

SHORT NON-REFEREED PAPER

FAMILY BY ENVIRONMENT INTERACTIONS FOR SUGARCANE YIELD IN SOUTH AFRICA

MBUMA NW^{1,2}, ZHOU MM^{1,2,3} AND VAN DER MERWE R²

¹South African Sugarcane Research Institute, P/Bag X02, Mount Edgecombe, 4300, South Africa

²University of the Free State, PO Box 339, Bloemfontein, 9300, South Africa

³School of Agriculture, Earth and Environmental Sciences, UKZN, Pietermaritzburg, South Africa

Ntombi.Mbuma@sugar.org.za Marvellous.Zhou@sugar.org.za

VanDerMerweR@ufs.ac.za

Introduction

Family evaluation involves using progeny data to determine family trait values. Families can be planted in several locations and over years to evaluate family by environment interactions (FE). Hogarth and Bull (1990) reported significant FL for cane and sugar yield from study of 35 families. Jackson *et al.* (1995) and Jackson and McRae (1998) proposed multi-location testing of families where significant genotype by environment interactions (GE) existed. Jackson *et al.* (1995) reported significant FL for cane yield and sugar yield in the Herbert Region of North Queensland, Australia, where GE were known to be important (Hogarth and Bull 1990). Studies by McRae and Jackson (1995) reported non-significant FL and FC for cane yield and sugar content in the Burdekin region of Australia. In Louisiana, Souza-Vieira and Milligan (1999) reported non-significant FL for cane yield components and suggested that family evaluation in Louisiana needed only to be conducted at one environment.

In South Africa, sugarcane is grown in three agro-climatic regions (irrigated, high altitude Midlands, and coastal regions) representing unique environmental conditions. The differences in the agro-climatic regions could result in trait values of a family varying from one region to another resulting in FE. Significant GE has been reported (Zhou *et al.*, 2011; Zhou *et al.*, 2012; Zhou and Gwata, 2015; Sengwayo *et al.*, 2017) suggesting potential existence of FE in South Africa. The objectives were to determine FE breeding parameters, family values across locations and traits controlling adaptability to different environments.

Materials and Methods

Family evaluation data were collected from plant, first and second ratoon crops of stage I 'mini-line' trials laid out in a randomised complete block design with three replications. The 44 families were made from 18 female and 18 male genotypes planted in 2013 in Midland humid soils 24 months at Bruyns Hill, Midlands sandy soils 24 months at Glenside, coastal 18 months at Gingindlovu, coastal 12 months at Empangeni, and irrigated 12 months at Pongola locations. Cane yield (kg) was estimated from stalk numbers, height (m) and diameter (cm) measured from the first 20 progenies in each family plot, the formula used to estimate cane yield assumed that the sugarcane stalk was a perfect cylinder with a density of 1.00 g/cm³ (Chang and Milligan, 1992). Data were analysed in the Statistical Analysis System (SAS Institute, 2014) using the linear mixed model for family by environment analysis:

$$Y_{ijklm} = \mu + L_i + R(L)_{ij} + F_k + FL_{ik} + FR(L)_{ijk} + C_l + CL_{il} + CR(L)_{ijl} + FC_{ik} + FLC_{ikl} + FRC(L)_{ijkl} + G(FRC(L))_{ijklm} \quad \text{Equation 1}$$

Where Y_{ijklm} = cane yield of the l^{th} genotype in the i^{th} location in l^{th} crop-years of the j^{th} replication, and k^{th} family random effects, μ = overall mean, L_i = fixed effect of i^{th} locations, $R(L)_{ij}$ = random effect of the j^{th} replications nested within i^{th} locations and is the experimental error for locations, F_k = fixed effect of families, FL_{ik} = fixed effect of the interaction between the k^{th} families and i^{th} locations, $FR(L)_{ijk}$ = random effects of the interaction of family by replication

nested within locations and is the experimental error for family and family by locations fixed effects, C_i = random effect of the i th crop-year, CL_{ij} = random effect between i th locations and the i th crop-year, $CR(L)$ = random effect of the interaction between i th crop-years and j th replications within i th locations, FC_{ki} = random effect of the interaction between k th family and i th crop-year, FLC_{iki} = random effect between the interaction of the with k th family, with i th location and i th crop-year, $FRC(L)_{ijkl}$ = random effect of the interaction j th replications by i th crop-years by k th family nested within i th locations, $G(FRC(L))_{ijklm}$ = random effects of genotype nested within the interaction effects of family with replication and with crop year nested within locations and is the residual error. Families, locations and crop years were assumed to be random. The families represent a random sample of possible families from stage I 'mini-line' trial. Locations represent a random sample of all possible locations representing sugarcane growing environments in South Africa. Crop year represents a random sample of the combined effect of year-to-year variability associated with ratooning of sugarcane.

BLUP analysis for the family effects used the linear mixed model:

$$Y_{ijk} = \mu + R_i + F_j + G(FR)_{k(ij)} \quad \text{Equation 2}$$

where Y_{ijk} = cane yield of the k th genotype recorded from j th family in the i th replication, R_i = random effect of the i th replication, $G(FR)_{k(ij)}$ = random effect of the k th genotype nested within the random interaction effect of the i th replication by the j th family.

A grouping of the data based on the breeding programme source (refers to the origin of genotypes that were used to make crosses) created a new design variable. The new data created with these categories (irrigated, Midlands, and coastal) were subjected to ANOVA and their mean values focused on trait adaptability to different locations.

Results and Discussion

Only the F, FL, FC and FLC variance components were interpreted because they influence family evaluation. The highly significant ($P < 0.001$) F variance for all traits indicated large genetic variability among the families for sugarcane yield present, regardless of the test environment of the populations (Table 1). The significant ($P < 0.01$) FL variance for cane yield, stalk number and diameter indicated that genetic variability among families varied across locations. The highly significant ($P < 0.001$) FC variance for stalk number suggested that there was a large crop-year effect on genetic variability among families. However, crop year effects and its interactions are confounded and unpredictable, and therefore not useful for guiding breeding and selection strategies (Ramburan, 2013; Zhou and Shoko, 2012). The FLC variance was largely non-significant ($P > 0.05$) for cane yield and stalk number, which indicated less influence of location specific crop-year effects on the traits.

BLUPs identified families such as TT1051, UU0332 and UU0312 for cane yield that showed the potential presence of broad adaptation of progenies because they produced high trait values in irrigated, coastal, and Midlands environments (results not shown). Family VV0701 for cane yield showed potentially specific adaptation to 12 month harvest cycles because their progenies produced high trait values only in irrigated and coastal short cycle. Families VV0390 and UU0198 for cane yield indicated specific adaptation of progenies to Midlands 24 months harvest cycle because they produced high traits values only in areas that represents slow crop growth caused by the long cold winters and short summers. Future research should consider the standard deviation within a cross as an important parameter when determining the value of a family and for potential exploitation via selection.

The irrigated, coastal and Midlands populations showed the most specific adaption for cane yield and stalk height because each population produced high trait values in locations that represents unique conditions (Figure 1). The coastal and irrigated populations showed the

broad adaption for stalk number and diameter, respectively, in diverse environments representing major agro-ecological regions of sugarcane production. Studies (Zhou, 2004) showed that stalk number had the strongest influence on cane yield. Therefore, these results could indicate potential opportunity to enhance the selection gains through transfer of genotype used in crosses across programmes.

Conclusions

Testing families in multi-locations was more important than across ratoons. BLUP estimates identified families (TT1051, UU0332 and UU0312) with significantly higher cane yields across locations, indicating potential presence of broad adaptation among progenies. Families VV0701 (irrigated), VV0390 (Midlands) and UU0198 (Midlands) for cane yield showed specific adaptability and could be exploited for niche breeding in sugarcane. The irrigated, coastal and Midlands populations showed the most specific adaptability for cane yield and stalk height.

Table 1. Family by environment interaction variance components (\pm standard error), mean and standard deviation (SD), coefficient of determination (R²) and coefficient of variation (CV) for cane yield (kg), stalk number, height and diameter.

Effect	Cane yield	Stalk number	Height	Diameter
L	32.48 \pm 32.49ns	5.46 \pm 8.77ns	0.0948 \pm 0.0975ns	0.0021 \pm 0.0103ns
R(L)	0.00 \pm 0.00	0.02 \pm 0.57ns	0.0003 \pm 0.0018ns	0.0003 \pm 0.0005ns
F	3.62 \pm 1.33**	17.87 \pm 4.56***	0.0079 \pm 0.0021***	0.0242 \pm 0.0056***
FL	4.28 \pm 1.29***	3.94 \pm 1.35**	0.0012 \pm 0.0012ns	0.0025 \pm 0.0011**
FR(L)	10.28 \pm 1.26***	11.57 \pm 1.45***	0.0124 \pm 0.0015***	0.0077 \pm 0.0011***
C	0.00 \pm 0.00	14.52 \pm 21.67ns	0.0000 \pm 0.0000	0.0394 \pm 0.0513ns
CL	34.12 \pm 18.10*	14.89 \pm 9.68ns	0.1033 \pm 0.0552*	0.0287 \pm 0.0166*
RC(L)	1.53 \pm 0.61**	0.95 \pm 0.60ns	0.0051 \pm 0.0022*	0.0008 \pm 0.0004*
FC	0.00 \pm 0.00	2.51 \pm 0.77***	0.0000 \pm 0.0000	0.0000 \pm 0.0000
FLC	0.79 \pm 0.55ns	0.00 \pm 0.00	0.0012 \pm 0.0007*	0.0012 \pm 0.0005*
FRC(L)	1.58 \pm 0.87*	0.00 \pm 0.00	0.0055 \pm 0.0007***	0.0000 \pm 0.0000
Residual	91.13 \pm 1.44***	119.49 \pm 1.84***	0.0657 \pm 0.0011***	0.0973 \pm 0.0015***
Trial mean \pm SD	16.57 \pm 9.59	26.78 \pm 11.04	1.48 \pm 0.26	2.21 \pm 0.31
R ²	0.57	0.43	0.81	0.53
CV	57.85	41.23	17.32	14.22

L = location; R(L) = replications within location; F = family; FL = family by location interaction; FR (L) = family by replications within location; C = crop; CL = location by crop-years interaction; CR(L) = crop by replications within location; FC = family by crop-years interaction; FLC = family by location by crop-years interaction, FRC(L) = family by replication by crop-years within location, ***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Not significant at P \geq 0.05

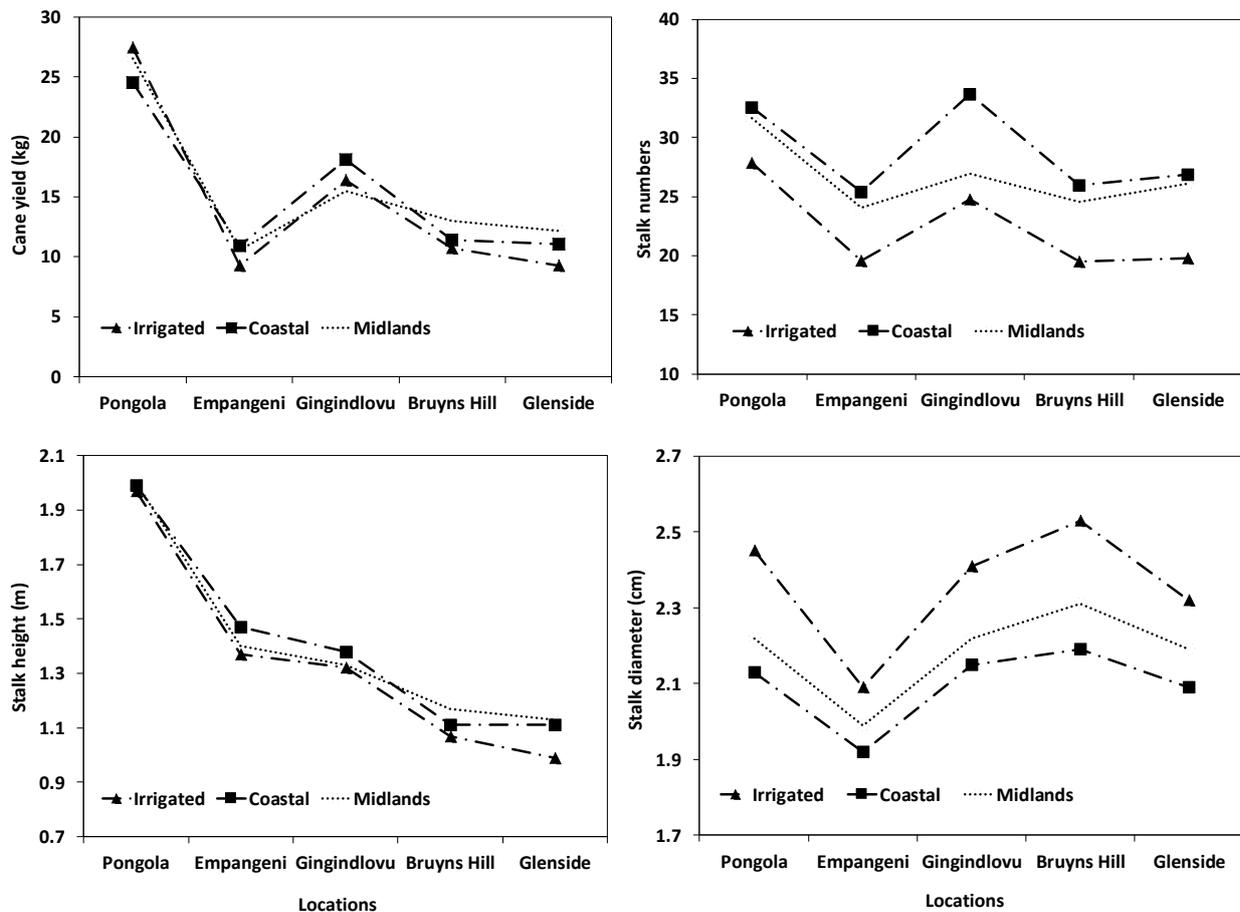


Figure 1. Trends in location by breeding source interaction for cane yield, stalk number, height and diameter.

Acknowledgements

The authors would like to thank the South African Sugarcane Research Institute (SASRI), the National Research Foundation (NRF), and the University of the Free State (UFS) for funding this project and SASRI plant breeding selection technicians for the management of the trials and data collection.

REFERENCES

- Chang YS and Milligan SB (1992). Estimating the potential of sugarcane families to produce elite genotypes using univariate cross prediction methods. *Theor Appl Genet* 84(5-6): 662-671.
- Hogarth DM and Bull JK (1990). The implications of genotype x environment interactions for evaluating sugarcane families. I: Effect on selection. In: Kang MS (Ed) *Genotype-by-Environment Interactions and Plant Breeding*. Baton Rouge: Louisiana State University, 335-346.
- Jackson PA and McRae TA (1998). Gains from the selection of broadly adapted and specifically adapted sugarcane families. *Field Crops Res* 59(3): 151-162.
- Jackson PA, McRae TA and Hogarth DM (1995). Selection of sugarcane families across variable environments. I: Sources of variation and an optimal selection index. *Field Crops Res* 43(2-3): 109-118.
- McRae TA and Jackson PA (1995). Genotype x environment interaction and selection of sugarcane families for the Burdekin River irrigation area: Final Report SRDC Project BS57S. Sugar Research Australia, 22 pp.
- Ramburan S (2013). A multivariate illustration and interpretation of non-repeatable genotype x environment interactions in sugarcane. *Field Crops Res* 157: 57-64.
- SAS Institute (2014). SAS/STAT user's guide, version 9.1.3. Cary, NC: SAS Institute.
- Sengwayo SH, Zhou MM and Labuschagne M (2017). Location and crop-year effects on sugarcane genotype performance for the coastal short cycle breeding programmes in South Africa. *S Afr J Plant Soil* 35(2): 79-87.
- Souza-Vieira ODE and Milligan SB (1999). Intrarow plant spacing and family x environment interaction effects on sugarcane family evaluation. *Crop Sci* 39(2): 358-364.
- Zhou MM (2004). Stalk population control of yield, quality and agronomic traits of sugarcane population in early selection stages. *Int Sugar J* 22(5): 14-20.
- Zhou MM and Gwata E (2015). Location effects and their implications in breeding for sugarcane yield and quality in the Midlands region in South Africa. *Crop Sci* 55(6): 2628-2638.
- Zhou MM and Shoko MD (2012). Simultaneous selection for yield and ratooning ability in sugarcane genotypes using analysis of covariance. *S Afr J Plant Soil* 29(2): 93-100.
- Zhou MM, Joshi SV and Maritz T (2012). Trends and implications of genotype by environment interaction in South African sugarcane breeding. *Journal of Crop Improvement* 26(2): 163-176.
- Zhou MM, Joshi SV, Maritz T and Koberstein H (2011). Components of genotype by environment interaction among SASRI regional breeding and selection programs and their implications. *Proc S Afr Sug Technol Ass* 84: 401-412.