrt{\sigma^2g} \times 100}{\text{Grand mean}}$$

$$PCV = \frac{\sqrt{\sigma^2p} \times 100}{\text{Grand mean}}$$

$$h^2 = \frac{\sigma^2g}{\sigma^2p}$$

$$GA = K \frac{\sigma^2g}{\sqrt{\sigma^2p}}$$

where: σ^2g = estimated genetic variance, σ^2e = pooled error variance, r = number of replications, K = selection differential and it was 2.06 at selection intensity of 5%.

3. Results and discussion

3.1. Analysis of variance

ANOVA revealed highly significant differences among the accessions for the traits indicating the presence of significant amount of variability among the traits studied except for the kernel elongation ratio (Table 2). Similar results were also reported by Allam et al. [8], Nirmaladevi et al. [9], Gampala et al. [10] and Kumar et al. [11] in their experiments. Mean performance for all traits is presented in Table 3.

Table 2. Analysis of variance (ANOVA) for grain quality traits.

Source of variation	Accession	Replication	Error
df	19 ^{ns}	2 ^{ns}	38 ^{ns}
Grain length	24.46**	0.47*	0.11 ^{ns}
Grain width	0.36**	0.01 ^{ns}	0.01 ^{ns}
Milled grain length	14.16**	0.06 ^{ns}	0.05 ^{ns}
Milled grain width	0.22**	0.002 ^{ns}	0.01 ^{ns}
Ratio MGL/MGW	3.95**	0.02 ^{ns}	0.03 ^{ns}
Grain length after cooking	13.92**	0.13 ^{ns}	0.06 ^{ns}
Kernel elongation ratio	0.004 ^{ns}	0.003 ^{ns}	0.003 ^{ns}

MGL = milled grain length, MGW = milled grain width, ns = no significant differences.

*Significant difference at 5% level, **Significant difference at 1% level in F-test.

Table 3. Mean performance for physical grain properties of tested accessions.

Accession	Grain length (mm)	Grain width (mm)	Milled grain length (mm)	Milled grain width (mm)	Ratio MGL/MGW	Grain length after cooking (mm)	Kernel elongation ratio
Fawng Nan	11.69±0.22	2.26±0.05	8.42±0.11	2.06±0.04	4.09±0.09	8.64±0.19	1.03±0.03
Khao Pra Quad	11.18±0.31	2.46±0.06	8.01±0.07	2.23±0.06	3.59±0.11	7.93±0.15	0.99±0.02
Kapuri	12.37±0.11	2.50±0.02	8.93±0.12	2.24±0.03	3.99±0.07	8.89±0.25	1.00±0.04
SML 242	11.81±0.37	2.37±0.09	8.84±0.10	2.13±0.04	4.16±0.12	8.83±0.12	1.00±0.01
Cho Ko To	13.28±0.39	2.63±0.09	8.90±0.24	2.34±0.06	3.81±0.08	9.23±0.13	1.04±0.04
Lalang	12.05±0.16	2.43±0.06	8.49±0.13	2.22±0.05	3.83±0.13	8.19±0.25	0.97±0.04
Ceysvoni	12.74±0.22	2.39±0.01	9.12±0.21	2.06±0.03	4.43±0.15	9.67±0.13	1.06±0.01
Padi Mosilou	12.03±0.27	2.45±0.08	8.18±0.14	2.29±0.15	3.59±0.19	8.11±0.10	0.99±0.03
Washabo	11.97±0.23	2.46±0.06	8.91±0.29	2.26±0.03	3.94±0.12	9.21±0.15	1.04±0.03
SML 81B-25	11.88±0.27	2.28±0.06	9.09±0.06	2.03±0.03	4.47±0.06	9.11±0.05	1.00±0.01
Ceylon 8	6.61±0.19	2.66±0.02	4.70±0.10	2.46±0.01	1.91±0.04	4.85±0.21	1.03±0.02
ARC7110	7.07±0.06	2.14±0.05	4.81±0.08	1.90±0.03	2.53±0.08	4.89±0.12	1.02±0.03
Rambai Kersik	6.30±0.04	2.92±0.03	4.30±0.04	2.59±0.04	1.66±0.04	4.41±0.04	1.0±0.01
Karok	6.73±0.08	3.63±0.03	4.79±0.12	3.08±0.04	1.55±0.03	4.83±0.18	1.01±0.02
Lembut Terong	6.13±0.05	2.74±0.09	4.20±0.05	2.42±0.01	1.73±0.03	4.35±0.03	1.04±0.02
Burung (1)	5.91±0.08	2.78±0.14	4.17±0.04	2.42±0.05	1.73±0.06	4.12±0.09	0.99±0.02
Ketitir	6.76±0.05	2.61±0.03	4.55±0.06	2.44±0.01	1.86±0.03	4.85±0.11	1.07±0.01
Banyak Anak 192	7.18±0.16	2.59±0.05	5.06±0.08	2.39±0.05	2.12±0.07	5.07±0.12	1.00±0.03
H8	6.47±0.23	2.82±0.11	3.93±0.12	2.55±0.11	1.54±0.03	4.34±0.14	1.11±0.07
Hsin Chu 56	7.00±0.13	3.21±0.03	4.64±0.08	2.78±0.12	1.67±0.06	5.08±0.04	1.09±0.03
Mean	9.36	2.62	6.60	2.34	2.91	6.73	1.02
LSD ($\alpha = 0.05$)	0.56	0.19	0.37	0.18	0.26	0.40	0.09

MGL = milled grain length, MGW = milled grain width.

3.2. Phenotypic and genotypic coefficient of variation

The estimates of PCV, GCV, h^2 and expected GA values as percent of mean are presented in Table 4. Based on the result, PCV values were higher than their corresponding GCV for all traits demonstrates that the variations expressed were not solely due to genotype, but also influenced by environment. However, the value difference between PCV and GCV for most of the traits studied is low which might be less influenced by the environment [11]. This findings is in line with other study that showed small gap of PCV and GCV value of grain properties on selected rice varieties/accessions [12–15].

3.3. Heritability and genetic advance

Heritability is important to determine trait response to phenotypic selection. Improvement of quantitative trait in plants requires reliable estimation of heritability for effective breeding program [16]. Moreover, h^2 is the relative magnitude of phenotypic and genotypic variance of the traits that gives an idea of the total variation accounted to genotypic effect [17]. High h^2 were observed in most of traits studied viz. grain length (98.66), grain width (91.67), milled grain length (98.95), milled grain width (87.50), milled grain length/width ratio (98.50) and milled grain length after cooking (98.93).

This finding is in line with other studies [8–11]. However, heritability value of kernel elongation ratio in this study is low (11.76) which might be contributed by the selection of materials with no notable accessions with kernel elongation trait. Most of other studies reported high heritability value

of this trait viz. 98% [8], 86% [3] and 91.88% [10]. Nevertheless, Devi et al. [15] reported moderate heritability value for kernel elongation ratio (59%) with low genetic advance (7.5%). Although the high heritability value shows the effectiveness of selection based on phenotypic performance, it does not demonstrate any indication to the amount of genetic progress for selecting the superior individuals which is possible by using genetic advance estimation [3].

Table 4. Variance components and heritability values for grain quality traits.

Parameters	σ^2_e	σ^2_g	σ^2_p	h^2	PCV	GCV	GA	GA%
Grain length	0.11	8.11	8.22	98.66	30.63	30.43	5.83	62.25
Grain width	0.01	0.11	0.12	91.67	13.22	12.66	0.65	24.97
Milled grain length	0.05	4.70	4.75	98.95	33.02	32.85	4.44	67.31
Milled grain width	0.01	0.07	0.08	87.50	12.04	11.26	0.51	21.69
Ratio MGL/MGW	0.02	1.31	1.33	98.50	39.63	39.33	2.34	80.41
Grain length after cooking	0.05	4.62	4.67	98.93	32.11	31.94	4.40	65.44
Kernel elongation	0.003	0.0004	0.0034	11.76	5.72	1.96	0.01	1.38

MGL = milled grain length, MGW = milled grain width, σ^2_e = error variance, σ^2_g = genotypic variance, σ^2_p = phenotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, h^2 (%) = broad sense heritability, GA = genetic advance, GA% = genetic advance as percent of mean.

High heritability with high genetic advance is demonstrated by grain length (62.25), milled grain length (67.31), milled grain length/width ratio (80.41) and milled grain length after cooking (65.44) that might indicate additive gene action. Furthermore, high heritability with low genetic advance is demonstrated by grain width (24.97), milled grain width (21.69). Kernel elongation ratio had low heritability with low genetic advance (1.38) that might suggest the traits is highly influenced by the environment and phenotypic selection may not be effective in that particular condition. The estimation of genetic advance is more useful as a selection tool when considered jointly with heritability estimates [19].

4. Conclusions

There is high variability of grain physical properties existed among the accessions studied. The genotypic and phenotypic variances may provide information for high grain quality breeding program. The highest heritability with the highest genetic advance value is demonstrated by milled grain length/width ratio trait that might give useful information as rice grain with long and slender properties as the main feature for development of high quality rice for local market. Moreover, more materials from germplasm need to be explored in order to exploit its desirable trait in breeding program and can be combined with application of marker-assisted selection (MAS) for low heritability traits.

5. References

- [1] Fitzgerald M, McCouch S and Hall R 2009 Not just a grain of rice: the quest for quality *Trends Plant Sci.* **14** 133–9
- [2] Sellappan K, Datta K, Parkhi V and Datta S K 2009 Rice caryopsis structure in relation to distribution of micronutrients (iron, zinc, β -carotene) of rice cultivars including transgenic indica rice *Plant Sci.* **177** 557–62
- [3] Nirmaladevi G, Padmavathi G, Kota S and Babu V R 2015 Genetic variability, heritability and correlation coefficients of grain quality characters in rice (*Oryza sativa* L.) *SABRAO J. Breed. Genet.* **47** 424–33
- [4] Bao J S, Xie J K and Xia Y 2001 Genetic analysis of cooked rice elongation in *indica* rice (*Oryza sativa* L.) *Acta Agron. Sin.* **27** 489–92

- [5] Ramaiah K 1985 *Grain Classification*
- [6] Murthy P S 1965 *Genetic Studies in Rice (Oryza sativa L.) with Special Reference to Contain Quality Features* (Orissa University of Agriculture and Technology)
- [7] Fathelrahman S A, Alsadig A I and Dagash Y I 2015 Genetic variability in rice genotypes (*Oryza sativa* L.) in yield and yield component under semi-arid zone (Sudan) *J. For. Prod. Ind.* **4** 21–32
- [8] Allam C R, Jaiswal H K, Qamar A, Venkateshwarlu C and Reddy Y 2015 Variability, heritability and genetic advance studies in some indigenous accessions of Basmati rice (*Oryza sativa* L.) *Electron. J. Plant Breed.* **6** 506–11
- [9] Gampala S, Singh V J and Chakraborti S K 2015 Analysis of variability and genetic parameter for grain quality attributes in high yielding rice (*Oryza sativa* L.) genotypes *The Ecoscan* **9** 411–4
- [10] Kumar V, Singh D and Singh R 2018 Assessment of genetic variability, heritability and genetic advance for yield and quality traits in Basmati (*Oryza sativa* L.) accessions of Himachal Pradesh *J. Pharmacogn. Phytochem.* **7** 1323–6
- [11] Kishore N S, Srinivas T, Nagabhushanam U, Pallavi M and Sameera S 2015 Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes *SAARC J. Agric.* **13** 99–108
- [12] Dhanwani R K, Sarawgi A K, Solanki A and Tiwari J K 2013 Genetic variability analysis for various yield attributing and genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.) *Suppl. Genet. Plant Breed.* **8** 1403–7
- [13] Vanisree S, Swapna K, Raju C D, Raju C S and Sreedhar M 2013 Genetic variability and selection criteria in rice *J. Biol. Sci. Opin.* **1** 341–6
- [14] Devi K R, Parimala K, Venkanna V, Lingaiah N, Hari Y and Chandra B S 2016 Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.) *Int. J. Pure Appl. Biosci.* **4** 250–5
- [15] Devi K R, Chandra B S, Lingaiah N, Hari Y and Venkanna V 2017 Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.) *Agric. Res. Commun. Cent.* **37** 1–9
- [16] Seyoum M, Alamerew S and Bantte K 2012 Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.) *J. Plant Sci.* **7** 13–22
- [17] Allard R 1960 *Principles of Plant Breeding* (New York: John Wiley and Sons Inc.)
- [18] Ramchander S, Ushakumari R and M P A 2015 Quality characteristics of rice mutants generated through gamma radiation in white ponni *Int. J. Agric. Sci.* **7** 714–8
- [19] Singh P and Narayana S S 1993 *Biometrical techniques in plant breeding* (New Delhi: Kalyani Publishers)