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GENETIC PARAMETERS AND SELECTION INDEX OF HIGH-YIELDING TOMATO F_2 POPULATIONS

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SUMMARY

Despite the increasing consumption of tomato (*Solanum lycopersicum* Mill.) in Indonesia, its yield capacity is lower than its demand. However, establishing high-yielding tomato varieties can overcome this. Strain in F_2 populations is the first step in assembling high-yielding tomato genotypes through systematic selection, one through using a selection index. The latest study aimed to identify the genetic diversity and the effectiveness of the selection index for high-yielding F_2 tomato population selection. The research took place from September to December 2021 at the Faculty of Agriculture Experimental Field, Hasanuddin University, Makassar, South Sulawesi, Indonesia. The study used an augmented design consisting of four blocks with complete randomization. Nine experimental units were used in this study, consisting of three F_2 lines plotted into four blocks with no repetition and three cultivars that repeated in each block as genotype check. The study of 15 growth parameters used analysis of variance, correlation, and path analysis. Results revealed that the selection index proved efficient in selecting the F_2 generation of tomato strain populations. Almost all the characters have the highest genetic diversity and showed potential for selection criteria usage. The total number of fruits (0.52), fruit diameter (0.32), and fruit weight (0.29) showed a direct influence on yield, and can serve as selection criteria for yield. The selection criteria were formulated into a selection index, producing 75 tomato strains potentially suitable as families in the F_3 generation.

Keywords: correlation, genetic parameters, path analysis, selection criteria, selection index tomato (*Solanum lycopersicum* Mill.)

Key findings: Lines selection in F_2 generation is critical in cultivar development, including the tomato (*Solanum lycopersicum* Mill.) crop. The study comprised the selection of promising tomato lines in F_2 and consecutively in the F_3 generation. The combination of several parameters to form a selection index on yield helped increase the effectiveness of selection. The selection index indicated 75 potential tomato lines for development in the F_3 generation.

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INTRODUCTION

Tomato (*Solanum lycopersicum* Mill.) is one of the leading horticultural commodities in Indonesia with economic and strategic values. This widely consumed plant is rich in nutrients and secondary metabolites that are essential for health, especially vitamins A and C and other important minerals (Wahyuni *et al*., 2014). Moreover, the high antioxidant content, known as lycopene, containing about 30–200 mg kg^{-1} of fresh fruit, is an added value of this fruit (Hasri, 2015).

Indonesia's tomato yield increased in the last three years, from 976,790 t (2018) to 1,020,333 t (2019) and 1,084,993 t (2020) (BPS, 2021). However, the tomato yield rate lags far below its yield potential (Wasonowati, 2010). Inappropriate cultivation techniques, pest and disease management, and the use of inappropriate cultivars revealed the major factors affecting yield. Therefore, these problems need progressive addressing, one of them by assembling superior tomato cultivars through plant breeding.

Plant breeding is essential in assembling high-yielding genotypes and increasing crop yield (Jambormias and Riry, 2009; Syukur *et al*., 2012). However, this concept anchors firmly on the broader genetic diversity of the existing populations. The more diverse population helps increase the selection effectiveness to achieve the plant breeding goals (Sa'diyah *et al*., 2009, 2013). Crossing the genotypes with distinct genetic backgrounds can attain increased genetic diversity. Farid *et al*. (2022) performed half-diallel crosses in genetically different tomato genotypes, resulting in suggested potential hybrids, i.e., Karina/Black Cherry, Karina/Mawar, and Mawar/Chung, with high yield and lycopene content, for further use in breeding programs. Their results revealed that these hybrids require future study in the F_2 generation to develop improved tomato cultivars with a higher yield.

Considering the F_2 generation has the highest level of genetic diversity hence, selection in this generation becomes crucial in assembling improved genotypes (Jameela *et al*., 2014). However, in the F_2 populations, the selection criteria used primarily determines the effectiveness of selection (Kristamtini *et al*., 2016). If the environment influences the selection criteria more, then the resulting genotype is considered too far from the potential cultivar, with an extended straining process (Wati *et al*., 2020). Hence, the selection criteria must have high heritability and direct gene action (Yudilastari *et al*., 2018) and relatively few genes (Phillips, 2008). The selection process needs to include several yield components to enhance the accuracy and stability of selection, especially if the yield as the main character is the basis of selection (Pramana *et al*., 2013). Furthermore, these supporting characters must have a strong association with a yield so that the estimation of the selection criteria for supporting yield is carried out systematically (Wirnas *et al*., 2006). Therefore, using several selection criteria with high genetic diversity to select F_2 populations in tomatoes needs implication, with the selection index as an important selection method to collectively use several yield contributing characters as selection criteria.

The selection index is a multiple linear regression equation that collects several selection criteria (Jambormias *et al*., 2014a). The concept of this index can be combined with character weighting, which is the priority value of the selection criteria (Amzeri *et al*., 2020). First, each selection criteria requires standardizing to equalize the degree among the characters, with the standardization estimates serving as the basis for producing index values for each line (Wening *et al*., 2018). This concept has shown effectiveness in the simultaneous selection of several characters. Several studies have reported the benefits of using the selection index in various crops (Sudika and Soemeinaboedhy, 2020; Harahap *et al*., 2019), including tomatoes (Okiarlis *et al*., 2016; Farid *et al*., 2022). Therefore, a selection index in the tomato F_2 populations approach proved applicable. The recent study aimed to determine the genetic diversity and the effectiveness of the selection index in selecting F_2 populations with higher yields in tomatoes.

MATERIALS AND METHODS

Genetic material and procedure

The research took place from September to December 2021 at the Faculty of Agriculture Experimental Field, Hasanuddin University, Makassar, South Sulawesi, Indonesia (5°07'40.1"S 119°28'52.2"E). The experiment proceeded in the augmented design with complete randomization as the environmental design. The augmented design continued in a population with a limited number of seeds and consisted of four blocks. Three F_2 tomato strains (Karina × Mawar, Mawar × Chung, and

Karina × Black Cherry) were used, with no repetition of each line in any block. For comparison purposes, three standard tomato cultivars, i.e., Karina, Mawar, and Chung, served as check genotypes. The parental cultivars also served as check genotypes with their F_2 populations and repeated in each block. Therefore, the use of nine experimental units ensued.

Planting seeds of F_2 tomato populations proceeded in the roasted husk and compost manure (1:1). The seeding took place in a greenhouse, afterward, Transfer of seedlings into polybags 14 days after sowing (DAS) occurred. Tomato seedlings received the AB mix solution (5 ml L^{-1}) at seven DAS. Two to three weeks after transplanting (WAP), planting seedlings followed on a soil bed size of 0.8 m × 7.5 m each, with a distance of 20 cm between beds. Following planting, the beds with plastic mulch attained holes 10 cm in diameter, with spacing at 40 cm × 80 cm. Thus, 18 plants per bed resulted.

Tomato crop maintenance consists of several activities, including watering twice daily until the soil looks moist. Replanting occurred at one WAP to replace abnormal and wilt seedlings. The replacement used the same age and genetic material. The first fertilization began at seven DAP once a week, using NPK Mutiara fertilizer at the rate of 10 g L^{-1} in the form of a solution applied around the plant roots. The leaf fertilizer application during vegetative and generative growth stages used Gandasil D and Gandasil B, respectively. Pruning proceeded by removing small shoots on the lower stem at least once a week. Weeding took place manually using a hoe and by applying herbicide (Gramoxone 2 g L^{-1} water). Pests and disease control also transpired once a week by spraying the insecticide Curacron 500 EC 2 cc L^{-1} and Lantracol fungicide g L^{-1}. Harvesting took two times a week on reddish yellow tomatoes that met the ready-to-harvest criteria, which continued for eight weeks.

Data analysis

Data recording through field observations proceeded in each experimental plot. Characters observed in this study included plant height, dichotomous height, stem diameter, flowering age, harvest age, number of bunch flowers, number of fruit bunches, total fruit number, fruit length, fruit diameter, fruit weight, number of cavities, Brix content, number of seed fruit, and yield total. The recorded data for the entire characters underwent analysis of variance (ANOVA) based on augmented design. Heritability predicted using ANOVA estimates basic. The determination of selection criteria progressed systematically through correlation and path analysis. Characters that were significantly different based on ANOVA and having a significant correlation with yield further continued evaluation using path analysis. The path analysis result becomes the basis of the best selection criteria determination. The action and detection of the number of genes used skewness (Zs) and kurtosis (Zk) analysis. Then, the path analysis estimates served as the basis for creating a selection index. The selection index ensued using the concept of Alsabah *et al*. (2019).

RESULTS

The results showed that the characters were significantly influenced by genotypes, check cultivars and their interactions, plant height, stem diameter, flowering age, harvest age, number of bunches, total fruit count, fruit length, fruit diameter, fruit weight, number of cavities, Brix content, number of seeds per fruit, and yield (Table 1). Meanwhile, the check cultivar and genotype and check cultivar interactions affected the number of bunch flowers relevantly, whereas the genotype and interaction between genotype and check cultivar impacted dichotomous height significantly. Based on the heritability values, all observed characters showed high heritability values, i.e., plant height (92.51), dichotomous height (91.01), stem diameter (91.75), flowering age (82.40), harvest age (83.81), number of bunches (99.03), fruit length (85.03), fruit diameter (93.14), fruit weight (98.61), number of cavities (91.50), Brix content (94.55), number of seeds per fruit (90.41), and yield (99.65). The total number of fruit characters (99.75) showed the highest heritability value. On the other hand, the number of bunch flowers (72.99) revealed the lowest one.

According to correlation analysis, yield-tomato yield showed a significant ($P \leq 0.05$) positive correlation with some characters, i.e., plant height (0.43), dichotomous height (0.23), stem diameter (0.25), number of flower bunches (0.20), number of fruit bunches (0.17), total fruit number (0.46), fruit length (0.20), fruit diameter (0.53), fruit weight (0.42), and number of cavities (0.21) (Table 2). Meanwhile, flowering age (-0.24) and

Table 1. Mean squares and heritability values for various characters in tomato.

Characters	Lines (L)	Check (C)	L vs C	CV	Vg	Vp	H^2
PH	1078.15**	969.22**	1579.98**	7.42	249.34	269.54	92.51
DH	119.43**	2.36ns	326.57**	8.87	27.17	29.863	91.01
DR	5.6519**	4.31*	26.50**	6.94	1.30	1.41	91.75
FD	9.75*	33.84**	11.19*	2.37	2.01	2.44	82.40
HD	10.08*	43.34**	16.90*	1.42	2.11	2.52	83.81
NF	0.72ns	18.02**	49.55**	10.54	0.13	0.18	72.99
NB	178.17**	2154.04**	444.36**	7.50	44.11	44.54	99.03
NFT	18854.20**	68377.80**	16100.40**	7.11	4701.60	4713.54	99.75
FL	13.69*	74.44**	415.36**	5.17	2.91	3.42	85.03
FD	40.06**	308.87**	18.17*	6.76	9.33	10.02	93.14
FW	86.82**	162.60**	69.90**	8.26	21.40	21.71	98.61
NC	3.49**	25.40**	1.93*	12.43	0.80	0.87	91.50
BR	3.30**	14.22**	73.82**	5.99	0.78	0.82	94.55
NS	1004.30**	12568.10**	127512**	19.95	226.99	251.08	90.41
PROD	41089.40**	9497.61**	14789.60**	6.10	10235.88	10272.35	99.65

Notes: ns: not significant, **; significant at α= 1%, *; significant at α= 5%; CV: Coefficient of variance; PH: plant height; DH: dichotomous height; DR: diameter of the rod; FD: flowering days; HD: harvest day; NF: number of flowers; NB: number of the bunch; NFT: number of fruit total; FL: fruit length; FD: fruit diameter; FW: fruit weight; NC: number of cavities; BR: Brix rate; NS: number of seeds; PROD: yield.

harvesting age (-0.24) had a significant ($P \leq 0.05$) negative correlation with yield. The path analysis showed a determination value of 0.403 for the model (Table 3). Total fruit number (0.52), fruit diameter (0.32), and fruit weight (0.29) had a significant positive direct effect on total yield. Meanwhile, plant height (0.12), dichotomous height (0.12), stem diameter (-0.03), flowering age (-0.03), harvest age (-0.02), number of bunch flowers (0.04), number of bunches (0.05), length of fruit (0.03) and the number of cavities (-0.07) did not have a significant direct effect on yield.

The image-based normality analysis revealed that fruit diameter had a relatively normal distribution (Figure 1). Populations among the three crosses (Karina × Black Cherry, Mawar × Chung, and Karina × Mawar) also had the same model and peak point for fruit diameter. However, total fruit number, weight, and yield characters have tended to skew to the right. Based on skewness and kurtosis, the total number of fruit (Zs = 18.86 and Zk = 40,526), fruit weight (Zs= 2.674 and Zk = -0.018), and yield (Zs = 11,517 and Zk = 16,874) revealed the highest Zs and Zk values (Table 4). The character fruit diameter has attained low Zs and Zk values, although the Zk value was insignificant.

The selection index values based on path analysis appear in Table 5. The selection index resulted from a combination of four parameters, i.e., yield, fruit diameter, fruit weight, and total fruit number. The selection index estimates showed that 75 tomato lines had positive index values. In addition, these lines had a better index compared with cultivars Karina, Chung, and Mawar. Based on the 75 tomato lines, six lines resulted from the cross combination of Karina × Black Cherry, 36 from Karina × Mawar, and 33 lines from Mawar × Chung.

DISCUSSION

Increasing plant breeding efficiency results from emphasizing genetic diversity, heritability, the correlation between characters, path analysis, and the number and action of genes that control a character at each implementation stage (Nzuve *et al*., 2014; Barmawi, 2007). The variance analysis results indicated a high diversity in the tomato F2 population for almost all characters. They strengthened the high heritability values for all growth and development characters. Both analyses align with Jambormias *et al*. (2014b); significant diversity and high heritability indicate better inheritance of the quantitative characters and opportunities for effective selection in the next generation. The instability of genotype performance to environmental change has the potential to become a limiter in the selection process (Navabi *et al*., 2006). The interaction between genotype and control can indicate the instability of the appearance of a cultivar in various environments (Dhillion *et al*., 2009; Dev *et al*., 2009). In general, significant variance is the initial basis for determining the effectiveness of a character selection character (Sabouri *et al*., 2008; Anshori *et al*., 2022; Litrico and Violle, 2015; Priyanto *et al*., 2018). Therefore, the source of

Table 2. Pearson correlation for selected characters of yield.

Characters	DH	DR	FD	HD	NF	NB	NFT	FL	FD	FW	NC	BR	NS	PROD
PH	0.27**	0.41**	-0.14*	-0.17*	0.17*	0.04ns	0.17*	0.22**	0.34**	0.22**	0.21**	0.26**	0.03ns	0.43**
DH		0.07ns	0.00ns	0.01ns	0.06ns	-0.07ns	0.07ns	0.13ns	0.06ns	0.06ns	-0.03ns	0.09ns	-0.06ns	0.23**
DR			0.03ns	-0.01ns	0.04ns	0.24**	0.39**	-0.05ns	0.09ns	-0.06ns	0.14ns	0.05ns	-0.02ns	0.25**
FD				0.95**	-0.23**	0.03ns	-0.04ns	-0.01ns	-0.28**	-0.16*	-0.15*	-0.12ns	-0.13ns	-0.24**
HD					-0.26**	0.03ns	-0.04ns	0.01ns	-0.27**	-0.16*	-0.12ns	-0.12ns	-0.13ns	-0.24**
NF						0.03ns	0.12ns	-0.05ns	0.14*	0.02ns	-0.07ns	0.12ns	0.29**	0.20**
NB							0.58**	-0.37**	-0.24*	-0.30**	-0.22**	-0.07ns	-0.06ns	0.17*
NFT								-0.25**	-0.10ns	-0.25**	-0.19*	-0.06ns	-0.10ns	0.46**
FL									0.40**	0.44**	0.15*	0.00ns	-0.18*	0.20*
FD										0.65**	0.61**	0.33**	0.09ns	0.53**
FW											0.45**	0.14*	0.19*	0.42**
NC												0.26**	0.18*	0.21**
BR													-0.09ns	0.13ns
NS														0.06ns
PROD														

Notes: ns: not significant, **; significant at α= 1%, *; significant at α= 5%; PH: plant height; DH: dichotomous height; DR: diameter of the rod; FD: flowering days; HD: harvest day; NF: number of flowers; NB: number of the bunch; NFT: number of fruit total; FL: fruit length; FD: fruit diameter; FW: fruit weight; NC: number of cavities; BR: Brix rate; NS: number of seeds; PROD: yield.

Table 3. Path analysis for tomato yield per plant based on the characters with the highest correlation with fruit yield.

Characters	PH	DH	DR	FD	HD	NF	NB	NFT	FL	FD	FW	NC	Correlation
PH	0.12	0.03	-0.01	0.00	0.00	0.01	0.00	0.09	0.01	0.11	0.06	-0.01	0.43**
DH	0.03	0.12	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.02	0.02	0.00	0.23**
DR	0.05	0.01	-0.03	0.00	0.00	0.00	0.01	0.2	0.00	0.03	-0.02	-0.01	0.25**
FD	-0.02	0.00	0.00	-0.03	-0.02	-0.01	0.00	-0.02	0.00	-0.09	-0.05	0.01	-0.24**
HD	-0.02	0.00	0.00	-0.03	-0.02	-0.01	0.00	-0.02	0.00	-0.09	-0.05	0.01	-0.24**
NF	0.02	0.01	0.00	0.01	0.01	0.04	0.00	0.06	0.00	0.04	0.01	0.00	0.20**
NB	0.01	-0.01	-0.01	0.00	0.00	0.00	0.05	0.30	-0.01	-0.08	-0.09	0.01	0.17*
NFT	0.02	0.01	-0.01	0.00	0.00	0.00	0.03	0.52**	-0.01	-0.03	-0.07	0.01	0.46**
FL	0.03	0.02	0.00	0.00	0.00	0.00	-0.02	-0.13	0.03	0.13	0.13	-0.01	0.20*
FD	0.04	0.01	0.00	0.01	0.01	0.00	-0.01	-0.05	0.01	0.32**	0.19	-0.04	0.53**
FW	0.03	0.01	0.00	0.01	0.00	0.00	-0.02	-0.13	0.02	0.21	0.29**	-0.03	0.42**
NC	0.03	0.00	0.00	0.01	0.00	0.00	-0.01	-0.1	0.01	0.2	0.13	-0.07	0.21**

Notes: numbers in bold indicate a direct effect, cross-print R2: 40.34, Res: Residual, PH: plant height, DH: dichotomous height, DR: diameter of the rod, FD: flowering days, HD: harvest day, NF: number of flowers, NB: number of the bunch, NFT: number of fruit total, FL: fruit length, FD: fruit diameter, FW: fruit weight, NC: number of cavities.

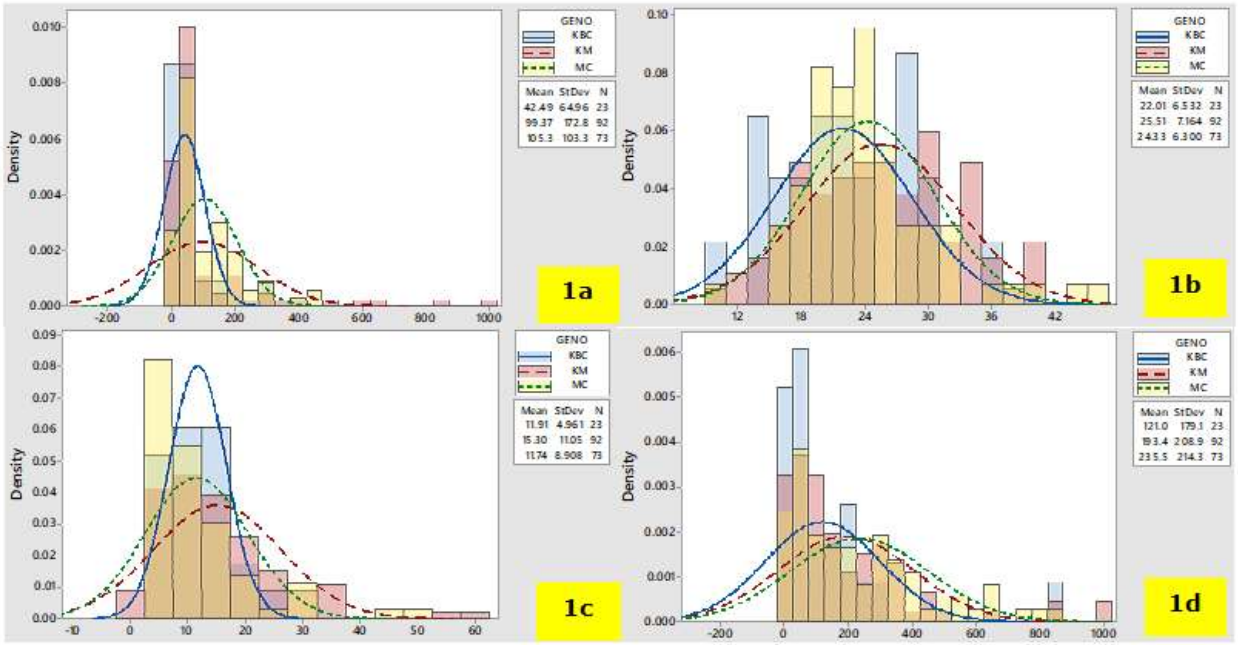

Figure 1. Distribution curve for the number of fruit total (NFT), b) distribution curve for fruit diameter (FD), c) distribution curve for fruit weight (FW), and d) distribution curve for yield.

Table 4. Estimation of gene action and gene number.

Variable	Skewness	Kurtosis	Zs	Zk	Gene Action	Gene Number
NFT	3.244	13.86	18.860**	40.526**	Additive, complementary epistasis	Few
FD	0.46	-0.0006	2.674**	-0.018ns	Additive, complementary epistasis	Many
FW	1.981	5.771	11.517**	16.874**	Additive, complementary epistasis	Few
PROD	1.769	3.402	10.285**	9.947**	Additive, complementary epistasis	Few

Notes: ns: not significant, **: significant at α= 1%, *: significant at α= 5%; NFT: number of fruit total; FD: fruit diameter; FW: fruit weight; PROD: yield; Zs = skewness standardization; Zk= kurtosis standardization; Kurtosis>3: a few genes; Kurtosis<3: many genes.

Table 5. Selection index based on the path analysis.

Genotype	Actual Value				Standardization				Selection Index
	PROD	NFT	FD	FW	PROD	NFT	FD	FW	
KM14	1016.30	161.30	38.10	31.50	3.93	0.47	1.98	1.86	4.76
KM9	1009.08	199.50	33.68	25.28	3.90	0.75	1.33	1.22	4.54
MC13	805.23	77.20	43.92	52.16	2.91	-0.13	2.84	3.98	4.08
KM8	863.54	172.30	34.64	25.05	3.19	0.55	1.47	1.19	3.83
KM29	831.16	186.30	33.42	22.31	3.04	0.65	1.29	0.91	3.62
MC33	847.04	440.80	24.76	9.61	3.12	2.49	0.02	-0.40	3.60
KBC8	848.12	300.50	27.46	14.11	3.12	1.48	0.42	0.07	3.55
MC11	656.97	74.20	46.46	44.24	2.20	-0.15	3.21	3.17	3.37
MC48	753.55	187.70	30.02	16.06	2.67	0.66	0.80	0.27	3.04
MC50	625.34	113.30	38.84	27.60	2.05	0.13	2.09	1.45	2.78
KM69	626.22	110.40	36.28	28.36	2.05	0.11	1.71	1.53	2.70
MC34	663.93	277.70	27.68	11.96	2.23	1.31	0.45	-0.15	2.61
MC17	602.08	164.50	32.10	18.30	1.94	0.50	1.10	0.50	2.38
KM53	443.06	858.60	27.02	2.58	1.17	5.49	0.36	-1.12	2.28
MC28	530.82	402.30	24.20	6.60	1.59	2.21	-0.06	-0.71	1.96
MC10	524.83	147.20	30.10	17.83	1.56	0.37	0.81	0.45	1.90
MC18	535.71	183.50	25.82	14.60	1.62	0.63	0.18	0.12	1.81
KM5	457.12	115.10	32.52	19.85	1.24	0.14	1.16	0.66	1.64
KM15	427.36	657.50	19.63	3.25	1.09	4.05	-0.73	-1.05	1.63

Table 5. (cont'd)

Genotype	Actual Value				Standardization				Selection Index
	PROD	NFT	FD	FW	PROD	NFT	FD	FW	
MC8	480.79	185.70	28.00	12.94	1.35	0.65	0.50	-0.05	1.61
MC14	376.71	61.70	40.60	30.51	0.85	-0.24	2.35	1.75	1.61
KM6	368.71	56.00	39.44	32.90	0.81	-0.28	2.18	2.00	1.55
KM13	360.68	51.90	39.42	34.73	0.77	-0.31	2.18	2.19	1.52
KM85	381.28	66.10	36.80	28.85	0.87	-0.21	1.79	1.58	1.47
KM25	354.65	56.70	39.36	31.27	0.74	-0.28	2.17	1.83	1.46
KM21	337.26	50.20	40.18	33.62	0.66	-0.32	2.29	2.07	1.42
KM65	484.52	35.50	27.24	13.93	1.37	-0.43	0.39	0.05	1.38
MC32	433.72	295.90	23.46	7.33	1.12	1.44	-0.17	-0.63	1.31
MC27	417.37	154.60	29.04	13.50	1.05	0.43	0.65	0.00	1.30
MC42	409.34	464.30	18.98	4.41	1.01	2.65	-0.82	-0.93	1.24
KM30	347.44	49.50	32.98	35.11	0.71	-0.33	1.23	2.23	1.22
KM82	310.20	25.00	26.52	62.04	0.53	-0.51	0.28	5.00	1.08
KM86	319.04	59.70	34.74	26.71	0.57	-0.26	1.49	1.36	1.06
KM63	246.85	975.30	15.14	2.48	0.22	6.33	-1.39	-1.13	1.06
MC9	361.16	127.50	28.12	14.17	0.78	0.23	0.52	0.07	0.97
KM35	314.87	66.00	33.38	23.86	0.55	-0.21	1.29	1.07	0.97
MC67	376.60	238.00	23.44	7.91	0.85	1.03	-0.17	-0.57	0.95
MC38	372.96	283.60	22.40	6.58	0.83	1.35	-0.32	-0.71	0.95
KM80	298.20	26.30	25.92	56.64	0.47	-0.50	0.19	4.44	0.94
KM71	307.99	602.00	18.89	2.56	0.52	3.65	-0.84	-1.12	0.94
KM32	297.78	63.60	33.68	23.40	0.47	-0.23	1.33	1.02	0.89
MC29	351.67	139.30	27.16	12.62	0.73	0.32	0.38	-0.09	0.88
KM73	365.40	221.90	22.68	8.23	0.80	0.91	-0.28	-0.54	0.85
KM10	272.65	58.60	35.56	23.27	0.35	-0.26	1.61	1.01	0.83
MC55	347.75	205.60	23.50	8.46	0.71	0.79	-0.16	-0.51	0.78
KM68	271.30	74.90	33.78	18.10	0.34	-0.15	1.35	0.48	0.71
MC12	367.89	53.60	21.24	20.59	0.81	-0.30	-0.49	0.73	0.70
MC19	278.19	73.80	32.16	18.85	0.38	-0.16	1.11	0.55	0.69
MC15	312.95	158.10	26.32	9.90	0.54	0.45	0.25	-0.37	0.66
KBC16	241.99	66.40	35.82	18.21	0.20	-0.21	1.65	0.49	0.64
KBC7	286.93	132.30	28.60	10.84	0.42	0.27	0.59	-0.27	0.59
MC7	304.37	152.30	25.62	9.99	0.50	0.41	0.15	-0.36	0.58
KM84	293.77	399.30	18.20	2.94	0.45	2.19	-0.94	-1.08	0.54
MC35	288.82	126.70	26.96	11.40	0.43	0.23	0.35	-0.21	0.54
MC30	302.46	264.00	20.00	5.73	0.49	1.21	-0.67	-0.79	0.48
MC68	278.95	47.50	23.82	29.39	0.38	-0.34	-0.11	1.64	0.47
KM3	233.93	47.40	30.70	24.66	0.16	-0.35	0.90	1.15	0.46
KM89	293.92	184.40	21.72	7.97	0.45	0.64	-0.42	-0.56	0.41
KM62	227.90	61.20	30.48	18.63	0.13	-0.25	0.86	0.53	0.37
MC31	274.62	215.50	21.82	6.37	0.36	0.86	-0.41	-0.73	0.35
MC71	295.88	178.50	19.00	8.29	0.46	0.60	-0.82	-0.53	0.31
KM36	197.55	44.30	32.36	22.31	-0.01	-0.37	1.14	0.91	0.31
KM70	237.40	77.80	27.84	15.25	0.18	-0.13	0.48	0.18	0.30
MC51	236.36	150.00	23.48	7.88	0.17	0.39	-0.16	-0.57	0.15
KM91	152.25	34.10	33.76	22.35	-0.23	-0.44	1.34	0.91	0.13
KBC1	181.88	54.20	30.86	16.77	-0.09	-0.30	0.92	0.34	0.13
KM24	233.30	325.30	17.20	3.59	0.16	1.65	-1.09	-1.02	0.11
MC26	225.29	130.40	24.34	8.64	0.12	0.25	-0.04	-0.50	0.11
MC46	161.10	41.20	32.52	19.54	-0.19	-0.39	1.16	0.63	0.10
KM1	159.64	40.90	31.48	19.50	-0.20	-0.39	1.01	0.62	0.06
KBC9	163.86	47.50	30.86	17.25	-0.18	-0.34	0.92	0.39	0.04
KBC21	186.43	89.40	28.42	10.43	-0.07	-0.04	0.56	-0.31	0.03
KM31	219.88	105.70	23.22	10.41	0.09	0.07	-0.20	-0.31	0.02
KM26	166.39	49.80	29.96	16.72	-0.16	-0.33	0.79	0.34	0.01
MC16	195.90	44.80	26.12	17.48	-0.02	-0.36	0.22	0.41	0.01
KARINA	106.91	93.57	21.80	13.48	-0.45	-0.01	-0.41	0.00	-0.56
MAWAR	152.75	30.23	32.08	14.73	-0.23	-0.47	1.10	0.13	-0.03
CHUNG	204.31	281.61	14.59	3.12	0.02	1.34	-1.47	-1.06	-0.20

Note: NFT: number of fruit total, FD: fruit diameter, FW: fruit weight, PROD: yield.

diversity is an essential requirement for line selection in augmented design. However, these findings also require association with the concept of heritability. The heritability value is high (>50%) due to low environmental or genetic diversity (Sutarman, 2013; Mangoendidjojo, 2012). High heritability values indicate a greater genetic influence than environmental factors and the selection to be more effective (Sami *et al*., 2013; Syukur *et al*., 2015).

The selection process for these three populations considerably showed adequate based on the analysis of variance and heritability. However, the use of all characters in the selection reduces selection effectiveness, so the yield characters and yield supporting characters have to align with the objectives of the breeding program as effective selection criteria (Sabouri *et al*., 2008; Mustafa *et al*., 2019; Anshori *et al*., 2021; Fadli *et al*., 2022; Farid *et al*., 2022). Determining the character as a selection criterion can be seen from the magnitude of the direct influence on the main character (Lelang, 2017). Selection criteria can be determined based on correlation and path analysis, with that concept also reported by Sabouri *et al*. (2008), Khapte and Jansirani (2014), Kumar *et al*. (2014), Mustafa *et al*. (2019), and Akbar *et al*. (2021).

In general, correlation shows a close relationship between two variables (As'ari, 2014). However, a significant correlation only shows a close relationship between characters but does not show a causal relationship. Hence, the use of path analysis can determine causal relationships and sort out the direct and indirect effects (Li, 1956; Singh and Chaudary, 2010; Kumar *et al*., 2014; Anshori *et al*., 2021; Gani *et al*., 1995), as well as, calculate the characters that contributed significantly to the increase in yield (Abdulkhaleq and Tawfiq, 2014). Still, the direct use of path analysis on many characters becomes inefficient, and it needs filtering with a significant correlation analysis on yield as the main character (Anshori *et al*., 2021, 2022). Both analyses showed that character, total fruit number, diameter, and weight directly influence yield. Reports of these results also came from Islam *et al*. (2015), Kumar *et al*. (2014), Ritonga *et al*. (2018), Mustafa *et al*. (2019), Alam *et al*. (2004), and Maurya *et al*. (2013). Therefore, these three characters can serve as selection criteria, with yield, with further in-depth analysis by the number and gene action approach.

Relatively quantitative characters are polygenic, hence, the genetic and environmental factors influence the phenotypic pattern of a character (Oktaviani *et al*., 2018). If each gene is independent, then the character is only influenced by environmental diversity. However, if the gene forms a dominant gene action pattern, the phenotype pattern is more dominated by the number of genes and their gene action (Napitupulu and Damanhuri, 2018). Testing the value of stickiness (skewness) and tapering (kurtosis) analyzes the number and action of genes.

If the skewness and kurtosis tests are not significantly different from 0, then the distribution is normal (Sayurandi and Woelan, 2016). The normal distribution in gene action is additive, and the additive character showed the independent nature of alleles passed down from generation to generation (Yudilastari *et al*., 2018). However, if the skewness test shows a significant z-test, then the population has additional action, namely, complementary epistasis (Zs is positive) and duplication epistasis (Zs is negative) (Roy, 2000; Rahayu *et al*., 2018). Epistasis is a complementary meaning that the genes at different loci control the character that interacts to produce a certain phenotype, where genes from one locus can mask the action of genes at other loci (Sobir and Syukur, 2015). No absolute inheritance of the epistasis appears because it occurs when an interaction between alleles at different loci happens (Sayurandi and Woelan, 2016). The presence of epistasis indicates that there are several unstable phenotypes to be passed on to the next generation so that selection becomes less effective (Sulistyowati *et al*., 2015).

Meanwhile, determining the number of genes involved employed kurtosis analysis. A kurtosis value (Zk) >3 indicates that the character has a *leptokurtic* and is controlled by a few genes. On the other hand, Zk <3 shows the character has a *platykurtic* and is controlled by many genes (Rahayu *et al*., 2018). The greater the number of genes get involved, the more complex the interaction of genes that control the characters (Fitriani *et al*., 2013). Based on the study results, the fruit diameter became more stable for selection, with a higher level of genetic diversity. Therefore, the line selection will prioritize the character of fruit diameter over the number of fruits and fruit weight. However, the priority value will not exceed the yield character priority as the main character in the selection index.

The selection index proceeds simultaneously using selected characters based on genetic parameters and their close

relationship with the main characters so that they can be compiled into an effective selection index (Wricke and Weber, 1985). The selection index development focuses on the selection criteria and the weighting of each selection criterion. In this study, setting the selection criteria used a systematic concept to determine the weight of each criterion. Several methods developed for the selection index include both subjective (Hidayatullah *et al*., 2018), objective (Anshori *et al*., 2021, 2022; Farid *et al*., 2021, 2022), and semi-objective (Sabouri *et al*., 2008; Alsabah *et al*., 2019). This study considered semi-subjective weighting as a good choice. It is due to the differences in the gene action among the selection criteria used while still prioritizing the character of the yield. This concept was also used by Alsabah *et al*. (2019) in selecting diploid black rice. Sabouri *et al*. (2008) also developed the concept using a direct effect on cross-section-based weighting. However, some subjective character weight is multiplied by two, considering the main priority. Based on this, the concept of Alsabah *et al*. (2019) can be applied in the development of weighting, where the character fruit diameter is multiplied by two as a stable character. Although, using this direct influence also needs correcting with the value of determination (Anshori *et al*., 2022). The selection index developed in this study is as follows:

Selection index = Yield + (2 × 0.32 × 0.4034) fruit diameter + (0.52 × 0.4034) total fruit number + (0.29 × 0.4034) fruit weight

or

Selection index = Yield + 0.258 fruit diameter + 0.21 total number of fruit + 0.117 fruit weight

The selection index showed 75 expected tomato lines, with two concepts involved in making the selection. The first was the comparison with control plants (Suwarno *et al*., 2009; Anshori *et al*., 2021, 2022), while the second was using positive values on index values as a basis for selection (Peternelli *et al*., 2017; Anshori *et al*., 2021; Padjung *et al*., 2021). Based on the parental genotypes, the cultivar Mawar showed good potential in forming the F_2 base populations. Furthermore, Bdr *et al*. (2020) and Farid *et al*. (2022) reported that the cultivar Mawar was the best parent in forming the hybrids. Therefore, these 75 lines can continue as families in the F_3 generation, especially the families generated from cultivar Mawar as one of the parents.

CONCLUSIONS

The study developed an effective selection index, then employed it on the F2 generation of tomato crosses. Almost all characters showed high genetic diversity, with potential as selection criteria. Characters of total fruit number, diameter, and weight showed the best selection criteria, with yield. The selection index formulation resulting from this study consists of yield + 0.258 fruit diameter + 0.21 total fruit + 0.117 fruit weight. The results of the selection index revealed 75 promising tomato strains for use as families in the F_3 generation.

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REFERENCES

Abdulkhaleq DA, Tawfiq SI (2014). Correlation and path coefficient analysis of yield and agronomic characters among some maize genotypes and their F_1 hybrids in diallel cross. *J. Zankoy Sulaiman* 16: 1-8.

Akbar MR, Purwoko BS, Dewi IS, Suwarno WB, Sugiyanta, Anshori MF (2021). Agronomic and yield selection of double haploid lines of rainfed lowland rice in advanced yield trials. *Biodiversitas* 22: 3006-3012.

Alam MZ, Bhuiya MAA, Muttaleb MA, Rashid MM (2004). Effect of alternating saline and non-saline condition on emergence and seedling growth of rice. *Pak. J. Biol. Sci*. 7(6): 883-890.

Alsabah R, Purwoko BS, Dewi IS, Wahyu Y (2019). Selection index for selecting promising doubled haploid lines of black rice. *SABRAO J. Breed. Genet*. 51(4): 430-441.

Anshori MF, Purwoko BS, Dewi IS, Ardie SW, Suwarno WB (2021). A new approach to select doubled haploid rice lines under salinity stress using indirect selection index. *Rice Sci*. 28: 368-378.

Anshori MF, Purwoko BS, Dewi IS, Suwarno WB, Ardie SW (2022). Salinity tolerance selection of double-haploid rice lines based on selection index and factor analysis. *AIMS Agric. Food*. 7(3): 520-535.

As'ari NP (2014). Proportion reduction in error (Pre) dalam Mengukur Asosiasi Penggunaan Kontrasepsi Hormonal terhadap Kejadian Hipertensi. Yogyakarta: Skripsi Fakultas Matematika dan Ilmu Pengetahuan Alam UNY.

Barmawi M (2007). Pola segregasi dan heritabilitas karakter ketahanan kedelai terhadap cowpea mild mottle virus populasi wilis X Mlg2521. *J. HPT Tropika* 7: 48-52. (in Indonesian).

Bdr MF, Anshori MF, Emanuella G, Pratiwi N, Ermiyanti I, Yovita V, Musdalifa, Nasaruddin (2020). High lycopene tomato breeding through the diallel crossing. *Agrotech. J*. 5: 63-72.

BPS (2021). Badan Pusat Statistik (BPS), Statistik Pertanian. Badan Pusat Statistik dan Direktorat Jenderal Hortikultura. (in Indonesian).

Dev J, Anand D, Kumari V, Sood VK, Singh A, Kaushal RP, Jenjiha JK, Sood OP (2009). Genotype x environment interaction for yield and maturity in soybean. *J. Crop Improv.* 36(1): 59-63.

Dhillion SK, Singh G, Gill BS, Singh P (2009). Stability analysis for grain yield and its components in soybean (*Glycine max* L. Merrill). *Crop Imp*. 36(1): 55-58.

Fadli M, Farid M, Yassi A, Nasaruddin, Anshori MF, Nur A, Suratman (2022). Evaluation of the advanced yield trial on tropical wheat (*Triticum aestivum* L.) mutant lines using selection index and multivariate analysis. *Biodiversitas* 23(1): 540-547.

Farid M, Anshori MF, Ridwan I, Dungga NE, Ermiyanti I (2022). Half diallel of F_1 tomato hybrid and its double cross-compatibility. *Biodiversitas* 23(4): 1813-1821.

Farid M, Nasaruddin, Musa Y (2021). Effective screening of tropical wheat mutant lines under hydroponically induced drought stress using multivariate analysis approach. *Asian J. Plant Sci*. 20: 172-182.

Fitriani L, Toekidjo, Purwanti S (2013). Keragaan lima kultivar cabai (*Capsicum annuum* L.) di-dataran medium. *J. Vegetalika* 2(2): 50-63. (in Indonesian).

Gani A, Suhartono, Rukidjo (1995). Evaluasi Sifat-Sifat Penentu Hasil Kacang Tanah (Arachis hypogaea L.) di Lahan Podzolik Merah Kuning. Pem. Penel. Sukarami. 24: 12-17. (in Indonesian).

Hasri (2015). Kandungan Likopen Buah Tomat (*Lycopersicum esculentum* L.) terhadap Waktu dan Suhu Pemanasan. Kimia FMIPA Universitas Negeri Makassar, Makassar. (in Indonesian).

Hidayatullah A, Purwoko BS, Dewi IS, Suwarno WB (2018). Agronomic performance and yield of doubled haploid rice lines in advanced yield trial. *SABRAO J. Breed. Genet*. 50(2): 42-53.

Islam MA, Raffi SA, Hossain MA, Hasan AK (2015). Analysis of genetic variability, heritability, and genetic advanced for yield associated characters in some promising advanced lines of rice. *Prog. Agric*. 26: 26-31.

Jambormias E, Patty JR, Laisina JKJ, Tutupary A, Madubun EL, Ririhena RE (2014a). Analisis genetik dan segregasi transgresif sifat berganda pada generasi F_2 persilangan kacang hijau mamasa lere butnem x lasafu lere butsiw. *J. Budidaya Pertanian* 10(2): 52-58. (in Indonesian).

Jambormias E, Riry J (2009). Penyesuaian data dan penggunaan informasi kekerabatan untuk mendeteksi segregan transgresif karakter kuantitatif pada tanaman menyerbuk sendiri (Suatu pendekatan dalam seleksi). *J. Budidaya Pertanian* 5: 11-18. (in Indonesian).

Jambormias E, Sutjahjo SH, Mattjik AA, Wahyu, Y, Wirnas D (2014b). Perluasan indeks seleksi nilai fenotipe untuk indeks seleksi nilai pemuliaan. *Bull. Agrohortic*. 2(1): 115-124. (in Indonesian).

Khapte PS, Jansirani P (2014). Genetic variability and performance studies of tomato (*Solanum lycopersicum* L.) genotypes for fruit quality and yield. *Trends in Biosci*. 7(12): 1246-1248.

Kumar V, Koshta N, Sohgaura N, Koutu GK (2014). Genetic evaluation of RILs population for yield and quality attributing characters in rice (*Oryza sativa* L.). *J. Agric. Technol*. 1(1): 43-51.

Lelang MA (2017). Uji Korelasi dan analisis lintas terhadap karakter komponen pertumbuhan dan karakter hasil tanaman tomat (*Lycopersicum esculentum* Mill). *J. Pertanian Konservasi Lahan Kering* 2(2): 33-35. (in Indonesian).

Li CC (1956). The concept of path coefficient and its impact on population genetics. *Biometrics* 12(2): 190-210.

Litrico I, Violle C (2015). Diversity in plant breeding: A new conceptual framework. *Trends in Plant Sci*. 20(10): 604-613.

Mangoendidjo W (2012). Dasar - Dasar Pemuliaan Tanaman. Yogyakarta: Kanisius. (in Indonesian).

Maurya RP, Bailey JA, Chandler JSA (2013). Impact of plant spacing and picking interval on the growth, fruit quality, and yield of okra (*Abelmoschus esculentus* (L.) Moench). *Am. J. Agric. For.* 1(4): 48-54.

Mustafa M, Syukur M, Sutjahjo SH, Sobir (2019). Inheritance study for fruit characters of tomato IPBT78 x IPBT73 using joint scaling test*. IOP Conf. Ser Earth Environ. Sci.* 382: 012009.

Napitupulu M, Damanhuri (2018). Keragaman genetik, fenotipe dan heritabilitas pada generasi F_2 hasil persilangan tanaman padi (*Oryza sativa* L.). *J. Produksi Tanaman* 6(8): 1844-1850. (in Indonesian).

Navabi A, Yang RC, Helm J, Spawer DM (2006). Can spring wheat growing mega-environments in the Northem great plain be dissected for representative locations or niche-adapted genotypes? *Crop Sci*. 46: 1107-1116.

Nzuve F, Githiri S, Mukunya DM, Gethi J (2014). Genetic variability and correlation studies of grain yield and related agronomic characters in maize. *J. Agric. Sci*. 6(9): 166-176.

Oktaviani E, Rostini N, Karuniawan A (2018). Penampilan fenotipik karakter hasil pada lima genotipe cabai rawit (*Capsicum frutescens* l.) di sukamantri, ciamis. Fakultas Pertanian Universitas Padjadjaran. (in Indonesian).

Padjung R, Farid M, Musa Y, Anshori MF, Nur A, Masnenong A (2021). Drought-adapted maize line based on morpho-physiological selection Index. *Biodiversitas* 22(9): 4028-4035.

Peternelli LA, Moreira EFA, Nascimento M, Cruz CD (2017). Artificial neural networks and linear discriminant analysis in early selection among sugarcane families. *Crop Breed. Appl. Biotechnol*. 17: 299-305.

Priyanto SB, Muhammad A, Andi TM (2018). Parameter genetik dan korelasi karakter komponen hasil jagung hibrida. *Bull. Penelitian Tanaman Serealia* 1(2). (in Indonesian).

Rahayu S, Suwarno WB, Ghulamahdi M, Aswidinnoor H (2018). Analysis of panicle morphology characters in F_2 and reciprocal F_2 populations of rice (*Oryza sativa* L.). *SABRAO J. Breed. Genet*. 50(1): 9-24.

Ritonga AW, Choizin MA, Syukur M, Maharijaya A, Sobir (2018). Short communication: Genetic variability, heritability, correlation, and path analysis in tomato (*Solanum lycopersicum*) under shading conditions. *Biodiversitas* 19(4): 1527-1531.

Roy D (2000). Plant Breeding Analysis and Exploitation of Variation. Narosa Publishing House. New Delhi, India.

Sa'diyah N, Basoeki TR, Putri AE, Maretha D, Utomo SD (2009). Korelasi, keragaman genetik, dan heritabilitas karakter agronomi kacang panjang populasi F_3 keturunan persilangan testa hitam x lurik. *J. Agrotropika* 14: 37-41. (in Indonesian).

Sa'diyah NM, Widiastuti, Ardian (2013). Keragaan, keragaman, dan heritabilitas karakter agronomi kacang panjang (*Vigna unguiculata*) generasi F_1. *J. Agrotek Tropika* 1(1): 32-37. (in Indonesian).

Sabouri H, Rabiei B, Fazlalipour M (2008). Use of selection indices based on multivariate analysis for improving grain yield in rice. *Rice Sci*. 15(4): 303-310.

Sami RA, Yeye MY, Usman IS, Hassan LB, Usman M (2013). Studies on genetic variability in some sweet sorghum (*Sorghum bicolor* L. Moench) genotypes. *Acad. Res. J. Agric. Sci. Res*. 1:1-6.

Sayurandi, Woelan S (2016). Pendugaan aksi gen pada karakter komponen hasil dan daya hasil lateks beberapa genotipe karet hasil persilangan tetua klon IAN 873 x PN 3760. *J. Penelitian Karet* 34(2): 141-150. (in Indonesian).

Singh RK, Chaudhary BD (2010). Biometrical Methods in Quantitative Genetic Analysis. New Delhi: Kalyani Publisher.

Sobir, Syukur M (2015). Genetika Tanaman. Bogor: IPB Press. (in Indonesian).

Sulistyowati Y, Trikoesoemaningtyas, Sopandie D, Ardhie SW, Nugroho S (2015). Estimation of genetic parameters and gene actions of sorghum (*Sorghum bicolor* L. Moench) tolerance to low P condition. *Int. J. Agron. Agric. Res.* 7:38-46.

Sutarman LW (2013). Heritabilitas pada Tanaman Kedelai (*Glycine max* L.). Universitas Lampung, Bandar Lampung. (in Indonesian).

Suwarno, Lubis E, Hairmansis A, Santoso (2009). Development of a package of 20 cultivars for blast management on upland rice. Advances in genetics, genomics, and control of Rice blast disease. Dordrecht (NL): Springer Netherlands, pp. 347-357.

Syukur MS, Sujiprihati, Yunianti R (2012). Teknik Pemuliaan Tanaman. Jakarta: Penebar Swadaya. (in Indonesian).

Syukur MS, Sujiprihati, Yunianti R (2015). Teknik Pemuliaan Tanaman Edisi Revisi. Jakarta: Penebar Swadaya. (in Indonesian).

Wahyuni S, Yunianti R, Syukur M, Witono JR, Aisyah SI (2014). Ketahanan 25 genotipe tomat (*Solanum lycopersicum* Mill.) terhadap pecah buah dan korelasinya dengan Karakter-karakter Lain. *J. Agron. Indonesia* 42(3): 195-202. (in Indonesian).

Wasonowati C (2010). Peningkatan produksi dan kualitas tomat (*Lycopersicon esculentum*) dengan sistem budidaya hidroponik. *J. Rekayasa* 3(2): 83-89. (in Indonesian).

Wricke G, Weber WE (1985). Quantitative Genetics and Selection in Plant Breeding. Berlin: Walter de Gruyter.

Yudilastari T, Syukur M, Sobir (2018). Pewarisan karakter hasil dan komponen hasil pada dua populasi persilangan cabai rawit hijau (*Capsicum annuum* L.). *J. Agron. Indonesia* 46(3): 283-289. (in Indonesian).