



Genetic Analysis and Distribution of F2 Population Variety of Tomato Crosses

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Abstract

The demand for tomatoes is increasing along with population growth. However, this demand needs to be supported by increasing tomato productivity. One way to increase this is the assembly of high-yielding tomato varieties. In the assembly of varieties, the F2 generation is a generation with high diversity. This becomes important in the process of evaluating and selecting tomato varieties. Genetic variants are the initial capital of plant breeding efforts, which are related to the assembly of varieties to increase the quantitatively and quality of the yield including fruit size, fruit quality and productivity by utilizing the heterotic phenomenon in the assembly of tomato varieties. A research was conducted to evaluate the diversity of generations of biparental crosses using an augmented design. The genotypes used were Mawar (30 plants), Karina (30 plants), F1 genotype of Mawar x Karina (25 plants), Mawar x Karina x Mawar (20 plants), Mawar x Karina x Karina (20 plants), and F2 genotype of Mawar x Karina (200 plants) which were divided into 4 blocks. The results show that the genetic diversity of the F2 population was highest in the characters of plant height, harvest age, fruit length and fruit diameter, with heritability values in the medium to high category

Keywords: F2 population, genetic diversity, tomato cross

A. Introduction

Tomato (*Lycopersicon esculentum* Mill) is a horticultural commodity whose fruit contains lots of vitamins C, A, K and minerals. Tomatoes are favored globally in the world, both consumed as processed foods and as fresh vegetables. This causes tomatoes to continue to develop into an

important commodity in international trade. As an agricultural country, Indonesia is ranked at 21st as a tomato producer in the world (Pusat Data dan Sistem Informasi Pertanian, 2014) with a harvested area of 54,780 hectares and total production in 2019 of 1,020,333 tons (KEMENTAN, 2021). Tomato cultivation in Indonesia is carried out by farmers in the lowlands to the highlands with varying areas. The large planting area and growing environment are good opportunities for tomato plant breeders to assemble superior varieties. Continuous increase in demand for tomatoes both in quantity and quality requires the availability of superior tomato varieties. The assembly of high-yielding tomato varieties can be done through plant breeding, including through artificial crosses (Hermanto R, Syukur M, Widodo, 2017).

Artificial crossing is the process of taking pollen from the male parent and placing it on the pistil of the female parent, each of which has its own advantages. The purpose of crosses is to produce offspring that combines superior characters. The success of the tomato plant breeding program is largely determined by the availability of various genetic sources of tomatoes and appropriate breeding methods. Exploration activities are one of the activities that can be carried out to provide genetic resources by utilizing local wisdom that exists in Indonesia (Sutjahjo, S.H., C. Herison, Sulastrini, Marwiyah, 2015).

Genetic diversity is the initial capital of plant breeding efforts, which is related to the assembly of varieties to improve yield in terms of fruit size, fruit quality and productivity by utilizing the heterotic phenomenon in the assembly of tomato varieties. This method is quite effective in increasing yields with high fruit quality and good nutritional content. The initial stage in determining the results of crosses between varieties is evaluating the general combining capacity (DGU) and special combining capacity (DGK). This information is needed to obtain a combination of parents that produces offspring that have the potential to have high yields and productivity (Sutjahjo et al., 2015)

According to Saputra, Helfi Eka Saputra, Dwi Wahyuni Ganefianti, Umi Salamah, Yenny Sariasih, Nico Dwi Ardiansyah (2019). the crossover method is a method of uniting each of the superior characters that exist in various genotypes in one genotype so as to produce an F2 population that can segregate maximally. Therefore, the estimation of genetic diversity, heritability, and the number of gene control groups of characters has been done extensively in this population. Analysis of this generation mean has been widely used to determine the type and magnitude of gene action involved in the inheritance of tomato characters. This can induce a superior diversity of tomato species and have a unique shape. However, in the process of observing data, the conventional method has a large bias if it is carried out with logs or lots of plants or fruit.

Therefore, technology in assisting the observation process is indispensable in minimizing observational bias. Genetic diversity and heritability are absolute requirements for the success of a plant breeding program. Genetic diversity can increase the possibility of getting a better genotype through selection. Character diversity and genotypic diversity are useful for knowing the pattern of grouping genotypes in certain populations based on the observed characters and can be used as the basis for selection activities (Agustina and Waluyo, 2017). Analysis of diversity can be done in various ways, namely using markers, one type of marker is morphology in plants. Heritability is a genetic parameter used to measure the ability of a genotype in a plant population to pass on its characters (Rachmadi, M., N. Hermiati, A. Baihaki, dan R. Setiamiharja, 1990). The indicator of the character is genetically controlled based on heritability values. Heritability estimates have functions including determining the success of selection, because they can provide clues that a trait is more influenced by genetic factors or environmental factors (Poehlman, J. M. and D.A. Sleeper, 1995).

Heritability is a genetic parameter used to measure the ability of a genotype in a plant population to pass on its characters. The heritability value has a function to determine the success of the selection, because it can provide an indication of a trait that is more influenced by genetic factors or environmental factors. Heritability values are expressed in fractions or percentages ranging from 0 to 1. The closer the value to 1, the higher the heritability value, on the other hand, the closer to the 0 value, the lower the heritability value (Syukur M, Sujiprihati S, Yuniaanti R., 2012).

A high heritability value indicates that genetic factors play a more important role in controlling a trait than environmental factors. Heritability determines the progress of selection, the greater the value of heritability, the greater the progress of selection, and vice versa. Selection characters must have high diversity and heritability, in order to obtain a target for selection progress (Lubis, K., S.H. Sutjahjo, M. Syukur, dan Trikoesoemaningtyas, 2014). According to Barmawi, M., A.

Yushardi, dan N. Sa'diyah (2013), genetic diversity and heritability are useful for predicting the genetic progress of selection.

Therefore, selection on the F2 population resulting from crossing black rice with white rice can give an indication of a high expected value of genetic progress, if the traits involved in the selection have high genetic diversity and heritability. Thus, selection is expected to result in high genetic advances for some of the desired agronomic characters. The purpose of this study was to determine the hope of genetic progress and the predictability of heritability (inheritance) of agronomic characters of the F2 generation of tomatoes from crosses with superior tomato varieties.

B. Methodology

This research was conducted at Experimental Farm, Hasanuddin University on April 2021. The materials used in this study were F2 tomato seeds from crosses (200 genotypes) and 4 comparison varieties, namely Black Cherry, Chung, Mawar, and Karina. The tools used in this research are shovel, hoe, scissors, meter, sieve, caliper, analytical balance, and camera.

1. Research Methods

The The research to evaluate the diversity of generations of biparental crosses was carried out with an augmented design, the genotypes used were 6 biparental generations consisting of P1 vegetable tomatoes (Mawar) 30 plants, P2 fruit tomatoes (Karina) 30 plants, F1 (Mawar x Karina) 25 plants, BCP1 (Mawar x Karina x Mawar) 20 plants, BCP2 (Mawar x Karina x Karina) 20 plants, and F2 (Mawar x Karina) 200 plants which was divided into 4 blocks.

Prior to planting, tomato seeds were sown using Rockwool for two weeks. Subsequently, seedlings were transferred to a 15x 20 cm small polybag for one month. Seedlings that grew well were transferred to the field with a plot size of 2x3 m and a spacing of 50 x50 cm. Fertilization using NPK, urea and SP36 were applied twice, ie 1 week after planting and 3 weeks after planting. Parameters observed were plant height, stem diameter, number of branches, harvest age, fruit fresh weight, fruit diameter, fruit length and fruit height.

2. Data Analysis

All observational data were analyzed by analysis of genetic parameters such as coefficients of genetic diversity, heritability, Skewness, and kurtosis (Singh and Chaudhary 2007; Syukur et al. 2012). Data analysis was performed using Microsoft Excel Software and SPSS v 22.

C. Result and Discussion

Based on the analysis in Table 1, the heritability values were analyzed based on the variance of all characters. There are 4 parameters having high heritability values, 2 parameters having medium heritability values, and 2 parameters having low heritability values. Meanwhile, the characters classified as having high heritability values were plant height (78.08%), stem length (64.37%), fruit height (62.83%), and fruit diameter (58.71%). The results of the analysis showed that the genetic diversity was wide for several characters in this population due to the different genetic backgrounds of the population and the selection would be directed at the characters of plant height, harvest age, stem diameter, stem length, fruit diameter, fruit height, fruit weight and number of branches. Understanding of the genetic background of the population is essential to initiate selection. One of the important components determining the success of a selection program in breeding is genetic diversity, so knowledge related to population genetic diversity is the main thing before starting the selection. According to Pinaria, A, A. Baihaki, R. Setiamihardja dan A.A. Daradjat. (1995), the genetic diversity of a population is influenced by the nature of the population, namely whether the population is a segregated generation from a cross, in what generation and how the genetic background is. In addition, the estimated value of heritability also needs to be known to predict the progress of a selection, whether it is influenced by genetics or the environment (Syukur M, Sujiprihati S, Siregar A., 2010).

Table 1. Results of the distribution of genetic variance values of tomato crosses

Characters	K	M	F1	F2	BCP1	BCP2	Heritability
TT	42.24	178.12	157.50	574.58	398.11	787.95	78.08
UP	6.09	76.90	252.30	143.00	134.11	611.01	21.84
DB	3.03	4.30	7.74	7.14	5.22	7.22	29.71
PB	82.08	17.67	35.40	126.42	27.35	24.88	64.37

DBU	98.99	26.83	37.97	132.23	15.95	27.43	58.71
TIB	63.21	27.27	40.09	117.10	26.16	17.81	62.83
JC	3.69	2.26	2.30	2.96	0.78	2.37	7.01
BB	153.88	48.01	31.72	64.70	45.67	60.86	0.00

Note: TT: Plant height, UP: Harvest age, DB: stem diameter, PB: fruit length, DBU: fruit diameter, TIB: fruit height, BB: fruit weight, JC: branch numbers

The estimated heritability values between parameters are presented in Table 1. A high heritability value indicates that there is a greater influence of genetic factors than environmental factors and has a great chance of being passed on to their offspring. According to Roy (2000), if the predictive value of heritability is high, the selection is carried out in the early generations because the selection progress will be large. On the other hand, if the heritability is low to moderate, the character needs to be fixed through selection. Genetic diversity and heritability are very useful in the selection process. This is in accordance with the opinion of Syukur (2010) which states that selection will be effective if the population has wide genetic diversity and high heritability. In addition to population variance information, the mean value of each genotype also plays a role in the effectiveness of selection in producing superior tomato varieties.

Table 2. The results of the significance value of the Skewness-Kurtosis Test

Characters	Median	Skewness	Kurtosis
TT	75.51	-0.04	-1.54
UP	120.04	-4.87	1.52
DB	8.57	2.01	4.38
PB	30.32	14.81	40.67
DBU	32.08	13.62	36.90
TIB	27.25	16.07	44.39
JC	4.87	2.67	-1.29
BB	17.63	3.29	0.32

Note: TT: Plant height, UP: Harvest age, DB: stem diameter, PB: fruit length, DBU: fruit diameter, TIB: fruit height, BB: fruit weight, JC: branch numbers.

Table 2 shows the mean population value and the results of the skewness and kurtosis analysis. Analysis of skewness and kurtosis is an approach to predict genetic control descriptively (Roy, 2000). The results of the observed population data distribution based on the data distribution curve on the character of plant height has a skewness of -0.04 and kurtosis -1.54, stem diameter has a skewness of 2.01 and a kurtosis of 4.38, the number of branches has a skewness of 2.67 and a kurtosis of -1.29 based on the value of skewness and kurtosis indicates that these characters are continuous and controlled by many genes. while the length of the fruit has a skewness of 14.81 and kurtosis of 40.67, the diameter of the fruit has a skewness of 13.62 and kurtosis of 36.90, the height of the fruit has a skewness of 16.67 and kurtosis of 44.39 and the weight of the fruit has a skewness of 3.29 and kurtosis of 0.32, indicating that the character is controlled by a few genes. Determination of the nature of the data and the number of genes that control it refers to Roy (2000) and Sihalo, A.N., Trikoesoemaningtyas, D. Sopandie, D. Wirnas. (2015), which state that the continuous distribution of data is a character controlled by many genes indicated by the kurtosis value of $-3 < \text{kurtosis} < 3$ (mesokurtic form), while characters controlled by a few genes are indicated by kurtosis values > 3 (leptokurtic form) or < -3 (platikurtic form).

The distribution of data that has a skewness value of zero indicates that the character is controlled by additive gene action, a positive skewness value indicates additive gene action has a complementary epistasis effect, while a negative skewness value indicates an additive gene control with a duplicate epistasis effect (Roy, 2000). Based on this, it can be said that the character of plant height is a character controlled by many genes with additive gene action with the effect of duplicate epistasis. Fruit diameter and fruit height are characters that are controlled by a few genes with additive gene action with complementary epistatic effects and harvest age characters are controlled by a few genes with additive gene action having duplicate epistasis effects.

D. Conclusion

High genetic diversity is an important aspect before selection. The genetic diversity of the F2 population was highest in the characters of plant height, harvest age, fruit length and fruit diameter, with heritability values in the medium to high category

E. References

- Agustina NI, Waluyo, B. (2017). Keragaman karakter morfo-agronomi Jurnal Agro 5(1), 2018 37 dan keanekaragaman galur- galur cabai besar (*Capsicum annum* L.). *Jurnal Agro*, 4(2), 120-130.
- Barmawi, M., A. Yushardi, dan N. Sa'diyah. (2013). Daya waris dan harapan kemajuan seleksi karakter agronomi kedelai Generasi F2 hasil persilangan antara Yellow bean dan Taichung. *J. Agrotek Tropika* 1(1):20-24.
- Hermanto R, Syukur M, Widodo. (2017). Pendugaan ragam genetik dan heritabilitas karakter hasil dan komponen hasil tomat (*Lycopersicum esculentum* Mill.) di dua lokasi. *J. Hort. Indonesia* 8(1): 31-38.
- KEMENTAN (2021). Produksi tomat menurut provinsi, tahun 2015-2019. Available at: <https://www.pertanian.go.id/home/index.php?show=repo&fileNum=318>. [15/11/2021].
- Lubis, K., S.H. Sutjahjo, M. Syukur, dan Trikoesoemaningtyas. (2014). Pendugaan parameter genetik dan seleksi karakter morfofisiologi galur jagung introduksi di lingkungan tanah masam. *J. Penelitian Pertanian Tanaman Pangan* 33(2): 122- 128.
- Pinaria, A, A. Baihaki, R. Setiamihardja dan A.A. Daradjat. (1995). Variabilitas genetic dan heritabilitas karakter-karakter biomassa 53 genotipe kedelai. *Zuriat* 6(2):88-92.
- Poehlman, J. M. and D.A. Sleeper. (1995). *Breeding Field Crops (Second Edition)*. Iowa State University Press. USA.
- Pusat Data dan Sistem Informasi Pertanian. (2014). Outlook komoditi tomat. Available at: <http://pusdatin.setjen.pertanian.go.id/tin ymcpuk/gambar/file/tomat2014.pdf>.
- Rachmadi, M., N. Hermiati, A. Baihaki, dan R. Setiamiharja. (1990). Variasi genetik dan heritabilitas komponen hasil dan hasil galur harapan kedelai. *Zuriat* 1(1):48-51.
- Roy, D. (2000). *Plant Breeding, Analysis and Exploitation of Variation*. Narosa Publishing House. New Delhi.
- Saputra, Helfi Eka Saputra, Dwi Wahyuni Ganefianti, Umi Salamah, Yenny Sariasih, Nico Dwi Ardiansyah. (2019). Estimasi Ragam Jumlah Kelompok Gen Pengendali Karakter dan Heritabilitas Tomat di Dataran Rendah. *J. Hort. Vol. 2, No. 10*.
- Sihaloho, A.N., Trikoesoemaningtyas, D. Sopandie, D. Wirnas. (2015). Identifikasi aksi gen epistasis pada toleransi kedelai terhadap cekaman aluminium. *J. Agron. Indonesia*. 43(1): 30-35.
- Singh, R.K., B.D. Chaudhary. (2007). *Biometrical Methods in Quantitative Genetic Analysis*. Reprinted. Kalyani Publisher, New Delhi, INA.
- Sutjahjo, S.H., C. Herison, Sulastrini, Marwiyah. (2015). Pendugaan keragaman genetik beberapa karakter pertumbuhan dan hasil pada 30 genotipe tomat lokal. *J. Hort.* 25(4): 304-310.
- Syukur M, Sujiprihati S, Siregar A. (2010). Pendugaan parameter genetik beberapa karakter agronomi cabai F4 dan evaluasi daya hasilnya menggunakan rancangan perbesaran (augmented design). *Jurnal Agrotropika*. 15 (1): 9-16.
- Syukur M, Sujiprihati S, Yuniaanti R. (2012). *Teknik Pemuliaan Tanaman*. Cet.1. Jakarta (ID): Penebar Swadaya.Thompson HC, WC Kelly. 1957. Veg.