

Genetic Variability and Gene Action for Several Traits in F₄ and F₅ Population of Rice

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ABSTRACT This study estimated the genetic variability and gene action of several traits in the F₄ and F₅ rice populations to determine a trait for selection program. The trait of date to flowering and date to harvesting had narrow genetic variability, whereas trait productive tillers, number of fertile grain, and total grains had moderate to wide genetic variability. Genetic variability in trait number of fertile grain and total grains showed decreased in F₅ generation compare to the F₄ generation, whereas trait productive tillers, date to flowering, and date to harvesting showed an increase. Additive gene action with duplicate and complementary epistasis was found in all traits, except for trait productive tillers only showed additive gene action with duplicate epistasis. Kurtosis less than 3 was found in all traits which indicate many genes control the traits. The number of fertile grain trait showed wide genetic variability which decreased in F₅ generation compare to the F₄ generation, and there is an additive gene action with duplicate epistasis. It indicates selection will be effective with the trait of number of fertile grain.

Keywords Genetic, Variability, Skewness, Kurtosis, Rice

INTRODUCTION

Rice is the main staple food of Indonesian people. Not only in Indonesia but also in more than half of the world's population is considered rice as the main food in the lived of people (Sala *et al.* 2015). It is necessary to make the production of rice continuously increased, until the people's need is fulfilled, especially in Indonesia. The increasing number of people in Indonesia causes the high conversion of rice fields into non-agricultural bases. Based on data (BPS, 2018) the area of rice fields decreased from 2013-2015 respectively by 8.12 million ha, 8.11 million ha, and 8.0 million ha. Responding to this problem, it is necessary to optimize the use of dry land for rice cultivation. There is a potential for dry land to be utilized for rice cultivation especially for upland rice cultivation (Hajoeningtjas and Purnawanto 2013).

There are two types of rice, it is lowland and upland rice. Lowland rice needs water during its growth, so it is must be always waterlogged especially in several critical phases which need a lot of water. Upland rice is the type of rice that can grow well in a dry land, but it has low production of yields when compared to lowland rice production (Mulyaningsih and Indrayani 2014). Cibogo varieties have an IR64 genetic background which is widely used by farmers because it can provide high yields (Sitaresmi *et al.* 2018), while Situ Bagendit varieties are the type of rice that can grow well in a dry land. Assembling new varieties of rice that have high yields and can grow in dry land can be done through crosses between superior lowland rice varieties and upland rice varieties.

Genetic variability has a very important role in the assembly of varieties (Saragih and Wirnas 2019). Variability in a population under the same cropping environ-

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ment indicates there are differences in the genotypes of individual plants. Gene action is the role of a gene to express a certain trait. Gene action and the number of genes that control traits can be known by calculating the value of skewness and kurtosis (Nachimuthu *et al.* 2014). Information about genetic variability and gene action is necessary to be known in a breeding program. Limited information regarding these parameters would detain the process of the breeding program. This research aimed to estimate genetic variability and gene action on several quantitative traits of rice and determines trait which can be used as selection criteria.

MATERIALS AND METHODS

The research was conducted in August-December 2020 at Greenhouse of the Faculty of Agriculture, Brawijaya Universitas. The research was conducted using F₄ and F₅ generation of rice from the crossing of Situ Bagendit with Cibogo varieties (SB × CB) which obtained from hybridization in the research of Adiredjo *et al.* (2019), the total number of plants for each population is 46 plants. And total plants for the elders are 18 plants for each Situ Bagendit and Cibogo varieties. Other materials used in this research are urea fertilizer, SP36 fertilizer, KCL fertilizer, and humus. The research was conducted without using an experimental design. The research was conducted by planting the plants

in the same environment without any replication, and the observation was made on each individual plant. Observations were made on several quantitative traits of rice, which are the total productive tillers, date to flowering, date to harvesting, a total of number of fertile grain and total grains. Data were analyzed using analysis of variance by calculating the average and variance of phenotypic, environment, and genetic. Furthermore, it is used to calculate the estimate of the genetic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in a broad sense (h²), and gene action. The estimates of GCV and PCV were calculated by using the following formula, according to (Hill, Singh and Chaudhary 1978):

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

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

Explanation:

GCV = genetic coefficient of variance

$\sigma^2 g$ = genetic variance

$\sigma^2 p$ = phenotypic variance

\bar{X} = average

The estimate of heritability was calculated by using the following formula, according to (Janick 2008):

Table 1. Genotype coefficient of variance and heritability of several traits in F₄ and F₅ generation.

Traits ²⁾	Generation	GCV (%) ³⁾	Categories	H ^{2x)}	Categories
PT	F ₄	11.8	Moderate	0.3	Moderate
	F ₅	14.7	Moderate	0.3	Moderate
DF (days)	F ₄	5.4	Narrow	0.8	High
	F ₅	2.8	Narrow	0.5	High
DH (days)	F ₄	2.4	Narrow	0.4	Moderate
	F ₅	1.2	Narrow	0.2	Moderate
NFG	F ₄	26.4	Wide	0.4	Moderate
	F ₅	24.3	Wide	0.2	Moderate
TG	F ₄	20.4	Wide	0.2	Moderate
	F ₅	26.6	Wide	0.4	Moderate

²⁾PT: productive tillers, FA: date to flowering, HA: date to harvesting, TPG: number of fertile grains, TG: total grains.

³⁾GCV: genetic coefficient of variance.

^{x)}H²: heritability in a broad sense.

$$h^2_{(BS)} = \frac{\sigma^2_g}{\sigma^2_p}$$

Explanation:

$h^2_{(BS)}$ = heritability in a broad sense

σ^2_g = genetic variance

σ^2_p = phenotypic variance

Analysis of gene action and total genes are known by calculating the value of skewness and kurtosis using Statistical Product and Service Solutions (SPSS) v16 software.

RESULTS

The results showed that low estimates of genotype coefficient of variance (GCV) were observed for the trait of date to flowering and date to harvesting, moderate estimates were observed for the trait of total productive tillers, whereas high estimates were observed for trait number of fertile grains and total grains (Table 1). The estimate of GCV is divided into 3 categories, *i.e.* narrow if the estimate of GCV is less than 10%, moderate if it is between 10-20%, and wide if it is more than 20%.

The results showed that moderate heritability was observed for all traits, except for trait date to flowering showed high heritability. The estimates of heritability show the proportion of genetic and environmental roles in influencing the appearance of traits. The estimate of heritability is presented in the numbers range of 0-1, greater genetic role indicates by higher heritability. Moderate to high heritability indicates the variability was influenced by genetic factors. The estimate of heritability is divided into 3 categories, *i.e.* low if $h^2 < 0.2$, moderate if h^2 between 0.2-0.5, and high if $h^2 > 0.5$.

The estimate of GCV and heritability showed decreases in all traits in the F₅ generation compared to the F₄ generation, except for traits total productive tillers and total grains showed increased. The decrease of GCV in the F₅ generation indicates selection will be effective.

The study of the distribution of quantitative traits showed non-normal distribution, which is indicated by the slope of the curve skewed to the right and left. All traits

showed platykurtic distribution, it is indicated by the peak of distribution are flatter than the normal distribution (Fig. 1). By knowing the skewness and kurtosis of traits it will provide information about genetic action and the number of genes controlling the traits.

The results showed traits such as total productive tillers, date to flowering in the F₄ generation, date to harvesting in the F₄ generation, number of fertile grains in the F₄ generation, and total grains in the F₅ generation were observed negative skewness. Positive skewness was observed for trait date to flowering in the F₅ generation, date to harvesting in the F₅ generation, number of fertile grains in the F₅ generation, and total grains in the F₄ generation. All traits showed kurtosis < 3. The statistical test of Z skewness and kurtosis showed all traits were observed not significantly different (Table 2).

DISCUSSION

A low estimate of GCV indicates there is no difference in the gene composition of these traits, it concludes the genetic deviations that appear are narrow. A low estimate of GCV indicates the population is considered to be similar, with the result that is not effective for selection (Rini *et al.* 2018). Low estimate of GCV is common in the next generation, it is due to the increasing of selfing (Jambormias 2009). Traits with moderate to high GCV are effective for selection. Traits with moderate GCV can be used as selection traits (Nurhidayah *et al.* 2017). A high estimate of GCV indicates the selection will be effective due to wide genetic deviations (Rini *et al.* 2018).

Moderate heritability indicates the traits can be inherited to their offspring although they can still be influenced by environmental changes (Seyoum *et al.* 2012). Traits with moderate heritability have the opportunity to be used as a selection program (Widyayanti *et al.* 2017). High heritability indicates the variability is influenced by genetic (Napitupulu and Damanhuri 2018), so it can be inherited to their offspring (Syukur *et al.* 2017).

The decrease of genetic variance from the previous generation is due to the presence of selfing (Samak *et al.* 2011). The frequency of heterozygosity in the population

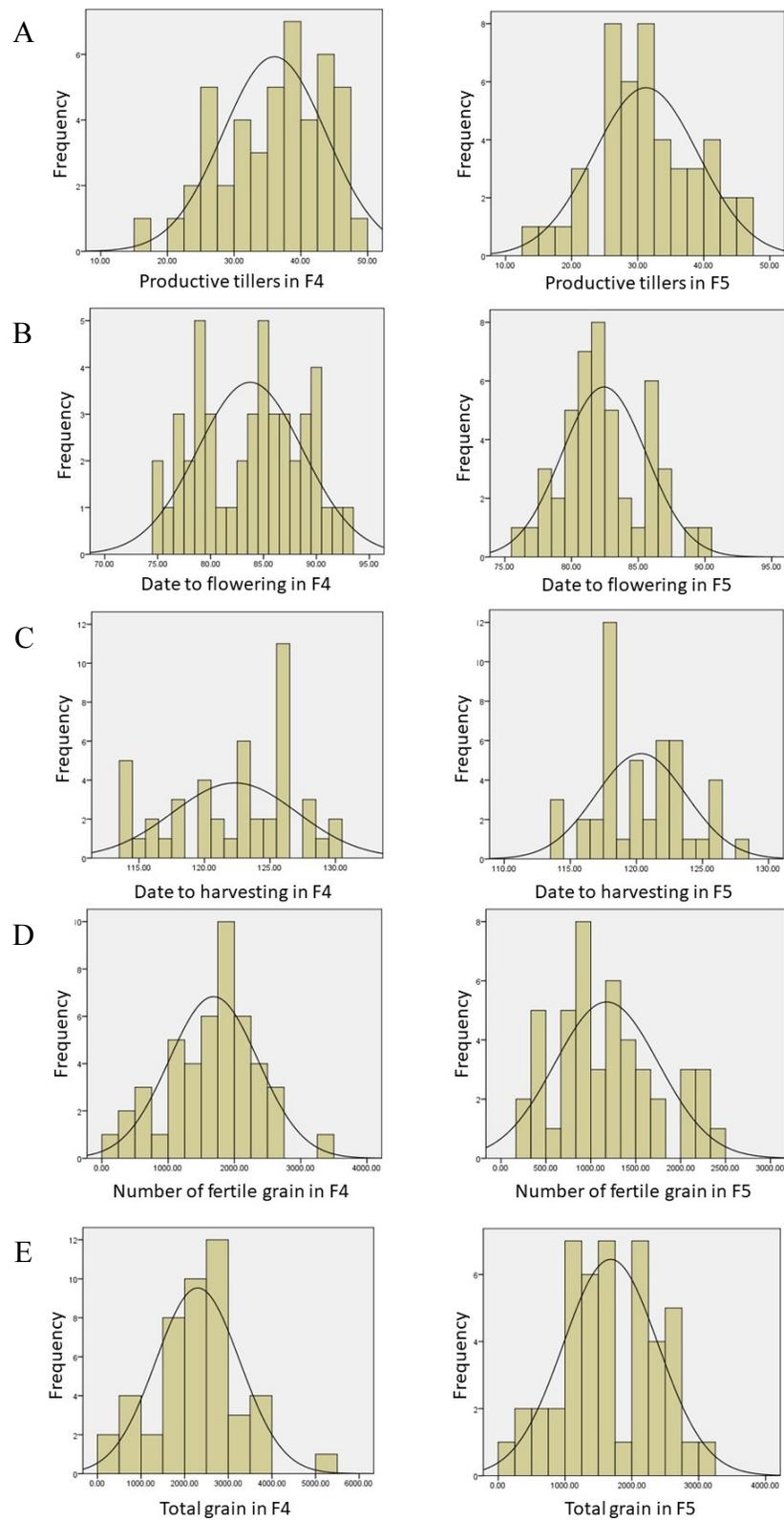


Fig. 1. Distribution of quantitative traits. (A) Total productive tillers. (B) Date to flowering. (C) Date to harvesting. (D) Number of fertile grain. (E) Total grains.

Table 2. The value of skewness and kurtosis for several quantitative traits in rice.

Trait ^{z)}	Generation	Sk ^{y)}	Z _s	Gene Action ^{x)}	Kc ^{w)}	Zk ^{v)}	Number of Genes
PT	F ₄	-0.43	-1.23 ^{tn}	AD + DE	-0.66	-0.96 ^{ns}	Polygenic
	F ₅	-0.06	-0.17 ^{tn}	AD + DE	-0.12	-0.17 ^{ns}	Polygenic
DF (days)	F ₄	-0.06	-0.17 ^{tn}	AD + DE	-1.12	-1.62 ^{ns}	Polygenic
	F ₅	0.32	0.91 ^{tn}	AD + KE	-0.26	-0.38 ^{ns}	Polygenic
DH (days)	F ₄	-0.41	-1.17 ^{tn}	AD + DE	-0.93	-1.35 ^{ns}	Polygenic
	F ₅	0.17	0.49 ^{tn}	AD + KE	-0.52	-0.75 ^{ns}	Polygenic
NFG	F ₄	-0.32	-0.91 ^{tn}	AD + DE	0.09	0.13 ^{ns}	Polygenic
	F ₅	0.37	1.1 ^{tn}	AD + KE	-0.56	-0.81 ^{ns}	Polygenic
TG	F ₄	0.19	0.54 ^{tn}	AD + KE	1.12	1.62 ^{ns}	Polygenic
	F ₅	-0.08	-0.23 ^{tn}	AD + DE	-0.65	-0.94 ^{ns}	Polygenic

^{z)}PT: productive tillers, FA: date to flowering, HA: date to harvesting, TPG: number of fertile grains, TG: total grains.

^{y)}Sk: the value of skewness.

^{x)}AD: additive, DE: duplicate epistasis, KE: komplementer epistasis.

^{w)}Kc: the value of kurtosis.

^{v)}Zk: the statistical of Z skewness and kurtosis, ns: not significant.

will decrease as well as the increase of selfing (Riry 2015). The increase of the estimate of GCV indicates there is a high environmental influenced. The increase of heritability indicates there is an accelerated fixation process, which is causing early homozygosity in the trait. Selection will be effective on this trait if it is done in the early generations. Furthermore, the decrease of heritability indicates there is an involvement of many loci in the inheritance of the traits, this indicates there is high genetic influence although the effect of a non-additive gene is be found (Samak *et al.* 2011).

Traits with negative skewness indicate there is duplicate gene action, it concludes at these traits will be effective if the selection is carried out in the advanced generation. Traits with positive skewness indicate there is complementary gene action, it concludes at these traits will be effective if the selection is carried out intensively from the early generation to the advanced generation (Jayaramachandran *et al.* 2010). The study of the number and action of genes is urgently needed to improve the efficiency of selection and breeding programs (Samak *et al.* 2011).

Negative skewed indicates there is duplicate epistasis gene action. Duplicate epistasis is an interaction of genes that only occurs if two genes produce the same material to form the same phenotype (Griffiths *et al.* 2012). Positive

skewed indicates there is complementary epistasis gene action. Complementary epistasis is an interaction of genes in which one gene requires another gene that has a metabolic function (Griffiths *et al.* 2012).

Kurtosis < 3 indicates traits are controlled by many genes (Isnaini *et al.* 2014). Traits that are controlled by many genes form an accumulation of different locus with each locus having a small and additive effect, so the possibility of environmental influence is low (Sulistyowati *et al.* 2016).

The results of the Z skewness and kurtosis test which are not significantly different indicate the data distribution in all traits was close to normal and controlled by many genes with additive gene action. Additive genes action indicates alleles of the parents are inherited to their offspring, so that effect similar traits between the offspring and the parents (Griffiths *et al.* 2012).

Quantitative traits of rice are generally influenced by many genes with the presence of additive and epistatic gene action. A high estimate of GCV with moderate to high heritability which decreased in number of fertile grains indicates high genetic influence than the environment. The presence of additive and epistasis duplicate gene action in number of fertile grains indicates selection will be effective in an advance generation.

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