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TRANSGRESSIVE SEGREGANT OF TOMATO F4 POPULATIONS BASED ON FRUIT YIELD AND LYCOPENE CONTENT

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SUMMARY

Lycopene is an essential antioxidant found in tomatoes (*Solanum lycopersicum* L.) that can inhibit and prevent cell damage in the body. Thus, enhancing lycopene content is one of the crucial objectives in tomato breeding. Efforts should focus on assembling the tomato with high fruit yield and good quality by conducting transgressive segregant selection through plant breeding programs. The study aimed to select tomato lines with the potential for transgressive segregation based on high fruit yield and lycopene content. The research began in an augmented design combined with factors comprising 54 non-repeated tomato lines, compared with four repeated standard cultivars (Mawar, Chung, Karina, and Tymoti). The tomato lines' planting into seven blocks had no repeats, while the check cultivars for comparison engaged in repeated planting in each block. The observations underwent the analysis of variance (ANOVA), path analysis, correlation, heritability (narrow sense), and transgressive segregants. Based on transgressive segregation, the high-yielding tomato lines selected bore analysis for lycopene content. Based on the plant height and productive bunches per plant (directly supporting the fruit yield), the 14 promising transgressive segregant families' selection comprised 10 MC crosses, MC10.10, MC10.4, MC11.4, MC12.3, MC27.12, MC27.7, MC29.4, MC35.7, MC74.12, and MC8.3 and four KM crosses, KM23.2, KM26.1, KM30.5, and KM.5.5. For increased lycopene content, the five F4 families MC10.10, MC27.12, MC35.7, KM23.2, and KM30.5 showed better performance wherein selecting 10 transgressive segregant lines resulted with high lycopene content and fruit yield.

Keywords: Correlation, heritability, lycopene content, transgressive segregant, tomato

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Key findings: Selected tomato (*Solanum lycopersicum* L.) lines are potentially transgressive segregants based on high fruit yield and lycopene. The results also revealed that the traits of plant height and productive bunches per plant directly influenced the fruit yield in tomatoes and showed 10 transgressive segregant lines with high fruit yield and lycopene content.

INTRODUCTION

Tomato (*Solanum lycopersicum* L.), as a source of vitamins and minerals, has the potential for development and cultivation in the tropics, especially useful for its high nutrition that can benefit the community. One of the valuable antioxidants found in tomatoes is lycopene, a phytochemical compound in the carotenoid group synthesized by plants and microorganisms, characterized by the red pigment color in the fruits (Myong Roh *et al.*, 2013). This phytochemical compound can easily prevent cell damage caused by free radicals and reduce the risk of various diseases, such as cancer, heart attack, and slow aging (Mu'nisa, 2012; Srivastava, 2017). Tomato yield over the past three years gradually increased from 1.085 million tons (2020) to 1.114 million tons (2021) and 1.117 m tons (2022). Meanwhile, the demand and consumption of tomatoes for household needs in Indonesia also continue to rise yearly, and tomato consumption by the household sector reached 677,970 tons in 2021, which was 6.93% higher than in 2020 (439,600 tons) (BPS, 2023).

With increased production and demand for tomatoes, their superior cultivars with good fruit production and quality are requisite through plant breeding programs (Saputra *et al.*, 2019; Ritonga *et al.*, 2017). The plant breeding program is one of the primary strategies to produce high-yielding tomato cultivars with good quality. Some breeding phases also include expanding genetic diversity, character stature analysis, selection, testing and evaluation, and release of cultivars. Crosses of selected tomato checks and F3 generations, segregated population options using a selection index based on narrow sense heritability and factor analysis, have been carried out by Farid *et al.* (2022a) on two crosses, namely, Mawar/Chung and Karina/Mawar. The selection of checks in this

study, depending on the advantages in each control, i.e., Mawar, Karina, and Tymoti, are tomato varieties with high production and highly familiar to the public. Meanwhile, the Chung variety is a cherry tomato type that can benefit as a source of lycopene.

Developing better tomato genotypes is ideal for increased yield and better nutritional quality since tomato is a crucial raw material for large-scale food industries (De Sio *et al.*, 2021). Obtaining the desired high-yielding cultivars through transgressive segregants' selection is one of the principal activities in plant breeding. Transgressive segregants' identification is one of the selection strategies to acquire high-yielding cultivars (Munarti *et al.*, 2022). Transgressive segregants' election in early generations for polygenic controlled and additively controlled characters provides an advantage for plant breeders because of less handling of the breeding material in later generations. In addition, it can also increase the selection efficiency in plant breeding. Transgressive segregants can be predictable and detectable within progenies of an early segregating generation. Expected transgressive segregants can be predicted at the F1 generation level, while the observed transgressive segregants are obtainable at the F2, F3, and F4 generations (Jambormias *et al.*, 2015).

High heritability, direct gene activity, and a few genes are requirements for the selection criteria (Constantin *et al.*, 2017). In particular, if the yield becomes the basis for selection, the selection procedure must incorporate several yield components to improve its accuracy and future stability (Fischer and Rebetzke, 2018). Additionally, for a methodical assessment of the selection criteria for supporting yield, these qualities must have a significant link with a tomato fruit yield (Fadhilah *et al.*, 2022). Transgressive segregant is a crucial preference strategy; thus, it is necessary to use numerous yield-

contributing features jointly as choice criteria when using multiple selection criteria with significant genetic variation to select F4 populations. Therefore, the latest study aimed to find tomato lines that can potentially become transgressive segregants based on high fruit yield and lycopene content.

MATERIALS AND METHODS

Breeding material and procedure

The promising research on the tomato (*Solanum lycopersicum* L.) transpired from September 2022 to January 2023 at the Experimental Farm of the Faculty of Agriculture, Hasanuddin University, Makassar City, Indonesia (5°07'39" S 119°28'59" E). This research employed an augmented design combined with a randomized complete block design (RCBD) arrangement. Augmented design is well suited to populations with a limited number of seeds. In the presented research, the main factor was the tomato genotypes divided into two groups: non-repeated genotypes and the check cultivars with replications. The non-repeated genotypes comprised 54 tomato lines from two biparental populations, Mawar/Chung (39 lines) and Karina/Mawar (15 lines), with limited seeds divided into seven blocks. However, the tomato check cultivars (Mawar, Chung, Karina, and Tymoti) had repeated plantings in each block.

The experiment first germinated tomato seeds previously selected from the F3 generation. The seeds, soaked for 30 minutes, attained transfer to the germination site. The seeds germinate for about a week. After germination, sowing tomato seeds continued on soil, roasted husk, and compost with a 1:1:1 volume ratio. The seeding took place inside a greenhouse, with the seedlings transferred into polybags, where 14 days after sowing (DAS), the seedling roots received an AB Mix at a dose of 5 ml L⁻¹ after seven days. Two to three weeks after transplanting (WAP), seedlings' planting on soil beds had a size of 0.8 m × 6 m, with a distance of 20 cm. The beds covered with black silver mulch bore 10 cm diameter holes for planting with the tomato

seeds. Each bed consisted of two rows, and each row consisted of eight plants, resulting in 16 plants per bed, while the spacing used was 80 cm within rows and 40 cm between the rows.

Maintenance of tomato crops consisted of several activities, including watering twice in the morning and evening until the soil moistens. At one WAP, seedlings with abnormal growth or wilted and attacked by pests or disease incur replacement with plants of the same age and breeding material. Replanting occurred in the evening so as not to experience a sudden temperature change by the plant. The first fertilization used the NPK Mutiara fertilizer at the rate of 10 g L⁻¹ at one WAP, with subsequent fertilization adding KNO₃ at the rate of 5 g L⁻¹ of water, given three and six WAP in a solution form applied around the plant roots. Fertilizer application on the leaf continued when entering the vegetative and generative phases using Gandasil D and B. Pruning ensued by removing small shoots on the lower stem at least once a week. Weed growth around the planting hole's manual removal also used the herbicide Gramoxone with a dose of 2 g L⁻¹ for weed control around the beds. Controlling pests and diseases received a once-a-week spraying of insecticide Curacron 500 EC at a concentration of 2 cc L⁻¹ and Antracol 70 WP at a dose of 2 cc L⁻¹. Harvesting followed twice a week on reddish yellow tomatoes with ready criteria to harvest for eight weeks.

Data recorded and analysis

The data recording through field observations ensued in each experimental subplot. The observed data comprised several parameters, i.e., plant height (cm), dichotomous height (cm), stem diameter (mm), number of branches (branch), flowering days (DAP), harvest day (DAP), number of flowers per bunch (flower), number of fruits per bunch (fruit), productive bunches per plant (bunches), fruit length, thickness, and diameter (mm), fruit weight (g), number of cavities (cavities), total dissolved solids (Brix), number of seeds per fruit (seed), and fruit yield (g). All the recorded data's averages

sustained a systematic analysis with several concepts.

The recorded data analysis employed the SAS 9.0 software based on augmented design, using the assessed variance's mean squares to determine the heritability of each characteristic. Significant mean differences for various traits continued assessment for correlation and path analysis. The attributes with a significant correlation with fruit yield proceeded further to evaluation using path analysis. The path analysis findings helped determine the best selection criteria. The narrow-sense heritability estimates with genetic advance were typically helpful in predicting the gain under selection than heritability estimates alone (Reddy and Jabeen, 2016). Selecting transgressive segregants in F4 populations depended on traits with a high value of narrow-sense heritability. Families selected through transgressive segregants have higher average values than the check genotypes. Apart from the average value, the variance value also requires consideration. A low variance rate indicates that the genotype is increasingly homogeneous (Maulida *et al.*, 2022).

Lycopene content analysis

The lycopene content analysis followed the methodology of Suwanarung (2016) with slight modifications. The process included the following: 1) dissolving fruit samples of 0.002 g in 1 ml of distilled water, continuing to vortex in a water bath at 30 °C for 5 min, and then adding a solution of 16 ml comprising hexane:ethanol:acetone (at a ratio 2:1:1); 2) the samples continued to vortex immediately for 5 min, then incubated out of bright light for 10 min; 3) afterward, adding 1 ml distilled water to each sample ensued and vortexed again for 5 min; 4) allowing the samples to stand for 10 min to separate phases and all air bubbles to disappear; and 5) analyzing samples to determine absorbance at 503 nm used spectrophotometry. In samples, the lycopene levels calculation employed the following equation: Lycopene (mg) = Abs_{503 nm} × 137.4.

RESULTS

The analysis of variance showed that all the growth and yield-related characteristics of tomato (*Solanum lycopersicum* L.) incurred significant effects with the diversity of advanced lines and check cultivars (Table 1). The results of the heritability values are available in Table 1. From the table, the growth and yield-related traits revealed high heritability values, i.e., plant height (92.04), dichotomous height (91.35), stem diameter (74.20), number of branches (93.27), flowering days (74.73), harvest days (94.20), productive bunches per plant (98.97), number of flowers per bunch (78.90), number of fruits per bunch (90.37), fruit length (89.77), fruit diameter (94.51), fruit weight (86.97), number of cavities (86.26), total dissolved solids (90.05), number of seeds per fruit (80.84), and fruit yield (97.65). However, the tomato fruit thickness emerged with a moderate heritability value (58.59).

The correlation analysis showed 12 characteristics significantly and positively correlated with the yield attributes, i.e., plant height (0.49), dichotomous height (0.16), stem diameter (0.30), number of branches (0.32), number of flowers per bunch (0.40), number of fruits per bunch (0.43), productive bunches per plant (0.39), fruit length (0.14), fruit thickness (0.19), fruit diameter (0.18), number of cavities (0.11), and number of seed per fruit (0.16) (Table 2). However, the variables flowering day (-0.01), harvest day (-0.07), and total dissolved solids (-0.09) had a negative correlation with fruit yield. According to path analysis, a determination value of 0.401 and a residual effect rate of 0.601 were evident for the model (Table 3). The plant height (0.401), number of fruits per bunch (0.136), and productive bunches per plant (0.225) have a substantial positive direct influence on fruit yield compared with other parameters. Meanwhile, the trait number of branches (-0.006) negatively affected the yield parameters. Inversely, the traits' stem diameter (0.024) and number of flowers per bunch (0.023) have a significant positive direct and relatively the same effect on yield attributes.

Table 1. Mean squares and heritability values in F4 tomato populations for various traits.

Characteristics	C	L	L × C	CV	VG	VP	H ² (%)
PH	621.81**	646.96**	4027.32**	7.58	119.10	129.39	92.04
DH	767.56**	126.91**	2165.01**	10.40	23.19	25.38	91.35
SD	39.17**	5.29**	76.1**	11.32	0.79	1.06	74.20
NB	234.38**	54.74**	67.25**	12.00	10.21	10.95	93.27
FD	114.32**	21.72**	34.42*	7.04	3.25	4.34	74.73
HD	387.33**	27.29**	366.21**	1.58	5.14	5.46	94.20
NFB	7.39**	2.17*	15.75**	12.06	0.34	0.43	78.90
NFrB	26.17**	2.54**	37.30**	11.75	0.46	0.51	90.37
PBP	371.03**	87.67**	654.62**	6.45	17.35	17.53	98.97
FL	262.03**	40.79**	55.95**	7.69	7.32	8.16	89.77
FT	160.42**	13.89*	56.76**	11.26	1.63	2.78	58.59
FrD	253.14**	62.65**	56.10**	7.90	11.84	12.53	94.51
FW	3663.14**	27.83**	14974.10**	17.51	4.84	5.57	86.97
NC	35.79**	2.46**	15.88*	12.75	0.42	0.49	86.26
TDS	3.12**	2.31**	1.88*	9.83	0.42	0.46	90.05
NS	6639.18**	829.95**	754.40*	20.29	134.18	165.99	80.84
Y	11368.44**	58565.19**	37756.72**	14.34	11438.02	11713.04	97.65

Notes: **: significant at $\alpha = 1\%$, *: significant at $\alpha = 5\%$, C: Check, L: Lines, L×C: interaction between Lines and Check, CV: Coefficient of variance, VG: Variance of genotypes, VP: Variance of phenotypes, H: Heritability, PH: plant height, DH: dichotomous height, SD: stem diameter, NB: number of branches, FD: flowering days, HD: harvest days, NFB: number of flowers per bunch, NFrB: number of fruits per bunch, PBP: productive bunches per plant, FL: fruit length, FT: fruit thickness, FrD: fruit diameter, FW: fruit weight, NC: number of cavities, TDS: total dissolved solids, NS: number of seeds per fruit, Y: yield.

Table 2. Pearson correlation analysis for selected characteristics of the tomato.

Characteristics	PH	DH	SD	NB	FD	HD	NFB	NFrB	PBP	FL	FT	FrD	FW	NC	TDS	NS	Y
PH	1.00																
DH	0.50**	1.00															
SD	0.40**	-0.03 ^{ns}	1.00														
NB	0.38**	-0.15**	0.43**	1.00													
FD	-0.03 ^{ns}	-0.03 ^{ns}	-0.03 ^{ns}	-0.04 ^{ns}	1.00												
HD	-0.03 ^{ns}	-0.12*	-0.02 ^{ns}	-0.06 ^{ns}	0.21**	1.00											
NFB	0.44**	0.17**	0.29**	0.39**	-0.10*	-0.07 ^{ns}	1.00										
NFrB	0.31**	-0.04 ^{ns}	0.27**	0.35**	0.00 ^{ns}	0.00 ^{ns}	0.68**	1.00									
PBP	0.15**	-0.24**	0.34**	0.49**	0.01 ^{ns}	-0.07 ^{ns}	0.47**	0.64**	1.00								
FL	0.33**	0.32**	-0.07 ^{ns}	-0.22**	0.14*	0.16**	-0.09 ^{ns}	-0.16**	-0.36**	1.00							
FT	0.41**	0.44**	-0.04 ^{ns}	-0.10*	0.02 ^{ns}	0.01 ^{ns}	0.05 ^{ns}	-0.10*	-0.30**	0.75**	1.00						
FrD	0.32**	0.32**	-0.07 ^{ns}	-0.17**	0.15**	0.09 ^{ns}	-0.05 ^{ns}	-0.14*	-0.31**	0.92**	0.77**	1.00					
FW	0.11*	0.38**	-0.23**	-0.10*	0.05 ^{ns}	-0.04 ^{ns}	-0.17**	-0.31**	-0.33**	0.54**	0.63**	0.59**	1.00				
NC	0.06 ^{ns}	-0.01 ^{ns}	-0.06 ^{ns}	-0.02 ^{ns}	0.20**	0.14*	-0.12*	-0.16**	-0.10 ^{ns}	0.48**	0.10*	0.46**	0.20**	1.00			
TDS	-0.10*	0.03 ^{ns}	-0.10*	-0.18*	0.03 ^{ns}	0.03 ^{ns}	-0.03 ^{ns}	-0.20**	-0.25**	0.11*	0.03 ^{ns}	0.06 ^{ns}	0.01 ^{ns}	0.12*	1.00		
NS	0.18**	0.20**	-0.01 ^{ns}	-0.21**	0.14*	0.12*	-0.06 ^{ns}	-0.02 ^{ns}	-0.11*	0.56**	0.33**	0.53**	0.25**	0.42**	0.00 ^{ns}	1.00	
Y	0.49**	0.16**	0.30**	0.32**	-0.01 ^{ns}	-0.07 ^{ns}	0.40**	0.43**	0.39**	0.14**	0.19**	0.18**	0.05 ^{ns}	0.11*	-0.09 ^{ns}	0.16**	1.00

Notes: ns: not significant correlation, **: significant correlation at $\alpha = 1\%$, *: significant at $\alpha = 5\%$, PH: plant height, DH: dichotomous height, SD: stem diameter, NB: number of branches, FD: flowering days, HD: harvest days, NFB: number of flowers per bunch, NFrB: number of fruits per bunch, PBP: productive bunches per plant, FL: fruit length, FT: fruit thickness, FrD: fruit diameter, FW: fruit weight, NC: number of cavities, TDS: total dissolved solids, NS: number of seeds per fruit, Y: yield.

Table 3. Path analysis based on the characteristics correlation with the fruit yield in tomato.

Characteristics	Direct effects	Indirect effects						Total effects
		PH	SD	NB	NFB	NFrB	PBP	
PH	0.401**	-	0.008	-0.011	0.072	-0.051	0.053	0.494
SD	0.024**	0.168	-	-0.013	0.048	-0.044	0.122	0.300
NB	-0.006**	0.162	0.008	-	0.063	-0.057	0.178	0.325
NFB	0.023**	0.188	0.006	-0.011	-	-0.110	0.171	0.404
NFrB	0.136**	0.132	0.005	-0.010	0.109	-	0.233	0.426
PBP	0.225**	0.063	0.006	-0.014	0.077	-0.105	-	0.388
Residual		0.601						

Notes: **: significant effect at $\alpha = 1\%$, PH: plant height, SD: stem diameter, NB: number of branches, NFB: number of flowers per bunch, NFrB: number of fruits per bunch, PBP: productive bunches per plant.

Table 4. Narrow-sense heritability of two tomato lines' populations.

Populations and genetic parameters	MC Populations				KM Populations			
	PH	NFrB	PBP	Yield	PH	NFrB	PBP	Yield
F3 based population (A)	134.50	7.90	15.13	337.29	127.55	7.01	18.02	526.43
F3 selected (B)	159.30	8.67	17.53	498.81	138.23	8.22	24.70	582.22
F4 selected (C)	151.01	5.22	16.85	318.48	148.24	5.27	26.46	449.00
Differential selection (S = B - A)	24.80	0.77	2.40	161.52	10.68	1.21	6.68	55.79
Selection gain (G = C - A)	16.51	-2.68	1.72	-18.81	20.69	-1.74	8.44	-77.43
h^2_{ns} (%) (G/S \times 100%)	66.57	-348.05(~0)	71.67	-11.65(~0)	193.73(~100)	-143.80(~0)	126.35(~100)	-138.79(~0)

Notes: PH: plant height, NFrB: number of fruits per bunch, PBP: productive bunches per plant, F3: folial 3, F4: folial 4, ~0 or 100: assumed.

The narrow-sense heritability analysis revealed that MC and KM tomato populations have the same pattern toward the plant height, number of fruits per bunch, productive bunches per plant, and fruit yield (Table 4). The MC and KM tomato populations provided narrow-sense heritability values of 66.57% and 193.73% (~100%), respectively, for plant height. For the number of fruits per bunch, the MC and KM populations owned the narrow-sense heritability of -348.05% (~0%) and -143.80% (~0%), respectively. For productive bunches per plant, the MC and KM populations gave narrow-sense heritability of 71.67% and 126.35% (~100%), respectively. Meanwhile, for the fruit yield feature, MC and KM tomato populations have narrow-sense heritability of -11.65% and -138.79% (~0%), respectively. Transgressive segregants selected simultaneously were the uniformed families with the best performance for various traits (Jambormias *et al.*, 2015).

The tomato check cultivar 'Chung' had a considerable plant height and productive bunches per plant and can serve as a value

threshold for selecting the tomato families. In the cultivar Chung, the average value and variance for the plant height were 95.11 and 17.36, respectively, and for productive bunches per plant, the values were 9.76 and 1.11, respectively. The transgressive segregant analysis showed the selection of 14 families based on the characteristics, plant height, and productive bunches per plant (Table 5). In the selected 14 tomato families, 10 were products of MC crosses, i.e., MC10.10, MC10.4, MC11.4, MC12.3, MC27.12, MC27.7, MC29.4, MC35.7, MC74.12, and MC8.3, while four promising families were notable in the KM crosses, i.e., KM23.2, KM26.1, KM30.5, and KM.5.5.

The results of lycopene content analysis of the tomato-selected transgressive segregant genotypes appear in Table 6. From the table, the lycopene content analysis obtained five families that have lines with lycopene content higher than the average value of selected cultivars and a lower variance value than the variance value in the tomato selected cultivar 'Chung,' i.e., MC10.10, MC27.12, MC35.7, KM23.2, and KM30.5. The

Table 5. Selected tomato families obtained from transgressive segregant of F4 populations based on plant height and productive bunches per plant.

No.	Families	PH		PBP		Yield	
		Average	Variance	Average	Variance	Average	Variance
1	MC10.10	7.42*	1.26a	7.42*	1.26a	704.12*	93.52a
2	MC10.4	6.62*	0.35a	6.62*	0.35a	894.25*	467.97a
3	MC11.4	6.17*	0.64a	6.17*	0.64a	521.27*	711.41a
4	MC12.3	6.13*	1.27a	6.13*	1.27a	599.28*	313.05a
5	MC27.12	7.08*	1.01a	7.08*	1.01a	1010.44*	382.75a
6	MC27.7	6.33*	1.03a	6.33*	1.03a	491.57*	765.10a
7	MC29.4	6.08*	0.79a	6.08*	0.79a	499.15*	290.21a
8	MC35.7	7.14*	0.81a	7.14*	0.81a	575.56*	702.58a
9	MC74.12	6.25*	1.14a	6.25*	1.14a	519.98*	761.86a
10	MC8.3	6.08*	0.88a	6.08*	0.88a	792.60*	204.30a
11	KM23.2	6.04*	1.25a	6.04*	1.25a	918.80*	613.78a
12	KM26.1	6.20*	1.14a	6.20*	1.14a	410.16*	816.74a
13	KM30.5	6.83*	1.24a	6.83*	1.24a	1812.37*	658.11a
14	KM5.5	7.53*	0.81a	7.53*	0.81a	605.30*	442.50a
15	MC9.2	73.25ns	130.21b	12.13*	59.55b	214.02ns	16234.37b
16	MC8.7	100.38*	270.84b	10.25*	27.36b	277.98ns	14071.15b
17	MC26.11	101.25*	88.92b	7.75ns	23.58b	160.96ns	624.46a
18	KM71.10	83.88ns	553.27b	6.25ns	7.36b	53.20ns	2129.91b
19	KM15.5	92.00ns	109.00b	7.00ns	4.00b	197.77ns	2366.46b
20	MC38.8	83.63ns	43.13b	24.13*	22.13b	352.86*	7220.49b
21	MC14.12	76.67ns	207.07b	6.67ns	4.67b	51.60ns	72.05a
22	MC51.2	107.00*	461.00b	7.60ns	3.30b	99.59ns	2562.26b
23	MC8.11	122.57*	67.95b	12.57*	23.62b	315.70*	28953.06b
24	KM35.1	79.67ns	330.33b	6.00ns	4.00b	105.77ns	54.92a
25	MC73.7	94.00ns	194.00b	9.00ns	2.40b	480.87*	23081.16b
26	MC38.1	83.63ns	43.13b	24.13*	22.13b	352.86*	7220.49b
27	MC33.5	89.00ns	435.33b	5.75ns	4.92b	124.24ns	3608.80b
28	MC10.7	113.38*	13.70a	20.00*	38.29b	318.67*	9236.87b
29	KM69.6	113.13*	768.70b	8.75ns	18.79b	287.30*	14491.98b
30	KM25.9	131.50*	419.68b	12.25*	11.58b	115.53ns	3714.66b
31	MC10.11	107.88*	132.41b	6.75ns	5.07b	56.91ns	805.99b
32	KM69.5	75.50ns	529.00b	7.25ns	4.92b	79.08ns	2720.21b
33	KM5.3	83.88ns	80.70b	23.25*	105.64b	258.52ns	13289.79b
34	MC30.10	115.25*	36.21b	5.13ns	7.55b	294.45*	4155.57b
35	MC9.5.1	119.38*	785.98b	13.88*	40.13b	134.77ns	3288.62b
36	MC38.2	81.88ns	164.98b	12.75*	6.50b	135.35ns	4423.60b
37	MC17.3	115.50*	85.43b	18.13*	12.70b	192.77ns	1748.39b
38	MC28.6	103.50*	13.71a	6.13ns	9.27b	288.67ns	3335.99b
39	KM69.4	80.00ns	374.86b	5.13ns	8.70b	78.18ns	5038.90b
40	MC74.11	103.38*	149.70b	19.38*	47.41b	120.63ns	3406.1b
41	MC32.11	93.80ns	296.70b	24.00*	66.00b	117.49ns	1493.58b
42	KM5.6	68.13ns	189.84b	26.00*	80.00b	320.42*	21616.66b
43	MC9.6	70.88ns	21.84b	22.88*	50.98b	173.63ns	7648.83b
44	MC129.5	118.88*	233.84b	9.38ns	8.84b	113.12ns	2454.15b
45	KM6.8	77.80ns	344.70b	25.80*	92.70b	184.23ns	15303.77b
46	MC14.10	95.60*	50.30b	5.00ns	6.00b	148.37ns	303.97b
47	MC9.4	115.88*	415.84b	20.00*	46.29b	264.55ns	25004.31b
48	KM15.3	69.38ns	44.27b	12.75*	13.07b	77.08ns	1134.43b
49	MC29.8	92.33ns	376.33b	15.00*	1.00a	93.94ns	60.56a
50	MC42.11	65.60ns	40.50b	11.00*	2.00b	49.30ns	66.59a

Table 5. (cont'd.)

No.	Families	PH		PBP		Yield	
		Average	Variance	Average	Variance	Average	Variance
51	MC15.7	132.71*	234.24b	26.29*	69.90b	234.38ns	3007.23b
52	MC15.1	76.83ns	105.37b	9.00ns	11.20b	170.23ns	3228.84b
53	MC10.6	95.14*	6.14a	31.71*	25.90b	311.47*	1417.08b
54	MC38.7	57.75ns	104.25b	23.00*	68.67b	91.62ns	2558.23b
Chung (*) (a)		95.11	17.36	9.76	1.11	279.85	831.15
Mawar		82.26	178.42	7.57	1.62	213.26	1058.50
Karina		72.89	83.64	6.60	1.54	197.15	2838.32
Tymoti		78.10	109.47	5.97	1.38	193.07	3413.52

Notes: MC: Mawar/Chung, KM: Karina/Mawar, *: significant high value Chung as the best check variety, a: value variance less significant or same to Chung as the best check variety, ns: less significant means than the best check variety, b: higher significant of value variance than Chung as the best check variety.

Table 6. Lycopene content of the selected tomato families obtained from transgressive segregant of F4 populations.

No.	Families	Average	Variance
1	MC10.10	43.88*	59.36a
2	MC10.4	85.56*	382.27b
3	MC11.4	42.93ns	1055.30b
4	MC12.3	40.70ns	404.896b
5	MC27.12	60.01*	131.43a
6	MC27.7	42.59ns	26.42a
7	MC29.4	30.57ns	247.89b
8	MC35.7	45.88*	69.48a
9	MC74.12	27.30ns	88.12a
10	MC8.3	67.83*	368.22b
11	KM23.2	105.85*	84.71a
12	KM26.1	46.16*	390.25b
13	KM30.5	105.60*	118.67a
14	KM5.5	30.42ns	723.03b
Chung (*) (a)		43.76	155.64
Mawar		39.25	173.52
Karina		38.07	211.81
Tymoti		34.74	182.24

Notes: *: significant high value with Chung as the best check variety, a: value variance less significant or same to Chung as the best check variety, ns: less significant means than the best check variety, b: higher significant of value variance than Chung as the best check variety.

results of the transgressive segregated lines analysis from five selected families with high lycopene content showed that 10 selected lines had higher lycopene contents and fruit yields than the standard cultivar 'Chung,' namely, MC10.10.1 (54.73 and 715.90), MC10.10.3 (53.58 and 698.21), MC27.12.4 (57.70 and 990.15), MC27.12.7 (74.18 and 982.15), MC35.7.1 (48.46 and 628.35), MC35.7.5 (58.46 and 585.89), KM23.2.2 (117.18 and 886.24), KM23.2.5 (114.21 and 938.12),

KM30.5.5 (120.89 and 1842.18), and KM30.5.6 (117.43 and 1786.73).

DISCUSSION

Considerable efficiency of plant breeding results from the relationship and linkage between genetic diversity, heritability, correlation between characteristics, and path analysis that controls the traits (Fadhilah *et al.*, 2022). Analysis of variance showed that overall

growth and production characteristics significantly influenced F4 tomato populations on lines, check cultivars, and interactions between lines and checks. The genetic diversity that exerts a significant influence plays a vital role in selecting promising populations for improving the desired traits. The study result is in line with the opinion of Priyanto *et al.* (2018), which states that high genetic diversity in tomato populations is crucial and necessary in the selection process, further enhancing the opportunities to combine the desired plant traits.

These results also agreed with Anshori *et al.* (2022), who stated that significant analysis of variance is the basis for determining the effectiveness of selection between strains and elders, which is vital in the selection process. Genetic diversity with significant influence was also evident in previous studies on genetic parameters and selection index in F2 populations of high-yielding tomatoes (Fadhilah *et al.*, 2022). Based on this, an in-depth analysis is relevant in correlation analysis, path analysis, narrow-sense heritability, and transgressive segregation selection to determine which strains include transgressive segregant lines.

Determining a characteristic as a selection criterion can be visible through the correlation between supporting traits and the main attribute to identify the appropriate selection criteria to improve the plant yield. Correlation between different characteristics can help plant breeders know how one attribute's influence can bring change or impact on the others (Hastini *et al.*, 2019). From the correlation analysis in Table 2, 12 characteristics exhibited positively correlated with fruit production, with a designation as essential yield-related traits. Production is rather complex, influenced by several factors and other attributes, requiring further scrutiny in the path analysis to know how much each parameter affects fruit production directly or indirectly.

Path analysis can help identify the most reliable and effective characteristics that can benefit genetic improvement to obtain high production and group desirable traits (Namdev and Rahul, 2018). Path analysis has reportedly

helped plant breeders develop appropriate methods to select superior genotypes in tomatoes (Singh *et al.*, 2018; Maurya *et al.*, 2020; Nevani and Sridevi, 2021; Tsgaye *et al.*, 2022; Panchbhai and Kulkarni, 2023) and cayenne peppers (Amas *et al.*, 2023). The results of path analysis showed that the traits displaying the broader direct influence on tomato fruit production were the plant height, number of fruits per bunch, and productive bunches per plant than other characters, and these three traits can be effective selection criteria with fruit production as the chief trait.

Genetic parameters and heritability also determined the effectiveness of a selection. Heritability is an estimation that measures the phenotype diversity of a genotype in a population due to the vital role of genetic factors in tomato crops (Widarsiono *et al.*, 2022). The heritability analysis of the tomato F4 population showed that all observed characteristics had high heritability (>50%), which means that the observed traits in this study more predominantly bore influence from genetic factors than environmental ones (Bdr *et al.*, 2020). A large genetic role can be evident through high heritability values for desirable traits in tomatoes (Hermanto *et al.*, 2017). Therefore, it becomes one of the bases in determining the effectiveness of the selection and assessment of a tomato population (Farid *et al.*, 2022a, b).

Narrow-sense heritability is the proportion of total additive variance of phenotypic variance, and it is also vital in the selection process in plant breeding, particularly in the selection of elite genotypes from the populations (Reddy and Jabeen, 2016). Narrow and broad sense heritability in the supporting production trait showed wider differences in heritability values, where the rate of the broad-sense heritability is normal (0%–100%), while the narrow-sense heritability values were lower to very high. Plant height and productive bunches per plant have lower values of the narrow-sense heritability in MC crosses, but KM crosses' broad-sense heritability values were very high. However, these three attributes still have positive heritability values, with classification as high, above 50% in both sets of crosses (Farhah *et al.*, 2022). The narrow-

Table 7. Transgressive segregant obtained from five tomato families with high lycopene content and fruit yield.

No.	F3 Families	F4 Lines	Lycopene Content (mg)	Yield (g)
1	MC10.10	MC10.10.1	54.73*	715.90*
2		MC10.10.2	46.10*	709.20*
3		MC10.10.3	53.58*	698.21*
4		MC10.10.4	34.34 ^{ns}	706.02*
5		MC10.10.5	35.72 ^{ns}	714.85*
6		MC10.10.6	46.48*	706.24*
7		MC10.10.7	41.60 ^{ns}	691.80*
8		MC10.10.8	38.46 ^{ns}	690.70*
9	MC.27.12	MC27.12.1	54.34*	998.95*
10		MC27.12.2	41.60 ^{ns}	1023.13*
11		MC27.12.3	53.74*	1024.52*
12		MC27.12.4	57.70*	990.15*
13		MC27.12.5	69.84*	1022.64*
14		MC27.12.6	68.69*	1031.52*
15		MC27.12.7	74.18*	982.15*
16	MC35.7	MC35.7.1	48.46*	628.35*
17		MC35.7.2	39.23 ^{ns}	549.42*
18		MC35.7.3	42.59 ^{ns}	568.58*
19		MC35.7.5	58.46*	585.89*
20		MC35.7.6	50.22*	551.66*
21		MC35.7.7	32.97 ^{ns}	572.25*
22		MC35.7.8	49.23*	572.77*
23	KM23.2	KM23.2.1	93.03*	917.07*
24		KM23.2.2	117.18*	886.24*
25		KM23.2.3	97.70*	958.63*
26		KM23.2.4	110.44*	904.15*
27		KM23.2.5	114.21*	938.12*
28		KM23.2.6	105.55*	933.97*
29		KM23.2.7	96.03*	922.01*
30		KM23.2.8	112.65*	890.19*
31	KM30.5	KM30.5.1	92.04*	1795.32*
32		KM30.5.2	103.03*	1792.68*
33		KM30.5.3	93.22*	1855.83*
34		KM30.5.4	112.97*	1793.02*
35		KM30.5.5	120.89*	1842.18*
36		KM30.5.6	117.43*	1786.73*
37		KM30.5.7	98.08*	1810.17*
38		KM30.5.8	107.15*	1823.06*
	Chung (*)		43.76	279.85
	Mawar		39.25	213.26
	Karina		38.07	197.15
	Tymoti		34.74	193.07

Notes: *: significant high value with Chung as the best check variety, ns: less significant means than the best check variety (Chung), bold value: lines that have high lycopene content and fruit yield.

sense heritability values for fruits per bunch and yield were negative, indicating these traits sustained environmental influences. In this existing research, the value of the narrow sense heritability was outside of a normal range. The reason is due to the difference in

cultivation climate between the current and previous populations. Also, the decrease in heritability suggests involving many loci in the traits' inheritance and the higher genetic influence of non-additive gene effects (Ardiarini *et al.*, 2022). Based on the analysis of genetic

diversity, heritability, narrow sense heritability, correlation, and path analysis conducted in this F4 generation, it was apparent that the plant height and productive bunches per plant traits were superior as selection criteria. These findings also align with Rohmawati *et al.* (2018), which states that plants with many fruits will affect fruit weight, plant height, and the number of bunches.

Transgressive segregation determination focuses on segregants with a better average value than comparison varieties, and the variance must be lower or the same as the control. In this case, the study used the variety Chung for the best comparison. Selecting according to plant height and productive bunches per plant parameters resulted in 14 tomato families with 104 lines chosen from two types of crosses, i.e., 10 families from Mawar/Chung crosses and four families from Karina/Mawar crosses. Mardi *et al.* (2022) also reported that transgressive segregants were the genotypes with a higher mean value than check genotypes, and the level of diversity was lower or equal to pure lines. Several studies have also carried out transgressive segregation estimations, including on wheat (Al-Bakry, 2021), mung bean (Jambormias *et al.*, 2015; Maulida *et al.*, 2022), sorghum (Munarti *et al.*, 2022), and chili (Karim *et al.*, 2022).

After transgressive segregation, the selected tomato lines' analysis for lycopene content progressed. Based on the assessment, five tomato families with 38 lines have the highest lycopene content compared with the tomato check cultivar 'Chung' (Table 7). In five selected families, 10 were the best lines with the highest lycopene content. Several studies ran on lycopene content in tomato populations and reported the same findings (Noviyandari *et al.*, 2019; Oktavia *et al.*, 2022). Lycopene can exist in red fruits, one of which is tomato, containing several benefits for health. Novita *et al.* (2015) reported that lycopene is a bright red pigment carotenoid found in tomatoes and other red fruits. This substance functions as an antioxidant, an antidote to free radicals, beneficial to health. Tomato fruits synthesize lycopene in large quantities during ripening,

which reaches 90 of the total carotenoid fraction.

CONCLUSIONS

The transgressive segregant analysis revealed effectivity in selecting tomato (*Solanum lycopersicum* L.) lines in F4 populations. Almost all characteristics showed the highest genetic diversity, with the potential as selection criteria. Based on the transgressive segregants, 14 families were potentially promising, in which five families consisting of 10 lines, i.e., MC10.10.1, MC10.10.3, MC27.12.4, MC27.12.7, MC35.7.1, MC35.7.5, KM23.2.2, KM23.2.5, KM30.5.5, and KM30.5.6, exhibited high lycopene content and fruit yield.

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