

Genetic diversity and gain quantitative characters of maize from index-based selection at two dry lands in Lombok, Indonesia

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Abstract. Sudika IW, Soemeinaboedhy IN, Sutresna IW. 2023. Genetic diversity and gain quantitative characters of maize from index-based selection at two dry lands in Lombok, Indonesia. *Biodiversitas* 24: 11-19. Genetic diversity and gain quantitative characters of maize from index-based selection at dry land is poorly reported. This research aims to study the genetic diversity and gain of several traits quantitative of the index-based selection at two dry lands in Amor-Amor and Pererenan, Lombok, Indonesia. A randomized block design with three replications was applied to design the experiment. The materials used is maize from nine populations, namely eight populations from the selection of index-based and one from the initial population. The data were analyzed for variance at the 5% significance level. The results showed that the genetic diversity of yields was categorized as moderate, and the weight of dry cobs harvested per plant was narrow in both locations. The genetic diversity of fresh stover weight per plant in Pererenan was wider than in Amor-Amor, but still in the same category, which was medium. These three traits had a significant genetic gain in the moderate category for both locations, except for the weight of fresh stover per plant, which was high in Pererenan. The dry seed weight per plant had a moderate genetic diversity and gain with a significant positive phenotypic correlation with yield. Yield and fresh stover per plant can still be increased through index-based selection by using dry seed weight per plant and fresh stover per plant in both locations.

Keywords: Genetic diversity, genetic gain, index-based selection, Lombok, maize

INTRODUCTION

The yields are quantitative traits influenced by many factors, such as fertilizer and the variety of maize seeds (Musundire et al. 2019; Aman et al. 2020). Besides that, the fresh stover weight of the maize plant is also important for animal feed (Crevelari et al. 2018). Therefore, both traits have been improved through index-based selection by Sudika et al. (2019) for eight cycles on dry land. Index selection is one of the selections for improving two or more traits at once in each cycle (Streck et al. 2017; Silva et al. 2020). This selection is based on economic value to determine the index of each plant (Zankrut 2021). Two characteristics of maize plants have economic value and are used for selection criteria, namely the weight of dry cobs harvested per plant and the weight of fresh stover per plant (Sudika and Soemeinaboedhy 2022).

The success of the selection is highly dependent on genetic diversity, heritability (Dar et al. 2015; Admire et al. 2018; Sadimantara et al. 2021; Rachman et al. 2022; Yali 2022), effectiveness of selection procedures and the environment (Azrai et al. 2016; Aci et al. 2018). The category of genetic diversity can be seen from the value of the coefficient of genetic diversity since this value measures the magnitude of the genetic variation of a trait (Lubis et al. 2014; Dar et al. 2015). The magnitude of the coefficient of genetic diversity is determined by the environment where the test is conducted because the environment affects the phenotypic variation of a trait (Aci et al. 2018; Golla et al. 2018). Several studies on genetic diversity in maize have been conducted by Dar et al.

(2015), Ferdoush et al. (2017), Admire et al. (2018), Hosang et al. (2020), and Padjung et al. (2021).

The amount of genetic diversity in each location will be a consideration for the next cycle of selection activities. Another consideration is the magnitude of the genetic gain (Covarrubias-Pazaran 2020). Genetic gain measures the effectiveness of the breeding program (Badu-Apraku et al. 2021). Abdulmalik et al. (2017) reported the response to the selection of maize yields and Dermail (2022) examined white sweet corn by index selection. Oloyede-Kamiyo (2019) stated that index-based selection was more efficient in increasing the resistance of maize plants to stem borer. Sudika and Soemeinaboedhy (2022) tested the results of index-based selection until the seventh cycle. de Santiago et al. (2019) tested 256 inbreds in 12 environments. Yani et al. (2022) tested local corn cultivars of East Nusa Tenggara. Other researchers have studied the index-based genetic gain in several species of plants, such as Silva et al. (2020) on sweet corn, Fellahi et al. (2020) on wheat, Smiderle et al. (2019) and Venmuhil et al. (2020) on rice, and de Azeredo et al. (2017) on sugarcane.

The genetic gain consists of direct and indirect genetic gain. In indirect genetic gain, the correlation coefficient between selected traits and other traits becomes very important (Ferdoush et al. 2017; Rai et al. 2021). The size of the genetic gain is not only determined by genetic diversity and selection procedures but also determined by the value of heritability (Amien et al. 2021). This research aims to study the genetic diversity and genetic gain of several traits quantitative of the index-based selection at two dry lands in Lombok, Indonesia.

MATERIALS AND METHODS

Study area

The experiment was carried out on dry land in Amor-Amor (North Lombok) and Pererenan (East Lombok), West Nusa Tenggara, Indonesia (Figure 1). Environmental conditions at research sites are shown in Table 1.

Research materials

The materials used in this experiment were 9 populations, namely eight populations from the selection of the index-based and one from the initial population. The population seeds from the selection of the first cycle to the eighth cycle have been produced by Sudika et al. (2018). The treatment codes are presented in Table 2.

Procedures

The experiment was designed in a randomized block design for each location. The number of repetitions for each location is 3 repetitions (blocks). The soil for the experiment in each location was tilled by plowing and harrowing once each, then leveled, 3 subplots (blocks) were made, and each block was divided into 9 treatment plots with a size of 3 x 4 m. Each treatment was planted in 5 rows, and each row contained 20 plants. The spacing used is 20 x 60 cm, one plant per hole. Fertilization with inorganic fertilizers was carried out twice, namely at planting and 28 days after planting (DAP). The dose of fertilizer every time was the same, namely Urea 100 kg ha⁻¹ and Phonska 150 kg ha⁻¹. At the time of planting, fertilization was carried out with Petroganik fertilizer at a dose of 500 kg ha⁻¹. Fertilization was done by spreading along the rows after the holes were filled with seeds.

The corn cob harvest was carried out according to the harvest criteria by Sunarti and Turang (2017), namely the cob and cob hairs were dry, the seeds were hard and shiny, and when massaged with nails, there was no mark left. The observed characteristics included yield (weight of dry seeds per plot), weight of dry cob harvested per plant and weight of fresh stover per plant, plant height, total number of leaves per plant, number of fresh leaves at harvest per plant, 50% anthesis, 50% silking, Anthesis Silking Interval (ASI), harvest age, length of cob, the diameter of cob, the weight of 1000 seeds, and weight of dry shelled seeds per plant (Sudika et al. 2019).

Data analysis

The data were analyzed by analysis of variance using the Minitab 18 program. The genetic diversity of each trait of each location was calculated based on the results of the analysis of variance (Anova) with the following formula Singh and Chaudhary (1985) as follows:

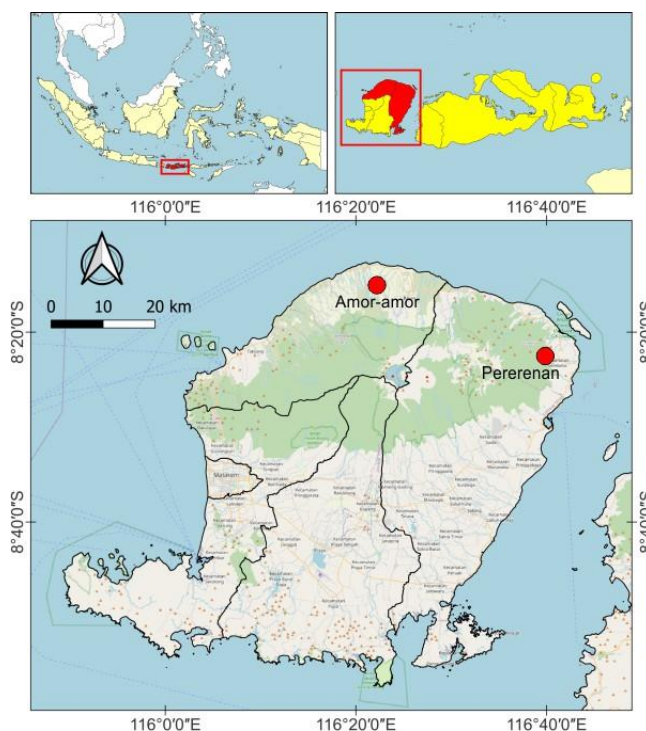


Figure 1. Map showing two study sites in Lombok Amor-Amor (North Lombok) and Pererenan (East Lombok), Indonesia

Table 2. Treatment codes and description

Treatment codes	Description
P0	Initial population
P1IS	The population of the first cycle selection
P2IS	The population of the second cycle selection
P3IS	The population of the third cycle selection
P4IS	The population of the fourth cycle selection
P5IS	The population of the fifth cycle selection
P6IS	The population of the sixth cycle selection
P7IS	The population of the seventh cycle selection
P8IS	The population of the eighth cycle selection

Table 1. Environmental conditions at the research sites

Descriptions	Pererenan (East Lombok)*	Amor-Amor (North Lombok)**
Altitude (m above sea level)	50	60
Soil texture	Sandy loam	Sandy loam
Minimum temperature January-April 2019 (Average±SD) (°C)	22.94±0.91	22.44±1.20
Maximum temperature January-April 2019 (Average±SD) (°C)	30.25±1.74	30.36±1.70
Minimum air humidity January-April 2019 (Average±SD) (%)	82.58±5.01	81.82±6.73
Maximum air humidity January-April 2019 (Average±SD) (%)	99.61±0.88	99.71±0.78
Rainfall by month (January-April 2019) (Average±SD) (mm)	163.40±65.05	304±268.87
Rainy days (January - April 2019) (Average±SD) (days)	11.50±3.11	14.00±6.68

Note: *Assessment Institute for Agricultural Technology (BPTP) Pringabaya, **Results from the research sites; SD: standard deviation

$$\sigma^2_G = \frac{(KT_P - KT_G)}{r}$$

$$\sigma^2_P = \sigma^2_G + KT_G$$

Where: σ^2_G is genetic diversity, KT_P is the middle square of treatment in the analysis of the variance model, KT_G is the mean square of the error, and r is the number of blocks. Testing of genetic diversity between two locations used the formula of Fitriani (2019), namely $F \text{ value} = \sigma^2_{G1} / \sigma^2_{G2}$; with σ^2_{G1} is the larger genetic diversity, and σ^2_{G2} is the smaller genetic diversity.

The breadth or narrowness of the genetic diversity of a trait was obtained from the Coefficient of Genetic Diversity (CGD) value category, using the formula developed by Azrai et al. (2016) as follows:

$$\text{CGD (\%)} = \frac{\sqrt{\sigma^2_G}}{\bar{x}} \times 100\%$$

Where: CGD is the Coefficient of Genetic Diversity, and \bar{x} is the general mean (mean of the initial population to the eighth cycle population). If the CGD value is $>20\%$, it means wide genetic diversity, 10-20% means moderate, and it narrows when the CGD is $<10\%$ (Lubis et al. 2014; Bartaula et al. 2019; Lamichhane et al. 2021).

The genetic gain of each trait was obtained from the linear regression coefficient, namely the value of b_1 in the linear regression equation (Covarrubias-Pazaran 2020; Meiryani 2021) as follows:

$$Y = b_0 + b_1 X$$

Where: Y , the predictive value of an index-based selection cycle; b_0 , initial population mean (P_0); b_1 , linear regression coefficient is the average genetic gain per cycle, and X is the selection cycle. The significance of the genetic gain was tested with the F test at a 5% significance level. The value of Genetic Gain (GG) was calculated by the formula: $GG = b_1 / P_0 \times 100\%$; with P_0 is the initial

population mean (Ferdoush et al. 2017), and then the values were categorized into 4 levels, namely: low (0 - $<3.3\%$), moderate (3.3 - $<6.6\%$), moderately high (6.6 - $<10\%$), and high ($>10\%$) (Karmana et al. 1990).

Heritability was calculated according to the formula proposed by Azrai et al. (2016), as follows:

$$H^2 = (\sigma^2_G / \sigma^2_P) \times 100 \%$$

Where: H^2 is a broad heritability, σ^2_G is genetic diversity, and σ^2_P is phenotypic diversity. Low heritability if $H^2 < 20\%$, moderate is 20-50%, and high if $H^2 > 50\%$ (Lubis et al. 2014; Azrai et al. 2016).

The value of the phenotypic correlation coefficient (r) between observed traits (X and Y) was carried out using the Paiman (2019) formula as follows:

$$r_{xy} = \frac{n \sum X_i Y_i - \sum X_i \sum Y_i}{\sqrt{n \sum X_i^2 - (\sum X_i)^2} \sqrt{n \sum Y_i^2 - (\sum Y_i)^2}}$$

Where: r_{xy} is the phenotypic correlation coefficient between trait X and trait Y . The criteria for the correlation coefficient (r) were determined according to Kurnia et al. (2021), namely $0 \leq r < 0.20$ is very weak; $0.20 \leq r < 0.40$ is weak; $0.4 \leq r < 0.60$ is moderate; $0.60 \leq r < 0.80$ is strong; and $0.80 \leq r < 1.0$ is very strong.

RESULTS AND DISCUSSION

Genetic diversity and coefficient of genetic diversity

The genetic diversity of dry cobs harvested weight per plant had the same genetic diversity between the two locations and was classified as narrow of 109.187 (with CDG, 8.50%) for Pererenan and 111.66 (with CDG 6.57%) for Amor-Amor (Table 3).

Table 3. The genetic diversity (σ^2_G) and the coefficient of genetic diversity (CGD) of all traits observed at each research site and the combination of the two sites

Observed traits	Pererenan			Amor-Amor			Fvalue	Combination		
	σ^2_G	CGD (%)	Category	σ^2_G	CGD (%)	Category		σ^2_G	CGD (%)	Category
Dry cobs harvested weight (g/plant)	109.187	8.50	Narrow	111.66	6.57	Narrow	1.02 ^{ns}	127.772	7.97	Narrow
Fresh stover weight (g/plant)	4184.89	19.33	Moderate	1170.53	11.52	Moderate	3.58*	2622.691	15.71	Moderate
Yield (dry seeds weight (kg/plot)	1.236	16.32	Moderate	0.675	11.86	Moderate	1.83 ^{ns}	0.962	14.15	Moderate
Plant height (cm)	276.135	8.52	Narrow	38.694	3.03	Narrow	7.14*	149.698	6.11	Narrow
Total number of leaves (sheet/ plant)	0.099	2.67	Narrow	0.214	3.78	Narrow	2.16 ^{ns}	0.174	3.47	Narrow
Number of fresh leaves at harvest (sheet/plant)	0.118	5.06	Narrow	0.289	7.20	Narrow	2.45*	0.199	6.21	Narrow
50% anthesis (days)	0.020	0.36	Narrow	0.027	0.39	Narrow	1.35 ^{ns}	0.012	0.27	Narrow
50% silking (days)	0.008	0.22	Narrow	0.021	0.32	Narrow	2.63*	0.004	0.14	Narrow
ASI (Anthesis Silking Interval) (days)	0.004	3.99	Narrow	0.004	3.99	Narrow	1.0 ^{ns}	0.010	4.20	Narrow
Harvest age (days)	0.003	0.108	Narrow	0.019	0.18	Narrow	6.33*	0.003	0.08	Narrow
Cob length (cm)	0.623	6.60	Narrow	0.252	3.80	Narrow	2.47*	0.492	5.57	Narrow
Cob diameter (cm)	0.043	4.88	Narrow	0.001	0.57	Narrow	43.0*	0.016	2.92	Narrow
1,000 seeds weight (g)	119.826	4.48	Narrow	115.433	4.26	Narrow	1.04 ^{ns}	118.288	4.38	Narrow
Dry seed weight (g/plant)	57.477	11.50	Moderate	78.225	10.82	Moderate	1.36 ^{ns}	71.537	11.46	Moderate

Note: *Significantly different from the F test at the 5% level, and ^{ns}not significantly different from the F test at the 5% level

The combination of the two locations was also narrow with a percentage of 7.97%. The weight of fresh stover per plant was wider in Pererenan compared to Amor-Amor, which was 4184.89 and 1170.53 respectively, with CGD values of 19.33% and 11.52%, and both were classified as moderate. In the combination of the two locations, the CGD value was 15.71%, and the genetic diversity was classified as moderate. The yields had the same genetic diversity between locations, and the combination was classified as moderate. The cob length between locations and the combination of the two locations had the same genetic diversity in the narrow category. The magnitude of the genetic diversity from Pererenan was 1.236 (16.32%) and Amor-Amor 0.675 (11.86%). Other traits with the same genetic diversity between locations were obtained in the total number of leaves per plant, 50% anthesis, ASI, the weight of 1,000 seeds, and the weight of dry seeds per plant. The genetic diversity of these traits was narrow, except that the dry seed weight per plant was classified as moderate. Plant height, number of fresh leaves at harvest, 50% silking, age of harvest, length of cob, and diameter of cob had different genetic diversity between locations, with all of them belonging to the narrow category.

Genetic gain, heritability, and phenotypic correlation

The genetic gain was significantly obtained on the traits of fresh stover per plant, the weight of dry cob harvested per plant, yield, plant height, the total number of leaves per plant, number of fresh leaves at harvest per plant, 50% anthesis, length of cob, the diameter of cob, weight of 1,000 seeds, and dry seed weight per plant for Pererenan (Table 4). The percentage of response category for a selection of fresh stover weight per plant was high of 10.90%, while yield and harvested dry cob weight were classified as moderate, respectively at 5.80% and 3.87%, and both were classified as moderate. The weight of dry cobs harvested per plant, the fresh stover weight per plant, and the yield at the Amor-Amor had a significant genetic gain with a moderate percentage of 3.63%, 5.23%, and

6.03%, respectively. The characteristics of 50% silking, ASI, and harvest age had no significant genetic gain at both locations, while 50% anthesis and cob diameter were not significant only in Amor-Amor. Based on the combination of the two locations, the genetic gain of harvested dry cob weight, fresh stover weight, yield, plant height, the total number of leaves per plant, number of fresh leaves at harvest per plant, and yield components were significant, while 50% anthesis, 50% cob hair growing age, ASI, and harvest age were not significant.

Heritability was high for Pererenan obtained from the weight of fresh stover per plant, yield, plant height, number of fresh leaves at harvest per plant, cob diameter, the weight of 1,000 seeds, and weight of dry seeds harvested per plant with a range of values 54.49% to 82.64% (Table 5). The weight of dry cobs harvested per plant and the length of the cobs were classified as moderate with values of 40.57% and 36.88%, respectively. The total number of leaves per plant, 50% anthesis, 50% silking, ASI, and harvest age were low, with a value range of 0.39% to 17.73%. High heritability for Amor-Amor was obtained for: the total number of leaves per plant, the number of fresh leaves at harvest, the weight of 1,000 seeds, and the weight of dry seeds per plant, with a range of values of 51.18 to 77.82%. The yield of fresh stover weight per plant, harvested dry cob weight per plant, plant height, and cob length were moderate, ranging from 27.75 to 49.87%. The 50% anthesis, 50% silking, ASI, harvest age, and cob diameter were classified as low, ranging from 0.67 to 14.29 for the site. In the combination of the two sites, high heritability was obtained in dry cobs harvested weight per plant, fresh stover weight per plant, yield (dry seed weight per plot), plant height, number of fresh leaves at harvest per plant, cob diameter, 1,000 seeds weight and dry seed weight per plant. The total number of leaves per plant and cob length have moderate heritability. Low heritability value was obtained in 50% anthesis, 50% silking, ASI, and harvest age.

Table 4. The average genetic gain per cycle of all observed traits at each research site-and the combination of the two sites

Observed traits	Genetic gain								
	Pererenan			Amor-Amor			Combination		
	F value	%	Category	F value	%	Category	F value	%	Category
Dry cobs harvested weight (g/plant)	4.163*	3.87	Moderate	4.363*	3.63	Moderate	4.263*	3.65	Moderate
Fresh stover weight (g/plant)	23.287*	10.90	High	11.987*	5.23	Moderate	17.63*	7.97	Moderately high
Yield (dry seeds weight (kg/plot)	0.421*	5.80	Moderate	0.338*	6.03	Moderate	0.380*	7.13	Moderately high
Plant height (cm)	6.023*	3.79	Moderate	2.856*	1.50	Low	4.440*	2.54	Low
Total number of leaves (sheet/ plant)	0.152*	1.38	Low	0.164*	1.42	Low	0.158*	1.40	Low
Number of fresh leaves at harvest (sheet/plant)	0.111*	1.85	Low	0.195*	3.13	Low	0.153*	2.50	Low
50% anthesis (days)	-0.126*	0.32	Low	0.072 ^{ns}	0.17	Low	-0.027 ^{ns}	0.13	Low
50% silking (days)	-0.105 ^{ns}	0.26	Low	-0.072 ^{ns}	0.16	Low	-0.089 ^{ns}	0.21	Low
ASI (Anthesis Silking Interval) (days)	0.021 ^{ns}	1.97	Low	-0.144*	3.61	Moderate	-0.062 ^{ns}	2.44	Low
Harvest age (days)	0.085 ^{ns}	0.11	Low	-0.039 ^{ns}	0.05	Low	0.023 ^{ns}	0.23	Low
Cob length (cm)	0.333*	3.23	Low	0.239*	2.00	Low	0.286*	2.57	Low
Cob diameter (cm)	0.069*	1.78	Low	0.041 ^{ns}	0.33	Low	0.042*	1.01	Low
1,000 seeds weight (g)	4.106*	1.86	Low	3.312*	147	Low	3.709*	1.66	Low
Dry seed weight (g/plant)	2.815*	4.92	Moderate	3.27*	5.22	Moderate	3.040*	5.08	Moderate

Note: *Significantly different from the F test at the 5% level, and ^{ns}not significantly different from the F test at the 5% level

The characteristics that have a very significant correlation with the results are fresh stover weight per plant, dry cobs harvested weight per plant, plant height, the total number of leaves per plant, cob length, cob diameter, 1,000 seeds weight and dry seed weight per plant each with moderate category (Table 6). No significant correlation with yield was obtained in character 50% anthesis, 50% silking, ASI dan harvest age with very weak category. Fresh stover weight had a very significant correlation with yield, plant height, number of fresh leaves at harvest per plant, cob length, cob diameter, 1,000 seeds weight, and dry seed weight per plant each with a moderate category. Fresh stover weight significantly correlated with dry cobs harvested weight per plant and the total number of leaves per plant in the weak category, whereas 50% anthesis, 50% silking, ASI, and harvest age did not significantly correlate in the very weak category. The weight of dry cobs harvested per plant correlated very significantly with most of the characteristics in the moderate category. The weight of dry cobs harvested per plant correlated with 50% anthesis, 50% silking, ASI, and harvest age in the very weak category. Weight of harvested dry cobs per plant correlated with the weight of the fresh stover per plant in the weak category.

The correlation between harvested dry cobs weight per plant and the number of selection cycles is presented in

Figure 2. The actual direct genetic gain for harvested dry cobs weight per plant per cycle is 4.263 g, which is linear. The determination value (R^2) of 0.827 indicates that as much as 82.7% of the selection cycle affects the value of harvested dry cob weight per plant.

The genetic gain per cycle of fresh stover weight per plant is 17.63 g with an R^2 value of 0.833 (Figure 3). It means that as much as 83.3% of the selection cycle affects the weight of fresh stover per plant. The genetic gain for traits that were not used as selection criteria is called a correlated genetic gain. Indirect genetic gain or correlated genetic gain is an increase in a trait due to the selection of other traits. Correlated genetic gains were found in yield, plant height, the total number of leaves per plant, number of fresh leaves at harvest per plant, 50% anthesis, 50% silking, ASI, harvest age, cob length, cob diameter, 1,000 seeds weight, and dry seed weight per plant. The size of the correlated genetic gain is highly dependent on the close correlation between these traits and the selected trait. The genetic gain is seen from the combination of the two locations because the correlation coefficient value is obtained from the combined data of the two locations.

The R^2 value of 0.978 indicates that 97.8% of the selection cycles influence the yields. It can be seen from the magnitude of the yields of each cycle that almost all of them are on the regression line (Figure 4).

Table 5. The broad sense heritability value (H^2) for each trait observed at each research site

Observed traits	Pererenan		Amor-Amor		Combination	
	H^2 (%)	Category	H^2 (%)	Category	H^2 (%)	Category
Dry cobs harvested weight (g/plant)	40.57	Moderate	35.60	Moderate	53.54	High
Fresh stover weight (g/plant)	82.64	High	41.41	Moderate	83.21	High
Yield (dry seeds weight (kg/plot)	58.85	High	49.87	Moderate	68.99	High
Plant height (cm)	74.38	High	27.88	Moderate	74.77	High
Total number of leaves (sheet/ plant)	17.73	Low	61.51	High	48.27	Moderate
Number of fresh leaves at harvest (sheet/plant)	54.49	High	67.57	High	74.33	High
50% anthesis (days)	3.67	Low	1.95	Low	1.59	Low
50% silking (days)	0.99	Low	1.62	Low	0.59	Low
ASI (Anthesis Silking Interval) (days)	0.67	Low	0.67	Low	2.60	Low
Harvest age (days)	0.39	Low	14.29	Low	1.39	Low
Cob length (cm)	36.88	Moderate	27.75	Moderate	48.14	Moderate
Cob diameter (cm)	75.28	High	3.49	Low	67.52	High
1,000 seeds weight (g)	65.12	High	77.82	High	80.37	High
Dry seed weight (g/plant)	64.53	High	51.18	High	73.46	High

Table 6. Phenotypic correlation coefficient values between yields, fresh stover weight (FSW), and harvested dry cob weight per plant (HDCW) with other characteristics

Observed traits	Correlation coefficient with					
	Yield	Category	FSW	Category	HDCW	Category
Yield (dry seeds weight (kg/plot)	1		0.54**	Moderate	0.47**	Moderate
Fresh stover weight (g/plant)	0.54**	Moderate	1		0.29*	Weak
Dry cobs harvested weight (g/plant)	0.47**	Moderate	0.29*	Weak	1	
Plant height (cm)	0.51**	Moderate	0.59**	Moderate	0.59**	Moderate
Total number of leaves (sheet/ plant)	0.48**	Moderate	0.26*	Weak	0.47**	Moderate
Number of fresh leaves at harvest (sheet/plant)	0.46**	Moderate	0.66**	Moderate	0.54**	Moderate
50% anthesis (days)	0.06 ^{ns}	Very weak	-0.16 ^{ns}	Very weak	0.19 ^{ns}	Very weak
50% silking (days)	0.02 ^{ns}	Very weak	-0.18 ^{ns}	Very weak	0.12 ^{ns}	Very weak
ASI (Anthesis Silking Interval) (days)	-0.05 ^{ns}	Very weak	-0.13 ^{ns}	Very weak	0.14 ^{ns}	Very weak
Harvest age (days)	0.10 ^{ns}	Very weak	-0.15 ^{ns}	Very weak	0.18 ^{ns}	Very weak
Cob length (cm)	0.51**	Moderate	0.43**	Moderate	0.69**	Moderate
Cob diameter (cm)	0.43**	Moderate	0.42**	Moderate	0.78**	Strong
1,000 seeds weight (g)	0.64**	Moderate	0.58**	Moderate	0.49**	Moderate
Dry seed weight (g/plant)	0.61**	Moderate	0.54**	Moderate	0.86**	Strong

Notes: *Significantly correlated ($P < 0.05$, $58 = 0.25$), **very significant ($P < 0.01$, $58 = 0.33$), ^{ns}not significantly correlated

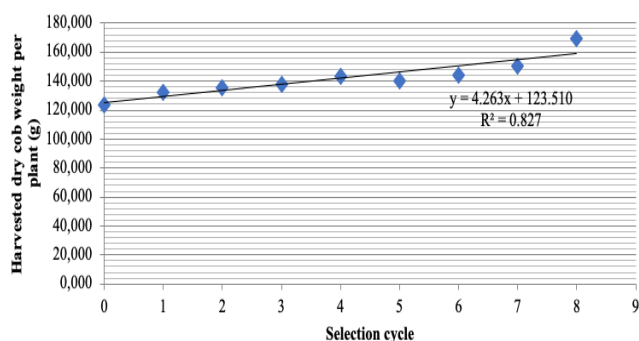


Figure 2. The correlation between harvested dry cob weight per plant and the number of selection cycles

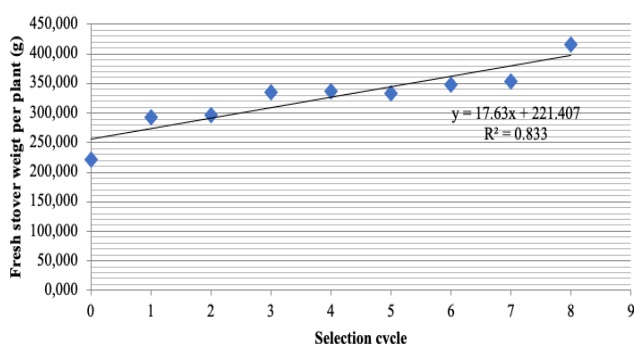


Figure 3. The correlation between fresh stover weight per plant and the number of selection cycles

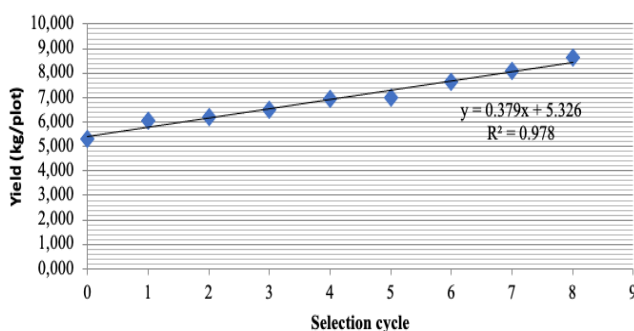


Figure 4. The yield correlation (dry seeds weight per plot) with the number of selection cycles

Discussion

Genetic diversity is very important in selection activities (Yali 2022). The magnitude of the genetic diversity of a location is a consideration for the place to be selected (Lubis et al. 2014). Selection is more successful if the genetic variety of the selected population is wider (Admire et al. 2018; Rachman et al. 2022). The genetic diversity of harvested dry cob weight per plant was the same between the two locations, and both were relatively narrow. Narrow genetic diversity indicates that subsequent selection for this trait will not be effective (Rachman et al. 2022). Azrai et al. (2016) reported the same result that the genetic diversity of harvest cob weight was narrow with a genetic diversity value of 0.11 and a CGD value of

7.751%. However, Lubis et al. (2014) found the opposite the genetic diversity of cob dry weight was high in acid soil.

The genetic diversity of fresh stover weight per plant in Pererenan was wider than in Amor-Amor. The existence of different genetic diversity between locations indicates that environmental conditions affect the gene expression of each population tested for this trait (Aci et al. 2018). It means that various environmental factors affect the expression of these trait genes (Golla et al. 2018; Amien et al. 2021). The environmental factor that has a big influence on dry land is rainfall. The ideal rainfall for maize plants is generally between 100 and 300 mm per month. The ideal altitude is 50 to 450 m asl., and the optimum temperature is 23° to 30°C (Putra 2018). The rainfall in Pererenan in February 2019 was 71 mm, smaller than the minimum requirement (Table 1). At that time, the plant began to enter the flowering phase. Lack of water during flowering in maize plants is a critical phase. Water stress at this time, in addition to increasing ASI, can also reduce crown weight (Jaya et al. 2020). The weight of the crown is a fresh stover and is called the phenotype. The variety of phenotypes is caused by genetic diversity and environmental diversity (Golla et al. 2018). The difference in genetic diversity of fresh stover indicates that each selected population has a different genetic response between the two locations (Freeman et al. 2019). The existence of a wider genetic diversity allows a greater genetic gain (Rachman et al. 2022).

Yield (dry seed weight per plot) is an improved trait, but is not a selection criterion. The genetic diversity of the yield was classified as moderate in both locations and combined with a CGD value of 16.32% for Pererenan, 11.86% Amor-Amor, and 14.15% at a combination of two locations. The genetic diversity of the yield between the two locations was the same, indicating that the genetic response of each selected population was the same in both locations. Golla et al. (2018) found that planting location did not affect yield. Belay (2018) obtained the same result that the genetic diversity was moderate with a CGD of 17.20%, and Admire et al. (2018) of 18.11%. Several studies have obtained high genetic diversity with CGD values of 20.00% or more, such as Adhikari et al. (2018) obtained a value of 21.96% on 13 maize genotypes from the National Maize Research Program, Rai et al. (2021) of 31.53%, Kandel et al. (2018) for a two-season average of 32.84%, Taiwo et al. (2020) of 27.71%, and Bartaula et al. (2019) of 51.24%. However, the narrow category was also obtained, such as Freeman et al. (2019) of 9.98%.

Plant height, number of fresh leaves at harvest per plant, 50% silking, harvest age, cob length, and cob diameter had different genetic diversity between locations. The category of genetic diversity for these traits in both locations was narrow, except that the dry seed weight per plant was classified as moderate. Azrai et al. (2016) found that genetic diversity was relatively narrow for plant height, cob hair growing age, harvest age, cob length, and cob diameter. Al-Amin et al. (2019) also got the same thing for plant height of 7.58%. Freeman et al. (2019) obtained a narrow genetic diversity for 50% silking, harvest age, and cob diameter with values of 4.64%, 3.10%, and 9.61%, respectively. Other traits with the same genetic diversity

between the two locations were obtained in the total number of leaves per plant, 50% of the age of panicle growing age, ASI, 1,000 seeds weight, and dry seeds weight per plant.

Genetic gain is distinguished into direct genetic gain and indirect genetic gain. The direct genetic gain is the magnitude of the increase in a trait per cycle for the selected trait (Covarrubias-Pazarán 2020), while the correlated genetic gain is a change in each cycle for the unselected trait. The magnitude of the direct genetic gain is strongly influenced by the genetic diversity and the heritability of these traits (Adhikari et al. 2018; Admire et al. 2018; Rutkoski 2019). The direct genetic gain in this study was the dry cob weight harvested per plant and the weight of fresh stover per plant (Sudika et al. 2019). Both traits had a significant genetic gain. The genetic gain of dry cob harvested weight and fresh stover weight per plant is a direct genetic gain. The genetic gain of dry cob harvested weight per plant between locations was the same, classified as moderate (Table 4). It is caused by the same genetic diversity between locations. Heritability is also important to determine the magnitude of the genetic gain (Amegbor et al. 2022). The heritability value of these traits also supports the genetic gain, classified as the same between locations, namely in the medium category, 40.57% and 35.60% (Table 5). Heritability is the proportion of genetic variants to phenotypic variants (Yali 2022). Moderate heritability indicates that variation in the population is caused partly by genetic diversity and partly by environmental variation. Lubis (2014) and Azrai et al. (2016) obtained moderate heritability of 34%, and Magar et al. (2021) of 44% for this trait.

Meiryani (2021) stated that the value of determination explains how much influence the independent variable has on the dependent variable. This percentage is quite high. It can be seen from the value of this trait that each cycle is close to a linear line. The change in the selection cycle towards more cycles also causes the higher weight of dry cobs harvested per plant (Figure 2) and yields (Figure 4). The genetic diversity of fresh stover weight per plant was higher in Pererenan than in Amor-Amor with the same category, namely moderate. The percentage of Pererenan CGD values tends to be higher than Amor-Amor. The effect of this genetic diversity is seen in genetic gain. Pererenan genetic gain was higher than in Amor-Amor, where the percentage in Pererenan was high, while in Amor-Amor it was moderate. The heritability value also supports a higher response to the selection of these traits, which is high of 82.64% for Pererenan, and moderate of 41.41% for Amor-Amor (Table 5).

The significant correlation coefficient of the weight of harvested dry cobs and the weight of fresh stover per plant with yields of 0.47 and 0.54 were positive, very significant, and classified as moderate (Table 6). Crevelari et al. (2018) obtained the same result that the yield with harvested dry cobs weight and fresh stover weight had a very significant correlation of 0.71 and 0.64, respectively. The correlation of yield with harvested dry cobs weight of 0.76 was obtained by Adhikari et al. (2018) and with fresh biomass of 0.89 on various maize lines by Mogesse (2021). The

existence of a very significant positive correlation between the two traits with the yields causes the real genetic gain to be quite high of 7.13%. Badu-Apraku et al. (2021) obtained that the genetic gain was 4.14% under normal conditions and 4.15% with water stress.

The effect of magnitude of correlation coefficient on the correlated genetic gain was also seen in several traits, namely 50% anthesis, 50% silking, ASI, and harvest age. These characteristics were not significantly correlated with the weight of dry cobs harvested and the weight of fresh stover per plant; both are very weak (Table 6). Chandana et al. (2018) obtained the same result that the yields were not significantly correlated with 50% anthesis, 50% silking, and ASI 0.041, 0.047, and 0.029 respectively. Kamal et al. (2020) obtained a value of -0.0692 for 50% anthesis, and -0.1686 for 50% silking. Khan et al. (2018) obtained different results, where the phenotypic correlation of seed yield with 50% male flowers and 50% female flowers was very significant of 0.495 and 0.421, respectively. The non-significant correlation of the four traits caused the correlated genetic gain to be not significant and relatively low at the combination of the two locations (Table 4). The correlated traits were classified as moderate with the selected traits (with harvested dry cob weight and fresh stover per plant), namely plant height, number of fresh leaves at harvest, length of cob, and weight of 1,000 seeds. The four traits had a real genetic gain even though the percentage of the genetic gain was relatively low (<5%). The dry seed weight per plant had a moderate correlation with fresh stover per plant, harvested dry cob weight per plant, and yield. This trait had a selection response of 3,040 g/plant/cycle with a moderate genetic gain percentage of 5.08% and greater than the genetic gain for dry cobs harvested weight per plant, which was 3.65% (Table 4).

The correlated genetic gain is not only affected by the value of the correlation coefficient, but also by genetic diversity and heritability, as described in the following characteristics. The high yield genetic gain was due to this trait having a high heritability value of 68.99% in a combination of locations. The same results of high heritability were obtained by Admire et al. (2018) of 67%; Dadzie et al. (2021) of 62.7%; Rai et al. (2021) of 64.68%; Magar et al. (2021) of 93%; Amegbor et al. (2022) of 97%; Belay (2018) of 76%; Kandel et al. (2018) of 75.5%; Kandel et al. (2019) of 87.36% and Taiwo (2020) of 73.31%. The genetic diversity of yield characteristics also supports a high genetic gain, which is classified as moderate with a CGD value of 14.15% in a combination of locations. Kandel et al. (2019) obtained the same results for classified as moderate with a CGD value of 15.46%.

The traits of 50% anthesis, 50% silking, ASI, and harvest age had a narrow genetic diversity at a combination of two locations, <5% (Table 3). The same thing was obtained by Taiwo et al. (2020) for genetic diversity, 50% anthesis and 50% silking were narrow with a CGD of 1.58 and 1.32, respectively. The heritability of the four traits was also low with a value of <20% at both locations (Table 5). This causes the correlated genetic gain of these four traits to be unreal and relatively low. Khan et al. (2018)

obtained different results with high heritability for 50% anthesis and 50% silking of 98% and 91%, respectively.

Dry seed weight per plant had a significant positive correlation with the yield of 0.61, while the correlation between harvested dry cobs and yields was 0.47 (Table 6). Hadi et al. (2021) obtained a correlation coefficient of 0.64. The heritability of dry seed weight per plant was high in both locations, and the combination of the two locations was 64.53%, 51.18%, and 73.46% (Table 5). Khan and Mahmud (2021) obtained the heritability of this trait of 64.11%, and Al-Amin et al. (2019) of 74.43%. High heritability for a trait in an environment provides a great opportunity to obtain a high genetic gain (Azrai et al. 2016; Rachman et al. 2022). Traits with high heritability can be used as selection criteria for index selection (Musundire et al. 2019). The genetic diversity of these traits is moderate, thus, they can be considered as selection criteria for the next cycle.

The length of the cob has a significant positive correlation with the results of 0.51, but the genetic diversity is narrow. Kamal et al. (2020) obtained the correlation coefficient of the results with the length of the cob of 0.63. Therefore, the dry seed weight trait per plant can be used as an index-based selection criterion to increase yields. The length and diameter of the cob had a narrow genetic diversity (Table 3), and the heritability was moderate. The phenotypic correlation coefficients of cob length and cob diameter were 0.51 and 0.43, respectively. Rai et al. (2021) also obtained the same results, namely the phenotypic correlation of the results with the length of the cob and the diameter of the cob was 0.49 and 0.45, respectively. The phenotypic correlation of yield with higher cob length was obtained by Bartaula et al. (2019) of 0.840, Yahaya (2021) of 0.790 in Kafanchan, and 0.727 in Kadawa, and Hadi et al. (2021) of 0.681. Genetic diversity is categorized as narrow (Table 2), and heritability for cob length and cob diameter is categorized as moderate (Table 5).

In conclusion, the genetic diversity of yield was moderate, and weight of dry cobs harvested per plant was narrow and both locations had the same genetic diversity. The genetic diversity of fresh stover weight per plant in Pererenan was wider than in Amor-Amor with the same category, which was medium. Significant genetic gain in the moderate category for both locations was obtained in the weight of dry cobs harvested per plant and yield. The weight of fresh stover per plant in Pererenan had a significant genetic gain with high and medium categories for Amor-Amor. Dry seed weight per plant had moderate genetic diversity and genetic gain and had a significant positive phenotypic correlation with yield. Other traits had narrow genetic diversity and low genetic gain. Yield and fresh stover per plant can still be increased through index-based selection by using dry seed weight per plant and fresh stover per plant in both locations.

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