



Genetic parameters and inbreeding depression of Half-Sib and Selfing families to developed as baby corn variety

Nailan Nabila, Yudiwanti Wahyu*, Winarso Drajad Widodo

Departement of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University, Bogor, Indonesia

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Abstract

Baby corn is kind of vegetable that has high nutritional value and safe to be consumed fresh or in canned, but baby corn variety isn't available in Indonesia. The objective of this study was to evaluated S_1 and HS families to be developed as baby corn variety. This study was conducted at Cikarawang experimental station, Bogor Agricultural University from May to December 2016, using eight open pollinated varieties as progenitor (S_0) and their inbreeding families (HS and S_1). Significant differences were found among genotypes on baby corn traits. Mean of inbreeding families were lower than their S_0 in baby corn traits except ear diameter. The best percentage of marketable baby corn was selfing families 37.56%. Inbreeding depression for S_1 families were higher than HS families. The highest inbreeding depression was number of ear per plant, 20.25% for HS and 25.52% for S_1 . The estimates of genetic effects (additive and dominance) for baby corn traits were specific in each S_1 genotypes. In general, the gene action was predominantly additive for all traits in S_1 families. Selfing families generated from Golden, Hawaii, Baruna, Lokal madura, and Mutiara were suggested to developed as open pollinated varieties, and S_1 families from Laksmi, Genjah melati, and Srikandi kuning were suggested to developed as hybrid varieties.

*Corresponding Author: Yudiwanti Wahyu ✉ yudiwanti@apps.ipb.ac.id

Introduction

Baby corn is unfertilized ear of maize which harvested early within 1-3 days after silking which has high nutritional value and free from pesticides so it safe for consume fresh or in canned (Dhasarathan *et al.*, 2012, 2015). Baby corn contained 90.03, 17.96, 2.13, 5.30 and 5.89 percent moisture, protein, fat, ash and crude fibre, respectively (Hooda and Kawatra 2013). Baby corn is valuable crop which gives good returns in short period of time and can grow as multiple cropping systems (Rani *et al.* 2017). Based on these informations, baby corn is belonging to prospective horticulture commodities to be developed, but breeding strategy for improvement of baby corn's production and quality is very limited in Indonesia. Indonesian farmers usually use field corn variety to produce baby corn due to the unavailability of baby corn variety. Another factor that causes low productivity is limited number of ears per plant and varied of ear baby corn size (Sutjahjo *et al.* 2005; Yudiwanti *et al.* 2010).

Number of ear per plant more than one (prolific) and ear size are important traits when constructing new baby corn variety. Prolific is controlled by recessive gene, so it will be expressed in phenotypes when its loci is homozygous (Harris *et al.*, 1976; Keller and waller 2002). Selfing is the method to increase homozygosity and decrease heterozygosity up to 50% per generation, but selfing can cause high inbreeding depression which can decrease plant's performance (Khasiani *et al.*, 2010). Another method to increase homozygosity with better performance in the same generation is sib-mating like half-sibs which can reduce the impact of inbreeding depression (Porcher *et al.* 2016). Baby corn breeding was initiated in the late 1970s. Some baby corn varieties have been produced such as VL-78 and HM-4 in India and Ki39, Ki40, PACB 421 and G-5414 in Thailand (Shahi and Gayatonde, 2017).

In Indonesia, we can't get baby corn variety that have been already registered. At the beginning of this study in constructing new baby corn variety, increasing homozygosity of prolific characters and baby corn quality will be reached by selfing and half-sib from field corn and sweet corn.

Aekatasanawan (2001) and Shahi and Gayatonde (2017) reported that sweet corn, field corn, popcorn, and silage corn can be used as genetic material in baby corn breeding. Population improvement by selfing and full-sibs selection have been used by Promson *et al.* (1990) to get baby corn variety with high productivity, good baby corn quality, and resistant to downy mildew. The objective of this study was to evaluated S_1 and HS families to be developed as baby corn variety.

Material and methods

Genetic materials

Eight open pollinated varieties consist of 4 field corns (Srikandi kuning, Lokal madura, Genjah melati, and Mutiara) and 4 sweet corns (Laksmi, Hawaii, Golden, and Baruna) were used as progenitor (S_0) to generate S_1 and HS families. HS and S_1 seeds were obtained by artificial pollination from 8 progenitors where conducted at Cikarawang experimental station on May-August 2016. S_1 seeds were produced through artificial pollination between male and female flower on same plant. HS seeds were produced by collecting bulk pollen from several plants and sib mating within population (Govindaraj *et al.*, 2016; Hallauler *et al.*, 1988). S_1 and HS genotypes were randomly selected one ear per genotypes to be evaluated.

Evaluation of production and quality traits of baby corn conducted at Cikarawang experimental station on October-December 2016. S_0 , HS, and S_1 from each genotypes were planted in single row with 0.75 x 0.25m in spacing. Baby corn traits were analyzed consist of: days to 50% tasseling (days after panting-DAP), plant height (cm), ear height (cm), number of ear per plant, weight of dehusked ear (g), weight of husked ear (g), ear diameter (mm), and ear length (cm).

Statistical analysis

S_0 , HS, and S_1 of each genotype were sampled in randomized complete block design with three replications to eliminate field variation. Baby corn traits were significantly different at significance level $\alpha=0.05$ and $\alpha=0.01$ followed by orthogonal contrast between HS vs S_0 , S_1 vs S_0 , and S_1 vs HS. All statistical analysis was performed using SAS 9.0.

Gardner's method which was cited by Arnhold *et al.* (2010); Grisales *et al.* (2014); De Freitas *et al.* (2016) was used to obtain the estimates of inbreeding depression and the average genetic components of the families, based on the dominant-additive model. Inbreeding depression (ID) for each baby corn traits from HS and S₁ families was obtained by the difference between the population average of each generation (S₀) and their inbreeding families (HS and S₁): ID_{HS} = $\bar{S}_0 - \overline{HS}$ and ID_{S₁} = $\bar{S}_0 - \bar{S}_1$. Percentage of inbreeding depression was obtained by %ID_{HS} = $\left(\frac{\bar{S}_0 - \overline{HS}}{\bar{S}_0}\right) \times 100$; %ID_{S₁} = $\left(\frac{\bar{S}_0 - \bar{S}_1}{\bar{S}_0}\right) \times 100$ Wherein ID = the estimated inbreeding depression; %ID = percentage of inbreeding depression; \bar{S}_0 = the average of progenitor; HS = the average of HS families; \bar{S}_1 = the average of S₁ families. The difference of inbreeding depression between HS and S₁ families based on t-test with significance level $\alpha=0.05$. The cumulative contribution of homozygous loci ($\mu+a$) in the combined average of the population was estimated by $\mu+a = 2\bar{S}_1 - \bar{S}_0$ and the contribution of heterozygous loci (δ) was estimated by $\delta = 2(\bar{S}_0 - \bar{S}_1)$.

Average degree of dominance (add) was estimated by $add = \frac{\delta}{\mu+a}$. When add = 0 the traits were belong to additive gene action, add < 1 traits were belong to partial dominance, add=1 traits were belong to complete dominance, and add>1 traits were belong to over dominance.

Result and discussion

Agronomic and quality traits performance

Analysis of variance, mean, and orthogonal contrast from S₀, HS and S₁ families were showed in Table 1. Mean of baby corn traits showed that HS and S₁ families were lower than their progenitors except ear diameter. Analysis of variance (Table 1) revealed highly significant differences among evaluated genotypes for baby corn traits.

The contrast between S₀ vs HS was statistically significant for baby corn trait except ear length, contrast between S₀ vs S₁ was statistically significant for baby corn traits except ear length and ear diameter, and contrast between HS and S₁, was statistically significant for ear height, weight husked ear, weight unhusked ear, and ear diameter (Table 1).

Table 1. Analysis of variance, mean, and orthogonal contrast of baby corn traits from progenitor (S₀), half-sib (HS), and selfing (S₁) families.

Traits	Mean square	Mean			Orthogonal contrast		
		S ₀	HS	S ₁	S ₀ vs HS	S ₀ vs S ₁	HS vs S ₁
DT	30.85**	51.83 ±3.02	53.67 ±3.90	54.08 ±3.36	39.67*	59.15**	1.87
PH	2500.57**	191.07 ±35.49	171.71 ±11.44	164.68 ±36.19	4186.40**	8904.01**	851.56
EH	2014.92**	97.55 ±30.81	86.93 ±18.59	80.72 ±32.85	1255.87**	3632.10**	596.79*
NE	0.88**	3.52 ±0.46	2.77 ±0.27	2.60 ±0.41	6.25**	10.22**	0.47
WDE	4156.93**	51.48 ±11.16	49.51 ±9.74	44.62 ± 11.10	14225.08**	41102.36**	6744.59**
WHE	78.78**	7.13 ±0.73	7.05 ±1.42	5.98 ±0.91	236.98**	851.86**	184.16**
ED	9.47*	13.74 ±0.70	14.35 ±1.34	13.57 ±0.96	10.05*	0.04	11.05*
EL	1.59**	8.32 ±0.24	7.95 ±0.68	7.19 ±0.76	1.24	1.63	0.02

DT: Days to 50% tasseling (DAP); PH: plant height (cm); EH: ear height (cm); NE: number of ears per plant; WDE: weight of dehusked ear (g); WHE: weight of husked ear (g); ED: ear diameter (mm); EL: ear length (cm); *, **: significant at 5% and 1%, respectively, according to F test for analysis of variance or orthogonal contrast.

Percentage of marketable baby corn for HS (81.25%) and S₁ (81.07%) were higher than their progenitors (79.47%). Grading of Baby corn based on CODEX standard were classified in three classes: class A, class B, and class C. Specifications for baby corn based on CODEX standard are 5-7 cm in length for class A, 7-9 cm in length for class B, and 9-12 cm in length for class C.

For all classes, the minimum width should not be less than 1.0cm, the maximum width not more than 2.0 cm, sharp tip ear, free of damage caused by pests and disease, regular arrangement of undeveloped kernels (ovules) (FAO, 2007). The majority of marketable baby corns were classified into class B. The percentage of marketable baby corn on class B were 56.00% for progenitor, 58.50% for HS, and 53.57% for S₁, respectively (Fig. 1).

Ideal genotype for baby corn was highest percentage of marketable baby corn in class A and the lowest rejected ears (Sutjahjo *et al.*, 2005). The highest percentage of class A in this study was selfing families, 37.56% of marketable ears (Fig 1). Yudiwanti *et al.* (2010), based on ear size, majority of harvested baby corn fulfilled CODEX standard requirements, but only one of all harvested baby corn per plant suitable for canned product.

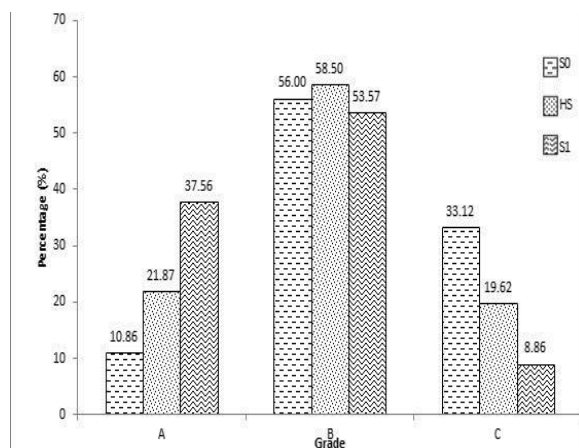


Fig. 1. Grading of marketable baby corn based on CODEX standard.

Estimated of Inbreeding depression and genetic parameters

Inbreeding depression and percentage of inbreeding depression of HS and S₁ families were presented in Table 2. Inbreeding depression was negligible for ear diameter in HS families (ID= -0.62). Inbreeding depression of S₁ was greater than HS families. The percentage of inbreeding depression ranged from 1.11% to 25.52% for S₁ families and 0.51% to 20.25% for HS families. The highest ID was number of ear per plant for HS and S₁ families (Tabel 2).

Inbreeding in cross-pollinated plant played a central role when constructing new varieties. Inbreeding depression (ID) was defined as the decrease in mean fitness of selfed offspring if compared with those produced by outcrossing between unrelated parents (Porcher and Lande, 2016).

Inbreeding occurred in baby corn traits that determined baby corn grading like length and diameter of ears. Inbreeding depression in the ear diameter wasn't significantly different between HS and S₁ families, but it was significantly different for ear length (Table 2).

Percentage of marketable ear classified to class A in S₁ and HS families were higher than their progenitors (Fig 1). Based on this study, plant breeder must gave more attention for the existence of inbreeding in baby corn size, so the percentage of marketable baby corn was not decrease due to baby corn size less than standard requirements. The effect of the inbreeding system especially selfing might be the fixation of deleterious gene leading to reduction of plant's performance, whereas in the half-sibs, greater heterozygosity would lead to the deleterious alel being hidden in heterozygote and the resultant effect would be good performance (Ajala *et al.*, 2009).

Genetic parameters and inbreeding depression of baby corn traits from each genotype in selfing families were presented in Table 3. There were differences of inbreeding depression (ID) value and percentage of inbreeding (%ID) among selfing genotypes in each baby corn traits. Inbreeding depression didn't be occurred in Golden for plant height (%ID = -0.14), ear height (%ID = -0.08), weight husked ears (%ID = -0.33), and ear diameter (%ID= 0.00), Hawaii for weight husked ears (%ID = -0.01) and ear diameter (%ID = -0.03), Lokal madura for ear diameter (%ID = -0.08), and Srikandi kuning for weight dehusked ears (%ID = -0.03) and ear diameter (%ID = -0.06) (Table 3). Positive and negative of inbreeding depression was influenced by type of action genes that control the expression of quantitative traits (Fox, 2005). Negative value in inbreeding depression indicated a large number of homozygous loci, which maintain genetic stability of the genotypes and leads to less depreciation in some traits performance (Botelho *et al.*, 2016).

Table 2. Inbreeding depression and percentage of inbreeding depression of baby corn traits from half-sibs (HS) and selfing (S₁) families.

Traits	Inbreeding depression		Percentage of inbreeding depression	
	HS	S ₁	HS	S ₁
PH	19.36 (a)*	26.39 (a)	8.22	13.14
EH	10.62 (a)	16.82 (a)	7.07	17.31
NE	0.75 (a)	0.92 (a)	20.25	25.52
WDE	1.97 (a)	6.86 (a)	2.94	11.46
WHE	0.08 (a)	1.15 (a)	0.51	15.61
ED	-0.62 (a)	0.17 (a)	-4.66	1.11
EL	0.36 (a)	1.12 (b)	4.38	13.60

PH: plant height (cm); EH: ear height (cm); NE: number of ears per plant; WDE: weight of dehusked ear (g); WHE: weight of husked ear (g); ED: ear diameter (mm); EL: ear length (cm);* the same letter in raw are not significantly different from each other based on t-test (p<0.05).

Table 3. Inbreeding depression (ID), percentage of inbreeding depression (%ID), estimates of the contribution of homozygous loci ($\mu+a$) and heterozygous loci (δ), and average degree of dominance (add) in Selfing families.

Families from	Plant height				
	ID	ID%	$\mu + a$	δ	Add
Baruna	42.10	0.23	99.98	84.21	0.84
Golden	-19.64	-0.14	182.78	-39.28	-0.21
Hawaii	14.16	0.09	130.13	28.32	0.22
Laksmi	59.94	0.31	70.79	119.87	1.69
Lokal Madura	14.88	0.06	232.99	29.77	0.13
Genjah melati	38.25	0.20	119.37	76.49	0.64
Mutiara	12.76	0.07	160.57	25.52	0.16
Srikandi kuning	48.66	0.24	109.73	97.32	0.89
Average	26.39	0.13	138.29	52.78	0.38
Families from	Ear height				
	ID	ID%	$\mu + a$	δ	add
Baruna	26.76	0.33	27.67	53.52	1.93
Golden	-4.89	-0.08	70.17	-9.78	-0.14
Hawaii	8.75	0.12	54.88	17.50	0.32
Laksmi	39.83	0.44	10.86	79.67	7.34
Lokal Madura	5.78	0.04	147.85	11.56	0.08
Genjah melati	20.59	0.20	64.37	41.17	0.64
Mutiara	10.32	0.11	72.60	20.64	0.28
Srikandi kuning	27.44	0.23	62.84	54.87	0.87
Average	16.82	0.17	63.90	33.64	0.53
Families from	Number of ear per plant				
	ID	ID%	$\mu + a$	δ	add
Baruna	0.40	0.10	2.90	0.81	0.28
Golden	0.67	0.03	1.67	1.33	0.80
Hawaii	0.42	0.09	2.38	0.83	0.35
Laksmi	1.30	0.21	0.79	2.60	3.28
Lokal Madura	0.67	0.04	1.66	1.35	0.81
Genjah melati	1.70	0.24	0.94	3.39	3.60
Mutiara	0.87	0.02	2.11	1.75	0.83
Srikandi kuning	1.29	0.14	1.05	2.57	2.45
Average	0.92	0.11	1.69	1.83	1.08
Families from	Weight of dehusked ear				
	ID	ID%	$\mu + a$	δ	add
Baruna	6.83	0.13	38.17	13.66	0.36
Golden	-12.88	-0.33	64.70	-25.77	-0.40
Hawaii	-0.24	-0.01	44.15	-0.49	-0.01
Laksmi	24.83	0.47	3.36	49.66	14.79
Lokal Madura	10.29	0.13	55.70	20.57	0.37
Genjah melati	14.20	0.28	21.50	28.41	1.32
Mutiara	2.79	0.06	40.14	5.58	0.14
Srikandi kuning	9.06	0.17	34.35	18.11	0.53
Average	6.86	0.11	37.76	13.72	0.36

Families from	Weight of husked ear				
	ID	ID%	$\mu + a$	δ	Add
Baruna	1.84	0.26	3.38	3.68	1.09
Golden	2.54	0.33	2.70	5.08	1.88
Hawaii	0.63	0.08	6.71	1.27	0.19
Laksmi	2.24	0.29	3.11	4.47	1.44
Lokal Madura	0.43	0.06	6.23	0.87	0.14
Genjah melati	0.42	0.08	4.76	0.85	0.18
Mutiara	1.23	0.18	4.52	2.47	0.55
Srikandi kuning	-0.18	-0.03	7.28	-0.36	-0.05
Average	1.15	0.16	4.84	2.29	0.47
Families from	Ear diameter				
	ID	ID%	$\mu + a$	δ	add
Baruna	0.72	0.05	13.01	1.45	0.11
Golden	0.05	0.00	13.47	0.10	0.01
Hawaii	-0.50	-0.03	15.40	-1.00	-0.07
Laksmi	1.32	0.09	11.96	2.64	0.22
Lokal Madura	-1.13	-0.08	15.61	-2.26	-0.14
Genjah melati	1.31	0.10	10.34	2.61	0.25
Mutiara	0.32	0.02	13.14	0.64	0.05
Srikandi kuning	-0.76	-0.06	14.31	-1.53	-0.11
Average	0.17	0.01	13.41	0.33	0.22
Families from	Ear length				
	ID	ID%	$\mu + a$	δ	add
Baruna	1.86	0.24	4.09	3.72	0.91
Golden	1.83	0.22	4.59	3.66	0.80
Hawaii	0.81	0.10	6.83	1.62	0.24
Laksmi	1.36	0.16	5.53	2.71	0.49
Lokal Madura	1.39	0.16	5.84	2.77	0.47
Genjah melati	0.55	0.06	7.36	1.10	0.15
Mutiara	1.02	0.12	6.29	2.04	0.32
Srikandi kuning	0.17	0.02	8.05	0.33	0.04
Average	1.12	0.14	6.07	2.24	0.37

All of baby corn traits in the selfing genotypes had positive value in the estimated contribution of homozygous loci ($\mu + a$) and in the estimated contribution of heterozygous loci (δ). In this study, traits would have negative value in inbreeding depression, if value of $\mu + a$ parameter was positive ($\mu + a > 0$), and value of δ parameter was negative ($\delta < 0$) (Table 3). The variation found in inbreeding depression was related to the nature of the traits, genetic complexity of traits, the geographical origin of the accession, and the degree of genetic heterozygosity in the S_0 genotypes (De Freitas *et al.*, 2016; Grisales *et al.*, 2014). There was closed negative relationship between parameter ID and $\mu + a$ with correlation value $r = -0.98^*$ (Pacheco *et al.*, 2002). The positive value of $\mu + a$ indicated the number of additive allele that controlled the expression of genes higher after selfing and the positive value of δ indicates dominance effect was in the sense of the genes favoring traits expression (Grisales *et al.*, 2014).

Almost baby corn traits were included into partial dominant in degree of dominance parameter except for number of ear per plant which was over dominance. Average degree dominance (add) of each traits were different among selfing genotypes (Table 3). The estimated contribution of heterozygous loci (δ) and the degree of dominance could suggest the presence of a few region with segregating recessives at several loci thus providing a great affected phenotypes performance (Edwards and Lamkey, 2002).

Plant breeders was suggested to give more attention in genetic factors and inbreeding depression when would construct baby corn variety which has high production and good quality traits (length and diameter of ears). Additive gene action in ear diameter for S_1 genotypes with add value -0.07 for Hawaii, -0.14 for Lokal madura, and -0.11 for Srikandi kuning, while another genotypes were partial dominance. Average degree of dominance for ear length from all of Selfing genotypes belonging to partial dominance (Table 3).

There were variances between S_1 genotypes for number of ear per plant. Selfing genotypes from Laksmi, Genjah melati, and Srikandi kuning were classified to over dominance and selfing genotypes from Golden, Hawaii, Baruna, and Lokal madura were classified to partial dominance. Based on this study, S_1 genotypes from Golden, Hawaii, Baruna, Lokal madura, and Mutiara were suggested to developed as open pollinated varieties (OPV) through recurrent selection and S_1 offspring from Laksmi, Genjah melati, and Srikandi kuning were suggested to developed as hybrid varieties. Population development and improvement using recurrent selection methods could be used as OPV (Aekatasanawan, 2001). Characters that have over dominance gene action could only fixed through hybrid variety to obtain superior genotypes (Sleper and Poehlman, 2006).

Conclusion

Means of Inbreeding families both half-sib and selfing families were lower than their progenitor for baby corn traits except ear diameter. There wasn't significantly difference of inbreeding depression value for half-sib and selfing families except for ear length. Inbreeding depression and percentage of inbreeding depression were different among selfing genotypes. Baby corn traits would has negative value in inbreeding depression, if value of $\mu + a$ parameter was positive ($\mu + a > 0$) and value of δ parameter was negative ($\delta < 0$). Selfing genotypes from Golden, Hawaii, Baruna, Lokal madura, and Mutiara were suggested to develop as open pollinated varieties, while Selfing genotypes from Laksmi, Genjah melati, and Srikandi kuning were suggested to develop as hybrid varieties.

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