Estimation of Genetic Parameters, Heritability, Genetic Advance and Heterosis in Sugarcane Families

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ABSTRACT

The present investigation was to estimate variance components, genetic parameters, broad-sense heritability, genetic advance and heterosis percentage for 9 agronomic traits of 142 bi-parent sugarcane family hybrids and 15 male parents used in this experiment. The experiments were conducted at three representative locations at Nakhon Pathom (KS), Nakhon Sawan (KL), and Nakhon Ratchasima (KN) from November 2013 to March 2015. Randomized complete block (RCB) design with 4 replications was employed. Results revealed that the variance components due to families and environments was relatively high, affecting higher heritability in most agronomic traits, especially the flowering percentage, stalk diameter, brix, stalk number, and stalk weight. When considering both broad-sense heritability and genetic advance, the mean percentage was relatively high in stalk number, stalk diameter and flowering, which should be highly effective traits for direct selection within these families. There were nine significant family groups based on heterosis percentage for seven traits. Among the offsprings, the male parents had a clear expression pattern which showed that the FG1 to FG4 came from the TByEFC energy-cane, while the FG5 to FG9 obtained mainly from sugarcane. The family x trait biplot drawing showed that heterosis percentage on the family group F99 and F102 correlated highly to cane yield and brix yield.

Keywords: heritability, genetic advance, heterosis, sugarcane.

INTRODUCTION

Sugarcane breeding programs in Thailand are mainly developed at the Office of the Cane and Sugar Board (OCSB), Department of Agriculture (DOA), and Kasetsart University (KU). Generally, sugarcane breeding programs in Thailand are using individual selection and family selection. The process of improving sugarcane variety was slow because of clone selection and evaluation that takes about 12-15 years to release a new variety (Kimbeng and Cox, 2003). For worldwide sugarcane breeding program, there were four selection methods, including individual selection, family selection, sequential selection, and regional selection.

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Individual selection used for early selection stage in sugarcane breeding programs. This method could be summarized as the clonal visual selection that correlated with cane yield and its components. While the **family selection** also evaluated at seedling stage and mass clones selection from within families. This method was used as method of indirect selection among seedling populations. Family selection method in sugarcane that the rejection or selection of entire population seedlings based on information derived from family plots. **Sequential selection** methods were family selection efficiency can be enhanced by adding individual selection within the best families, In this case, the selection criterion used within families is based on individual deviation from the mean value of its corresponding family. While the **regional selection** used for breeding programs have adopted specific strategies for development of varieties for broad range of environments or for specific environment. (Kimbeng and Cox, 2003). It is widely practiced in early selection stage in Australia (Stringer *et al*., 2010), the United States (Stringer *et al*., 2011), India (Shanthi *et al*., 2008), Brazil (Silva *et al*., 2002), South African (Zhou *et al*., 2012), and China (Tang *et al*., 2017). Family selection was evaluated using planted in replicated plots across several locations. It could collect information over ratoon crops by evaluating genotype by environment interaction effects (Zhou and Lichakane, 2012). The major agronomic traits are essential in sugarcane family selection that stalk number, stalk height, stalk diameter, cane yield, sucrose content, and sugar yield. They are the primary traits selected for early stages (Zhou, 2014; Silveira *et al*., 2015), indicates the potential of these traits to benefit from the family selection. Consequently, using family selection for these traits was expected to increase broad-sense heritability and get to higher predicted selection gains (Pedrozo *et al*., 2011). Zhou (2014) studied the potential of evaluating cane yield of sugarcane family estimated using agronomic traits compared to individual selection. The result showed family selection percent predicted gains and broad-sense heritability were more prominent than for individual selection. Stringer *et al.* (2010) proposed the family selection shown to be superior to individual selection, the selection of families instead of that of individual clones, followed by the selection of the best genotypes within the best families so that the heritability of yield-related traits in families was higher than in individual plants. In general, family selection based on broad adaptation, or based on mean yield across all sites, gave the best gains from selection in most environments. Considering clone performance at individual sites, genetic correlation with average family yield across all sites was more significant than the correlation with the family yield at particular sites (Jackson and McRae, 1998).

This study aimed to evaluate the impact of family selection for agronomic traits using data available and determine the magnitude of sugarcane family x environment interaction to optimize methods for selecting among family in breeding programs. This experiment's objective was to estimate variance components, genetic parameters, broad-sense heritability, genetic advance, and heterosis percentage for nine traits in selection at the seedling stage. They also allowed displays of the relationship among families and agronomic characters through the family x trait biplot.

MATERIALS AND METHOD

The experiments were conducted at three representative locations at Nakhon Pathom (KS), Nakhon Sawan (KL), and Nakhon Ratchasima (KN) from November 2013 to March 2015. Each site was conducted in a randomized complete block (RCB) design with 4 replications. A total of 142 bi-parent sugarcane family hybrid and 15 male parents were used in the experiment. All sugarcane families breed from 93 female parents classified into 67 exotic and 26 Thai varieties derived from the germplasm collection of the Sugarcane Breeding Project, Kasetsart University (Table 1). The male parents were used as testers comprised of Thai sugarcane and TByEFC (Tiphuyae Banyang Energy and Forage Cane) varieties. These sugarcane varieties were developed through breeding programs of 3 government offices, viz. the Office of the Cane and Sugar Board (K88-92), the Department of Agriculture (UT1 and Ehaew), and Kasetsart University (TBy20-0214, TBy20-1300, TBy26-1255, and Kps01-12). The TByEFC-varieties are the interspecific hybrids with special agronomic characters, such as many stalks, extended plant height, and thin stalk diameter. In contrast, five Thai sugarcane varieties, TBy20-0214, TBy20-1300, TBy26-1255, Ehaew, and Kps01-12 represent the high brix values, whereas K88-92 and UT1 are characterized by predominant stalk diameter and stalk weight. Therefore, the breeder can use them as a parental tester in these agronomic traits. The planting seedling family was in a single row plot of 22.5 meters long and 1.5 meters between rows with 30 seedlings per family per plot. Data collected on nine agronomic traits, namely number of stalks (STKNO, thousand stalks ha-1), single stalk weight (STKWT, kg), stalk height (STKHT, m), stalk diameter (STKDIA, cm), brix value (BRIX, %), and cane yield (CYLD, ton ha-1). While brix yield (BYLD, ton brix ha-1), percent of flowering (PFLW, %) and percent of smut disease (PSMUT, %) were calculated as follow:

BYLD = (CYLD x BRIX)/100
PFLW = [(number of flowering stools)/(total number of stools)] x 100
PSMUT = [(number of smut stools)/(total number of stools) x 100

Statistical analysis

The statistical model for the combined ANOVA across locations as follow:

$$Y_{ijk} = \mu + L_i + R_{i(j)} + F_k + FL_{ik} + e_{ik(j)}$$

where Y_{ijk} was the value observed for the *k*th family in the *i*th location and *j*th replication, was the overall mean, $R_{i(j)}$ was the effect of *j*th replication within the *i*th location, F_k was the effect of the *k*th family, FL_{ik} was the interaction effect between the *k*th family and the *i*th location, and $e_{ik(j)}$ was the residual.

The variance components were estimated using the mixed model with the restricted maximum likelihood (REML). The families, replications within locations, and family x location interaction were considered to be random effects, while locations were regarded as fixed effects. The phenotypic (σ^2_G) and genetic (σ^2_P) variance based on plot averages were obtained from the formulae,

$$\sigma^2_P = \sigma^2_f + \sigma^2_{fl}/l + \sigma^2_e/lr$$
$$\sigma^2_G = \sigma^2_f$$

when σ^2_f was the variance due to differences among families, σ^2_f was the variance due to interaction of families and locations, and σ^2_e was the residual.

The phenotypic (PCV), genotypic (GCV) and environmental (ECV) coefficient of variation and index of variation (IV) were estimated for each trait according to Johnson *et al.* (1955):

$$\mathrm{PCV} = [\sqrt{\sigma^2_P} / \bar{X}] \text{ x } 100$$
$$\mathrm{GCV} = [\sqrt{\sigma^2_G} / \bar{X}] \text{ x } 100$$
$$\mathrm{ECV} = [\sqrt{\sigma^2_e} / \bar{X}] \text{ x } 100$$
$$\mathrm{IV} = \mathrm{GCV} / \mathrm{ECV}$$

The PCV and GCV values greater than 20% were considered as high, values between 10 and 20% to be medium, and values less than 10% were considered to be low. (Deshmukh *et al.*, 1986).

Broad-sense heritability (h^2_B) and standard errors (S.E.) of h^2_B for all agronomic traits were estimated in accordance with Becker (1992):

$$h^2_B = [\sigma^2_G/\sigma^2_P] \text{ x } 100$$

$$\mathrm{S.E.}(h^2_B) = \sqrt{\frac{2(1-h^2_B)^2[1+h^2_B(n-1)]}{n(n-1)(f-1)}}$$

The heritability values greater than 80% were considered very high, values 60% to 79% are moderately high, values from 40% to 59% were medium and values less than 40% were low (Singh *et al*, 2005).

Genetic advance (GA) and genetic advance as the percentage of mean (GAM) were determined as described by Johnson *et al.* (1955):

$$\mathrm{GA} = k(\sigma_P)h^2_B$$
$$\mathrm{GAM} = (\mathrm{GA}/\bar{X}) \text{ x } 100$$

Where: k = the selection differential (k=2.6652 at 1% selection intensity); σ^2_P = the phenotypic standard deviation of the trait; X = grand mean of the trait. The genetic advance as a percentage of the mean; values 0-10% were low, 10-20% are moderate and above 20% were high (Johnson *et al.*, 1955).

The percent of heterosis based on the male parents used to assess the prominence of the hybrid in the agronomic traits of the offspring that calculated from the following formula:

$$\text{Male parent heterosis (\%)} = \frac{F_1 - \text{Male parent}}{\text{Male parent}} \text{ x} 100$$

Where: F1 = mean of a family; Mp = male parental value

Table 1 Female and male parents of the 142 sugarcane families

Fam.	Female	Male	Fam.	Female	Male
F1	Co245	TByEFC05-0014	F44	Ja64-19	TByEFC05-0810
F2	CP50-11	TByEFC05-0014	F45	NCo387	TByEFC05-0810
F3	CP51-11	TByEFC05-0014	F46	SP50	TByEFC05-0810
F4	CP51-13	TByEFC05-0014	F47	LK92-11	TByEFC05-0895
F5	CP77-418	TByEFC05-0014	F48	LK95-118	TByEFC05-0895
F6	F175	TByEFC05-0014	F49	UT5	TByEFC05-0895
F7	Fiji105	TByEFC05-0014	F50	CP29-211	TByEFC05-1264
F8	IAC49131	TByEFC05-0014	F51	CP77-403	TByEFC05-1264
F9	IRK67-1	TByEFC05-0014	F52	Fiji105	TByEFC05-1264
F10	MP96-273	TByEFC05-0014	F53	IAC49131	TByEFC05-1264
F11	N52-211	TByEFC05-0014	F54	IAC52-15	TByEFC05-1264
F12	N52-219	TByEFC05-0014	F55	IRK67-1	TByEFC05-1264
F13	N6	TByEFC05-0014	F56	N52-211	TByEFC05-1264
F14	Phil63-17	TByEFC05-0014	F57	N52-219	TByEFC05-1264
F15	ROC5	TByEFC05-0014	F58	TByEFC05-0836	TBy20-0214
F16	LF78-960	TByEFC05-0033	F59	TByEFC05-1083	TBy20-0214
F17	LF89-149	TByEFC05-0033	F60	TByEFC05-1211	TBy20-0214
F18	M34/45	TByEFC05-0033	F61	K97-27	TBy20-0214
F19	NCo310	TByEFC05-0033	F62	LK95-127	TBy20-0214
F20	Phil6607	TByEFC05-0033	F63	K93-347	TBy20-1300
F21	PR763035	TByEFC05-0033	F64	K97-27	TBy20-1300
F22	PT43-52	TByEFC05-0033	F65	Phil65-33	TBy20-1300
F23	TBy22-0663	TByEFC05-0069	F66	PS41	TBy20-1300
F24	F148	TByEFC05-0069	F67	Q107	TBy20-1300
F25	F162	TByEFC05-0069	F68	TBy22-0663	TBy26-1255
F26	K93-219	TByEFC05-0069	F69	B76718	TBy26-1255
F27	Kwt3	TByEFC05-0069	F70	BL22	TBy26-1255
F28	M147/44	TByEFC05-0069	F71	CAC57-11	TBy26-1255
F29	My5514	TByEFC05-0069	F72	CAC57-66	TBy26-1255
F30	Waya	TByEFC05-0069	F73	Co1148	TBy26-1255
F31	H38-2915	TByEFC05-0080	F74	Co775	TBy26-1255
F32	H47-4991	TByEFC05-0080	F75	CP29-291	TBy26-1255
F33	H59-3775	TByEFC05-0080	F76	CP75-109	TBy26-1255
F34	IAC48-65	TByEFC05-0080	F77	D158-41	TBy26-1255
F35	TBy23-0201	TByEFC05-0222	F78	DB671760	TBy26-1255
F36	TBy23-0421	TByEFC05-0222	F79	DB7160	TBy26-1255
F37	TBy24-0039	TByEFC05-0222	F80	F162	TBy26-1255
F38	K97-29	TByEFC05-0222	F81	H47-4991	TBy26-1255
F39	KU50	TByEFC05-0222	F82	H59-3775	TBy26-1255
F40	Q84	TByEFC05-0222	F83	IAC48-65	TBy26-1255
F41	ROC24	TByEFC05-0222	F84	K99-72	TBy26-1255
F42	SP701406	TByEFC05-0222	F85	LF89-149	TBy26-1255
F43	UT4	TByEFC05-0222	F86	M34/45	TBy26-1255

Table 1 Cont.

Fam.	Female	Male	Fam.	Female	Male
F87	My5514	TBy26-1255	F115	CAC57-11	Kps01-12
F88	Phil63-17	TBy26-1255	F116	Co1148	Kps01-12
F89	Phil6607	TBy26-1255	F117	Co775	Kps01-12
F90	PR763035	TBy26-1255	F118	CP75-109	Kps01-12
F91	PSA63	TBy26-1255	F119	D158-41	Kps01-12
F92	PT43-52	TBy26-1255	F120	DB671760	Kps01-12
F93	ROC24	TBy26-1255	F121	F162	Kps01-12
F94	SP701406	TBy26-1255	F122	H38-2915	Kps01-12
F95	SP758110	TBy26-1255	F123	H47-4991	Kps01-12
F96	UT4	TBy26-1255	F124	H59-3775	Kps01-12
F97	TBy22-0877	Ehaew	F125	LF78-960	Kps01-12
F98	H47-4991	Ehaew	F126	LF89-149	Kps01-12
F99	K90-77	Ehaew	F127	M147/44	Kps01-12
F100	M147/158	Ehaew	F128	M34/45	Kps01-12
F101	Phil65-33	Ehaew	F129	NCo310	Kps01-12
F102	SP80	Ehaew	F130	Phil63-17	Kps01-12
F103	TBy20-0214	K88-92	F131	Phil6607	Kps01-12
F104	Co245	K88-92	F132	PT43-52	Kps01-12
F105	CP48-103	K88-92	F133	Q66	Kps01-12
F106	CP52-48	K88-92	F134	Q84	Kps01-12
F107	F151	K88-92	F135	Singapore	Kps01-12
F108	LF89-205	K88-92	F136	UT4	Kps01-12
F109	M147/158	K88-92	F137	TBy22-0663	UT1
F110	NCo293	K88-92	F138	K83-74	UT1
F111	Phil56-226	K88-92	F139	K88-65	UT1
F112	Phil65-33	K88-92	F140	My5514	UT1
F113	ROC7	K88-92	F141	Q130	UT1
F114	BL22	Kps01-12	F142	ROC3	UT1

The hierarchical cluster analysis using data from the percent of heterosis on seven agronomic traits of 142 bi-parent sugarcane family hybrids was calculated by the square euclidean distance and Ward's clustering method. A two-way table of family and trait's heterosis was analyzed using the principal component analysis to capture the essence of the data in a few main component (PCs) axes that convey the most variation. The first two PCs axes describe the amount explained variation of the total variation and drawn the biplot diagram to explore the relationship among family and their traits' heterosis.

RESULT AND DISCUSSION

Components of variance and variation

Estimates of variances components and their genetic parameters are given in (Table 2). Variance components of the families, family x location, and environment for each trait show their contribution to the total variance. Variance components for families were relatively higher than the environmental effect in PFLW, STKDIA, BRIX, STKNO, and STKWT, respectively. Zhou and Lichakane (2020) reported the large variability in some quality traits, especially having relatively high heritability for brix similar earlier studies in South Africa (Bond, 1977) and Brazil (Pedrozo *et al*., 2011). The PCV values ranged from 6.06% to 115%, while the GCV values ranged from 4.48% to 91.57%. According to classification of the coefficient of variation by Deshmukh *et al*. (1986), it found that high PCV and GCV values were observed in PFLW (108.81% and 91.57%, respectively) and PSMUT (115% and 61.25%, respectively), for high PCV and moderate GCV were observed in the STKNO (22.10% and 18.22%, respectively), CYLD (23.68% and 15.35%, respectively) and BYLD (24.14% and 15.66%, respectively), for moderate PCV and GCV were observed in STKWT (17.84% and 14.64%, respectively); therefore, these sugarcane families exhibited wider genetic variation for 6 agronomic traits. High GCV and PCV for TCH (tons cane per hectare) were also found by Singh and Sangwan (1980) and Mehareb *et al*. (2017). At the same time, low PCV and GCV were observed in 3 traits, STKHT (7.54% and 4.48%, respectively), STKDIA (9.21% and 8.32%, respectively), and BRIX (6.06% and 5.20%, respectively). Therefore, the breeders should find a high variability of genetic sources for these three traits to make improvements. The ECV values ranged from 2.81% to 97.33%. The IV values had the highest for STKDIA, followed by PFLW, BRIX, STKNO, and STKWT, respectively. These indicated that the genetic variation is more significant than environmental variation in these five traits.

Heritability and genetic advanced

The heritability values ranged from 28.37% to 81.54% while ranging values of the GA are 0.27 to 22.08, ranging values of the GAM is 7.09% to 205.38% (Table 2). Broad-sense heritability was high in STKDIA, BRIX, PFLW, and STKNO. The result was consistent with Mehareb *et al*. (2017) reports in stalk weight and diameter. The moderate broad-sense heritability found in CYLD was 42.01, having near the value of heritability on a family basis in cane yield, reported by Skinner *et al*. (1987). This means that selection for cane yield on a family basis will be largely effective in original seedlings (Stringer *et al*., 2010). However, heritability should be considered together with the GAM. The agronomic traits that exhibit high heritability and GAM could be used as a powerful tool in the selection process. High heritability and GAM were observed in STKNO (67.94% and 40.02%), STKDIA (81.54% and 20.02%), and PFLW (70.82% and 205.38%), respectively, high heritability

Table 2 Estimated variance components and genetic parameters for 9 agronomic traits of the 142 sugarcane families

Parameter	Agronomic traits								
	STKNO	**STKHT**	**STKDIA**	**STKWT**	**BRIX**	**PFLW**	**PSMUT**	**CYLD**	**BYLD**
σ^2_f	100.60	78.83	0.04	0.02	0.92	96.95	2.01	36.42	1.28
σ^2_f	4.72	20.11	0.00	0.00	0.06	19.85	0.00	0.55	0.00
σ^2_e	42.74	124.72	0.01	0.01	0.27	20.09	5.07	49.71	1.77
σ^2_P	148.06	223.66	0.05	0.02	1.25	136.9	7.07	86.68	3.05
h^2_B	67.94	35.24	81.54	67.35	73.70	70.82	28.37	42.01	42.08
S.E.(h^2_B)	0.0068	0.0101	0.0042	0.0069	0.0058	0.0063	0.0101	0.0098	0.0082
PCV	22.10	7.54	9.21	17.84	6.06	108.81	115.00	23.68	24.14
GCV	18.22	4.48	8.32	14.64	5.20	91.57	61.25	15.35	15.66
ECV	11.87	5.63	3.52	10.13	2.81	41.69	97.33	17.93	18.37
IV	153.41	79.50	236.58	144.52	185.04	219.66	62.93	85.59	85.24
GA	22.03	14.05	0.48	0.27	2.19	22.08	2.01	10.43	1.96
GAM	40.02	7.09	20.02	32.02	11.91	205.38	86.95	26.51	27.08

and moderate GAM in were found STKWT (67.35% and 32.02%, respectively), whereas moderate heritability and GAM in CYLD 42.01% and 26.51%) and BYLD 42.08% and 27.08%, respectively. The resultsshowed a relatively high percent of heritability for brix as 73.7 in which similar studies by Leite *et al.* (2009) showed high heritability of 0.66, 0.88, and 0.86 for brix, TSH (tons stalk of stalk per hectare), TBH (tons of brix per hectare), respectively. Pedrozo et al. (2011) reported the heritability of brix was relatively low, but the heritability of CYLD and BYLD found in these studies were near similar to TSH and TBH, respectively. These authors point out that the variation in heritability estimates in the different studies may have arisen from differences in several aspects, including breeding populations, the environments evaluated, and the experimental design. From the results of the study, it can be concluded that highly effective direct selection within these sugarcane families can be made for most agronomic traits, viz. STKNO, STKDIA, PFLW, and STKWT, since exhibited high heritability and high range of variation.

Heterosis

The percent of heterosis on male parents for all agronomic traits was calculated (data not shown). Cluster analysis using traits' heterosis percentage for all 142 sugarcane families was classified into 9 different family groups (Figure 1). The results showed that most male parents between FG1 and FG4 breed from the series of TByEFC energy-cane genotypes, whereas 5 family groups between FG5 and FG9 breed from Thai sugarcane genotypes. The biggest family group, FG5, contained 31 families, followed by FG2, FG8, FG7, FG1, FG3, FG6, FG4, and FG9 had 21, 21, 16, 15, 15, 14, 7, and 2 families, respectively (Table 3). The dendrogram showed cluster FG9 closely relationship with FG6 and FG8, but it was a higher distance to another cluster (Figure 1). The FG9 group provided high positive percent of heterosis in almost agronomic traits, except STKDIA. In contrast, FG6 and FG8 had negative percent of heterosis in STKWT and STKDIA (Table 4). In comparison, FG4 provided positive percent of heterosis in most agronomic traits, except STKNO. These implied that the progenies that breed from female parents exhibited superior characteristics in most traits. The FG1 and FG3 groups showed positive percent of heterosis in STKWT, STKDIA, and BRIX, but their heterosis is negative in STKNO, STKHT, CYLD, and BYLD. The FG2 has the percent of heterosis similar to the FG1 and FG3 in all agronomic traits but a positive in BYLD.

Family x Trait biplot.

The biplot of family and their traits' heterosis, the two principle components explained 88.21% of the total variation that it was apparently showed sufficient amount of the total variation, indicating the biplot was applicable to the results in this experiment (Figure 2). The more significant variation shown in STKNO, STKWT, BYLD, and CYLD, respectively, indicated by their vectors' relatively more extended length. The narrow angles between the traits showed a strong correlation between them. The results can divide the traits into 4 groups, (T1) STKDIA, BRIX, STKHT; (T2) CYLD and BYLD, (T3) STKWT; and (T4) STKNO, that the traits within the same group had a high positive correlation among them. There is a very high negative correlation between STKWT and STKNO, indicated by the opposite vector's direction. The family F99 and F102 had long vectors and having very narrow acute angles with CYLD and BYLD; therefore, these families had the highest positive percent of heterosis for both agronomic traits. In this study, the TByEFC energy-cane (sugarcane x S. spontaneum) genotypes used as male parents gave a better hybrid performance in the most agronomic traits. In an earlier study in India, Anbanandan and Eswaran (2018) reported that the intergeneric hybrids (Badila x *E. arundinaceus* and Co86032 x *E. arundinaceus*) performed better based on the mean performance for traits cane yield and its components.

Table 3 The nine family groups using data from the percent of heterosis based on the male parent for seven agronomic traits

Family Groups	No. of Families	Family members
FG1	15	F1, F7, F15, F16, F17, F18, F19, F20, F22, F24, F28, F30, F40, F52, F56
FG2	21	F2, F3, F4, F5, F6, F8, F9, F10, F11, F12, F13, F14, F21, F25, F29, F37, F38, F39, F41, F42, F103
FG3	15	F23, F26, F31, F32, F34, F36, F45, F47, F48, F49, F50, F51, F53, F54, F57
FG4	7	F27, F33, F43, F44, F46, F55, F62
FG5	31	F35, F66, F68, F74, F85, F86, F95, F96, F110, F111, F112, F113, F116, F117, F118, F120, F121, F123, F124, F125, F127, F131, F132, F133, F134, F135, F138, F139, F140, F141, F142
FG6	14	F58, F59, F60, F61, F84, F88, F97, F98, F100, F104, F105, F107, F114, F119
FG7	16	F63, F73, F75, F77, F78, F80, F87, F90, F91, F92, F93, F94, F108, F109, F122, F128
FG8	21	F64, F65, F67, F69, F70, F71, F72, F76, F79, F81, F82, F83, F89, F101, F106, F115, F126, F129, F130, F136, F137
FG9	2	F99, F102

Table 4 The mean value and standard deviation (std.) of the percent of heterosis on 7 agronomic traits in each of 9 family groups.

Group	Statistics	STKNO	STKWT	STKHT	STKDIA	BRIX	CYLD	BYLD
FG1	Mean	-49.7	7.2	-22.6	13.3	14.1	-48.6	-41.4
	Std.	10.9	14.4	13.7	9.0	9.8	8.7	9.8
FG2	Mean	-18.6	14.1	-15.3	12.8	17.3	-12.8	2.4
	Std.	14.0	12.6	5.1	7.2	8.2	13.5	16.2
FG3	Mean	-44.4	58.4	-0.9	25.3	1.3	-13.6	-13.7
	Std.	8.6	22.1	10.8	15.2	10.9	16.1	11.9
FG4	Mean	-11.3	63.8	2.2	19.8	8.6	36.8	47.4
	Std.	15.5	17.9	8.1	8.8	8.3	7.4	8.4
FG5	Mean	10.2	-21.0	3.0	-14.7	3.2	-14.0	-11.4
	Std.	16.4	9.3	7.5	7.4	11.2	8.8	12.0
FG6	Mean	67.0	-5.3	8.9	-18.6	14.8	42.4	62.1
	Std.	34.0	20.7	8.9	6.7	10.1	21.5	23.5
FG7	Mean	9.0	-41.0	-10.5	-22.2	6.3	-36.0	-32.2
	Std.	15.6	6.8	9.2	4.8	7.2	10.5	11.4
FG8	Mean	36.1	-21.2	5.2	-18.6	5.5	8.4	14.5
	Std.	16.8	13.5	11.7	5.0	7.0	10.1	11.2
FG9	Mean	88.0	62.1	24.2	-7.4	14.2	171.8	210.5
	Std.	28.4	20.1	7.5	2.3	2.5	4.4	1.5

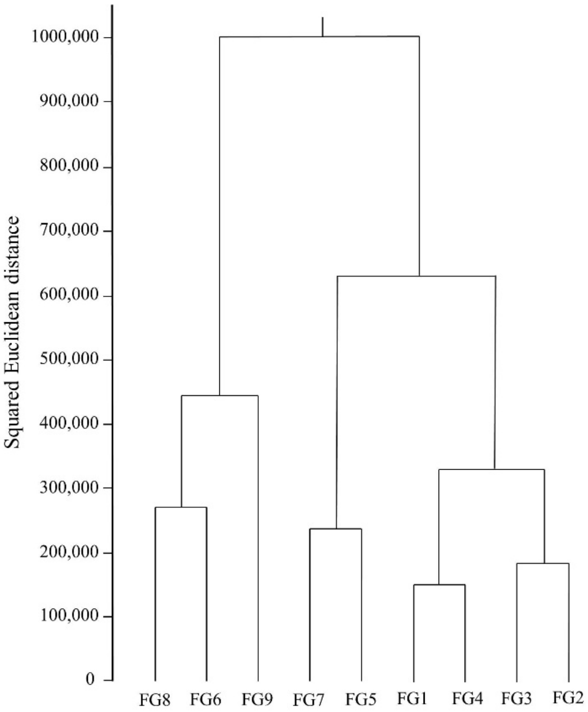

Figure 1 Dendrogram of nine sugarcane family groups calculated by the data from the male parent heterosis on seven agronomic traits

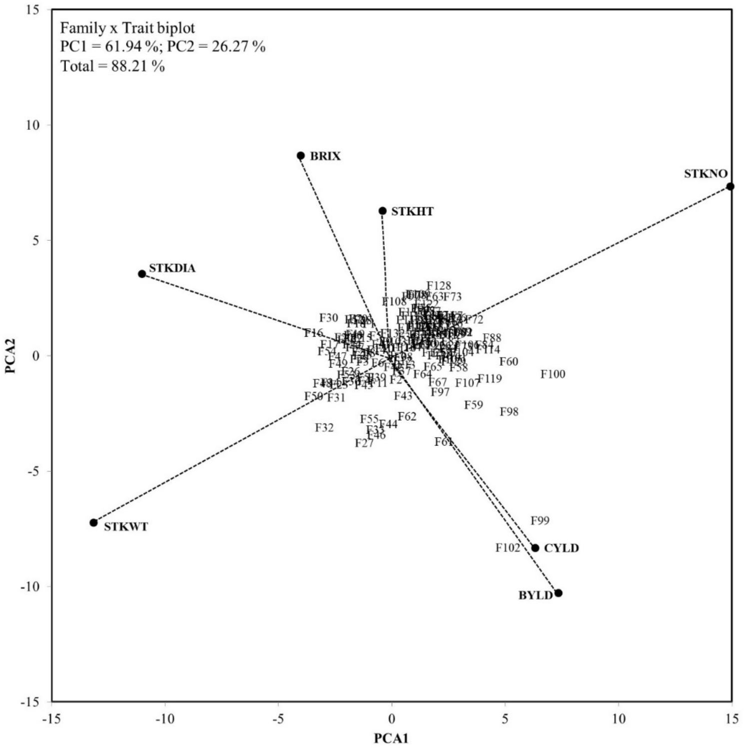

Figure 2 The biplot showing the position of families and the vectors of 7 traits' heterosis, such as the number of stalks (STKNO), single stalk weight (STKWT), stalk height (STKHT), stalk diameter (STKDIA), brix value (BRIX), cane yield (CYLD), and brix yield (BYLD)

CONCLUSION

The proportion of the variance components due to families and environments was relatively high, affects higher heritability in most agronomic traits, especially the flowering percentage, stalk diameter, brix, stalk number, and stalk weight. When considering both broad-sense heritability and genetic advance as the mean percentage were relatively high in the stalk number, stalk diameter, and flowering percentage, these traits should be highly effective directly selecting within these families. There were nine significant family groups base on the percent of heterosis for seven traits. In the offspring, the male parents had a clear expression pattern, which found that the FG1 to FG4 came from the TByEFC energycane, while the FG5 to FG9 obtained mainly from Thai sugarcane. The family x trait biplot drawing shows that the percent of heterosis on the family group F99 and F102 highly correlated to cane yield and brix yield. The new explores from this research were the fundamental for developed breeding sugarcane in Thailand. That can be used as a database on sugarcane breeding program to enhance cane yield and conserve the environment.

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