SUGARCANE FAMILY AND INDIVIDUAL CLONE SELECTION BASED ON BEST LINEAR UNBIASED PREDICTORS (BLUPS) ANALYSIS AT SINGLE STOOL STAGE

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Abstract

A field trial was carried out to evaluate 544 sugarcane clones (genotypes) and 3 check cultivars under un-replicated augmented design with eight unbalanced blocks at Giza Agricultural Research Station, Egypt (latitude of 30° 0' N, and longitude of 31° 12' E) in 2016/2017 seasons. The present work deals with the estimation of variance components, heritability, prediction accuracy and efficiency of selection in a population of 19 sugarcane families at single stool stage of breeding program using REML/BLUP (Restricted Maximum Likelihood/Best Linear Unbiased Prediction). Based on one-way and augmented block design without replication, the results showed low genetic variability among the evaluated families in stalk length, diameter, weight and number per stool. The narrow-sense heritability estimates ranged between the lowest (5.98%) for stalk number/stool to the highest (52.06%) for Brix%. Analysis of variance revealed significant differences among the evaluated clones for all the traits. The mean estimated through components via BLUP facilitated the selection of six families; number (1, 10, 3, 9, 17 and 2) as superior ones, respectively. The use of the augmented block design without replication in family selection experiments proved inadequate due to the low estimates of selective accuracy and family mean heritability. Owing to the large number of families and the use of the REML/BLUP procedure, either using or not using the checks in the analysis did not alter the estimated genetic parameters. Based on the individual BLUP in sugarcane selection, high differences within family for the yield main components were detected. The highest genotypic effects and high-predicted values for stalk weight per stool were recorded by the sugarcane clones number (375, 495, 31 and 359), while the highest for Brix% were recorded by clone's number (429, 259, 432 and 258). The results suggested that individual clone selection by BLUP procedure could indicate a higher number of promising clones for quantitative traits within families with high genotypic effects.

Key words: Sugarcane, REML/BLUP, family and individual selection, variance components, heritability, predictive accuracy

Introduction

The major challenge in breeding programs is the efficient selection of genotypes in the early stages. In Egypt, the sugarcane breeding program comprises uses several sequentially planted selection stages to identify and select the best clones within each cross. Sugarcane (*Saccharum spp.)* is a clonally propagated crop; genetic variability is created by crossing selected female and male parents. Selection is the cornerstone of plant breeding and is practiced across all stages of the sugarcane breeding program (Skinner et al. 1987). Sugarcane selection cycle starts with the hybridization of parents. Cross appraisal or progeny-tests are often used to focus selection for the best individuals from the best crosses (Cox et al. 1996; Barbosa et al. 2005). The first stage of selection involves evaluation of segregated seedlings planted from true seeds obtained after crossing. Referred to as the seedling stage (single stools stage), this is the only stage established from true seeds. The seedlings are evaluated either as individuals or in

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family plots. The statistical methods used in the early stages of sugarcane selection are the BLUP individual (Best Linear Unbiased Predictor) as shown by (Resende 2002). Kimbeng and Cox (2003) reported that the selection of families using BLUP led to the identification of new superior families, which would further lead to the selection of superior clones for commercial purposes. Chang and Milligan (1992) opined that BLUP was reliable in predicting the potential of a cross to produce elite progeny in sugarcane. Resende (2007) indicated that the ideal selection strategy for sugarcane would be to predict genotypic values by BLUP. Castro et al. (2016) confirmed that the BLUP procedure demonstrated great efficiency in selecting individuals in sugarcane families during the initial phase of genetic breeding programs.

BLUP method assumes genetic values are unobservable random effects and those genetic variances and covariance are known. Since for the latter assumption, this is never the case, this technique is in practice only an approximation of BLUP (Kennedy 1981). However, under normality, replacing the unknown variances by their restricted maximum likelihood (REML) estimate results is a very close approximation of BLUP (Gianola and Fernando 1986). The BLUP or mixed model methodology was developed and applied by breeders in the forest and some fruit species improvement (Resende 2001). Piepho et al. (2008) provided the basis for BLUP/REML or simply, the BLUP method. This method would predict a more accurate genotypic value, which is important for the selection of new varieties, or even the genetic values (additive effects) for the selection of progenies. Carvalho (2012) concluded that BLUP established a high correlation with different additive variance and heritability values. The higher values of heritability combined with the higher values of additive showed that the most efficient method was BLUP. Oliveira et al. (2011) and Almeida et al. (2014) used the BLUP to assay bi-parental crosses, estimate genetic parameters and predict the genotypic values of sugar cane families by analyzing individuals within families. Silva et al. (2015) pointed out that, for BLUP, the clones are selected by their own predicted genetic effects and the clones still have to be chosen based on individual phenotypes, such an approach

Table 1. Description of the bi-parental crosses and selfed populations of sugarcane

No. of Cross	Family pedigree		No. of Clones	No. of Cross	Family pedigree		No. of Clones
	Female	Male			Female	Male	
1	CP67-412 x selfing		1-50	12	BO18 x Crystallina		390-401
2	EH94-119-72 x selfing		51-100	13	CP57-614 x selfing		402-413
3	IK76-99 x selfing		101-150	14	CP67-412 x IK76-99		414-429
4	EH94-119-72 x BO18		151-200	15	EH94-181-1 x CP67-412		430-458
5	IK76-99 x EH94-119-72		201-250	16	CP57-614 x BO19		459-487
6	Cristallina x BO18		251-300	17	CP57-614 x IK76-66		488-497
7	IK76-66 x EH94-119-72		301-350	18	CP57-617 x BO18		498-522
8	BO18 x EH94-181-1		351-354	19	EH94-181-1 x CP67-412		523-544
9	BO18 x selfing		355-368	Check 1	G. 84-47		C_1
10	CP67-412 x EH94-119-72		369 to 379	Check 2	Phil. 8013		C_2
11	CP57-614 x IK76-99		380 to 389	Check 3	G.T. 54-9		C_3

Data were obtained from Sugar Crops Res. Institute, ARC at Giza.

approximately coincides with the within-family selection component, thus, the methods can, in fact, lead to the selection of almost the same set of clones. The present study aimed at utilizing REML/BLUP technique to evaluate a large number of sugarcane clones at seedling stage and to select sugarcane families and elite individual clones in the augmented block design as well as to estimate the heritability and prediction.

Materials and methods

Plant material

The single stool trial was established from biparental cross seedlings in the middle of April during 2016 season. A total of 544 sugarcane seedlings (clones) of 14 bi-parental crosses and 5 selfed populations were transplanted after the age of 3 months for evaluation in a single stool stage at the breeding nursery at Sugar Crops Research Institute, Giza Governorate (Table 1).

Experimental details

The experimental plant materials were laid out in an augmented design (Design II) with eight blocks to evaluate 544 sugarcane clones obtained from 14 crosses and 5 selfs (in a single stool) along with three checks. Each block consisted of 17 rows with each row of 4 m in length and 1m in width and 1 m between seedlings. Therefore, each block included 68 clones as well as three check cultivars viz. G.T.54-9, Phil.8013, and G.84-47 that grown in three rows within each block. After 12 months from seedling transplanting, data were recorded on stalk length, stalk diameter, stalk number per stool, stalk weight per stool and hand refractometer Brix%.

Statistical analysis

In the first model of analysis, the checks were not applied. Then, data were analyzed via a one-way (no blocking) analysis of variance (between and within families), and examined the residual plot. Apart from individual random errors, the only possible differences in the data could appear from individual treatment effects, leading to a model

Y = mean + treatment effect + error

The *F* test depends heavily on normally distributed data, and percentages are unlikely to be normally distributed, so the *P*-value is somewhat unreliable. Normality data test was applied to the data set (19 families) to verify the Normality.

Data recorded on cultivars *viz.* G.T.54-9, Phil.8013 and G.84-47, which were used as checks. In the first

Table 2. Structure of ANOVA for one-way (no blocking) analysis and augmented design-II.

Source of variation (SOV)	df	SS	MS	EMS	*F*
Between families	f-1	SS_f	MS_f	$\sigma^2_e + (c/f)\sigma^2_f$	MS_f / MS_e
Within families (error)	t-f	SS_e	MS_e	σ^2_e	
Total	t-1	SS_t			
Blocks (b)	b-1	SS_b	MS_b		MS_b / MS_e
Entries	n-1	SS_n	MS_n	$\sigma^2_e + b\sigma^2_n$	MS_n / MS_e
Clones (g)	g-1	SS_g	MS_g		MS_g / MS_e
Checks (c)	c-1	SS_c	MS_c		MS_c / MS_e
Checks *vs.* clones	1	SS_{cg}	MS_{cg}		MS_{cg} / MS_e
Error	(c-1) (b-1)	SS_e	MS_e	σ^2_e	

analysis model, an augmented design II (Federer and Searle 1976), which holds considerable promise for evaluation of large breeding materials, was used. Augmented design incorporates the provision of accommodating single replication of all treatments (Table 2) by spreading it over all the blocks (b), while a set of checks (c), numbering three are replicated in each block. Randomization was done in such a way that all the checks (c) and a part of test lines fall only once in each block. The equal number of test clones was planted in each block to facilitate augment statistical analysis.

Secondly, analyses with and without the use of the genetic relationship matrix were carried out by best linear unbiased predictor (BLUP) analysis**.** REML/BLUP analysis was based on a mixed linear model (Piepho et al. 2008) using Genstat computer package version 17.

The mixed model equations were used to calculate the BLUPs of the genetic values of each family for the studied traits, considering the genetic relationship matrix described below:

$Y = X\beta + Zu + e$

Where: *Y* is the vector of observations (i.e. phenotypic data)

B and *u* are the vectors of fixed and random effects, respectively.

X and *Z* are the associated design matrices.

e is the random residual error.

Based on BLUBs analysis, the best 25 sugarcane clones for stalk weight per stool were selected (5% selection intensity) and forwarded for evaluation in the next stage (clonal stage).

Estimation of genetic parameters

For estimation of genetic parameters, there are three models for REML/BLUP joint analysis in relation to the use of checks (augmented, REML/ Fixed and REML/BLUP)**.** The method proposed by (Henderson 1975) use the least squares equations and variance components. In balanced data, it is rather simple to estimate variance components, by setting the "Mean Squares" equal to their expectations. Those expectations are linear functions of the variance components. REML (Restricted ML) estimators maximize the likelihood estimation of the parameters are calculated based on the mixed model equations. REML/BLUP model for an augmented (as unbalanced) design (using or not using checks) with different regular treatments (fixed and random effects), was applied.

Genotypic (σ^2_g) and phenotypic (σ^2_p) components of variance were estimated according to the following formulae: $\sigma^2_g = MS_c - MS_{e,}$ and $\sigma^2_p = \sigma^2_g + MS_e$. Both genotypic and phenotypic coefficient of variability was computed for each trait according to the method suggested by Burton and De Vane (1953). Heritability in broad-sense (h^2_b %) was computed for each trait as the ratio of genetic variance to the total variance as suggested by Hanson et al. (1956). The estimation of variance components (within and between family components) is attributed to specific effects. Full-sib variance is due to differences between families. The variance component represents the family variance (σ^2_f), which is half of the additive genetic variance. Heritability in narrow-sense (h^2_n %) was computed for each trait as the ratio of additive genetic variance ($2\sigma^2_f$) to the total variance ($\sigma^2_f + \sigma^2_e$). Expected genetic gains as absolute and relative % of mean (GA %) was calculated according to Falconer (1981) at 5% selection intensity.

Results and discussion

Sampling at the single stool stage is too labor-intensive to be followed as a routine procedure in breeding programs. On this account, an individual selection using individual and family information

Table 3. One way ANOVA (no blocking) for the studied traits of 19 sugarcane families

SOV	df	Stalk length	Stalk diameter	Brix%	Stalk No./stool	Stalk weight/ stool
Between crosses (families)	18	2973.05**	0.36**	38.32**	73.65*	21.05**
Within crosses (error)	525	1427.59	0.06	3.46	39.11	10.30
Total	543	4401.00	0.42	41.80	112.80	31.35
h^2_n%: narrow-sense heritability		7.29%	29.74%	52.06%	5.98%	7.03%

* and ** significant at 0.05 probability level, respectively.

(individual BLUP) is restricted at this stage of the sugarcane improvement.

Analysis of variance

As shown in Table (3)**,** the analysis of variance based on one-way, revealed highly significant differences among the evaluated 19 families for all the traits. The variation within clones (544 clones) is largely due to differences between families; therefore, these clones are expected to give high cane and sugar yields in the next stage of selection. Darwish et al. (2017), who obtained a range of variability between the tested families.

Results in Table (4) revealed that analysis of variance based on augmented block design exhibited highly significant differences among the tested clones. Moreover, the checks versus clones for all studied traits indicated the existence of large variability among each group and considerable improvement could be obtained by selection for these traits. These results were reported by Tahir et al. (2014) and Abu-Ellail et al. (2017), who observed significant differences in the contrast of the checks vs. clones for most traits. Evaluation at family level was not proved suitable due to the low heritability values (Table 4), as the heritability% at

Table 4. Mean squares of augmented block design for studied traits in sugarcane in 2016/2017 season

SOV	df	Stalk length	Stalk diameter	Brix%	Stalk No./ stool	Stalk weight/ stool
Blocks	7	2010.70**	0.649**	41.72**	111.40**	34.12**
Entries	546	1478.23**	0.097**	4.34**	40.67**	19.06**
Clones	543	1454.90**	0.062**	4.08**	38.82**	10.22**
Checks (2)		2128.70**	1.032**	36.72**	26.55**	19.23**
Checks *vs.* Clones	1	12844.00**	17.346**	83.95**	1073.7**	4819.41**
Error	14	140.90	0.016	1.19	0.06	0.08

* and ** significant at 0.05 probability level, respectively

the level of family means were 7.29, 29.74, 52.06, 5.98 and 7.03% for stalk length, stalk diameter, stalk number/stool, Brix% and stalk weight/stool, respectively. An augmented experimental design is an unbalanced design, which divides a large set of experimental clones into small incomplete blocks. In each incomplete block, a set of checks was included; and these checks are used to estimate the error mean square and the block effect for reducing the error.

Family selection

Several research and simulation studies have shown that the combined family and individual clone selection is a practical and cost-efficient method of selection in the early stage of sugarcane trials. The data in Table 5 revealed that the family number 1 had the highest value of 20.27% and 7.83 kg for Brix% and stalk weight per stool, respectively, which was significantly higher than the lowest one (family number 11), by about

Table 5. Mean performance of 19 sugarcane families for stalk length, stalk diameter, Brix %, and stalk number/stool and stalk weight/stool in single stool stage in 2016/2017 seasons

Family No.	No. of clones / family	Stalk length (cm)	Stalk diameter (cm)	Brix %	Stalk No./ stool	Stalk weight / stool (kg)
1	50	267.90	2.06	20.27	14.34	7.83
2	50	269.50	2.35	19.29	10.66	6.75
3	50	284.10	2.44	19.26	11.54	7.15
4	50	271.98	2.38	19.14	10.60	6.40
5	50	270.15	2.27	19.28	10.26	6.11
6	50	275.09	2.22	19.29	9.90	5.64
7	50	283.65	2.36	19.15	9.34	5.45
8	4	263.75	1.98	17.18	12.25	5.55
9	14	280.00	2.30	20.21	13.04	6.83
10	11	287.99	2.45	19.58	9.68	7.52
11	10	297.30	1.89	15.32	8.30	4.61
12	12	277.08	2.29	15.86	9.75	5.47
13	12	253.75	2.44	17.20	10.25	5.08
14	16	267.08	2.40	15.75	9.63	5.63
15	29	291.62	2.02	18.67	10.78	5.64
16	29	251.38	2.31	18.97	9.19	5.32
17	10	272.67	2.37	19.50	11.40	6.81
18	25	267.07	2.35	17.45	9.06	5.39
19	22	269.00	2.39	18.32	7.85	5.55
Grand mean ± Sd		273.74± 12.26	2.28± 0.08	18.5± 0.61	10.5±2.07	6.10±1.07
LSD 0.05		24.65	0. 16	1.21	4.07	2.10

4.95% and 3.22 kg, respectively. Based on the results, six families; viz., 1, 10, 3, 9, 17, and 2, recorded the highest mean performance over the grand mean of 19 families for most of the important traits, pointing to selection between and within these families. Family selection involves the selection or rejection of whole families of seedlings based on information derived from family plots (Falconer and Mackay 1996). After family selection, the individual seedling selection is restricted to elite families. (Hogarth and Mullins 1989). The selection of families instead of that of individual clones was done, followed by the selection of the best genotypes within the best families, is more efficient as the heritability of yield-related traits in families is higher. Thus, it is preferable to prioritize the selection of promising families followed by individual selection of clones in the best families (Stringer et al. 2011).

Individual clone selection

The individual selection that aims at the establishment of clones within each family is based on visual criteria that involve a series of agronomical traits. The performance of 544 sugarcane clones evaluated at single stool stage are summarized in Figure (1) for stalk length, stalk diameter, stalk No./stool, stalk weight/stool and Brix% (Figure comprised of three group ranges). Concerning to the highest values over checks mean, there were 150, 0, 35, 61 and 3 clones recorded the highest values for stalk length, stalk diameter, stalk No./stool, Brix% and stalk weight/stool, respectively and these clones are superior to checks. In the second group, the clones with values ranged between checks mean and clones mean for stalk length, stalk diameter, stalk No./stool, Brix% and stalk weight/stool was 157, 250, 260, 108 and 149 clones, respectively. However, 137, 294, 249, 375 and 392 clones recorded lower values compared to clone mean. These results showed a wide range of variability among the tested clones for all studied traits, indicating that the selection of genotypes within this stage is possible for the traits under study. Similar results were reported by Tahir et al. (2014), who

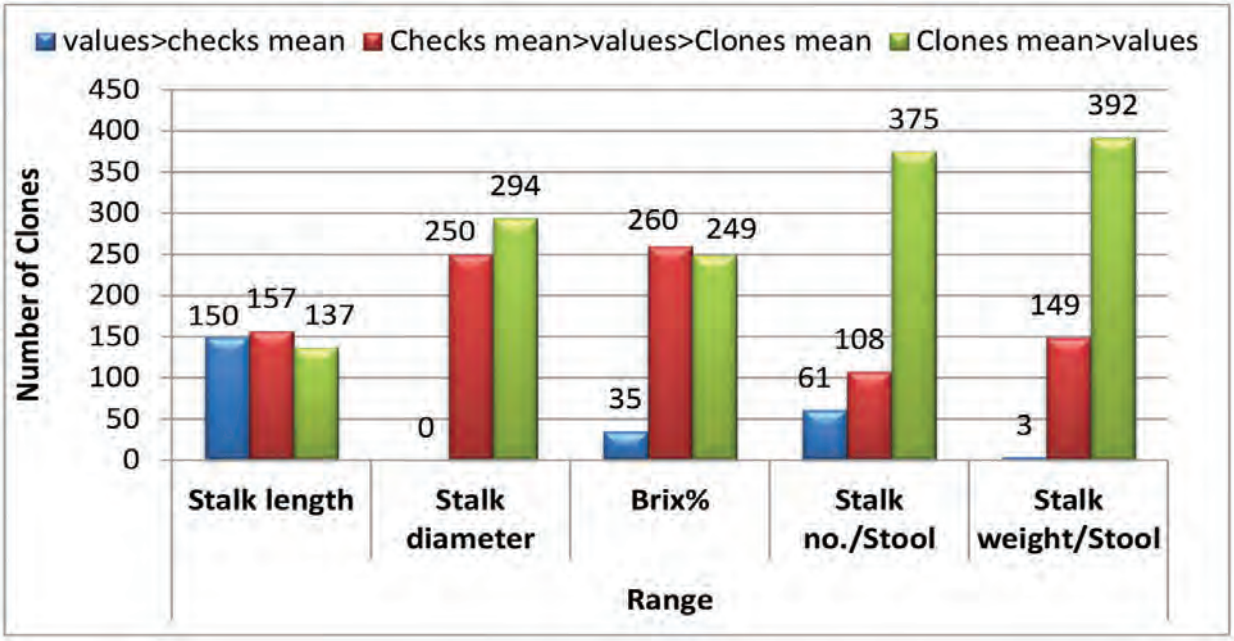

Fig. 1. Frequency distribution of stalk length, stalk diameter, stalk No./stool, stalk weight/stool and Brix% for the 544 evaluated sugarcane clones at single stool stage

Table 6. Variance components, genetic parameters and model type in three joint analyses (REML/ BLUP) of augmented design in sugarcane families in 2016/2017 seasons

Model (No.)	Traits	Variance components			h_b^2%	GA% 5%	Mean Blocks/ Checks/ Treatment	Model type
		σ^2_e	σ^2_g	σ^2_{ph}				
Augmented (544)	Stalk length	140.9	1337.4	1478.3	90.47	26.56	269.8	Random / Absence / Random
	Stalk diameter	0.02	0.08	0.10	83.50	26.46	1.85	
	Brix %	1.19	3.16	4.35	72.60	16.89	18.47	
	Stalk No. / stool	0.06	40.61	40.67	99.85	130.65	10.04	
	Stalk weight /stool	0.08	18.98	19.06	99.58	154.14	5.81	
REML/ Fixed (544)	Stalk length	124.70	1338.3	1463.0	91.48± 0.028	26.75	269.80	Random / Fixed / Random
	Stalk diameter	0.01	0.06	0.07	80.13± 0.05	23.50	1.85	
	Brix %	1.45	2.71	4.16	65.17± 0.106	14.84	18.47	
	Stalk No. / stool	0.06	40.12	40.18	99.85± 0.001	126.4	10.33	
	Stalk weight /stool	0.08	11.62	11.70	99.28± 0.002	120.6	5.81	
REML/ BLUP (547)	Stalk length	123.9	1343.0	1466.9	91.55 ± 0.028	26.81	268.79	Random/ Random/ Random
	Stalk diameter	0.02	0.04	0.06	66.58 ± 0.11	18.56	1.82	
	Brix %	1.58	2.52	4.11	61.42± 0.126	13.90	18.40	
	Stalk No. / stool	0.06	40.07	40.13	99.85± 0.001	126.3	10.33	
	Stalk weight /stool	0.09	10.51	10.60	99.17± 0.003	114.60	5.81	

σ^2_g: genotypic variance, σ^2_p: phenotypic variance, σ^2_e: environmental variance, n: number of evaluated genotypes, h^2_b%: individual broad-sense heritability, and GA%: genetic advance percent.

showed a broad range of variability in the tested genotypes at a single stool stage. Most commonly, individual selection is used for early selection in sugarcane breeding programs. This method can be summarized as the individual visual selection of clones for traits correlated with sugarcane yield and health (Barbosa et al. 2014).

Estimating heritability and predicted accuracy

The use of augmented block design for the evaluation of sugarcane families was not reliable due to the low heritability values at the level of family means (Table 3). Alternative methods have recently been suggested, which may increase the efficiency in the analyses of the augmented block design via mixed models (Federer et al. 2001). Thereby, it is possible to adjust the environmental effects, recover the genetic inter-block information, as well as estimate the variance components by the REML method. Results of the three models for REML/BLUP joint analysis in relation to the use of checks are presented in Table (6). In the first analysis model, the checks were not used. In the second model, checks G.T.54-9, Phil.8013 and G.84-47 were used as fixed. Meanwhile, the checks were used as random in the third analysis model. Broad-sense heritability (h_b^2 %) estimates were obtained for all studied traits to demonstrate that the relative influence of genotypic variance (σ^2_g) in determining phenotypic variance (σ^2_p) was more important for all studied traits among the three models. High broad-sense heritability (h_b^2 %) estimates were observed with 72.60, 65.17 and 61.42% for stalk number/stool among the three models (augmented, REML/Fixed and REML/BLUP), respectively. The important juice quality trait Brix % recorded the lowest estimated values (72.60, 65.17 and 61.42%) among the three models. These results suggested that there was genetic variability within family and it is possible to select the best clones through individual selection, especially for stalks number/stool, stalks weight/stool and stalk length. These results were in agreement with (Olivera et al. 2008), who suggested that the presence of genetic variability give the viability of potential selection.

The most important functions of heritability estimates in the genetic studies of quantitative traits are their predictive role. Possible advance through selection based on heritability estimates and genetic advance in a population provide information about the expected gain (GA %). Results presented in Table (6) revealed varied significance for the expected genetic gain in the studied traits among the three models (augmented, REML/Fixed and REML/BLUP). The results demonstrated that the highest genetic advance % was recorded for stalk weight/stool (154.14, 120.60 and 114.60%) and stalk number/stool (130.65, 126.40 and 126.30%) in all the three models. Meanwhile, Brix % trait recorded the lowest values (16.89, 14.84 and 13.90) for all the models. These results indicated the possibility of practicing selection of clones to enhance both stalk weight/stool and stalk number/stool and for identifying high yielding genotypes (Abu-Ellail et al. 2017). It was noticed that one-way (no blocking) analysis of variance (between and within families) revealed large relative differences between families (highest residual values). Furthermore, the large residual error indicates the need to optimize experimental designs to improve experimental efficiency. In augmented design (incomplete blocks) error mean square and the block effect are estimated and the block effect is estimated from the replicated mean values of the check and then removed from the means of the evaluated clones. This procedure reduces error and increases precision. Meanwhile, it is possible to adjust the environmental effects, recover the genetic inter-block information via REML method and increasing the efficiency (Federer et al. 2001).

Table 7. Predicted genetic effects (g_j) and genotypic values ($\mu + g_j$) of the highest selected 25 sugarcane clones in descending order using BLUP method for the studied traits in 2016/2017 seasons

No.	Stalk length			Stalk diameter			Brix %			Stalk no./stool			Stalk weight/stool		
	Clone No.	$\mu + g_j$	g_j	Clone No.	$\mu + g_j$	g_j	Clone No.	$\mu + g_j$	g_j	Clone No.	$\mu + g_j$	g_j	Clone No.	$\mu + g_j$	g_j
1	**113**	341.31	72.39	**C3**	3.30	1.17	**C3**	22.32	3.92	**150**	43.70	33.62	**150**	33.84	28.56
2	**252**	340.5	71.58	**C2**	2.98	0.86	**429**	21.22	2.82	**495**	39.86	29.78	**495**	24.34	19.07
3	**59**	340.27	71.35	268	2.61	0.49	**259**	21.14	2.74	**445**	36.01	25.93	**31**	21.93	16.65
4	**245**	337.45	68.53	**319**	2.62	0.49	**432**	21.01	2.60	**359**	35.86	25.78	**C3**	21.41	16.13
5	**436**	333.91	64.99	**176**	2.60	0.48	**258**	20.93	2.52	**31**	34.35	24.27	**C2**	19.12	13.85
6	**452**	332.38	63.47	**C1**	2.61	0.48	**40**	20.86	2.46	**200**	34.35	24.27	**359**	19.05	13.77
7	**301**	331.82	62.90	**345**	2.58	0.46	**302**	20.83	2.42	**83**	33.82	23.75	**445**	19.01	13.74
8	**439**	330.86	61.94	457	2.58	0.46	**349**	20.82	2.42	**251**	33.07	22.99	**200**	19.02	13.65
9	**325**	328.78	59.86	**535**	2.56	0.44	**364**	20.82	2.42	**339**	33.03	22.95	**100**	18.93	13.48
10	**381**	328.46	59.545	**378**	2.56	0.44	**444**	20.79	2.39	**120**	32.83	22.75	**248**	18.76	13.18
11	**326**	325.72	56.80	**412**	2.55	0.43	**204**	20.75	2.34	**38**	32.71	22.64	**C1**	18.46	12.48
12	**377**	325.42	56.50	**471**	2.56	0.43	**350**	20.71	2.31	**475**	31.01	20.94	**38**	17.76	12.38
13	**244**	325.25	56.33	167	2.55	0.42	**360**	20.71	2.31	**188**	30.35	20.27	**65**	17.66	11.36
14	**380**	323.89	54.971	**190**	2.57	0.42	**255**	20.71	2.30	**248**	30.07	19.99	**143**	16.64	11.12
15	**222**	323.73	54.811	**394**	2.53	0.41	**355**	20.60	2.20	**531**	29.87	19.80	**339**	16.39	10.67
16	**290**	322.68	53.757	**404**	2.53	0.41	**357**	20.60	2.20	**122**	29.83	19.75	**122**	15.95	9.59
17	**372**	320.84	51.925	**415**	2.52	0.40	**362**	20.50	2.09	**100**	27.83	17.75	**181**	14.65	9.38
18	**374**	320.84	51.925	418	2.53	0.40	**482**	20.48	2.07	**436**	26.02	15.94	**436**	14.37	9.09
19	**125**	318.44	49.519	**159**	2.52	0.40	**489**	20.48	2.07	**114**	25.84	15.76	**500**	14.32	9.04
20	**430**	317.45	48.527	**512**	2.51	0.39	**343**	20.39	1.98	**143**	25.36	15.28	**475**	14.17	8.89
21	**49**	317.4	48.48	**215**	2.51	0.39	**354**	20.39	1.98	**253**	25.08	15.00	**139**	14.16	8.88
22	**181**	315.17	46.256	**175**	2.49	0.37	**376**	20.39	1.98	**288**	25.04	14.97	**413**	14.07	8.79
23	**243**	314.58	45.664	484	2.48	0.36	**397**	20.39	1.98	**413**	25.02	14.95	**531**	14.02	8.74
24	**110**	313.86	44.945	**491**	2.49	0.36	**205**	20.38	1.98	**407**	24.87	14.79	**24**	13.99	8.71
25	**203**	313.66	44.737	**332**	2.48	0.35	**254**	20.38	1.98	**24**	24.73	14.65	**390**	13.99	8.71

The relative efficiency, based on *F* test of predictive heritability estimates for the studied traits error variances in Table (7), manifested insignificant *F*-test for the second and third models (REML/ Fixed and REML/BLUP), confirming that these models are statistically identical. Similar findings were reported by Barbosa et al. (2005), who mentioned that the adoption of REML analysis was expected to improve precision.

Estimates of the predicted genetic values *via* BLUP analysis

In sugarcane breeding program, the greatest genetic variability exists in the seedling generation (Molenaar et al. 2017). A single plant represents each seedling and individual. Augmented designs are applied in the current study since they are suitable for testing un-replicated treatments. Most of the clones (544 clones) had high values for the traits studied; therefore, selection of the best 25 sugarcane clones (5% selection intensity) was done based on stalk weight/stool employing BLUP analysis. The significant variance components suggested that the parents selected for crossing might have contributed significantly to the variability among progenies for cane yield components. Generally, the smaller standard error had attributed to the variability, suggesting the potential existence of genetic effects. The large residual error variances suggested high levels of noise in the data. The genotypic effects and genotypic values of the best 25 sugar cane clones from the 544 selected clones resulted from BLUP analysis for studied traits are presented in Table 7. As described by Zhou and Mokwele (2015), BLUP refers to the estimates of genotype breeding value relative to the population mean.

Clones with high genotypic effects and high genotypic values varied from one trait to another, for example, sugarcane clones number 113, 252, 59 and 245 had the highest genotypic effects and high predicted values ($\mu + g_{.j}$) for stalk length, while sugarcane clones number 268, 319, 176 and 345 had the highest genotypic effects and high predicted values for stalk diameter (Table 7). For stalk number/stool, the highest genotypic effects were recorded by clone's number 31, 495, 445 and 359. The highest genotypic effects and high predicted values for total soluble solids (Brix %) were recorded by the clones number 429, 259, 432 and 258. Meanwhile, stalk weight/stool, genetic effects and, genotypic values were recorded by the clones number 375, 495, 31 and 359, indicating that these clones may have the superiority for cane yield in advanced stages of selection. Exploiting of BLUB analysis for selection of superior families or individuals of sugarcane was reported by many researchers such as Carvalho (2012); Barbosa et al. (2014); Silva et al. (2015); Castro et al. (2016) and Mbuma et al. (2018). Despite the results of the BLUP procedure are unbiased, and its predicted genetic values are adjusted, the aforementioned unbalance contributed to different accuracy in the prediction of the genetic values and increased the predicted genetic values of the most tested (Resende 2002). Bressiani (2001) estimated differences within-family selection for the main components of stalk yield and Brix%, associated with each family and he found varied significant between clones for those traits. The selection by the individual BLUP in sugarcane improvement should be applied as suggested by McRae et al. (1998).

Conclusion

Overall, we can conclude that low genetic variability among the evaluated families was observed in the one-way analysis (without replication) and the additive effects were predominant to explain the genetic variation among families. The augmented block design (without replication) was not proved appropriate for the experiments of family selection for the evaluated population. The REML/BLUP

method proved to be suitable for the estimation of genetic parameters and the prediction of important genetic values for family selection in sugarcane improvement. BLUP estimates identified the elite genotypes viz., numbers 31, 495, 445, 359, 429, 259, 432 and 258 that had significantly higher stalk weight/stool and Brix%, indicating that these clones can be evaluated in next stages of selection and locations. Results of the present work should encourage breeders to select elite clones with higher genetic gains for stalk weight/stool and Brix percentage.

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