Family and parent evaluation for sugarcane yield in early stage breeding populations in South Africa

By

Ntombokulunga Wedy Mbuma

Dissertation submitted in partial fulfilment of the requirements in respect of the Master's Degree qualification in the Department of Plant Sciences (Plant Breeding) in the Faculty of Natural and Agricultural Sciences at the University of the Free State Bloemfontein

November 2016

Supervisor: Dr R van der Merwe
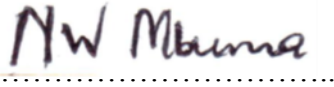**Co-supervisor: Prof MM Zhou**

DECLARATION

I, Ntombokulunga Wedy Mbuma, declare that the Master's Degree research dissertation that I herewith submit for the Master's Degree qualification in Plant Breeding at the University of the Free State, is my independent work, and that I have not previously submitted it for a qualification at another institution of higher education.

I, Ntombokulunga Wedy Mbuma, hereby declare that I am aware that the copyright is vested in the University of the Free State.

I, Ntombokulunga Wedy Mbuma, declare that all royalties as regards to intellectual property that was developed during the course of and/or in connection with the study at the University of the Free State, will accrue to the University.

I, Ntombokulunga Wedy Mbuma, hereby declare that I am aware that the research may only be published with the dean's approval.

23 November 2016

………………………..   …………………….

Signature   Date

ACKNOWLEDGEMENTS

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS AND SI UNITS

asl	Above sea level
BLUP	Best linear unbiased prediction
BML	Humic soil mini-lines
BP	Bi-parental
cm	Centimetre
CV	Coefficient of variation
°C	Degrees Celsius
DF	Degrees of freedom
DAFF	Department of Agricultural Forestry and Fisheries
F	Family
FAOSTAT	UN Food and Agriculture Organization Corporate Statistical Database
Gs	Predicted selection gains
GxE	Genotype x environment interaction
H	Broad-sense heritability
IGS	Individual genotype selection
K	Potassium
kg	Kilogram
m	Meter
MO	Males only
MP	Melting pot
N	Nitrogen
P	Phosphorus
PCA	Principal component analysis
PC1	Principal component 1
PC2	Principal component 2

PC3   Principal component 3

PC4   Principal component 4

SAS   Statistical analysis system

SASA   South African Sugar Association

SASRI   South African Sugarcane Research Institute

S.E.   Standard error

SML   Sandy soil mini-lines

stdev   Standard deviation

%Gs   Percent predicted selection gains

UNICA   The Association of Caribbean Universities and Research Institutes

USA   United States of America

R^2 Coefficient of determination

σ^2_F Family variance

σ^2_{FR} Family by replication variance

$\sigma^2_{G(F)}$ Genotype nested within family variance

$\sigma^2_{G(FR)}$ Residual variance

σ^2_R Replication variance

CHAPTER 1

INTRODUCTION

Sugarcane (*Saccharum* spp. hybrids) is grown in KwaZulu-Natal and Mpumalanga provinces of South Africa where it contributes significantly to the economy of the country. It provides approximately 79,000 direct jobs and 350,000 indirect jobs supporting the livelihoods of nearly a million people (SASA 2013/2014). Research to support the production of sugarcane is carried out by the South African Sugarcane Research Institute (SASRI) based in Durban. Sugarcane breeding is a major research focus of SASRI as varieties are an important input in sugarcane production.

The objectives of sugarcane breeding include developing varieties that produce high cane yield, high sucrose content (components of sugar yield, the commercial product), adaptability, ratooning ability, disease and pest resistance, and desirable agronomic characteristics (Jackson 2005). SASRI operates seven regional breeding programmes; two for the Midlands region, four for the coastal regions and one for the irrigated region (Nuss 1998; Zhou 2013). After crossing, generated populations are tested through four stages namely mini-lines, single lines, observation trials and advanced variety trials. In the mini-lines and single lines, the genotypes are not replicated while in the observation and variety trials, the genotypes are replicated (Zhou 2013). Variety trials are also planted at several locations to test for genotype by environment interaction (GxE) (Parfitt 2005; Zhou 2013).

Sugarcane millable stalks are the primary raw material produced by the farmer that is processed by the mills to produce sugar. Cane yield is the primary measure of productivity at the farm and forms a key selection criterion in sugarcane breeding. Cane yield is determined by the number of millable stalks, stalk height and stalk diameter (Chang and Milligan 1992a, 1992b). Breeding and selection methods to improve cane yield would therefore also focus on these yield components.

Sugarcane is a complex polyploid where autopolyploidy, aneuploidy and other complex chromosome and genetic combinations are known to exist. In addition, most commercial traits in sugarcane are controlled by many genes resulting in large influences of GxE

(Jackson and Hogarth 1992; Falconer and Mackay 1996; Jackson and McRae 1998). The effects of GxE are particularly large in early stages of sugarcane breeding where genotypes are not replicated, and are known to influence the efficiency of selecting for individual plants in sugarcane breeding (Skinner et al. 1987). Several methods can be used to increase selection efficiency and these include experimental designs and statistic models that account for competition effects among the individual genotypes (Zhou 2009).

In early years of sugarcane breeding, the proven cross system was used to evaluate the potential of families to produce elite progenies (Heinz and Tew 1987). The proven cross system was widely used in Australia, South Africa and other several breeding programmes (Heinz and Tew 1987; Skinner et al. 1987). The proven cross system depends on the number of genotypes, developed from a cross that are advanced to the later stage of breeding and selection. Crosses from which a large number of individuals are advanced were defined as elite families. The disadvantage of the proven cross system is the unavailability of the statistical tests for comparing families. The proven cross system further requires a number of years to determine the value of a cross or family (Kimbeng and Cox 2003).

Earlier studies in Australia (Hogarth et al. 1990) showed that larger genetic gains could be achieved when family selection was applied in Stage I (mini-lines) of sugarcane breeding. During family selection, the whole population of progenies within the family are selected or rejected based on family values and other family parameters (Falconer and Mackay 1996). Individual genotype selection (IGS) will only be done within the selected families. In Stage I, replication of individual genotypes is not possible because of limited planting material and the large areas of land required if material was available. However, at Stage I, families can be replicated providing an opportunity for evaluating family comparisons. Furthermore, family data can be used to identify and select superior parents used at the time of crossing. Family evaluation and selection have been practised in Australia (Hogarth et al. 1990; Jackson et al. 1995a, 1995b; Cox and Stringer 1998; Kimbeng et al. 2000, 2001; Stringer et al. 2011), Brazil (De Resende and Barbosa 2006; Pedrozo et al. 2011), India (Shanthi et al. 2008; Babu et al. 2009), USA (Milligan and Legendre 1990; Chang and Milligan 1992a, 1992b) and South Africa (Bond 1977, 1989; Zhou and Lichakane 2012; Zhou 2014, 2015; Zhou and Mokwele 2015). Preliminary studies in South Africa (Zhou 2014) and other countries (Barbosa et al. 2005) showed larger predicted genetic gains from

family selection compared to individual genotype selection particularly for yield traits. However, studies on comparing family selection with individual selection as well as comparing family selection among breeding programmes are limited.

Since the inception of family selection for yield in South African sugarcane breeding programmes, limited studies have been done to determine the benefits and progress that have been achieved from family selection (Zhou 2014). Limited studies have compared the differences in family selection parameters among breeding programmes as well as compared individual selection with family selection across family selection cycles. This is attributed to the difficulty of measuring individual plant data compared to family data particularly where manpower costs are high. Yet, the comparison is important when justifying the use of family selection over individual genotype selection. Very little information is known about the estimates of predicted selection gain as well as the optimum selection rate for families (for the different traits) and selection rate of genotypes within families. These parameters are important in determining the efficiency of breeding methods. Also, limited studies have determined the breeding values of parents using family data. However, the use of family data to evaluate parents is expected to provide better comparison among parents as well as to determine the best parent combinations at the time of crossing.

1.1 OBJECTIVES OF THE STUDY

The objectives of this study were:

1. To compare family selection with individual genotype selection for cane yield and yield components at early stages of selection for humic and sandy soil breeding programmes in the Midlands region of South Africa.
2. To evaluate and identify elite families for cane yield, determine the optimum family selection rate and identify ideal trait combinations among the elite families.
3. To use best linear unbiased prediction (BLUP) to identify superior parents using family data and to determine the proportion of superior parents within populations in the Midlands breeding programmes.

1.2 REFERENCES

Babu C, Koodalingam K, Natarajan US, Shanthi RM, Govindaraj P (2009) Interrelationships of sugarcane yield and quality components and their utility in family selection. Madras Agriculture Journal 96:309-313

Barbosa MHP, Resende MDV, Bressiani JA, Silveira LCI (2005) Selection of sugarcane families and parents by REML/BLUP. Crop Breeding Application Biotechnology 5:443-450

Bond RS (1977) The mean yield of seedlings as a guide to the selection potential of sugarcane crosses. Proceedings of the International Society of Sugar Cane Technologists 16:101-110

Bond RS (1989) Observations on family selection in the Mount Edgecombe sugarcane breeding programme. Proceedings of the South African Sugar Technologists' Association 63:132-135

Chang YS, Milligan SB (1992a) Estimating the potential of sugarcane families to produce elite genotypes using bivariate methods. Theoretical and Applied Genetics 84:633-639

Chang YS, Milligan SB (1992b) Estimating the potential of sugarcane families to produce elite genotypes using univariate cross prediction methods. Theoretical and Applied Genetics 84:662-671

Cox MC, Stringer JK (1998) Efficacy of early generation selection in a sugarcane improvement programme. Proceedings of the Australia Society of Sugar Cane Technologists 20:148-153

De Resende MDV, Barbosa MHP (2006) Selection via simulated individual BLUP based on family genotypic effects in sugarcane. Pesquisa Agropecuária Brasileira 41:421-429

Falconer DS, Mackay TFC (1996) Introduction to quantitative genetics. 4th Edition. Longman, UK. pp. 371

Heinz DJ, Tew TL (1987) Hybridization procedures. In: Heinz DJ (ed), Developments in Crop Science 11: Sugarcane improvement through breeding. Elsevier, New York. pp. 313-342

Hogarth DM, Braithwaite MJ, Skinner TC (1990) Selection of sugarcane families in the Burdekin district. Proceedings of the Australian Society of Sugar Cane Technologists 12:99-104

Jackson PA (2005) Breeding for improved sugar content in sugarcane. Field Crops Research 92:277-290

Jackson PA, Bull JK, McRae TA (1995a) The role of family selection in sugarcane breeding programmes and the effect of genotype x environment interactions. Proceedings of the International Society of Sugar Cane Technologists 22:261-269

Jackson PA, Hogarth DM (1992) Genotype x environment interactions in sugarcane. Patterns of response across sites and crop-years in North Queensland. Australian Journal of Agricultural Research 43:1447-1459

Jackson PA, McRae TA (1998) Gains from selection of broadly adapted and specifically adapted sugarcane families. Field Crops Research 59:151-162

Jackson PA, McRae TA, Hogarth DM (1995b) Selection of sugarcane families across variable environments. II. Patterns of response and association with environmental factors. Field Crops Research 42:109-118

Kimbeng CA, Cox MC (2003) Early generation selection of sugarcane families and clones in Australia. A review. Journal of the American Society of Sugar Cane Technologists 23:20-39

Kimbeng CA, McRae TA, Cox MC (2001) Optimizing early generation selection in sugarcane breeding. Proceedings of the Australian Society of Sugar Cane Technologists 24:488-493

Kimbeng CA, McRae TA, Stringer JK (2000) Gains from family and visual selection in sugarcane, particularly for heavily lodge crops in the Burdekin region. Proceedings of the Australian Society of Sugar Cane Technologists 22:163-169

Milligan SB, Legendre BL (1990) Development of a practical method for sugarcane cross appraisal. Journal of the American Society of Sugar Cane Technologists 11:59-68

Nuss KJ (1998) Aspects considered in the search for new farms for the Experiment Station. Proceedings of the South African Sugar Technologists' Association 72:42-45

Parfitt RC (2005) Release of sugarcane varieties in South Africa. Proceedings of the South African Sugar Technologists' Association 79:63-71

Pedrozo CA, Barbosa MHP, Da Silva FL, De Resende MDV, Peternelli LA (2011) Repeatability of full-sib sugarcane families across harvests and the efficiency of early selection. Euphytica 182:423-430

Shanthi RM, Bhagyalakshmi KV, Hemaprabha G, Alarmelu S, Nagarajan R (2008) Relative performance of the sugarcane families in early selection stages. Sugar Tech 10:114-118

Skinner JC, Hogarth DM, Wu KK (1987) Selection methods, criteria, and indices. In: Heinz DJ (ed), Sugarcane improvement through breeding. Elsevier, Amsterdam, Netherlands. pp. 409-453

South African Sugar Association (SASA) (20013/2014) South African Sugar Industry Directory pamphlet. pp. 54

Stringer JK, Cox MC, Atkin FC, Wei X, Hogarth DM (2011) Family selection improves the efficiency and effectiveness of selecting original seedlings and parents. Sugar Tech 13:36-41

Zhou MM (2009) Statistical methods and models for analysing sugarcane (*Saccharum* species hybrids) plant breeding data. Dissertation. Louisiana State University and Agricultural and Mechanical College. pp. 199

Zhou M (2013) Conventional sugarcane breeding in South Africa: Progress and future prospects. American Journal of Plant Sciences 4:189-196

Zhou M (2014) Family evaluation for sugarcane yield using data estimated from stalk number, height, and diameter. Journal of Crop Improvement 28:406-417

Zhou M (2015) Selection for *Eldana saccharina* borer resistance in early stages of sugarcane breeding in South Africa. American Journal of Plant Sciences 6:2168-2176

Zhou M, Lichakane ML (2012) Family selection gains for quality traits among South African sugarcane breeding populations. South African Journal of Plant and Soil 29:143-149

Zhou M, Mokwele A (2015) Family versus individual plant selection for stem borer (*Eldana saccharina*) resistance in early stages of sugarcane breeding in South Africa. South African Journal of Plant and Soil 33:89-96

CHAPTER 2

LITERATURE REVIEW

2.1 HISTORY AND ECONOMIC IMPORTANCE OF SUGARCANE

2.1.1 World history

Sugarcane (*Saccharum officinarum* L.) is a plant that accumulates high sucrose content in its stalk and is a perennial grass that does not tolerate severe frost (Long and Spence 2013; Friesen et al. 2014). Its centre of origin is in Southeast Asia around New Guinea where farmers chewed sugarcane plant for its sweet juice (Barnes 1974; Fauconnier 1993). The earliest known sugar production began in Northern India (Barnes 1974). Currently, the crop is grown in south-western Europe, Africa, Asia, Australia, USA, Mexico and Southern America (FAOSTAT 2014). It is grown between 22°N and 22°S and some up to 33°N and 33°S of the equator extending from tropical to subtropical zones (Bull and Glasziou 1979).

The crop is planted to approximately 27.18 million hectares with total production of 1, 899 million metric tons (FAOSTAT 2014). Brazil has the highest area planted to sugarcane (10.87 million hectares) (UNICA 2015). Sugarcane cultivation plays a significant role in the economy of many countries. Brazil, India and China are prominent producers of sugar while India and China are major consumers of sugar and these countries control the world markets (Gopinathan 2010). Of the world sugar, 70% is from sugarcane and 30% from sugar beet (Anonymous 2007; Statista 2014).

2.1.2 History of sugarcane in South Africa

In South Africa, sugarcane has been grown and milled for over 154 years (Richardson 1982). It is grown along the east coast, between 25°33'S and 30°93'S, and between 29°92'E and 32°32'E and is grown under a diverse range of environmental conditions (Ramburan 2012). Sugarcane is grown in KwaZulu-Natal, Mpumalanga and Eastern Cape provinces of South Africa where it contributes significantly to the economy. It provides approximately 79,000 direct jobs and 350,000 indirect jobs supporting the livelihoods of nearly a million people (DAFF 2011; SASA 2013/2014). Despite growing sugarcane in a relatively diverse conditions, the sugar industry generates an estimated annual direct income of R12 billion (Maloa 2001). South Africa is ranked among the top 10 sugar

exporters in the world. Approximately 20 million tons of sugarcane are processed annually producing 2.5 million tons of sugar. Fifty percent of sugar is produced for local consumption. The sugar industry is made up of 15 mills situated in KwaZulu-Natal and Mpumalanga (Figure 2.1) (Maloa 2001; DAFF 2011). Sugar is an important source of energy while bagasse (mainly fibre) is burned to produce electricity to run the sugar mills. Molasses (another waste product) is distilled to produce ethanol.

2.2 TAXONOMY AND BOTANY

2.2.1 Taxonomy of *Saccharum* complex

Sugarcane is classified under the genus *Saccharum* L., a member of the tribe *Andropogoneae*, like maize and sorghum and the family of *Poaceae*, like rice (Dillon et al. 2007). Members of this tribe use the C4 carbon fixation photosynthesis (Fageria et al. 2011). The genus *Saccharum* consists of six species including two wild species (*S. spontaneum* and *S. robustum*) and four cultivated species (*S. sinese, S. barberi, S. edule* and *S. officinarum*) (Daniels and Roach 1987). There are four closely related interbreeding genera (*Erianthus* section *Ripidum*, *Miscunthus* section, *Narenga* and *Slerostachya*) forming the *Saccharum* complex (Mukherjee 1954, 1957; Daniels and Roach 1987). The *Saccharum* complex is characterised by high heterozygosity, high incompatibility and high levels of polymorphism (Grivet et al. 1996; Cordeiro et al. 2000). Currently, modern sugarcane genotypes are mostly hybrids of different species of the genus *Saccharum* and related genera.

2.2.2 Botany of sugarcane

The sugarcane plant is made up of four parts that is the root system, stalks, leaves and inflorescence. Sugarcane is propagated vegetatively from the stalk that is cut and planted. Cuttings that are used for planting should have at least three buds to prevent apical dominance. The buds and root primordia give rise to the plant and its root system (Van Dillewijn 1952). Primary, secondary, tertiary and higher order tillers develop into millable stalks. Tillering and stalk characteristics such as stalk number, stalk height and stalk diameter are genotype specific (Matsuoka and Stolf 2012). Sugarcane stalks grow above the ground to allow the development of leaves and flowers. The sugarcane stalk is composed of different numbers of nodes and internodes depending on the variety. The node is where the leaf attaches to the stalk and is where the bud and root primordial are located

(Verheye 2010). Stalk elongation is facilitated by cell division and expansion. The bottom of the stalk has a higher sucrose content than the top of the stalk (Miller et al. 2012).

Figure 2.1 Sugarcane growing areas, mills and SASRI research stations (Anonymous 2003)

2.3 SUGARCANE GENETICS

2.3.1 Genetics of species

Sugarcane species have a complex genome and are characterised by high levels of polyploidy. For example, the chromosome number of *S. officinarum* is 2n=80 with a basic chromosome number of ten. *Saccharum spontaneum* has a chromosome number of 2n=40 to 128 (Sreenivasan et al. 1987), with a basic chromosome number of eight (D'Hont et al. 1998). *Saccharum robustum* is a diverse sugarcane species and is known to have 2n=60 and 2n=80 chromosome numbers. *Saccharum barberi* and *S. sinense* are intergeneric hybrids produced by interbreeding of other species. *Saccharum barberi* has a chromosome number of 2n=111 to 120 and *S. sinense* have 2n=80 to 124 chromosome numbers (Daniels and Roach 1987), and are hybrids of the *Saccharum* spp. complex. *Saccharum edule* is a cultivated species is a product from introgression breeding of *S. officinarum* or *S. robustrum* with other species. The chromosome number of *S. edule* is 2n=60 to 80 with aneuploidy prevalent (Daniels and Roach 1987). Modern genotypes are made up of 70 to 80% of chromosomes derived from *S. officinarum* and 10 to 20% are from *S. spontaneum*, and 10 to 20% from recombination (Grivet et al. 1996; Piperidis et al. 2001).

2.3.2 Polyploidy in sugarcane

Sugarcane hybrids are polyploids made up of two genomes. Sugarcane polyploidy ranges from eight to 14 copies of chromosomes, with individual chromosomes and alleles in varying numbers (Rossi et al. 2003). The genome of the modern sugarcane interspecific hybrids is highly polyploid (~12x), characterized by frequently unbalanced numbers of chromosomes which is also known as "aneuploidy" (D'Hont 2005). The nature of polyploidy varies with sugarcane species. For example, *S. edule* is a form of aneuploidy. *S. officinarum* is complex polyploid, and it is both allopolyploid and autopolyploid (Sreenivasan et al. 1987) which behaves like a diploid (Stevenson 1965).

2.3.3 Implications of polyploidy in sugarcane breeding

High polyploidy levels in sugarcane are associated with high vigour, high biomass yields and wide adaptation (Premachandran et al. 2011). Polyploids have a large number of cells and they tend to survive better in unfavourable environmental conditions than their diploid counterparts (Comai 2005). Polyploid species have the advantage of maintaining high levels of genetic variation, through incorporated genetic diversity of several diploid and polyploid parents (Comai 2005; Acquaah 2007; Premachandran et al. 2011). Another

advantage is the genome reshuffling with more genetic complexity that occurs during further hybridization of polyploid genotypes. Genome reshuffling is a source of genetic variability in polyploid populations (Premachandran et al. 2011). Seedling populations tend to be highly variable and sugarcane breeders use a wide range of parents to increase variability (Verheye 2010).

2.4 HISTORY OF SUGARCANE BREEDING

2.4.1 Early years

The first sugarcane breeding programmes began in Java and Barbados in 1888 due to the outbreak of viral sereh disease. Earliest reports of viable sugarcane were in Java (1858) and Barbados (1859). Prior to that, the sugarcane flower was believed to be infertile. Due to the outbreak of sereh disease, sugarcane breeding aimed to develop genotypes resistant to the disease via interspecific hybridization. The interspecific hybridization between *S. officinarum* (high sucrose genotype) and *S. spontaneum* (disease resistance genotype) resulted in modern sugarcane genotypes a process known as nobilization (Stevenson 1965; Sreenivasan et al. 1987). One of the earliest genotypes, POJ2878 was produced by nobilization (Jackson 2005). Other genotypes from interspecific hybridization such as POJ2864, POJ2364, Co206 and Co213 revolutionised sugarcane production (Santchurn 2010).

2.4.2 Flowering and pollen fertility in sugarcane

Due to low pollen fertility in sugarcane, South Africa and other subtropical countries depended on imported families from tropical countries such as India during early years of their breeding programmes (Brett 1953; Zhou 2013). In the 1940s, after experimentation, it was discovered that fertile pollen could be obtained by keeping flowers in the glasshouse at temperatures above 20ºC. Further research on photoperiod of sugarcane resulted in increased flowering and pollen fertility. This discovery ushered a new era of sugarcane breeding in South Africa and other subtropical countries (Brett 1949, 1954; Brett and Harding 1974).

2.5 HISTORY OF SUGARCANE BREEDING IN SOUTH AFRICA

2.5.1 Early years

SASRI was established in 1925 with the aim of importing, testing and releasing adaptable varieties with high yield, high sucrose content and varieties that are resistant to pest and diseases (Nuss 1998). The imported varieties were tested for adaptability to South African growing conditions. However, the majority of imported varieties were susceptible to major disease and pests.

Later, in the 1930s, SASRI imported crosses from several breeding programmes with the aim of selecting for genotypes adapted to South Africa's growing conditions. The first batch of crosses was from Canal Point that produced 47 seedlings. In 1932, SASRI imported from Mauritius, a cross between POJ2878 and Uba. In 1936, three crosses of POJ2725 X C02l4, POJ2725 X C028l and P0J2725 X C0301 were imported from Coimbatore, India (Nuss and Brett 1995). Once in 1938 and again in 1944, a cross Co421 X Co312 was imported from Coimbatore, India (Brett 1950). The variety NCo310 was released in 1945 from the 1938 import and the variety NCo376 was released in 1955 from the 1944 import (Nuss and Brett 1995). Because of their wide adaptability and superior yield, NCo310 and NCo376 became the most widely grown varieties in South Africa and other neighbouring countries.

To increase flowering and pollen fertility, SASRI constructed a glasshouse (1966) and photoperiod house (1971). The photoperiod house and glasshouse each has three photoperiod treatments. The photoperiod house is used to generate male genotypes, which are genotypes that produce higher quantities of viable pollen, while the glasshouse is used to produce female parents with less or no pollen. The glasshouse has also been partitioned into cubicles where crossing is carried out by pairing female and male parents.

2.5.2 Recent developments

SASRI breeding and selection programmes changed over the years with establishment of research stations in the major agro-ecological regions of South Africa (Nuss 1998; Zhou 2013). Crosses are made at Mount Edgecombe in Durban and seedlings, germinated in the glasshouse, are later transplanted at the respective research stations for testing and selection (Tables 2.1 and 2.3). The purpose of different locations was to ensure that released varieties are stable and adapted to different growing conditions. There are three agro-climatic zones

in South Africa, including the irrigated, coastal and high altitude zones. In South Africa, sugarcane is harvested between 12 and 24 months of age depending on the region (Ramburan 2012). SASRI breeding programmes were restructured in 1993 after the loss of Central Field research station due to urbanisation. The dry-land selection programmes were replaced by more representative sites for their agro-climatic zones.

Table 2.1 SASRI breeding programmes used before 1993

Selection site	Year acquired	Region	Age in months	Number of seedlings	Number of single lines
Pongola	1965	Irrigated North	12	50,000	4000
Mtunzini	Mid-1950s	Coast	12	25,000	2000
Shaka's Kraal	Mid-1950s	Coast	12	25,000	2000
Central Field					
Station	1965	Coast	18	25,000	2000
Mt Edgecombe	1925	Coast	12	25,000	2000
Holly Bros	1965	Midlands	24	9000	700

Source: Zhou (2013)

2.5.3 Current breeding programmes

After the restructuring of breeding programmes in 1993, SASRI programmes' size were increased from 160,000 to 250,000 seedlings per annum (Table 2.2). The breeding programmes aimed at developing and releasing varieties adapted to different agro-ecological regions. The breeding programmes start with parent selection. Selection of parents to be used in breeding programmes is based on genotype potential to produce high proportions of progenies with high trait values. The SASRI breeding programme selects parents according to specific traits including yield, quality, ratooning ability, agronomic performance, freedom from diseases and resistance to insect pests. Parents are selected from local or imported germplasm (Zhou 2013). Parents selected from wild germplasm are used to broaden the genetic diversity of sugarcane populations and to provide novel sources of important traits (Zhou 2013). Each year the selected elite parents are planted in the glasshouse and photoperiod house to induce flowering for crossing. Three mating designs are used for crossing. Bi-parental, males only (polycrosses) and melting pot (polycrosses) are used to generate segregating populations. In bi-parental crosses, the female and male

parents are known, while in polycrosses, the male parent is unknown. Males only polycrosses involve inter-crossing of at least two male parents while melting pot is where several male parents pollinate a single female parent.

Table 2.2 SASRI research stations representing different agro-climatic zones and the sizes of the breeding programmes

Research station	Region	Age in months	Number of seedlings	Number of lines
Pongola	Irrigated	12	50,000	4,000
Empangeni	Coastal short cycle high potential	12	50,000	4,000
Gingindlovu	Coastal short cycle average potential	12	25,000	2,000
Gingindlovu	Coastal long cycle average potential	18	25,000	2,000
Kearsney	Coastal long cycle high potential	16-18	50,000	4,000
Bruyns Hill	Humic soil	24	25,000	2,000
Glenside	Sandy soil	24	25,000	2,000

Source: Zhou (2013)

A five-stage testing and selection programme is used for variety development (Table 2.3). The aim of the programmes is to ensure that the variety to be released is adapted to all the agro-climatic regions in South Africa. Field evaluation and selection takes between 12 to 19 years from seedlings to release a new commercial variety (Zhou 2013). Over 20 years, significant progress have been made in developing and releasing more than 62 improved sugarcane varieties (Zhou 2013).

2.6 SUGARCANE SELECTION METHODS
2.6.1 Mass or individual selection
In early stages of selection, mass- or individual selection is used to identify plants (seedlings) by their phenotypic values (Bressiani et al. 2005). Mass selection is based on traits with high heritability estimates such as sucrose content (Brix%) and disease resistance. Hogarth et al. (1997) reported gains achieved through individual selection for traits with high heritability. Further, they pointed out that individual selection is not highly efficient when selecting traits with low heritability in early stages. Early stage selection is associated with low levels of efficiency due to the confounding effects of GxE and

competition effects among the individual genotypes (Skinner 1971; 1982). Experimental precision at early stages of selection is low due to the lack of replication of individual genotypes (Skinner et al. 1987; McRae and Jackson 1995; Kimbeng and Cox 2003; Oliveira et al. 2013).

The above mentioned confounding effects cannot be practically solved by replication because of the large number of seedlings involved and the small amount of breeding material in early stages of selection (Zhou et al. 2013b). However, there are methods that can be used to increase selection efficiency and these include experimental designs and statistic models that account for effects of inter-plot competition.

In sugarcane breeding, several methods have been used to evaluate seedling populations to identify elite individual genotypes. These include path coefficient analysis (Kang et al. 1989; Milligan and Legendre 1990; De Sousa-Vieira and Milligan 2005), spatial analysis (Edmé et al. 2007), artificial neutral network models (Zhou et al. 2011) and logistic regression models (Zhou et al. 2013a). Path coefficient analysis is used to determine traits to focus on during selection. Spatial analysis can be used to increase the precision of estimating genetic potential and genetic gains from selection by accounting and removing spatial variability from phenotypic values. Artificial neutral network models are used to identify individual seedlings that have the best combination of traits to produce high yield. Logistic regression models have been applied as a decision support tool for selection among individuals as well as among unreplicated, early stage clonal plots.

Table 2.3 Summary of the variety selection in breeding programmes at SASRI

Selection stage	No. of years	No. of clones per site/total	Trial design	Number of reps	Number of crops	Selection rate (%)	Selection criteria
Stage 1 Seedlings	0	50 000 x 5 250 000	Replication of plotted seedlings	3	1	70	Family values, visual assessment, freedom from disease and other important traits
Stage 2 Mini-lines	1	35 000 x 5 157 000	Replications of family	3	1	11	Yield, sucrose content, pest and disease resistance
Stage 3 Single lines	2	4000 x 5 20 000	Replications of family	3	1	10	Sucrose content, sucrose yield, pests and disease resistance
Stage 4 Observation	3-5	400 x 5 2000	Lattice, 2 x 8 m	3	2	10	Combined analysis for high yield, sucrose, pests and disease
Stage 5 Advance variety	6-10	40 x 5 200	Lattice, 5 x 8 m x 5 trials	3	3	-	Combined analysis across sites and crops
Bulking	11-15	1-2	-	-	-	-	-

Source: Zhou (2013)

2.6.2 Proven cross and parents

The proven cross system was used in sugarcane breeding to identify genotypes to be used in future crosses (Skinner et al. 1987). The proven cross system has been widely used in Australia (Heinz and Tew 1987), South Africa (Skinner 1982), Indonesia (Sukarso 1986) and other countries. This system focused on old, selected elite crosses with little attention given to new crosses, creating a bias against new crosses (Walker 1963). The proven cross system uses no statistical analysis for comparing crosses. Furthermore, with the proven cross system, breeders waited for years to evaluate family potential because individual genotypes within the selected elite families differed significantly from the expectations based on family means (Skinner et al. 1987; Milligan and Legendre 1990; Kimbeng et al. 2000). Experimental parents that make up the proven crosses are referred to as proven parents.

2.6.3 Family selection

Accepting or rejecting entire progenies from a cross, based on family values, is referred to as family selection. Family selection was proved superior to individual genotype selection for traits with low heritability such as sugarcane yield (Jackson and McRae 1998; Kimbeng and Cox 2003; Pedrozo et al. 2011; Zhou 2014). Previous studies (Kimbeng et al. 2000; Shanthi et al. 2008; Zhou 2014) reported low heritability estimates for cane yield and its components, which indicate the potential of these traits to benefit from family selection. Jackson (2005) reported higher gains from family selection for cane yield than for sucrose content.

Family selection in sugarcane was originally described by Hogarth (1971). Despite this research, family selection could not be implemented because of the high cost of weighing seedling plots. During that time, family plots had to be hand-cut and weighed manually (Kimbeng et al. 2000; Kimbeng and Cox 2003; Stringer et al. 2011). It was not until mobile weighing machines were developed in Australia (Hogarth and Mullins 1989) that family selection was adopted in Australian sugarcane breeding programmes (Kimbeng et al. 2000). Cox and Hogarth (1993) reported that family selection was used to identify elite families using data from replicated family plots. Higher trait values are expected from individual genotypes within the elite families (Cox and Hogarth 1993; Kimbeng et al. 2000; Kimbeng and Cox 2003).

In Australia, family plots made up of replicated seedlings are planted in replicated plots. At crop maturity, the replicated plots are sampled to obtain stalks from which cane quality values are estimated in the laboratory. The family plots are weighed at crop maturity to obtain yield data. The data is analysed to identify elite families. Family selection is followed by selecting individual genotypes within the selected families in the ratoon crops. In South Africa, cane yield components (stalk number, stalk height and stalk diameter) are measured on seedlings in a family plot. The yield component measurements are used to estimate cane yield of the family plot. Further, a random stalk sample is also taken from each family plot and used to estimate cane quality parameters. The estimated cane yield and cane quality data is analysed to determine elite families. Individual genotype selection is carried out in the selected elite families in the plant crop. This non-destructive sampling allows data and selection to be done in the same crop. Further, weighing machines that are used in Australia are considered more expensive in South Africa compared to yield measurements because of relatively lower manpower costs.

Currently, family selection in sugarcane breeding is practiced to different extents in Australia (Jackson et al. 1995; Kimbeng et al. 2000; Kimbeng and Cox 2003), USA (Tai et al. 2003), Brazil (Pedrozo et al. 2011) and India (Shanthi et al. 2008). Sugarcane breeding programmes in Indonesia (Sukarso 1986), South Africa (Bond 1989; Zhou and Lichakane 2012; Zhou et al. 2013b; Zhou 2014, 2015; Zhou and Mokwele 2015), Florida (Tai and Miller 1989), Cuba (Ortiz and Cabellero 1989), Hawaii (Wu and Tew 1989) and Lousiana (Chang and Milligan 1992a, 1992b) have also adopted family selection.

2.6.4 Advantages of family selection

Families can be replicated in trials and across locations in early stages of selection while individual genotypes cannot be replicated due to limited planting material. Furthermore, progeny data from replicated families can be used to evaluate family by environment interactions when families are planted across locations and data is collected across ratoons. The data used to evaluate progeny performances can also be used to identify and select elite parents for future use in crosses as well as determine the best parent combinations at the time of crossing (Cox and Stringer 1998; Shanthi et al. 2008; Zhou et al. 2013b). The benefits and theoretical impacts were further described in several studies (Hogarth and Mullins 1989; Tai and Miller 1989; Hogarth et al. 1990; Chang and Milligan 1992a, 1992b;

Jackson et al. 1995; Jackson and McRae 1998; Stringer et al. 2011; Zhou and Lichakane 2012; Zhou et al. 2013b; Zhou 2014).

2.6.5 Family selection in South Africa

The building of glasshouses and photoperiod houses in the 1970s resulted in more crosses to be made for breeding purposes (Bond 1977). Family evaluation offered the opportunity to screen and select elite crosses from which progeny selection would be done. The first study on family evaluation (Bond 1977) aimed to determine whether the mean yield of seedlings could indicate the potential of the family to produce superior individual genotypes. Evaluation of single stools showed differences in estimated mean yield. A strong positive correlation (r=0.69) between the number of seedlings selected from a family and the mean yield for the family indicated that seedling yield could be used to predict the potential performance of a family. Results further showed that environmental effects were large in original seedling populations and influenced the precision of selection. Further investigation was done on the subsequent selection stage to determine whether family characteristics from seedlings could predict the performance of genotypes selected for advanced stages (Bond 1989). There was a positive correlation (r=0.33) between yield measured at single stools and the yield measured at single lines, which indicated that breeding populations at seedling stages could be used to predict clonal performance at clonal stages.

Low heritability estimates for quality traits, reported by Bond (1989), indicated the potential of these traits to benefit from family evaluation and selection. Additive genetic effects were demonstrated which indicated the potential benefit of family evaluation and selection for quality traits (Lingle et al. 2010). Previous studies on family selection focused on individual populations and did not evaluate trends over time (Bond 1977, 1989). A study by Zhou and Lichakane (2012) evaluated families across selection cycles for quality traits which provided insight into trends over time. The study reported large variability among families across the populations over time, which highlighted the potential of selecting for superior families within these populations. The consistent increase in heritability and predicted gains upon selection with progressing selection cycles indicated the advantage of using family selection. A similar trend was observed among family populations from the very early stage of selection in a study reported by Zhou et al. (2013b). The study further concluded that recurrent selection could be used to enhance breeding for quality traits.

Brix% cane consistently showed increasing heritability and predicated selection gains. Results suggested that sucrose content (Brix%) estimates could be used to evaluate the variability within family populations because Brix% can be measured quicker and at lower cost with a hand held refractometer (Zhou and Lichakane 2012; Zhou et al. 2013b).

Family selection for cane yield remained unexplored because of the cost of weighing family plots in South Africa where automatic weighing machines are not available. A study was done to explore estimating cane yield from its components; stalk numbers height and diameter (Zhou 2014). The non-destructive sampling enables individual selection in the plant crop. Results showed a strong correlation (r=0.89) between the actual and estimated yield, an indication that yield components could be used to estimate cane yield. This study (Zhou 2014) also explored the advantages of family over individual genotype selection. Results showed that families produced larger broad-sense heritability and higher predicted selection gains than individual genotypes, indicating the superiority of family selection in improving yield trait values. The study further investigated the optimum sample size of seedlings required to estimate family parameters. It was concluded that yield data, collected from 10 seedlings per plot in each of the four replications per family, would be sufficient for evaluating family performances. This sample size was considered to cost considerably less than weighing the family plots.

The slow improvement, complexity and possibly quantitative genetic control of Eldana resistance (Nuss 1998) indicated the potential for Eldana resistance to benefit from family selection. A study by Zhou and Mokwele (2015) was done to examine the potential of evaluating sugarcane families for Eldana resistance. Results showed that families produced higher broad-sense heritability estimates and predicted selection gains than individual genotypes, indicating the potential of increasing genetic gains from Eldana resistance breeding. In addition, elite families and parents could be identified and therefore breeding and selection for Eldana could be improved using family evaluation.

Since 2010, data on family evaluation for cane yield using estimates from stalk number, height and diameter has been collected from several trials. Preliminary studies (Zhou 2014) demonstrated the potential of using yield estimates for family evaluation. The available data provided an opportunity to further quantify the benefits of family evaluation and selection. Further, little is known on the proportion of elite families and parents in South

African breeding populations. Such knowledge will guide family evaluation and selection as well as provide a benchmark on the future improvements expected after implementation of family evaluation. Determining elite parents for use in future crosses will further optimise crossing and cross combinations and strengthen South African breeding programmes. With this study, a gap in knowledge required by the South African breeding programmes will be filled. Thus, the current study will (a) compare family selection with individual genotype selection for cane yield and yield components at early stages of selection for humic and sandy soil breeding programmes in the Midlands region of South Africa. (b) Evaluate and identify elite families for cane yield, determine the optimum family selection rate and identify ideal trait combinations among the elite families. (c) Use BLUP to identify superior parents using family data and to determine the proportion of superior parents within populations in the Midlands breeding programmes.

2.7 REFERENCES

Acquaah G (2007) Principles of plant genetics breeding. Blackwell Publishing Ltd. pp. 569

Anonymous (2003) Plant breeding, crossing and selection Programmes. South African Sugar Association Experiment Station. pp. 12

Anonymous (2007) CAY mia sugarcane crop. Sugar and sugarcane R. & D. Centre. http://giongmia.files.wordpress.com/2007/01/sugarcane-crop-ebook.pdf. Accessed 3 June 2016

Barnes AC (1974) Composition of the sugarcane. The Sugarcane 2nd edition. Aylesbury: Leonard Hill Books. pp. 412-413

Bond RS (1977) The mean yield of seedlings as a guide to the selection potential of sugarcane crosses. Proceedings of the International Society of Sugar Cane Technologists 16:101-110

Bond RS (1989) Observations on family selection in the Mount Edgecombe sugarcane breeding programme. Proceedings of the South African Sugar Technologists' Association. pp. 132-135

Bressiani JA, Vencovsky R, Burnquist WL (2005) Modified family selection in sugarcane. Proceedings of the International Society of Sugar Cane Technologists 25:459-467

Brett PGC (1949) Further reports on sugarcane breeding in South Africa. Experiment Station, South African Sugar Association. pp. 108-114

Brett PGC (1950) Investigations on sugarcane breeding in Natal during 1949. Experiment station, South African Sugar Association. pp. 99-105

Brett PGC (1953) Temperature and ovule fertility of sugarcane in Natal. Proceedings of the International Society of Sugar Cane Technologists. pp. 463-465

Brett PGC (1954) The first ten years of sugarcane breeding in Natal. Experiment station, South African Sugar Association. pp. 141-145

Brett PGC, Harding RL (1974) Artificial induction of flowering in Natal. Proceedings of the International Society Sugar Cane Technologists 15:55-66

Bull TA, Glasziou KT (1979) Sugarcane. In: Lovett JV, Lazenby A (eds), Australian field crops Volume 2: Tropical Cereals, Oilseeds, Grain Legumes and Other Crops. Angus and Robertson Publishers. pp. 95-113

Chang YS, Milligan SB (1992a) Estimating the potential of sugarcane families to produce elite genotypes using bivariate prediction methods. Theoretical and Applied Genetics 84:633-639

Chang YS, Milligan SB (1992b) Estimating the potential of sugarcane families to produce elite genotypes using univariate cross prediction methods. Theoretical and Applied Genetics 84:662-671

Comai L (2005) The advantages and disadvantages of being polyploid. Nature Reviews Genetics 6:836-846

Cordeiro GM, Taylor GO, Henry RJ (2000) Characterisation of microsatellite markers from sugarcane (*Saccharum* sp.), a highly polyploid species. Plant Science 155:161-168

Cox MC, Hogarth DM (1993) The effectiveness of family selection in early stages of a sugarcane improvement program. In: Imrie BC, Hacker JB (eds), Focused plant improvement: Towards responsible and sustainable agriculture. Proceedings of the of the Australian Plant Breeding Conference. pp. 53-54

Cox MC, Stringer JK (1998) Efficacy of early generation selection in a sugarcane improvement program. Proceedings of the Australian Society of Sugar Cane Technologists 20:148-153

Daniels J, Roach BT (1987) A review of the origin and improvement of sugarcane. Copersucar International Sugarcane Breeding Workshop. pp. 1-32

Department of Agricultural Forestry and Fisheries (DAFF) (2011) Employment and production area: A profile of the South African sugar market value chain. pp. 5-8

De Sousa-Vieira O, Milligan SB (2005) Interrelationships of cane yield components and their utility in sugarcane family selection: path coefficient analysis. Interciencia 30:93-96

D'Hont A (2005) Unraveling the genome structure of polyploids using FISH and GISH: examples of sugarcane and banana. Cytogenetic Genome Research 109:27-33

D'Hont A, Ison D, Alix K, Roux C, Glaszmann JC (1998) Determination of basic chromosome numbers in the genus *Saccharum* by physical mapping of ribosomal RNA genes. Genome 41:221-225

Dillon SL, Shapter FM, Robert HJ, Cordeiro G, Izquierdo L, Lee SL (2007) Domestication to crop improvement: genetic resources for sorghum and *Saccharum* (*Andropogoneae*). Annals of Botany 5:975-989

Edmé SJ, Tai PYP, Miller JD (2007) Relative efficiency of spatial analyses for non-replicated early-stage sugarcane field experiments. Journal of the American Society Sugar Cane Technologists 27:89-104

Fageria KN, Baligar VC, Jones CA (2011) Growth and mineral nutrition of field crops, 3rd edition. Taylor and Francis group: CRC press. pp. 23

FAOSTAT (2014) Crop Production Data, Food and Agriculture Organization of the United Nations, available online at http://faostat.fao.org/site/567/default.aspx#ancor. Accessed 9 May 2016

Fauconnier R (1993) Sugarcane. Macmillan Press Ltd, London. pp. 140

Friesen PC, Peixoto MM, Busch FA, Johnson DC, Sage RF (2014) Chilling and frost tolerance in *Miscanthus* and *Saccharum* genotypes bred for cool temperate climates. Journal of Experimental Botany 65:3749-3758

Gopinathan MC (2010) Research and technology transfer strategies for the next decade an Indian example. Proceedings of the International Society of Sugar Cane Technologists 27:1-15

Grivet L, D'Hont A, Roques D, Feldmann P, Lanaud C, Glaszmann JC (1996) RFLP mapping in cultivated sugarcane (*Saccharum* spp.): genome organization in a highly polyploid and aneuploid interspecific hybrid. Genetics 142:987-988

Heinz DJ, Tew TL (1987) Hybridization procedures. In: Heinz DJ (ed), Developments in Crop Science 11: Sugarcane improvement through breeding. Elsevier, New York. pp. 313-342

Hogarth DM (1971) Quantitative inheritance studies in sugarcane. II. Correlations and predicted responses to selection. Crop and Pasture Science 22:103-109

Hogarth DM, Braithwaite MJ, Skinner JC (1990) Selection of sugarcane families in the Burdekin district. Proceedings of the Australian Society of Sugar Cane Technologists 12:99-104

Hogarth DM, Cox MC, Bull JK (1997) Sugarcane improvement: past achievements and future prospects. Crop improvement for the 21st century. Research signpost, Trivandrum, India. pp. 29-56

Hogarth DM, Mullins RT (1989) Changes in the BSES plant improvement program. Proceedings of the International Society of Sugar Cane Technologist 20:956-961

Jackson PA (2005) Breeding for improved sugar content in sugarcane. Field Crops Research 92:277-290

Jackson PA, Bull JK, McRae TA (1995) The role of family selection in sugarcane breeding programmes and the effects of genotype x environment interactions. Proceedings of the International Society of Sugar Cane Technologists 22:261-270

Jackson PA, McRae TA (1998) Gains from selection of broadly adapted and specifically adapted sugarcane families. Field Crops Research 59:151-162

Kang MS, Sosa O, Miller JD (1989) Path analysis for percent fiber, and cane and sugar yield in sugarcane. Crop Science 29:1481-1483

Kimbeng CA, Cox MC (2003) Early generation selection of sugarcane families and clones in Australia. A review. Journal of the American Society of Sugar Cane Technologists 23:20-39

Kimbeng CA, McRae TA, Stringer JK (2000) Gains from family and visual selection in sugarcane, particularly for heavily lodged crops in the Burdekin region. Proceedings of the Australian Society of Sugar Cane Technologists 22:163-169

Lingle SE, Johnson RM, Tew TL, Viator RP (2010) Changes in juice quality and sugarcane yield with recurrent selection for sucrose. Field Crops Research 118:152-157

Long SP, Spence AK (2013) Toward cool C_4 crops. Annual Review of Plant Biology 64:701-722

Maloa MB (2001) Sugarcane: A case as development crop in South Africa. SARPN conference on Land Reform and Poverty Alleviation in Southern Africa Pretoria. pp. 12

Matsuoka S, Stolf R (2012) Sugarcane tillering and ratooning: key factors for a profitable cropping. Sugarcane: Production, Cultivation and Uses. Nova Science Publishers, Inc, Hauppauge, New York, USA. pp. 137-157

McRae TA, Jackson PA (1995) Selection of sugarcane families for the Burdekin River irrigation area. Proceedings of the Australian Society of Sugar Cane Technologists 17:134-141

Miller JD, Gilbert RA, Odero DC (2012) Sugarcane Botany: A brief view. University of Florida. pp. 2-4

Milligan SB, Legendre BL (1990) Development of a practical method for sugarcane cross appraisal. Journal of the American Society of Sugar Cane Technologists 11:59-68

Mukherjee SK (1954) Revision of the genus *Saccharum*. Bulletin of the Botanical Society. Bengal 8:143-148

Mukherjee SK (1957) Origin and distribution of *Saccharum*. Botanical Gazette. pp. 55-62

Nuss KJ (1998) Aspects considered in the search for new farms for the Experiment Station. Proceedings of the South African Sugar Technologists' Association 72:42-45

Nuss KJ, Brett PGC (1995) The release of variety NCo310 in 1945 and its impact on the sugar industry. Proceedings of the South African Sugar Technologists' Association 69:1-8

Oliveira RA, Daros E, Resende MDV, João, Filho JCB, Zambon JLC, Ruaro L (2013) Early selection in sugarcane family trials via BLUP and BLUPIS procedure. Acta Scientiarum Agronomica 35:427-434

Ortiz R, Caballero A (1989) Effectiveness of early sugarcane selection procedures in Cuba. Proceeding of the International Society of Sugar Cane Technologists 20:932-937

Pedrozo CA, Barbosa MHP, da Silva FL, de Resende MDV, Peternelli LA (2011) Repeatability of full-sib sugarcane families across harvests and the efficiency of early selection. Euphytica 182:423-430

Piperidis G, D'Hont A, Hogarth DM (2001) Chromosome composition analysis of various *Saccharum* interspecific hybrids by genomic in situ hybridization (GISH). Proceedings of the Australian Society of Sugar Cane Technologists 2:565–566

Premachandran MN, Prathima PT, Lekshmi M (2011) Sugarcane and polyploidy: a review. Journal of Sugarcane Research 1: 1-5

Ramburan S (2012) Sugarcane and the South African industry. A review. The nature and causes of sugarcane genotype x environment interaction: Integrated approaches to analysis and interpretations. PhD thesis. University of the Free State, South Africa. pp. 166

Richardson P (1982) The Natal sugar industry, 1849–1905: An interpretative essay. The Journal of African History. 23: 515-527

Rossi M, Araujo PG, Paulet F, Garsmeur O, Dias VM, Chen H, Van Sluys MA, D'Hont A (2003) Genomic distribution and characterization of EST-derived resistance gene analogs (RGAs) in sugarcane. Molecular Genetics and Genomics 269:406-419

Santchurn D (2010) The related genera: A review. Evaluation and selection of different types of sugarcane varieties for multi-purpose use from a population of inter-specific derived clones in Mauritius. PhD Thesis. University of the Free State, South Africa. pp. 140

Sreenivasan TV, Ahloowalia BS, Heinz DJ (1987) Cytogenetics. In: Heinz DJ (ed), Sugarcane improvement through breeding. Elsevier, Amsterdam, the Netherlands. pp. 211-251

Shanthi RM, Bhagyalakshmi KV, Hemaprabha G, Alarmelu S, Nagarajan R (2008) Relative performance of the sugarcane families in early selection stages. Sugar Tech 10:114-118

Skinner JC (1971) Selection in sugarcane: A review. Proceedings of the International Society of Sugar Cane Technologists 14:149-162

Skinner JC (1982) Efficiency of bunch-planted and single-planted seedlings for selecting superior families in sugarcane. Euphytica 31:523-537

Skinner JC, Hogarth DM, Wu KK (1987) Selection methods, criteria and indices. In: Heinz DJ (ed), Sugarcane Improvement through Breeding. Elsevier. pp. 409-453

South African Sugar Association (SASA) (2013/2014) South African Sugar Industry Directory pamphlet. pp. 49

Statista (2014) Statistics and facts about the sugar industry, available online at www.statista.com. Accessed 7 July 2016

Stevenson (1965) Genetics and the breeding of sugarcane. Longman, London, UK. pp. 284

Stringer JK, Cox MC, Atkin FC, Wei X, Hogarth DM (2011) Family selection improves the efficiency and effectiveness of selecting original seedlings and parents. Sugar Tech 13:36-41

Sukarso G (1986) Assessment of family selection in original seedlings of sugarcane at Pasuruan. Proceedings of the International Society of Sugar Cane Technologists 19:440-446

Tai PYP, Miller JD (1989) Family performance at early stages of selection and frequency of superior clones from crosses among Canal Point cultivars of sugarcane. Journal of American Society of Sugar Cane Technologists 9:62-70

Tai PYP, Shine JM, Miller JD, Edmé SJ (2003) Estimating the family performance of sugarcane crosses using small progeny test. Journal of the American Society of Sugar Cane Technologists 23:61-70

UNICA (2015) Brazilian sugarcane industry association, UNICADATA, available online at http://www.unica.com.br/unicadata. Accessed 24 February 2017

Van Dillewijn C (1952) Botany of sugarcane. HH Veenaman and Zonen, Wageningen, Netherlands. pp. 371

Verheye W (2010) Growth and production of sugarcane. Soil, Growth and Plant Production 2:1-10

Walker DIT (1963) Family performance at early selection stages as a guide to the breeding programme. pp. 469-482

Wu KK, Tew TL (1989) Evaluation of sugarcane crosses by family yields. Proceedings of the International Society of Sugar Cane Technologists 20:926-931

Zhou M (2013) Conventional sugarcane breeding in South Africa: Progress and future prospects. American Journal of Plant Sciences 4:189-196

Zhou MM (2014) Family evaluation for sugarcane yield, using data estimated from stalk number, height and diameter. Journal of Crop Improvement 28:406-417

Zhou M (2015) Selection for *Eldana saccharina* borer resistance in early stages of sugarcane breeding in South Africa. American Journal of Plant Sciences 6:2168-2176

Zhou MM, Kimbeng CA, Tew TL, Gravois KA, Pontiff P (2011) Artificial neural network models as a decision support tool for selection in sugarcane: A case study using two seedling populations. Crop Science 51:1-11

Zhou MM, Kimbeng CA, Tew TL, Gravois KA, Pontif M, Bischoff KP (2013a) Logistic regression models to aid selection in early stage of sugarcane breeding. Euphytica 191:415-428

Zhou MM, Lichakane LM (2012) Family selection gains for quality traits among South African sugarcane breeding populations. South African Journal of Plant and Soil 29:143-149

Zhou MM, Lichakane ML, Josh SV (2013b) Family evaluation for quality traits in South African sugarcane breeding programmes. Sugar Cane International 115:418-430

Zhou M, Mokwele A (2015) Family versus individual plant selection for stem borer (*Eldana Saccharina*) resistance in early stages of sugarcane breeding in South Africa. South African Journal of Plant and Soil 33:89-96

CHAPTER 3

COMPARING FAMILY WITH INDIVIDUAL GENOTYPE SELECTION FOR SUGARCANE YIELD IN SOUTH AFRICA

3.1 ABSTRACT

Family selection is the positive selection of an entire population of individuals from a cross and is widely practiced in sugarcane breeding. The objective of this study was to compare family with individual genotype selection (IGS) for cane yield, stalk number, stalk height and stalk diameter for humic and sandy soil breeding programmes in South Africa. Data on stalk number, height and diameter, collected from seedling progenies, were used to estimate cane yield. Both family and individual genotype effects for all traits produced significant (P<0.001) variance components. Family variance was 1.2 to 5.0 times that of individual genotype variance indicating larger variability among families than individual progenies. Families produced larger broad-sense heritability (H) estimates (25 to 90%) compared to individual genotypes (1.6 to 23.5%) suggesting that selecting superior families would be more accurate than selecting individual genotypes. Populations grown on humic soil produced higher family H (58 to 90%) compared to sandy soil populations (24 to 90%) which indicated a higher precision of family selection in humic soil. Families produced higher predicted selection gains (%Gs) (9 to 59%) compared to individual genotypes (1 to 12%) which indicated higher efficiency associated with family selection. Humic soil populations produced higher average family %Gs (45%) compared to sandy soil populations (25%) suggesting better selection efficiency. Significant family and individual genotype variances indicated that family selection, followed by IGS within selected families, will increase efficiency in the first stages of sugarcane breeding. The larger family variance, higher H and higher %Gs indicated superiority of family compared with IGS in the breeding programme.

Keywords: Family selection, variance components, broad-sense heritability, predicted gains

3.2 INTRODUCTION

Family selection is the positive selection of the entire progenies from a family or cross based on progeny data collected from family plots (Falconer 1960; Falconer and Mackay 1996). Families can be replicated in trials and across locations in early stages of selection while individual genotypes cannot be replicated due to limited planting material. Family selection is expected to increase selection gains for traits with low heritability and which are controlled by quantitative genes with additive effects such as cane yield (Pedrozo et al. 2011). Low heritability estimates for cane yield components have been reported in previous studies (Kimbeng et al. 2000; Shanthi et al. 2008; Zhou 2013, 2014) which indicated the potential of these traits to benefit from family selection. Studies have shown that gains from family selection were higher for cane yield than for sucrose content (Jackson et al. 1995).

Family selection has been widely practiced in other crops such as soybean (Streit et al. 2001), rice (Santos et al. 2002), forage (Casler and Brummer 2008), potatoes (Melo et al. 2011) and maize (Noor et al. 2013). In sugarcane, research on family selection was first reported by Walker (1963). Research on the benefits of family selection was later described by Hogarth (1971) in studies done in Australia where family selection was adopted when automatic weighing machines became available (Hogarth and Mullins 1989). Today, family selection is routinely practiced in Stage I trials in Australia. The benefits of family selection were further described in several studies (Kimbeng et al. 2000; Kimbeng and Cox 2003; Zhou 2013, 2014). To date, family selection is practiced to different extents in Australia (Cox and Stringer 1998; Kimbeng et al. 2000, 2001; Stringer et al. 2011), India (Shanthi et al. 2008; Babu et al. 2009), Brazil (De Oliveira et al. 2013), South Africa (Zhou et al. 2013b; Zhou 2014) and USA (Milligan and Legendre 1990; Chang and Milligan 1992a, 1992b).

Before family selection was implemented, sugarcane breeders depended on the proven cross system to identify superior genotypes that could be used at the time of crossings (Heinz and Tew 1987). The proven cross system defined elite families as the ones that produced high germination rates, with large numbers of seedlings that are advanced to later stages of breeding programme. The elite families were planted repeatedly with large numbers of seedlings with the hope to produce more elite progenies. Genotypes that produced elite families were used more frequently to make crosses. The result was an

increase in the bias towards new crosses or crosses with fewer seedlings (Walker 1963). However, the proven cross system lacked statistical tests to validate the elite families. Further, with the proven cross system, breeders waited for a long period at least 10 to 24 years of advanced data from Stage I to V to determine the quality of families.

Family selection is extensively used in all Australian sugarcane breeding programmes, where 20 plants per plot are routinely planted in the first selection stage (Kimbeng and Cox 2003). The families are replicated three times. Whole family plots are harvested and weighed using a mechanical harvester and automatic weighing machines. Sucrose content is estimated using eight stalks, one from each of the eight randomly chosen stools in a plot. Families are ranked by a net merit grade and no information is taken from the individual genotypes of the family during the plant crop evaluation. About 40 to 50% of families with the highest ranking are selected and described as elite families. In the first ratoon crop, individual seedling selection is practiced only on the selected elite families (Park et al. 2007). The rest of the families are discarded.

Family evaluation data has also been used to evaluate other aspects of breeding programmes. Family data can be used to identify superior parents for future crosses as well as to determine the best parent combinations for crossing (Chang and Milligan 1992a, 1992b; Stringer et al. 1996; Cox and Stringer 1998; Balzarini 2000; Shanthi et al. 2008; Zhou et al. 2013b). Breeding values of parents can be estimated from family data (Atkin et al. 2009) which provide breeders with information to objectively evaluate the quality and evolution of parental populations over time.

Previous studies on family selection in Australia were based on data from mechanically harvested family plots. Therefore, no data on individual genotype plots was collected. At SASRI, family selection for quality traits is based on family plot data with no data from individual seedlings. While family selection advantages are known, there is limited data to validate the magnitude of improvement derived from family selection. Little is known of the comparison between family and individual genotype selection. This is partly attributed to the difficulty of measuring individual plant data compared to family data particularly where manpower costs are high. However, the comparison is important when justifying the use of family over individual plant selection. Additionally, gains from family selection and those from individual selection could be additive, thus resulting in larger gains in breeding

programmes. The objective of this study was to compare family with individual genotype selection for cane yield and yield components at early stages of selection for humic and sandy soil breeding programmes in the Midlands region of South Africa.

3.3 MATERIALS AND METHODS

3.3.1 Experimental material

Crosses are made in the glasshouse at Mount Edgecombe research station (29.7°S, 31.03°E, 96 m asl) in Durban. The crossing take place between May and August every year. The crosses used in this study were made between 2007 and 2011. The number of crosses (or families) planted in a trial ranged from 102 to 163. The numbers of male and female parents that were used to generate families (crosses) are shown in Table 3.1. Three mating designs were used to generate crosses namely bi-parental, males only and melting pot. Bi-parental crosses are where one female parent is crossed to one male parent. Males' only crosses involve inter-crossing of at least two male parents and collecting seed from all the parents. Melting pot is where several male parents pollinate a single female parent. In the males' only and melting pot, the source of pollen is always unknown. On average, 245 seedlings were grown from each cross. However, because of variable seed set at the time of crossing, variable germination percentage and seedling survival in the nursery, there were variable seedling numbers per cross (ranging from 45 to 378 per cross). This varying number of seedlings is typical at Stage I in sugarcane breeding.

Table 3.1 Location, numbers of families, parents and cross type for each trial

Location	Trial	Families	Female	Male	MO/MP	BP
Bruyns Hill	BML10	102	38	22	54	48
Bruyns Hill	BML11	113	47	31	60	53
Bruyns Hill	BML12	111	35	32	66	45
Glenside	SML10	121	38	23	82	39
Glenside	SML11	163	92	45	76	87
Glenside	SML12	112	36	34	59	53

BML = Humic soil mini-line, SML = Sandy soil mini-line, MO = Males only, MP = Melting pot, BP = Bi-parental.

3.3.2 Experimental design, seedling establishment and management

Seedlings were germinated from true seed (seed fuzz) in the glasshouse at Mount Edgecombe. A week after germination, the seedling trays were taken from the glasshouse

and grown outside to harden off. When seedlings were five weeks old, they were transplanted into air-bricks laid out on a concrete slab. At planting into air-bricks, the families were laid out in a randomised complete block design with three replications per family. The seedlings (genotypes) from each family was divided into three sets. The three sets were randomly assigned to the three replications. Therefore the families were replicated but the individual genotypes within a family were not replicated. The overall design resulted in two plot levels, the family plot (made up of the total number of genotypes) and the genotype plot within a family plot containing individual seedlings.

The growing conditions in the air-bricks are uniform because of similar and uniformly prepared growth media and uniform irrigation and therefore no carry over effects were expected. The growth media was made up of a mixture of sand, soil and bagasse compost in a ratio of 1:1:2. Seedlings were irrigated three times a day to prevent moisture stress. Fertiliser (N:P:K = 5:1:5) was applied weekly at a rate of 10 kg per hectare to achieve optimum growth and replenish nutrients lost to leaching. Seedlings were left to grow in the air-bricks for 10 months until they produced mini-stalks. At 10 months age, the seedlings produced at least 1 m long stalks.

3.3.3 Experimental sites and trial establishment

From each seedling, vegetative stalks were harvested by cutting at the base and topping at the natural breaking point. Cane setts were planted in the field using the same trial design used in air bricks. Cane setts were planted in a 1 m long plot with a 1.1 m row-spacing in a tram-line fashion. Tram-line refers to a system where two adjacent rows are planted followed by an unplanted row. A 2.2 m spacing was left between the two tram-line rows, which is equivalent to one unplanted row.

Two trials (at Bruyns Hill and Glenside) were respectively planted in the field across three consecutive years in 2010 (BML10, SML10), 2011 (BML11, SML11) and 2012 (BML12, SML12) (Table 3.1). Trial series BML10, BML11 and BML12 were humic soil, mini-lines trials. Trial series SML10, SML11 and SML12 were sandy soil, mini-lines trials. Trials were established at Bruyns Hill (1012 m above sea level, 30°41"E, 29°25"S) and Glenside (985 m above sea level, 30°46'30"E, 29°20'45"S) research stations (Table 3.1). Bruyns Hill is located on humic soil that is rich in organic matter with a high clay content, while Glenside is located on sandy soil. Humic soil has more than 5% organic matter, while sandy

soil possesses less than 2% organic matter (Van Antwerpen et al. 2013). Data collected from soil pits (Ramburan et al. 2012) showed that the humic soil had an effective rooting depth of 60 to 80 cm. Humic soil contained 18 to 36% clay, 4.0 to 6.5% soil organic matter and soil N mineralisation of 3.0 to 3.15%. In contrast, the sandy soil had an effective rooting depth of 40 to 60 cm, and contained 10 to 15% clay, 1.2 to 1.8% soil organic matter and 1.0 to 1.5% soil N mineralisation.

3.3.4 Data collection

Family cane yield was estimated from yield components (stalk number, stalk height and stalk diameter) measured from a sample of the first 20 individual genotypes per plot (Zhou 2013). The number of millable stalks was counted for each seedling. Stalk height was measured from the ground level to the topmost visible dewlap of a cane stalk. Stalk diameter was measured using a digital calliper at the centre of each of the three stalks. Cane yield (kg) was calculated from stalk number, stalk height and stalk diameter using the following formula (Chang and Milligan 1992a):

$$\text{Cane yield} = ndr^2\pi h \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\text{Equation 3.1}$$

Assuming that the sugarcane stalks are perfect cylinders, in which d is the density considered equal to 1 g cm^{-3}, n = number of stalks, h = stalk height in metres, r = radius of stalk in centimetres and $\pi = 22/7$.

3.3.5 Data analysis

Data were analysed using mixed procedure of Statistical Analysis System (SAS Institute 2014). The estimates of variance components, standard errors and probability tests were calculated using the COVTEST option of PROC MIXED. The following statistical linear mixed model was used for family analysis:

$$Y_{ijk} = R_i + F_j + FR_{ij} + G(FR)_{k(ij)} \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots \text{Equation 3.2}$$

where Y_{ijk} = cane yield of the kth genotype recorded from j^{th} family in the ith replication, R_i = random effect of the ith replication, F_j = random effect of the jth family, FR_{ij} = random interaction effect of the ith replication by the jth family, $G(FR)_{k(ij)}$ = random effect of the kth

genotype nested within the random interaction effect of the ith replication by the jth family and was also residual error.

The following linear mixed model was used for individual genotype analysis:

$$Y_{ijk} = G(F)_{k(j)} + G(FR)_{k(ij)}$$ ………………..…………….……………….…….……….Equation 3.3

where $G(F)_{k(j)}$ = random effects of kth genotype nested within the jth family, $G(FR)_{k(ij)}$ = random effect of the kth genotype nested within the random interaction effect of the ith replication by the jth family and was also residual error.

The estimate of broad-sense heritability (H) for family was calculated as:

$$H_F = \frac{\sigma_F^2}{(\sigma_F^2 + \frac{\sigma_{FR}^2}{r} + \frac{\sigma_{G(FR)}^2}{rg})}$$ ………………………………………………….……………Equation 3.4

The broad-sense heritability (H) for individual genotype was calculated as:

$$H_G = \frac{\sigma_{G(F)}^2}{(\sigma_{G(F)}^2 + \sigma_{G(FR)}^2)}$$ …………………………………………..…………..Equation 3.5

where σ_F^2 = variance component of the family effects, $\sigma_{G(F)}^2$ = variance component of individual genotype nested with the family, σ_{FR}^2 = variance component of the interaction effect of replication by family, $\sigma_{G(FR)}^2$ = residual variance component, r = the number of replications and g = the number of seedlings sampled per plot. The standard error (SE) for H was estimated using (Becker 1992):

$$SE = \sqrt{\frac{2(1-H)^2\,[1+H(q-1)]^2}{q(q-1)(n-1)}}$$ ………………………………………………….Equation 3.6

where q = the number of observations per family, H = broad-sense heritability and n = the number of families in trials.

Predicted selection gain (Gs) was estimated using the formula described by Allard (1960):

$$Gs = K\sigma_F H \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\text{Equation 3.7}$$

where K = family selection intensity, σ_F = family phenotypic standard deviation and H = broad-sense heritability. Family selection intensity (K) was assumed to be 30% while selection intensity for individual genotypes is 10%, the expected selection intensity in Stage I.

3.4 RESULTS

3.4.1 Cane yield

For cane yield, the families in all trials (except SML10) produced highly significant (P<0.001) family variance components (σ^2_F) (Table 3.2). BML10, BML11 and BML12 respectively produced larger family variance than SML10, SML11 and SML12 trials. Family by replication interaction variance component (σ^2_{FR}) was highly significant (P<0.001) for all trials. The residual variance component ($\sigma^2_{G(FR)}$) for families was highly significant (P<0.001) for all trials and this component increased from BML10 to BML12 as well as from SML10 to SML12. The replication variance component (σ^2_R) was non-significant (P>0.05) across all trials. With individual genotype selection, all genotype nested within family variance ($\sigma^2_{G(F)}$) components were highly significant (P<0.001) for all trials except BML11 (significant at P<0.01) and SML10 (not significant with P>0.05). The residual variance ($\sigma^2_{G(FR)}$) components for individual genotypes were highly significant (P<0.001) across all trials and this component increased from BML10 to BML12 as well as from SML10 to SML12. The variance components for families were 8 to 22% larger than that for individual genotypes across trials. The individual genotype residual variance ($\sigma^2_{G(FR)}$) was consistently larger than the family residual variance ($\sigma^2_{G(FR)}$) across all trials. The individual residual variance ($\sigma^2_{G(FR)}$) was 7 to 21% larger than the family residual variance ($\sigma^2_{G(FR)}$).

For cane yield, broad-sense heritability (H) estimates and predicted selection gains (Gs and %Gs) of families were larger than that of individual genotypes in all trials (Table 3.2 and Figure 3.1). The family broad-sense heritability ranged from 0.25 to 0.78. The BML trials (0.59 to 0.78) produced higher family broad-sense heritability estimates than the SML trials (0.25 to 0.55). The broad-sense heritability for individual genotypes ranged from 0.02 to

0.10. The BML trials (0.07 to 0.10) produced larger individual broad-sense heritability estimates than the SML trials (0.02 to 0.09). The broad sense heritability of families was six to 12 times larger than that of individual genotypes.

The percent predicted family selection gains (%Gs) for the BML trials (38.20 to 54.38%) were larger than that of the SML trials (17.76 to 28.81%). The percent predicted selection gains for individual genotypes for the BML trials (7.06 to 12.25%) were larger than that of the SML trials (1.97 to 6.79%). The percent predicted selection gains for families were four to nine times larger than those for individual genotype selection. The R^2 values as well as the coefficient of variation (CV%) for individual genotype selection were larger than those for family selection across all trials.

3.4.2 Stalk number, height and diameter

The replication variance components (σ^2_R) for families were not significant (P>0.05) for stalk number, stalk height and stalk diameter across all trials (Tables 3.3, 3.4, 3.5). The family variance components (σ^2_F) were highly significantly (P<0.001) across trials except for stalk number (significant at P<0.01) and stalk diameter (significant at P<0.05) in SML10. The family by replication variance (σ^2_{FR}) and residual variance components ($\sigma^2_{G(FR)}$) were highly significant (P<0.001) across all trials. Family variance components (σ^2_F) were generally larger than family by replication interaction variance components (σ^2_{FR}) for stalk number and stalk diameter. The opposite trend was observed for stalk height. For families, the residual variance ($\sigma^2_{G(FR)}$) was the largest. For individual genotypes, genotype nested within family ($\sigma^2_{G(F)}$) and the residual variance ($\sigma^2_{G(FR)}$) were highly significant (P<0.001) across trials, except for SML10 (significant at P<0.05) and SML11 (not significant with P>0.05) for stalk number. Family variance (σ^2_F) was larger than genotype nested within family variance ($\sigma^2_{G(F)}$) for stalk number (BML11, BML12 and SML11), stalk height (BML10, BML11, BML12 and SML10) and stalk diameter (BML10, BML11, BML12, SML10 and SML11). Residual variance ($\sigma^2_{G(FR)}$) for families was lower than residual variance ($\sigma^2_{G(FR)}$) for individual genotypes. Individual genotypes produced higher CV% and higher R^2 values than families.

The broad-sense heritability (H) and predicted selection gains (Gs and %Gs) of families were larger than that of individual genotypes for stalk number, stalk height and stalk diameter for all trials (Tables 3.3, 3.4, 3.5 and Figures 3.2, 3.3). Humic soil populations

generally produced larger H, Gs (except for stalk height in SML11) and %Gs values than sandy soil populations for both family and individual genotype selection. In humic soil trials, the highest broad-sense heritability values were observed for stalk diameter while stalk height had the lowest. In sandy soil trials, stalk diameter showed the highest broad-sense heritability estimates while stalk number had the lowest. The %Gs for families were highest for stalk number and lowest for stalk diameter in both humic and sandy soil trials. For humic soil trials, individual genotypes generally showed the highest %Gs for stalk number and the lowest for stalk diameter while for sandy soil trials the predicted selection gain was generally highest for stalk height and lowest for stalk diameter.

Table 3.2 Variance components, broad-sense heritability (H), predicted selection gain (Gs), coefficient of determination (R^2) and coefficient of variation (CV) for cane yield (kg) for family (F) and individual genotypes selection (IGS) in humic (BML) and sandy (SML) soil, mini-line series planted in 2010, 2011 and 2012

Statistic	BML10	BML11	BML12	SML10	SML11	SML12
Family						
σ^2_R	0.16±0.18ns	0.15±0.17ns	6.49±5.39ns	0.72±0.63ns	1.52±1.08ns	3.76±3.39ns
σ^2_F	2.49±0.52***	2.41±0.61***	6.00±1.13***	0.35±0.26ns	1.38±0.39***	3.62±1.16***
σ^2_{FR}	2.09±0.33***	3.32±0.47***	3.08±0.55***	2.35±0.34***	2.33±0.35***	6.99±1.06***
$\sigma^2_{G(FR)}$	18.98±0.38***	27.47±0.53***	40.78±0.80***	14.34±0.28***	17.36±0.34***	37.00±0.78***
H_F	0.70±0.03	0.59±0.11	0.78±0.02	0.25±0.03	0.55±0.03	0.54±0.03
Gs	3.56	3.58	5.77	1.08	2.68	3.82
%Gs	54.38	39.10	38.20	17.76	28.81	25.88
Mean±stdev	6.55±4.36	9.16±5.24	15.11±6.39	6.10±3.79	9.29±4.17	14.77±6.08
R^2	0.24	0.22	0.29	0.23	0.24	0.28
CV	66.54	57.26	42.27	62.08	44.89	41.17
Individual genotypes						
$\sigma^2_{G(F)}$	2.31±0.37***	2.21±0.49**	4.93±0.80***	0.29±0.26ns	1.13±0.29***	4.15±0.83***
$\sigma^2_{G(FR)}$	21.34±0.52***	31.03±0.72***	49.10±1.14***	17.29±0.41***	20.54±0.47***	44.71±1.16***
H_{IGS}	0.10±0.02	0.07±0.02	0.09±0.02	0.02±0.01	0.05±0.01	0.09±0.02
Gs	0.80	0.65	1.12	0.12	0.42	1.00
%Gs	12.25	7.06	7.44	1.97	4.50	6.79
Mean±stdev	6.55±4.66	9.16±5.52	15.11±7.0	6.10±4.17	9.29±4.56	14.77±6.70
R^2	0.43	0.43	0.43	0.44	0.42	0.49
CV	71.15	60.32	46.37	68.28	49.10	45.35
$\sigma^2_F / \sigma^2_{G(F)}$	108	109	122	121	122	87
H_F/H_{IGS}	700	843	867	1250	1100	600
%Gs$_{(F)}$/ %Gs (IGS)	444	554	513	901	640	381

σ^2_R = Replication variance, σ^2_F = Family variance, σ^2_{FR} = Family by replication variance, $\sigma^2_{G(FR)}$= Residual variance, $\sigma^2_{G(F)}$ = Genotype nested within family variance, ***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Not significant at P≥0.05
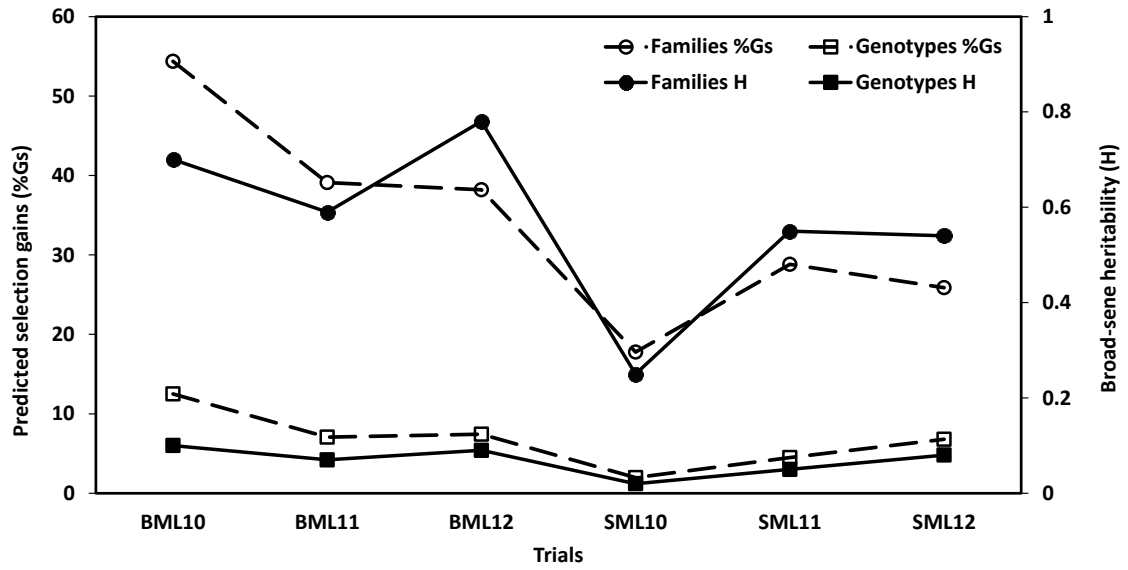
Figure 3.1 Trends for cane yield predicted selection gain (%Gs) and broad-sense heritability (H) for both families and individual genotypes for humic (BML) and sandy (SML) soil trial

Table 3.3 Variance components, broad-sense heritability (H), predicted selection gain (Gs), coefficient of determination (R^2) and coefficient of variation (CV) for stalk number for family (F) and individual genotypes selection (IGS) in humic (BML) and sandy (SML) soil, mini-line series planted in 2010, 2011 and 2012

Statistic	BML10	BML11	BML12	SML10	SML11	SML12
Family						
σ^2_R	0.04±0.09ns	0.54±0.57ns	8.53±7.11ns	0.22±0.27ns	5.76±3.97ns	2.58±2.64ns
σ^2_F	4.31±0.83***	9.16±2.15***	12.64±2.33***	1.41±0.59**	7.02±1.75***	13.26±2.89***
σ^2_{FR}	1.96±0.44***	8.72±1.44***	5.52±1.01***	3.72±0.65***	5.55±1.06***	10.40±1.73***
$\sigma^2_{G(FR)}$	41.63±0.83***	103.55±2.01***	77.43±1.52***	41.94±0.81***	69.15±1.37***	75.66±1.61***
H_F	0.75±0.03	0.64±0.03	0.80±0.02	0.40±0.04	0.69±0.03	0.73±0.03
Gs	5.62	7.60	8.18	3.00	6.62	7.35
%Gs	45.53	30.52	32.52	22.51	25.39	26.69
Mean±stdev	12.35±6.45	24.90±10.18	25.16±8.80	13.34±6.48	26.06±8.31	27.53±8.70
R^2	0.18	0.19	0.27	0.16	0.21	0.30
CV	52.26	40.88	34.97	48.54	31.89	31.60
Individual genotypes						
$\sigma^2_{G(F)}$	4.70±0.74***	7.60±1.77***	9.84±1.51***	1.61±0.71*	1.46±1.07ns	17.02±1.97***
$\sigma^2_{G(FR)}$	43.23±1.05***	113.22±2.62***	90.91±2.12***	45.55±1.09***	81.44±1.87***	83.55±2.45***
H_{IGS}	0.10±0.02	0.06±0.02	0.10±0.02	0.03±0.01	0.02±0.01	0.17±0.03
Gs	1.14	1.17	1.63	0.41	0.28	2.68
%Gs	11.55	4.71	6.49	3.05	1.06	9.75
Mean±stdev	12.35±6.62	24.90±10.58	25.16±9.50	13.34±6.75	26.06±8.96	27.53±9.01
R^2	0.43	0.43	0.44	0.45	0.42	0.55
CV	53.63	42.46	37.74	50.63	34.37	32.68
$\sigma^2_F/\sigma^2_{G(F)}$	92	120	128	88	481	78
H_F/H_{IGS}	750	1067	800	1333	3450	429
%Gs$_{(F)}$/%Gs$_{(IGS)}$	394	1252	501	738	2395	274

σ^2_R = Replication variance, σ^2_F = Family variance, σ^2_{FR} = Family by replication variance, $\sigma^2_{G(FR)}$ = Residual variance, $\sigma^2_{G(F)}$ = Genotype nested within family variance,***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Not significant at P≥0.05

Table 3.4 Variance components, broad-sense heritability (H), predicted selection gain (Gs), coefficient of determination (R^2) and coefficient of variation (CV) for stalk height for family (F) and individual genotypes selection (IGS) in humic (BML) and sandy (SML) soil, mini-line series planted in 2010, 2011 and 2012

Statistic	BML10	BML11	BML12	SML10	SML11	SML12
Family						
σ^2_R	0.0042±39.97ns	0.0013±0.0011ns	0.0107±0.0088ns	0.0108±0.0086ns	0.0013±0.0011ns	0.0066±0.0058ns
σ^2_F	0.0160±39.27***	0.0090±0.0021***	0.0062±0.0015***	0.0098±0.0028***	0.0087±0.0018***	0.0068±0.0058***
σ^2_{FR}	0.0260±31.73***	0.0138±0.0017***	0.0068±0.0010***	0.0206±0.0025***	0.0072±0.0010***	0.0080±0.0017***
$\sigma^2_{G(FR)}$	0.0755±15.13***	0.0537±0.0010***	0.0527±0.0010***	0.0562±0.0010***	0.0409±0.0008***	0.0557±0.0013***
H_F	0.61±42	0.61±0.03	0.66±0.37	0.55±0.04	0.73±0.02	0.64±0.03
Gs	19.5786	0.1627	0.1771	0.1466	0.1953	0.1792
%Gs	18.9862	20.5975	14.8814	13.9654	23.5357	14.2196
Mean±stdev	1.03±0.27	0.79±0.23	1.19±0.23	1.05±0.23	0.83±0.02	1.26±0.24
R^2	0.40	0.34	0.30	0.44	0.34	0.28
CV	26.64	29.33	19.32	22.49	24.27	18.71
Individual genotypes						
$\sigma^2_{G(F)}$	0.0133±19.06***	0.0078±0.0011***	0.0026±0.0009**	0.0079±0.0015***	0.0103±0.0010***	0.0073±0.0013***
$\sigma^2_{G(FR)}$	0.1063±25.84***	0.0685±0.0016***	0.0685±0.0016***	0.0873±0.0022***	0.0484±0.0011***	0.0658±0.0017***
H_{IGS}	0.11±0.02	0.10±0.02	0.04±0.01	0.08±0.02	0.18±0.02	0.10±0.02
Gs	6.3965	0.0466	0.0170	0.0424	6.8611	0.0455
%Gs	6.2030	5.8945	1.4254	4.0420	8.2267	3.6097
Mean±stdev	1.03±0.33	0.79±0.26	1.19±0.26	1.05±0.29	0.83±0.02	1.26±0.26
R^2	0.44	0.45	0.39	0.48	0.50	0.50
CV	31.76	33.13	22.11	27.96	26.68	20.30
$\sigma^2_{F}/\sigma^2_{G(F)}$	120	115	238	124	84	93
H_F/H_{IGS}	554	610	1650	687	406	640
%Gs(F)/%Gs$_{(IGS)}$	306	349	1044	345	286	394

σ^2_R = Replication variance, σ^2_F = Family variance, σ^2_{FR} = Family by replication variance, $\sigma^2_{G(FR)}$ = Residual variance, $\sigma^2_{G(F)}$ = Genotype nested within family variance,***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Not significant at P≥0.05

Table 3.5 Variance components, broad-sense heritability (H), predicted selection gain (Gs), coefficient of determination (R^2) and coefficient of variation (CV) for stalk diameter for family (F) and individual genotypes selection (IGS) in humic (BML) and sandy (SML) soil, mini-line series planted in 2010, 2011 and 2012

Statistic	BML10	BML11	BML12	SML10	SML11	SML12
Family						
σ^2_R	0.0002±0.0003ns	0.0000	0.0027±0.0023ns	0.0003±0.0004ns	0.0011±0.0009ns	0.0000
σ^2_F	0.0088±0.0018***	0.0154±0.0024***	0.0305±0.0048***	0.0086±0.0015*	0.0080±0.0017***	0.0235±0.0038***
σ^2_{FR}	0.0060±0.0010***	0.0027±0.0006***	0.0063±0.0011***	0.0038±0.0007***	0.0026±0.0011***	0.0040±0.0011***
$\sigma^2_{G(FR)}$	0.0657±0.0013***	0.0616±0.0012***	0.0854±0.0017***	0.0544±0.0010***	0.0902±0.0018***	0.0737±0.0015***
H_F	0.73±0.03	0.88±0.02	0.90±0.01	0.78±0.02	0.75±0.02	0.89±0.01
Gs	0.2210	0.2541	0.3017	0.2090	0.2619	0.2802
%Gs	8.9472	10.6332	11.9232	9.0851	11.3882	12.1277
Mean±stdev	2.47±0.26	2.39±0.25	2.53±0.29	2.30±0.23	2.30±0.30	2.31±0.27
R^2	0.22	0.27	0.34	0.23	0.15	0.31
CV	10.39	10.38	11.57	10.24	13.09	11.72
Individual genotypes						
$\sigma^2_{G(F)}$	0.0081±0.0013***	0.0134±0.0013***	0.0290±0.0022***	0.0086±0.0011***	0.0074±0.0015***	0.0236±0.0021***
$\sigma^2_{G(FR)}$	0.0718±0.0017***	0.0658±0.0015***	0.0945±0.0022***	0.0581±0.0014***	0.0928±0.0022***	0.0776±0.0021***
H_{IGS}	0.10±0.02	0.17±0.03	0.24±0.03	0.13±0.02	0.07±0.01	0.23±0.03
Gs	0.0483	0.0773	0.1283	0.0547	0.0392	0.1150
%Gs	1.9559	3.2350	5.0692	2.3779	1.7055	4.9803
Mean±stdev	2.47±0.27	2.39±0.26	2.53±0.31	2.30±0.24	2.30±0.30	2.31±0.28
R^2	0.45	0.49	0.52	0.51	0.47	0.58
CV	10.83	10.71	12.12	10.55	13.00	11.90
$\sigma^2_F / \sigma^2_{G(F)}$	108.64	114.92	105.17	100	108.11	99.58
H_F / H_{IGS}	730	518	375	600	1071	387
%Gs $_{(F)}$/ %Gs $_{(IGS)}$	457	329	235	382	668	243

σ^2_R = Replication variance, σ^2_F = Family variance, σ^2_{FR} = Family by replication variance, $\sigma^2_{G(FR)}$ = Residual variance, $\sigma^2_{G(F)}$ = Genotype nested within family variance, ***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Not significant at P≥0.05
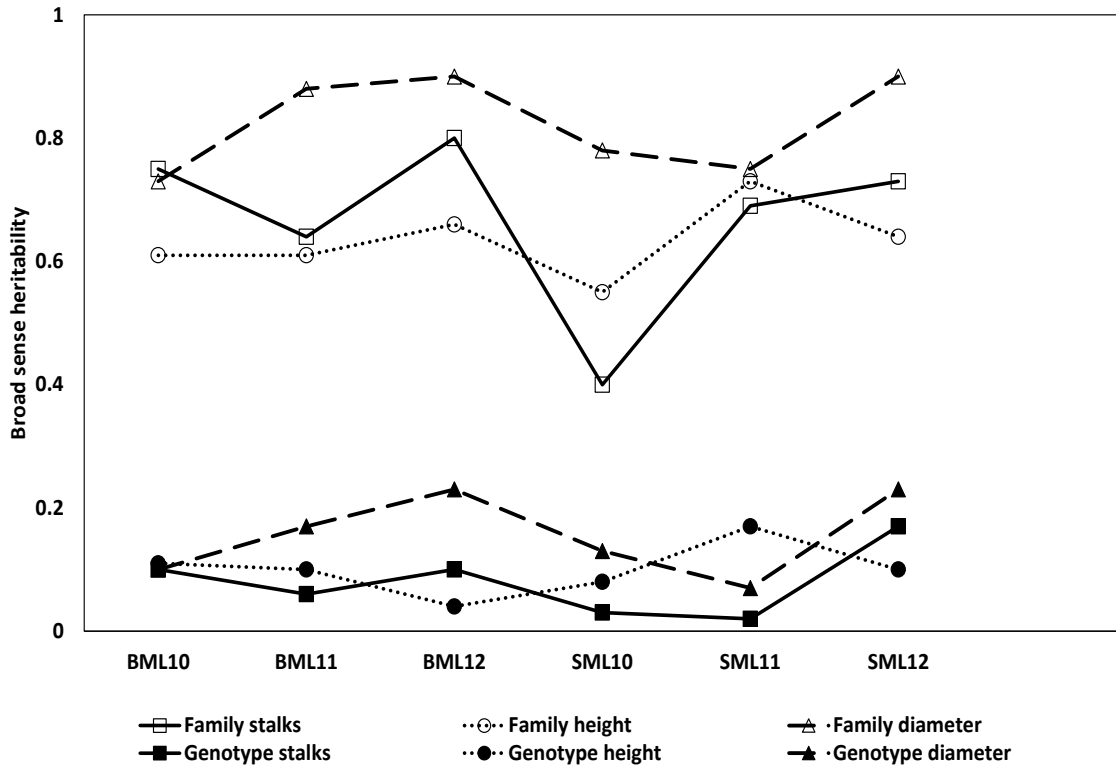
Figure 3.2 Trends in broad sense heritability for families and individual genotypes in humic (BML) and sandy (SML) soil trials
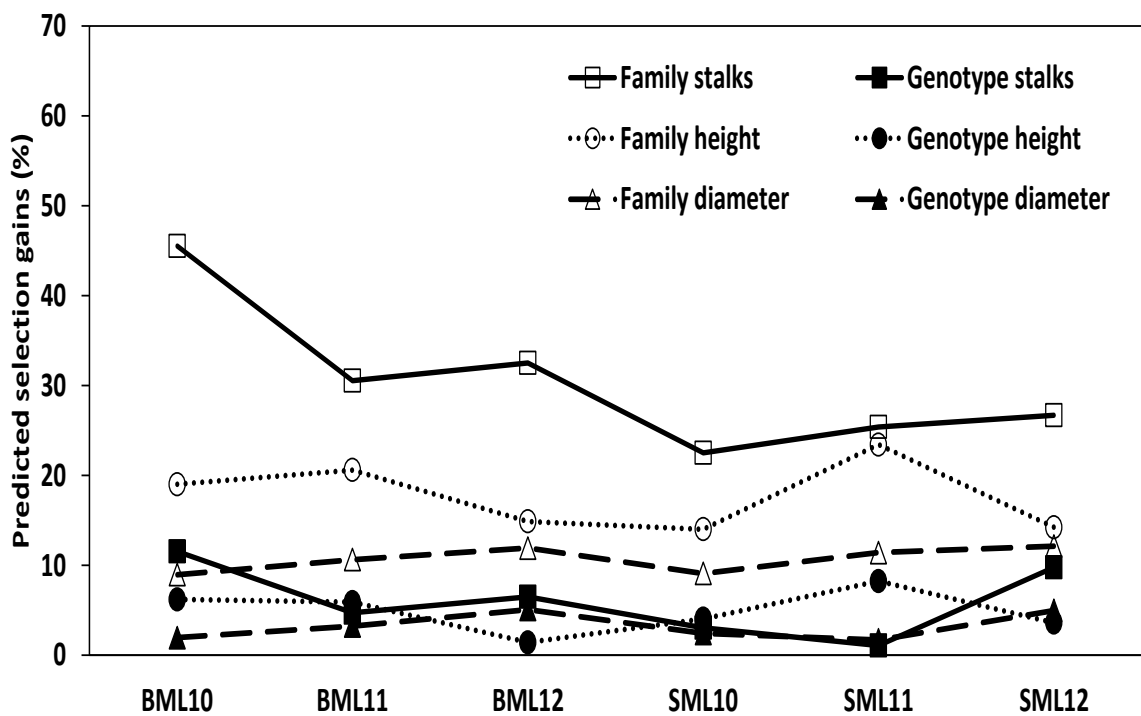
Figure 3.3 Trends in predicted selection gains for families and individual genotypes in humic (BML) and sandy (SML) soil trials

3.5 DISCUSSION

Families had higher predicted selection gains, higher broad-sense heritability estimates and larger variances than individual genotypes highlighting superiority of family compared to individual genotype selection in sugarcane breeding. The benefits of family selection are derived from larger genetic variability, ability to discriminate between superior and inferior families and the higher expected genetic gains. Previous studies on family selection by Cox and Stringer (1998), Kimbeng and Cox (2003) and Shanthi et al. (2008) demonstrated significant differences among families but none of these studies compared family to individual genotype selection. This study is the first to comprehensively quantify the benefits of family compared to individual genotype selection. All breeding parameters for families were higher than those for individual genotype selection indicating expected increased selection efficiency from adopting family selection in sugarcane breeding. The advantages of family selection compared to individual genotype selection are enhanced because families can be replicated whereas individual genotypes cannot be replicated. Individual genotypes cannot be replicated because of insufficient breeding material and this further decreases the precision of evaluating individual plant data. Individual genotypes cannot be replicated because of larger numbers which require much larger areas of land to achieve replication.

The cane yield for families produced at least six times higher broad-sense heritability estimates compared to individual genotypes for all trials. Broad-sense heritability is the proportion of genetic variance that is attributed to the amount of phenotypic variation in the population (Falconer 1960; Zhou and Joshi 2012). Results indicated that families contributed larger proportions of genetic variation compared to individual genotypes. The larger proportion of phenotype attributed to genetic variation showed that selection of families with superior genetic performance would be more effective than selecting individual genotypes with superior genetic make-up. The trend was the same for stalk number, stalk height and stalk diameter indicating that characterising populations through families was more accurate than through individual genotypes within the populations. Results confirm previous studies that showed family evaluation and selection was superior to individual genotype selection (Zhou 2014; Zhou and Mokwele 2015). Selecting for cane yield in families would be at least six times more accurate than through individual genotypes. Results further suggested that using family selection, populations that produce

high cane yield can be selected with higher precision than using individual genotype selection. Using family selection in sugarcane breeding increases significantly the identification of superior populations which should ultimately increase genetic gains for cane yield components.

Family predicted selection gain for yield was at least four times that for individual genotypes indicating that higher yield populations were advanced using family selection. Predicted selection gains are an indication of potential genetic gains that can be expected from selecting a proportion of individuals or a population of individuals. Results suggest that larger gains would be achieved through family compared to individual genotype selection. The trend was the same for stalk number, height and diameter indicating that improvement in cane yield would be accelerated using family selection. These results are in agreement with a study by Zhou (2014) which showed that yield components could provide an adequate discriminating ability for determining family differences. Because of higher precision of family selection, the advanced populations would generally be more superior and this result in more efficient utilisation of resources in later stages of genotype testing. Higher predicted gains that lead to higher genetic gains, when carried out over several cycles of sugarcane breeding, are expected to accelerate recurrent selection for target yield traits.

The larger family variance indicated larger genetic variability among families than among individual genotypes. Selection in plant breeding takes advantage of variability within populations (Allard 1960). Higher family genetic variability indicates that superior families can be easily identified from populations. Further, the lower genetic variability among individuals indicates that most of the variability could be caused by effects of random environmental error on the genotypes. Genotypes at this stage of sugarcane breeding are planted in small plots which result in higher inter-plot competition. Inter-plot competition has been identified among sugarcane individual genotypes in unreplicated single row trials in several studies (Skinner 1961; McRae and Jackson 1998). The effect of environmental error further increases the variability as well as the masking of true genetic expression. In contrast, families are generally planted in larger plots that are less susceptible to competition among families. Further, replication of families allows for field variability to be accounted for, unlike individual genotypes where field variability has a larger influence on individuals. Results suggest that variability among families was larger and more

important than among individuals within populations, and this provide a potential to increase selection of superior populations in sugarcane breeding.

The residual variance for individual genotypes was larger than that of families highlighting the lower precision associated with individual genotype evaluation compared to family evaluation. The residual variance for genotypes compared to families was largest for stalk height, indicating the lower accuracy of comparing populations for height using individual genotype data due to the confounding effect of environmental error. Results further suggested that height could be mostly influenced by inter-plot competition among genotypes than in families. Genotypes are planted in unreplicated single row plots of one row by 1 m long and therefore high inter-plot competition is expected. Several studies on the efficiency of using single-row plots for sugarcane breeding have been conducted (Skinner 1961; Jackson and McRae 2001). These studies concluded that, in trials which use single-row plots, inter-plot competition could bias estimates of genotype trait values and may reduce genetic progress. Further, during individual genotype evaluation and selection, a lot of bias is given to stalk height (because of easy visual appreciation for height), a parameter more susceptible to inter-plot competition, further confounding the effectiveness of individual genotype selection. Therefore, family evaluation and selection would reduce the impact of random environmental error on selection. The large residual variance for individual genotypes was associated with higher CV% indicating larger variability within the genotype data compared to family data.

Cane yield had higher predicted selection gains than stalk number, height and diameter suggesting that selecting for cane yield directly was more efficient than through its components. During individual genotype selection for advancement, sugarcane breeders visually evaluate each individual genotype for optimum combination of stalk number, height and diameter. Genotypes perceived to have the desired optimum combination, that is high number of stalks that are taller and thicker, are generally selected and advanced to the next stage of variety testing. Results suggest that such an approach, particularly based on limited or no data may not be entirely efficient. It appeared that the individual components have lower predicted selection gains and some possess lower broad-sense heritability than cane yield, indicating that they may be more prone to environmental error. Further, visual selection is known to be biased (Kimbeng and Cox 2003) and therefore, visually determining the optimum combination of traits maybe inaccurate (Zhou et al. 2010,

2013b). Studies using logistic regression models indicate that an unbiased statistical approach is more accurate. In this study, aiming to select for cane yield directly is more accurate.

In practice, family evaluation is followed by family selection to identify elite families from which individual genotype selection for advancement to the next stage is carried out. While results have shown the superiority of family selection, results also indicated that individual genotype variances were significant. Although individual genotypes had low predicted selection gains and broad-sense heritability estimates, these values were significant. Before family evaluation and selection were adopted, progress in genetic gains was achieved in sugarcane breeding, albeit at considerably lower levels of efficiency (Skinner 1982). Therefore, using the strategy of family evaluation to firstly identify elite families and then secondly applying efficient individual genotype selection within the selected families is expected to accelerate genetic gains in sugarcane breeding. Assuming that predicted selection gains from families and individual genotypes are additive, the combined application of family followed by individual genotype selection should benefit from the expected additive nature of the genetic gains. However, applying other approaches to selection for individual genotypes in elite populations such as logistic regression models (Zhou et al. 2013a) would further increase efficiencies in sugarcane breeding.

Humic soil populations had higher broad-sense heritability estimates and higher predicted selection gains compared to sandy soil populations suggesting higher efficiencies in humic than sandy soil. Humic soil is more uniform in terms of soil depth, organic matter and clay content than sandy soil. Humic soil is deeper with higher organic matter and clay content than sandy soil (Van Antwerpen et al. 2013). Therefore, less variability in the fields is evident from humic compared to sandy soil. Further, a deeper soil with higher water holding capacity reduces the impact of moisture stress on the crop in humic soil resulting in more uniform growth compared to sandy soil (Zhou and Gwata 2016). Therefore, less impact of environmental error is expected from humic soil than sandy soil. Further, the terrain in the fields where humic soil populations were grown was less rugged compared to where sandy soil populations were grown, further reducing the impact of environment error in humic soil.

Percent predicted selection gains were highest for stalk number and lowest for stalk diameter suggesting that during visual selection within elite families, focus should be on stalk number followed by stalk height and least on stalk diameter. A previous study (Zhou 2004) showed that stalk number had the strongest influence on yield. Other studies on path coefficient analysis (Mariotti 1973; Chaudhary and Singh 1994; Chaudhary and Joshi 2005; Tyagi et al. 2012; Smiullah et al. 2013; Sanghera et al. 2015) showed similar results. Studies using logistic regression models in early selection stages of sugarcane breeding (Zhou et al. 2013a) showed the strong influence of stalk number on sugarcane yield.

The consistently high residual variance in all trials indicated that a large proportion of the variability was not accounted for by the experimental design. Currently, a randomised complete block design is being used for all trials. Trials are generally planted in large areas, spanning from four to six hectares. The large within block variability could have contributed to the large residual error. By improving design efficiency and adopting incomplete block designs such as lattices would probably increase the efficiency in these trials. Such designs can account for within block variability and thus reduce residual variance and increasing the efficiency of comparing families. Statistical modelling of plant-to-plant competition and variability within blocks could also be used to reduce the residual variance. Large numbers of families are evaluated at early stages of sugarcane breeding and selection. This increases the importance of experimental design efficiency. According to Durner (1989), the plot size plays a significant role in determining field experimental precision. In this study, a family was replicated three times and a sample of first 20 seedlings per family plot was used. Zhou (2014) concluded that yield data collected from 10 seedlings per plot in each of the four replications per family would be sufficient for evaluating family performances. Other suggestions range from 20 to 150 plants per family (Wu et al. 1977, 1978; Mariotti et al. 1981; Barbosa et al. 2001). In addition, the lower R^2 values and larger CV% values observed in the current study is an indication of the larger variability in the data, leading to a poor detection of family differences. Therefore, this study indicated the need to optimise the replications and sample sizes for family trials.

3.6 CONCLUSIONS

Families had larger variability, higher broad sense heritability estimates and higher predicted selection gains than individual genotypes, highlighting the potential of using

family selection to accelerate genetic gains in sugarcane breeding. Selecting families directly for cane yield was more efficient than through the yield components indicating that visual selection, which focuses on the yield components, was less accurate. Stalk height was more susceptible to field variability and inter-plot competition suggesting that visual selection without family evaluation would be inefficient particularly because of the bias towards taller plants during selection. Combined gains from family and individual genotypes are expected to increase genetic gains from adopting family selection in sugarcane breeding. Humic soil populations had larger variability, higher broad sense heritability estimates and higher predicted selection gains compared to sandy soil populations, indicating the efficacy of family evaluation in comparing two breeding populations.

3.7 REFERENCES

Allard RW (1960) Principles of plant breeding. John Wiley and Sons, New York. pp. 414

Atkin FC, Dieters MJ, Stringer JK (2009) Impact of depth of pedigree and inclusion of historical data on the estimation of additive variance and breeding values in a sugarcane breeding program. Theoretical and Applied Genetics 119:555-565

Babu C, Koodalingam K, Natarajan US, Shanthi RM, Govindaraj P (2009) Interrelationships of sugarcane yield and quality components and their utility in family selection. Madras Agricultural Journal 96:309-313

Balzarini MG (2000) Biometrical models for predicting future performance in plant breeding. PhD Dissertation. Louisiana State University, Louisiana, USA. Biometrics 44:705-715

Barbosa MPH, Peternelli LA, Silveira LCI (2001) Plot size in sugarcane family selection experiments. Crop Breeding and Applied Biotechnology 1:271-276

Becker WA (1992) Manual of quantitative genetics, 5th edition. Pullman, WA: Academic Enterprises. pp. 189

Casler MD, Brummer EC (2008) Theoretical expected genetic gains for among-and-within-family selection methods in perennial forage crops. Crop Science 48:890-902

Chang YS, Milligan SB (1992a) Estimating the potential of sugarcane families to produce elite genotypes using bivariate prediction methods. Theoretical and Applied Genetics 84:633-639

Chang YS, Milligan SB (1992b) Estimating the potential of sugarcane families to produce elite genotypes using univariate cross prediction methods. Theoretical and Applied Genetics 84:662-671

Chaudhary AK, Singh JRP (1994) Correlation and path coefficient analysis studies in early maturing clone of sugarcane (*Saccharum* spp. Complex). Cooperative Sugar 25:305-307

Chaudhary RR, Joshi BK (2005) Correlation and path coefficient analysis in sugarcane. Nepal Agricultural Research Journal 6:24-27

Cox MC, Stringer JK (1998) Efficacy of early generation selection in a sugarcane improvement program. Proceedings of the Australian Society of Sugar Cane Technologists 20:148-153

De Oliveira RA, Daros E, de Resende MDV, Filho JCB, Zambon JLC, Ruaro L (2013) Early selection in sugarcane family trials via BLUP and BLUPIS procedures. Acta Scientiarum Agronomy 35:427-434

Durner EF (1989) OPS: a computer program for estimating optimum plot size for field research. HortScience 24:1040

Falconer DS (1960) Introduction to quantitative genetics. Oliver and Boyd, London. pp. 365

Falconer DS, Mackay TFC (1996) Introduction to quantitative genetics 4th edition. Longman Group Ltd, UK. pp. 480

Heinz DJ, Tew TL (1987) Hybridization procedures. In: Heinz DJ (ed), Developments in Crop Science 11: Sugarcane improvement through breeding, Elsevier, New York. pp. 313-342

Hogarth DM (1971) Quantitative inheritance studies in sugarcane II. Correlations and predicted responses to selection. Australian Journal of Agricultural Research 22:103-109

Hogarth DM, Mullins RT (1989) Changes in the BSES plant improvement program. Proceedings of the International Society of Sugar Cane Technologists 20:956-961

Jackson PA, Bull JK, McRae TA (1995) The role of family selection in sugarcane breeding programs and the effect of genotype x environment interactions. Proceedings of the International Society of Sugar Cane Technologists 22:261-269

Jackson P, McRae TA (2001) Selection of sugarcane clones in small plots. Effects of plot size and selection criteria. Crop Science 41:315-322

Kimbeng CA, Cox MC (2003) Early generation selection of sugarcane families and clones in Australia: A review. Journal of the American Society of Sugar Cane Technologists 23:20-39

Kimbeng CA, McRae TA, Cox MC (2001) Optimising early generation selection in sugarcane breeding. Proceedings of the International Society of Sugar Cane Technologists 24:488-493

Kimbeng CA, McRae TA, Stringer JK (2000) Gains from family and visual selection in sugarcane, particularly for heavily lodged crops in the Burdekin region. Proceedings of the Australian Society of Sugar Cane Technologists 22:163-169

Mariotti JA (1973) The influence of environment on the relationship between yield and its components in sugarcane. Proceedings of the International Society of Sugar Cane Technologists 32:19-22

Mariotti JA, Scandaliaris J, Ahmed MA, Cuenya MI (1981) Análisis del comportamiento familiar en progenies híbridasdecaña de azucar. Revista Industrial y Agrícola de Tucumán 58:1-14

McRae TA, Jackson PA (1998) Competition effects in selection trials. Proceedings of the Australian Society of Sugar Cane Technologists 20:154-161

Melo DS, Pinto CABP, Peixouto LS, Neder DG, de Assis JC (2011) Early selection of full-sib potato families. Ciência e Agrotecnologia 35:1101-1109

Milligan SB, Legendre BL (1990) Development of a practical method for sugarcane cross appraisal. Journal of the American Society of Sugar Cane Technologists 11:59-68

Noor M, Shahwar D, Rahman H, Ullah H, Ali F, Iqbal M, Sha LA, Ullah I (2013) Change in heritability estimates due to half-sib family selection in the maize variety Pahari. Genetics and Molecular Research 12:1872-1881

Park S, Jackson PA, Berding N, Inman-Bamber G (2007) Conventional breeding practices within the Australian sugarcane breeding program. Proceedings of the Australian Sugar Cane Technologists 29:113-121

Pedrozo CA, Barbosa MHP, da Silva FL, de Resende MDV, Peternelli LA (2011) Repeatability of full-sib sugarcane families across harvests and the efficiency of early selection. Euphytica 182:423-430

Ramburan S, Zhou MM, Labuschagne M (2012) Investigating test site similarity, trait relations and causes of genotype by environment interactions of sugarcane in the Midlands region of South Africa. Field Crops Research 129:71-80

Sanghera GS, Tyagi V, Kumar R, Thind KS, Sharma B (2015) Genetic variability, association and their dissection through path analysis for cane yield and its component traits in early maturing sugarcane clones. Journal of Science 5:28-34

Santos GP, Soares AA, Ramalho MAP (2002) Performance of upland rice families selected from segregant populations. Crop Breeding and Applied Biotechnology 2:237-246

SAS Institute (2014) SAS/STAT user's guide, version 9.1.3. Cary, NC: SAS Institute

Shanthi RM, Bhagyalakshmi KV, Hemaprabha G, Alarmelu S, Nagarajan R (2008) Relative performance of the sugarcane families in early selection stages. Sugar Tech 10:114-118

Skinner JC (1961) Sugarcane selection experiments 2. Competition between varieties. Technical Communications, Bureau of Sugar Experiment Stations, Queensland 1:1-26

Skinner JC (1982) Efficiency of bunch-planted and single-planted seedlings for selecting superior families in sugarcane. Euphytica 31:523-537

Smiullah, Khan FA, Ijaz U, Abdullah (2013) Genetic variability of different morphological and yield contributing traits in different accession of *Saccharum officinarum* L. Universal Journal of Plant Science 1:43-48

Streit LG, Fehr WR, Welke GA, Hammond EG, Cianzio SR (2001) Family and line selection for reduced palmitate, saturates, and linolenate of soybean. Crop Science 41:63-67

Stringer JK, Cox MC, Atkin FC, Wei X, Hogarth DM (2011) Family selection improves the efficiency and effectiveness of selecting original seedlings and parents. Sugar Tech 13:36-41

Stringer JK, McRae TA, Cox MC (1996) Best linear unbiased prediction as a method of estimating breeding value in sugarcane. In: Wilson JR, Hogarth DM, Campbell JA, Garside AL (eds), Sugarcane: Research Towards Efficient and Sustainable Production, CSIRO Division of Tropic Crops and Pastures, Brisbane, Australia. pp. 39-41

Tyagi VK, Sharma S, Bhardwaj SB (2012) Pattern of association among cane yield, sugar yield and their components in sugarcane (*Saccharum officinarum* L.). Journal of Agricultural Research 50:29-38

Van Antwerpen R, Wettergreen T, Van der Laan M, Miles N, Rhodes M, Weigel A (2013) Understanding and managing soil in the South African sugar industry. South African Sugarcane Research Institute. Durban, South Africa. pp. 176

Walker DIT (1963) Family performance at early selection stages as a guide to the breeding programme. Proceedings of the International Society of Sugar Cane Technologists 11:469-483

Wu KK, Heinz DJ, Meyer HK, Ladd SL (1977) Selection studies in sugarcane (*Saccharum* spp. hybrids): III. A method to determine sample size for the estimation of population variance. Theoretical and Applied Genetics 51:29-33

Wu KK, Heinz DJ, Meyer HK, Ladd SL (1978) Minimum sample size for estimating progeny mean and variance. Crop Science 18:57-62

Zhou MM (2004) Stalk population control of yield, quality and agronomic traits of sugarcane population in early selection stages. International Sugar Journal 22:14-20

Zhou MM (2013) Realised selection gains for cane yield, sucrose content and sugar yield among South African breeding programmes. Proceedings of the South African Sugar Technologists' Association 86:273-285

Zhou MM (2014) Family evaluation for sugarcane yield using data estimated from stalk number, height, and diameter. Journal of Crop Improvement 28:406-417

Zhou MM, da Silva JA, Kimbeng CA, White WH (2010) Cross resistance between the Mexican rice borer and the sugarcane borer (*Lepidoptera*: Crambidae): A case study using sugarcane breeding populations. Crop Science 50:1-9

Zhou MM, Gwata ET (2016) Quantifying sugarcane cultivar genetic gains in the Midlands region of South Africa. Agronomy Journal 108:342-348

Zhou MM, Joshi SV (2012) Trends in broad sense heritability and implications for sugarcane breeding in South Africa. Sugar Tech 14:40-46

Zhou MM, Kimbeng CA, Tew TL, Gravois KA, Pontif M, Bischoff KP (2013a) Logistic regression models to aid selection in early stages of sugarcane breeding. Sugar Tech 16:150-156

Zhou MM, Lichakane ML, Joshi SV (2013b) Family evaluation for quality traits in South African sugarcane breeding programmes. International Sugar Journal 115:418-430

Zhou MM, Mokwele A (2015) Family versus individual plant selection for stem borer (*Eldana saccharina*) resistance in early stages of sugarcane breeding in South Africa. South African Journal of Plant and Soil 33:89-96

CHAPTER 4

IDENTIFYING ELITE FAMILIES AND DETERMINING OPTIMUM FAMILY SELECTION RATES IN SUGARCANE BREEDING

4.1 ABSTRACT

Family selection in sugarcane has shown to increase genetic gains for traits controlled by several genes such as cane yield when compared to individual genotype selection at early selection stages. The objectives of this study were to evaluate and identify elite families for cane yield, to determine optimum family selection rates and to identify ideal trait combinations among the family groupings. Stalk number, stalk height and stalk diameter were measured on a sample of 20 individual genotypes per plot in each of the three replications per family and the data were used to calculate cane yield. Data were analysed for family, group and family within group effects using SAS mixed models. Results indicated highly significant differences (P<0.0001) for family and group effects for all traits. The highly significant differences (P<0.0001) observed for family within group effects for diameter indicated large variability for families within the different cane yield groups. Principal component analysis indicated that selection for stalk number and stalk height, rather than stalk diameter, would lead to an increase in cane yield. The humic soil populations produced a significantly (P<0.05) higher proportion of elite families compared to the sandy soil populations. The optimum selection rate for humic soil trials was 30% while that for sandy soil trials it was 25%, suggesting that more elite families were obtained from humic soil compared to sandy soil populations.

Keywords: Sugarcane, family evaluation, cane yield components, predicted selection gains, optimum selection rates

4.2 INTRODUCTION

Family evaluation involves collecting data from progenies within family plots and using the data to determine family values. The family values are used to identify families that possess higher trait values which are also known as elite families. The advantage of family evaluation and selection is that families can be replicated across locations which provide an opportunity for evaluating family comparisons whereas individuals cannot be replicated.

This is because of the small amount of seed material available to be planted for individual genotypes as well as the large numbers of seedlings involved at the early stages of sugarcane breeding. Individual genotype selection is therefore restricted to the selected families. Previous studies have shown that family selection, rather than individual genotype selection, resulted in higher genetic gains for quantitative traits such as cane yield at the early stages of sugarcane breeding (Hogarth 1971; Cox et al. 1996; Kimbeng and Cox 2003; Stringer et al. 2011; Barbosa et al. 2012). Thus, the selected or elite families are expected to produce a large number of superior individual genotypes with high cane yield.

Prior to family selection, the proven cross system was used to evaluate and identify superior families (Skinner et al. 1987). The proven cross system defined superior families based on the proportions of seedlings and genotypes advanced to later stages of the selection programme as a statistic to determine the value of a family. The proven cross system has been extensively used in sugarcane breeding programmes (Heinz and Tew 1987; Skinner et al. 1987). As a result, the proven cross system was biased towards the old rather than the new crosses (Zhou 2009) because they would have higher advancement rates. Crosses with high germination rates were most likely to be repeatedly replanted in large numbers of seedlings with the expectation to generate more elite progenies. The drawback of the proven cross system was that it lacked statistical comparison among families. The proven cross system required a number of years to determine whether a cross was elite or not (Milligan and Legendre 1990; Kimbeng and Cox 2003). Crosses with high germination rates had higher advancement rates and would be considered elite at the expense of new crosses or crosses with fewer seedlings. The lack of statistics to compare crosses resulted in a lack of objectivity when determining elite families.

Family selection has been used in sugarcane breeding programmes in Australia (Hogarth et al. 1990; Cox and Hogarth 1993a, 1993b; Cox and Stringer 1998; Kimbeng et al. 2000, 2001a, 2001b; Stringer et al. 2011), India (Shanthi et al. 2008; Babu et al. 2009), Hawaii (Wu and Tew 1989), Cuba (Ortiz and Cabellero 1989), Brazil (Bressiani et al. 2005; De Resende and Barbosa 2006; Pedrozo et al. 2011), South Africa (Bond 1977, 1989; Zhou and Lichakane 2012; Zhou et al. 2013b; Zhou 2014, 2015), Indonesia (Sukarso 1986) and USA (Milligan and Legendre 1990; Chang and Milligan 1992a, 1992b). Family evaluation data has also been used to determine the best parent combinations at the time of crossing as well as to identify elite parents for future crosses (Chang and Milligan 1992a, 1992b;

Cox and Stringer 1998). The family data is effective in evaluating parent's performances in complex genome plants such as sugarcane (Stringer et al. 2011).

Despite the wide adoption of family selection, there is no established optimum family selection rate. To date, limited research has investigated the optimum family selection rate. In Australia, approximately 40% of tested families are selected as elite families (Kimbeng and Cox 2003). However, there has been no evidence on how this figure was determined. Considering the wide adoption of family evaluation and selection in sugarcane, there is a need to determine methods for estimating optimum family selection rates. Further, such research will determine if the optimum family selection rate is static across breeding populations as well as over time. The objectives of this study were to evaluate and identify elite families for cane yield, determine the optimum family selection rate and identify ideal trait combinations among the elite families.

4.3 MATERIALS AND METHODS

The experimental material, experimental design, seedling establishment and management, experimental sites and trial establishment, and data collection used for this study were the same as described in Chapter 3, sections 3.3.1 to 3.3.4.

4.3.1 Data analysis

Data were analysed using mixed procedure of Statistical Analysis System (SAS Institute 2014). The estimates of variance components, standard errors and probability tests were calculated using the COVTEST option of PROC MIXED. Best linear unbiased predictors (BLUP) analysis for the family effects used the linear model:

$$Y_{ijk} = \mu + R_i + F_j + G(FR)_{k(ij)} \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots..\text{Equation 4.1}$$

where Y_{ijk} = cane yield of the kth genotype recorded from j^{th} family in the ith replication, μ = grand mean, R_i = random effect of the ith replication, F_j = random effect of the family, $G(FR)_{k(ij)}$ = random effect of the kth genotype nested within the random interaction effect of the ith replication by the jth family and was also residual error. The degrees of freedom for the BLUP were estimated using Satterthwaite's procedure (Freund and Wilson 2003) and used to perform an appropriate t-test.

The following linear mixed model was used for family fixed effects analysis:

$$Y_{ijk} = \mu + R_i + F_j + RF_{ij} + G(FR)_{k(ij)} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\text{.Equation 4.2}$$

where Y_{ijk} = cane yield of the kth genotype recorded from j^{th} family in the ith replication, μ = grand mean, R_i = random effect of the ith replication, F_j = fixed effect of the jth family, FR_{ij} = random interaction effect of the ith replication by the jth family, $G(FR)_{k(ij)}$ = random effect of the kth genotype nested within the random interaction effect of the ith replication by the jth family and was also residual error.

After analysis, families were ranked using BLUP values from lowest (large negative values) to highest (large positive values). The ranked families were then divided into groups based on magnitudes of their P-values (Table 4.1).

Table 4.1 Summary of the BLUP P-values, family subgroups and their yield groups

BLUP values (negative or positive)	BLUP P-values	Family subgroups	Yield groups
Positive	$P<0.0001$	PP0001	Elite
Positive	$P<0.001$	PP001	Elite
Positive	$P<0.01$	PP01	Elite
Positive	$P<0.05$	PP05	Elite
Positive	$P>0.05$	PPNS	Average
Negative	$P>0.05$	PNNS	Average
Negative	$P<0.05$	PN05	Non-elite
Negative	$P<0.01$	PN01	Non-elite
Negative	$P<0.001$	PN001	Non-elite
Negative	$P<0.0001$	PN0001	Non-elite

Family groupings were done for each trial. The new data for each trial, created with these groupings, were subjected to analysis of variance using the following linear mixed model:

$$Y_{ijkl} = \mu + R_i + C_j + F(C)_{kj} + RF(C)_{ijk} + G(FR(C))_{ijkl}\ldots\ldots\ldots\ldots\ldots\ldots\ldots\text{.Equation 4.3}$$

where Y_{ijkl} = cane yield of the lth genotype in the ith replication of the kth family within the jth group, μ = grand mean, R_i = random effect of the ith replication, C_j = fixed effect of the jth group of families, $F(C)_{kj}$ = fixed effect of the kth family nested within the jth group, $RF(C)_{ijk}$ = random interaction effect of the ith replication by the kth family nested within the jth group and is the error term for testing the group effect, $G(FR\ (C))_{ijkl}$ = individual l^{th} genotype nested within the interaction effect of the ith replication by the jth family, which in turn is nested within the jth group and is also the residual error.

Selection gain (Gs) was estimated using the formula described by Allard (1960):

$$Gs = K\sigma_F H \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots \text{Equation 4.4}$$

where K = family selection intensity, σ_F = family phenotypic standard deviation and H = broad-sense heritability. The optimum selection rate was determined by estimating the selection gain, using family selection intensity (K) ranging from 1 to 100%, while the σ_F and H were kept constant.

4.4 RESULTS

4.4.1 Family fixed effects

The family effects F-values for BML10, BML11 and BML12 were very highly significant (P<0.0001) for cane yield (Table 4.2). SML11 and SML12 trials had highly significant (P≤0.001) family effects F-values, while that of SML10 was significant (P<0.05). The F-values for sandy soil trials increased from SML10 to SML12. Trials BML11 and BML12 had highly significant (P<0.0001) F-values for stalk number, while BML10 was non-significant (P>0.05). For sandy soil, SML11 and SML12 were very highly significant (P<0.0001) while SML10 was highly significant (P<0.001) for stalk number. The F-values for stalk number across all trials increased from SML10 to SML12 as well as from BML10 to BML12. The F-values for stalk height were very highly significant (P<0.0001) for both humic and sandy soil trials. The humic soil F-values increased from BML10 to BML12. Stalk diameter F-values were very highly significant (P<0.0001) for both humic and sandy soil trials. The F-values in humic soil trials increased from BML10 to BML12. Humic soil trials generally produced larger F-values compared to sandy soil trials for cane yield, stalk number, stalk height and stalk diameter. Generally stalk height had the highest R^2 values,

while stalk number had the lowest values. Cane yield had the highest CV% values while stalk diameter had the lowest CV% values.

Table 4.2 Family F-values, their P-values, coefficient of variation (CV) and coefficient of determination (R^2) for cane yield and yield components for the humic (BML) and sandy (SML) soil trial series planted in 2010, 2011 and 2012

Effect	BML10	BML11	BML12	SML10	SML11	SML12
Cane yield						
Family	F=3.13	F=2.41	F=3.94	F=1.38	F=1.66	F=1.88
	P<0.0001	P<0.0001	P<0.0001	P=0.0283	P=0.0010	P=0.0002
R^2	0.24	0.22	0.29	0.22	0.24	0.28
CV	66.55	57.27	42.27	62.09	44.89	41.17
Mean±stdev	6.55±4.36	9.16±5.24	15.11±6.39	6.11±3.79	9.31±4.17	14.77±6.08
Stalk number						
Family	F=0.39	F=2.75	F=4.35	F=1.68	F=2.38	F=3.06
	P=0.3473	P<0.0001	P<0.0001	P=0.0011	P<0.0001	P<0.0001
R^2	0.18	0.19	0.27	0.15	0.21	0.29
CV	52.22	40.88	34.97	48.54	31.91	31.59
Mean±stdev	12.35±6.45	24.90±10.18	25.16±8.80	13.34±6.47	26.06±8.31	27.53±8.71
Stalk height						
Family	F=2.39	F=2.47	F=2.65	F=1.97	F=2.73	F=2.31
	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001
R^2	0.40	0.37	0.31	0.44	0.35	0.28
CV	25.65	29.32	19.32	22.49	24.26	18.71
Mean±stdev	1.03±0.27	0.79±0.23	1.19±0.23	1.05±0.24	0.83±0.20	1.26±0.24
Stalk diameter						
Family	F=3.46	F=7.78	F=8.34	F=4.11	F=2.89	F=7.36
	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001
R^2	0.22	0.27	0.34	0.23	0.15	0.31
CV	10.38	10.38	11.57	10.22	13.09	11.72
Mean±stdev	2.46±0.26	2.39±0.25	2.52±0.29	2.27±0.23	2.29±0.30	2.31±0.27

4.4.2 Group fixed effects

Group fixed effects were highly significant (P<0.0001) across all trials for all traits (except for stalk diameter in SML10 was significant at P=0.0083) (Table 4.3). The group F-values for cane yield, stalk number and stalk diameter in sandy soil trials increased from SML10 to SML12. Stalk diameter F-values in humic soil trials increased from BML10 to BML12, while stalk number F-values in humic soil trials decreased from BML10 to BML12. Across all trials the family within group F-values for cane yield were not significant (P>0.05). The family within group F-values for stalk number for the humic soil trials were non-significant in BML10 (P=0.5387) but significant in BML11 (P=0.0014) and highly significant in BML12 (P<0.0001). Sandy soil trials showed a similar pattern where the family within group F-value for stalk number was non-significant in SML10 (P=0.6176) but significant in SML11 (P=0.0008) and highly significant in SML12 (P<0.0001) respectively. The family within group F-values for stalk number increased from BML10 to BML12 as well as from SML10 to SML12. The family within group F-values for stalk height for humic soil trials were non-significant in BML10 (P=0.6558) and BML11 (P=0.0895) but highly significant in BML12 (P<0.0001). For sandy soil, the family within group F-values were non-significant in SML10 (P=0.6281) but significant in SML11 (P=0.0098) and SML12 (P=0.0470). The family within group F-values for stalk height in humic soil trials increased from BML10 to BML12. The family within group F-values for stalk diameter was highly significant (P<0.0001) for both humic and sandy soil trials.

Generally, larger and significant F-values among groups were associated with lower and non-significant F-values for families within groups. This trend was conspicuous across all traits. Cane yield, with highly significant F-values, produced non-significant family within group F-values, while the yield components with lower F-values produced larger and highly significant family within group F-values.

Table 4.3 Group and F(Group) (family within group) F-values, their P-values, coefficient of variation (CV) and coefficient of determination (R^2) for cane yield and yield components for the humic (BML) and sandy (SML) soil trial series planted in 2010, 2011 and 2012

Effect	BML10	BML11	BML12	SML10	SML11	SML12
Cane yield						
Group	F=33.40	F=24.16	F=37.75	F = 14.69	F=18.34	F=20.49
	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001
F(Group)	F=0.15	F=0.54	F=0.64	F=0.30	F=0.56	F=0.31
	P=1.0000	P=0.9997	P=0.9929	P=1.0000	P=0.9997	P=1.0000
R^2	0.24	0.22	0.29	0.22	0.24	0.28
CV	66.55	57.27	42.27	62.09	44.89	41.17
Mean±stdev	6.55±4.36	9.16±5.24	15.11±6.39	6.11±3.79	9.31±4.17	14.77±6.08
Stalk number						
Group	F=32.83	F=15.18	F=13.28	F=11.58	F=12.17	F=13.63
	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001
F(Group)	F=0.98	F=1.64	F=3.32	F=0.95	F=1.68	F=2.09
	P=0.5387	P=0.0014	P<0.0001	P=0.6176	P=0.0008	P<0.0001
R^2	0.18	0.19	0.27	0.15	0.21	0.29
CV	52.22	40.88	34.97	48.54	31.91	31.59
Mean±stdev	12.35±6.45	24.90±10.18	25.16±8.80	13.34±6.47	26.06±8.31	27.53±8.71
Stalk height						
Group	F=16.71	F=16.83	F=12.33	F=13.39	F=20.19	F=13.82
	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001
F(Group)	F=0.93	F=1.25	F=1.90	F=0.94	F=1.47	F=1.35
	P=0.6558	P=0.0895	P<0.0001	P=0.6281	P=0.0098	P=0.0470
R^2	0.40	0.37	0.31	0.44	0.35	0.28
CV	25.65	29.32	19.32	22.49	24.26	18.71
Mean±stdev	1.03±0.27	0.79±0.23	1.19±0.23	1.05±0.24	0.83±0.20	1.26±0.24
Stalk diameter						
Group	F=6.33	F=8.58	F=13.26	F=2.59	F=4.78	F=14.91
	P<0.0001	P<0.0001	P<0.0001	P=0.0083	P<0.0001	P<0.0001
F(Group)	F=3.08	F=7.76	F=7.54	F=4.11	F=2.66	F=6.63
	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001	P<0.0001
R^2	0.22	0.27	0.34	0.23	0.15	0.31
CV	10.38	10.38	11.57	10.22	13.09	11.72
Mean±stdev	2.46±0.26	2.39±0.25	2.52±0.29	2.27±0.23	2.29±0.30	2.31±0.27

4.4.3 Least square means for family group effects

The levels of significant differences among the groups were investigated by least square means of the groups (Table 4.4). The elite group of families (PP0001, PP001, PP01 and PP05) produced significantly (P<0.05) higher cane yield compared to the non-elite (PN05, PN01, PN001 and PN0001) group of families in both humic (BML) and sandy (SML) soil trials. Trials BML10 and BML12 showed that PPNS produced significantly (P<0.05) higher cane yield than PNNS. A consistent decrease in cane yield was observed for the group of families from PP0001 to PN0001 (Figure 4.1). The mean cane yield increased from BML10 and SML10 (lowest cane yield trials) to BML12 and SML12 (the highest cane yield trials).

The elite group of families for trials BML10 and BML11 produced significantly (P<0.05) more stalks than the non-elite group of families. Trial BML10 produced significantly (P<0.05) more stalks for PPNS than PNNS. The stalk number decreased consistently from PP0001 to PN0001 (Figure 4.1). Trials BML10 and SML10 produced fewer stalks than BML11, BML12, SML11 and SML12.

Stalk height of the elite group of families was significantly (P<0.05) taller than for the non-elite group in all trials except for BML12. Stalk height decreased consistently from PP0001 to PN0001 across all trials (Figure 4.1). BML11 and SML11 produced the shortest stalks while BML12 and SML12 produced the tallest stalks.

The elite group of families produced significantly (P<0.05) thicker stalks than the non-elite group for both BML12 and SML12 trials. There was no consistent increase or decrease trend in values for stalk diameter from PP0001 to PN0001 families (Figure 4.1). BML trials produced thicker stalks than SML trials. The yield components that showed higher and significant F-values for family within group effects, such as stalk number and stalk diameter, also showed lower differences in trait values between elite and non-elite group of families.

Table 4.4 The least square means for family group effects for cane yield and its components in humic (BML) and sandy (SML) soil trials

Class	BML10	BML11	BML12	SML10	SML11	SML12
Cane yield						
PP0001	9.54a	12.96a	21.54a	9.28a	11.63a	19.53a
PP001	8.73ab	12.88a	19.00ab	8.14ab	10.83ab	18.10ab
PP01	8.36b	12.58a	17.24bc	7.73abc	10.56ab	17.81ab
PP05	7.82bc	10.92b	16.31c	7.49bc	10.36ab	16.84bc
PPNS	7.10c	9.95bc	15.92c	6.46cd	9.56bc	15.40cd
PNNS	5.67d	8.36cd	13.75d	5.47de	8.37cd	13.65de
PN05	4.79de	7.41de	13.40d	3.99ef	6.93de	12.12ef
PN01	4.54e	6.37e	12.24de	3.76f	6.86e	11.26f
PN001	3.81ef	6.06e	10.64ef	3.97ef	6.13de	10.09f
PN0001	3.25f	6.05e	9.90f	3.76f	5.70e	10.03f
Stalk number						
PP0001	15.37a	28.15abc	27.53b	18.34a	28.43a	29.21abcd
PP001	15.63a	30.48a	31.35a	13.18bcde	27.02ab	30.80ab
PP01	14.75a	29.35ab	27.80b	14.50bc	28.01ab	32.02a
PP05	12.57b	26.89bcd	25.75bcd	15.05b	26.53abc	29.91abc
PPNS	13.13b	26.24cd	26.41bc	13.72bcd	25.87abc	28.38bcd
PNNS	11.20c	24.39de	23.74d	12.59cdef	25.54bcd	27.13cd
PN05	10.92cd	22.56ef	25.06cd	11.01ef	24.09cde	26.85d
PN01	9.73de	19.32g	24.48cd	11.96def	22.57e	19.91e
PN001	9.22ef	21.34fg	20.04e	11.07ef	22.75de	20.33e
PN0001	8.43f	20.91fg	20.62e	10.92f	17.76f	21.92e
Stalk height						
PP0001	1.21ab	1.00ab	1.28b	1.24ab	0.99a	1.41a
PP001	1.21abc	0.91bc	1.39a	1.36a	0.95ab	1.33bc
PP01	1.10bc	1.02a	1.23bc	1.22bc	0.89bc	1.40ab
PP05	1.24a	0.90cd	1.19cd	1.17bc	0.89bc	1.27cd
PPNS	1.10cd	0.81de	1.19cd	1.09cd	0.83cd	1.26cd
PNNS	0.98de	0.75ef	1.16d	1.01de	0.77de	1.24de
PN05	0.85fg	0.71fg	1.17cd	0.84f	0.69ef	1.17ef
PN01	0.91ef	0.66g	1.15de	0.76f	0.67f	1.14f
PN001	0.87fg	0.64g	1.06f	0.88ef	0.78d	1.12f
PN0001	0.79g	0.78fg	1.09ef	0.81f	0.75def	1.15f

Table 4.4 Continued.

Stalk diameter

PP0001	2.51a	2.41bc	2.64a	2.24abcd	2.26bcd	2.45a
PP001	2.40d	2.44ab	2.53b	2.27abc	2.31abc	2.38b
PP01	2.50a	2.45a	2.53b	2.31a	2.27bcd	2.25b
PP05	2.47ab	2.39bc	2.57ab	2.28abc	2.33ab	2.38b
PPNS	2.48ab	2.41bc	2.54b	2.30ab	2.35a	2.35b
PNNS	2.48ab	2.38c	2.52bc	2.26abc	2.28abc	2.27c
PN05	2.46abc	2.38c	2.44cd	2.23bcd	2.27bcd	2.38c
PN01	2.45bcd	2.30d	2.37de	2.18d	2.25cd	2.47c
PN001	2.33e	2.30d	2.52bc	2.21cd	2.20d	2.21c
PN0001	2.40cd	2.27d	2.32e	2.23bcd	2.27bcd	2.21c

Values followed by different letters are significantly different at P<0.05

4.4.4 Principal component analysis

To visualise the performance of the group of families in the humic and sandy soil trials, the data for yield and yield components was subjected to principal components analysis (PCA). More than 90% of the variation in the data was explained by principal component 1 (PC1) and principal component 2 (PC2) (Figure 4.2). Only results from PC1 and PC2 were interpreted since they explained most of the variation in the data (Table 4.5). For all humic soil trials, cane yield, stalk number and stalk height contributed average values for PC1 biplot. For sandy soil trials (SML11 and SML12), cane yield, stalk number and stalk height contributed average values for PC1 while for SML10, only cane yield and stalk height contributed average values for PC1 biplot. PC2 was strongly and positively influenced by stalk diameter for all humic and sandy soil trials. In SML10, PC2 was strongly and negatively influenced by stalk number.
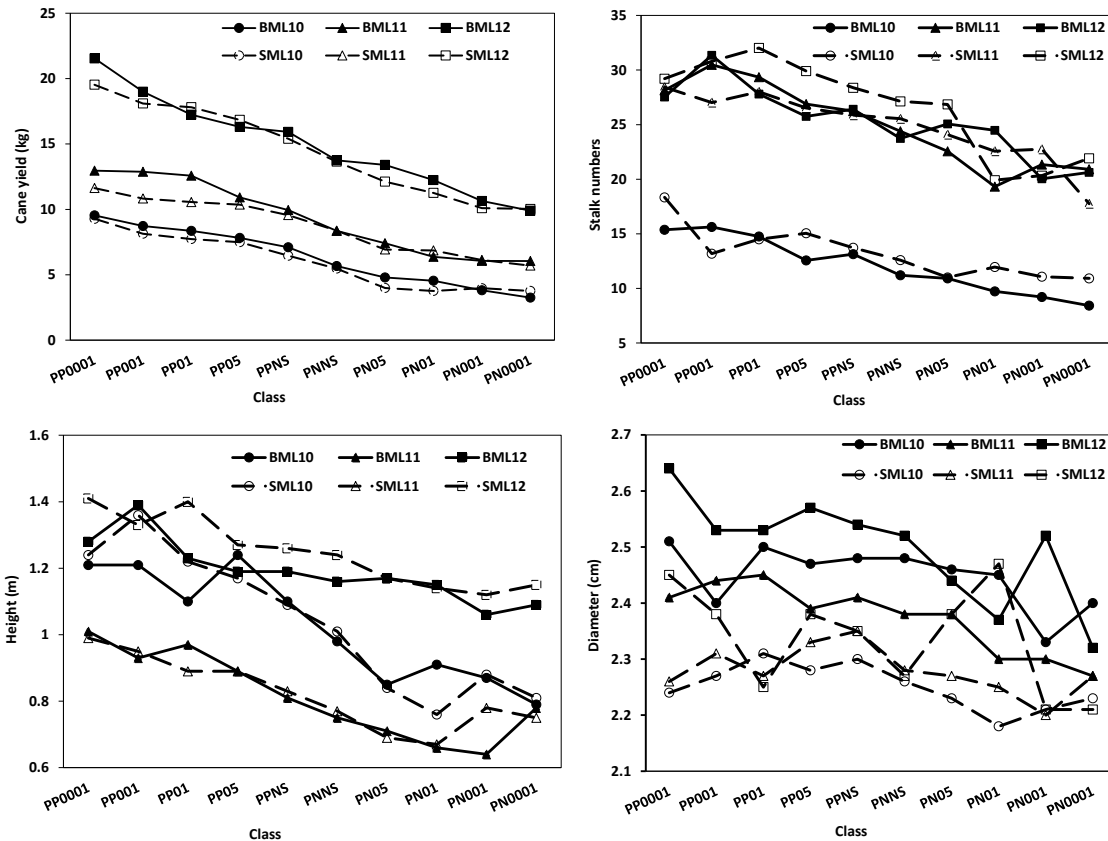
Figure 4.1 Trends in least square means for family group effects in humic (BML) and sandy (SML) soil trials

The plot of PC1 against PC2, distinguishes the 10 groups of families based on their potential traits (Figure 4.2). The PP0001, PP001, PP01, PP05 and PPNS were displayed on the positive side of PC1, indicating that these groups have high values for cane yield, stalk number and stalk height for populations planted in both humic and sandy soil trials. The PN05, PN01, PN001, PN0001 and PNNS were displayed on the negative side of PC1, indicating that these groups have low values of cane yield, stalk number and stalk height for population planted in both humic and sandy soil trials. Results indicated that PC1 could classify the 10 groups into two major groups namely; the elite (PP0001, PP001, PP01, PP05 and PPNS) and non-elite (PNNS, PN05, PN01, PN001 and PN0001) groups.
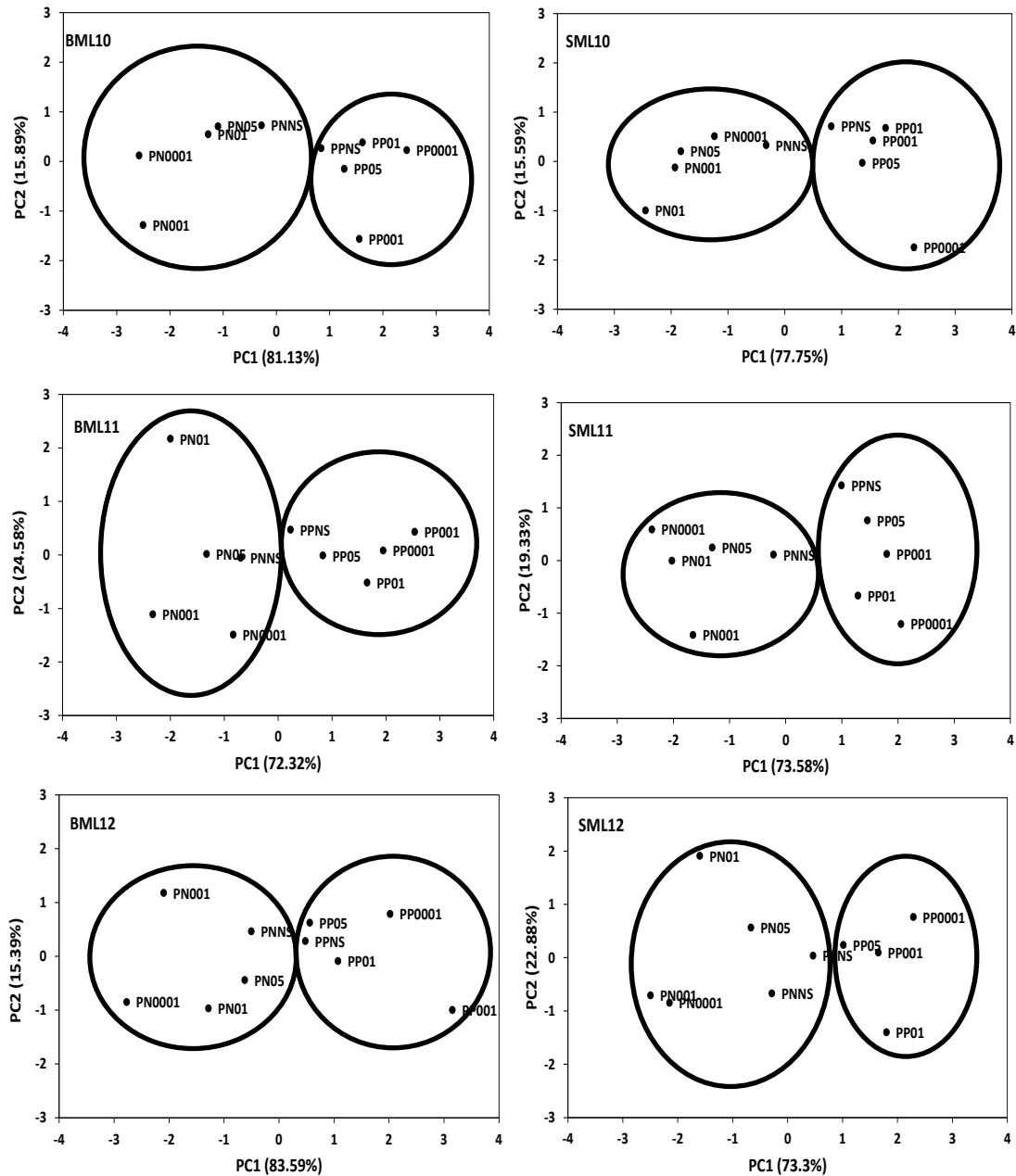
Figure 4.2 Biplot analysis for principal component 1 (PC1) on the x-axis plotted against and principal component 2 (PC2) on the y-axis for families grown in humic (BML) and sandy (SML) soil trials

The variation in PC2 was less than that in PC1 (Figure 4.2). PC1 values ranged from -4 to 4 while PC2 values ranged from -3 to 3. Two distinct clusters were observed in all trials. The cluster on the positive scale of PC1 was largely made up of family groups that produced higher cane yield, with higher stalk numbers and taller stalks. The cluster on the negative side of the PC1 scale was made up of groups of families that produced lower cane yield with fewer and shorter stalks. On the PC1 scale, the family groups were largely ranked

from highest to lowest yield, confirming that PC1 was an average of yield, stalk numbers and stalk height. Within clusters, on the PC2 scale, the variability was a factor of stalk diameter. High yielding genotypes can possess either thin or thick stalks, and the same was true for low yielding genotypes. PC2 was a positive factor of stalk diameter. Results indicated that elite and non-elite families could have either thin or thick stalks. The elite families in humic soil trials appeared to possess thicker stalks compared to those in sandy soil trails.

Table 4.5 Eigenvectors for principal component (PC) analysis

Traits	BML10				SML10			
	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4
Cane yield	0.55	-0.15	-0.10	-0.82	0.55	-0.22	-0.04	-0.80
Stalk number	0.53	-0.21	-0.67	0.48	0.48	-0.62	0.38	0.49
Stalk height	0.52	-0.29	0.73	0.32	0.52	0.20	-0.76	0.34
Stalk diameter	0.38	0.92	0.07	0.07	0.44	0.72	0.52	0.08
	BML11				SML11			
Cane yield	0.59	0.00	0.00	-0.81	0.58	-0.11	0.03	-0.81
Stalk number	0.57	-0.10	0.71	0.41	0.53	-0.21	-0.73	0.38
Stalk height	0.57	-0.09	-0.71	0.41	0.53	-0.25	0.68	0.44
Stalk diameter	0.11	0.99	0.00	0.08	0.33	0.94	0.02	0.11
	BML12				SML12			
Cane yield	0.55	-0.02	-0.13	-0.83	0.58	0.00	-0.22	-0.79
Stalk number	0.52	-0.32	0.75	0.24	0.54	-0.25	0.78	0.18
Stalk height	0.52	-0.32	-0.64	0.46	0.56	-0.17	-0.57	0.57
Stalk diameter	0.39	0.89	0.03	0.23	0.24	0.95	0.10	0.15

BML = Humic soil trials, SML = Sandy soil trials, PC1 = Principal component 1, PC2 = Principal component 2, PC3 = Principal component 3, PC4 = Principal component 4

4.4.5 Proportions of elite families and optimum selection rates

To determine the number of elite families, BLUP analysis was performed. The families that had significant (P<0.05) and positive BLUP values for cane yield were classified as elite families. A sample of BLUP values and their related statistics are presented in Table 4.6. As described by Zhou (2014) and Zhou and Mokwele (2015), BLUP refers to the estimates

of individual family value relative to the population mean. BLUP estimates can be positive or negative indicating that a family produced higher or smaller values than the grand mean, respectively. In this study families were classified into elite [with significant ($P<0.05$) positive BLUP values], average [with non-significant ($P>0.05$) negative or positive BLUP values], and non-elite [with significant ($P<0.05$) negative BLUP values] families.

Table 4.6 Sample output for family, best linear unbiased prediction (BLUP) of cane yield in relation to the grand mean, standard error (S.E.) of BLUP, t-statistics (t-stats), degrees of freedom (DF) and probability of a larger t-stats (P>t) of sugarcane families grown in humic soil trials (BML10)

Family	Female	Male	BLUP	S.E.	t-stats	DF	P>t
UU0038	98S0290	MO	-0.54	0.60	-0.89	176	0.3718
UU0049	98S0290	MP	1.98	0.55	3.62	176	0.0003
UU0113	99S1082	95H0130	0.48	0.58	0.84	176	0.4029
UU0134	97B0451	98S0590	1.51	0.58	2.61	176	0.0091
UU0135	95H0517	98S0590	0.19	0.58	0.33	176	0.7452
UU0137	00S1407	98S0113	-1.88	0.77	-2.43	176	0.0151
UU0140	98S0113	97B0272	2.29	0.58	3.95	176	<.0001
UU0141	96H0231	97B0272	1.77	0.58	3.06	176	0.0022
UU0142	98S0113	82H0397	-1.51	0.58	-2.61	176	0.0092
UU0199	97B0707	MO	1.25	0.58	2.16	176	0.0307
UU0227	99B1889	MO	-0.14	0.58	-0.25	176	0.8054
UU0273	96H0259	95H0039	3.13	0.58	5.40	176	<.0001
UU0277	98S0590	MO	0.95	0.58	1.65	176	0.0991
UU0280	97B0707	MO	0.72	0.58	1.25	176	0.2106
UU0283	99B1889	MO	-1.79	0.58	-3.07	176	0.0021
UU0309	95H0039	MP	-1.40	0.59	-2.36	176	0.0182

MO = Males only, MP = Melting pot

The proportions of families that produced significantly ($P<0.05$) higher BLUP values (elite families) were counted for all trials (Table 4.7). The number of elite families in BML (humic soil) trials were generally more than those in SML (sandy soil) trials. The number of elite families in each trial was divided by the total number of families in the trial to give

a percent value of elite families. The percent elite families in BML trials ranged from 18 to 29% and those in SML trials ranged from 12 to 23%.

Table 4.7 Proportion of elite families in the humic (BML10, BML11, BML12) and sandy (SML10, SML11, SML12) soil populations

Trial	Family	Elite families	%Elite
BML10	102	30	29.4
BML11	113	20	18.0
BML12	111	25	22.5
SML10	121	19	16.0
SML11	163	20	12.3
SML12	112	26	23.2
Total	722	140	19.4

To determine optimum family selection rate, the predicted family selection gain for each trial is plotted against family selection rates (Figures 4.3 and 4.4). The optimum selection rates varied with breeding programmes. Humic soil breeding programme trials had higher family selection rates compared to sandy soil breeding programme trials. In humic soil trials, the %Gs decreased rapidly with an increase in selection rate up to 30% (Figure 4.3). Beyond 30% (from 40 to 100%) selection rate, the %Gs decreased marginally suggesting that the likely family selection rate was around 30%. In sandy soil trials, the %Gs decreased rapidly with an increase in selection rate (Figure 4.4). Beyond 25% (from 30 to 100%) selection rate, the %Gs decreased marginally in all trials suggesting that the likely optimum family selection rate was around 25%.
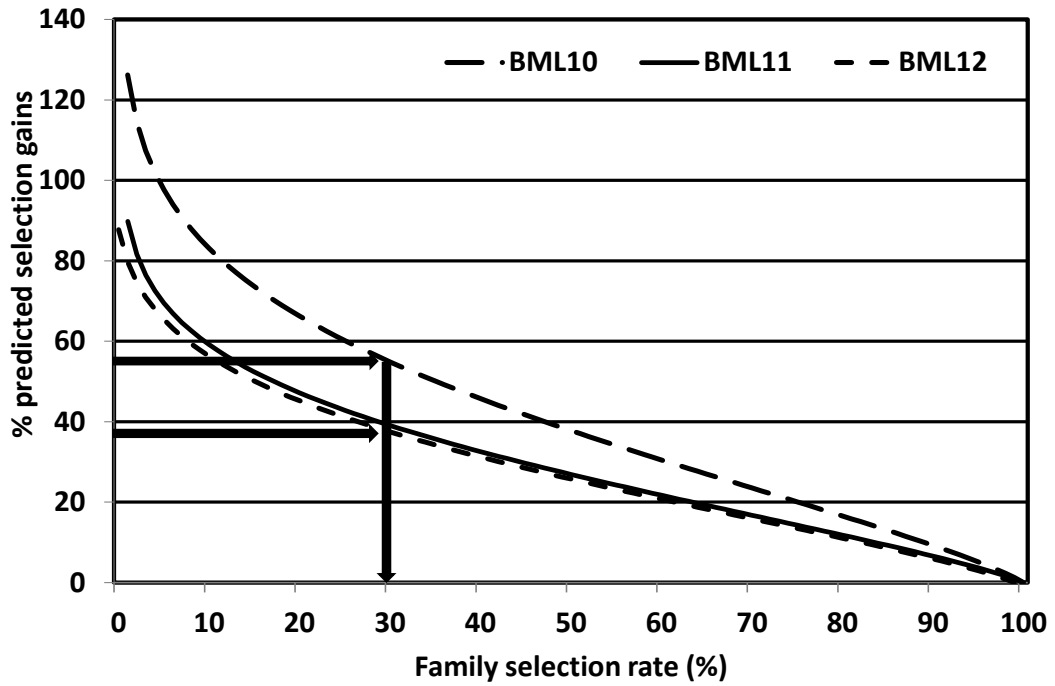
Figure 4.3 Predicted selection gain (%Gs) values plotted against family selection rates for cane yield in humic soil populations (BML10, BML11 and BML12)
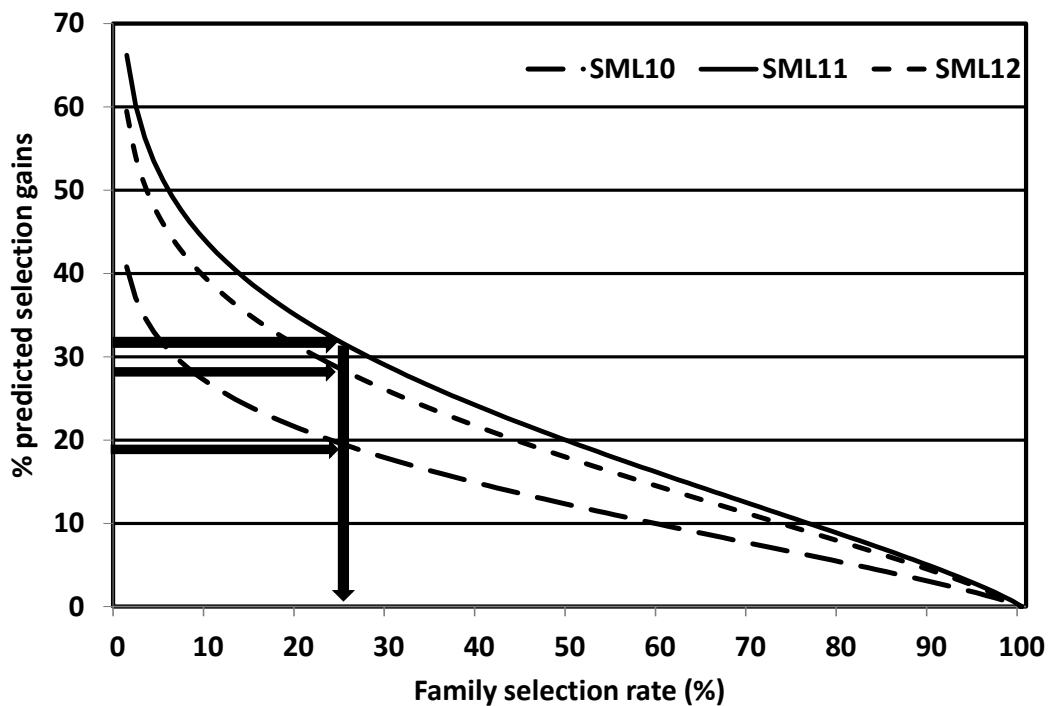
Figure 4.4 Predicted selection gain (%Gs) values plotted against family selection rates for cane yield in sandy soil populations (SML10, SML11 and SML12)

4.5 DISCUSSION

The significant family effects F-values for all traits in all trials indicated that selection for families with superior trait values would be effective in both the humic and sandy soil breeding programmes. The effectiveness of family selection in sugarcane breeding has been demonstrated in several studies (Cox and Hogarth 1993b; Cox and Stringer 1998; Kimbeng et al. 2000, 2001a, 2001b; Stringer et al. 2011). The higher F-values observed for humic soil populations compared to sandy soil populations highlighted the differences between the populations. Results indicated a greater potential for identifying superior families that possess high cane yield in humic soil trials compared to sandy soil trials. Humic soil are more uniform and deeper, with higher organic matter and clay content than sandy soil. The higher F-values observed for the humic soil populations could also be explained by the origin of the populations and cycles of recurrent breeding and selection. The humic soil breeding programme was established in the 1970s while the sandy soil breeding programme was established in 1997 (Nuss 1998). Therefore, the humic soil populations have benefited from 47 years of recurrent breeding and selection compared to just 19 years for the sandy soil breeding and selection programme. Further, the sandy soil breeding populations originated from the humic soil breeding programme and is currently in the stage of screening and development to produce adapted populations. Therefore, the lower F-values highlight the presence of a significant proportion of genetic background that is not adapted to sandy soil conditions. Further cycles of breeding and selection are expected to increase the adaptability of the sandy soil breeding populations and increase genetic variability of traits.

The highly significant group effects indicated that families could be categorised according to trait values. Results suggested that families could be categorised into groups ranging from superior trait values to those with inferior trait values. The grouping also highlights the potential to identify and select elite families as well as identify and discard inferior families. The objective of family selection is to identify elite families from where individual genotype selection will be focused (Cox and Hogarth 1993b; Kimbeng and Cox 2003; Melo et al. 2011). The group effects F-values were largest for cane yield and lower for the yield components. This suggested that selection of elite families would be more effective when selection is directly applied for cane yield rather than the individual yield components. This result is particularly significant because it highlights why in Australia (Kimbeng et al. 2000;

71

Kimbeng and Cox 2003) family selection, based on harvesting whole plots of families using automatic weighing machines (Hogarth and Mullins 1989), has been effective. However, use of automatic weighing machines may be expensive and unaffordable for smaller breeding programmes where such an investment in equipment is considered uneconomical (Stringer et al. 2011; Zhou 2014). Therefore, estimating cane yield through yield components remains the most viable and practical approach for smaller and resource limited breeding programmes. Further studies on logistic regression models by Zhou et al. (2013a) suggested that selection for yield, through its components may be more efficient and research to evaluate families through yield components using logistic regression models is needed.

Results showed that for traits, where F-values for groups were large and highly significant, the families within groups were largely non-significant; indicating that family groups were created by combining families with similar mean values. For cane yield, family within group was non-significant across all trials suggesting that the majority of the variability was among the groups and not families within groups. The opposite was true for the yield components were families within group differences were significant. These differences were highly significant across all trials for stalk diameter. These observations have significant implications for family selection and individual genotype selection among the selected families. Firstly, the main objective is to identify superior families for cane yield, which can be done with high precision because of highly significant group F-values for cane yield. The second objective would be to select for elite families that possess desirable combinations of yield components. The second level of family selection can be achieved by utilising the knowledge of path coefficient analysis (Kang et al. 1989; De Sousa-Vieira and Milligan 1999, 2005).

Research in sugarcane has shown that the largest contributor to cane yield is stalk number (Singh and Sharma 1997; Zhou 2004; Kumar and Singh 2005). Therefore, families with a high stalk population are likely more superior to those with lower stalk populations particularly in subtropical regions of countries such as South Africa (Zhou and Shoko 2012). Stalk population has been found important for adaptability and ratooning ability particularly in subtropical breeding programmes such as for South Africa (Zhou and Shoko 2012) and USA (Milligan et al. 1996). Further selection should be done among those families with high stalk populations and genotypes with generally taller stalks. Finally,

families with numerous and taller stalks should be screened for stalk diameter. Stalk diameter had the largest F-values for families within groups suggesting that the superior families could possess a wide range of stalk thickness. The combination of yield components can be decided based on path coefficient studies and prior knowledge of combinations that impact greater yield and adaptability in a breeding programme.

The least square mean values showed high discrimination among the groups for cane yield suggesting that identification of high yielding families would be accurate. Families with cane yields higher than the population mean produced significantly higher cane yields compared to those that produced cane yields below the population mean. This suggests that lower yielding families could be eliminated more accurately with low risk of discarding elite families and progenies. While stalk population and stalk height values decreased from high cane yielding to low cane yielding families, the decline was less consistent and in some populations the decrease was gradual. This indicates variability for stalk populations and stalk height within families and provides the opportunity to select the best combinations within elite families. Stalk diameter showed a slight decrease from high cane yielding to low cane yielding families indicating that stalk diameter was well distributed within each group of families. Therefore, families can be selected for stalk diameter only if they possess high yielding traits. Results highlighted that within groups of families, particularly elite families, different trait combinations exist for exploitation during family selection.

Stalk height produced the highest R^2 values compared to other traits which suggested that the statistical model used accounted for the majority of variability of the data for stalk height. Probably, environmental variables had larger influences on cane yield, stalk number and stalk diameter than stalk height. Stalk diameter, followed by stalk height, had the lowest CV% while cane yield had the highest CV%, suggesting larger variability in the data for cane yield compared to the yield components. The variability in data obtained from the yield components could cumulatively contribute to the larger CV% and variability of cane yield data.

Elite families, defined as families that produce significantly higher cane yields than the population mean, generally produce higher cane yield, higher stalk populations and taller stalks compared to the non-elite families. The trend was consistent across all trials suggesting that high trait values for cane yield, stalk population and stalk height were

required for elite families. However, with stalk diameter, it appears that the elite and non-elite families could have similar stalk diameter values. This result, suggesting that stalk diameter was less important in determining cane yield, was also reported in path coefficient analysis studies (James 1971; Kang et al. 1989; Zhou 2004; Chaudhary and Joshi 2005; Tyagi et al. 2012). Results may further indicate that after identifying elite families, focus should be on families that possess high stalk populations and taller stalks; traits that are also known from path coefficient analysis that contribute to cane yield.

Results from PCA showed that cane yield, stalk number and stalk height contributed positively to PC1 indicating that differentiating between elite and non-elite families was largely from these yield components. Elite families were characterised by high cane yield, high stalk population and taller stalks, while the opposite was true for non-elite families. PC2 was a factor positive for stalk diameter indicating that, within the groups of families, variability for stalk diameter was large. The PCA showed that either thin or thick stalks were present among elite and non-elite families. The differences among elite families between humic and sandy soil populations could be defined by stalk diameter. Elite humic soil families were more likely to possess thicker stalks, while sandy soil populations were likely to have thinner stalks; a potential adaptation difference to the growing conditions. Humic soil growing conditions are more favourable with less moisture and nutrient stress, while sandy soil are more prone to water and nutrient stress. The result suggests that thin stalks impart hardiness and adaptability to harsher growing conditions compared to thick stalks. Results validate why N31, a thin and tall stalk population variety, has shown superior adaptability to sandy soil conditions compared to N48, which is a thick stalked variety that is more adapted to humic soil conditions. This knowledge is particularly important to guide future selection in sandy soil trials.

The PCA graphics indicated the large variability for cane yield and yield components among the group of families in the Midlands breeding programmes. The PCA graphics further visually emphasised that the positioning and adaptability of the group of families across field trials were discriminated by stalk diameter. Results further indicated that, among the group of families that produced significantly high cane yield than the population mean, there was a group of families that is characterised by thin stalks. Therefore, in order to increase cane yield, focus should be put on improving stalk number and stalk height because stalk diameter does not influence cane yield production. Results are in conformity

with the findings from the studies carried out in Lousiana (Gravois et al. 1991; Milligan et al. 1996). Groups of families (clustered for high mean values) which are on the positive scale of PC1 could be used to improve the sugarcane yield components through breeding and selection.

The humic soil populations produced a 36.3% higher proportion of elite families than the sandy soil populations suggesting the superiority of humic soil populations. The humic soil breeding programme has been in existence for 47 years while the sandy soil breeding programme was established 19 years ago (Nuss 1998). The longer cycles of breeding and selection for the humic soil populations have resulted in better genetic background and better accumulation of additive genes for yield compared to the sandy soil populations. Further, when the sandy soil breeding programme was established, there was no suitable source of parental material to initiate the breeding programme. Consequently parents for the breeding programme were derived mainly from the humic soil and other SASRI breeding programmes. Most of these were less adapted and are still being developed for suitability. In the Midlands region, sugarcane is grown for 24 months to maturity and therefore, fewer cycles of breeding and selection are realised in a short period of time, further impacting the recurrent selection benefits for the sandy soil programme. Results also suggest that with the adoption of family evaluation and selection in Midlands breeding programmes, higher selection gains will be achieved. A study by Zhou and Gwata (2016) showed higher genotype genetic gains for cane yield in humic soil programmes compared to sandy soil programmes, indicating that higher proportions of elite families would translate to higher genetic gains at genotype release.

The optimum selection rates were 30% for humic soil populations and less than 25% for the sandy soil populations. Results suggest that optimum family selection rates are different between populations and certainly variable across breeding programmes. The variability in optimum family selection rates could be caused by the quality of the populations, where breeding programmes with a long history are likely to have higher proportions of optimum family selection rates compared to those just starting, as in the case for the humic and sandy soil breeding programmes. Results are different from the optimum family selection rates reported in Australia (Kimbeng and Cox 2003) of around 40%. The modelled optimum family selection rates were higher than the estimates proportions of elite families in the populations.

The proportions of elite families were determined from families which produced significantly higher cane yields than the population mean. The optimum selection rate was estimated using predicted selection gains which take into account within family variability, and the ability to identify families. Families may have lower means but have larger within family variability and therefore they possess high segregation for traits and are more ideal for selection of elite genotypes. Humic soil populations had a higher optimum selection rate and proportions of elite families than sandy soil populations suggesting that both values are indicative of the quality of the population, and the potential of breeding populations to possess high value families.

4.6 CONCLUSIONS

The highly significant family effects F-values indicated the potential effectiveness of family selection. Results further indicated the potential to identify and select elite families as well as to identify and discard non-elite families. The highly significant group effects F-values indicated families could be categorised according to trait values. From the principal component analysis, it is clear that number of stalks and stalk height contributed most to cane yield. Therefore, stalk number and stalk height are important traits to consider when selecting and evaluating families for sugarcane yield. Stalk diameter varied widely within both elite and non-elite families. The humic soil populations produced a higher proportion of elite families and had a higher optimum selection rate compared to the sandy soil populations. Results indicated that humic soil populations had a greater potential in increasing gains for cane yield through family selection.

4.7 REFERENCES

Allard RW (1960) Principles of plant breeding. New York, John Wiley and Sons. pp. 414

Babu CK, Koodalingam US Natarajan RM, Shanthi, Govindaraj P (2009) Interrelationships of sugarcane yield and quality components and their utility in family selection. Madras Agricultural Journal 96:309-313

Barbosa MHP, Resende MDV, Dias LAS, Barbosa GVS (2012) Genetic improvement of sugar sugarcane for bioenergy: The Brazilian experience in network research with RIDESA. Crop Breeding and Applied Biotechnology 12:87-98

Bond RS (1977) The mean of yield seedlings as a guide to the selection potential of sugarcane crosses. Proceedings of the International Society of Sugar Cane Technologists 16:101-110

Bond RS (1989) Observations on family selection in the Mount Edgecombe sugarcane breeding programme. Proceedings of the South African Sugar Technologists' Association 63:132-135

Bressiani JA, Vencovsky R, Burnquist WL (2005) Modified family selection in sugarcane. Proceedings of the International Society of Sugar Cane Technologists 25:459-467

Chang YS, Milligan SB (1992a) Estimating the potential of sugarcane families to produce elite genotypes using bivariate prediction methods. Theoretical and Applied Genetics 84:633-639

Chang YS, Milligan SB (1992b) Estimating the potential of sugarcane families to produce elite genotypes using univariate cross prediction methods. Theoretical and Applied Genetics 84:662-671

Chaudhary RR, Joshi BK (2005) Correlation and path coefficient analysis in sugarcane. Nepal Agricultural Research Journal 6:24-27

Cox MC, Hogarth DM (1993a) Progress and changes in the South Queensland variety development program. Proceedings of the International Society of Sugar Cane Technologists 15:251-255

Cox MC, Hogarth DM (1993b) The effectiveness of family selection in early stages of a sugarcane improvement program. In: Imrie BC, Hacker JB (eds), Focused plant improvement: Towards responsible and sustainable agriculture. Proceedings of the Tenth Australian Plant Breeding Conference. pp. 53-54

Cox MC, McRae TA, Bull JK, Hogarth DM (1996) Family selection improves the efficiency and the effectiveness of a sugarcane improvement program. In: Wilson JR, Hogarth DM, Campbell JA, Garside AL (eds), Sugarcane: Research towards Efficiency and Sustainable Production. CSIRO division. Tropical Crops and Pastures, Brisbane. pp. 42-43

Cox MC, Stringer JK (1998) Efficacy of early generation selection in a sugarcane improvement program. Proceedings of the Australian Society of Sugar Cane Technologists 20:148-153

De Resende MDV, Barbosa MHP (2006) Selection via simulated individual BLUP based on family genotypic effects in sugarcane. Pesquisa Agropecuária Brasileira, Brasilia 41:421-429

De Sousa-Vieira O, Milligan SB (1999) Intra-row spacing and family x environment effects on sugarcane family evaluation. Crop Science 39:358-364

De Sousa-Vieira O, Milligan SB (2005) Interrelationships of cane yield components and their utility in sugarcane family selection: Path coefficient analysis. Interciencia 30:93-96

Freund RJ, Wilson WJ (2003) Statistical methods. New York Academic Press 22:3-1187

Gravois KA, Milligan SB, Martin FA (1991) Indirect selection for increased sucrose yield in early sugarcane testing stages. Field Crops Research 26:67-73

Heinz DJ, Tew TL (1987) Hybridization procedures. In: Heinz DJ (ed), Developments in Crop Science 11: Sugarcane improvement through breeding. Elsevier, New York. pp. 313-342

Hogarth DM (1971) Quantitative inheritance studies in sugarcane II. Correlations and Predicted response to selection. Australian Journal of Agricultural Research 22:103-109

Hogarth DM, Braithwaite MJ, Skinner TC (1990) Selection of sugarcane families in the Burdekin district. Proceedings of the Australian Society of Sugar Cane Technologists 12:99-104

Hogarth DM, Mullins RT (1989) Changes in the BSES plant improvement programme. Proceedings of the International Society of Sugar Cane Technologists 20:956-961

James NI (1971) Yield components in random and selected sugarcane populations. Crop Science 11:906-908

Kang MS, Sosa O, Miller JD (1989) Path analysis for percent fiber, and cane and sugar yield in sugarcane. Crop Science 29:1481-1483

Kimbeng CA, Cox MC (2003) Early generation selection of sugarcane families and clones in Australia: A review. Journal of the American Society of Sugar Cane Technologists 23:20-39

Kimbeng CA, Froyland D, Appo D, Corcoran A, Hetherington M (2001a) An appraisal of early generation selection in central Queensland sugarcane improvement program. Proceedings of the International Society of Sugar Cane Technologists 23:129-135

Kimbeng CA, McRae TA, Cox MC (2001b) Optimising early generation selection in sugarcane breeding. Proceedings of the International Society of Sugar Cane Technologists 24:488-493

Kimbeng CA, McRae TA, Stringer JK (2000) Gains from family and visual selection in sugarcane, particularly for heavily lodged crops in the Burdekin region. Proceedings of the Australia Society of Sugar Cane Technologists 22:163-169

Kumar N, Singh JRP (2005) Path analysis in sugarcane under different environmental conditions. Indian Sugar 55:57-60

Melo DS, Pinto CABP, Peixouto LS, Neder DG, de Assis JC (2011) Early selection of full-sib potato families. Ciência e Agrotecnologia 35:1101-1109

Milligan SB, Legendre BL (1990) Development of a practical method for sugarcane cross appraisal. Journal of the American Society of Sugar Cane Technologists 11:59-68

Milligan SB, Martin FA, Gravois KA (1996) Inheritance of sugarcane ratooning ability and the relationship of younger crop traits to older crop traits. Crop Science 36:45-60

Nuss KJ (1998) Aspects considered in the search for new farms for the Experiment Station. Proceedings of the South African Sugarcane Technologists' Association 72:42-45

Ortiz R, Caballero A (1989) Effectiveness of early sugarcane selection procedures in Cuba. Proceeding of the International Society of Sugar Cane Technologists 20:932-937

Pedrozo CA, Barbosa MHP, da Silva FL, de Resende MDV, Peternelli LA (2011) Repeatability of full-sib sugarcane families across harvests and the efficiency of early selection. Euphytica 182:423-430

SAS Institute (2014) SAS/STAT user's guide, version 9.1.3. Cary, NC: SAS Institute

Shanthi RM, Bhagyalakshmi KV, Hemaprabha G, Alarmelu S, Nagarajan R (2008) Relative performance of the sugarcane families in early selection stages. Sugar Tech 10:114-118

Singh P, Sharma ML (1997) Cause and effect of relationship in clonal population of sugarcane. Seventh All India Congress of Cytology and Genetics. pp. 25-32

Skinner JC, Hogarth DM, Wu KK (1987) Selection methods, criteria, and indices. In: Heinz DJ (ed), Sugarcane improvement through breeding. Elsevier, Amsterdam, Netherlands. pp. 409-453

Stringer JK, Cox MC, Atkin FC, Wei X, Hogarth DM (2011) Family selection improves the efficiency and effectiveness of selecting original seedlings and parents. Sugar Tech 13:36-41

Sukarso G (1986) Assessment of family selection in original seedlings of sugarcane at Pasuruan. Proceedings of the International Society of Sugar Cane Technologists 19:440-446

Tyagi VK, Sharma S, Bhardwaj SB (2012) Pattern of association among cane yield, sugar yield and their components in sugarcane (*Saccharum officinarum* L.). Journal of Agricultural Research 50:29-38

Wu KK, Tew TL (1989) Evaluation of sugarcane crosses by family yields. Proceedings of the International Society of Sugar Cane Technologists 20:926-931

Zhou MM (2004) Breeding stalk population control of yield, quality and agronomic traits of sugarcane population in early selection stages. International Sugar Journal 22:20-26

Zhou MM (2009) Statistical methods and models for analysing sugarcane (*Saccharum* species hybrids) plant breeding data. Dissertation. Louisiana State University and Agricultural and Mechanical College. pp. 199

Zhou MM (2014) Family evaluation for sugarcane yield using data estimated from stalk number, height and diameter. Journal of Crop Improvement 28:406-417

Zhou M (2015) Selection for *Eldana saccharina* borer resistance in early stages of sugarcane breeding in South Africa. American Journal of Plant Sciences 6:2168-2176

Zhou MM, Gwata ET (2016) Quantifying sugarcane cultivar genetic gains in the Midlands region of South Africa. Agronomy Journal 108:342-348

Zhou MM, Kimbeng CA, Tew TL, Gravois KA, Pontif M, Bischoff KP (2013a) Logistic regression models to aid selection in early stages of sugarcane breeding. Sugar Tech 16:150-156

Zhou MM, Lichakane ML (2012) Family selection gains for quality traits among South African sugarcane breeding populations. South African Journal of Plant and Soil 29:143-149

Zhou MM, Lichakane ML, Joshi SV (2013b) Family evaluation for quality traits in South African sugarcane breeding programmes. International Sugar Journal 115:418-430

Zhou MM, Mokwele A (2015) Family versus individual plant selection for stem borer (*Eldana saccharina*) resistance in early stages of sugarcane breeding in South Africa. South African Journal of Plant and Soil 33:89-96

Zhou MM, Shoko MD (2012) Simultaneous selection for yield and ratooning ability in sugarcane genotypes using analysis of covariance. South African Journal of Plant and Soil 29:93-100

CHAPTER 5

DETERMINING ELITE PARENTS FOR SUGARCANE YIELD USING FAMILY SELECTION DATA

5.1 ABSTRACT

The success of a sugarcane breeding programme can be determined by the choice of parents, crosses made and progeny testing. The objectives of this study were to use best linear unbiased prediction (BLUP) to identify superior parents from family data and to determine the proportion of superior parents within populations in the Midlands breeding programmes. Data on stalk number, height and diameter, collected from 20 seedling progenies per plot in each of the three replications per family, were used to estimate cane yield. Family data was analysed using Statistical Analysis System (SAS) mixed models to estimate the breeding values of parents. Significant (P<0.05) female and male variances indicated that the large variability observed among progenies could be attributed to the variability among parents. Using BLUP estimates, female (82H0397, 96H0259, 98B0460, 98S0290, 98H0590, 98S1362 and N52) and male (02S0639, 82H0397, 97B0272, 98B0460, 98B1889 and N52) parents have been identified that produced progenies with significantly (P<0.05) higher cane yield in humic and sandy soil populations. The identified parents potentially are elite parents that could be used in building a core germplasm pool of genotypes that produce elite progenies. Humic soil populations contained a higher proportion of elite parents compared to the sandy soil populations; probably due to longer cycles of recurrent breeding and selection. Results have highlighted the deficiency in basing parent selection on breeding values instead of mid-parent values because the majority of parents with high mid-parent values produced progenies with significantly lower yield. The proportion of elite parents was low at 20% (females) and 10.6% (males) for humic soil populations and 12.7% (females) and 9.8% (males) for sandy soil populations. This suggested that intensive parent evaluation and development is required for these populations.

Keywords: Best linear unbiased prediction, sugarcane yield, parents, progenies

5.2 INTRODUCTION

Selection of parents forms the foundation of all breeding programmes. The parent combinations made at the time of crossing ultimately determines the quality of progeny produced when crosses are planted in the field (Chang and Milligan 1992a, 1992b; Stringer et al. 1996; Cox 1996; Cox and Stringer 1998; Balzarini 2000). Therefore, parent evaluation is critical in any plant breeding programme. Crossing with elite parents is expected to increase genetic gains in populations over time because of a higher accumulation of additive genes (Stringer et al. 2011; Zhou 2015). In sugarcane breeding, crossing with parents known to produce progenies with high trait values is very important because genetic recombination and segregation occurs only at crossing (Skinner et al. 1987; Barbosa et al. 2001; Kimbeng and Cox 2003). Thereafter, subsequent stages are planted from vegetative material with no further recombination.

In the early years of sugarcane breeding, the proven cross and proven parent systems were used to identify genotypes to be used in crosses (Heinz and Tew 1987). The proven cross system depends on the number of genotypes that is being advanced from a cross as well as the stage of advancement reached by individual genotypes. Crosses, from which large numbers of individuals are advanced, are considered elite families. Parents used to generate the elite crosses are then considered elite parents. The elite crosses are repeated more frequently, in the hope of generating more elite progenies. As a result, the elite parents are used more frequently in crosses resulting in an increased bias towards crosses and parents designated as elite, with little attention given to new crosses with limited advancement data. This bias eventually leads to potentially narrowing genetic diversity of parent and progeny populations.

The first disadvantage of the proven cross and proven parent system was that crosses with higher germination rates, and therefore larger number of seedlings planted, were likely to be declared elite crosses. Their parents were also likely to be declared elite. Crosses and parents with lower germination rates had a lower likelihood of being classified as elite crosses and elite parents because fewer of their progenies were advanced to later stages. The second disadvantage was associated with the lack of a statistic to compare performances among crosses and parents when determining whether a cross or a parent was elite (Zhou 2009). Numbers of advanced genotypes from different germination rates were

the only data available for classifying crosses and parents. This major weakness meant that a cross could be classified as elite in one year but later as non-elite. The third disadvantage was associated with the length of time taken to determine whether crosses or parents were elite. Considering that sugarcane is a perennial plant, it takes at least 12 to 24 months in South Africa from planting to harvest of a trial. Advancements from Stage I to V can take at least 10 to 24 years before the quality of crosses and parents could be determined. Therefore, the long period means that breeders will go for long periods without knowing if their parent selection and cross combinations are producing desirable populations (Milligan and Legendre 1990; Kimbeng and Cox 2003).

Considering that the purpose of cross- and parent evaluation is to advise on cross combinations, lengthy periods (before sufficient data is available to quantify the quality of crosses and parents) meant lengthy delays in improving cross combinations and parents. In addition, breeders are required to build up a collection of superior parents that would contribute to the gene pool for future breeding programmes. Such a collection of superior parents will change when new, high quality parents replace the old and less desirable parents. With the proven cross system, it would be difficult (and sometimes take lengthy periods) to shift the genetic potential of parents because more crosses could be made with elite parents at the expense of testing new parents. This creates a bias that is self-perpetuating.

At SASRI, parents are currently chosen based on the proven parent system as well as genetic values. Family data has been collected in the last four years and will eventually replace the proven cross and parent system in evaluating and identifying superior parents for use in future crosses. The use of family data, to evaluate parents, is expected to provide better comparisons among parents and continuous evaluation of old and new parents used in crosses. Therefore, the objectives of this study were to use best linear unbiased prediction (BLUP) to identify superior parents using family data from six Stage I trials and to determine the proportions of superior parents within these populations.

5.3 MATERIALS AND METHODS

The experimental material, experimental design, seedling establishment and management, experimental sites and trial establishment, and data collection used for this study were the same as described in Chapter 3, sections 3.3.1 to 3.3.4.

5.3.1 Data analysis

Data were analysed using mixed procedure of Statistical Analysis System (SAS Institute 2014). The estimates of variance components, standard errors and probability tests were calculated using the COVTEST option of PROC MIXED. BLUP analysis for the parental effects was done using the linear model:

$$Y_{ijkl} = \mu + R_i + F_j + M_k + G(FRM)_{l(ijk)} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots..\text{Equation 5.1}$$

where Y_{ijkl} = cane yield of the lth genotype in the ith replication of the jth female and k^{th} male parent random effects, μ = grand mean, R_i = random effect of the ith 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 ith replication by the jth female parent by the kth 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.

The female and male parents in each trial were grouped based on BLUP values. After analysis, the parents were ranked using BLUP values from lowest (large negative values) to highest (large positive values). The ranked parents were then divided into groups based on magnitudes of their P-values. Parents were grouped into elite, average, and non-elite cane yield groups. The data from these groups were subjected to analysis of variance using the following linear mixed model:

$$Y_{ijklm} = \mu + R_i + C_j + F(C)_{k(j)} + M(C)_{l(j)} + G(FRM\ (C))_{m(ijkl)} \ldots\ldots\ldots\ldots\ldots...\text{Equation 5.2}$$

where Y_{ijklm} = cane yield of the mth genotype in the ith replication of the kth female and l^{th} male parent within the jth group, μ = grand mean, R_i = random effect of the ith replication, C_j = fixed effect of the jth group of parents, $F(C)_{k(j)}$ = random effect of the kth female parent nested within the jth group, $M(C)_{l(j)}$ = random effect of the lth male parent nested with j^{th} group, $G(FRM\ (C))m_{(ijkl)}$ = individual m^{th} genotype nested within the interaction effect of the ith replication by the kth female parent by the lth male parent, which in turn is nested within the jth group and is also the residual error.

The proportions of superior parents were determined based on the BLUP values with their probability levels. Parents with positive BLUP values at P<0.05 were considered as elite parents while parents with negative BLUP values at P<0.05 were considered as poor parents for cane yield.

5.4 RESULTS

The female variance effects were highly significant (P<0.001) in BML10, BML11, BML12, SML11 and significant (P<0.01) in SML10 and SML12 (Table 5.1). The male variance effects were highly significant (P<0.001) in SML12, significant at P<0.01 in BML11 and BML12 and significant at P<0.05 in BML10, SML10 and SML11. The female effects produced in most cases larger variances and smaller standard error (SE) compared to the male effects. The residual error variance effects were highly significant (P<0.001) for all trials and were larger than both female and male variance effects across all trials.

Table 5.1 Covariate parameter estimates for female and male effect, residual error and their standard error (S.E.) for the humic (BML) and sandy (SML) soil breeding programmes

Trial	Female	Male	Residual
	Estimate ± S.E.	*Estimate ± S.E.*	*Estimate ± S.E.*
BML10	1.80±0.52***	1.12±0.52*	21.32±0.42***
BML11	1.97±1.35***	1.35±0.56**	30.93±0.59***
BML12	4.86±1.42***	5.54±1.90**	44.93±0.86***
SML10	0.50±0.18**	0.55±0.25*	16.36±0.31***
SML11	1.69±0.43***	0.88±0.49*	19.40±0.38***
SML12	2.29±0.78**	7.36±2.18***	43.03±0.89***

***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05

The BLUP analysis was used to generate potential breeding values for the female and male parents in BML (humic soil) and SML (sandy soil) trials. The BLUP estimates and their related statistics are presented in Tables 5.2 to 5.7. As described by Zhou (2014a) and Zhou and Mokwele (2015), BLUP refers to the estimates of family breeding value relative to the population mean. BLUP estimates can be positive or negative indicating that a family produced higher or smaller values than the grand mean, respectively.

In this study parents were classified into elite [with significant (P<0.05) positive BLUP values], average [with non-significant (P>0.05) negative or positive BLUP values], and non-elite [with significant (P<0.05) negative BLUP values] parents. Polycrosses such as males only (MO) and melting pot (MP) were not classified into elite, average or non-elite parents for cane yield because the source of pollen for these crosses is unknown.

Female parents 96H0590, 98S0590, 99S1504, 98B0460, 99S1362, 96H0259 and 99B1659 had progenies that produced significantly (P<0.05) higher cane yield compared to the grand mean for the BML10 populations (Table 5.2). Male parents 99B1889 and 95H0039 produced progenies with significantly (P<0.05) higher cane yield compared to the grand mean. Female parents 98S0113, N48, 97B0740, 95H0517, 95H0039, 98S0082, 95H0130 and 99S0089 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean. Male parents 98S0290 and N48 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean.

Female parents 97B0931, 00B0094, 99B1979, 96H0289, 94H0102, 99B0325 and 00B1735 produced progenies that had significantly (P<0.05) higher cane yield compared to the grand mean in BML11 (Table 5.3). Male parents 97B0931, 82H0397 and 96H0320 produced progenies that had significantly (P<0.05) higher cane yield compared to the grand mean. Female parents 95H0130, 97B0740, 95L0828, 91L1198, 96H0320, 86H0048 and 00B1741 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean. Male parent 99B1439 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean.

Female parents 95H0039, 93H0460, 82H0397, 00B1741, 00B1431, N52, 01B0586 and 01B0742 produced progenies that had significantly (P<0.05) higher cane yield compared to the grand mean in BML12 (Table 5.4). Male parents 02S0639, 96H0289, 00B0379 and 85L1612 produced progenies with significantly (P<0.05) higher cane yield compared to the grand mean. Female parents 97B0272, 96H0289, 99S0176, 00B1056, 91M1610, 96H0320, 99B1439 and 00B1244 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean. Male parents 99B1439, 90H0525, 87L0573, 80M0922 and CP701133 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean.

Table 5.2 Female and male best linear unbiased prediction (BLUP), standard error of BLUP (S.E.), t-stats (t-statistic) and probability of a larger t-statistic (P>t) for the humic soil (BML10) populations

Female	BLUP	SE	t-stats	P>t	Female	BLUP	S.E.	t-stats	P>t
96H0590	2.68	0.59	4.57	<.0001	97B0740	-1.04	0.36	-2.93	0.0034
98S0590	1.55	0.49	3.13	0.0017	00S1407	-1.06	0.91	-1.17	0.2420
99S1504	1.54	0.59	2.61	0.0091	95H0517	-1.11	0.45	-2.49	0.0129
98B0460	1.45	0.33	4.33	<.0001	95H0039	-1.39	0.49	-2.87	0.0041
98B0202	1.31	0.92	1.42	0.1557	98S0082	-1.41	0.48	-2.91	0.0036
79H0469	1.22	0.67	1.82	0.0693	95H0130	-2.53	0.36	-7.09	<.0001
99S1362	1.20	0.48	2.53	0.0115	99S0089	-3.10	0.75	-4.13	<.0001
96H0259	1.19	0.38	3.17	0.0015					
99B1659	0.88	0.36	2.47	0.0137	**Male**	**BLUP**	**S.E.**	**t-stats**	**P>t**
98S0290	0.85	0.47	1.82	0.0685	99B1889	1.78	0.59	3.04	0.0024
99B1022	0.79	1.09	0.72	0.4704	95H0039	1.10	0.43	2.59	0.0097
98S0311	0.74	0.92	0.81	0.4185	98B0460	0.81	0.87	0.93	0.3499
96H0231	0.74	0.53	1.40	0.1628	98S0590	0.81	0.51	1.57	0.1159
97B0451	0.47	0.40	1.18	0.2364	97B0272	0.75	0.46	1.64	0.1003
93H0119	0.42	0.41	1.02	0.3056	99S0089	0.49	0.94	0.52	0.6035
86H0048	0.38	0.63	0.61	0.5451	95H0517	0.46	0.49	0.93	0.3540
97B0707	0.38	0.37	1.02	0.3085	96H0259	0.46	0.87	0.53	0.5942
97B0208	0.37	0.92	0.40	0.6884	99S1043	0.23	0.87	0.26	0.7918
82H0397	0.20	0.59	0.34	0.7354	96H0590	0.12	0.66	0.19	0.8500
97B0272	0.17	0.92	0.19	0.8528	99B1659	0.11	0.87	0.12	0.9028
99S1082	0.12	0.92	0.13	0.9000	99S1504	0.08	0.68	0.11	0.9103
99B0325	-0.03	0.61	-0.05	0.9611	95H0130	0.07	0.87	0.08	0.9341
99B0112	-0.54	0.59	-0.92	0.3598	82H0397	-0.32	0.50	-0.64	0.5204
99B1889	-0.66	0.38	-1.70	0.0883	MO	-0.34	0.30	-1.13	0.2575
N31	-0.67	0.92	-0.73	0.4664	MP	-0.38	0.38	-1.02	0.3099
98S0030	-0.67	0.51	-1.32	0.1857	95H0170	-0.42	0.87	-0.48	0.6315
98S0113	-0.76	0.36	-2.09	0.0370	99B0325	-0.75	0.42	-1.76	0.0784
99S1043	-0.77	0.85	-0.91	0.3603	98S0290	-1.07	0.52	-2.06	0.0392
98S0330	-0.88	0.61	-1.44	0.1502	98S0330	-1.09	0.66	-1.66	0.0971
N48	-1.00	0.42	-2.36	0.0182	98S0113	-1.14	0.77	-1.47	0.1410
89H0568	-1.02	0.61	-1.66	0.0977	N48	-1.76	0.50	-3.54	0.0004

MO = Males only, MP = Melting pot

Table 5.3 Female and male best linear unbiased prediction (BLUP), standard error of BLUP (S.E.), t-stats (t-statistic) and probability of a larger t-statistic (P>t) for the humic soil (BML11) populations

Female	BLUP	SE	t-stats	P>t	Female	BLUP	S.E.	t-stats	P>t
97B0931	2.81	0.67	4.18	<.0001	N48	-1.34	1.01	-1.32	0.1864
00B0094	2.68	0.51	5.24	<.0001	95L0828	-1.45	0.55	-2.63	0.0087
99B1979	2.25	0.48	4.71	<.0001	85HM86	-1.52	1.06	-1.43	0.1518
96H0289	1.70	0.63	2.70	0.0070	91L1198	-1.56	0.68	-2.28	0.0224
94H0102	1.54	0.55	2.80	0.0051	96H0320	-1.61	0.54	-2.98	0.0029
99B0325	1.27	0.51	2.51	0.0120	86H0048	-2.33	0.80	-2.92	0.0035
00B1735	1.17	0.51	2.31	0.0211	00B1741	-2.41	0.49	-4.96	<.0001
96H0588	1.14	0.67	1.69	0.0904					
99B1659	1.06	0.94	1.12	0.2639	**Male**	**BLUP**	**S.E.**	**t-stats**	**P>t**
95H0059	0.98	0.80	1.22	0.2210	97B0931	2.04	0.69	2.95	0.0032
98B0460	0.91	0.73	1.25	0.2127	82H0397	1.45	0.46	3.13	0.0018
94H0031	0.89	0.50	1.77	0.0775	96H0320	1.38	0.65	2.11	0.0351
98B0114	0.84	0.68	1.22	0.2220	92L0429	1.18	0.67	1.74	0.0815
99B1047	0.76	1.03	0.74	0.4612	99B0325	1.16	0.76	1.53	0.1263
00B1706	0.73	0.52	1.39	0.1641	00B1244	0.75	0.89	0.84	0.4000
99B1844	0.68	0.67	1.02	0.3087	94H0102	0.52	0.96	0.54	0.5896
00B1431	0.50	0.69	0.73	0.4664	95L1446	0.44	0.76	0.58	0.5595
00B1056	0.49	0.56	0.87	0.3849	00B0094	0.33	0.64	0.51	0.6102
86H0437	0.39	0.99	0.39	0.6951	99B1979	0.32	0.60	0.52	0.6021
91W1460	0.25	1.13	0.22	0.8271	MO	0.29	0.34	0.86	0.3897
99B1439	0.23	0.69	0.34	0.7360	00B1431	0.27	0.53	0.51	0.6107
93H0094	0.12	0.95	0.12	0.9026	95H0059	0.27	0.94	0.28	0.7780
97B0707	0.02	0.37	0.05	0.9610	97W0181	0.17	1.01	0.17	0.8676
89H0568	-0.06	0.50	-0.13	0.9001	97B0107	0.09	0.54	0.17	0.8640
98B0202	-0.14	1.03	-0.13	0.8933	CP701133	-0.02	0.54	-0.04	0.9697
92H0193	-0.19	0.65	-0.29	0.7691	95L0828	-0.09	0.96	-0.10	0.9218
85H0428	-0.22	1.02	-0.21	0.8322	80M0922	-0.15	0.95	-0.15	0.8773
81L1629	-0.23	0.50	-0.46	0.6468	85H0428	-0.16	0.69	-0.23	0.8199
96H0220	-0.28	0.55	-0.51	0.6130	N48	-0.17	0.58	-0.29	0.7711
93H0460	-0.40	0.50	-0.79	0.4300	MP	-0.20	0.39	-0.52	0.6001
97B0107	-0.53	0.45	-1.17	0.2409	96H0289	-0.21	0.65	-0.32	0.7453
N19	-0.59	0.90	-0.65	0.5154	98G0115	-0.32	0.83	-0.39	0.6975
82H0397	-0.80	0.45	-1.79	0.0743	88L0046	-0.64	0.93	-0.69	0.4895
CP701133	-0.90	0.53	-1.69	0.0903	88M0777	-0.81	0.71	-1.15	0.2503
71L0416	-0.98	0.88	-1.11	0.2669	00B1735	-0.90	0.71	-1.26	0.2079
98B0532	-1.12	0.63	-1.77	0.0760	77F0790	-1.04	0.98	-1.07	0.2865
95H0130	-1.13	0.56	-2.02	0.0437	96E0439	-1.10	0.86	-1.29	0.1986
00B1244	-1.18	0.68	-1.73	0.0828	95H0553	-1.26	0.69	-1.82	0.0693
97B0272	-1.21	0.78	-1.56	0.1186	01G0498	-1.39	0.72	-1.92	0.0545
97B0740	-1.24	0.41	-3.03	0.0025	99B1439	-2.17	0.52	-4.15	<.0001

MO = Males only, MP = Melting pot

Table 5.4 Female and male best linear unbiased prediction (BLUP), standard error of BLUP (S.E.), t-stats (t-statistic) and probability of a larger t-statistic (P>t) for the humic soil (BML12) populations

Female	BLUP	SE	t-stats	P>t	Male	BLUP	S.E.	t-stats	P>t
95H0039	4.23	1.35	3.13	0.0017	02S0639	4.66	1.00	4.66	<.0001
93H0460	3.81	0.68	5.63	<.0001	96H0289	2.58	1.22	2.11	0.0347
82H0397	3.56	0.61	5.85	<.0001	01S1749	2.12	1.37	1.55	0.1222
00B1741	2.58	1.06	2.44	0.0149	00B0379	2.07	1.02	2.02	0.0431
00B1431	2.54	0.89	2.84	0.0045	85L1612	1.90	0.89	2.12	0.0338
N52	2.29	0.60	3.83	0.0001	N52	1.66	1.42	1.17	0.2421
01B0586	1.93	0.71	2.72	0.0066	00B1741	1.52	0.83	1.82	0.0681
01B0742	1.73	0.49	3.50	0.0005	02B0228	1.39	0.95	1.46	0.1452
85H0428	1.39	0.86	1.61	0.1065	00S1919	1.23	1.66	0.74	0.4572
02B0228	0.99	0.72	1.37	0.1706	N31	1.23	0.85	1.46	0.1451
97B0107	0.91	1.67	0.55	0.5854	01S1637	1.11	0.95	1.17	0.2428
92H0193	0.72	1.33	0.54	0.5866	01S1672	1.11	0.71	1.58	0.1152
89H0568	0.52	0.88	0.59	0.5522	82H0397	1.04	1.69	0.62	0.5381
00S1919	0.41	0.86	0.47	0.6352	99B1979	0.87	0.92	0.95	0.3433
99B1979	0.30	0.56	0.54	0.5872	MP	0.59	0.51	1.14	0.2528
01B1377	0.05	0.97	0.06	0.9548	MO	0.50	0.54	0.94	0.3496
00B0379	-0.06	1.67	-0.04	0.9712	N48	0.29	1.35	0.22	0.8271
00S1247	-0.13	0.59	-0.22	0.8247	IK7650	0.02	2.04	0.01	0.9905
02B1571	-0.20	0.73	-0.27	0.7883	00S1368	-0.15	0.88	-0.18	0.8605
90H0525	-0.60	0.69	-0.87	0.3849	85L0102	-0.38	2.02	-0.19	0.8502
94H0031	-0.60	0.93	-0.64	0.5198	97B0272	-0.72	1.10	-0.65	0.5141
96H0220	-0.65	1.49	-0.43	0.6651	01B1377	-0.75	1.70	-0.44	0.6583
00S0664	-0.70	1.52	-0.46	0.6442	US56158	-0.78	1.51	-0.52	0.6059
86H0437	-0.78	0.59	-1.32	0.1884	95H0039	-1.05	0.95	-1.10	0.2695
00B1941	-0.87	0.89	-0.98	0.3291	97B0107	-1.20	0.95	-1.26	0.2066
97B0272	-1.37	0.53	-2.59	0.0097	99B1439	-1.74	0.86	-2.01	0.0443
96H0289	-1.76	0.69	-2.55	0.0107	00B1941	-2.03	1.67	-1.21	0.2247
00B0094	-1.80	1.05	-1.71	0.0869	99K0784	-2.56	1.34	-1.91	0.0559
86H0048	-2.00	1.22	-1.64	0.1003	90H0525	-2.88	0.81	-3.55	0.0004
99S0176	-2.18	0.96	-2.28	0.0227	87L0573	-3.17	1.16	-2.72	0.0065
00B1056	-2.40	0.61	-3.95	<.0001	80M0922	-3.87	1.24	-3.12	0.0018
91M1610	-2.46	0.69	-3.56	0.0004	CP701133	-4.63	1.42	-3.25	0.0012
96H0320	-2.46	1.11	-2.21	0.0270					
99B1439	-3.14	0.76	-4.15	<.0001					
00B1244	-3.81	0.93	-4.10	<.0001					

MO = Males only, MP = Melting pot

Female parents 82H0397, 98B0460, 98S0590 and 98S0290 produced progenies that had significantly (P<0.05) higher cane yield compared to the grand mean in SML10 (Table 5.5). Male parents 99B1889 and 99S1504 produced progenies that had significantly (P<0.05) higher cane yield compared to the grand mean. Female parents 99S0176, 95H0517, 95H0130 and 89H0568 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean. Male parents MO, 95H0517 and 98S0290 produced families that had significantly (P<0.05) lower cane yield than the grand mean.

Female parents 95H0167, 99S1362, 98S0311, 96H0259, 97B0707, 98S0030, 95H0517, 95L1446, 92L0429 and 99S1043 produced progenies that had significantly (P<0.05) higher cane yield compared to the grand mean in SML11 (Table 5.6). Male parents 82H0397 and 97B0272 produced progenies that had significantly (P<0.05) higher cane yield compared to the population (grand) mean. Female parents 96H0398, 85H0428, 95H0039, 96H0296, 93H0115, 85H0363, N42, 95H0130 and 85L1374 produced progenies that had significantly (P<0.05) low cane yield compared to the grand mean. No male parents were observed that produced progenies that had significantly lower cane yield compared to the grand mean.

Female parents N52, 82H0397, 01S1428, 00S1958, 01S1637 and 95H0059 produced progenies that had significantly (P<0.05) higher cane yield compared to the grand mean in SML12 (Table 5.7). Male parents N52, US56158, 00B1244, 95H0059, 02S1314 and 02S0639 produced progenies that had significantly (P<0.05) higher cane yield compared to the grand mean. Female parents 85H0428, 00B1741, 01S1672, 01S1749 and 95H0553 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean. Male parents 99B1979, 85L1612, 01S1428, 00B1941, N48, 99S0176 and 01S1681 produced progenies that had significantly (P<0.05) lower cane yield compared to the grand mean.

Table 5.5 Female and male best linear unbiased prediction (BLUP), standard error of BLUP (S.E.), t-stats (t-statistic) and probability of a larger t-statistic (P>t) for the sandy soil (SML10) populations

Female	BLUP	SE	t-stats	P>t
82H0397	1.50	0.40	3.78	0.0002
98B0460	0.94	0.33	2.86	0.0042
98S0590	0.73	0.33	2.18	0.0296
98S0290	0.56	0.28	2.01	0.0447
99S1362	0.54	0.28	1.95	0.0515
95H0170	0.47	0.35	1.35	0.1770
98S0311	0.43	0.50	0.86	0.3893
79H0469	0.42	0.56	0.75	0.4553
98S0082	0.39	0.26	1.51	0.1302
86H0048	0.37	0.51	0.73	0.4656
99S1082	0.31	0.37	0.84	0.4021
N48	0.28	0.53	0.54	0.5926
97B0740	0.28	0.33	0.85	0.3963
96H0231	0.26	0.36	0.71	0.4772
99B1659	0.21	0.32	0.66	0.5090
92H0188	0.18	0.47	0.39	0.6948
96H0590	0.14	0.33	0.42	0.6766
98S0330	0.12	0.30	0.42	0.6754
N31	0.11	0.44	0.25	0.8024
99B1889	0.10	0.42	0.23	0.8172
96H0259	0.00	0.35	0.01	0.9935
99S1043	-0.05	0.25	-0.22	0.8288
97B0272	-0.10	0.58	-0.17	0.8634
99S0712	-0.11	0.31	-0.35	0.7292
98S0030	-0.11	0.29	-0.38	0.7039
95H0039	-0.12	0.32	-0.38	0.7013
99S1504	-0.21	0.33	-0.64	0.5242
98B0202	-0.25	0.53	-0.46	0.6422
98S0113	-0.27	0.25	-1.10	0.2719
99S0089	-0.32	0.33	-0.99	0.3206
00S1407	-0.41	0.31	-1.35	0.1768
90H0525	-0.43	0.48	-0.90	0.3697

Female	BLUP	S.E.	t-stats	P>t
99B0112	-0.47	0.56	-0.84	0.4021
93H0119	-0.77	0.56	-1.38	0.1671
99S0176	-0.96	0.35	-2.74	0.0061
95H0517	-1.11	0.35	-3.16	0.0016
95H0130	-1.13	0.33	-3.40	0.0007
89H0568	-1.52	0.57	-2.65	0.0080

Male	BLUP	S.E.	t-stats	P>t
99B1889	1.52	0.41	3.67	0.0002
96H0259	0.97	0.57	1.70	0.0887
99S1504	0.90	0.37	2.44	0.0146
98B0460	0.71	0.43	1.65	0.0980
96H0231	0.54	0.47	1.17	0.2439
95H0039	0.43	0.34	1.24	0.2145
98S0113	0.40	0.35	1.12	0.2610
99S1043	0.16	0.47	0.35	0.7263
98S0082	0.04	0.51	0.09	0.9309
96H0590	-0.04	0.50	-0.07	0.9405
MP	-0.08	0.23	-0.36	0.7184
99B1659	-0.11	0.59	-0.19	0.8518
99B0325	-0.14	0.35	-0.41	0.6807
95H0130	-0.25	0.36	-0.71	0.4792
98G1178	-0.28	0.39	-0.72	0.4738
94L1039	-0.34	0.53	-0.65	0.5129
82H0397	-0.38	0.31	-1.21	0.2270
97B0272	-0.45	0.33	-1.39	0.1636
N48	-0.53	0.39	-1.37	0.1699
MO	-0.58	0.22	-2.68	0.0074
95H0170	-0.63	0.52	-1.21	0.2261
95H0517	-0.78	0.39	-2.02	0.0438
98S0290	-1.06	0.47	-2.26	0.0236

MO = Males only, MP = Melting pot

Table 5.6 Female and male best linear unbiased prediction (BLUP), standard error of BLUP (S.E.), t-stats (t-statistic) and probability of a larger t-statistic (P>t) for the sandy soil (SML11) populations

Female	BLUP	SE	t-stats	P>t	Female	BLUP	S.E.	t-stats	P>t
95H0167	2.28	0.38	5.96	<.0001	88H0167	-0.16	1.25	-0.13	0.8953
99S1362	1.96	0.57	3.47	0.0005	88H0173	-0.16	1.25	-0.12	0.9012
98S0311	1.93	0.33	5.85	<.0001	88H0179	-0.18	1.25	-0.15	0.8832
96H0259	1.85	0.56	3.33	0.0009	96L0679	-0.18	1.01	-0.18	0.8587
97B0707	1.68	0.81	2.08	0.0372	92L0434	-0.18	1.25	-0.15	0.8845
98S0030	1.48	0.49	3.03	0.0025	95H0170	-0.20	0.71	-0.29	0.7745
95H0517	1.47	0.35	4.26	<.0001	90H0525	-0.21	0.31	-0.66	0.5066
95L1446	1.30	0.52	2.48	0.0133	88H0178	-0.23	1.25	-0.18	0.8536
97B0740	1.27	0.80	1.58	0.1141	92L0432	-0.23	1.25	-0.19	0.8531
N16	1.13	0.70	1.61	0.1066	88H0166	-0.26	0.56	-0.46	0.6479
92L0429	1.03	0.44	2.35	0.0187	95H0553	-0.27	0.51	-0.53	0.5962
92L0431	0.97	1.25	0.78	0.4363	88H0170	-0.28	1.25	-0.23	0.8199
76H0376	0.84	0.87	0.96	0.3358	88H0169	-0.30	1.25	-0.24	0.8084
99S1043	0.82	0.41	1.97	0.0488	88H0177	-0.36	1.25	-0.29	0.7710
94H0031	0.80	0.71	1.14	0.2555	92L0430	-0.37	1.25	-0.30	0.7650
92H0193	0.73	0.89	0.82	0.4107	88H0171	-0.41	1.25	-0.33	0.7443
97W0181	0.73	0.39	1.87	0.0609	00B0094	-0.50	0.88	-0.57	0.5718
95W1786	0.55	0.52	1.06	0.2895	99S1472	-0.56	0.64	-0.87	0.3837
99S1082	0.52	0.30	1.72	0.0846	00B1056	-0.65	0.95	-0.68	0.4963
98S0330	0.46	0.57	0.82	0.4148	99S0712	-0.65	0.37	-1.77	0.0767
99S0176	0.42	0.29	1.43	0.1519	99B1844	-0.99	0.81	-1.23	0.2175
82H0397	0.38	0.38	1.00	0.3192	97B0197	-1.06	0.61	-1.72	0.0848
91L1198	0.38	0.45	0.84	0.4020	85L1056	-1.20	1.03	-1.17	0.2432
86H0437	0.37	0.65	0.57	0.5712	88M0777	-1.20	0.97	-1.23	0.2180
N45	0.37	0.40	0.95	0.3442	96H0398	-1.21	0.52	-2.33	0.0201
88H0174	0.33	1.25	0.27	0.7900	85H0428	-1.27	0.49	-2.61	0.0092
92L0433	0.31	1.25	0.25	0.8060	95H0039	-1.29	0.66	-1.96	0.0496
00S1407	0.21	1.09	0.19	0.8477	96H0296	-1.31	0.58	-2.24	0.0248
97B0272	0.19	0.82	0.24	0.8128	93H0115	-1.64	0.47	-3.51	0.0005
99B0325	0.15	0.39	0.38	0.7059	85H0363	-2.05	0.80	-2.56	0.0105
97B0931	0.06	0.80	0.07	0.9442	N42	-2.06	0.68	-3.04	0.0023
99S0854	0.04	0.55	0.08	0.9370	95H0130	-2.38	0.69	-3.44	0.0006
88H0175	0.02	1.25	0.01	0.9885	85L1374	-2.43	0.70	-3.49	0.0005
88H0168	-0.06	1.25	-0.05	0.9589					
85L1612	-0.07	0.51	-0.13	0.8953	**Male**	**BLUP**	**S.E.**	**t-stats**	**P>t**
88H0172	-0.08	1.25	-0.06	0.9486	82H0397	1.47	0.62	2.39	0.0169
88H0176	-0.08	1.25	-0.06	0.9486	97B0272	1.16	0.47	2.45	0.0144
86H0048	-0.09	0.50	-0.17	0.8655	97B0107	1.03	0.80	1.29	0.1964
92L0435	-0.10	1.25	-0.08	0.9360	99B0325	1.01	0.70	1.45	0.1480
89H0568	-0.11	0.60	-0.19	0.8509	96H0289	0.53	0.72	0.73	0.4654

MO = Males only, MP = Melting pot

Table 5.6 Continued.

Male	BLUP	SE	t-stats	P>t	Male	BLUP	S.E.	t-stats	P>t
MO	0.40	0.29	1.38	0.1683	82H0398	-0.09	0.92	-0.09	0.9258
85H0428	0.34	0.61	0.56	0.5788	82H0410	-0.10	0.92	-0.10	0.9172
88M0777	0.30	0.59	0.50	0.6148	82H0409	-0.12	0.92	-0.13	0.8961
95H0059	0.26	0.67	0.39	0.6973	MP	-0.15	0.31	-0.48	0.6282
00B1244	0.19	0.88	0.22	0.8269	82H0401	-0.15	0.92	-0.16	0.8720
82H0405	0.17	0.92	0.19	0.8505	82H0400	-0.16	0.92	-0.17	0.8638
85H0363	0.08	0.58	0.15	0.8835	82H0408	-0.19	0.92	-0.21	0.8368
85H0605	0.06	0.71	0.08	0.9382	82H0402	-0.21	0.92	-0.23	0.8174
CP701133	0.06	0.62	0.09	0.9252	93H0460	-0.25	0.71	-0.36	0.7197
99S0176	0.01	0.49	0.01	0.9908	99B1979	-0.34	0.82	-0.41	0.6795
82H0406	0.01	0.92	0.01	0.9919	95H0039	-0.43	0.74	-0.59	0.5577
82H0399	-0.03	0.92	-0.04	0.9709	92L0429	-0.52	0.42	-1.24	0.2158
82H0403	-0.04	0.92	-0.05	0.9636	76H0376	-0.74	0.62	-1.19	0.2351
82H0407	-0.04	0.92	-0.05	0.9636	00B1941	-0.89	0.61	-1.45	0.1466
82H0404	-0.08	0.92	-0.09	0.9300	99B1439	-1.21	0.76	-1.59	0.1114
N51	-0.09	0.84	-0.11	0.9107	90H0525	-1.24	0.75	-1.66	0.0978

MO = Males only, MP = Melting pot

Table 5.7 Female and male best linear unbiased prediction (BLUP), standard error of BLUP (S.E.), t-stats (t-statistic) and probability of a larger t-statistic (P>t) for the sandy soil (SML12) populations

Female	BLUP	S.E.	t-stats	P>t	Male	BLUP	S.E.	t-stats	P>t
N52	2.87	0.55	5.19	<.0001	N52	4.16	1.57	2.65	0.0081
82H0397	2.64	0.74	3.57	0.0004	US56158	4.08	1.11	3.66	0.0003
01S1428	1.97	0.61	3.21	0.0013	00B1244	4.00	1.03	3.88	0.0001
00S1958	1.85	0.56	3.28	0.0011	95H0059	3.64	1.24	2.94	0.0032
01S1637	1.61	0.69	2.34	0.0192	N31	2.67	1.66	1.61	0.1080
95H0059	1.35	0.62	2.17	0.0304	02S1314	2.66	1.10	2.42	0.0158
87L0573	1.29	1.35	0.96	0.3376	02S0639	2.58	0.86	2.99	0.0028
02S1314	1.08	0.57	1.90	0.0570	82H0397	1.66	1.09	1.53	0.1257
85L0102	0.82	0.53	1.54	0.1226	93H0094	1.58	1.08	1.46	0.1430
93H0094	0.78	0.80	0.97	0.3323	01B0586	1.56	1.11	1.41	0.1580
85L1612	0.51	0.52	0.97	0.3306	85H0605	1.36	0.96	1.42	0.1568
86H0437	0.47	0.59	0.80	0.4250	00B1741	0.95	0.75	1.26	0.2064
00S0664	0.46	1.16	0.40	0.6897	96H0289	0.75	1.01	0.74	0.4575
92L0429	0.36	0.89	0.40	0.6869	97B0107	0.68	1.09	0.63	0.5309
01S1681	0.29	0.48	0.62	0.5385	88M0777	0.65	1.13	0.58	0.5643
91H0460	0.03	1.35	0.02	0.9851	85H0428	0.36	1.09	0.33	0.7436
01S1430	-0.07	0.89	-0.08	0.9391	MP	0.27	0.59	0.46	0.6474
76H0376	-0.07	1.07	-0.07	0.9480	87L0573	0.08	1.56	0.05	0.9586
02S0639	-0.18	0.62	-0.29	0.7699	99B1659	0.05	1.38	0.04	0.9706
97B0272	-0.21	0.60	-0.36	0.7212	92L0429	-0.12	1.08	-0.11	0.9112
88M0777	-0.29	0.75	-0.38	0.7003	04K1388	-0.73	1.12	-0.65	0.5130
99B0325	-0.31	1.06	-0.29	0.7708	MO	-0.77	0.55	-1.40	0.1602
98S0330	-0.42	1.17	-0.36	0.7180	CP701133	-1.00	1.48	-0.67	0.5005
99S1472	-0.71	1.06	-0.67	0.5015	01S1672	-1.57	1.27	-1.24	0.2160
90H0525	-0.77	1.36	-0.57	0.5694	99B1979	-1.90	0.88	-2.15	0.0313
00S1247	-0.81	0.89	-0.91	0.3630	97B0272	-1.91	1.87	-1.02	0.3079
02S0097	-1.14	1.09	-1.04	0.2966	01S1749	-2.17	1.45	-1.50	0.1339
99S0176	-1.18	0.78	-1.50	0.1325	85L1612	-2.38	0.97	-2.46	0.0138
00B0379	-1.30	1.10	-1.18	0.2384	76H0376	-2.48	1.65	-1.51	0.1315
85H0428	-1.36	0.54	-2.53	0.0114	01S1428	-2.51	0.99	-2.55	0.0109
00B1741	-1.38	0.70	-1.97	0.0492	00B1941	-2.58	0.85	-3.03	0.0025
01S0213	-1.43	1.04	-1.37	0.1710	N48	-3.21	1.00	-3.22	0.0013
01S1672	-1.54	0.54	-2.87	0.0041	99S0176	-4.48	1.25	-3.58	0.0004
86H0048	-1.58	0.89	-1.77	0.0771	01S1681	-5.95	0.96	-6.18	<.0001
01S1749	-1.60	0.56	-2.85	0.0043					
95H0553	-2.04	0.75	-2.71	0.0067					

MO = Males only, MP = Melting pot

The elite groups of female and male parents produced both significantly (P<0.05) higher cane yield compared to the non-elite group of parents in both BML and SML trials (Table 5.8). There was a consistent decrease in cane yield from elite to non-elite groups of parents. The order of the magnitude of the classification (from largest to smallest) was elite>average>non-elite for both female and male parents. A consistent increase in cane yield, produced by both groups of female and male parents, was observed form BML10 to BML11 to BML12 as well as from SML10 to SML11 to SML12.

Table 5.8 Female and male parent classification by least square means generated by best linear unbiased prediction (BLUP) procedure for cane yield in humic (BML) and sandy (SML) soil populations

Trial	Classification	Female	Male
BML10	Elite	7.79a	7.98a
	Average	6.82b	6.44b
	Non-elite	5.18c	5.36c
BML11	Elite	10.65a	10.61a
	Average	8.65b	9.04b
	Non-elite	7.22c	6.86c
BML12	Elite	16.76a	16.82a
	Average	13.83b	14.49b
	Non-elite	12.05c	11.34c
SML10	Elite	7.96a	7.76a
	Average	7.64b	6.22b
	Non-elite	6.77c	5.74c
SML11	Elite	10.08a	10.68a
	Average	8.63b	8.90b
	Non-elite	7.06c	6.19c
SML12	Elite	17.82a	19.73a
	Average	15.86b	15.63b
	Non-elite	14.15c	12.46c

Values followed by different letters are significant different at P<0.05

The proportions of female and male parents that produced significantly (P<0.05) higher BLUP values (elite parents) were counted for all trials (Table 5.9). The total number of elite female parents in BML (humic soil) trials was more than that of SML (sandy soil) trials, except for the total number of elite female parents in BML11 which was less than for the SML11. BML and SML trials produced more or less the same number of elite male parents. The numbers of elite female and male parents in each trial were divided by the total number of female and male parents in the trial to give a percent value of elite parents. The percentage of elite female parents in BML trials ranged from 14.9 to 32.0% while in SML trials it ranged from 10.9 to 16.7%. The percentage of elite male parents in BML trials ranged from 9.1 to 12.5% while in SML trials it ranged from 4.4 to 17.6%.

Table 5.9 Proportions of elite parents for cane yield for the humic (BML) and sandy (SML) soil populations

Trial	Female			Male		
	Total	**Elite**	**%Elite**	**Total**	**Elite**	**%Elite**
Humic soil breeding programme						
BML10	38	7	18.4	22	2	9.1
BML11	47	7	14.9	31	3	9.7
BML12	25	8	32.0	32	4	12.5
Total	110	22	20.0	85	9	10.6
Sandy soil breeding programme						
SML10	38	5	13.2	23	2	8.7
SML11	92	10	10.9	45	2	4.4
SML12	36	6	16.7	34	6	17.6
Total	166	21	12.7	102	10	9.8

5.5 DISCUSSION

The significant female and male variance components suggested that the parents that have been selected for crossing contributed significantly to variability among progenies for cane yield. Generally, the female effects produced larger variances and smaller standard error compared to the male effects and this suggested that most of the variability in progenies were probably attributed to variability among female parents. Results suggest the potential existence of dominance or maternal effects. Zhou (2015) reported stronger maternal effects

compared to paternal effects and this highlight the difficulty of synchronising sugarcane genotypes flowering during crossing. The large residual error variances (larger than both the female and male effects) suggested that most of the variability observed in the data was not contributed by the female and male parents. The large variability could be attributed to large spatial variability associated with the large trial characteristic of this stage in plant breeding trials. The large variability could also be due to non-additive genetic variation caused by complex genome of sugarcane. Further, the large residual error indicates the need to optimise experimental designs to improve trial efficiency. Currently, the randomised block design is used which may not be appropriate for trials with more than 100 crosses. Adoption of an alpha lattice design is expected to improve efficiency. The alpha lattice designs can account for within block variability and thus reduce error variance and increasing the efficiency of comparing families.

In both humic and sandy soil populations, female parents 82H0397 (BML12, SML10, SML12), 96H0259 (BML10, SML11), 98B0460 (BML10, BML11, SML10), 98S0290 (BML10, SML10), 98H0590 (BML10, SML10), 99S1362 (BML10, SML10, SML11) and N52 (BML12, SML12) produced progenies that had significantly higher cane yield compared to the population mean in at least more than two trials, indicating that these parents were potentially elite parents for the Midlands breeding programmes. Male parents 02S0639 (BML12, SML12), 82H0397 (BML11, SML11), 98B0460 (BML10, SML10), 98B1889 (BML10, SML10) and N52 (SML12) produced progenies with significantly higher cane yield compared to the population mean suggesting that these were potentially elite male parents. According to Barbosa et al. (2005), it is important to know the breeding values of parent genotypes to allow a greater combining ability. Thus, the identified elite parents could in return be crossed with other parents as well as among each other in order to examine the specific combining ability for further crossings (Barbosa et al. 2005). Parents 82H0397, 98B0460 and N52 appeared as both elite male and female parents. Results may indicate that both 98B0460 and N52 are likely to be true elite male parents that excel in pollen production. In breeding trials, it has been frequently observed that progeny plots from crosses including N52 and 98B0460 are frequently more vigorous with better combinations of other commercial traits such as good agronomic appearance and low disease symptoms. However, they are frequently used in polycrosses where seed is collected from their flowers and thus act as female parents. Results indicate that all the

above parents could be retained as elite parents to be used in building a core germplasm pool of known genotypes that produce elite progenies.

Genotypes 00B1244 (BML12, SML11), 00B1741 (BML11, SML12), 85H0428 (SML11, SML12), 86H0048 (BML11, SML12), 95H0039 (BML10, SML11), 95H0130 (BML10, SML10, SML11), 95H0517 (BML10, SML10), 96H0320 (BML11, BML12), 97B0740 (BML10, BML11), and 99S0176 (BML12, SML10) when used as female parents, produced progenies with significantly lower cane yield compared the population mean in at least two trials suggesting that these genotypes were inferior parents for the Midlands breeding programmes. Genotypes 98S0290 (BML10, SML10), 99B1439 (BML11, BML12) and N48 (BML10, SML12), when used as male parents, produced progenies with significantly lower cane yield compared the population mean in at least two trials. Genotype N48 produced consistently lower yielding progenies when used both as a female and male parent; a testimony to its poor performance as a parent. Despite the poor performance of genotype N48 as a parent according to Zhou (2014b), genotype N48 produced high sucrose content in humic soil and high cane yield in sandy soil. Results suggest that N48 possesses a high genetic value but a low breeding value. Genotypes that produced inferior progenies can potentially be discarded from the gene pool because of their limited contribution to the Midlands breeding programmes as parents. It is recommended that parent selection be focused only on genotypes that produced elite progenies for sugarcane yield. Similar results were obtained from a study carried out in South Africa involving selection for Eldana borer resistance using family data (Zhou and Mokwele 2015). Furthermore, the average parents could be used in future crosses only if they possess high breeding values for quality, ratooning ability, and insect pest and disease resistance.

Parent selection and crossing at SASRI is currently based on mid-parent values. The assumption is that genotypes that possess high genetic values will ultimately produce progenies with high genetic values. However, results suggested that some parents with high genetic values do not produce progenies with high genetic values. This indicated that a high genetic value does not necessarily mean a genotype possess a high breeding value. Breeding values refer to the ability of genotypes to pass on genes to their progenies (Wei et al. 2012). Therefore, future parent selection should be based on breeding values rather than genetic values. Results highlighted the need to intensify evaluation of parents using family data, not only for the Midlands breeding programmes but also for other SASRI breeding

programmes. The evaluation will ultimately identify elite parents that would form the basis of future sugarcane breeding in South Africa. The identified elite parents can be the core gene pool to which new parents are added after testing each year, while older parents with comparatively lower breeding values are eliminated.

The elite group of female and male parents significantly produced higher cane yield compared to the non-elite group of parents in both BML and SML trials, indicating that the groups were predictable. There was a consistent decrease in cane yield from elite to non-elite groups of parents. Results indicated that the non-elite parents could be discarded with minimal genetic loss from the breeding programmes. Results further highlighted the effectiveness of using family data to generate breeding value estimates of parents involved in crosses (Kimbeng and Cox 2003).

The numbers of elite female parents in BML trials were more than those in SML trials. The sandy soil breeding programme started only more recently in 1997, while the humic soil programme started 40 years ago and was relocated to the current research station (Nuss 1998). The sandy soil breeding programme started with parents derived from the humic soil programme and other breeding programmes. Therefore, the sandy soil breeding programme has had fewer cycles of recurrent selection compared to the humic soil breeding programme, and thus has fewer elite parents.

There appeared to be higher numbers of elite parents in later series compared to earlier series for both humic and sandy soil trials suggesting a potential increase in the number of elite families with cycles of breeding. Results suggested that future cycles of recurrent selection will have higher proportions of elite parents. A study by Zhou (2014b) has shown an increase in yield produced by newer genotypes compared to older genotypes which indicates the potential effectiveness of recurrent selection for cane yield. Further, results suggested that with focussed parent evaluation, the development and identification of elite parents will accelerate, resulting in increased efficiency in these breeding programmes. This trend has been observed for studies in Australia (Atkin et al. 2009) and in South Africa (Zhou 2015).

5.6 CONCLUSIONS

The significant female and male variance components indicated the effectiveness of using family data to estimate the breeding values of parents that were used in crosses. The significant female and male parent's variance effects were also associated with variability for cane yield among parents suggesting the existence of genetic variability among parents. Parents producing progenies that had significantly higher cane yield were identified from the family data in both humic and sandy soil populations and those parents can be used for building a germplasm pool for sugarcane yield. BLUP estimates identified female parents (82H0397, 96H0259, 98B0460, 98S0290, 98H0590, 98S1362 and N52) and male parents (02S0639, 82H0397, 97B0272, 98B0460, 98B1889 and N52) that produced progenies with significantly higher cane yield in humic and sandy soil populations, indicating that these parents were potentially elite parents in these populations.

Parents were classified into elite, average and non-elite where the non-elite parents can be discarded for future crosses and selection. Results from this study should encourage breeders to make new crosses using the selected elite parents from where higher genetic gains for sugarcane yield are expected. Humic soil populations had higher proportions of elite parents compared to sandy soil populations probably due to longer cycles of recurrent breeding and selection. The proportions of elite parents were 20% (females) and 10.6 (males) for humic soil populations and 12.7% (females) and 9.8% (males) for sandy soil populations, suggesting intensive parent evaluation and development was required in these populations.

5.7 REFERENCES

Atkin FC, Dieters MJ, Stringer JK (2009) Impact of depth of pedigree and inclusion of historical data on the estimation of additive variance and breeding values in a sugarcane breeding program. Theoretical and Applied Genetics 119:555-565

Balzarini MG (2000) Biometrical models for predicting future performance in plant breeding. PhD Dissertation. Louisiana State University, Louisiana, USA. Biometrics 44:705-715

Barbosa MHP, Peternelli LA, Silveira LCI (2001) Plot size in sugarcane family selection experiments. Crop Breeding and Applied Biotechnology 1:271-276

Barbosa MHP, Resende MDV, Bressiani JA, Silveira LCI, Peternelli LA (2005) Selection of sugarcane families and parents by REML/BLUP. Crop Breeding and Applied Technology 5:443-450

Chang YS, Milligan SB (1992a) Estimating the potential of sugarcane families to produce elite genotypes using bivariate prediction methods. Theoretical and Applied Genetics 84:633-639

Chang YS, Milligan SB (1992b) Estimating the potential of sugarcane families to produce elite genotypes using univariate cross prediction methods. Theoretical and Applied Genetics 84:662-671

Cox MC (1996) Optimum family selection for net merit grade in stage 2 trials BS45S. Bureau of sugar experiment stations Queensland, Australia. Sugar Research Australia Ltd. pp. 1-19

Cox MC, Stringer JK (1998) Efficacy of early generation selection in a sugarcane improvement programme. Proceedings of the Australian Society of Sugar Cane Technologists 20:148-153

Freund RJ, Wilson WJ (2003) Statistical methods. New York Academic Press 22:3-1187

Heinz DJ, Tew TL (1987) Hybridization procedures. In: Heinz DJ (ed), Developments in Crop Science 11: Sugarcane improvement through breeding. Elsevier, New York. pp. 313-342

Kimbeng CA, Cox MC (2003) Early generation selection of sugarcane families and clones in Australia: A review. Journal of the American Society of Sugar Cane Technologists 23:20-39

Milligan SB, Legendre BL (1990) Development of a practical method for sugarcane cross appraisal. Journal of the American Society of Sugar Cane Technologists 11:59-68

Nuss KJ (1998) Aspects considered in the search for new farms for the Experiment Station. Proceedings of the South African Sugar Technologists' Association 72:42-45

SAS Institute (2014) SAS/STAT user's guide, version 9.1.3. Cary, NC: SAS Institute

Skinner JC, Hogarth DM, Wu KK (1987) Selection methods, criteria and indices. In: Heinz DJ (ed), Sugarcane improvement through breeding. Elsevier. pp. 409-453

Stringer JK, Cox MC, Atkin FC, Wei X, Hogarth DM (2011) Family selection improves the efficiency and effectiveness of selecting original seedlings and parents. Sugar Tech 13:36-41

Stringer JK, McRae TA, Cox MC (1996) Best linear unbiased prediction as a method of estimating breeding value in sugarcane. In: Wilson JR, Hogarth DM, Campbell JA

and Garside AL (eds), Sugarcane: Research towards efficient and sustainable production. CSIRO Division of Tropical Crops and Pastures, Brisbane, Australia. pp. 39-41

Wei X, Jackson P, Atkin F, Cox M, Piperidis G, Parfitt R (2012) How well are the predicted breeding values of parental clones associated with family performance in the BSES-CSIRO sugarcane breeding program? Proceedings of the Australian Society of Sugar Cane Technologists 34:1-6

Zhou MM (2009) Statistical methods and models for analysing sugarcane (*Saccharum* species hybrids) plant breeding data. PhD Dissertation. Louisiana State University and Agricultural and Mechanical College. pp. 199

Zhou MM (2014a) Family evaluation for sugarcane yield, using data estimated from stalk number, height and diameter. Journal of Crop Improvement 28:406-417

Zhou MM (2014b) Cultivar genetic gains for sugarcane yield, sucrose content and sugar yield in the Midlands region breeding programmes. Proceedings of the South African Sugar Technologists' Association 87:419-431

Zhou M (2015) Selection for *Eldana saccharina* borer resistance in early stages of sugarcane breeding in South Africa. American Journal of Plant Sciences 6:2168-2176

Zhou M, Mokwele A (2015) Family versus individual plant selection for stem borer (*Eldana saccharina*) resistance in early stages of sugarcane breeding in South Africa. South African Journal of Plant and Soil 33:89-96

CHAPTER 6

GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS FOR FUTURE RESEARCH

6.1 GENERAL DISCUSSION

Family evaluation was adopted to increase genetic gains for cane yield in SASRI breeding programmes. Family data for stalk number, stalk height and stalk diameter was collected during the last four years and used to estimate cane yield. Preliminary studies (Zhou 2014) demonstrated the potential of using yield estimates for family evaluation. However, greater understanding of the potential of family selection is required to unlock the potential genetic gains in cane yield using family evaluation. To investigate the benefits and progress of family evaluation at early stages of selection, three study areas were identified namely; family versus individual genotype selection (Chapter 3), family evaluation (Chapter 4) and parent evaluation (Chapter 5).

This study showed that family selection for all traits (cane yield, stalk number, height and diameter) was superior to individual genotype selection producing larger variability, higher broad-sense heritability and higher predicted selection gains. Results indicated that an increase in genetic values for cane yield and its components could be accelerated using family selection rather than individual genotype selection. Cane yield had higher predicted selection gains compared to yield components, indicating that selection of families directly for cane yield was more efficient than through the yield components. Stalk height consistently produced higher CV% values suggesting that more precision was necessary in the measurement of height. In addition, the study showed that data collected from yield components was sufficient in determining family differences. However, cane yield is known to correlate with yield components as demonstrated by path coefficient studies (Risch 2000).

In practice, family evaluation leads to the selection of elite families followed by the selection of superior genotypes within elite families. Of great interest is that while results have shown the superiority of family selection, results also indicated that individual genotype variances were significant. This was a strong evidence that a combination of

family selection followed by individual genotype selection could be more effective and efficient than family selection alone.

The family gains for humic soil populations were more than those for sandy soil populations, indicating that high proportions of elite families for cane yield were advanced in humic rather than in sandy soil breeding populations. This could be due to differences in soil type since humic soil is more uniform and deeper, with higher organic matter and clay content compared to sandy soil. Therefore, less impact of GxE is expected from humic soil compared to sandy soil. This further enhances the ability to identify superior families and genotypes on humic soil. In addition, the humic soil breeding programme has been in existence for over 40 years and has benefited from several cycles of genetic recombination's compared to the sandy soil breeding programme, which was established 20 years ago (Nuss 1998).

There were significant differences among families and group of families which indicated the ability of using progeny performance data to determine differences among sugarcane families in humic and sandy soil breeding populations. Based on the variation observed among families for cane yield, families were divided into three groups (elite, average and non-elite) using BLUP estimates. Generally, the means of cane yield significantly decreased from the elite to the non-elite group of families. The elite group of families represented families that produced significant higher cane yield compared to the population mean. The non-elite group of families represented families that produced significant lower cane yield compared to the population mean. The elite group produced significant higher cane yield than the average groups, whereas the average groups produced significant higher cane yield than non-elite groups. It is suggested that individual genotype selection be concentrated on the progenies from elite families, whereas the non-elite families should be discarded. It is also recommended that the average group should not be discarded but preferably be used as a group of family that is known to possess progenies with high breeding values for agronomic, quality, and pest and disease resistance traits.

Principal component analysis provided an efficient way of summarising the whole data set by compressing the different correlated variables into fewer dimensions. The total variation explained by the first two PCs was more than 90%. The first PC emphasised on cane yield, stalk number and stalk height while the second PC emphasised on stalk diameter. It became

clear that in an attempt to increase cane yield the focus should be on improving stalk number and stalk height rather than stalk diameter. Using BLUP analysis, selection based on family data in the plant crop of original seedlings, was effective in identifying elite families for cane yield. Humic soil populations produced higher proportions of elite families compared to sandy soil populations. Results indicated that populations grown in humic soil had a greater potential of increasing gains for cane yield through family selection. The optimum selection rate for humic soil populations was higher than for sandy soil populations.

This study showed highly significant female and male variance components which indicated that parents were contributing significantly to variability among progenies for cane yield. Parents were divided into three groups (elite, average and non-elite) for cane yield using BLUP estimates. The elite parents produced families with higher cane yield than the average parents, whereas the average parents produced families with higher cane yield than the non-elite parents. Results indicated that the non-elite parents could be discarded with minimal genetic loss from the breeding programmes. In the Midlands breeding programmes (humic and sandy soil), the sandy soil breeding programme is the youngest, therefore fewer recurrent selection has occurred (Nuss 1998) and thus has fewer elite parents. Thus, dedicated recurrent selection for cane yield is required for the sandy soil breeding programmes.

Generally, the proportions of elite parents (both females and males) were low for humic (30.6%) and sandy (22.5%) soil populations because the majority of parents with high genetic values produced families with significantly low cane yield compared to the population mean. This study revealed that some parents with high genetic values do not produce progenies with high genetic values. This indicated that a high genetic value does not necessarily mean a genotype possesses a high breeding value. Therefore, it is recommended that future parent selection should be based on breeding values rather than genetic values. Information on breeding values will be informative for parent selection, germplasm development, introgression breeding and parent combinations at a time of crossing.

Generally there was a large residual error in all trials, indicating that large variability was not accounted for by experimental designs. This large residual error indicated the need to

optimise experimental designs to improve trial efficiency. It was concluded that the randomised complete block design, which was used for all these trials, may not be appropriate for trials with more than 100 families (crosses). In an attempt to improve design efficiency, the adoption of an alpha lattice design could increase the efficiency in trials.

6.2 CONCLUSIONS

Family selection was more effective than individual genotype selection since it produced higher variability, higher heritability and larger predicted selection gains across all trials in both humic and sandy soil breeding programmes. Selecting families directly for cane yield was more efficient than through its components. Stalk height was more susceptible to inter-plot competition among individuals compared to families and this indicates the potential of stalk height to benefit from family selection. Combined gains from both family selection and individual genotype selection are expected to increase the genetic gains for yield in sugarcane breeding. The significant differences among families and group of families indicated the effectiveness of family selection and the potential of identifying and selecting elite families as well as discarding the non-elite families. Principal component analysis showed that number of stalks and stalk height contributed the most to cane yield. Therefore, stalk number and stalk height are important traits to consider when selecting and evaluating families for sugarcane yield. Elite families were identified using BLUP estimates. The humic soil populations produced a higher proportion of elite families and had a higher optimum selection rate compared to the sandy soil populations.

The significant female and male variance components indicated the effectiveness of using family data to estimate the breeding values of parents that were used in crosses. Elite parents for cane yield were identified using BLUP estimates from family data in both humic and sandy soil breeding populations. Elite parents can be used to build a core germplasm while the non-elite parents can be discarded for future breeding and selection. There were lower proportions of elite parents for both humic and sandy soil populations indicating a need for parent evaluation and development for these populations.

6.3 RECOMMENDATIONS FOR FUTURE RESEARCH

1. This study demonstrated the advantages of family over individual genotype selection for cane yield in the Midlands breeding programmes. Further studies are needed to investigate the benefits of family evaluation and selection for cane yield across the other SASRI breeding programmes.

2. Gains achieved by family selection at early stages of selection could be further enhanced by combining family selection with individual genotype selection in two steps; first selection of elite families and then individual selection. Thus, there is a need for research to evaluate the gains from combination of family and individual selection. This will allow for investigating the subsequent selection stages to determine whether family traits could predict the performance of genotypes advanced to later stages of the SASRI breeding programme.

3. Although yield components provided sufficient discriminating ability to determine family differences, family genetic interrelationships for the yield traits are still not known. Further studies are needed to determine the family phenotypic and genetic correlations among yield traits as well as establish path coefficients across different populations.

4. The current study has determined the optimum family selection rates for the Midlands breeding programmes. Therefore, further studies should focus on determining if the optimum family selection rates are static across the SASRI breeding populations.

5. Future studies should intensify evaluation of parents using family data, not only for the Midlands breeding programmes but also for other SASRI breeding programmes. The evaluation will identify elite parents that would form the basis of sugarcane breeding and such information can also be used for the development of sugarcane germplasm in South Africa.

6. Further studies are required to quantify the field variability in the original seedlings trials and accommodate them during experimental design.

7. Genetic populations studied in three years and in two environments are different. Therefore, it would be important to consider future research to study the same pool of families in contrasting environment, over different years.

6.4 REFERENCES

Nuss KJ (1998) Aspects considered in the search for new farms for the Experiment Station. Proceedings of the South African Sugar Technologists' Association 72:42-45

Risch NJ (2000) Searching for genetic determinants in the new millennium. Nature 405:847-856

Zhou MM (2014) Family evaluation for sugarcane yield, using data estimated from stalk number, height and diameter. Journal of Crop Improvement 28:406-417

ABSTRACT

Family selection provides the potential to improve gains for quantitative traits with low heritability such as cane yield at early selection stages. Family evaluation data can also be used to identify superior parents for use in future crossing. The objectives of the study were to compare family with individual genotype selection for cane yield components; to identify and determine the proportions of elite families for sugarcane yield; to determine the optimum family selection rate and identify ideal trait combinations among the elite families; to identify superior parents using family data and determine the proportion of superior parents within populations in the Midlands breeding programmes. Family data on stalk number, stalk height and stalk diameter were collected from a sample of the first 20 genotypes per family plot. Family yield data were analysed using Statistical Analysis System (SAS) linear mixed models. Family variance was 1.2 to 5.0 times that of individual genotype variance indicating larger variability among families compared to individual progenies. Families produced larger broad-sense heritability estimates (25 to 90%) than individual genotypes (1.6 to 23.5%) suggesting that selection for superior families would be more accurate than for individual genotypes. Families produced higher predicted selection gains (9 to 59%) compared to individual genotypes (1 to 12%) which indicated that family selection would be more efficient. Results indicated highly significant differences ($P<0.0001$) for family and group effects for all traits. The highly significant differences ($P<0.0001$) observed for family within group effects for stalk diameter indicated large variability for families within the different cane yield groups. The humic soil populations produced a significantly ($P<0.05$) high proportion of elite families and the higher optimum selection rate (30%) compared to sandy soil trials (25%) suggested that humic soil populations contained more elite families compared to sandy soil populations. Using BLUP estimates, female (82H0397, 96H0259, 98B0460, 98S0290, 98H0590, 98S1362 and N52) and male (02S0639, 82H0397, 97B0272, 98B0460, 98B1889 and N52) parents produced progenies with significantly ($P<0.05$) high cane yield compared to the population mean in both humic and sandy soil populations. The identified elite parents could be used in building a core germplasm pool of genotypes that produce elite progenies. Humic soil populations contained a higher proportion of elite parents (30.6%) compared to sandy soil populations (22.5%) which is probably due to longer cycles of recurrent breeding and selection in humic soil breeding programmes. The low proportions of elite parents for

both humic and sandy soil populations obtained suggest that intensive parent evaluation and development is required.

OPSOMMING

Familie-seleksie het die potensiaal om vordering vir kwantitatiewe eienskappe met lae oorerflikhede, soos rietopbrengs in 'n vroeë seleksiestadium, te bevorder. Familie-evaluasie data kan ook gebruik word om beter ouers te identifiseer wat gebruik kan word in toekomstige kruisings. Die doelwitte van hierdie studie was om familie- en individuele genotipe seleksie met mekaar te vergelyk ten op sigte van rietopbrengs-komponente; om die proporsies "elite" families te evalueer en te bepaal vir rietopbrengs; om die optimale familie-seleksie tempo te bepaal en om die ideale eienskapkombinasies tussen families te identifiseer; om beter ouers te identifiseer deur gebruik te maak van familie-data en om die proporsie beter ouers binne die Midlandse telingsprogramme te identifiseer. Familie-data in terme van aantal stele, steelhoogte en steeldeursnee is versamel vanaf die eerste 20 genotipes per familie-plot. Familie-opbrengs data is ontleed deur gebruik te maak van Statistiese Analise Stelsel (SAS) se lineêre gemengde modelle. Familie-variansie was 1.2 tot 5.0 keer dié van individuele genotipe variansie en dit toon aan dat groter veranderlikheid tussen families voorgekom het as tussen individuele nageslagte. Families het groter breë sin oorerflikheidsskattings (25 tot 90%) gelewer in vergelyking met individuele genotipes (16 tot 23.5%) en dit toon aan dat seleksie vir beter families meer akkuraat sal wees as vir individuele genotipes. Families het hoër verwagte seleksie-vorderings (9 tot 59%) gelewer in vergelyking met individuele genotipes (1 tot 12%) wat aanngetoon het dat familie-seleksie meer effektief sal wees. Resultate het aangetoon dat daar hoogs betekenisvolle verskille (P<0.0001) vir familie- en groepeffekte vir alle eienskappe voorgekom het. Die hoogse betekenisvolle verskille (P<0.0001) vir familie- en groepeffekte vir steeldeursnee het aangetoon dat daar groot veranderlikheid tussen families binne die verskillende rietopbrengsgroepe was. Die humusgrond-populasies het 'n betekinsvolle (P<0.05) hoër proporsie "elite" families geproduseer en die hoër optimum seleksietempo (30%) invergelyking met sandgrond proewe (25%) het voorgestel dat die humusgrond populasies meer "elite" families vervat het as die sandgrond populasies. Deur gebruik te maak van BLUP skattings het vroulike (82H0397, 96H0259, 98B0460, 98S0290, 98H0590, 98S1362 en N52) en manlike (02S0639, 82H0397, 97B0272, 98B0460, 98B1889 en N52) ouers nageslagte geproduseer wat betekenisvol (P<0.05) hoë rietopbrengste in beide humus- en sandgrond populasies gelewer het. Die geïdentifiseerde "elite" ouers kan gebruik word om 'n kern kiemplasmapoel van genotipes te bou wat weer "elite" nageslagte kan produseer. Humusgrond populasies het 'n hoër proporsie "elite" ouers (30.6%) vervat in vergelyking

met sandgrond populasies (22.5%) wat waarskynlik toegeskryf kan word aan die langer seleksiesiklusse van herhalende teling en seleksie in humusgrond telingsprogramme. Die lae proporsies "elite" ouers wat voogekom het vir beide humus- en sandgrond populasies stel voor dat intensiewe ouerevaluasie en ontwikkeling benodig word.

Sleutelwoorde: Suikerriet, familie, individuele genotipe, ouers, opbrengs, verwagte seleksie vordering