Inheritance study for fruit characters of tomato IPBT78 x IPBT73 using joint scaling test

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Abstract. The increase of tomato production can be done through the improvement of superior genotypes that have high production components even though they are planted in the lowlands. Information on components' inheritance of tomato production in the lowlands is very important to determine the effective selection method for the development of lowland tomatoes. This study aimed to study the pattern of components' inheritance of tomato products in the lowlands. This study used an analysis of six generations, namely P1, P2, F1/F1R, BCP1, BCP2, and F2 through a joint scaling test. The results showed that the characters of fruit length, fruit diameter, fruit size, weight per fruit, fruits number per plant were controlled by many genes, and there were no maternal effects. Gene action for fruit length character was duplicate epistasis and additive dominance, for fruit diameter characters were additive dominance and complementary epistasis, duplicate epistasis and additive dominance for fruit size characters, duplicate epistasis and additive dominance for fruit size characters, duplicate epistasis for per fruit weight, several fruits per plant and fruit weight per plant.

1. Introduction

Increased tomato production in Indonesia through extensification leads to less fertile lands and shifts to lowland planting. Shifting tomato planting area to the lowlands causes a risk of decreasing the quality and production of the fruit. Low production in the lowlands is partly due to the limited high yielding potential varieties [1, 2]. Lowlands have high temperatures. High temperatures not only have an impact on fruit ripening but also fruit growth rates on tomatoes [3]. An increase in temperature of 2-40°C from the optimum temperature reportedly affects gamete development and inhibits fruit formation, thereby reducing tomato production [4, 5, 6].
The utilization of superior adaptive varieties to environmental conditions in the lowlands is the right solution to obtain tomatoes that are capable of high production even though they are planted in the lowlands. The assembly of superior varieties is done through improving the characteristics of tomatoes in the lowlands. Efforts to improve these characters require literature study on character inheritance and must be chosen based on the heritability value [7]. The study of character inheritance is the basis for determining an effective and efficient selection method to obtain superior varieties based on the desired character [8]. The success of plant assembly is largely determined by appropriate methods and selection criteria [9, 10, 11]. Therefore, research in the production components inheritance on tomatoes is important to do. This study aims to determine the inheritance pattern of production components. Thus it can recommend the right selection method for assembling tomato varieties with high production in the lowlands.

2. Methods
This study used six generation method (biparental). The populations of P1, P2, F1, and F1R were 20 plants, F2 with ± 200 plants, BCP1 and BCP1 were 80 plants. Each of these populations was planted simultaneously.

Seeding was carried out on a tray containing sterile seedling media. Land management and making beds were carried out simultaneously during seeding activities. Planting was conducted after the tomato seeds were 30 days old after the seedling. Plots of beds were made with a size of 5 m x 1 m for each experiment unit with a distance between beds of 50 cm. Then each bed was given 20 kg of manure and 0.5 kg of chalk. After giving chalk and manure for two weeks, the beds were covered with black silver plastic mulch and a planting hole with a distance of 50 cm x 50 cm was created.

Character data of production components were analyzed by observing maternal influence, a number of genes controlling character, degree of dominance, estimation of effective factors, estimation of genetic components by using joint scaling test, and determining the heritability value.

3. Results and Discussions
The population median of the characters was fruit length, fruit diameter, fruit size and weight per fruit at IPBT78 x IPT73, namely female parent (P1) was higher than the male parent population (P2). The median values of BCP1, BCP2, and F2 were between the median values of the two parents. The median values of F1 and F1R populations were also between the averages to the two parents (Table 1).

The homogeneous variance test results (f test) and the maternal effect by using the median value difference test (t-test) showed that there were no significant differences between F1 and F1R for the observed characters (Table 2). The t-test results that are not significant indicate that there is no maternal effect and only genes in the nucleus that control the inheritance of these characters, hence for further analysis, F1 and F1R can be combined.

| Population | Fruit Length | Fruit Diameter | Fruit Size | Weight per fruit | Number of Fruits per Plant |
|------------|--------------|----------------|------------|------------------|---------------------------|
| P1         | 54.07 ±4.97  | 54.07 ± 4.96   | 46.55 ± 5.07 | 43.41 ± 5.20     | 35.80 ± 3.52              |
| P2         | 26.81 ±2.56  | 26.81 ± 2.56   | 36.76 ± 4.55 | 37.90 ± 8.42     | 44.20 ± 5.05              |
| BCP1       | 42.58 ± 7.18 | 42.58 ± 7.17   | 42.32 ± 7.11 | 41.11 ±15.29     | 39.13 ± 10.09             |
| BCP2       | 31.19 ±6.11  | 31.19 ± 6.11   | 36.83 ± 4.88 | 36.17 ± 13.56    | 40.89 ± 10.09             |
| F2         | 37.17 ± 7.64 | 37.17 ± 7.64   | 38.02 ± 7.01 | 33.68 ± 15.28    | 42.77 ± 11.13             |

P1: female parent, P2: male parent, BCP1: Backcross to female parent (F1 x P1), BCP2: backcross to male parent (F1 x P2), F2: second generation
The character ratio potential value of fruit length and number of fruits per plant are in the range of 0 to 1 (Table 3). The potential ratio value that is in the range 0 to 1 means that the F1 average is greater than the average of the two parents but smaller than the average parent with the highest value [12]. This shows that the character of fruit length and number of fruits per plant are controlled by the action of partial dominance genes. This is consistent with the results of the research of [13] that the number of fruits per plant is inherited by a partial dominance. The character ratio potential value of fruit diameter, fruit size, and weight per fruit are in the range of 0 to 1 (Table 3). This value indicates that the F1 average is between the averages of the two parents which means that the fruit diameter, fruit size, and weight per fruit is controlled by overdominance gene action.

The approach to predicting genetic control can be descriptive estimation using skewness and kurtosis. The distribution of data with zero skewness values reflects that the character is controlled by additive gene action, positive skewness is additive gene action as the influence of complementary epistasis, while for negative skewness reflects control of additive genes with the effect of duplicate epistasis. The characters controlled by many genes are indicated by the value of \(-3 < \chi^2 < 3\) (mesokurtic), while characters controlled by fewer genes are indicated by kurtosis> 3 (platykurtic) or <-3 (leptokurtic) [14]. The number of genes controlling fruit diameter character in all cross combinations is at least one gene (Table 3). This shows that the minimum number of effective factors involved in controlling fruit characters is one. All characters observed had positive skewness, and the kurtosis value was mesokurtic \((-3 < \chi^2 < 3\) (Table 3). This shows that the characters are controlled by many genes with additive gene action as the influence of complementary epistasis. The joint scaling test indicated that the assumption of the additive-dominance genetic model was not satisfied in any one of the characters studied, wherein all the tested parameters and \(\chi^2\) values were significant [15]. The most compatible model based on the combined scale test is a model that shows the smallest value of \(\chi^2\) and smaller than the \(\chi^2\) table \((\text{prob} < 0.05\) [16]. Genetic model compatible for the character of fruit length, fruit diameter, fruit size was additive x dominance \((m [d] [h])\) The most compatible model for weight per fruit and number of fruits per plant was additive-dominant with the influence of additive x additive and dominant x dominant \((m[d][h][i][ l])\) (Table 4).
The genetic model compatible for fruit length, fruit diameter, and fruit size was the dominance additive model (m [d] [h]). If the dominance additive genetic model (m [d] [h]) is compatible, there is no need to proceed to test other models because the model is the most compatible [16]. This shows that these characters have no epistasis effect. The negative dominance effect means that the shorter fruit expression (IPB T73) is more dominant for large fruit diameter (IPB T73), and smaller fruit size (IPB T73) is dominant for the size of large fruit (IPB T78). Fruit length characters are controlled by genes that work additively [17].

On the weight character per fruit, the dominance influence was positive, which means that the fruit weight of IPBT78 was dominant on the fruit weight of IPBT73. Additive and dominance influences in the opposite direction with the effect of the interaction, thus the gene action that has more influence on the weight per fruit was duplicate epistasis. The character of the number of fruits per plant had additive and dominance component. S Additive and negative dominance effects indicate that fewer fruits per plant (IPBT78) was more dominant for a large number of fruits (IPBT73). The dominance additive effect was in the opposite direction to the influence of the interaction. Hence gene action which had more influential was duplicate epistasis. The results obtained are not compatible, there is no need to proceed to test other models because the model is the most compatible [16].

Table 4. Genetic model compatibility using joint scaling test

| Cross Combination | Fruit Length | Fruit Diameter | Fruit Size | Weight per Fruit | Number of Fruits per Plant |
|-------------------|--------------|----------------|------------|------------------|-----------------------------|
|                   | χ²cal | m [d] | χ²cal | m [d] | χ²cal | m [d] | χ²cal | m [d] | χ²cal | m [d] | χ²cal |
| Fruit Length      | 40.031* | 43.93* | 41.98* | 20.79* | -5.94* | -5.195* | -6.29* | -42.50* | 19.52* | -33.46* |
| Fruit Diameter    | 49.3*   | 49.05* | 49.5*   | 3.20*   | -5.94* | -5.195* | -6.29* | -42.50* | 19.52* | -33.46* |
| Fruit Size        | 41.98*  | 49.05* | 49.5*   | 3.20*   | -5.94* | -5.195* | -6.29* | -42.50* | 19.52* | -33.46* |
| Weight per Fruit  | 20.79*  | 3.50*  | 42.50*  | 19.52*  | -33.46* |
| Number of Fruits per Plant | 50.52* | -3.43* | -22.29* | 10.78* | -13.57* |

Table 5. Estimating genetic components to determine gene action

| Cross Combination | Genetic Component |
|-------------------|-------------------|
|                   | m | d | h | i | j | l |
| Fruit Length      | 40.031* | 12.93* | -5.94* | - | - | - |
| Fruit Diameter    | 43.93* | -3.20* | -5.195* | - | - | - |
| Fruit Size        | 41.98* | 4.95* | -6.29* | - | - | - |
| Weight per Fruit  | 20.79* | 3.50* | 42.50* | 19.52* | -33.46* |
| Number of Fruits per Plant | 50.52* | -3.43* | -22.29* | 10.78* | -13.57* |

The degree of dominance for fruit length, fruit diameter, and fruit size was the dominance additive model (m [d] [h]). If the dominance additive genetic model (m [d] [h]) is compatible, there is no need to proceed to test other models because the model is the most compatible [16]. This shows that these characters have no epistasis effect. The negative dominance effect means that the shorter fruit expression (IPB T73) is more dominant for the long fruit (IPB T78), smaller fruit diameter (IPB T78) is more dominant for large fruit diameter (IPB T73), and smaller fruit size (IPB T73) is dominant for the size of large fruit (IPB T78). Fruit length characters are controlled by genes that work additively [17].

On the weight character per fruit, the dominance influence was positive, which means that the fruit weight of IPBT78 was dominant on the fruit weight of IPBT73. Additive and dominance influences in the opposite direction with the effect of the interaction, thus the gene action that has more influence on the weight per fruit was duplicate epistasis. The character of the number of fruits per plant had additive and dominance component. S Additive and negative dominance effects indicate that fewer fruits per plant (IPBT78) was more dominant for a large number of fruits (IPBT73). The dominance additive effect was in the opposite direction to the influence of the interaction. Hence gene action which had more influential was duplicate epistasis. The results obtained are not by the results of the [18] who reported that character inheritance of the number of fruits followed the dominance additive gene action model.

4. Conclusion

The character of fruit length, fruit diameter, fruit size, weight per fruit, number of fruits per plant were controlled by many genes, and there was no maternal effect. The degree of dominance for fruit length character was partial and dominance recessive, on fruit diameter character was partial recessive, partial dominance and overdominance, on the fruit size character was partial dominance, and overdominance, the weight character per fruit was partial dominance and overdominance, in the
character of the number of fruits per plant was partial dominance and the character of fruit weight per plant was partial dominance and overdominance. Gene action for fruit length characters was duplicate epistasis and dominance additive, for fruit diameter character was dominance additive and complementary epistasis, duplicate epistasis and dominance additives for fruit size character, duplicate epistasis for per fruit weight, number of fruits per plant and fruit weight per plant.

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