Performances and Genetic Parameters Estimation of Yield and Yield Related Traits in Sweet Corn Inbred Lines Selected for Better Adaptation to Organic Cropping System

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Abstract— Limited number of sweet corn varieties specifically bred for organic cropping system has brought about the organic sweet corn growers use hybrid varieties supposedly grown under high agrochemical inputs cropping system. The objective of the present study was to evaluate the performance of sweet corn inbred lines and to estimate the genetic parameters as to the development of varieties suitable for organic cropping systems. Eight inbred lines of S5generation previously selected for yield and adaptability to organic conditions were evaluated in a randomized block design with seven replications. Performances and genetic parameter estimation were addressed to plant height, the number of leaves, stalk diameter, ear length, ear diameter, kernel row number, kernel number per row, and ear yield per plant. Significant variations were found among the inbred lines for all traits studied. Similar features were also found within the inbred line, except stalk diameter showed non-significant within-line variation. Evaluation of mean values indicated that CAPS 2 exhibited the best plant growth performances and produced reasonably high ear yield. CAPS 5 produced the highest ear yield along with superior ear length, ear diameter, and kernel row number. Broad sense heritability (h^2_B) were ranged from low to moderate with the higher estimates found on ear length (0.43) and ear yield per plant (0.40). Based on the estimates of genetic advance as percent of the population mean (GAM), moderate improvement can be expected from ear length (13.37%) and ear yield per plant (20.86%) by selecting the top 5% of the inbred line populations.

Keywords— sweet corn inbred lines; organic cropping system; heritability; genetic advance.

I. INTRODUCTION

The recent increase in consumer concern on food quality, food health, and environmental sustainability to a large extent has contributed to a substantial development in the organic sweet corn production system. Some studies have been conducted to provide scientific background for attaining success in crop production, including the use of organic inputs and crop management. A variety of organic materials has been claimed to be potential alternatives to inorganic fertilizers in providing plant nutrients for sweet corn [1]–[3]. Similarly, there are some technologies for coping with pest, disease, and weed problems suited for organic crop production [4]–[6]. Apart from these facts, the development of organic sweet breeding is still in its infancy [7], [8].

Breeding of sweet corn for developing varieties best suited for organic production must deal with multiple objectives to meet both the growers' and consumers' demands. For the growers, the varieties for organic production should have comparable ear yield to varieties designed for conventional production. Moreover, morphological characteristic of ear and kernel, as well as chemical composition of the kernel is important to the consumers and industrial processing [9], [10]. For these reasons, selection and evaluation during inbred lines development should be carried out under organic environments to facilitate an objective judgment in each step of the breeding program.

The organic cropping system is characterized by avoidance of using of artificial fertilizers, synthetic pesticides, growth hormones, and genetically modified organism in the crop production [11]. Such system implies that plant selection under organic conditions is challenging as the plant performances to a large extent are dictated by limited nutrients availability in the soil, weed competition, and pests and diseases suppression [12]. Consequently, the plant's selection under organic cropping system during the inbred development should be addressed to full exploitation of genetic potential existing in the breeding population.

Like other open pollinated crops, hybrid varieties are the targeted products of sweet corn breeding program and combining ability (CA) test plays an essential step in identifying potential combiners and hybrid combinations. CA test is commonly carried out at the earlier generation of inbreeding, vis., S_3 , or S_4 generation [13]. However, such a

test involves considerable effort and resources commonly practiced by large seed companies. Therefore, delayed CA tests until later generations are not uncommon with the assumption that continuing selection on inbred line *per se* for the traits with additive inheritance till S_5 or S_6 generation would reduce the number of inbred lines should be tested for CA [14]. This study aims to evaluate the variability of eight sweet corn inbred lines that previously selected under an organic cropping system. This study also aims to estimate the genetic parameters as to the determination of inheritance modes of yield and yield corresponding traits and to assess the progress that could be expected from the selection practices.

II. MATERIALS AND METHOD

A. Location and Characteristic of the Experimental Site

The experiment was run on an organic research land at Sukamarga, Rejang Lebong Regency, Bengkulu Province, Indonesia (Longitude. $102^{\circ}30'$ E., Latitude. $3^{\circ}29'$ S., Altitude 618 m.a.s.l,). The soil type is *inceptisol*, with soil pH=5.6. The site had been used for organic vegetable production in two consecutive years before the current experiment.

B. Plant Materials and Experimental Design

Eight sweet corn inbred lines (CAPS 2, CAPS 3, CAPS 5, CAPS 15, CAPS 17A, CAPS 17B, CAPS 22, and CAPS 23) were used in this experiment. The lines were the fifth generation of *selfing* (S_5), as shown in Table 1, and developed through selection program under organic cropping management. Each line was randomly allocated to the experimental units according to a randomized complete block design with seven replications. Seeds from each line were shown in a double row plot of 4 m long with a plant-to-plant distance of 20 cm and the rows-to-row distance of 70 cm.

TABLE I
THE PEDIGREE OF INBRED LINES USED IN THE STUDY

No.	Line Pedigree					
1	CAPS 2	BS - 1-2-1-1-2				
2	CAPS 3	GD -2-2-1-1-2				
3	CAPS 5	MTO C-2-1-1-3				
4	CAPS 15	SB-1-5-1-4-2				
5	CAPS 17A	SG -2-1-1-2-1				
6	CAPS 17B	SG -2-4-1-31				
7	CAPS 22	BM -3-3-1-3-2				
8	CAPS 23	SI -2-1-1-8-1				

C. Crop Management

A week before sowing, the land was prepared manually using hoes, and cow manure at 15-ton ha⁻¹ was added to the soil as the basal fertilizer. Additional fertilizer was applied by spraying the plants four times during the plant growth period with two weeks interval using liquid organic fertilizer [15], [16]. The soil of each plant row was risen at 4 WAP (weeks after planting) using the inter-row soil. Plant water was supplied as necessary from the adjacent irrigation facility. No agrochemical products were applied during the experimentation. Similarly, no control measure was taken for pest and disease as their infestations were negligible. Weeds were controlled manually using hoes. Ears were thinned two days following pollination to leave a single ear per plant. Ears were harvested at 30 days after silking as the husk had turned dark green, silks turned dark brown, and kernels fully developed and oozed milky sap when pinched with fingernails.

D. Measurements and data collection

Five plant samples were randomly selected from each plot to produce the experimental data. The data were collected for plant height, the number of leaves, stalk diameter, ear length, ear diameter, kernel-row number, kernel number per row, and ear yield per plant (weight of ear with husk per plant). Plant height was measured from the soil surface to the plant tip. The number of leaves was counted from all leaves arisen on the plant, including the flag leaf. Ear length was measured from the basal to the tip of the husk. Ear diameter was measured as the girth of the ear. Kernel-row-number was the number of kernel-row formed in the ear. Kernel number per row was measured as the average number of kernels formed in each kernel row. Ear yield was measured on the single plant by weighing the produced ear, including the husk, on a digital balance.

E. Data analysis

The collected data were subjected to analysis of variance to reveal the significant variations among and within the inbred lines on the traits studied, following the procedure as described by [17] with the linear additive model for the analysis as:

$$Y_{ijk} = \mu + \tau_i + \rho_j + \tau \rho_{ij} + \epsilon_{ijk} \tag{1}$$
 $(i=1,\,2,\,...,8;\,j=1,\,2,\,...,7;\,k=\!\!1,\,2,\,...,5)$

where Y_{ijk} : the observation made on the kth individual plant in ith line row and jth block. μ : the overall mean; τ : the fixed effect of the ith line; β j is the effect of the jth block, a random variable with mean zero and variance σ^2_{β} ; $\tau\beta_{ij}$: the experimental error, measuring the variation among plant samples within the line. The genetic parameters were estimated from the mean-squares [18] as given below in Table 2:

TABLE II Genetic Parameters

Source	Degree of freedom	Sum of square	Mean square	Expected mean square
Block	r-1	SSB	MS _B	$\sigma_E^2 + g \sigma_B^2$
Among line	g-1	SS _{AL}	MS _{AL}	$\sigma^2_E + r \sigma^2_G$
Within line	(r-1)(g-1)	SS_{WL}	MS _{WL}	σ_{E}^{2}
Error	rg (s-1)	SSE	MS _E	σ_{s}^{2}

$$\sigma 2E = MS$$
 within line (2)

 $\sigma 2G = (MS \text{ among line} - MS \text{ within line}) / 7$ (3)

$$\sigma 2P = \sigma 2G + \sigma 2E \tag{4}$$

where σ_{E}^{2} : environmental variance, σ_{G}^{2} : genotypic variance, and σ_{P}^{2} : phenotypic variance.

The phenotypic and genotypic coefficient of variations were estimated using the formula suggested by [19] given as:

$$PCV = \sqrt{\sigma_P^2} / \overline{X} \times 100\%$$
 (5)

$$GCV = \sqrt{\sigma_{\rm G}^2} / \overline{X} \times 100\% \tag{6}$$

where PCV: phenotypic coefficient of variation, GCV: genotypic coefficient of variation, and \overline{X} : the general mean of the corresponding trait.

Broad-sense heritability was estimated following [20] as

$$h2B = \sigma 2G / \sigma 2P \tag{7}$$

where h_B^2 is classed as low (<30%), moderate (30 – 60%), and high (>60%).

The genetic advances were predicted using the formula given by [21] as:

$$GA = i \cdot \sqrt{\sigma_P^2} \cdot h2B$$
 (8)

$$GAM = GAM = GA / \overline{X} \times 100\%$$
(9)

where GA: genetic advance, GAM: genetic advance as a percentage of the trait grand mean, i = 2.063 for 5% selection intensity. GAM is classed as low (<10%), moderate (10 – 20%), and high (>30%).

III. RESULTS AND DISCUSSION

A. Variability of the population

The overall performances of the population under study were shown in Table 3. Mean and range values, along with their coefficient of variation (CV), indicated the existence of considerable variability in the population for most of the traits with stalk diameter being the highest. Such features provide an initial signal that the population consisted of a wide range of plant types to warrant a large scope and flexibility for practicing selection based on the phenotypic performances. The mean squares derived from analysis of variance (Table 4) revealed significant genotypic effects among the lines and shared the largest portions of the total variability of all traits. These confirmed that the examined lines were readily exploitable for improvement through selection. The existence of high significant within-line variation for most traits, excepting stalk diameter, indicated that plant-to-plant uniformity within each line had not been reached. The genetic materials used in this study were S5 generations, and, theoretically, they should have been nearly homozygous in most of the linked loci [22] to produce more homogeneous phenotypes within each line [23].

Nevertheless, a continued inbreeding process is required to bring the lines into highly inbred and homozygous in all loci. Spatial variability in soil fertility could also be a possible explanation for such plant-to-plant variations. A study conducted by [24] showed that the distribution of fertility in organic soil was heterogeneous with an irregular pattern.

TABLE III Overall Performances of Eight Sweet Corn Inbred Lines as Grown under Organic Cropping System

Trait	Minimum	Maximum	Mean	CV (%)
Plant height (cm)	2.38	255	202.19	10.07
Number of leaves	9	14	11.77	7.87
Stalk diameter (cm)	1.3	2.9	2.36	18.84
Ear length (cm)	19.5	39	28.10	10.08
Ear diameter (mm)	37.14	69.29	52.63	8.05
Kernel-row No	10	19	14.07	10.09
Kernel no. per row	19	50	30.19	15.63
Ear yield per plant (g)	122	426	252.43	17.96

B. Mean Performances of the Lines

The mean values depicted in Fig. 1 to Fig. 3 indicated that the inbred lines varied substantially in the growth performances and readily exploited for particular breeding programs, such as improved biomass for Stover silage, sugar, and bioethanol productions [25, 26]. Within this context, CAPS 2 was identified as the best lines for distinctively exhibiting the tallest stature, the largest number of leaves, and larger stalk diameter. A path analysis carried out by [27] indicated that plant height and stalk diameter had a positive direct contribution to ear yield by 31.0% and 17.7%, respectively, implying that both traits had an amenable role in the plant yield. A closer inspection of the remaining lines, it was revealed that CAPS 3, CAPS 17, could serve as alternative lines to CAPS2.



Fig. 1 Mean values of plant height row in 8 sweet corn inbred lines as tested using LSD at P < 0.05

TABLE IV MEAN SQUARES FROM ANALYSIS OF VARIANCE FOR EIGHT TRAITS IN EIGHT INBRED LINE AS GROWN UNDER ORGANIC CROPPING SYSTEM

Source	df	Plant height	Number of leaves	Stem diameter	Ear length	Ear diameter	Kernel- row no.	Kernel no. per row	Ear yield per plant
Block	6	1016.98	0.36	3.73	10.05	62.97	4.45	10.96	9985.16
Among line	7	4305.77*	6.79**	9.44**	281.46**	326.59**	10.87^{**}	275.97**	59998.76**
Within line	42	1636.07**	1.53**	2.37	22.69**	46.70**	3.48**	61.26**	4862.82**
Error	224	414.28	0.86	1.92	8.03	17.93	2.02	22.28	2055.00

* and ** significant at P < 0.05 and P < 0.01, respectively



Fig. 2 Mean values of 8 sweet corn inbred lines for the number of leaves as tested using LSD at P < 0.05



Fig. 3 Mean values of 8 sweet corn inbred lines for the number of leaves as tested using LSD at P < 0.05

Fig. 4 to Fig. 7 displays the mean performances for yield and its related components of the inbred lines. In reference to ear yield per plant, CAPS 5 was identified as a superior line, followed by CAPS 2, CAPS 3, CAPS 17A, and CAPS 17B. CAPS 5 was also characterized by high ear diameter, kernel-row number, and kernel number per row. These results suggested a strong indication that CAPS 17A, CAPS 2, CAPS3, CAPS 5, and CAPS 17B could serve as potential parents for improving growth performances and plant yield.



Fig. 4 Mean values of ear diameter in 8 sweet corn inbred lines as tested using LSD at P < 0.05





Fig 6. Mean values of kernel number per row in 8 sweet corn inbred lines as tested using LSD at P < 0.05



Fig. 7 Mean values of ear yield per plant in 8 inbred corn lines as tested using LSD at P < 0.05

C. The Estimate of genetic parameters

Table 5 presents the genetic parameters estimated for all traits studied. The highest phenotypic coefficient of variation (CVP) and genotypic coefficients of variation (CVG) was recorded on stalk diameter, as followed by ear yield per plant. The rest of the traits had low to moderate CVP with low CVG. In all cases, the magnitudes of CVP) were larger than the corresponding CVG with the sizeable difference between them. The difference between CVP and CVG indicates the sensitivity to environmental fluctuations [28]; the wider the difference implies that the traits would be more sensitive to environmental variability, and vise-versa.

TABLE V GENETIC PARAMETERS ESTIMATED FROM EIGHT TRAITS IN EIGHT INBRED LINES AS GROWN UNDER AN ORGANIC CROPPING SYSTEM

Trait	CVP (%)	CVG (%)	H_{B}^{2}	GA	GAM (%)
Plant Height	13.21	5.08	0.15	8.17	4.04
Number of leaves	9.03	3.47	0.15	0.32	2.74
Stalk diameter	63.02	19.57	0.10	0.30	12.54
Ear length	15.14	9.90	0.43	3.76	13.37
Ear diameter	10.61	5.60	0.28	3.21	6.10
Kernel row no.	11.22	3.53	0.10	0.32	2.29
Kernel no. per row	19.74	8.81	0.20	2.45	8.11
Ear yield per plant	25.49	16.06	0.40	52.67	20.86

The estimate of broad-sense heritability (H_B^2) denotes the relative contribution of the heritable portion of a trait variability and provides measures to the plant breeder in deciding the optimal selection strategies under a given environment [29]. The broad-sense heritability across traits was ranged from low to moderate ($0.10 < H_B^2 < 0.43$), with the highest estimate, which was recorded on ear length. In the previous study, higher H_B^2 estimates were reported for most of the traits currently studied [30]. This disagreement was not surprising as H_B^2 is not only the property of the trait being studied but also the population being sampled in each environment [31].

The estimate of genetic advance (GA) measures the expected gain from selecting the best performance genotypes for a given trait [32]. The range of GA varied from 0.30 to 52.67. The highest GA was observed on-ear yield per plant (52.67), whereas the lowest GA was observed on stalk diameter (0.30). GA values of different traits are not comparable due to a unit of measurement dependency. To facilitate comparison in the selection gain among different traits, GA expressed as genetic advance as percent of the population mean (GAM) is commonly preferred. Ear yield per plant showed the highest GAM (20.86%), indicating that a sizeable yield improvement could be gained by selecting the top 5% of the breeding population. By applying the same selection pressure, notable improvements could also be expected for stalk diameter (12.54%) and ear length (13.37%). The rest of the traits would have slow selection progress, as indicated by low GAM (< 10%).

Combining information gained from H_B^2 and GAM would reveal the mode of inheritance for a given trait [33] and, in turn, they would affirm the selection strategy to be implemented. In the present study, moderate H_B^2 coupled with moderate GAM were observed on ear length and ear yield per plant, indicating that both additive and nonadditive gene actions controlled the expression of the traits. The remaining traits had low H_B^2 with low GAM, indicating that expression of these traits was prominently controlled by non-additive gene action. Having known that non-additive gene action was predominant in governing the expression for most of the desired traits, a recurrent selection system should be considered for their improvement in the successive generations [34], [35].

IV. CONCLUSION

Considerable variations in yield and its related traits were observed to warrant further improvement of the sweet corn breeding materials. CAPS 17A, CAPS 2, CAPS3, CAPS 5, and CAPS 17B were identified as potential inbred lines for utilization in developing new sweet corn varieties better adapted for organic environment. Elucidation of the genetic merit of variations, however, indicated that selection progress could be hindered by the involvement of non-additive genes and great environmental influence. Recurrent selection, therefore, was considered to be the most appropriate method for improving overall plant performances.

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