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

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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      | Indica      | IRRI                 |
| MRGB00698   | Khao Pra Guad 55-2-133 | Indica | Thailand             |
| MRGB00653   | Kapuri         | Indica      | Suriname             |
| MRGB01727   | SML 242        | Indica      | Suriname             |
| MRGB10778   | Ceysvoni       | Indica      | Suriname             |
| MRGB01846   | Washabo        | Indica      | Suriname             |
| MRGB01726   | SML 81B-25     | Indica      | Suriname             |
| MRGB01873   | ARC7110        | Indica      | India                |
| MRGB09874   | Padi Mosilou   | Indica      | East Malaysia (Sabah) |
| MRGB03532   | Rambai Kersik  | Indica      | East Malaysia (Sarawak) |
| MRGB03337   | Karok          | Indica      | East Malaysia (Sarawak) |
| MRGB05031   | Padi Lalang    | Indica      | Peninsular Malaysia  |
| MRGB05022   | Lembut Terong  | Indica      | Peninsular Malaysia  |
| MRGB01154   | Burong 1       | Indica      | Peninsular Malaysia  |
| MRGB00694   | Ketitir        | Indica      | Peninsular Malaysia  |
| MRGB00174   | Banyak Anak 192 | Indica   | Peninsular Malaysia  |
| MRGB00490   | H 8            | Indica      | Sri Lanka            |
| MRGB00280   | Ceylon 8       | Indica      | Sri Lanka            |
| MRGB00533   | Hsin Chu 56    | Japonica    | Taiwan               |
| MRGB00348   | Cho Ko To      | Japonica    | 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 ($\sigma^2g$) and phenotypic ($\sigma^2p$) 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:

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

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

where: $r$ = number of replications, $\sigma^2e$= 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: $\sigma^2g$ = estimated genetic variance, $\sigma^2e$ = 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.

| 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.
henotypic and genotypic variance of the traits that
might be less influenced by the environment.

Moreover, 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].

| Parameters                  | σ²e  | σ²g  | σ²p  | h²   | 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, σ²e = error variance, σ²g = genotypic variance, σ²p = phenotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, h² (%) = 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.

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