Inheritance study for yield components of pepper
(*Capsicum annuum* L.)

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Abstract. An inheritance study for yield components character of pepper was done in population derived from IPB C120 and IPB C5 crosses, i.e. F2, F1, first back crosses generation including the two parents. Broad-sense heritability was high for days to flowering, days to harvest, fruit weight, fruit length, fruits diameter, number of fruit per plant, yield; and medium for pedicel length and pericarp thickness. Narrow-sense heritability was high for days to harvest, fruit length; medium for days to flowering, fruit weight, pedicel length, fruit diameter, pericarp thickness; and low for number of fruit per plant and yield. The significant scaling test and joint scaling tests indicated the presence of epistasis gene actions. The additive-dominant models with the effect of additive-additive and additive-dominant interaction were fit for days to harvest character and fruit diameter. The additive-dominant models with the effect of additive-additive and dominant-dominant interaction were fit for pericarp thickness, number of fruit per plant and yield. The additive-dominant with influence of interaction additive-dominant and interaction dominant-dominant was fit for days to flowering, pedicel length and fruit length.

Keywords: epistasis, gene action, heritability, inheritance, yield components

1. Introduction

Peppers (*Capsicum annuum* L.) are widely grown as a spices and vegetables. Peppers are classified as the second most important vegetables in the world in *solanaceae* group after tomato [1]. The average of pepper productivity in the world is 17.76 ton ha⁻¹ in 2013 [2], while productivity potency that can be achieved is about 18-24.2 ton ha⁻¹ [3]. Increased productivity of pepper in the world can be done by the development of high yielding varieties of pepper, which can be obtained from plant breeding programs.

Genetic diversity is a key factor of the successfullness of a breeding program. The source of genetic diversity can be obtained by the introduction, hybridization, mutation or even by genetic engineering. Up to now, hybridization or croses of two pure lines are the most common techniques used in plant breeding activities. It will result the F1 heterozygous offspring and the next segregation will appear in the F2 generation [4]. Information regarding the inheritance of qualitative and quantitative characters is very important to do selections from crossing population to develop new promising varieties. Inheritance analysis of qualitative and quantitative character can predict the number of genes that control any particular characters, gene actions, and other genetic informations [5], thus selection will be more effective and efficient.

Heritability is one of the genetic information that can be used to predict the effect of genetic and/or enviromental factors to plant phenotypes. The character with high heritability values indicate that the...
plant phenotypes are more influenced by genetic factors that can be inherited. This character can be controlled by either additive, dominant or epistasis gene actions. According to [6], genetic variance comprise of additive variance (V_A), dominant variance (V_D) and epistatic variance (V_I). Additive genetic variance is a major effect of similarities among relatives (among parent with offsprings). Variance is the average of the gene, the function of the degree which changes in phenotype due to selection. Dominant genetic variance is the main effect of dissimilarity among relatives. These variances are the main basis for heterosis and specific combining ability. The effects of additive genes with greater than a dominant gene in character will provide information that its character can be inherited to progeny and it can be concluded that the appearance of each character observed is affected by additive gene action [7]. Epistasis is variance of gene between locus interaction and often also referred to as non-allelic gene interaction.

The genetic information, such as the gene actions, genetic variability, heritability and other information very useful in the selection process, so that the selection can be more effective and efficient [8]. Moreover, pattern of inheritance, genetic variability and heritability of a character is an important genetic parameters related to the selection process and merger of important characters in a genotype [9]. [10] stated that genetic information and efficiency in plant breeding program is required to improve yield productivity. Generation mean analysis is a tool that can be used to study other models of genetic effects outside of additive-dominant model [11]. Explanations for additive and dominant gene actions for the planning in plant breeding programs with highly efficient could be obtained from comparative assessment of the linear components, which comprise of additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l]. Study of inheritance yield component characters become important in maximizing used genetic potential in the effective breeding programs. The objectives of this study were obtained yield component characters inheritance information of chili.

2. Materials and methods
This research was conducted from September 2013 to July 2014 for the F2 population development and from August to December 2014 for the field trial at Leuwi Koppo Field Station of Bogor Agricultural University in Bogor, Indonesia.

Biparental crossing design was used in this research, which consisted of 40 plants for each parents, 40 plants of F1, 40 plants of reciprocal first generation (F1R), 100 plants of backcross (BCP1 and BCP2), and 300 plants of F2. The parents used in this study were IPB C120 (curly pepper type) and IPB C5 (chilli pepper type). The characters observed in this study were yield components i.e. Days to flowering (Days After Transplanting), days to harvest (Days After Transplanting), fruit weight (g), pedicel length (cm), fruit length (cm), fruit diameter (mm), pericarp thickness (mm), number of fruits per plant, and yield (g tan^{-1}).

The data were subjected to analysis as follows:

2.1. Estimation of heritability
Estimation of heritability consists of broad-sense heritability [12,6] and narrow-sense heritability [13] using this formula:
$$h^2_{bs} = \frac{VF2 - (VF1 + VP1 + VP2)/3}{VF2}$$

$$h^2_{ns} = \frac{2VF2 - (VBCP1 + VBCP2)}{VF2}$$

Note:

$h^2_{bs}$ = Broad-sense heritability

$h^2_{ns}$ = Narrow-sense heritability

$VF1$ = Variance of F1

$VF2$ = Variance of F2

$VP1$ = Variance of P1

$VP2$ = Variance of P2

$VBCP1$ = Variance of backcross P1

$VBCP2$ = Variance of backcross P2

2.2. Gene effects

Three parameter models described by [14], namely: $A=2BCP1-P1-F1$; $B=2BCP2-P2-F1$; $C=4F2-2F1-P1-P2$ were used in individual scaling test to estimate the suitability of additive-dominant models. If the individual scale test results was not suitable with additive-dominant models, we then continued with the joint scaling tests ($m = \frac{1}{2}P1 + \frac{1}{2} P2 + 4F2 - 2BCP1 - 2BCP2; [d] = \frac{1}{2}P1 - \frac{1}{2}P2; [h]=6BCP1 + 6BCP2 - 8F2 - F1 - \frac{1}{2}P1 - 1\frac{1}{2}P2; [i]=2BCP1 + 2BCP2 - 4F2; [j]=2BCP1 - P1 - 2BCP2 + P2; [l]=P1 + P2 + 2F1 + 4F2 - 4BCP1 - 4BCP2$) to add contribution of epistasis (non-allelic gene interaction). This test generated the estimation of the three parameters: mean ($m$), additive effect ($d$), dominance effect ($h$) and also produce the estimation for the three parameters epistasis additive x additive interaction ($i$), additive x dominance interaction ($j$) and dominance x dominance interaction ($l$).

3. Result and discussion

3.1 Results

3.1.1. Heritability. Broad-sense heritability ($h^2_{bs}$) and narrow-sense heritability ($h^2_{ns}$) obtained in this study were presented in Table 1. Broad-sense heritability ranged from 0.37 (moderate) to 0.89 (high). High broad-sense heritability in this study was found for days to flowering, days to harvest, fruit weight, fruit length, fruit diameter, number of fruit, yield and moderate recorded for the character of the pedicel length and pericarp thickness (table 1). The narrow-sense heritability ranged from 0.19 (low) to 0.86 (high). High narrow-sense heritability was found for days to harvesting and fruit length, moderate recorded for days to flowering, fruit weight, pedicel length, and fruits diameter and pericarp thickness character. Low narrow-sense heritability was found for number of fruits per plant and yield (table 1).

| Characters            | $h^2_{bs}$ | $h^2_{ns}$ |
|-----------------------|------------|------------|
| Days to flowering     | 0.57       | 0.44       |
| Days to harvest       | 0.89       | 0.86       |
| Fruit weight          | 0.72       | 0.46       |
| Pedicel length        | 0.49       | 0.27       |
| Fruit length          | 0.81       | 0.57       |
| Fruit diameter        | 0.71       | 0.48       |
| Pericarp thickness    | 0.37       | 0.33       |
| Number of fruits per plant | 0.60   | 0.19       |
| Yield                 | 0.60       | 0.22       |
3.1.2. Scaling test. Significant scaling test on A, B and C indicated the presence of epistatic or the interaction non-allelic (table 2). The value A of all characters showed significant value except for yield indicating that the means models of additive-dominate genetic model was not appropriate. Although the value A for yield was non-significant, additive-dominant models could be used since the value of C for yields was significant. According to [15], if the model is not fit to the dominant additive models, it needs to be tested to other models that involved in the non-allelic interaction.

Table 2. Scaling test for yield component character.

| Character                  | A     | B     | C     |
|----------------------------|-------|-------|-------|
| Days to flowering          | 9.629 | **    | 5.543 | **    | 14.760 | **    |
| Days to harvest            | 13.409| **    | 9.166 | **    | 45.718 | **    |
| Fruit weight               | -4.842| **    | -2.588| **    | -18.959| **    |
| Pedicel length             | -1.531| **    | -0.458| **    | -2.161 | **    |
| Fruit length               | -6.741| **    | -4.960| **    | -13.325| **    |
| Fruit diameter             | -3582 | **    | -2.044| **    | -14.073| **    |
| Pericarp thickness         | -0.18 | **    | -0.057| ns    | -0.749 | **    |
| Number of fruit per plant  | 37.426| **    | 39.388| **    | 146.428| **    |
| Yield                      | 2.461 | ns    | 39.658| ns    | -213.872| *     |

Significant value of A and B indicates the presence of i, j and l type of gene interaction. Significant value of C indicates the presence of l type of gene interaction. A significant $\chi^2$ value indicates the inadequacy of three parameter model. * $P<0.05$, ** $P<0.01$ respectively.

3.1.3. Joint scaling test. Parameters of genetic model according to [14] were used to test the type of interaction between loci. Genetic models are appropriate when the $\chi^2$ values were not significantly different. However if they have several non-significant, $\chi^2$ values, seeing predictive can be used to predict of the appropriate model. Genetic model that might be appropriate for the character of days to flowering, pedicel length and fruit length is additive-dominant model with effects additive x dominance interaction and dominance x dominance interaction with five components, namely m [d] [h] [i] [j] [l] (table 3). The model of additive-dominant effect additive x additive interaction and additive x dominance interaction were fit for the days to harvesting, fruit weight and fruit diameter with five components, namely m [d] [h] [i] [j] (table 3). Genetic model that was fit for pericarp thickness, number of fruit per plant and yield character is additive-dominant model with effect additive x additive interaction and dominance x dominance interaction with five components, namely m [d] [h] [i] [l] (table 3).

Refers to [16], the fitness of the parameters of genetic model can be predicted from the significant value of character, such as: m, [d], [h], [i] [j], and [l] indicates a gene action additive, dominant and epistasis well as their interactions. If the value of [h] and [l] are significant and have the same sign referred to as type complementation. If the value of [h] and [l] significant and have different sign referred to as type duplication [14]. In this study the character of days to flowering, pedicel length, fruit length and number of fruit per plant had complementation gene interactions (table 4). Characters fruit weight, pericarp thickness and yield has a duplicate gene interactions for [h] and [l] with different direction (table 4).
Table 3. Value of genetic parameters on yield component character.

| Model | Days to flowering | Days to harvest | Fruit weight | Pedicel length | Fruit length | Fruit diameter | Pericarp thickness | Number of fruit per plant | Yield |
|-------|------------------|----------------|-------------|----------------|-------------|---------------|-------------------|--------------------------|-------|
| m [d] | 180.980**        | 169.107**      | 519.085**   | 173.132**      | 200.506**   | 62.514**      | 157.876**         | 23.145**                 |
| m [d] **| 151.670**        | 110.392**      | 519.047**   | 149.832**      | 200.506**   | 60.95**       | 124.004**         | 11.624**                 |
| m [d] [h] | 52.935**        | 1.435 ns         | 6.343 *     | 55.827**      | 33.650**    | 3.395 ns      | 5.021 ns          | 0.127 ns                 |
| m [d] [h] [i] | 145.283**        | 110.038**      | 519.047**   | 122.097**      | 200.490**   | 58.32**       | 122.498**         | 11.504**                 |
| m [d] [h] [j] | 12.487**         | 22.09**        | 133.162**   | 8.356**       | 65.372**    | 33.561**      | 22.498**          | 9.806**                  |
| m [d] [h] [k] | 41.142**         | 0.696 ns        | 20.543 ns   | 125.772**     | 65.592**    | 32.981**      | 22.213**          | 9.806**                  |

m = means; d = additive effect; h = dominant effect; i = effect additive x additive interaction; j = effect additive x dominant interaction; l = effect dominant x dominant interaction; **=highly significant; *=significant; ns = non significant at $\alpha = 5\%$

Table 4. Estimates of gene effect on yield component character.

| Gene Effect | Days to flowering | Days to harvest | Fruit Weight | Pedicel length | Fruit length | Fruit diameter | Pericarp thickness | Number of fruit per plant | Yield |
|-------------|------------------|----------------|-------------|----------------|-------------|---------------|-------------------|--------------------------|-------|
| m           | 31.190**         | 98.187**       | 4.801**     | 3.562**        | 9.244**     | 9.244**       | 1.237**           | 115.343**                | 375.182**|
| [d]         | 0.768 ns         | 1.757 ns       | -7.251**    | 0.079 ns       | 1.027**     | -7.472**      | -0.684**          | 8.806 ns                 | -159.803**|
| [h]         | -4.138**         | -33.091**      | 1.120**     | 0.662**        | 3.646**     | 7.864**       | 0.479**           | -46.716**                | 393.470**|
| [i]         | 0.412 ns         | -23.143**      | 11.529**    | 0.172 ns       | 1.531 ns    | 8.447**       | 0.512**           | -69.614**                | 255.991**|
| [j]         | 2.043 ns         | 1.127**        | -0.536**    | -0.891**       | -0.769**    | -0.061**      | -0.981**          | -18.598 ns               | -298.110**|
| [l]         | -15.583**        | 0.569 ns       | -4.100**    | 1.817**        | 10.17**     | -2.821**      | -0.274**          | -7.201 ns                | -298.110**|

m = means; d = additive effect; h = dominant effect; i = effect additive x additive interaction; j = effect additive x dominant interaction; l = effect dominant x dominant interaction; **=highly significant; *=significant; ns = non significant at $\alpha = 5\%$
3.2 Discussion

Most of the broad-sense heritability are high. Several studies of chili also showed that the broad-sense heritability is high for the days to flowering [17,18], days to harvest [18,19], fruit weight and fruit length [20,21,22,23], fruit diameter [20,21,23], number of fruit per plant [24,25] and yield [23]. The moderate broad-sense heritability in of pedicel length and pericarp thickness characters in our study is slightly different from the results of [20] and [21]. Different population used in these studies might be the most contributed factors for these differences.

In our study, narrow-sense heritability value of the number fruit per plant was much lower compared to its broad-sense heritability value. Several studies have also shown similar results [26,27]. This indicates that the proportion of additive variance is smaller than the dominant variance. Narrow-sense heritability of the days to harvest and fruit length were high. Characters of days to flowering, fruit weight and fruit diameter has moderate narrow-sense heritability. In fact, several studies show different results, such as [18] where the narrow-sense heritability of the days to harvest is high and the fruit diameter is low, and the result of [20] and [21] where the fruit weight had a high narrow-sense heritability.

Broad-sense and narrow-sense heritability of pedicel length and pericarp thickness is moderate and yield is low. This is different with previous studies such as [20] and [21] where the narrow-sense heritability of pedicel length and pericarp thickness is high. [23] also reported that the narrow-sense heritability of yield is high. Differences in the results of these studies can be due the different population used in each study. Similar to fruit length and days to harvest, narrow-sense heritability indicates an additive effect is greater than the dominant effect.

Estimation of the heritability is important to predict if the characters are affected more by genetic or by environmental factors. High heritability indicates that genetic factors have greater influence compared with environment on phenotypic appearance of a plant. High narrow sense heritability plays an important role in increasing effectiveness of selection [6].

Model of additive-dominant with effects of additive x dominance interaction and dominance x dominance interaction for the days to flowering and the fruit length are equal with the result of [1]. [28] also report on the fitness of an additive-dominant model with the effects of additive x dominance interaction and dominance x dominance interaction for fruit length character. Genetic model of days to harvest in this study was additive-dominant with effect of additive-additive interaction and additive-dominant interaction. The same thing was shown by [29], where the days to harvest character was affected by the additive-additive interaction and additive-dominant interaction. Fruit diameter and fruit weight character were fit with the model of additive-dominant with effect of additive-additive interaction and additive-dominant interactions. [21] and [1] reported that the fruit diameter and fruit weight characters is also influenced by the additive-additive interaction and additive-dominant interaction. The fitted genetic model for pericarp thickness, number of fruit per plant and yield additive-dominant with effect of additive-additive interaction and dominant-dominant interaction. Same result was found on [1] on the pericarp thickness character and [16] on the number of fruit per plant and yield characters.

Based on our results here, the breeding program of our pepper population can be continued by utilizing the heterosis effects to develop hybrid varieties since the non-additive gene effects were bigger in those characters. According to [1] interaction of gene complementation selection in early generations of segregation will not provide a major contribution to improvement of these characters. While according to [16] modified of bulk selection is recommended if there are gene interactions complementary, where selection is carried after homozygosity level is already high enough. Complementary will increase heterosis, whereas duplication causing heterosis down. In this study gene effect of duplicates found in fruit weight, pericarp thickness and yield characters. This will reduce the benefits that occurred from heterozygosity caused cancellation of dominant and epistasis effect [30]. In this case, delay the selection will be more effective to get a better selection response.
Based on this study, all kinds of gene action was found. This condition will increase the characters standard selection procedure that can be done to exploit additive gene effect. However, at the same time, precautions should be bear in mind so that the dominant gene effect will not disappear in the hopes of the dominant effects collected. According to [31] reciprocal recurrent selection of breeding seems to be best method because it will make use of three types of gene effects which are additive, dominant and epistasis which result accumulation of the desired recombinant at the next recombinant.

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