Expected genetic progress of F2 resulted from crossovers of paddy Situ Patenggang variety with IPB 3S variety

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Abstract. This study aims to determine the expected genetic progress of the F2 population resulting from the crossing of Situ Patenggang variety with IPB 3S variety, which was carried out in the experimental garden of the Faculty of Agriculture, University of Mataram, Nyur Lembang Village, Narmada District, West Lombok Regency in July to December 2018. The material used in this study is Situ Patenggang varieties, IPB 3S varieties, Inpari 32 varieties, F1 resulting from the crossing of Situ Patenggang varieties with IPB 3S varieties and F2 selfing from F1. Using Augmented design with RAK models. Analysis of Hope Genetic Progress (KGH) allegedly using the formula Knight (1979). The results showed that the high expected genetic progress value was found in the characters of productive tillers, number of non-productive tillers, number of seeds containing panicle, number of empty seedlings, and weight characteristics of 1000 seeds, while genetic progress was quite high in the length of panicle characters.

1. Introduction

Paddy (Oryza sativa L.) is a major food crop for almost half of world’s population, including in Indonesia. Rice, as the staple food which consumed by nearly 90% of Indonesians, contain more good nutrients than any other staple foods [1,2].

The Center of Statistics Bureau (BPS, 2015) reported that rice’s production at West Nusa Tenggara in 2015 is 2,417,392 tonnes of dry unhusked rice (GKG), or it was increased to 290,755 tonnes if compared to the production in 2014, i.e., 2,116,637 tonnes of GKG [3]. Along with the growing population, the productivity of high-yielding rice is demanded to meet the needs of the community [4].

Any variety of kinds of rice are continuing to develop by researchers to get the best rice’s variety than before. Varieties of rice that used are Situ Patenggang and IPB 3S. The Situ Patenggang can be cultivated at the rice field or the dry one at rainy season has scented more than Pandang Wangi, and also easier to be husked manually (rampek) rather than the other variety, i.e. IPB 3S. The Situ Patenggang has a weakness at their production result, with its yield only ranging at 3,6 – 5,6 tonnes per ha, the IPB 3S potentially have a high yield production ranging to 10 – 13 tonnes per ha, so that it needs to get fix at their genetic variety by crossovers the Situ Patenggang with the IPB 3S.

To assemble the best varieties of rice, the genetic parameters like a variety of genetics, heritability, and expected genetic progress is needed to know. The expected value of the genetic progress must
know in estimating how much value-added of certain traits due to the selection of the average population value. The genetic wide variation and high heritability value are a few of requirements that will lead the result to be effective.

This study aims to know the expected genetic progress on F2 population, which was the result of the crossover of Situ Patenggang and IPB 3S.

2. Methods
The experiment was conducted at ExFarm in Faculty of Agriculture, Universitas Mataram, Nyur Lembang Village, District of Narmada, Lombok Barat, West Nusa Tenggara Province, from July to December 2018. The used materials are Situ Patenggang variety, IPB 3S (Sudharmawan’s collection) F1 and F2 as the result of crossover between Situ Patenggang and IPB 3S, and also Inpari 32 variety (controller). The action plan using Augmented design with Random Group Plan (RAK) which looping three times. The formula of the genetic variation analysis ($\sigma_g^2$), phenotype variations ($\sigma_p^2$) and heritability is as follow (Suharsono and friends, 2006):

$$\sigma_g^2 = \frac{\sum_{i=1}^{n} (x_i - \mu)^2}{N}$$

$x_i$ = the value plant’s observation of-I

$\mu$ = median of population

$N$ = number of observed plants

$$\alpha_f^2 = \frac{n1 \sigma_{F1}^2 + n2 \sigma_{F2}^2}{n1 + n2}$$

$$\sigma_g^2 = \alpha_f^2 - \alpha_e^2 ;$$

$$h^2 = \frac{\sigma_g^2}{\sigma_f^2} \times 100\% ;$$

$h^2$ = wide meaning of heritability

$\sigma_g^2$ = genotype variations

$\sigma_f^2$ = phenotype variations

$\sigma_{F2}^2$ = variations’ value at F2 population

$\sigma_{F1}^2$ = variations’ value at F1 population

The genetic progress (KG) and the expected genetic progress (KGH) is using a formula (Knight, 1979):

$$KG = h^2 \times i \times \sigma_f$$

$$KGH = \frac{KG}{X} \times 100\%$$

KG = the genetic progress,

KGH = the expected genetic progress,

$X$ = common average,

$i$ = 10% of selection intensity (=1,76)

$\sigma_f$ = standard deviation of phenotype

$h^2$ = wide meaning of heritability.

3. Results and Discussion

3.1. Results
In Table 1, the character shows the phenotype variations such as the plant’s height, a total of productive tillers, the number of contained and empty seeds, also the weight of 1000 seeds, while the characters that showed a narrow phenotype variation were found in the long panicle characters and the number of non-productive tillers.
Table 1. Phenotype variations’ value.

| Character(s)                        | $\sigma^2_g$ | $\sigma_g$ | $2\sigma_g$ | Criteria  |
|-------------------------------------|--------------|------------|-------------|-----------|
| Plant’s height                      | 120.05       | 10.95      | 21.91       | Wide      |
| Panicle length                      | 2.93         | 1.71       | 3.43        | Narrow    |
| Total of productive tillers        | 46.89        | 6.85       | 13.69       | Wide      |
| Total of non-productive tillers    | 1.25         | 1.12       | 2.24        | Narrow    |
| Contained seeds per panicle         | 124.32       | 11.15      | 22.30       | Wide      |
| Empty seeds per panicle             | 12.36        | 3.52       | 7.03        | Wide      |
| Weight of 1000 seeds               | 5.42         | 2.32       | 4.64        | Wide      |

The wide phenotype variation if $\sigma^2_g > 2\sigma_f$, while the narrow phenotype variation if $\sigma^2_g < 2\sigma_f$ (Anderson and Bancroft, 1952 in Wahdah, 1996).

Table 2. Genotype variations’ value.

| Character(s)                        | $\sigma^2_g$ | $\sigma_g$ | $2\sigma_g$ | Criteria  |
|-------------------------------------|--------------|------------|-------------|-----------|
| Plant’s height                      | 118.58       | 10.88      | 21.77       | Wide      |
| Panicle length                      | 1.83         | 1.35       | 2.71        | Narrow    |
| Total of productive tillers        | 33.02        | 5.75       | 11.49       | Wide      |
| Total of non-productive tillers    | 0.98         | 0.99       | 1.98        | Narrow    |
| Contained seeds per panicle         | 98.84        | 9.94       | 19.88       | Wide      |
| Empty seeds per panicle             | 10.99        | 3.32       | 6.63        | Wide      |
| Weight of 1000 seeds               | 5.02         | 2.24       | 4.48        | Wide      |

In Table 2, the character shows genetics wide variety at its plant’s height, total of productive tillers, the number of contained and empty seeds, also the weight of 1000 seeds, meanwhile, the narrow genotype variations can be seen at its panicle length and non-productive tillers. The wide genotype variation if $\sigma^2_g > 2\sigma_f$, while the narrow genotype variation if $\sigma^2_g < 2\sigma_f$ (Anderson and Bancroft, 1952 in Wahdah, 1996).

In Table 3, all characters show a high heritability value alongside with its value of expected genetics progress, except the length of panicle, which seems to have only quite high value.

Table 3. The heritability value and expected genetics progress.

| Character(s)                        | $h^2$  | Criteria of 1 | %KGH | Criteria  |
|-------------------------------------|--------|---------------|------|-----------|
| Plant’s height                      | 0.98   | High          | 22.76| High      |
| Panicle length                      | 0.63   | High          | 7.07 | Quite high|
| Total of productive tillers        | 0.70   | High          | 33.3 | High      |
| Total of non-productive tillers    | 0.79   | High          | 195.95| High     |
| Contained seeds per panicle         | 0.79   | High          | 12.54| High      |
| Empty seeds per panicle             | 0.89   | High          | 44.53| High      |
| Weight of 1000 seeds               | 0.92   | High          | 13.78| High      |
3.2. Discussion

The wide genetic variation is the successful key of a selection. This can be considered as if the wider the genetic variation is, the bigger the opportunity to increase the expected cell/genetic frequency and vice versa. The use of seeds in this study is known to be F2 seed. According to Poespodarsono (1998), the F2 generation is the one who has wider and high variations so that it can push the chances to a succeed selection [5]. Allard (1960); Hallauer (1987); and Ayalneh and friends (2012) said that the wide variations of genetic is a required process of an effective on-going selection, because it provides unimpeded at the selection process of some genotypes, thereby increasing the chances of a successful selection [6–8]. The effectiveness of selection is inseparable from the value of genetic parameters, namely: heritability and genetic progress.

Table 1 and 2 show that the phenotype and genotype variations are diverse, both from the narrow and wide sides. It is considered as wide if its value is twice more than the standard deviation. Meanwhile, it can be categorized as narrow if the value is two times below or equal to its standard deviation [9].

The wide variety of value indicates that the inheritance of upcoming traits is big enough (100%), which can be found on its height, productive tillers, contained and empty seeds per panicle, and the weight of 1000 seeds, meaning that the genetic factor on those characteristics plays a big role than the environmental factor [10]. The wide range of genetic diversity caused by a diversified character. It probably came from the old generation of Situ Patenggang with IPB 3S, which have a different characteristic and its higher level of segregation.

The result of the wide variations, both on phenotype and genotype, shows a big opportunity of selecting the expected characters. While for the narrow genetic variations only contained in the panicle length and non-productive tillers, which caused by using the genotype characters whose character is limited. According to Paramita (2014), the precarious genetic variations signed that the observed trait could have similar appearances, so if there is any selection obtained to those plants, it will be an ineffective result because in achieving the genetic progress is very much low [11].

The wide variation of genetic marks the selection effectiveness or successful of a plant breeding. The wider its genetic variations on the population, the more variety of traits could mirror the genetic control on it. Highly genetic control on some traits could lead to a bigger chance to get a better genotype through a rigorous selection process. Hamdi et al. (2003) and Jalata et al. (2011), said that genetic progress is an important part of determining the expected value of a single election cycle. The value of expected genetic progress (KGH) differs between the character’s appearance on the average population of its successor and the predecessor [12,13]. The difference between genotype variations’ value is an estimator of a character’s selection process which will have an impact to fixing the plant’s genotype on a certain selection intensity [14].

The expected progress valued in Table 3 ranging from 7.07% to 195.09%, with the highest criteria to all characters except the panicle length whose value in progress only scored with 7.07%. Categorizing these criteria according to Mangoendidjojo (2003), whereas the expected genetic progress value can be considered high if it has achieved more than 10%, high enough if its value is below or equal to 10% and more than 6.6%, quite low if its value is ranging less than 6.6% or more than 3.3% and very low if the value is below or equal to 3.3% or greater than 0 [15].

The high value of genetic progress in a character indicates that it is supported by genetic factors, so it is allowed to facilitate the progress selection. This is consistent with a study conducted by Martono (2009), which revealed that the high value of heritability of a character followed by genetic variations shows that its appearance determined by its genetic factor [16]. Therefore, the selection process on this population could be more efficient and effective because it gives hope to the genetic progress. Thus, its selection at resulting in the best quality of genotype, can be applied to those characters.

According to Hapsari and Adie (2010), the effectiveness in selecting a character is when the genetic progress is high and supported by its highly valued heritability [17]. The high value in heritability follows by its high percentage of expectation to some characters could also potentially give a positive response to the improvement’s effort on it. To Falconer and Mackay (1996), a character
whose progress is high is always followed by the high value of wide-meaning heritability, and potentially could be fixed with a selection on its early generation [18]. Therefore, these characters which its progress values are high and supported with a wide range of variety can be selected through a pedigree method. The method is usually applied to identify the difference between a family, which was considered a homozygote (Poespodarsono, 1998) [5]. The estimated method is based on diversifying components that can be used to know the genotype differences between the resulted crossovers and the self-pollinated plant.

4. Conclusion
The crossover between Situ Patenggang variety with IPB 3S variety have resulted from a population which has a high heritability value and expected genetic progress at all characters, such as plant’s height, the total of productive and non-productive tillers, contained and empty seeds for each panicle, and at the weight of 1000 seeds. The expected genetics value is quite high only in long panicles.

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