

The selection index of S3 corn convergent breeding population based on multivariate analysis

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Abstract. Makmur, Farid M, Ala A, Mandja K, Anshori MF, Fadhilah AN. 2024. *The selection index of S3 corn convergent breeding population based on multivariate analysis. Biodiversitas 25: 1097-1103.* Corn is one of the most important and strategic food crops in the world, including Indonesia. Increasing corn production through a plant breeding program by assembling hybrid varieties begins with developing a convergent breeding population and index selection. The research aims to identify genetic variance and the effectiveness of selection indices in selecting high-yield S3 cross populations. The research was carried out in Rea Village, Binuang Sub-District, Polewali Mandar District, West Sulawesi from July to November 2022. The research used an augmented design with four blocks. Sixty-six lines were derived from 4 double cross populations and 8 populations of the S3 generation multiple-cross population, as well as 9 check varieties (NK7328, Pioneer 36, Bisi 18, Bisi 2, NK99, Nasa 29, JH45, Bisi 9, and NK212) were used in this study. The results indicate that the length of cobs (5.98;73.59%), length of seed cobs (7.06; 79.46%), weight of 100 seeds (7.75; 89.30%), and weight of seeds per cob (7.84; 65.59%) have moderate genetic variance and high heritability. The characteristics of stem diameter, yield percentage, and weight of seed per cob were effectively used in the selection index formulation. Based on the index selection, there were 14 potential corn lines with a good performance, recommended for the next hybridization stage.

Keywords: Double cross, magic population, maize, lines, yield

Abbreviations: CV: Coefficient of Variance, VG: Variance of Genotype, VP: Variance of Phenotype, GDC: Genetic Diversity Coefficient

INTRODUCTION

Corn (*Zea mays* L.) is one of the essential food crops in the world and has a strategic role in the economy of a country, including Indonesia. Indonesia's corn productivity is around 5.2 tons ha⁻¹ and has experienced a low increase of around 0.20% from 2021 to 2022. This is not comparable to the production potential of varieties that can achieve yields of 10-12 ton ha⁻¹ (BPS-statistics Indonesia 2023). Therefore, variety development is always carried out in Indonesia, both hybrid varieties and open pollinated varieties (Azizah et al. 2017; Amas et al. 2021).

Variety development can be done through plant breeding programs. This program is a dynamic and sustainable activity in increasing plant productivity (Jambormias et al. 2015). In general, maize breeding is directed at the formation of hybrid varieties and free-pollinated varieties (Masuka et al. 2017). However, hybrid varieties are the dominant varieties to be developed (Padjung et al. 2021). In current developments, population formation can be carried out using the concept of convergent breeding to obtain genetic diversity in a population (Syukur et al. 2015). It is based on combining several generations of lines resulting from crosses with different characteristics to form a new population (Huang et al. 2015), to increase the efficiency of the breeding program to get more profitable

cross combinations (Siswati et al. 2015). This also allows new combinations of traits to occur from the interaction of genes from a group of different parents, especially in corn hybrids, which have the concept of heterosis.

Selfing in the third generation (S3) is one of the initial generations that carry out the process of breeding through artificial self-pollination in order to produce pure lines that act as parents in forming hybrid varieties (Acquaah 2015). S3 selfing is considered to have relatively high diversity, even though the population has experienced an increase in homozygosity and a decrease in line diversity in the population (Wulan et al. 2017). Therefore, breeding in this generation is essential because the population will continue to experience inbreeding depression in the next generation, so a practical concept is needed in the selection process in the S3 generation (Mawikere et al. 2015).

Selection criteria are characters that are closely related to breeding objectives and are the basis for the selection process. However, selection with a multi-character concept needs to consider genetic parameters and the concept of combining the selection characters. The use of genetic diversity and heritability are genetic parameters that must be known in selection (Priyanto et al. 2018; Anshori et al. 2022). In addition, the use of productivity as the main character is controlled by many genes, so the effectiveness of selection needs to include several production-supporting

characters to increase the stability and accuracy of selection (Kassahun et al. 2013; Fellahi et al. 2018; Padjung et al. 2021). These supporting characters must have a strong relationship with productivity characters, so that the estimation of productivity supporting selection criteria is carried out systematically (Silva et al. 2020; Padjung et al. 2021; Amegbor et al. 2022; Akfindarwan et al. 2023). Therefore, the use of several selection criteria with high genetic diversity is important in selection. One selection method that can collect several selection criteria effectively is the selection index.

The selection index is a multiple linear regression equation of selection criteria with specific weight values (Simeão et al. 2015; Fadhilah et al. 2022). The selection index method is a selection method that was developed with the aim of being able to select superior genotypes according to the desired goals (Hapsari 2014). The weighting value can be a priority value between selection criteria. This concept is considered adequate in multi-character-based selection. A crucial thing in developing a selection index is determining the weight values in the selection index (Amzeri et al. 2020). This can be done through heritability and statistical approaches, such as principal components analysis. Principal component analysis can combine selection criteria into a dimension with specific eigenvector values as weight values (Ramos et al. 2014; Gazal et al. 2017). Therefore, the concept of index formation can also be applied to the S3 corn screening process. This research aims to determine the selection criteria and index for S3 corn lines and to select potential lines that can proceed to the hybridization stage.

MATERIALS AND METHODS

Plant materials and experimental design

The plant materials or genotypes used in this study were S3 convergent breeding lines and check varieties. Convergent breeding lines were generated from 4 populations double cross and 4 population of multiple cross of the S3 generation (Table 1). In addition, nine check varieties were also used, namely NK7328, Pioneer 36 (P36), Bisi 18 (B18), Bisi 2

(B2), NK99, Nasa 29 (N29), JH45, Bisi 9 (B9), and NK212. This research was arranged in an augmented design, with the randomized completed block design as its environmental design. All lines as non-repeating factors were distributed into 4 blocks, while all check varieties were repeated in all blocks. This combination generated 97 experimental units (61 units for lines + 36 units for check) and each experimental unit planted 30 individual plants, so there were 2910 individual plants.

Field experiment

The research was carried out from July to November 2022 in Rea Village, Binuang District, Polewali Mandar Regency, West Sulawesi with altitude of 24 m above sea level. These locations have rainfall patterns of 426 mm for July, 69 mm for August, 161 mm for September, 403 mm for October, and 345 for November 2022 Land preparation began with cleaning the land from weed residues, then plowing the land. The land was then made into 4 blocks with dimensions of 6,5 m x 35 m and a distance between blocks of 100 cm. For each experimental unit, there were two rows or 30 plants. Two seeds were sown in each plant hole with a spacing of 70 x 20 cm. After 2 weeks, thinning and replanting were carried out in each hole, so that each hole only contained one plant.

Fertilization, irrigation, weeding, hilling, disease and insect control are maintenance activities in this research. Fertilization was carried out three times using urea, SP36, and Phonska fertilizer at the ages of 7 Days After Planting (DAP), 35 DAP, and 50 DAP. Irrigation is carried out every 10 days until harvest, depending on weather conditions. Weeding was carried out when the plants were 10 DAP and 35 DAP by cleaning the weeds around the corn plants. Hilling was carried out when the plants were 35 DAP by raising the mound and loosening the soil. Pest and disease control were carried out by spraying pesticide.

Selfing was carried out to the S3 lines on 10 plants per line, and 20 other plants were allowed to reproduce open-pollinated for evaluation. On other hands, the check varieties were allowed to open-pollinate. Harvesting was done at the cobs have experienced physiological maturity (black spots at the base of seed) or around 100 DAP.

Table 1. The lines detail as unrepeated genotypes

Label	The crossing details	Population	Number of lines
DC1	(P36 F1/B9 F1)	Double cross	9
DC2	(B9 F1/P36 F1)	Double cross	3
DC3	(NK7328 F1/HJ28 F1)	Double cross	5
DC4	(HJ28 F1/NK7328 F1)	Double cross	13
MC1	P36/B9//NK7328/JH28//B18/JH45//N29/B2	Multiple cross	13
MC2	B9/P36//HJ28/NK7328//HJ28//B18//N29/B2	Multiple cross	10
MC5	HJ28/NK7328//B9/P36//N29/B2//HJ28/NK7328	Multiple cross	6
MC7	NK7328/HJ28//P36/B9//B2/N29//B18/JH45	Multiple cross	2
Sum of selected lines from S1			61

Note: DC: Double Cross, MC: Multiple Cross

Observation parameters and data analysis

The parameters observed were plant height, number of leaves, stem diameter, cob height, male flowering age, female flowering age, anthesis silking interval, diameter of cobs, length of cobs, length of seed cobs, number of rows per cob, number of seeds per row, weight of 100 seeds, yield percentage, and weight of seeds per cob. The data obtained were analyzed using variance analysis according to *augmented design* (Federer and Raghavarao 1975; You et al. 2016; Fadhilah et al. 2022; Malaquias et al. 2022). The ANOVA results are the basis for determining character's broad sense heritability according to Lestari et al. (2012), where the heritability classification was divided into three, namely high (>50%), moderate (20-50%) and low (<20%) (Acquaah 2015; Syukur et al. 2015; Fadhilah et al. 2022). Besides broad heritability, determination of genotypic coefficient of variability (GCV) also was analyzed by following formula of $GCV = \sqrt{(\sigma_g)/X} \times 100\%$, where σ_g = Genetic variance and X = Mean of populations. The GCV criteria also consisted of three, namely great (>14.5%), moderate (5-14.5%), and narrow (0-5%) (Milligan et al. 1996). The selection criteria are determined systematically through Pearson correlation analysis and path analysis to determine the close relationship between supporting characters and the main characters, then combined into a selection index based on the direct influence of cross-prints.

RESULTS AND DISCUSSION

Variance analysis

The results of variance analysis showed that almost all characters were influenced by genotype, check and the comparison of lines and check (lines vs check), except for several characters. The character number of leaves and stem diameter are influenced by lines and comparison of line and check. The character of male flowering age and female flowering age is only influenced by check variance. Meanwhile, the Anthesis Silking Interval (ASI), diameter of cobs, number of rows per cobs, and weight of cobs have been influenced by check and comparison line vs check variance (Table 2). Based on the overall character, coefficient of variance values range from 5.38-14.58.

Genetic variance coefficient and heritability

The Genetic Diversity Coefficient (GDC) in Table 3 shows that almost all of the observed characters have relatively narrow GDC values ranging from 0.68-4.73, except for the character's length of cobs (5.98), length of seed cobs (7.06), weight of seeds per cob (7.84), and weight of 100 seeds (7.75) with a medium GDC value. Based on the heritability value, the weight of 100 seeds character has the highest heritability (89.30). At the same time, the Anthesis Silking Interval (ASI) has the lowest heritability (4.20).

Correlation among selected traits

The results of the correlation analysis showed that the characters that were significantly positively correlated with the weight of seeds per cob character were stem diameter

(0.84**), cob height (0.60**), diameter of cobs (0.81**), length of cobs (0.73**), number of rows per cob (0.50**), number of seeds per row (0.78**), weight of 100 seeds (0.40**), and yield percentage (0.78*). The character that was significantly negatively correlated with the character of weight of seeds per cob was the character plant height (-0.10**), male flowering age (-0.47**) and female flowering age (-0.32**). In addition, the characters that do not correlate with the characteristics of weight of seeds per cob, namely the number of leaves, Anthesis Silking Interval (ASI), weight of cob, and length of seed cobs (Table 4).

Path analysis and selection index value

The path analysis results show a determination value of 0.6183 for the path analysis model (Table 5). Based on the path analysis results, stem diameter (0.28), diameter of cobs (0.20) and yield percentage (0.37) had a sizeable direct influence on the characteristics of weight of seeds per cob. The selection index value based on path analysis (Table 6) is formed from a combination of four characters, namely stem diameter, diameter of cobs, yield and weight of seeds per cob. Therefore, the selection index developed in this research is,

Selection Index = weight of seeds per cob + (0.28 x 0.6183 x stem diameter) + (0.37 x 0.6183 x yield percentage)

Based on this selection index, there were 5 lines resulting from the double cross and 9 lines resulting from the multiple crosspopulation, which have positive index values, and almost all of the selected lines have better index values than comparison varieties.

Table 2. Analysis of variance from Augmented design to the growth characteristics of S3 generation corn

Character	Source of variation			CV
	C	L	L vs C	
PH	620.54**	189.16**	4766.97**	5.53
NL	0.92ns	1.13**	25.12**	6.63
SD	1.30ns	2.42*	15.42**	5.53
CH	281.25**	111.92**	10250.93**	5.38
MFA	40.57*	18.11ns	11.27ns	7.64
FFA	49.04*	17.53ns	13.46ns	7.74
ASI	4.30**	0.28ns	2.90**	13.70
WC	478.37*	322.13ns	4607.67**	14.58
DC	14.60*	4.96ns	71.18**	5.51
LC	9.08**	6.48**	48.47**	8.02
LSC	5.37**	7.64**	11.49*	8.04
NRC	7.85**	1.56ns	8.31*	7.89
NSR	21.79**	13.48**	76.97**	6.98
W100S	6.49*	8.42**	23.63**	6.01
Y	101.77*	66.98*	280.27**	9.15
WSC	474.38**	167.80**	1061.06**	12.69

Note: **: Significant effect on 1% level, *: Significant effect on 5% level, ns: Not significant, L: Lines, C: Check, CV: Coefficient of Variance, PH: Plant Height, NL: Number of Leaves, SD: Stem Diameter, CH: Cob Height, MFA: Male Flowering Age, FFA: Female Flowering Age, ASI: Anthesis Silking Interval, DC: Diameter of Cobs, LC: Length of Cobs, LSC: Length of Seed Cobs, NRC: Number of Rows per Cob, NSR: Number of Seeds per Row, WSC: Weight of Seeds per Cob, W100S: Weight of 100 Seeds, Y: Yield, WSC: Weight of Seed per Cob

Discussion

The results of the analysis of variance in this study showed that differences in genotypes and comparison between genotypes and checks had a significant to very significant effect on the 10 observed characters. These characters can then be used as a basis for determining the effectiveness of a selection. In general, significant variance is the initial basis for determining the effectiveness of selection on a character, and the source of line diversity, as well as comparison between lines and checks, are essential assessments in the line selection process (Litrico and Violle 2015; Fellahi et al. 2018; Priyanto et al. 2018; Anshori et al. 2022). The coefficient of diversity value for each character ranges from 5.38-14.58. Therefore, based on these aspects of consideration, the characteristics of plant height, number of leaves, stem diameter, cob height, length of cobs, length of seed cobs, number of seeds per row, weight of seeds per cob, weight of 100 seeds, and yield are appropriate characters for further analysis as a candidate for selection criteria in the distribution process.

The results of the Genetic Diversity Coefficient (GDC) analysis show that there are 12 genotypes with narrow GDC values and 4 genotypes with medium GDC values. In the S3 population resulting from crosses, the segregation that occurs begins to decrease compared to the previous generation, so the genetic diversity obtained will be narrower. In addition, heritability estimation can show whether a character is controlled by genetic or environmental factors so that it can be seen to what extent the character can be passed on to subsequent offspring (Syukur et al. 2015).

Almost all of the observed characters are dominated by heritability values in the medium and high categories, so it can be said that these characters show a more significant genetic influence than their environmental influence. Characters that show high heritability values and broad GDC can be continued at the selection stage. However, if there are characters with narrow GDC values, they can still be considered if the heritability value in the population remains high (Rosyidah et al. 2016). The heritability value

can be used to determine selection progress, where the higher the heritability value of a character, the greater the selection progress that can be achieved through the selection of that character (Hidayatullah et al. 2018). However, if the character is not closely related to the main objective, namely WSC, then the character is not worthy of being used as a selection criterion. Therefore, the relationship between the main character and other characters in this study is known through correlation analysis and path analysis.

Table 3. Genetic diversity coefficient and heritability

Character	VG	VP	GDC		Heritability	
			(%)	Criteria	Character	VG
PH	21.08	37.83	2.78	Narrow	55.72	High
NL	0.13	0.23	3.39	Narrow	55.84	High
SD	0.23	0.48	2.35	Narrow	47.45	Moderate
CH	17.32	22.38	4.45	Narrow	77.37	High
MFA	0.60	3.62	1.46	Narrow	16.45	Low
FFA	0.15	3.51	0.76	Narrow	4.31	Low
ASI	0.002	0.06	1.18	Narrow	4.20	Low
WC	22.20	64.43	4.73	Narrow	34.46	Moderate
DC	0.07	0.99	0.68	Narrow	7.04	Low
LC	0.95	1.30	5.98	Moderate	73.59	High
LSC	1.21	1.53	7.06	Moderate	79.46	High
NRC	0.07	0.31	1.91	Narrow	23.23	Moderate
NSR	1.50	2.70	3.50	Narrow	55.79	High
W100S	1.50	1.68	7.75	Moderate	89.30	High
YP	6.56	13.40	4.01	Narrow	48.99	Moderate
WSC	22.01	33.56	7.84	Moderate	65.59	High
ASI	22.20	64.43	4.73	Narrow	34.46	Moderate

Note: VG: Variance of Genotypes, VP: Variance of Phenotypes, GDC: Genetic Diversity Coefficient, PH: Plant Height, NL: Number of Leaves, SD: Stem Diameter, CH: Cob Height, MFA: Male Flowering Age, FFA: Female Flowering Age, ASI: Anthesis Silking Interval, DC: Diameter of Cobs, LC: Length of Cobs, LSC: Length of Seed Cobs, NRC: Number of Rows per Cob, NSR: Number of Seeds per Row, WSC: Weight of Seeds per Cob, W100S: Weight of 100 Seeds, BY: Yield Percentage, WC: Weight of Cob. The bold letter indicated the best heritability among growth parameters

Table 4. Pearson correlation for the selected traits in maize

	PH	NL	SD	CH	MFA	FFA	ASI	WC	DC	LC	LSC	NRC	NSR	W100S	YP
NL	0.05ns														
SD	-0.04ns	0.03ns													
CH	-0.12ns	0.001ns	0.62**												
MFA	-0.09ns	-0.08ns	-0.47**	-0.25**											
FFA	-0.08ns	0.003ns	-0.30**	-0.12*	0.55**										
ASI	0.02ns	0.04ns	-0.04ns	-0.01ns	0.04ns	0.09ns									
WC	0.26ns	0.02ns	0.06ns	0.01ns	-0.07ns	-0.10ns	0.03ns								
DC	-0.02ns	0.05ns	0.80**	0.51**	-0.57**	-0.40**	-0.11*	0.06ns							
LC	-0.04ns	0.05ns	0.72**	0.53**	-0.46**	-0.29**	-0.07ns	0.09ns	0.78**						
LSC	-0.003ns	-0.004ns	-0.01ns	-0.06ns	-0.08ns	-0.11*	0.07ns	-0.05ns	0.06ns	-0.07ns					
NSC	-0.02ns	-0.004ns	0.52**	0.30**	-0.27**	-0.14**	-0.00004ns	0.09ns	0.51**	0.40**	-0.02ns				
NSR	-0.10*	0.01ns	0.78**	0.58**	-0.40**	-0.27**	-0.08ns	0.03ns	0.80**	0.72**	-0.06ns	0.48**			
W100S	-0.02ns	-0.02ns	0.41**	0.34**	-0.18**	-0.11*	-0.04ns	-0.07ns	0.43**	0.37**	0.03ns	0.13**	0.40**		
YP	-0.26**	0.03ns	0.63**	0.49**	-0.33**	-0.18**	-0.05ns	-0.53**	0.60**	0.52**	0.03ns	0.33**	0.60**	0.35**	
WSC	-0.10*	0.05ns	0.84**	0.60**	-0.47**	-0.32**	-0.05ns	0.09ns	0.81**	0.73**	-0.04ns	0.50**	0.78**	0.40**	0.78**

Notes: **: Significant effect on 1% level, *: Significant effect on 5% level, ns: Not significant, PH: Plant Height, NL: Number of Leaves, SD: Stem Diameter, CH: Cob Height, MFA: Male Flowering Age, FFA: Female Flowering Age, ASI: Anthesis Silking Interval, DC: Diameter of Cobs, WC: Weight of Cobs, LC: Length of Cobs, LSC: Length of Seed Cobs, NRC: Number of Rows per Cob, NSR: Number of Seeds per Row, W100S: Weight of 100 Seeds, YP: Yield Percentage, WSC: Weight of Seeds per Cob

Table 5. Path analysis for maize based on the traits with the highest correlation to weight of seeds per cob

Traits	SD	CH	DC	LC	NRC	NSR	W100S	PY	Res
SD	0.28	0.03	0.16	0.07	0.03	0.04	-0.004	0.23	0.84
CH	0.17	0.05	0.10	0.05	0.02	0.03	-0.003	0.18	0.60
DC	0.22	0.03	0.20	0.08	0.03	0.04	-0.004	0.22	0.81
LC	0.20	0.03	0.16	0.10	0.02	0.04	-0.004	0.19	0.73
NRC	0.15	0.01	0.10	0.04	0.06	0.02	-0.001	0.12	0.50
NSR	0.22	0.03	0.16	0.07	0.03	0.05	-0.004	0.22	0.78
W100S	0.11	0.02	0.09	0.04	0.01	0.02	-0.01	0.13	0.40
PY	0.18	0.02	0.12	0.05	0.02	0.03	-0.004	0.37	0.78

Notes: Numbers in bold indicate a direct effect, cross-print R2: 61.83, Res: Residual, SD: Stem Diameter, CH: Cob Height, DC: Diameter of Cob, LC: Length of Cob, NRC: Number of Rows per Cob, NSR: Number of Seeds per Row, W100S: Weight of 100 Seeds, YP: Yield Percentage

Table 6. The best lines selected based on the total number of fruit characters

Lines	Actual value		Standardization			Index selection	
	WSC	SD	BY	WSC	SD		PY
MC1.5.2.5	98.8	20.41	69.22	2.69	-0.07	0.57	2.81
MC2.3.8.4	96.67	20.06	71.09	2.54	-0.29	0.75	2.66
MC2.23.1.3	91.68	23.08	64.06	2.2	1.55	0.05	2.48
MC1.5.7.5	90.37	21.18	70.25	2.11	0.4	0.67	2.33
MC2.22.9.2	93.46	19.27	68.59	2.32	-0.76	0.5	2.30
DC2.7.14.2	87.7	20.44	70.77	1.93	-0.05	0.72	2.09
DC2.12.3.2	84.24	20.41	76.88	1.69	-0.07	1.33	1.98
MC5.2.6.2	85.87	19.72	72.07	1.8	-0.49	0.85	1.91
DC4.27.5.3	86.03	22.24	59.1	1.81	1.04	-0.44	1.89
DC4.24.13.1	82.91	23.2	63.41	1.6	1.62	-0.01	1.88
MC5.1.4.1	84.35	20.6	69.19	1.7	0.04	0.56	1.84
DC2.25.6.1	86.6	18.98	69.08	1.85	-0.94	0.55	1.81
MC1.5.4.1	83.06	21.66	61.41	1.61	0.69	-0.21	1.68
MC2.22.4.3	79.08	20.53	75.69	1.34	0	1.21	1.62
P6 (NASA 29)	80.87	20.45	67.72	1.46	-0.05	0.42	1.55
P7 (JH 45)	79.94	21.48	63.88	1.4	0.58	0.04	1.51
DC1.10.5.1	77.66	18.7	80.15	1.24	-1.11	1.65	1.43
MC1.42.5.1	74.02	18.04	94.06	0.99	-1.51	3.03	1.42
DC1.15.3.1	74.07	20.52	81.69	0.99	0	1.8	1.40
DC4.9.5.4	77.43	20.25	72.67	1.22	-0.17	0.91	1.40
MC5.2.9.2	70.83	19.51	91.74	0.77	-0.61	2.8	1.30
DC1.25.10.1	76.78	19.37	73.17	1.18	-0.7	0.96	1.28
DC4.51.4.2	71.41	19.93	84.57	0.81	-0.36	2.09	1.23
DC4.41.4.1	68.97	25.11	66.71	0.64	2.77	0.32	1.19
DC1.21.3.3	67.34	25.8	64.71	0.53	3.19	0.12	1.11
MC5.2.10.4	77.84	19.1	62.1	1.25	-0.86	-0.14	1.07
DC4.36.1.5	73.86	20.58	66.72	0.98	0.03	0.32	1.06
MC1.37.14.3	73.5	20.38	67.18	0.96	-0.09	0.36	1.03
P1(NK7328)	75.34	21.16	56.74	1.08	0.38	-0.67	0.99
MC2.9.1.1	70.98	21.03	67.34	0.78	0.31	0.38	0.92
MC5.5.8.3	69.63	19.97	76.01	0.69	-0.34	1.24	0.91
DC3.8.8.2	72.55	18.18	74.05	0.89	-1.42	1.05	0.88
DC1.8.4.4	68.95	18.77	78.09	0.64	-1.07	1.45	0.79
DC4.38.14.4	70.18	22	58.64	0.73	0.89	-0.48	0.77
MC2.23.5.4	66.1	21.24	72.67	0.45	0.43	0.91	0.73
MC1.11.6.4	67.81	21.94	64.18	0.56	0.86	0.07	0.72
MC2.23.3.1	69.76	19.02	70.36	0.7	-0.92	0.68	0.70
P3 (BISI 18)	65.29	21.34	71.8	0.39	0.49	0.82	0.66
DC1.1.24.3	66.79	20.97	68.74	0.49	0.27	0.52	0.66
DC1.27.6.2	63.8	20.11	80.82	0.29	-0.25	1.72	0.64
MC1.48.1.2	65.87	20.11	68.84	0.43	-0.25	0.53	0.51
DC4.42.12.3	68.79	19.87	60.63	0.63	-0.4	-0.29	0.49
MC7.1.2.5	66.1	20.53	65.41	0.45	0	0.19	0.49
MC5.10.7.1	54.84	22.87	87.88	-0.33	1.42	2.42	0.47
MC1.24.6.5	66.16	20.68	62.87	0.45	0.09	-0.06	0.45

MC1.48.6.1	59.24	20.41	81.92	-0.02	-0.07	1.83	0.39
DC3.33.15.3	63.21	22.59	57.22	0.25	1.25	-0.63	0.32
P4 (BISI 2)	65.92	20.28	59.42	0.43	-0.15	-0.41	0.31
MC7.2.8.1	66.51	19.87	59.02	0.48	-0.4	-0.45	0.31
DC4.19.7.4	60.13	21.06	72.71	0.04	0.32	0.91	0.30
DC4.53.2.3	60.1	19.73	78.25	0.04	-0.49	1.46	0.29
MC1.34.5.1	63.68	19.17	69.32	0.28	-0.82	0.58	0.27
DC4.31.3.1	66.84	16.6	71.34	0.5	-2.38	0.78	0.27
MC2.34.11.2	62.99	21.46	59.92	0.23	0.57	-0.36	0.25
MC1.10.2.5	63.02	18.9	71.06	0.24	-0.99	0.75	0.24
MC1.11.7.3	64.8	20.41	57.93	0.36	-0.07	-0.55	0.22
MC2.1.6.3	70.63	17.89	50.33	0.76	-1.6	-1.31	0.18
MC1.11.3.4	63.56	19.2	65.15	0.27	-0.8	0.16	0.17
DC1.10.6.5	63.21	20.35	60.42	0.25	-0.11	-0.31	0.16
DC1.1.6.5	58.82	23.19	60.02	-0.05	1.61	-0.35	0.15
DC3.31.10.1	59.83	22.16	61.58	0.02	0.99	-0.19	0.15
P2 (PIONEER36)	62.82	20.76	57.77	0.22	0.14	-0.57	0.11
MC2.23.9.3	66.67	17.56	60.18	0.49	-1.8	-0.33	0.10
DC3.32.14.4	59.24	23.08	56.82	-0.02	1.55	-0.67	0.10
DC4.26.6.5	65.14	19.27	55.03	0.38	-0.76	-0.84	0.06
DC4.37.2.1	59.8	20.82	62.16	0.01	0.18	-0.13	0.01
DC3.1.14.2	53.75	21.46	76.38	-0.4	0.57	1.28	-0.01
P5 (NK 99)	57.41	20.03	58.16	-0.15	-0.3	-0.53	-0.32
P8 (BISI 9)	56.37	20.87	56.37	-0.22	0.21	-0.71	-0.35
P9 (NK 212)	54.74	20.68	61.82	-0.33	0.09	-0.17	-0.35

Note: WSC: Weight of Seeds per Cob, SD: Stem Diameter, YP: Yield Percentage

The results of previous analyzes indicate that almost all observed characters can become selection characters, however the use of all observed characters in selection can reduce the effectiveness of the selection itself, so main characters and supporting characters are needed that are in line with the plant breeding program (Mustafa et al. 2019; Anshori et al. 2021; Fadli et al. 2022; Farid et al. 2022). Determining character as a selection criterion can be seen based on the correlation between the main character and supporting characters, as well as the magnitude of the direct influence of the supporting character on the main character, which can be done through correlation and path analysis (Khapte and Jansirani 2014; Mustafa et al. 2019; Akbar et al. 2021). The use of correlation analysis and path analysis has been widely carried out on various types of plants, such as Maize (Pavlov et al. 2015; Amas et al. 2021; Magar et al. 2021; Pranay et al. 2022), tomatoes (Singh et al. 2018; Maurya et al. 2020; Nevani and Sridevi 2021; Fadhilah et al. 2022; Tsagaye et al. 2022; Panchbhai and

Kulkarni 2023), and chilies (Luitel et al. 2013; Amas et al. 2023).

The results of this study indicate that almost all observed characters can become selection characters. However, the use of all observed characters in selection can reduce the effectiveness of the selection itself, so main characters and supporting characters are needed that are in line with the plant breeding program (Mustafa et al. 2019; Anshori et al. 2021; Fadli et al. 2022; Farid et al. 2022). Determining character as a selection criterion can be seen based on the correlation between the main character and supporting characters, as well as the magnitude of the direct influence of the supporting character on the main character, which can be done through correlation and path analysis (Khapte and Jansirani 2014; Mustafa et al. 2019; Akbar et al. 2021). However, this character needs to consider its heritability value. Based on the heritability value, the DC character is a character that has low heritability, while SD and percentage of results have moderate heritability with values close to 50%. This indicates that the SD and percentage results can be considered for inclusion in the selection index.

In this research, the selection criteria have been determined with a systematic concept, so determining the weighting for each selection criterion is the main thing at this stage. Several methods for developing selection indices include subjective (Hidayatullah et al. 2018), objective (Anshori et al. 2021, 2022; Farid et al. 2021, 2022) or semi-subjective (Alsabah et al. 2019). The semi-subjective weighting development method is considered to be the right choice in this research. However, the use of direct influence also needs to be corrected by the determination value (Anshori et al. 2019).

The selection index results in Table 6 show that there were 24 lines identified a good performance. The identification was based on 2 selection concepts, namely by comparison with check variety (Anshori et al. 2021, 2022) and by use positive value in the index value as a basis for selection (Peternelli et al. 2017; Anshori et al. 2021, 2022; Padjung et al. 2021). The effectiveness of this approach combination was also applied by Anshori et al. (2021, 2022). Therefore, these 14 corn lines are worth recommending being passed on to the S4 generation.

In conclusion, the use of selection indices based on multivariate analysis is considered effective in the systematic selection of convergent breeding S3 maize populations. The effective selection index formulation in this study was seed weight per ear + (0.28 x 0.6183 x stem diameter) + (0.30 x 0.6183 x ear diameter) + (0.37 x 0.6183 x yield). The results of index selection show that 14 S3 lines of convergent breeding corn can be inherited by the S3 generation. These lines need to be tested with within-family analysis of variance to discern potential transgressive segregation.

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