

SHORT, NON-REFEREED PAPER

EVALUATING BREEDING VALUES OF GENOTYPES IN SUGARCANE BREEDING USING BEST LINEAR UNBIASED PREDICTION (BLUP)

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Abstract

Breeding values (BV) refer to the ability of a genotype to produce progenies with high trait values when crossed with other genotypes and are used to predict the breeding performance of parental genotypes in sugarcane breeding. The objective of this study was to use best linear unbiased prediction (BLUP) to determine breeding values of parental genotypes for cane yield. Data were collected from a family evaluation trial planted in the Midlands on sandy soil in 2013. The families consisted of 31 female and 19 male parents. Cane yield was estimated from stalk numbers, height and diameter measured from the first 20 progenies per plot. BLUP analysis, which provides comparison of genotypes to population means, was done using SAS mixed models. There were significant female ($P=0.0019$) and male ($P=0.0093$) variances which indicated that the large genetic variability among progenies was associated with parents. Female parents 02S1314 (2.87, $P<0.0001$), 85H0428 (1.82, $P=0.0057$), 02S0674 (1.75, $P=0.0004$) and male parents B74713 (6.48, $P<0.0001$), 02B1047 (3.04, $P=0.0031$), and 99S1504 (1.84, $P=0.0244$) had significantly higher BV suggesting the ability to produce high yielding progenies. Female parent 85H0428 had higher BV when crossed with parents derived from Midlands humic soil (3.31, $P<0.0001$) and coastal long average potential (3.47, $P=0.005$) regions, suggesting broad general combining ability and BV. Male parent B74713 had significantly higher BV when crossed with parents derived from irrigated (5.00, $P<0.0001$) and coastal (1.88 to 4.62, $P<0.05$) regions, suggesting wider general combining ability. BLUP analysis successfully identified parents with high BV across breeding programmes.

Keywords: breeding values, parents, progenies, sugarcane yield

Introduction

Parent selection is the first step in a breeding programme. Selection of parents to be used in breeding programmes is based on the genotype's breeding value in order to sustain the genetic progress. Genetic combinations of selected parents influence the genetic variability among progeny populations (Balzarini, 2000). Therefore, parent evaluation will enhance the breeding efficiency because only genotypes with high breeding values will be used when crossing. Currently, the challenge in sugarcane breeding is predicting the potential of a genotype to produce high value progenies and this is largely attributed to the complexity of the sugarcane genome. The genome of the modern sugarcane hybrids derived from *Saccharum officinarum* and *spontaneum* are highly polyploidy, highly heterozygous, and are characterised by frequently unbalanced numbers of chromosomes, which is also known as 'aneuploidy' (D'Hont, 2005). The heterozygous and complex polyploid nature of sugarcane species results in high genetic variability of progenies produced from crosses (Premachandran et al., 2011). The prediction of progeny and parent performance is difficult due to unpredictable

chromosome transmission during crossing (Grivet and Arruda, 2001; Mudge *et al.*, 2009). In sugarcane breeding, the family evaluation data which is measured from the first stage of a four-stage selection programme (in South Africa) in the field is used to evaluate breeding values of parents.

Breeding values refer to the ability of a genotype to produce progeny with high trait values when crossed with other genotypes and are used to predict the breeding performance of genotypes as a parent in sugarcane. Knowledge of the breeding values of genotypes is expected to increase the quality of progenies, optimise crossing and reduce breeding costs. The objective of this study was to use best linear unbiased prediction (BLUP) to determine breeding values of genotypes for cane yield.

Materials and Methods

Family evaluation data were collected from stage 1 'mini-line' trials laid out in a randomised complete block design with three replications. The families were made up of 31 female and 19 male parents. The trial was established in 2013 at Glenside research station (997 m altitude, 29°20'S; 30°46'E) in a sandy soil breeding programme. Cane yield was estimated from stalk numbers, height (m) and diameter (cm) measured from the first 20 progenies in each family plot (Chang and Milligan, 1992). The BLUP analysis was done to generate potential breeding values for the female and male parents in sandy soil trial, using the mixed procedure of the Statistical Analysis System (SAS Institute, 2014).

$$Y_{ijkl} = \mu + R_i + F_j + M_k + G(FRM)_{l(ijk)} \quad \text{Equation 1}$$

where Y_{ijkl} = cane yield of the l th genotype in the i th replication of the j th female and k th male parent random effects, μ = grand mean, R_i = random effect of the i th replication, F_j = random effect of the female parent, M_k = random effect of the male parent, $G(FRM)_{l(ijk)}$ = individual l th genotype nested within the interaction effect of the i th replication by the j th female parent by the k th male parent and is also the residual error. The degrees of freedom for the BLUP were estimated using Satterthwaite's procedure (Freund and Wilson, 2003) for an appropriate t-test.

Results and Discussion

There were significant female ($P=0.0019$) and male ($P=0.0093$) variances for cane yield (Table 1), which indicated that progeny yield was associated with females and males. Males produced larger variance and larger standard errors compared to the female effects, suggesting that males were contributing more to variability among progenies. The residual error variance was larger than for both females and males, which indicated a very large influence of environment and other variables (Zhou and Mokwele, 2015).

BLUP refers to the estimates of breeding value relative to the population mean. The BLUP estimates can be significant ($P<0.05$) positive or negative indicating that a parent genotype produced higher or smaller values than the population mean, respectively. Females 02S1314 (2.87, $P<0.0001$), 85H0428 (1.82, $P=0.0057$), 02S0674 (1.75, $P=0.0004$) and males B74713 (6.48, $P<0.0001$), 02B1047 (3.04, $P=0.0031$), and 99S1504 (1.84, $P=0.0244$) had significantly higher breeding values for cane yield than the population mean (Table 2).

Female 85H0428 had higher breeding values for cane yield when crossed with different males and progenies evaluated in humic soil (3.31, $P<0.0001$) and coastal long average potential (3.47, $P=0.0050$), suggesting broad general combining ability. Male B74713 had higher breeding values when crossed with different females and tested in irrigated breeding programmes (5.00, $P<0.0001$) and coastal (1.88 to 4.62, $P<0.05$) breeding programmes.

Table 1. Covariance parameter estimates for cane yield for female, male, residual error effect, their standard error (S.E.), population mean and standard deviation (SD), Z-value and the probability for larger Z-value for the sandy soil population planted in 2013.

Covariance parameter	Estimate	Standard Error	Z Value	Pr > Z
Female	1.90	0.66	2.90	0.0019
Male	5.58	2.37	2.35	0.0093
Residual	44.51	0.90	49.69	<0.0001
Mean±SD	11.02±6.37			

Table 2. Female and male best linear unbiased prediction (BLUP) values for cane yield, standard error (S.E.) of BLUP, t-stats (t-statistic) and probability of a larger t-statistic (Pr>|t|) for the sandy soil populations planted in 2013.

Female	BLUP	S.E	t-stats	Pr > t	Male	BLUP	S.E	t-stats	Pr > t
02S1314	2.87	0.54	5.31	<0.0001	B74713	6.48	1.20	5.38	<0.0001
85H0428	1.82	0.66	2.77	0.0057	02B1047	3.04	1.03	2.95	0.0031
02S0674	1.75	0.50	3.53	0.0004	99S1504	1.84	0.81	2.25	0.0244
85L1612	1.49	0.94	1.59	0.1116	76H0255	1.01	1.08	0.93	0.3502
02S0582	1.25	0.96	1.31	0.1917	93H0094	0.98	1.30	0.76	0.4494
76H0376	1.22	0.77	1.60	0.1095	00B1198	0.73	1.02	0.71	0.4772
01S1430	0.91	0.49	1.85	0.0640	02S0928	0.21	1.26	0.16	0.8698
93H0094	0.88	0.98	0.90	0.3687	WI82498	0.09	1.50	0.06	0.9522
03S0767	0.81	0.53	1.53	0.1250	MP	-0.18	0.64	-0.29	0.7720
03S0282	0.79	0.55	1.43	0.1522	00B1189	-0.28	1.07	-0.26	0.7928
01S1428	0.62	0.89	0.70	0.4839	03S2040	-0.32	0.84	-0.38	0.7008
98S0290	0.57	0.57	1.00	0.3194	MO	-0.49	0.65	-0.75	0.4533
03S0283	0.31	0.48	0.63	0.5259	02S0639	-1.29	1.05	-1.23	0.2192
03S2040	0.15	0.57	0.27	0.7903	99B1979	-1.51	0.97	-1.56	0.1192
02S0639	-0.08	0.44	-0.19	0.8489	03S0472	-1.57	0.95	-1.66	0.0978
03S0379	-0.13	0.70	-0.19	0.8504	00B1941	-1.65	1.07	-1.54	0.1230
00S1247	-0.23	0.82	-0.28	0.7758	01S1681	-2.00	1.00	-2.01	0.0446
01S1637	-0.27	0.45	-0.61	0.5444	N37	-2.38	1.56	-1.53	0.1260
01S1672	-0.32	0.51	-0.63	0.5302	02B0918	-2.69	1.12	-2.41	0.0160
02S0558	-0.47	0.80	-0.59	0.5531					
00S0664	-0.51	0.58	-0.89	0.3733					
86H0430	-0.78	0.86	-0.90	0.3678					
02S0928	-0.78	0.45	-1.74	0.0819					
02S0679	-1.24	0.79	-1.57	0.1160					
97B0272	-1.28	0.77	-1.66	0.0967					
96H0652	-1.29	0.69	-1.88	0.0597					
03S0472	-1.43	0.65	-2.20	0.0279					
01S1681	-1.61	0.63	-2.55	0.0108					
76H0255	-1.64	0.87	-1.89	0.0593					
00S1958	-2.22	0.62	-3.58	0.0004					

Conclusions

Genotypes (02S1314, 85H0428, 02S0674, B74713, 02B1047, and 99S1504) with high breeding values were identified from progeny data and such genotypes are desirable for building a core germplasm pool of parents that are known to produce superior progeny for cane yield in sandy soil breeding programmes. Genotypes with high breeding values across breeding populations such as 85H0428 are present in South African Sugarcane Research Institute (SASRI) germplasm and could be used to guide future crossing for adaptability in multiple agro-ecological sugarcane growing areas.

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