Tomato F3 lines development and its selection index based on narrow-sense heritability and factor analysis

MUH FARID, MUHAMMAD FUAD ANSHORI♥, IFAYANTI RIDWAN

Department of Agronomy, Faculty of Agriculture, Universitas Hasanuddin. Jl. Perintis Kemerdekaan Km 10, Tamalanrea, Makassar 90245, South Sulawesi, Indonesia. Tel./fax.: +62-853-11236019, ♥email: fuad.pbt15@gmail.com

Abstract. *Farid M, Anshori MF, Ridwan I. 2022. Tomato F3 lines development and its selection index based on narrow-sense heritability and factor analysis. Biodiversitas 23: 5790-5797.* The F3 is the early selection generation that has a good heritability and heredity pattern in a segregated population. The aims of this study are to identify the effectiveness of forming a selection index based on narrow-sense heritability and factor analysis and to select potential tomato F3 lines to be continued in the F4 generation. The research was arranged by an augmented design combined with a randomized complete block design as the environmental design. The research factors consisted of non-repeated genotypes, i.e. the lines with a limited number of seeds consisting of 75 lines and repeated genotypes as comparison varieties consisting of three varieties (Mawar, Tymoty, and Karina). The lines that were not repeated were divided into 5 blocks, while the check varieties were planted repeatedly in each block. The effective selection criteria in this study were the yield, fruit weight, number of branches, and total fruit number. The priority character besides yield in this study is fruit weight with high and normal narrow-sense heritability. The index selection results from this study showed that there were a good 32 tomato lines to be continued in the F4 generation. t was considered effective in the selection of tomato lines of the F3 generation.

Keywords: Factor analysis, index selection, narrow-sense heritability, *Solanum lycopersicum*, tomato lines

INTRODUCTION

Hybridization is the most common method of creating high diversity (Holme et al. 2019; Afifah et al. 2021; Lopez-Gomollon et al. 2022), including tomato plants as one crop of significant economic prospects (Quinet et al. 2019). The effectiveness of hybridization is highly dependent on the genetic background of the crossed parents. The farther the genetic distance between the two parents, the higher or wider the diversity of the resulting lineage (Wei et al. 2018). Farid et al. (2022) have performed crosses of various tomato parental lines with different genetic backgrounds, especially on the shape of the fruit and its lycopene content. The research has entered the F3 generation, hence the selection of these lines must be carried out systematically with a good accuracy approach. Single selection with productivity is considered very risky because the yield is polygenic with a complex genetic pattern (Anisa et al. 2022). This indicates that multi-character selection needs to be carried out systematically on the F3 tomato population (Medico et al. 2020). One approach that can be used in multi-character selection is the index selection approach.

The index selection approach is an effective approach in multicharacter-based selection. The effectiveness of this approach has been reported by Authrapun et al. (2021), Olivieri et al. (2021), and Farid et al. (2021). Basically, index selection uses index values from a combination of several selection criteria with specific weighting values (Wang and Chen 2016). The crucial thing in the formation of this index is the determination of effective selection criteria and the basis for their weighting values (Akbar et al. 2021; Anshori et al. 2021). The more selection criteria involved, the less directed the selection direction. So, the determination of the selection criteria must be adjusted to the objectives of the various development and narrow-sense heritability (Acquaah 2007; Reddy and Jabeen 2016). Narrow-sense heritability has an important role in determining the effectiveness of genetic gain (Syukur et al. 2015), so it should be considered in forming the selection index. In addition, assigning a weighted value, including considering narrow-sense heritability, will determine the priority of these criteria in selection (Reddy and Jabeen 2016). Based on this, the determination of selection criteria and their weighting in the selection index needs to be done systematically through a series of statistical approaches and narrow-sense heritability.

The formation of a selection index with a statistical approach can be conducted through factor analysis. Factor analysis can compress complex data dimensions into simpler dimensions by optimizing the large internal covariance on each dimension (Ebrahimnejad and Rameeh 2016). The concept of this analysis is to identify a significant internal relationship between the main character and its supporting characters (Ali et al. 2015), so that the selection process with a combination of these characters becomes more focused (Oliveira et al. 2016; Barth et al. 2022). The effectiveness of this analysis has also been reported by Farid et al. (2020) in predicting secondary characters in wheat, also in Arifuddin et al. (2021) and Anshori et al. (2022) in predicting selection criteria in rice screening against salinity stress. Based on this, the

application of factor analysis in the formation of the selection index can also be applied in the selection of tomato lines of the F3 generation. This concept could be more effective if it is combined with narrow-sense heritability information in each selection criteria. Therefore, the aims of this study were to identify the effectiveness of forming a selection index based on narrow-sense heritability and factor analysis; and to select potential tomato lines to be continued in the F4 generation.

MATERIALS AND METHODS

The research was conducted at the Horticultural Seed Center, Bonto-bonto, Gowa Regency (-5.28892,119.56012) from April to September 2022. This study used an Augmented Design and a randomized complete block design as the environmental design. The main factor in this study was the genotype which was divided into two groups, namely the non-repeated genotype and the repeated genotype. The non-repeated genotypes were 54 tomato lines from two biparental populations, namely Karina x Mawar (27 lines) and Mawar x Chung (27 lines), with a limited number of seeds. The plotting of non-repeated genotypes was divided into four blocks. While the repeated genotype used three check varieties (Mawar, Tymoty, and Karina) that were planted repeatedly in each block. Based on this, there were 90 experimental units in this study.

Research procedure

The seedling was carried out in a greenhouse using roasted husk and compost as a planting medium in a 1:1 ratio. AB mix nutrient solution was applied when seedlings were 7 days after sowing (DAS) with a dose of 5 ml L^{-1}. At 14 DAS, seedlings were transferred to polybags and then to beds at 2-3 weeks after planting (WAP). The beds used were 0.8 x 5 m, with a distance of 20 cm between beds covered with black silver mulch and 10 cm diameter holes were made for planting seedlings. Each bed consisted of 2 lines and each line consisted of 12 plants, resulting in 24 plant beds. The spacing used was 40 cm in rows and 80 cm between rows and the distance between lines in the beds was 100 cm. Maintenance consists of several activities, namely watering twice a day until the soil looks moist. At one WAP, seedlings experienced abnormal growth, were wilted and attacked by pests or diseases were replaced with plants of the same age and genetic code. The first fertilization was carried out at the next 7 days after planting (DAP) given once a week, using NPK Mutiara fertilizer at a dose of 10 g L^{-1} in the form of a solution and applied around the plant roots. Additional fertilizers were applied using Gandasil D fertilizer in the vegetative phase and Gandasil B in the generative phase. Pruning was conducted by removing small shoots on the lower stem at least once a week. Weeding was carried out every two weeks to remove weeds that interfere with plant growth, manually by hand, hoe, or by the application of the herbicide Gramoxone with a dose of 2 g L^{-1} of water. Pest and disease control was carried out once a week, using the insecticide Curacron 500 EC with a concentration of 2 cc L^{-1} and antracol fungicide with a concentration of 2 g L^{-1}, by spraying on the plant surface. Harvesting was conducted twice a week on sunny days on tomatoes that are reddish yellow and have met the criteria for ready to harvest (Ritonga et al. 2018), which are carried out for 8 weeks.

Parameter observation and data analysis

The parameters observed in this study were plant height, dichotomous height, stem diameter, number of branches, flowering days, harvest days, number of flowers per inflorescence, number of fruits per inflorescence, number of inflorescence, number of total fruit, fruit length, fruit diameter, fruit weight, number of cavities, total dissolved solids, number of seeds per fruit and the yield (Ritonga et al. 2018). These observations were analyzed systematically with several concepts. The ANOVA was analyzed with SAS 9.0 software and estimation of broad sense heritability using formula of You et al. (2016) (Table 1). Significant characters in ANOVA were analyzed further in factor analysis. In factor analysis, the highest diversity of productivity in factor dimensions is the key to determining the best factor dimensions for the formation of the selection index (Anshori et al. 2022). Then, the selection index is corrected based on the realized heritability in narrow-sense based on selection gain and differential selection (G/Sx 100%) (Syukur et al. 2015). Characters that had high and normal values of narrow heritability were weighted doubled, whereas, characters with negative values were folded 0.5. The index formulation becomes the basis for selecting the best line to be continued in the F4 generation.

RESULTS AND DISCUSSION

Analysis of variance was more focused on three sources of performance, namely control, strain and comparison of control lines. The results of the analysis show that almost all characters were significantly affected by the diversity of controls, the lines, and the comparison of control lines (Table 2).

However, there are some characters that are only influenced by two or one or even not at all influenced by the three types of diversity sources. The character of the number of flowers per inflorescence and fruit length was significantly affected by the diversity of controls and the comparison of control lines, while the diversity of lines showed an insignificant effect.

Table 1. Analysis of variance based on Augmented design model 1

Source	df	MS	EMS
Genotype (G)	g-1	A_{ii}	$Ve+Vg$
Control (C)	t-1	B_{ii}	$Ve+nK^2_c$
Error	rc+2m-t	C_{ii}	Ve

Notes: df: degrees of freedom; MS: mean square; EMS: expected mean square; g: number of genotypes; t: number of control genotypes; n: average number of replicates for each control genotype (see formula (7) in text); r and c are the number of rows and columns, respectively; and m is the number of replicates for two subplot controls

The stem diameter character was strongly influenced by the variety of lines and the comparison of the control lines, while there was no significant variation in the control variance of these characters. The dichotomous height character was only significantly affected by the diversity of the control-line comparisons. In fact, harvest age is the only character that was not influenced by the three sources of diversity.

The results of the heritability analysis are also shown in Table 2. Based on the table, the character of the number of flowers per bunch (42.46%) is the only character that has a heritability value of lower than 50%. On the other hand, other characters have high heritability values (> 50%). Meanwhile, characters with heritability values reaching a value of 90% and above were the number of branches

(98.03%), the number of bunches (97.90%), the number of total fruits (98.94), fruit weight (99.25%), the number of fruit cavities (92.25%), and yield (98.87%).

The result of factor analysis shows that there are six optimal factors with a total level of diversity of 0.818 or 81.8% (Table 3). The productivity character has a communality of 0.83 or 83% of the production data that has been collected in factor analysis. The fifth factor is the factor dimension with the highest yield loading factor value (-0.738) compared to other factor dimensions. The characters of the number of branches (-0.153), fruit weight (-0.132) and the number of total fruits (-0.298) are characters that have the same factor loading direction as yield and the value is considered quite good on the dimensions, of these factors.

Table 2. Mean squares and heritability values traits in F3 tomato lines population

Character	C	L	LvsC	Error	CV	VG	VP	H (%)
PH	1907.43**	1339.51**	5401.07**	142.39	8.92	239.42	267.90	89.37
DH	118.68ns	92.64ns	2800.15**	45.18	14.34	9.49	18.53	51.23
SD	2.99ns	4.45*	431.88**	1.69	8.79	0.55	0.89	61.98
NB	28.12**	78.81**	86.46**	1.55	14.69	15.45	15.76	**98.03**
FD	129.46**	37.61**	298.78**	9.08	5.16	5.71	7.52	75.87
HD	55.21ns	41.16ns	35.43ns	19.54	5.08	4.32	8.23	52.52
NFI	3.87**	1.05ns	349.99**	0.60	8.21	0.09	0.21	42.46
NFrI	2.41**	0.94*	279.62**	0.26	6.54	0.14	0.19	72.22
NI	146.05**	32.98**	446.25**	0.69	5.15	6.46	6.60	97.90
NTF	10658.43**	225.74**	15202.19**	2.39	8.54	44.67	45.15	**98.94**
FL	377.79**	23.56ns	228.79**	4.94	8.66	3.72	4.71	79.02
FD	582.45**	57.42**	441.98**	9.27	10.77	9.63	11.48	83.86
FW	1220.71**	107.25**	1562.46**	0.80	5.27	21.29	21.45	**99.25**
NC	30.31**	4.61**	101.45**	0.36	8.80	0.85	0.92	92.25
TDS	0.35*	0.30**	99.01**	0.07	5.60	0.05	0.06	76.92
NS	8.43**	4.31**	73.82**	0.85	9.48	0.69	0.86	80.39
Yield	8189.58**	7812.39**	43058.41**	88.19	7.54	1544.84	1562.48	**98.87**

Notes: **: significant effect on 1% level, *: significant effect on 5% level, ns: not significant, L: Lines, C: 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 day, NFI: number of flowers per inflorescence, NFrI: number of fruits per inflorescence, NI: number of the inflorescence, NTF: number of total fruits, FL: fruit length, FD: fruit diameter, FW: fruit weight, NC: number of cavities, TDS: total dissolved solids, NS: number of seeds per fruit

Table 3. Factor analysis of significant growth characters in F3 tomato lines

Variable	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Communality
PH	0.050	-0.050	-0.037	-0.025	0.078	0.538	0.657
SD	0.008	-0.030	0.208	-0.575	0.096	0.259	0.820
NB	0.007	0.048	-0.146	-0.626	-0.153	-0.215	0.863
FD	0.089	-0.014	-0.698	0.047	-0.036	-0.087	0.788
NFrI	0.055	-0.403	-0.396	-0.108	-0.066	0.103	0.765
NI	0.046	-0.561	-0.017	-0.006	0.061	0.097	0.837
FD	0.220	-0.016	-0.024	-0.011	-0.047	0.001	0.937
FW	0.239	-0.092	-0.045	-0.027	-0.132	-0.056	0.861
NC	0.234	-0.053	-0.038	-0.038	-0.109	-0.038	0.905
TDS	0.062	-0.394	0.242	0.144	-0.007	-0.224	0.760
NTF	-0.142	-0.009	0.172	-0.073	-0.298	-0.113	0.761
NS	0.120	0.006	-0.141	-0.021	0.318	-0.569	0.715
Yield	0.093	0.009	-0.097	-0.057	-0.738	0.042	0.830
Variance	4.508	1.689	1.357	1.333	1.289	1.273	11.448
% Var	0.322	0.121	0.097	0.095	0.092	0.091	0.818

Notes: PH: plant height, SD: stem diameter, NB: number of branches, FD: flowering days, NFI: number of fruits per Inflorescence, NI: number of the Inflorescence, NTF: number of total fruits, FD: fruit diameter, FW: fruit weight, NC: number of cavities, TDS: total dissolved solids, NS: number of seeds per fruit. The yellow background is the selected criteria selection for the F3 tomato line populations

The results of the narrow-sense heritability show that KM and MC populations have the same pattern toward a number of branches, fruit weight, the number of total fruits, and yield (Table 4). For the number of branches, KM and MC populations have narrow-sense heritability at 147.55 % and 198.57 %, respectively. For the fruit weight, KM and MC populations have narrow-sense heritability at 58.03 % and 52.69 %, respectively. For the number of total fruits, both KM and MC populations have narrow-sense heritability at -476.78% and -216.35 %, respectively. Meanwhile, for the yield, KM and MC populations have narrow-sense heritability at -38.73% and -69.08 %, respectively.

The results of the index selection are shown in Table 5. Based on the table, there are 32 lines that have a positive index value. In addition, based on a comparison to the best control, line KM14 (1.74) is the only one that has a better index value than the Mawar variety (1.35) as the best comparison variety in this study. Meanwhile, based on a comparison with the lowest control variety, Karina (0.44), there were 16 tomato lines that had a better index value than the Karina variety.

Discussion

The results of the analysis of variance show that the tomato F3 population in this study provided significant diversity in almost all growth characters. Meanwhile, some characters that are not influenced by the three sources of diversity at once, still have the opportunity to be included in further analysis. This is because the deeper analysis in this study only focused on the diversity of lines and the comparison of lines versus controls. This concept has also been reported by Nur (2021) in predicting the character of the selection process of evaluation and selection of maize based on the augmented design. Principally, the augmented design is focused on predicting the diversity of lines based on control varieties as the basis for error and environmental variability (Williams et al. 2011). This indicates that the use of controls with relatively consistent phenotypes is the key to evaluating lines in this design. In addition, the diversity of control-linear comparisons is also one of the considerations in the effectiveness of the evaluation and selection process. The source of the variance of the control-line comparison which was not significant, indicated that there was no difference between the control and the lines so the selection was considered less effective for these characters. Therefore, based on these considerations, the character of plant height, stem diameter, number of branches, flowering age, number of fruits, number of bunches, fruit diameter, fruit weight, number of cavities, brix content, total fruit number, number of seeds per fruit, and yield are characters that need to be analyzed further as a candidate for selection criteria in the formation of a selection index.

The formation of the selection index is based on the concept of Alsabah et al. (2019), Anshori et al. (2021), Akbar et al. (2021), and Anshori et al. (2022). Although they formed a selection index based on principal component analysis (PCA), however, the basic concepts of PCA and relative factor analysis have the same basis. Both analyzes compress data with large dimensions into a new, simpler dimension (Mattjik and Sumertajaya 2011), so that the PCA principle can be applied to factor analysis. Meanwhile, the concept of forming the selection index in question is the use of factor dimensions that collect the highest diversity (factor loading or eigenvalue) of the main characters as the basis for forming the selection index (Anshori et al. 2022).

The main character in this study is yield, therefore the determination of the best dimension in the formation of the selection index is based on this character. Based on the results of factor analysis, the dimension of factor 5 is the dimension that collects the greatest diversity in yield characteristics compared to other factor dimensions. This indicates that this dimension is the basis for determining the selection criteria and their weighting. Even though the dimension factor is 5, the yield character has a negative value. However, according to Jolliffe and Jorge (2016) and Anshori et al. (2022) a negative value on the eigenvalue or factor loading, in this case, only shows the direction of variance. This indicates that the character selected as the selection criteria is a character with a negative direction such as productivity. However, not all characters with a negative variance direction are selected to be selected characters. The selection is based on the value of the largest loading factor. This is the difference between PCA analysis and factor analysis. In addition to condensing data, factor analysis will also optimize large internal covariance and reduce or eliminate small internal covariance between characters on a dimension (Ebrahimnejad and Rameeh 2016).

Table 4. Narrow-sense heritability on two tomato lines population

Parameter	KM Population				MC Population			
	NB	FW (g)	NTF	Yield (g)	NB	FW (g)	NTF	Yield (g)
F2 based population (A)	6.39	15.13	98.95	193.59	6.68	11.71	105.10	235.18
F2 selected (B)	7.33	22.44	116.51	374.30	7.93	16.68	146.11	396.09
F3 selected (C)	7.78	19.37	15.24	123.60	9.15	14.33	16.37	124.03
Differential selection (S = B-A)	0.94	7.31	17.56	180.71	1.24	4.97	41.01	160.90
Selection gain (G= C-A)	1.39	4.24	-83.71	-69.99	2.46	2.62	-88.72	-111.15
h^2_{ns} (%) (G/Sx 100%)	147.55	58.03	-476.78	-38.73	198.57	52.69	-216.35	-69.08

Note: NB: number of branches; FW: fruit weight; NTF: number of total fruits, F2 &F3: folial 2 & folial 3

Table 5. A selection index of F3 tomato lines population

Rank	Genotype	Real values				Z-values				Index
		NB	FW	NFT	Yield	NB	FW	NFT	Yield	
1	KM14	4.89	31.10	9.17	252.51	-0.55	1.86	-0.73	3.22	1.74
2	Mawar	7.62	40.27	26.54	167.342	-0.11	3.13	1.09	1.07	1.35
3	KM36	7.69	20.90	22.16	187.50	-0.10	0.45	0.63	1.58	0.84
4	MC17	53.44	9.85	26.69	109.56	7.20	-1.07	1.11	-0.39	0.82
5	MC71	9.24	17.38	24.75	193.48	0.14	-0.03	0.91	1.73	0.80
6	KM25	6.38	28.86	15.49	154.77	-0.31	1.55	-0.07	0.75	0.79
7	MC50	5.56	27.21	15.45	158.17	-0.44	1.32	-0.07	0.84	0.74
8	MC35	9.18	15.26	15.78	191.84	0.13	-0.33	-0.04	1.69	0.71
9	KM85	6.44	26.32	16.16	150.18	-0.30	1.20	0.00	0.63	0.65
10	Tymoty	3.2	30.728	17.19	137.978	-0.82	1.81	0.11	0.33	0.62
11	MC31	9.18	20.14	20.03	162.08	0.14	0.35	0.41	0.94	0.61
12	MC67	6.56	24.10	16.71	152.49	-0.28	0.90	0.06	0.69	0.60
13	KM86	6.96	23.60	16.00	152.15	-0.22	0.83	-0.01	0.68	0.59
14	MC42	8.22	16.42	35.05	173.83	-0.02	-0.17	1.99	1.23	0.56
15	KM15	9.67	23.35	6.22	142.69	0.21	0.79	-1.04	0.45	0.56
16	KM1	7.56	22.58	6.75	149.15	-0.12	0.68	-0.98	0.61	0.54
17	KM68	7.26	21.27	8.05	154.36	-0.17	0.50	-0.85	0.74	0.53
18	KM35	9.23	32.90	8.93	103.06	0.14	2.11	-0.75	-0.56	0.52
19	Karina	7.168	23.338	21.192	137.114	-0.19	0.79	0.53	0.30	0.44
20	MC12	5.70	18.38	12.94	156.65	-0.42	0.11	-0.33	0.80	0.41
21	MC46	8.00	20.89	5.92	132.95	-0.05	0.45	-1.07	0.20	0.33
22	KM9	7.21	18.83	6.94	141.02	-0.18	0.17	-0.96	0.40	0.31
23	KM91	4.70	11.49	18.27	171.61	-0.58	-0.85	0.23	1.18	0.27
24	MC68	9.18	10.25	23.23	161.98	0.13	-1.02	0.75	0.93	0.25
25	MC48	5.56	14.11	15.83	155.59	-0.44	-0.48	-0.03	0.77	0.24
26	KM70	7.99	18.98	12.36	118.14	-0.05	0.19	-0.39	-0.18	0.13
27	MC7	8.24	22.60	9.41	102.01	-0.01	0.69	-0.70	-0.58	0.11
28	KM21	7.82	20.85	10.78	105.18	-0.08	0.45	-0.56	-0.50	0.07
29	KM32	7.06	16.46	8.13	124.25	-0.20	-0.16	-0.84	-0.02	0.07
30	KM10	8.22	27.09	6.84	78.82	-0.02	1.31	-0.97	-1.17	0.06
31	KM30	6.47	18.26	24.20	115.79	-0.30	0.09	0.85	-0.23	0.04
32	MC13	6.11	10.68	14.13	145.61	-0.36	-0.96	-0.21	0.52	0.03
33	MC8	9.22	12.50	15.93	129.20	0.14	-0.71	-0.02	0.10	0.02
34	KM26	8.49	16.17	13.99	115.59	0.02	-0.20	-0.22	-0.24	0.01
35	KM82	5.61	17.51	16.88	117.04	-0.44	-0.01	0.08	-0.20	0.00
36	MC9	8.11	8.93	24.88	133.14	-0.04	-1.20	0.92	0.20	-0.10
37	MC11	6.09	14.86	10.43	112.67	-0.36	-0.38	-0.60	-0.31	-0.12
38	KM3	9.35	10.72	20.61	113.15	0.16	-0.95	0.47	-0.30	-0.19
39	MC16	7.72	11.96	20.21	112.48	-0.10	-0.78	0.43	-0.32	-0.19
40	KM89	10.28	10.54	20.28	109.79	0.31	-0.98	0.44	-0.39	-0.20
41	KM5	12.44	2.44	71.02	135.20	0.66	-2.10	5.76	0.26	-0.21
42	KM31	7.62	13.84	12.52	101.65	-0.11	-0.52	-0.38	-0.59	-0.22
43	MC15	6.11	11.26	8.85	114.79	-0.36	-0.88	-0.76	-0.26	-0.23
44	MC38	6.95	16.64	17.05	88.52	-0.22	-0.14	0.10	-0.92	-0.26
45	MC32	9.14	9.97	7.78	108.34	0.13	-1.06	-0.87	-0.42	-0.27
46	KM24	9.31	14.50	11.43	90.19	0.16	-0.43	-0.49	-0.88	-0.27
47	KM62	9.65	16.50	15.29	72.71	0.21	-0.15	-0.09	-1.32	-0.35
48	MC26	7.38	13.54	13.28	89.70	-0.15	-0.56	-0.30	-0.89	-0.35
49	MC18	9.66	11.32	17.75	91.25	0.21	-0.87	0.17	-0.85	-0.36
50	MC51	4.33	11.45	8.94	103.69	-0.64	-0.85	-0.75	-0.54	-0.37
51	KM69	7.95	14.35	15.80	82.12	-0.06	-0.45	-0.03	-1.09	-0.38
52	KM73	8.27	19.40	10.57	56.71	-0.01	0.25	-0.58	-1.73	-0.43
53	KM8	5.56	24.14	6.78	41.88	-0.44	0.90	-0.98	-2.10	-0.46
54	MC19	4.97	9.86	13.14	96.81	-0.54	-1.07	-0.31	-0.71	-0.48
55	MC14	5.80	11.85	14.28	57.64	-0.40	-0.80	-0.19	-1.70	-0.75
56	MC29	9.45	8.02	16.71	62.90	0.18	-1.33	0.06	-1.57	-0.75
57	MC10	7.94	7.46	16.91	51.53	-0.06	-1.40	0.08	-1.86	-0.92

Notes: NB: number of branches, FW: fruit weight, NTF: number of total fruits, KM: Karina x Mawar population, MC: Mawar x Chung population

Based on this basis, the characters that deserve to be used as selection criteria are the number of branches (-0.153), fruit weight (-0.132), total fruit number (-0.298) and yield (-0.738). Although according to Taherdoost et al. (2020), the best character in a factor dimension is a character with a loading factor above 0.32. However, based on the pattern of factor loading values on the factor dimension 5, the value -0.1 becomes a barrier between characters with small internal covariance and large internal covariance. This is the basis for selecting the four characters as the selection criteria. Meanwhile, the number of cavities was not included as a selection criterion because the loading factor value was around -0.1 or -0.109 to be exact.

The selection of the number of branches, fruit weight and total fruit number as selection criteria was also supported by other research reports. The results of the research of Islam et al. (2010), Kumar and Paliwal (2016), Khapte and Jansirani (2014), Ritonga et al. (2018), and Mustafa et al. (2018) showed that the diversity of characters in the number of total fruits was strongly related to the diversity of tomato productivity. The research of Islam et al. (2010), Khapte and Jansirani (2014), Ritonga et al. (2018), Mustafa et al. (2018), Alam et al. (2019) and Maurya et al. (2020) reported the diversity of bo characters individual fruit bots also affect the diversity of tomato productivity in segregated populations. In addition, based on Bojarian et al. (2018), the diversity of the two characters detected has the same direction of diversity and magnitude of factor loading in factor analysis. The results of these reports indicate that the character of the number of total fruits and the weight of individual fruits are effective to be used as selection criteria for the companion of the yield. Meanwhile, the number of branches is relatively not widely reported by several studies. However, according to Maurya et al. (2020), the number of branches has a good correlation with productivity, so it has the potential to affect productivity diversity. This is also supported by a fairly good loading factor value. Therefore, based on these considerations, the character of the number of branches, fruit weight and total fruit number is very suitable to be used as a basis for forming a selection index with productivity.

The loading factor on the 5th-factor dimension can be the basis for determining the weight of the selection criteria in the selection index. However, determining the selection weights in segregated populations needs to pay attention to the narrow sense of heritability. The determination of the narrow-sense heritability can be based on the comparison of selection gain from the F3 generation to the differential selection of its F2 generation (Syukur et al. 2015; Evans et al. 2018). Based on the narrow-sense heritability, the value of narrow heritability has a different range with broad heritability, except for the fruit weight. The number of branches, the number of total fruits, and the yield have values outside of the normal range of heritability (0%-100%). It indicates three characters have over or underestimation in a narrow sense of heritability (Wang et al. 2013; Evans et al. 2018). Although, the number of branches togeher with fruit weight have positive heritability values and are higher than 50% in two tomato line populations, these can be categorized as high heritability (Acquaah 2007; Syukur et al. 2015). The high narrow-sense heritability can indicate that the selection in F2 is more dominated by additive gene role (Polderman et al. 2015), so the character with high narrow-sense heritability can be effective selection criteria. However, the number of branches is considered less effective than fruit weights. The overestimate of this character is caused by wielding in F3 being less intensive than the F2 generation. The number of samples per line is larger than F2 generation and the lack of labor is the reason for the less intensive wiping done in the F3 generation, so the number of branches is less able to be a good selection character compared to fruit weight. However, the number of branches is still better than the character of the number of total fruits and yield which has a negative narrow-sense heritability value. The negative heritability of the number of total fruits and yield characters indicated that both characters were still highly influenced by environmental influences (Wang et al. 2013; Evans et al. 2018). Although, these results cannot be separated from other influences, such as the dominant influence and epistasis. However, a too-low narrow-sense heritability value (negative) indicates a high environmental difference between the F2 and F3 generations (Tenesa and Haley 2013; Evans et al. 2018), where the F2 generation environment is more optimal than the F3 generation. Therefore, the character of fruit weight is prioritized in this selection, so that the concept of priority on the selection index is conducted semi-objectively.

The semi-objective concept in forming the selection index is done by doubling the factor loading value on the factor dimension 5. This concept has been reported by Alsabah et al. (2019) on the selection of dihaploid black rice lines. The results of this study used the multiplication of 3 on the productivity character eigenvectors based on the comparison of the ratio between productive tillers and the yield in several previous studies. This concept can also be applied to this research. In this research, the factor loading of fruit weight, as a priority character, is multiplied by two, the factor loading of the number of branches is multiplied by 1, while the factor loading of the number of total fruits and the yield is multiplied by 0.5. Therefore, the formulation formed is:

Selection index = (0.5x0.738) yield + 0.153 NB + 2 x 0.132 FW +(0.5 x 0.298) NFT
Selection index = 0.369 yield + 0.153 number of branches + 0.264 fruit weight + 0.149 number of total fruits

Based on the results of the index, there are 32 lines that can be recommended to be further analyzed in the next generation. Although, selection can be made based on comparisons with control varieties (Suwarno et al. 2009; Anshori et al. 2021; Anshori et al. 2022), however, consider that F3 is still at the beginning of the generation, so the selection is not carried out strictly. Therefore, these 32 lines are preferred as the lines that will be continued in the F4. However, 14 lines that were better than the

comparison varieties of Karina were further selected for their transgressive segregation characteristics in the F4.

In summary, the selection index based on narrow-sense heritability and factor analysis was considered effective in the selection of tomato lines of the F3 generation. The effective selection criteria in this study were the yield, fruit weight, number of branches, and total fruit number. The priority character besides yield in this study is fruit weight with high and normal narrow-sense heritability. The selection index formulation formed was 0.369 yield + 0.153 number of branches + 0.264 fruit weight + 0.149 number of total fruits. The results of the index selection show that there are 32 tomato lines from the F3 generation that are eligible to be passed on to the F4 generation. Meanwhile, 14 lines of them recommended analyzing transgressive segregation in the F4 generation.

ACKNOWLEDGEMENTS

REFERENCES

Acquaah G. 2007. Principles of Plant Genetics and Breeding. Blackwell Publishing, Oxford.

Afifah EN, Murti RH, Wahyudhi A. 2021. Evaluation of a promising tomato line (*Solanum lycopersicum*) derived from mutation breeding. Biodiversitas 22: 1863-1868. DOI: 10.13057/biodiv/d220432.

Akbar MR, Purwoko BS, Dewi IS, Suwarno WB, Sugiyanta, Anshori MF. 2021. Agronomic and yield selection of doubled haploid lines of rainfed lowland rice in advanced yield trials. Biodiversitas 22: 3006-3012. DOI: 10.13057/biodiv/d220754.

Alam MdS, Huda MdN, Rahman MdS, Azad AKM, Rahman MdM, Molla MM. 2019. Character association and path analysis of tomato (*Solanum lycopersicum* L.). J Biosci Agric Res 22 (1): 1815-1822.

Ali F, Kanwal N, Ahsan M, Ali Q, Bibi I, Niazi NK. 2015. Multivariate analysis of grain yield and its attributing traits in different maize hybrids grown under heat and drought stress. Scientifica 563869. DOI: 10.1155/2015/563869.

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.

Anisa WN, Afifah EN, Murti RH. 2022. Selection of tomato breeding lines based on morphological traits associated with high yield potential in double-cross population. Biodiversitas 23 (6): 2973-2980. DOI: 10.13057/biodiv/d230624.

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. DOI: 10.1016/j.rsci.2021.05.007.

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. DOI: 10.3934/agrfood.2022032.

Arifuddin M, Musa Y, Farid M, Anshori MF, Nasaruddin N, Nur A, Sakinah AI. 2021. Rice screening with hydroponic deep-flow technique under salinity stress. SABRAO J Breed Genet 53 (3): 435-446.

Authrapun J, Lertsuchatavanich U, Kang D. 2021. Selection for improving field resistance to capsicum chlorosis virus and yield-related traits using selection indices in peanut breeding. Acta Sci Agric 5 (6): 22-31. DOI: 10.31080/ASAG.2021.05.1001.

Barth E, de Resende JTV, Mariguele KH, de Resende MDV, da Silva ALBR, Ru S. 2022. Multivariate analysis methods improve the selection of strawberry genotypes with low cold requirement. Sci Rep (2022) 12: 11458. DOI: 10.1038/s41598-022-15688-4.

Bojarian M, Asadi-Gharneh HA, and Golabadi M. 2018. Factor analysis, stepwise regression, and path coefficient analyses of yield, yield associated traits, and fruit quality in tomato. Intl J Veg Sci 25: 542-553. DOI: 10.1080/19315260.2018.1551260.

Ebrahimnejad S, Rameeh V. 2016. Correlation and factor analysis of grain yield and some important component characters in spring bread wheat genotypes. Cercetări Agronomice în Moldova 165: 5-15. DOI: 10.1515/cerce-2016-0001.

Evans ML, Tahmasbi R, Jones M, Vrieze S, Abecasis GR, Das S, Bjelland DW, de Candia TR, Yang J, Goddard ME, Visscher PM, Keller MC. 2018. Narrow-sense heritability estimation of complex traits using identity-by-descent information. Heredity 121: 616-630. DOI: 10.1038/s41437-018-0067-0.

Farid M, Nasaruddin, Musa Y, Anshori, MF, Ridwan I, Hendra J. 2020. Genetic parameters and multivariate analysis to determine secondary traits in selecting wheat mutant adaptive on tropical lowlands. Plant Breed Biotechnol 8 (4): 368-377. DOI: 10.9787/PBB.2020.8.4.368.

Farid M, Nasaruddin, Anshori MF, Musa Y, Iswoyo H, Sakinah AI. 2021. Interaction of rice salinity screening in germination and seedling phase through selection index based on principal components. Chile J Agric Res 81: 368-377. DOI: 10.4067/S0718-58392021000300368.

Farid M, Anshori MF, Ridwan I, Dungga NE, Ermiyanti I. 2022. Half diallel of F1 tomato hybrid and its double cross-compatibility. Biodiversitas 23 (4): 1813-1821. DOI: 10.13057/biodiv/d230413.

Holme IB, Gregersen PL, Brinch-Pedersen H. 2019. Induced genetic variation in crop plants by random or targeted mutagenesis: Convergence and differences. Front Plant Sci 10: 1468. DOI: 10.3389/fpls.2019.01468.

Islam BMR, Ivy NA, Rasul MG, Zakaria M. 2010. Character association and path analysis of exotic tomato (*Solanum lycopersicum* L.) genotypes. Bangladesh J Plant Breed Genet 23 (1): 13-18. DOI: 10.3329/bjpbg.v23i1.9313.

Jolliffe IT, Jorge C. 2016. Principal component analysis: a review and recent developments. Philos Trans R Soc A 374: 20150202. DOI: 10.1098/rsta.2015.0202.

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

Kumar P, Paliwal A. 2016. Heterosis breeding for quality improvement in tomato (*Lycopersicon esculentum* Mill.) for cultivation in mid hills of Uttarakhand. Intl J New Technol Res 2: 75-78.

Lopez-Gomollon S, Müller SY, Baulcombe DC. 2022. Interspecific hybridization in tomato influences endogenous viral sRNAs and alters gene expression. Gen Biol 23: 120. DOI: 10.1186/s13059-022-02685-z.

Mattjik AA, Sumertajaya IM. 2011. Multivariate Analysis Using SAS. Statistika F-MIPA Institut Pertanian Bogor, Bogor. [Indonesian]

Maurya AK, Yadav RK, Singh AK, Deep A, Yadav V. 2020. Studies on correlation and path coefficients analysis in bread wheat (*Triticum aestivum* L.). J Pharmac Phytochem 9 (4): 524-527.

Medico APD, Cabodevila VG, Vitelleschi MS, Pratta GR. 2020. Characterization of tomato generations according to a three-way data analysis. Bragantia 79 (1): 8-18. DOI: 10.1590/1678-4499.20190047.

Mustafa M, Syukur M, Sutjahji SH, Sobir. 2018. Determination of selection criteria for tomato (*Solanum lycopersicum* L.) yield component in the lowland based on path analysis. Agrotech J 3 (1): 34-41. DOI: 10.31327/atj.v3i1.556.

Nur A, Riadi M, Yassi A, Farid M, Anshori MF, Akfindarwan AK. 2021. Selection and evaluation the corn lines from multiple-cross progeny based on targeted selection environment on acid soil. IOP Conf Ser Earth Environ Sci 911 (1): 012016. DOI: 10.1088/1755-1315/911/1/012016.

Oliveira GHF, Amaral CB, Silva FAM, Dutra SMF, Marcanato MB, Moro GV. 2016. Mixed models and multivariate analysis for selection of superior maize genotypes. Chilean J Agric Res 76 (4): 427-431. DOI: 10.4067/S0718-58392016000400005.

Olivieri F, Graci S, Francesca S, Rigano MM, Barone A. 2021. Accelerating the development of heat tolerant tomato hybrids through a multi-traits evaluation of parental lines combining phenotypic and genotypic analysis. Plants (Basel) 13 (10): 2168. DOI: 10.3390/plants10102168.

Polderman TJC, Benyamin B, de Leeuw CA, Sullivan PF, van Bochoven A, Visscher PM, Posthuma D. 2015. Meta-analysis of the heritability of human traits based on fifty years of twin studies. Nat Genet 47: 702-709. DOI: 10.1038/ng.3285.

Quinet M, Angosto T, Yuste-Lisbona FJ, Blanchard-Gros R, Bigot S, Martinez J-P, Lutt S. 2019. Tomato fruit development and metabolism. Front Plant Sci 10: 1554. DOI: 10.3389/fpls.2019.01554.

Reddy VR, Jabeen F. 2016. Narrow-sense heritability, correlation and path analysis in maize (*Zea mays* L.). SABRAO J Breed Genet 48 (2): 120-126.

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. DOI: 10.13057/biodiv/d190445.

Suwarno, Lubis E, Hairmansis A, Santoso. 2009. Development of a package of 20 varieties for blast management on upland rice. In: Wang GL, Valent B (eds). Advances in Genetics, Genomics and Control of Rice Blast Disease. Springer Netherlands, Dordrecht.

Syukur M, Sujiprihati S, Yunianti R. 2015. Plant Breeding Techniques. Penebar Swadaya, Depok. [Indonesian]

Taherdoost H, Sahibuddin S, Jalaliyoon N. 2014. Exploratory factor analysis: Concepts and theory. In: Jerzy B (ed). Advances in Applied and Pure Mathematics 27, WSEAS. Mathematics and Computers in Science and Engineering Series, 978-960-474-380-3. 02557344.

Tenesa A, Haley CS. 2013. The heritability of human disease: estimation, uses and abuses. Nat Rev Genet 14: 139-149. DOI: 10.1038/nrg3377.

Wang K, Chen Z. 2016. Stepwise regression and all possible subsets regression in education. Electron Intl J Educ Arts Sci 2: 60-81.

Wang Y, Vik OJ, Omholt SW, Gjuvsland AB. 2013. Effect of regulatory architecture on broad versus narrow-sense heritability. PLoS Comput Biol 9(5): e1003053. DOI: 10.1371/journal.pcbi.1003053.

Wei X, Zhang J. 2018. The optimal mating distance resulting from heterosis and genetic incompatibility. Sci Adv 4 (11): eaau5518. DOI: 10.1126/sciadv. aau5518.

Williams E, Piepho HP, Whitaker D. 2011. Augmented p-rep designs. Biometrical J 53: 19-27. DOI: 10.1002/bimj.201000102.

You MK, Song Q, Jia G, Cheng Y, Duguid S, Booker H, Cloutier S. 2016. Estimation of genetic parameters and their sampling variances for quantitative traits in the type 2 modified augmented design. Crop J 4: 107-118. DOI: 10.1016/j.cj.2016.01.003.