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Selection criteria and index analysis for the S2 maize lines of double-crosses

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Abstract. *Akfindarwan AK, Farid M, Syaiful SA, Anshori MF, Nur A. 2023. Selection criteria and index analysis for the S2 maize lines of double-crosses. Biodiversitas 24: 192-199.* This study aimed to determine the selection criteria and the selection index for the S2 maize lineage from double cross crosses and to select the potential lines that could be continued in the S3 generation. The research was carried out in the field from July to November 2020 at the Experimental Farm of the Agriculture Faculty, Hasanuddin University, Tamalanrea District, Makassar City, South Sulawesi. The maize lines used were derived from 4 double cross populations of S1 generation, namely: DC1 (P36/B9//NK7328/JH2) with 19 genotypes, DC2 (B9)/HJ28/NK728), DC3 (B18/B2/B2/N29), and DC4 (JH45/B19/N29/B2). The results of this study revealed that the selection criteria suitable for this population were the weight of seeds per cob, peel cob weight, and weight of 100 seeds. Furthermore, the selection index analysis showed that there were 61 promising lines for F2 double cross maize that had a positive index value, while based on the Z value, there were 44 lines that had a better index value than the best parents. Therefore, it is recommended that the 61 S2 Maize lines from double crosses be further tested on to the S3 generation.

Keywords: Gene action, selection index, principal component, self-pollinating population, *Zea mays*

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important food crops and has a strategic role in the economic condition of several countries, including Indonesia. Maize has a multipurpose function as a source of food, feed, and industrial raw materials (Moelyohadi et al. 2012). The production of maize in Indonesia has continued to increase in recent years, but the increase is not predominantly due to increased productivity; thus, there is still a great opportunity for boosting national corn production by increasing corn productivity. One of the practical efforts to increase corn productivity is through the assembly of hybrid maize varieties (Takdir et al. 2007; Yasin and Malik 2014).

The development of hybrid maize needs pure lines that can be generated through self-pollination over generations. The S2 selfing generation is one of the earliest generations of the straining process through artificial self-pollination. Self-pollination (selfing) in breeding aims to produce pure lines that can be used as parents in forming hybrid varieties (Acquaah 2015). Selfing in the second generation (S2) is considered to have a reasonably high diversity, even though the population has experienced an increase in homozygosity and a decrease in the diversity of lines in the population (Acquaah 2009). The nature of heterosis and inbreeding depression is the basis for the diversity of the generational population, so the effectiveness of this diversity has been determined by the number of parents and the genetic distance between these parents (Barmawi et al. 2013). This generation's stressed condition is crucial because the population will continue to experience inbreeding depression in the next generation, so an effective concept is needed in the selection process for the S2 generation. One of them is determining selection criteria (Efendi et al. 2016).

The selection criteria are the characters closely related to the breeding objectives and are the basis for the selection process. The determination of selection criteria is always focused on increasing productivity (Padjung et al. 2021; Anshori et al. 2022). However, productivity is controlled by many genes, so its relative stability is influenced by the environment and genetic-by-environment interactions (Fellahi et al. 2018). Moreover, the crop evaluation was mostly done in a single location, so the determination of secondary characters related to productivity needs to be determined to maintain the main character’s stability (Dwi 2020). Therefore, selection based on multi-characters is a solution in an effective lineage process, including the S2 generation of double-crossing maize (Riddle et al. 2006).

Selection with a multi-character concept needs to consider genetic parameters and the concept of the combination of these selection characters in selection. Heritability and gene action are two genetic parameters that must be known in selection (Anshori et al. 2022). Heritability is the value of estimating the magnitude of genetic diversity in influencing phenotype diversity (Acquaah 2009; Syukur et al. 2015). However, heritability estimates carried out in one generation is broad, so it needs to be closer to other parameters, such as gene action. Gene action is a pattern of interactions between alleles in character (Roy 2000). Gene action affects the allele potential of a trait when passed on to the next generation (Barabaschi et al. 2016). Therefore, the combination of heritability and gene action becomes important in determining the selection concept so that the breeding becomes effective and targeted (Anshori et al. 2022).

Mixing character selection can be done with the selection index. The selection index is a multiple linear regression equation with a specific weighted value from the selection criteria (Simeao et al. 2015). The weighting value can be a priority value between selection criteria, which is crucial in developing the selection index. This can be done through statistical approaches, such as principal component analysis. Principal component analysis can combine selection criteria into a dimension with specific eigenvector values as weighting values (Ramos et al. 2014; Gazal et al. 2017). Therefore, the concept of forming this index can also be applied in this S2 corn planting process. This study aimed to determine the selection criteria and index for the S2 maize lineage from double crosses and to select the potential lines that could be continued in the S3 maize generation.

MATERIALS AND METHODS

Research site, materials and design

The research was carried out from July to November 2020 at the Experimental Farm of the Agriculture Faculty, Hasanuddin University, Tamalanrea District, Makassar City, South Sulawesi, Indonesia. The research was arranged in an Augmented Design divided into 3 blocks. Augmented design is a design that was carried out on a population with a limited number of seeds. Each line was not repeated in every block. On the other hand, the check varieties were repeated according to the number of blocks. The lines used were derived from 4 double cross populations of S1 generation, namely: DC1 (P36/B9//NK7328/JH2) with 19 genotypes, DC2 (B9/P36//HJ28/NK7328) with 24 genotypes, DC3 (B18 /JH45//B2/N29) as many as 37 genotypes, and DC4 (JH45/B18//N29/B2) as many as 47 genotypes, so there were 127 genotypes. Each genotype consisted of 15 individuals per row, so there were 1905 individuals. The check varieties used were JH 45, Bima 9, NASA 29, and Bisi 2, which were repeated 3 times according to the number of blocks.

Research procedure

Land preparation was started with land clearing, followed by plowing the ground using a tractor. The experimental field was divided into 3 blocks of 3.5 m x 33 m, each with a between-block distance of 100 cm. Planting was done by making a single planting hole with a spacing of 70 cm x 20 cm. Each row consisted of 1 line with 15 plants planted with 2 seeds in each planting hole. Maintenance activities included fertilization, irrigation, replanting dead plants or ungerminated seeds, thinning, weeding, hoarding, and controlling pests and diseases. Fertilization was carried out 3 times at, respectively, 7 days after planting (DAP), 35 DAP, and 50 DAP, using urea, SP36, and Phonska fertilizers. Irrigation was carried out at a 10-day interval from panting to harvest, depending on weather conditions. Plants with poor growth or dead were replaced at 7 DAP. Thinning was done at 10 DAP to retain only one plant per hole. Weeding was done when the plants were at 10 DAP and 35 DAP by cleaning weeds around the maize plants.

Mounding was done when the plants were 35 DAP by elevating the mounds and loosening the soil to allow better soil aeration. Pest control was carried out by spraying insecticides to prevent/reduce the leaf caterpillar attacks. Selfing was performed on 10 maize plants per genotype; the other 5 were allowed to interbreed for evaluation. Selfing was started by covering the cob using plastic before the hair on the tip of the cob emerged. After the cob hairs emerged, they were cut to retain only 1 – 1.5 cm long. After that, pollen or pollen from male flowers was placed on the cob hairs of the same plant. The female flower was then covered. Harvesting was done by taking the corn cobs on each plant by turning or breaking the cobs.

Observations and data analysis

The plant characteristics observed in this research were plant height, cobs height, number of leaves, stem diameter, male flowering age, female flowering age, anthesis silking interval, peeled cobs weight, cobs diameter, cobs length, length of peeled cob, number of seeds per row, the weight of seeds per cob, and weight of 100 seeds. The observed data were subjected to analysis of variance (ANOVA) according to the augmented design. The ANOVA results served as the basis for determining the heritability of characters. Selection criteria were determined systematically through a normality test, skewness kurtosis, and correlation analysis. First, the selection criteria were combined into an index with weighted values from principal component analysis. Then, the weighting was corrected by the proportion value of PCA and correlation analysis. Finally, the fixed yield index was used in the double cross F2 maize selection process.

RESULTS AND DISCUSSION

Results

Analysis of variance in Table 1 shows that the variance source of lines had a significant effect on plant height, cob height, steam diameter, peel cobs weight, number of seeds per row, the weight of 100 seeds, and weight of seeds per cob. The Check variety showed no significant effect on the observed variables, indicating no significant difference among the check varieties on the observed variables. Meanwhile, the characters of plant height and cobs height were significantly different between the check and the lines, but the check and lines differed significantly on other observed variables. Heritability values of plant height, cob height, number of leaves, stem diameter, peeled cobs weight, cobs length, length of peeled cobs, number of seeds row, the weight of 100 seeds, and weight of seeds per cobs were considered high. In contrast, those of days of male flowering and cobs diameter were moderate. The characters with low heritability were days of female flowering and anthesis silking interval (ASI).

Figure 1 shows the results of the correlation analysis of several characters employing data from the lines evaluated. The character of the number of seeds per row was positively correlated with stem diameter (0.173). The weight of the cob seed (0.616) and 100 seed weight (0.282) each was positively correlated with the weight of the peel cob's weight. The weight of 100 seeds was positively correlated with the weight of the cob seeds (0.341), and the character of the number of seeds per row (0.199) was positively correlated with the weight of 100 seeds. A negative correlation was observed between the character of the number of rows of seeds with the weight of the peeled cob (-0.131) and the character of the number of rows of seeds with the weight of the cob seeds (-0.070).

The results of the image-based normality test are shown in Figure 2. The seed weight per cob (Figure 2A), the peel cob weight (Figure 2B), and the weight of 100 seeds (Figure 2C) showed the normal distribution curve. Although, the weight of 100 seeds has a relative skewness on the right than the others. The skewness and kurtosis values were, respectively, 0.0701 and 0.0603 for the seed weight per cob, 0.3164 and -0.1299 for peeled cob weight, and -0.4920 and 0.5010 for the weight of 100.

Table 1. Analysis of variance and genetic parameters of observed characters

Character	Means Square			VG	VP	CV	H (%) lines
	L	C	L vs. C				
PH	502.63943**	101.64136ns	126.17328ns	149.00	167.55	3.76	88.93
CH	239.64446*	43.4479ns	30.72406ns	64.37	79.88	5.95	80.59
NL	0.46658417ns	0.81194ns	42.30027606**	1.00	1.36	7.56	73.23
SD	3.1632141*	0.23065ns	202.1582095**	0.71	1.05	4.64	67.43
DMF	11.302318ns	7.3029ns	716.466073**	1.82	3.77	4.54	48.39
DFF	10.664896ns	3.848519ns	624.011379**	0.57	3.55	5.35	16.02
ASI	0.22433139ns	0.22433ns	12.90830274**	0.01	0.07	18.28	7.49
PCW	974.8765*	307.7345ns	2957.3389**	266.65	324.96	8.16	82.06
DC	12.451319ns	16.6845ns	290.625416**	1.06	4.15	7.64	25.57
LC	4.5371149ns	0.3745111ns	124.84265448**	1.08	1.51	7.00	71.73
LSC	5.2879626ns	0.4464111ns	44.313618**	1.14	1.76	9.53	64.49
NSR	1.4379762**	0.2312306ns	74.070966**	0.42	0.48	3.22	87.38
W100S	19.927697**	1.633031ns	132.233129**	5.82	6.64	5.15	87.58
WSC	1191.0183*	255.9973ns	1415.7027*	339.48	397.01	11.67	85.51

Note: **: significant effect on 1% level, *: significant effect on 5%, ns: not significant, L: Lines, C: Check, CV: Coefficient of variance, Vg: Variance of genotypes, Vp: Variance of phenotypes, H: Heritability, PH: plant height, CH: cob height, NL: number of leaves, SD: stem diameter, MFA: days of male flowering, DFF: days of female flowering, ASI: anthesis silking interval, PCW: peel cobs weight, DC: diameter of cobs, LC: length of cobs, LSC: length of peeled cobs, NSR: number of seeds per row, W100S: weight of 100 seeds, WSC: weight of seeds per cob

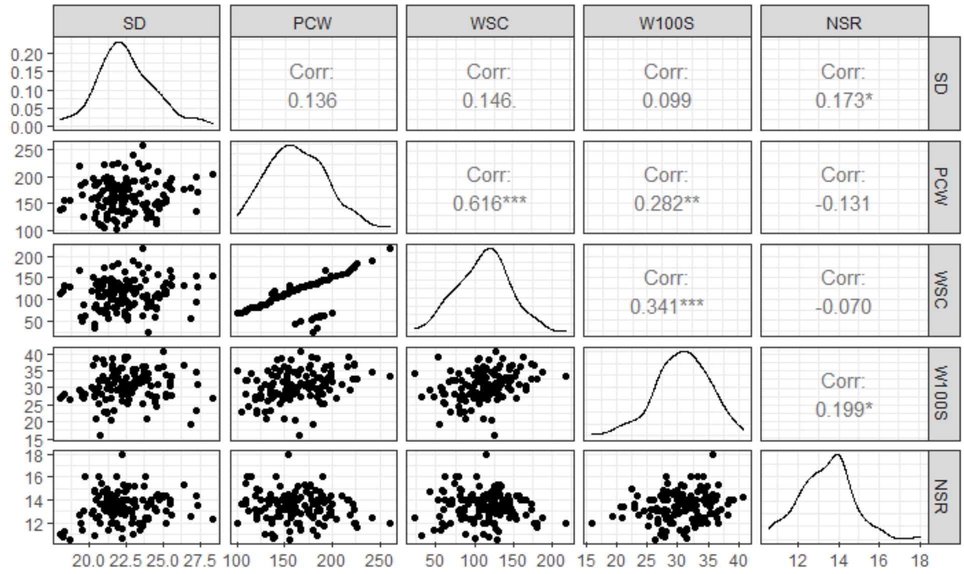

Figure 1. Pearson correlation for selected characters that are significant to the variance source on lines (L) and lines vs. check (L vs. C) (***: significant at 0.1% level, **: significant at 1% level, *: significant at 5%.

The results of the principal component analysis are shown in Table 2. Based on the analysis, the proportion of PC1 is 0.615, PC2 is 0.258, and PC3 is 0.127. The eigenvector value on the character of the weight of the peeled cob was 0.618, the weight of seeds per cob was 0.636, and the weight of 100 seeds was 0.462. The main component 1 (PC1) is the PC mostly responsible for the observed variability, i.e., 0.615 or 61.50%, so, in this study, the selection index was on PC1.

The results of the selection index based on PCA analysis (Table 3) showed that there were 61 promising lines for F2 double cross maize with a positive index value, while based on the Z value, there were 44 lines with a better index value than the best parents. In addition, the parental index value identified BISI 2 variety (0.16) as the best/highest while JH 45 variety (0.14) was the lowest parent index.

Table 2. Principal Component Analysis of maize production character S2 generation

Variable	**PC1**	**PC2**	**PC3**
PCW	0.618	-0.392	0.682
WSC	0.636	-0.261	-0.726
W100S	0.462	0.882	0.089
Eigenvalue	1.8457	0.7739	0.3805
Proportion	0.615	0.258	0.127
Cumulative	0.615	0.873	1

Notes: PCW: PCW: peel cobs weight, WSC: weight of seeds per cob, W100S: weight of 100 seeds

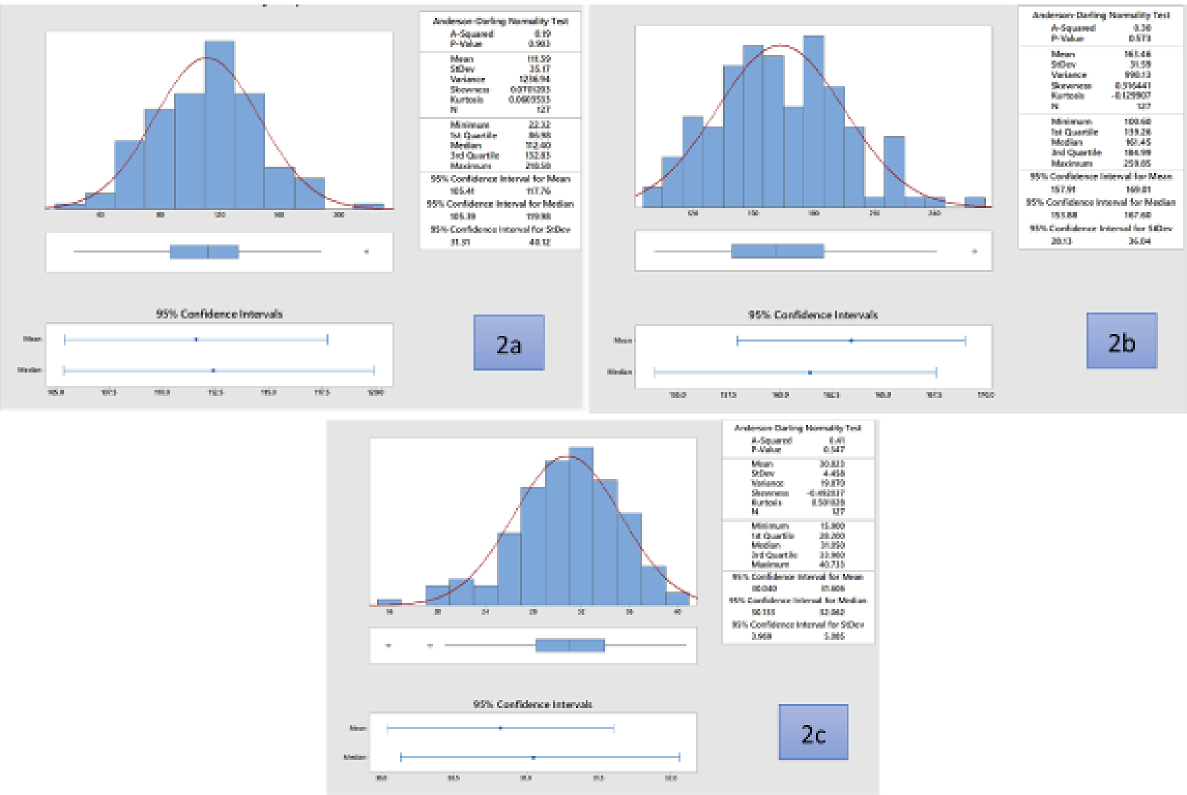

Figure 2. Test of Normality, Skewness, and Kurtosis. A. Character distribution curve of seed weight per cob, B. Character distribution curve of Peeled Cob Weight, C. Character distribution curve of the weight of 100 seeds

Table 3. Selection of S2 maize lines based on the index value

Rank	Genotype	Real Values			Z Value			Index
		PCW	WCS	W100S	PCW	WCS	W100S	
1	DC3.31	259.85	218.58	33.58	3.11	3.08	0.65	1.68
2	DC2.14	241.30	188.38	34.50	2.51	2.21	0.86	1.26
3	DC4.10	225.79	181.38	32.75	2.02	2.01	0.46	1.09
4	DC2.4	224.20	180.42	32.51	1.97	1.98	0.41	1.07
5	DC4.15	223.42	177.66	36.63	1.94	1.90	1.34	1.07
6	DC3.38	222.62	173.71	37.11	1.92	1.79	1.45	1.02
7	DC4.5	221.34	173.64	32.42	1.87	1.78	0.39	0.98
8	DC4.50	216.60	162.39	38.87	1.72	1.46	1.85	0.88
9	DC2.26	219.03	167.14	29.44	1.80	1.60	-0.29	0.87
10	DC3.15	215.75	159.94	36.15	1.69	1.39	1.23	0.83
11	DC1.7	192.60	165.82	30.50	0.95	1.56	-0.05	0.75
12	DC3.24	210.42	156.76	30.80	1.52	1.30	0.02	0.73
13	DC4.17	198.99	153.24	34.56	1.16	1.19	0.87	0.66
14	DC1.6	198.14	152.28	33.24	1.13	1.17	0.57	0.64
15	DC2.16	198.11	149.49	36.67	1.13	1.09	1.35	0.63
16	DC4.40	203.77	153.63	26.80	1.31	1.21	-0.89	0.63
17	DC2.22	197.62	146.93	32.20	1.11	1.01	0.34	0.57
18	DC3.14	193.15	145.28	36.35	0.97	0.96	1.28	0.56
19	DC2.21	196.35	146.01	33.10	1.07	0.99	0.54	0.56
20	DC3.39	191.06	144.89	35.42	0.90	0.95	1.07	0.54
21	DC4.8	196.82	146.18	29.35	1.09	0.99	-0.31	0.53
22	DC3.2	193.03	145.26	31.96	0.97	0.96	0.28	0.53
23	DC4.2	189.61	143.28	32.10	0.86	0.91	0.31	0.49
24	DC3.27	188.60	142.54	30.06	0.82	0.89	-0.15	0.46
25	DC3.36	186.49	140.85	32.96	0.76	0.84	0.51	0.45
26	DC3.5	184.24	136.50	38.50	0.68	0.71	1.76	0.43
27	DC2.12	184.51	139.65	33.08	0.69	0.80	0.53	0.43
28	DC4.3	180.03	135.98	31.98	0.55	0.70	0.29	0.36
29	DC4.49	184.30	136.68	27.46	0.69	0.72	-0.74	0.35
30	DC4.22	176.70	133.10	36.66	0.44	0.61	1.35	0.35
31	DC4.16	177.11	134.59	31.05	0.45	0.66	0.08	0.32
32	DC4.51	175.47	131.19	35.73	0.40	0.56	1.14	0.31
33	DC2.32	176.53	132.83	30.87	0.44	0.60	0.03	0.30
34	DC3.34	173.06	130.58	33.32	0.32	0.54	0.59	0.28
35	DC4.45	176.48	132.71	27.80	0.43	0.60	-0.66	0.28
36	DC1.26	166.99	127.78	40.73	0.13	0.46	2.27	0.27
37	DC4.31	174.33	130.65	31.31	0.37	0.54	0.14	0.27
38	DC3.11	175.10	130.85	29.84	0.39	0.55	-0.20	0.26
39	DC3.20	171.76	129.49	31.04	0.28	0.51	0.07	0.24
40	DC4.34	171.49	129.36	30.50	0.27	0.50	-0.05	0.24
41	DC3.37	166.53	127.76	35.23	0.11	0.46	1.02	0.23
42	DC3.18	167.45	129.04	31.49	0.14	0.49	0.17	0.22
43	DC3.17	167.39	127.88	31.53	0.14	0.46	0.18	0.21
44	DC3.10	163.81	125.00	33.70	0.03	0.38	0.68	0.17
45	P4	155.66	131.14	28.04	-0.23	0.56	-0.61	0.16
46	DC1.20	163.35	123.75	34.27	0.01	0.34	0.80	0.16
47	DC4.12	164.21	125.85	30.26	0.04	0.40	-0.10	0.16
48	DC1.27	164.07	125.84	30.30	0.04	0.40	-0.10	0.16
49	DC4.55	161.45	122.32	34.42	-0.05	0.30	0.84	0.14
50	P3	155.64	129.91	26.40	-0.23	0.52	-0.98	0.14
51	DC4.11	160.20	121.94	34.58	-0.09	0.29	0.88	0.13
52	DC3.41	161.83	123.46	28.69	-0.04	0.33	-0.46	0.11
53	DC2.18	156.20	117.70	38.20	-0.22	0.17	1.70	0.09
54	DC3.33	159.08	119.83	30.12	-0.12	0.23	-0.14	0.07
55	DC3.9	165.35	126.31	15.90	0.08	0.42	-3.36	0.06
56	DC2.33	159.13	119.90	28.20	-0.12	0.23	-0.57	0.05
57	DC1.2	159.08	118.46	30.12	-0.12	0.19	-0.14	0.05
58	DC3.22	156.90	117.86	31.19	-0.19	0.17	0.11	0.04
59	DC4.48	153.89	115.15	35.84	-0.29	0.09	1.16	0.03
60	DC4.9	160.56	122.30	20.58	-0.08	0.30	-2.30	0.03
61	DC4.36	157.16	118.04	28.78	-0.19	0.18	-0.44	0.03
62	DC1.8	153.40	114.43	35.35	-0.31	0.07	1.05	0.02
63	DC3.28	153.17	114.10	35.75	-0.31	0.06	1.14	0.02
64	DC4.39	152.90	114.10	32.96	-0.32	0.06	0.51	-0.01
70	P2	139.74	118.06	27.80	-0.75	0.18	-0.66	-0.06
77	P1	136.74	112.16	27.14	-0.84	0.01	-0.81	-0.15

Notes: PCW: PCW: peel cobs weight, WSC: weight of seeds per cob, W100S: weight of 100 seeds

Discussion

This research showed that the stem diameter, peeled cobs weight, number of seeds per row, the weight of 100 seeds, and weight of seeds per cob could be used as the basis for line selection. According to Amin (2021), the significant difference between the variances of the lines and the check varieties has a good basis for estimating the selection character in the augmented design. If one of these sources is insignificant, then the selection process is considered less effective. In general, the diversity of the lines is the key to selection. Although there was a significant difference among the lines, the pooled line data were not significantly different from the control/check varieties. Thus, the chances of getting the expected line are low because the basis of breeding is to find better lines than the existing varieties. Therefore, the five characters are considered potential as selection criteria. In addition, this potential is also supported by high heritability values for the five characters. According to Acquaah (2009), Syukur et al. (2015), and Anshori et al. (2022), a high heritability value becomes one of the indicators in the selection of an effective character selection. Therefore, it is suitable to analyze further the characteristics of stem diameter, peeled cobs weight, number of seeds per row, the weight of 100 seeds, and weight of seeds per cobs for determining good selection criteria for S2 maize planting in double cross crosses.

The estimation of effective selection criteria is closely related to the purpose of breeding. Generally, the breeding program aims to increase plant productivity (Syukur et al. 2015; Ruswandi et al. 2020; Olanrewaju et al. 2021). In this research, seed weight per cob is an indicator of increasing productivity, so this character becomes the main character in the selection. This indicates that the potential selection criteria are the characters significantly related to seed weight per cob. Based on this research, the peeled cob's weight and the weight of 100 seeds became characters that were significantly correlated with the weight of seeds per cob. Similar results were also reported by Aman et al. (2020); Padjung et al. (2021), Yahaya et al. (2021) on the weight of 1000 grains; and Nataraj et al. (2014) and Fadhli et al. (2020) on the weight of the peeled cob. Therefore, the peeled cob's weight and the weight of 100 seeds can be used as selection criteria, along with the weight of seeds per cob in the planting of this research.

The determination of selection criteria also must be separated from the action of genes on each character. Gene action becomes important information in inheritance patterns from generation to generation (Fitz and Cavalli 2022). The concept of gene action can be predicted through the analysis of normality, skewness, and kurtosis (Rahayu et al. 2018; Hastini et al. 2021). Based on this analysis, the character of the peeled cob's weight, the weight of 100 seeds, and the weight of seeds per cob showed a normal distribution, indicating that the three characters have additive gene action with many genes involved in controlling the traits. In general, additive gene action is an independent and stable gene action. The action of these genes is related to the independent ability of an allele in determining the phenotype of a fixed character (Zhang et al. 2021), so the merging of two alleles in a gene is arithmetic (Acquaah 2009). The inheritance stability of additive gene action is very well used in straining from generation to generation. Additive gene action differs from epistasis, which is identical to allele interaction, so the phenotype from one generation to another is unstable (Benildo 2019). In addition, the large number of genes involved indicates a wide diversity in character selection (Rahayu et al. 2018). It will increase the effectiveness of the selection process. Therefore, the three characters can be recommended as practical selection criteria in the S2 maize lineage from double-cross crosses. The three selection criteria were then formulated as a selection index. The selection index could be formed using principal component analysis. The use of principal component analysis has been widely reported in determining the weight of selection criteria (Alsabah et al. 2019; Akbar et al. 2019; Tirtana et al. 2021; Padjung et al. 2021).

Based on the PCA analysis in this research, PC1 has a good dimension in forming the selection index (Farid et al. 2021). This is based on the eigenvalue that exceeds 1, while PC2 and PC3 have eigenvalues below 1. According to Jolliffe and Cadima (2016), the value of 1 in the eigenvalue is the limit of the effectiveness of a dimension in collecting multi-character diversity in PCA analysis. This is because the variation in the normal distribution of a character is 1, so if a PC has an eigenvalue of 1, it means that there is at least 1 character with wide diversity following the normal distribution (Mattjik and Sumertajaya 2011). Therefore, the eigenvector value on PC1 can be used as the basis for the weighting of the selection index, namely the selection index = 0.636 weight of seeds per ear + 0.618 peeled cobs weight + 0.462 weight of 100 seeds. However, this index still needs to be corrected with other factors, such as gene action and correlation to the main character.

The main characters in the selection are still prioritized over the secondary characters (Olanrewaju et al. 2021). This indicates that the weighting of the selection index on secondary characters needs to be corrected through the PCA proportion of variance (Padjung et al. 2021; Anshori et al. 2022) and correlation analysis (Sabouri et al. 2008). Although correlation analysis is still considered rough (Anshori et al. 2022), it is quite effective on relatively few secondary characters. In addition, it can also optimize the use of the correlation coefficient through the value of determination. In general, the value of determination is the probability of a model or an independent character in determining the dependent character or other related characters (Chicco et al. 2021). So, the corrected index can characterize the optimal conditions in the lineage selection. Therefore, the use of the value of determination needs to be applied to the formation of the selection index of this research. Based on the correlation determination value, the selection index formed is

Selection Index = (0.636 x 0.615) weight of seeds per cob + (0.618 x 0.615 x 0.379) peeled cobs weight + (0.462 x 0.615 x 0.116) weight of 100 seeds

or,

Selection Index = 0.391 weight of seeds per cob + 0.144 peeled cobs weight + 0.033 weight of 100 seeds

The selection index analysis selected 61 lines in this research. This selection was based on two considerations: the positive index value and the comparison with control varieties. Both concepts have been reported by Peternelli et al. (2017), Padjung et al. (2021), and Anshori et al. (2022) for the use of positive indices and Lubis and Hairmansis (2009) for comparison with control varieties. However, using the basic positive index value in this research is considered more suitable for the S2 generation stage in the selection. This is based on the number of selected lines reaching about 50% of the total existing lines. Furthermore, the selection of lines in the early generations should be flexible so that the selection of the expected lines has a great chance with an increase in selection progress that is relatively consistent in each generation. Therefore, it is recommended that the 61 S2 maize lines from double cross crosses be passed on to the S3 generation.

In conclusion, the effective selection criteria on S2 double crosses maize were the weight of seeds per cob, the peeled cobs weight, and the weight of 100 seeds. These three criteria have additive gene action and were effectively combined as a corrected selection index. The selection index formed was 0.391 seed weight per cob + 0.144 peeled cobs weight + 0.033 weight of 100 seeds. Meanwhile, the selected lines based on the index were 61 S2 maize lines. These lines are recommended to be passed on to the S3 generation.

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