Evaluating families and breeding values of parental populations in sugarcane

By

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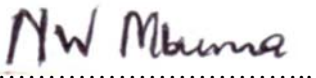
DECLARATION

"I, Ntombokulunga Wedy Mbuma, declare that the Doctoral research thesis that I herewith submit for the Doctoral Degree qualification Philosophiae Doctor 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."



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Signature Date

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TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS AND SI UNITS

asl	Above sea level
B	Breeding programme
BC	Breeding programme by crop year interaction
BL	Breeding programme by location interaction
BLC	Breeding programme by location by crop year interaction
BR(L)	Breeding programme by replication interaction within location
BRC(L)	Breeding programme by replication by crop year interaction within location
G(BRC(L))	Genotype nested within breeding programme by replication by crop year interaction within location
BLUP	Best linear unbiased prediction
BP	Bi-parental
BV	Breeding values
C	Crop year
c	Number of crop years
°C	Degrees Celsius
CL	Crop year by location interaction
CLCAP	Coastal long cycle average potential
CLCHP	Coastal long cycle high potential
cm	Centimetre
CR(L)	Crop year by replication within location
CSCAP	Coastal short cycle average potential
CSCHP	Coastal short cycle high potential
CV	Coefficient of variation
F	Family

FAOSTAT	UN Food and Agriculture Organization Corporate Statistical Database
FC	Family by crop year interaction
FE	Family by environment interaction
FL	Family by location interaction
FLC	Family by location by crop year interaction
FR(L)	Family by replication interaction within location
FRC(L)	Family by replication by crop year interaction within location
g	Number of seedlings/genotypes sampled per plot
G(FRC(L))	Genotype nested within family by replication by crop year interaction within location
Gs	Predicted selection gains
GxE	Genotype by environment interaction
H	Broad-sense heritability
K	Potassium
kg	Kilogram
L	Location
l	Number of locations
m	Meter
MO	Males only
MP	Melting pot
N	Nitrogen
P	Phosphorus
SAS	Statistical analysis system
SASEX	South African Sugar Experiment Station
SASRI	South African Sugarcane Research Institute
S.E.	Standard error
SD	Standard deviation

% Gs	Percent predicted selection gains
USA	United States of America
r	Number of replications
R^2	Coefficient of determination
RCBD	Randomised complete block design
R(L)	Replication within location
σ^2_F	Family variance
σ^2_{FC}	Family by crop year variance
σ^2_{FL}	Family by location variance
σ^2_{FLC}	Family by location by crop year variance
$\sigma^2_{FR\,(L)}$	Family by replication within location variance
$\sigma^2_{FRC(L)}$	Family by replication by crop year within location 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

ABSTRACT

Sugarcane is a complex crop which is under complex genetic control where chromosomes get eliminated after crossing, resulting in progeny performance deviating from the expected based mid-parent values. ~~The~~ early stage of sugarcane breeding is generally associated with low levels of precision and selection efficiency due to the significant genotype by environment interaction effects and competition among genotypes. The general aim of this study was to evaluate sugarcane families and assess the breeding values (BV) of genotypes to increase crossing and selection efficiency in sugarcane breeding programmes. The objectives were; to 1) determine the magnitude~~s~~ of variability in family variance components, 2) broad-sense heritability (H) and to evaluate their implications in breeding for cane yield, 3) to evaluate BV of genotypes using best linear unbiased prediction (BLUP), 4) to determine the range of BV among the SASRI gene pool, 5) to investigate family by environment interaction and evaluate its implications in sugarcane varietal development breeding. Family data on stalk number, stalk height and stalk diameter were sampled from the first 20 genotypes per family plot across the SASRI regional breeding programmes and were used to calculate cane yield.

Highly significant ($P< 0.001$) family and individual genotype variance in all the populations except CLCAP, indicated the existence of large genetic variability among the populations. Families produced larger variances and H estimates than individual genotypes, indicating that selection of superior families would be more effective than selecting among individual genotypes. The humic soil (68%), CLCHP (57%), CSCHP (57%) and irrigated (53%) populations had higher family H estimates for cane yield than sandy soil (42%), CLCAP (37%) and CSCAP (43%) populations, indicating the importance of family evaluation and the potential improved genetic gains through family selection, first followed by individual selection within those families in different ecological conditions and identification of location specific families. Low H estimates in sandy soil, CLCAP and CSCAP populations indicated a low proportion of genetic variability and thereby a potentially low selection efficiency among these populations. Significant ($P < 0.05$) female and male variances indicated ~~that~~ the presence of enormous genetic variability among progenies which was inherited from both the parents. Genotypes (82H0397, 85H0428, N52, B74713, 87W0629, 01G1662, 88W1323, 02K1657, 87L0573, 97E0474, N31, 93E0888, 03U1030, 06T3608,

96W0246, WI82498 and 79F0779) with high BV produced progenies with high cane yield when crossed with diverse genotypes, which indicate their general combining ability and these combiners can be utilised in base broadening programmes. Genotypes with high BV can be used to build a core germplasm /gene pool of best combiners that are known to produce high cane yielding progenies. The numbers of genotypes with high breeding values in CSCHP (29.4%), CLCHP (28.0%), humic soil and irrigated (26.0%) populations were higher compared to those in sandy soil (22.9%), CSCAP (21.0%) and CLCAP (18.4%) populations. Significant ($P<0.01$) family and family by location variance for cane yield, stalk number and diameter indicated the existence of location specific variability among families for these traits. The family by crop year and family by location by crop year interaction variances were non-significant ($P>0.05$). Evaluating families in multi-locations proved to be the need of the hour than its performance across ratoon crops. BLUP estimates identified elite families with significantly higher cane yield across locations and which were location specific compared to population mean. Results from this research could be used to guide future crossing (trait combinations) and selection at early stages of breeding thereby enhancing breeding efficiency

Key words: genetic variability, broad-sense heritability, breeding values, progenies, genotypes, family by environment interactions, cane yield traits, variance

CHAPTER 1

INTRODUCTION

Sugarcane (*Saccharum* hybrids spp) is a perennial crop that grows in warm tropical and subtropical environments. In South Africa, sugarcane contributes significantly to the economy producing sugar for local and export market. Research in plant breeding to support the production of sugarcane is carried out by South African Sugarcane Research Institute (SASRI) based at Mount Edgecombe, Durban. The objective of the SASRI breeding programmes is to develop and release high yielding varieties that are well adapted to diverse agro-ecological regions where sugarcane is grown in South Africa. SASRI operates seven regional breeding programmes; two for the high altitude Midlands region (24 months harvest cycle), four for the coastal area (12 to 18 months harvest cycle) and one for the irrigated region (12 months harvest cycle), each representing unique growing conditions.

Sugarcane cultivars are interspecific hybrids that have one of the most complex genomes among the plant species. It is a complex polyploid (allopolyploid and aneuploid) with chromosome numbers of hybrids ranging from 100 to 130 (Sreenivasan et al. 1987) and its complex genome interferes in breeding and slow down the genetic improvement. Due to limited control of genetic transmission during crossing, it is difficult to predict progeny performance. Most of the commercial traits such as cane yield and quality traits (dry matter, fibre, Brix, purity, sucrose content, ERC) are controlled by several genes, which result in large genotype by environment (G x E) interaction effects (Jackson and Hogarth 1992; Falconer and Mackay 1996; Jackson and McRae 1998). The effects of G x E are larger in early stages of sugarcane breeding because individual genotypes are planted in unreplicated small plots. The large effects of G x E reduces heritability and correspondingly selection efficiency. Due to the complex nature of sugarcane genome, accurate prediction of progeny performance at early stage of selection is not possible in sugarcane. Family evaluation has been proposed as one of the breeding strategy to increase heritability and correspondingly selection efficiency and selection gains in early stages of sugarcane breeding.

Family evaluation and selection in sugarcane breeding involves the positive selection of a whole population of progenies from a cross based on data collected from family plots

(Kimbeng and Cox 2003). In family evaluation, the selection for superior individual plants is focused within elite families where a higher proportion of superior genotypes exists. Families can be replicated across trials and locations providing an opportunity to compare families and evaluate family by environment interaction to identify stable families. Family evaluation and selection is reported to increase the efficiency of breeding for quantitative traits (Hogarth et al. 1990). Furthermore, family mean data is used to evaluate the potential of individual genotypes for their use as parents in hybridization.

Research on family evaluation started as early as in seventies in Australia (Hogarth 1971). Family evaluation and selection in sugarcane is practiced to different magnitudes 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. 2013; 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 evaluation and selection. In South Africa, family evaluation started in 1999 (Zhou and Lichakane 2012) for quality traits (dry matter, fibre, Brix, purity, sucrose content, ERC) and in 2011 for sugarcane yield (Zhou 2014) and work is being strengthened to have better selection efficiency methods in breeding trials.

The delay in implementing family evaluation for cane yield in South Africa was due to non-availability of automatic weighing machines and methods for collecting yield data, which is associated with high costs. In 2010, South Africa investigated the use of yield components (stalk number, stalk height and stalk diameter) to estimate cane yield (Zhou 2014) and the research showed that cane yield as estimated from stalk number, stalk height and stalk diameter is reliable and can be used to determine family genetic values and its worthiness for further use.

Comprehensive analysis of family data is needed to optimise family evaluation and selection in early generation stages, assess the variability and genetic parameters such variance components, broad sense heritability, predicted selection gains, and breeding values across diverse breeding populations and to evaluate the potential of genotypes to produce high yield progenies when used as parents during crossing. Research to quantify the proportion of elite

or superior families is limited but is essential to increase family selection efficiency. In Australia, the best 40% of the crosses were identified as elite families (Kimbeng and Cox 2003), but have not been statistically validated across breeding programmes. Breeding values refer to the ability of a genotype to pass its genes to progenies. Evaluating the breeding values of genotypes will thus provide objective parameters to select genotypes to be used as parents during crossing.

1.1 RESEARCH HYPOTHESIS

1. Family breeding parameters such variance components, broad sense heritability, and predicted selection gains are uniform across the seven SASRI breeding programmes.
2. The proportions of elite genotypes used in making crosses across the seven SASRI breeding programmes are similar.
3. Breeding values of all genotypes are similar among SASRI sugarcane populations.
4. There is no family by environment interaction across the seven SASRI breeding programmes.

1.2 RESEARCH OBJECTIVES

1. Determine the magnitude of variability in family variance components, broad-sense heritability and predicted selection gains, and evaluate their implications in breeding for cane yield.
2. Estimate the breeding values of genotypes by using best linear unbiased prediction (BLUP) and determine their advantages and importance in selection procedures.
3. Determine the breeding values and potential of genotypes/parents for SASRI germplasm collection and evaluate their worthiness for further utilization in base broadening programmes.
4. Investigate family by environment interaction and its implication in sugarcane breeding.

1.3 EXPECTED OUTCOMES

1. Family evaluation breeding parameters such variance components, broad-sense heritability and predicted selection gains across SASRI breeding programmes.

2. Estimates of breeding values for genotypes in the germplasm collection used for crossing.
3. Identification of proportions of genotypes with high breeding values among SASRI breeding programmes.
4. Significance of family by environment interaction in South Africa and identification of location specific families and stable genotypes.

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CHAPTER 2

LITERATURE REVIEW

2.1 ORIGIN, HISTORY AND PRODUCTION OF SUGARCANE

Sugarcane originated in Southeast Asia and its domestication started around 6000 BC (Barnes 1974) in New Guinea, where *Saccharum officinarum* was planted in gardens. The earliest known commercial sugarcane cultivation started in Northern India (Barnes 1974) and spread to other tropical and sub-tropical regions of the world. Sugarcane is now grown in southern Europe, Africa, Asia, Australia, USA, Mexico and South America (FAOSTAT 2014). Most of the sugarcane is grown between latitudes 30°N and 30°S of the equator (Bull and Glasziou 1979).

Sugarcane is an important source of food, fuel, fodder and fibre. Green tops of sugarcane are used as fodder for cattle in India (Singh and Katiyar 2016). The main by-products of sugar production are molasses and bagasse. Molasses are used as stock feed and for the production of ethanol (Zuurbier and Van de Vooren 2008), while bagasse (fibre) can either be burned to produce steam and/or electricity to run the sugar mills, or used in the production of cardboard, fibre board, furfural and wall board (Almazan et al. 1998). The sugar refining process also generates waste known as a filter cake or filter press. The filter cake is nutrition rich and also used as a substitute for lime in crop production (Allen and Padayachee 2011).

Approximately 75% of world's sugar is produced from sugarcane. In 2016/2017 (Figure 2.1), 170.8 million metric tons of sugar were produced worldwide (Statista 2018). The top ten sugar producing countries (Brazil, India, China, Thailand, Mexico, Pakistan, Colombia, Indonesia, Philippines, and USA) represents 75% of the world sugar production. Brazil is the top producer of sugar contributing 25% to the world production (FAOSTAT 2015). South Africa is ranked among the top 15 sugar producing countries in the world.

World sugar trade averages 60 million tonnes/year (International Sugar Organization 2018) with 60% as raw sugar. The 10 major raw sugar exporters are with Brazil, Thailand, Australia, Guatemala, Mexico, India, Cuba, Swaziland, Argentina and El Salvador

accounting for 92% in 2016. Brazil contributed 45% of exports in 2016. Africa imported 14 million of the 72 million metric tonnes world export in 2015/2016 and exported 4 million tonnes in 2015/2016 compared to 69 million metric tonnes of the world export. In 2018/2019, approximately 178.93 million metric tons of sugar were produced in total worldwide.

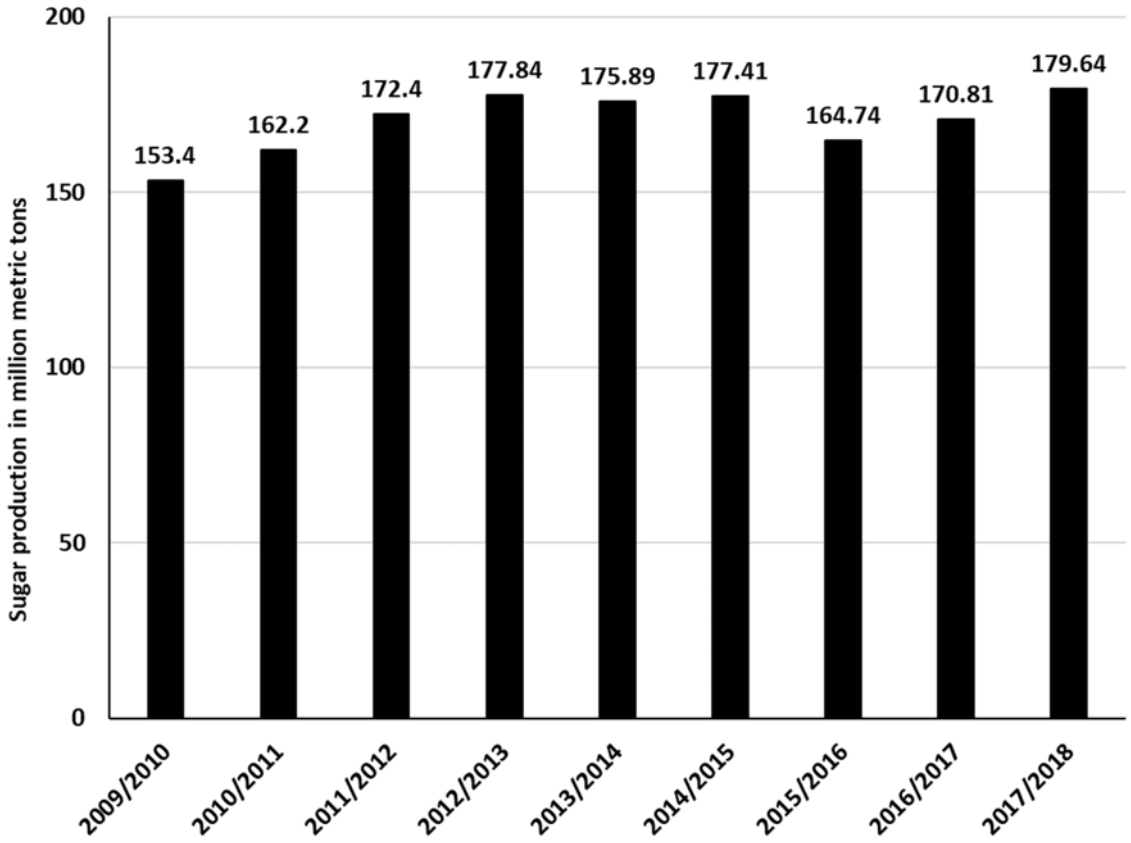

Figure 2.1 Sugar production worldwide from 2009/2010 to 2017/2018 (in million metric tons)

2.2 HISTORY AND PRODUCTION OF SUGARCANE IN SOUTH AFRICA

In South Africa, sugarcane cultivation and processing started around 1848 (O'Reilly 1998). It is cultivated between 25°33'S and 30°93'S, and 29°92'E and 32°32'E (Ramburan 2012) and grown in KwaZulu-Natal, Mpumalanga and Eastern Cape provinces where it contributes to the local economies (Maloa 2001). The sugar industry employs 79000 people directly and 350000 indirectly (South African Sugar Industry Directory 2015) and generates a revenue of R16 billion (South African Sugar Industry Directory 2016/2017).

There are 21889 registered sugarcane growers who produce 19 million tons of sugarcane, which are processed by 14 sugar mills to produce 2.3 million tons of sugar. About 76% of the sugar is marketed in the South African Customs Union (Botswana, Lesotho, Namibia, South Africa and Swaziland) and the remainder is exported to Africa, Asia and the USA (South African Sugar Industry Directory 2015).

2.3 SUGARCANE TAXONOMY, BOTANY AND GENETICS

Sugarcane is a tall perennial grass that belongs to the *Saccharum* genus in the Poaceae family (Cai et al. 2005; Chinnadurai 2017) comprising six species, namely *S. officinarum*, *S. spontaneum*, *S. robustum*, *S. barberi*, *S. sinense* and *S. edule* (D'Hont et al. 1998). The genus is characterised by high levels of polyploidy and variable chromosome numbers (Sreenivasan et al. 1987). The *Saccharum* complex includes related genera such as *Erianthus, Sclerostachya, Narenga* and *Miscanthus*) (Mukherjee 1957; Daniels and Roach 1987).

The sugarcane plant is made up of stem, leaves and root system. Each stem is composed of a series of nodes and internodes, each node bearing a leaf in the axil on which a bud is present and on germination the roots arise from root primordia and shoot from the bud. The root primordia germinate to produce the roots that support plant growth. The buds below the ground germinate to produce secondary, tertiary and higher order tillers which develop into millable stalks (Bull 2000). Tillering and stalk characteristics such as stalk height and stalk diameter are controlled by genetic and environmental factors (Smit et al. 2004). The terminal point of the stalk can develop into flowers.

Sugarcane is a polyploid (Sreenivasan et al. 1987; Grivet et al. 1996). *Saccharum* species have different chromosome numbers, for example, *S. officinarum* is an decaploid (2n = 80) with a basic chromosome number of 10. *S. spontaneum* is octoploid with a basic chromosome number of eight with a chromosome number ranging from 2n = 40 to 128. *S. robustum* has chromosome numbers ranging from 2n = 60 to 200. *S. barberi* has chromosome number ranging from 2n = 111 to 120. Chromosome numbers for *S. sinense* range from 2n = 80 to 124, while for *S. edule* the chromosome number ranges from 2n = 60 to 80 with aneuploidy forms (Buzacott 1965; Daniels and Roach 1987).

Modern sugarcane cultivars, which were originally derived from a cross between *S. officinarum* and *S. spontaneum*, are considered allopolyploid/aneuploid hybrids and are also comprised of a large number of chromosomes which ranges from 2n = 99 to 130 (Butterfield et al. 2001). Cytogenetic studies have clearly shown that the genomes of modern hybrids comprises 70 to 80% of *S. officinarum* chromosomes, 10 to 20% of *S. spontaneum* and 10 to 20% recombinants between the two species (D'Hont et al. 1998; Piperidis et al. 2001; D'Hont 2005).

2.4 HISTORY OF SUGARCANE BREEDING

2.4.1 Sugarcane breeding in the world

Sugarcane improvement through breeding started in Java and Barbados in 1888, following the observation in 1854 that sugarcane flowers could produce viable seeds (Stevenson 1965). Sugarcane breeding aimed to develop genotypes resistant to diseases, with higher sugar yield, better ratooning ability and adaptability to unfavourable growing conditions through interspecific hybridization (Roach 1972, 1986). The interspecific hybridisation between *S. officinarum* (noble canes: high sucrose) and *S. spontaneum* (disease resistance, high biomass and wide adaptability) have resulted in modern sugarcane cultivars, a process known as nobilisation (Stevenson 1965; Sreenivasan et al. 1987). Varieties produced by Proefstation Oost Java, identified as POJ varieties became the initial sources of germplasm in other breeding programmes. POJ 2878 was one of the popular genotypes produced by nobilisation (Jackson 2005). Coimbatore in India (1912) established a sugarcane breeding programme, producing Co varieties that were grown and used as germplasm in other countries, including South Africa.

2.4.2 Sugarcane breeding in South Africa

2.4.2.1 Early years

In South Africa, the first sugar was produced in 1852 from a noble cane, *S. officinarum*. The sugar industry depended on regular imports of varieties but most were susceptible to diseases, such as sugarcane mosaic virus (Brett 1950; Zhou 2013). In the 1880s, variety Uba (*S. sinens*e), imported from China, was resistant to sugarcane mosaic virus (Barnes 1964). However, after more than 32 years of commercial production, Uba succumbed to streak virus (Barnes 1964). In 1925, the South African Sugarcane Experimental Station (SASEX) (currently known as South African Sugarcane Research Institute, SASRI) was established at Mount Edgecombe with the aim of importing, testing and releasing adaptable

varieties with high yield, high sucrose content and resistance to pests and diseases (Nuss 1998).

Many imported genotypes were not adaptable in South Africa and often were susceptible to pests and diseases. As a result of failure of the imported varieties, SASRI breeding started with the objective of developing varieties adaptable to local growing conditions. Due to low winter temperatures (Brett 1947) and pollen infertility, crosses could not be effected in South Africa. Therefore initial crosses were imported from several countries such as India, Mauritius, Barbados and Florida. Few promising varieties were produced from imported crosses. Crosses between Co 421, Co 312 (imported from Coimbatore, India in 1938) and N44 (Brett 1950) produced famous varieties such as NCo 310 that was released in 1945 and NCo 376 that was released in 1955 (Nuss and Brett 1995).

2.4.2.2 Sugarcane flowering and pollen survival

Sugarcane naturally exhibits variable flowering patterns and infertile pollen in sub-tropical environments such as South Africa (Berding et al. 2007). Flowering occurs in winter when temperature~~s~~ fluctuate below 20°C, the minimum required for pollen survival (Brunkhorst 2003; Horsley and Zhou 2013). The optimum temperatures for development of inflorescence and pollen are 28°C during the day and 23°C at night (Horsley and Zhou 2013). Day temperatures above 31°C and night temperatures below 18°C reduces flowering and pollen production (Brett and Harding 1974; Moore and Nuss 1987; Horsley and Zhou 2013; Zhou 2013).

Research on flowering aspects done in South Africa (Brett 1947, 1951) led to the construction of the glasshouse (1966) and photoperiod house (1971) (Nuss 1982; Zhou 2013) that maintain temperature above 20^{o}C (Brett 1947, 1951; Zhou 2013). Both the photoperiod house and glasshouse are used for artificial photoperiod treatments to ~~initiate~~ induce flowering while the glasshouse is also used as a crossing facility.

2.4.2.3 SASRI sugarcane breeding programmes before 1997

At SASRI, crossing started in 1945 when temperature control experiments (Brett 1947, 1951) showed pollen survival could be achieved by maintaining temperatures above 20^{o}C. Coastal breeding programmes were established at Shakaskraal (North coast), Mtunzini in Zululand and Central field station near Durban in the 1950s (Table 2.1) and were followed

by irrigated breeding based at Pongola research station in 1965, and the Midlands breeding programme in the 1970's. In 1993, SASRI breeding programmes were reviewed after loss of Central field station due to urban expansion. Replacing Mtunzini and Shakaskraal (high soil variability) stations with more representative breeding stations were recommended (Nuss 1998).

Table 2.1 Original breeding sites used in SASRI breeding programmes

Location	Established	Region	Harvest cycle	Seedlings
Pongola	1965	Irrigated	12 months	50000
Mtunzini	1950	Coast	12 months	25000
Shakas Kraal	1950	Coast	12 months	25000
CFS	1965	Coast	18 months	25000
Mount Edgecombe	1925	Coast	12 months	25000
Holly Bros	1965	Midlands	24 months	9000

2.4.2.4 SASRI sugarcane breeding programmes after 1997

Following the recommendations to replace the research stations in the rain-fed region, new research stations were acquired in 1997. The new research stations (Table 2.2) were Bruyns Hill and Glenside, representing the humic and sandy soils breeding programmes, respectively in the Midlands region. The humic soil breeding programme is based on rich soils, characterised by having more than 5% organic matter, while sandy soil have less than 2% organic matter (Van Antwerpen et al. 2013). Kearsney research station was established to represent the coastal long cycle high yield potential programme, Gingindlovu to represent coastal long and short cycle average yield potential programmes and Empangeni research station representing the coastal short cycle high yield potential programme (Nuss 1998). As a result, the number of breeding programmes operated by SASRI increased from six to seven. Each breeding programme represented each of the major agro-ecological regions of sugarcane cultivation in South Africa (Figure 2.2).

Table 2.2 Current SASRI breeding research stations and their breeding programmes

Research station	Region	Programme	Crop age	Seedlings
Pongola	Irrigated	Irrigated	12 months	50000
Empangeni	Coast	Short high potential	12 months	50000
Gingindlovu	Coast	Short average potential	12 months	25000
Gingindlovu	Coast	Long average potential	16-18 months	25000
Kearsney	Coast	Long high potential	18 months	50000
Bruyns Hill	Midlands	Humic soil	24 months	25000
Glenside	Midlands	Sandy soil	24 months	25000

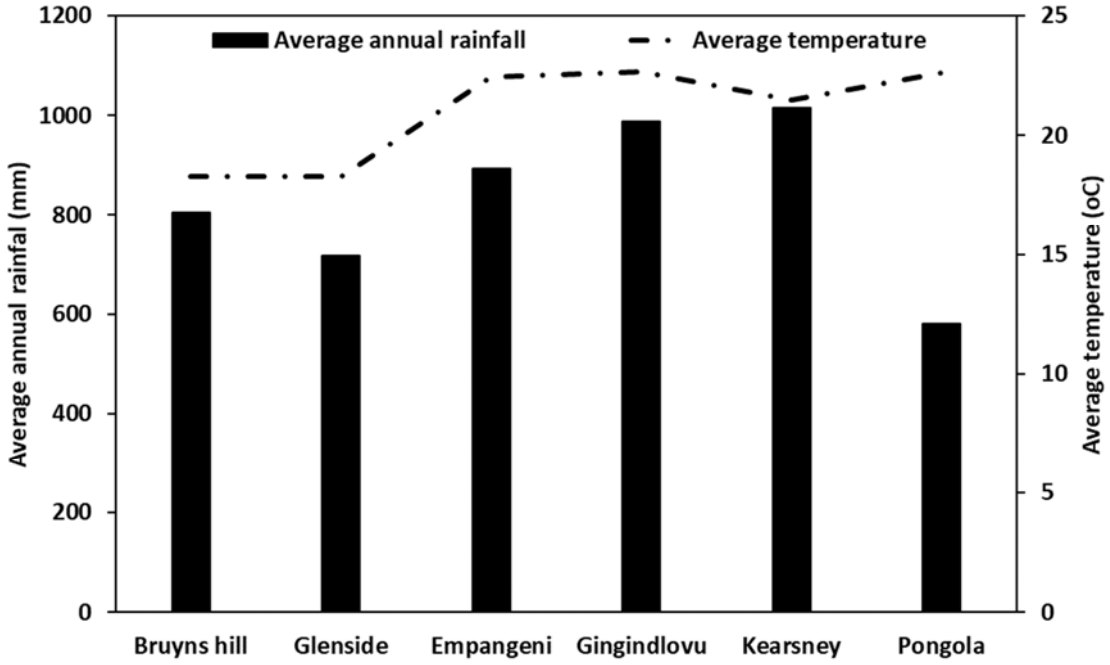

Figure 2.2 Climatic conditions of the different agro-ecological regions for sugarcane production in South Africa

2.4.2.5 Stages of the sugarcane breeding programmes

SASRI breeding programmes have five stages namely crossing, mini lines, single lines, observation, and variety trials (Table 2.3). Breeding programmes start by parental selection and crossing genotypes possessing desirable traits and of choice. Depending on the

breeding objectives, the genotypes to be used in the crosses can be selected either from local, imported or from wild germplasm. The seedlings obtained are distributed to all SASRI regional breeding programmes to undergo field evaluation and selection.

The mini-lines is the first field evaluation stage where progenies from several crosses are planted in 1 m long plots and evaluated for yield, quality, agronomic, pest and disease traits. At this stage, families are replicated while progenies within families are not replicated. The single lines stage is the second field evaluation where genotypes selected from mini-lines are each planted in 8 m unreplicated single row plots. Data collected in the plots are used to determine the genotypes to be advanced to variety observation trials and this is the first stage with replication. The genotypes are planted in two row plots of 8 m length and three replications. Yield, quality, agronomic, pest and disease data were recorded to evaluate the performance of genotypes in the plant and first ratoon crops. Selected genotypes are planted in varietal trials, established at five or six locations with each genotype planted in at least three replications per trial and data collected in the plant, first, second or third ratoon crops. Selected varieties are recommended for release. Field evaluation and selection takes between 12 years (12 months cycle) to 19 years (24 months cycle) from seedlings to release of a new commercial variety (Zhou 2013).

2.5 SELECTION METHODS IN SUGARCANE BREEDING

2.5.1 Mass selection

Mass selection refers to selection of an individual plant, based on the phenotype of each plant in a mixed population (Bressiani et al. 2005). In early stages of sugarcane breeding, mass selection considers traits with high heritability such as is the case with disease infection, flowering and juice Brix % and visual selection of clones for traits correlated with sugarcane yield. Sufficient gains were achieved through mass selection for traits with high heritability (Hogarth et al. 1997). However, mass selection is not efficient when selecting for traits with low heritability such as cane yield (Simmonds 1996). Several studies on various crops such as potatoes (Benavente and Pito 2012), maize (Viana 2007), apple (Hajnajari et al. 2012) and sugarcane (Hogarth 1971) have indicated that yield have low heritability . The early stage of breeding is known to be associated with low levels of selection efficiency due to the high genotype by environment interaction and competition effects among individual genotypes (Skinner 1971). Individual plants are not replicated at early stages, resulting in a low experimental precision.

Table 2.3 SASRI breeding programme stages

Stage	Genotypes	Plot	Replications	Crop	Year	Selection %
Seedling	250000	1 Plant	Families x 3	1	0	70
Mini-line	157000	1 row x 1 m	Families x 3	1	1	11
Single lines	20000	1 row x 8 m	Families x3	1	2	10
Observation	2000	2 rows x 8 m	3	2	3-5	10
Variety trials	200	5 rows x 8 m	>3 reps	3	6-10	
Bulking	1-2				11-15	

Source: Zhou (2013)

The significant large genotype by environment interaction, high competition effects among genotypes and low experimental precision at early stages of breeding cannot be practically resolved by replicating because of the large number of individual genotypes involved as well as insufficient plant material (Zhou 2009). However, suitable experimental designs and statistical models that account for inter-plot competition can be used to increase selection efficiency.

Several methods such as path coefficient analysis (De Sousa-Vieira and Milligan 2005), spatial analysis (Edmé et al. 2007), artificial neutral networks models (Zhou et al. 2011) and logistic regression models (Zhou et al. 2013a) have been explored in sugarcane breeding to increase selection efficiency at early stages. Path coefficient analysis is used to determine traits to focus on during selection. Spatial analysis was used to increase the precision of estimating genetic values by accounting and removing spatial variability from phenotypic values (Edmé et al. 2007; Bian et al. 2017). Artificial neutral network models predict individual seedlings that have the best combination of traits that would increase yield. Logistic regression models (Zhou et al. 2013a; Zhou 2018) are a decision support tool for selecting genotypes in un-replicated clonal plots.

2.5.2 Proven cross system

The proven cross system was used in sugarcane breeding to evaluate crosses (Skinner et al. 1987) in Australia (Heinz and Tew 1987), South Africa (Skinner 1982), Indonesia (Sukarso 1986) and other countries. The proven cross system depends on the number of genotypes

in a cross that are advanced across stages. Crosses with large numbers of individuals advanced, are considered elite families. This system was biased against new crosses (Walker 1963). The proven cross system uses no systematic statistical analysis for comparing crosses. Furthermore, with the proven cross system, breeders had to wait 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).

2.5.3 Family evaluation

Family evaluation involves collecting data from progenies of crosses and using the data to determine family values (Kimbeng and Cox 2003). Family evaluation has been widely used 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), maize (Noor et al. 2013) and sugarcane (Kimbeng and Cox 2003). Family evaluation and selection have shown to reduce breeding cycles in perennial crops such as Eucalyptus and other tree crops (Marques junior et al. 1996; Baudouin et al. 1997; Apiolaza 2009).

Family selection refers to accepting or rejecting entire progenies from a cross, based on family mean values. Family evaluation and selection proved superior to mass selection of individual genotype for traits with low heritability such as sugarcane yield by many workers (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 evaluation and selection in sugarcane was first described by Hogarth (1971). Despite their research, family evaluation and selection could not be easily implemented due to high cost involved in weighment of seedling plots. During that period, 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 (Hogarth and Mullins 1989) family evaluation was adopted in Australia (Kimbeng et al. 2000). Cox and Hogarth (1993) reported that family evaluation was used to determine 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).

To date, family evaluation and selection have been implemented in several sugarcane breeding programmes including Australia (Jackson et al. 1995; Kimbeng et al. 2000; Kimbeng and Cox 2003), Brazil (Pedrozo et al. 2011), India (Shanthi et al. 2008), (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; Tai et al. 2003), Cuba (Ortiz and Cabellero 1989), Hawaii (Wu and Tew 1989) and Louisiana (Chang and Milligan 1992a, 1992b).

In Australia, family plots of seedlings are replicated and at crop harvest, the replicated plots are sampled to obtain stalks from which cane quality (dry matter, fibre, Brix, purity, sucrose content, ERC) values are estimated in the laboratory. The family plots are harvested and weighed to estimate yield and the data are analysed to determine family means which are used for selection. Individual genotypes are selected from families with high mean values in the ratoon crop. In South Africa, stalk number, stalk height and diameter are measured from the first 20 seedlings in a family plot and used to estimate cane yield with a formula that assume that sugarcane stalks are a perfect cylinder in which a density if 1.00 g/cm^3. At harvest age, stalks are randomly sampled from each family plot and analysed in the laboratory to determine cane quality traits (Schoonees-Muir et al. 2009). The estimated cane yield and cane quality data (dry matter, fibre, Brix, purity, sucrose content, ERC) are analysed to determine high trait value families and individual elite genotypes are selected within the elite families in the same crop (Zhou 2014).

The advantages of family evaluation and selection is that families are replicated in trials and across locations in early stages of breeding compared to individual genotypes which cannot be replicated due to limited planting material. Furthermore, progeny data from replicated families can be used to evaluate family by environment interactions for families planted across locations (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). The same data can determine breeding values (Cox and Stringer 1998; Shanthi et al. 2008; Zhou et al. 2013b).

2.5.4 History of family evaluation in South Africa

With family evaluation in South Africa (Bond 1977) the mean cane yield of seedlings were used to predict the value of a cross. A phenotypic correlation (r = 0.69) between the number of seedlings selected and the mean yield for the family indicated potential of family evaluation. Further research has shown a phenotypic correlation (r = 0.33) between yield in breeding stages 1 and 2 (Bond 1989).

Bond (1989) suggested that quality traits (dry matter, fibre, Brix, purity, sucrose content, ERC) may benefit from family evaluation and selection. A study by Zhou and Lichakane (2012) showed benefits of family evaluation for quality traits (dry matter, fibre, Brix, purity, sucrose content, ERC). Zhou and Mokwele (2015) showed the benefits of family and parent evaluation for *Eldana saccharina* stem borer. Zhou (2014) showed that cane yield (estimated from stalk number, stalk height, and stalk diameter and assumed that sugarcane stalk is a perfect cylinder in which a density is 1.00 g/cm^3) was suitable for family evaluation and selection compared to individual selection. Mbuma et al. (2017) also demonstrated identification of superior families for cane yield and its components.

2.5.5 Parent evaluation

2.5.5.1 Proven parent system

The proven parent system use the number of seedlings advanced to determine superior parent genotypes (Heinz and Tew 1987; Skinner et al. 1987). The system was biased towards older parents that were planted more frequently as well as those with higher germination rates. Another disadvantage was associated with the lack of a statistic tool to compare the performance of genotypes in crosses. The proven parent system took several years to determine productive parents due to accumulation of advanced varietal trial data over long period of time.

2.5.5.2 Breeding value

Breeding values were used long ago in animal breeding to estimate a cow or bull's genetic merit for a trait using the best linear unbiased prediction (BLUP) (Henderson 1977, 1984). Breeding values refer to the ability of a genotype to produce progenies with high trait values when crossed with other genotypes. In crop plants, the early research on breeding values focused on forestry breeding (White and Hodge 1989). Breeding values are helpful to predict additive genetic effects particularly in complex genomes such as sugarcane.

Breeding values are being used in maize (Vivek et al. 2017), soybean (De Carvalho et al. 2008), peach (De Souza and Byrne 2000) and sugarcane (Chang and Milligan 1992a, 1992b; Atkin et al. 2009; Atkin 2010; Zhou and Mokwele 2015). In sugarcane, breeding values were estimated from family data (Stringer et al. 1996), predicted using pedigree data (Atkin et al. 2009), and used in selection of parents (Jackson 2016).

2.6 GENETIC VARIANCE, HERITABILITY, PREDICTED SELECTION GAINS AND BEST LINEAR UNBIASED PREDICTION (BLUP)

Genetic variance refers to the heritable proportion of the total phenotypic variance and the genotypic variance (the variance due to genetic variation) can be subdivided into three components such as additive genetic variance, dominance variance, and epistasis variance. The magnitude of the variance attributed to the genotype in the population determines the extent of genetic improvement of that population through selection and influences breeding and selection strategies. The genetic variance is used to determine the heritability of the population of a given trait.

Heritability is the ratio of genetic to phenotypic variance and is used in plant and animal breeding to quantify the precision of selection in field trials (Piepho and Mohring 2007). There are two types of heritability, namely broad-sense and narrow-sense heritability. Broad sense heritability (H) refers to the degree to which the phenotype of an individual is controlled by its genotype (Falconer 1960). It is expressed as the proportion of the total genetic variance (additive, dominance, and epistasis) to the total phenotypic variance in a population. In breeding clonally propagated crops such as sugarcane and banana, where segregation events are limited to time of crossing, broad-sense heritability are evaluated in subsequent testing stages only (Zhou and Joshi 2012). In contrast, narrow-sense heritability is a measure of the proportion of additive genetic variation to phenotypic variation in a given population for a given trait (Falconer and Mackay 1995). It is expressed as the ratio of additive genetic variance to phenotypic variance (Wei and Jackson 2016). Because the additive component of genetic variance determines the response to genetic effects that can be utilised and predicted easily during crossing, the breeding values in a breeding programme are estimated through narrow-sense heritability. The broad sense and narrow-sense heritability estimates are always in the range of 0 to 1. The closer the heritability estimates are to 1, the larger the proportion of the phenotype explained by the genotype.

Therefore, in sugarcane breeding, narrow-sense heritability can be exploited at crossing and broad-sense heritability is exploited during selection stages.

The broad-sense heritability is an important breeding parameters because it is used to determine the predicted selection gains at a given selection intensity. Predicted selection gains refer to the genetic improvement of the traits that can be expected in subsequent generations (Wolie et al. 2013). The broad-sense heritability and predicted selection gains enable breeders to understand the effect of selection on genetic improvement, to identify the strengths and the weaknesses of the breeding population and to determine the efficiency of current breeding strategies. These quantitative genetics parameters enable the breeders to identify traits that are responsive to genetic improvement through selection in a breeding population.

The BLUP method is used to accurately predict the breeding values of parental genotype in animal and plants. The main advantage of the BLUP over other statistical methods is that it can accommodate a highly unbalanced data sets, such as those generated from routine sugarcane progeny evaluation trials (Stringer et al. 2011; Zhou and Mokwele 2015). Chang and Milligan (1992a, 1992b) reported use of BLUP to predict cross performance. The BLUP has been increasingly used to identify and select parents and crosses, and to design new crosses in Australia (Atkin et al. 2009, Atkin 2010; Jackson 2016), South Africa (Zhou 2014; Zhou and Mokwele 2015), and Brazil (Moreira and Peternelli 2015). Further research (Piepho et al. 2008; Atkin et al. 2009) has reported that the BLUP estimated from pedigree data was more accurate than estimates from independent single trial.

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CHAPTER 3

COMPARING FAMILY WITH INDIVIDUAL GENOTYPE VARIANCE AMONG SUGARCANE BREEDING POPULATIONS

3.1 ABSTRACT

Family evaluation data obtained from progenies are used to determine traits values of family mean and identify superior families in comparison with population mean. After family evaluation, best individual genotypes are selected within the elite families. The ability to detect significant genetic differences among families depends on the variance associated with the means. The objectives of this study were to compare family with individual genotype variance components among different breeding populations, to compare trends in variances over time and across breeding populations, and to evaluate their implications in breeding for cane yield. Data were collected from the Midlands humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP), and irrigated populations, planted from 2010 to 2015. Data on stalk number, stalk height and stalk diameter were used to estimate cane yield, measured from the first 20 mini-lines in each family plot, and analysed using the linear mixed models of the Statistical Analysis System (SAS) to estimate variance components. Family and individual genotype variance were highly significant ($P<0.001$) indicating large genetic variability. Family variance was larger than individual genotype variance, indicating larger genetic variability among families and scope for exploitation of heterotic segregants for genetic enhancement. The humic soil, sandy soil, CLCHP and irrigated populations recorded high family variances which implies a very efficient and unbiased family selection compared to CLCAP, CSCHP and CSCAP populations and in identification of families with a higher frequency of superior clones. The lower variances or less genetic variation among Midlands sandy soil, CLCAP and CSCAP populations suggested narrow genetic diversity among the parents utilised in crossing and lay emphasis on attempting more number of divergent crosses for Midlands region. The rationale for family selection is not to produce superior families with commercial value but rather to identify families. Hence, identification of promising families with the maximum potential of producing

economically viable genotypes would be of great interest and usefulness to the sugarcane breeders.

Key words: Family, individual genotypes, genetic variability, selection efficiency

3.2 INTRODUCTION

Commercial sugarcane cultivars are complex polyploids and aneuploids, which were derived from inter-specific hybridisation between *Saccharum officinarum* and *Saccharum spontaneum* polyploid species (Butterfield et al. 2001; Da Silva and Bressiani 2005; Premachandran et al. 2011) in the 18th century (Price 1963). The heterozygous and complex polyploid genetic make-up of sugarcane hybrids produces high genetic variability among progenies within crosses (Premachandran et al. 2011). The progenies are genetically different due to the heterozygous nature of the parents (Vettore et al. 2001). There is low prediction of family and progeny performance because of the complex and variable chromosome transmission during crossing (Grivet and Arruda 2001; Mudge et al. 2009). Large number of genotypes are planted in smaller plots and tested in early stages of plant breeding trials. The small plots result in large inter-plot competition and significant genotype by environment interaction, which in turn reduces selection efficiency (Jackson and McRae 2001). Family evaluation and selection is thereby explored to increase selection efficiency. Individual genotypes are selected from high cane yield families while inferior families are discarded (Kimbeng and Cox 2003).

Studies on family evaluation and selection research were reported 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 2014a) and superior families and individuals were selected for further evaluation. Preliminary studies in South Africa (Zhou 2014a) and other countries (Barbosa et al. 2005; Shanthi et al. 2008; Kimbeng et al. 2000) showed larger gains from family selection for yield compared to individual genotype selection.

Family evaluation involves collecting data from progenies within family plots and analysing the data to determine trait values of a family (Kimbeng and Cox 2003). During

family evaluation and selection, the whole population of progenies within the family are selected or rejected based on family means and family breeding parameters such as genetic variability, heritability and predicted selection gains (Falconer and Mackay 1996). With family evaluation, the selection for superior individual plants is focused within the best families where a greater chance of identifying superior genotypes exists. The breeding Stage I "mini-lines" is the first field evaluation stage where progenies from several crosses are planted in 1 m long plots and evaluated for cane yield components (stalk number, stalk height, and stalk diameter), quality (dry matter, fibre, Brix, purity, sucrose content, ERC), pest and disease traits. At this stage, families are replicated while progenies within families are not replicated because of limited planting material and the large number of genotypes involved.

One of the advantages is that families can be replicated in trials and across locations while individual genotypes cannot be replicated due to limited planting material and the large numbers planted. Family data are used to evaluate genotypes for parent selection. Family evaluation has previously shown to increase genetic gain for traits with low heritability such as cane yield (Bond 1989; Kimbeng et al. 2000; Shanthi et al. 2008; Pedrozo et al. 2011; Zhou 2014a).

The magnitude of genetic variability sets the limit of improvement of a crop through breeding (Falconer 1989; Roach 1989; Hogarth et al. 1981). Variance components can provide an estimate of genetic variability in a population (Chaudhary 2001; Zhou and Lichakane 2012; Zhou et al. 2013; Zhou 2014a; Ebid et al. 2015).

The South African Sugarcane Research Institute (SASRI) operates seven regional breeding programmes (Table 3.1) which were established to develop varieties for the main agro-ecological regions of South Africa (Nuss 1998; Parfitt 2005; Zhou 2013a). These breeding programmes are focussed for both rain-fed and irrigated sugarcane growing regions. The rain-fed region is subdivided into the Midlands and coastal regions. The Midlands region is represented by the sandy and humic soil breeding programmes which are characterised by a high altitude, long and cold winters, and prolonging crop maturity to approximately 20 to 24 months harvest age. The coastal long cycle breeding programme is divided into coastal long cycle high potential (CLCHP) and coastal long cycle average potential (CLCAP) programmes. These two breeding programmes were established to develop high

yielding and late maturing varieties that can be harvested at the crop age of 16 to 18 months, and the breeding programmes are established in areas where Eldana damage is endemic and Eldana resistance is required. The coastal short cycle breeding programme is divided into coastal short cycle high potential (CSCHP) and coastal short cycle average potential (CSCAP) programmes. These were established to develop high yielding and early maturing varieties that can be harvested at the crop age of 10 to 12 months in areas where sugarcane is normally harvested at 18 months. The CSCHP is located in high potential areas due to highly distributed rainfall and deep fertile soils, while the CSCAP is located in average potential areas, having low rainfall, shallow soils and high Eldana predation. The irrigated breeding programme is located in areas with a high temperature, and a combination of irrigation and high heat units accelerates crop maturity, allowing it to be harvested at a crop age of 12 months.

Table 3.1 SASRI regional breeding programmes

Research station	Breeding programme	Harvest cycle	Altitude (m)	Latitude	longitude
Pongola	Irrigated	12	308	27°24'S	31°35'E
Empangeni	Coastal short cycle high potential	12	102	28°43'S	31°53'E
Gingindlovu	Coastal short cycle average potential	12	93	29°1'S	31°36'E
Gingindlovu	Coastal long cycle average potential	16-18	93	29°1'S	31°36'E
Kearsney	Coastal long cycle high potential	16-18	241	29°17'S	31°16'E
Bruyns Hill	Humic soil	24	1012	29º42'S	30º68'E
Glenside	Sandy soil	24	997	29°20'S	30°46'E

The differences in agro-ecological regions as well as the differences among the populations used to start the breeding programmes are expected to influence the magnitude of breeding parameters. Further, some breeding programmes are more than 50 years old (such as the irrigated programme) while others are relatively young (over 20 years). Some breeding programmes such as the Midlands programmes have longer cycles because of 24 months cutting age. Thus, a study of family and genotype variances is necessary to examine the differences among the breeding programmes over time and their potential to identify location suitable cultivars. Therefore, the objectives of this study were to compare family to individual genotype variance trends over time among different breeding populations and to evaluate their implications in breeding for cane yield.

3.3 MATERIALS AND METHODS

3.3.1 Experimental material

Sugarcane families (crosses) included in this study were made at Mount Edgecombe research station (96 m altitude; 29°42', 31°2'E) located in Durban, KwaZulu-Natal province of South Africa. The families included in this study were developed between May and August during 2007 to 2015 crop seasons. Three mating designs were used to generate, bi-parental, males only and melting pot families. Bi-parental mating involves crossing one female parent with a male parent. Males' mating involves inter-crossing of at least two male parents and collecting seed from all genotypes in which the identity of the pollen donor is unknown. Melting pot technique is one where several male parents pollinate a single female parent.

3.3.2 Experimental design, seedling establishment and management

Seedlings were germinated from true seed (seed fuzz) in the glasshouse at Mount Edgecombe research station. A week after germination, the seedlings in trays were transferred outside the glasshouse for hardening. At five weeks age, seedlings 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 (RCBD) with three replications per family. The seedlings (genotypes) from each family were divided into three sets and each set was randomly assigned to a replication. The families were replicated but the individual genotypes within a family were not. 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 which contained individual seedlings.

The growing conditions in the air-bricks were even because of uniform growth media and irrigation and, therefore, no residual effects were expected. The growth media was a mixture of sand, soil and bagasse compost in the 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 1 m long stalks.

3.3.3 Experimental sites and trial establishment

From each seedling, l m long vegetative stalks were cut at the base and topped at the natural breaking point. Cane setts were planted in the field using the same experimental design used in air-bricks. Cane setts were planted in a 1 m long plot. For the Midlands trials, a 1 m spacing between two rows was used and 2 m (equivalent to one unplanted row) was left between the two tramline rows. For coastal trials, the spacing was 1.2 m between rows and 2.4 m between tramlines, while for the irrigated trials, the spacing was 1.4 m between rows and 2.8 m between tramlines. Tram-line refers to a system where two adjacent rows are planted, followed by an unplanted row.

The number of families planted in each trial ranged from 85 to 290. The total number of families in the Midlands humic soil was 453, Midlands sandy soil was 592, coastal long cycle high potential was 911, coastal long cycle average potential was 580, coastal short cycle high potential was 887, coastal short cycle average potential was 622, and irrigated was 1088. On average, 245 seedlings/individual genotype populations were sown from each cross/family. However, because of variable seed set at the time of crossing and variable germination percentage and seedling survival in the nursery, there were variable seedling numbers per cross planted in the field, ranging from 45 to 378. This varying number of seedlings is typical at Stage I in sugarcane breeding. The trials were planted in the field during 2010 to 2015 crop seasons across the seven regional breeding programmes (Table 3.2). The Midlands trials were established at Bruyns Hill (1012 m altitude; 29º25’S, 30º68’E) and Glenside (997 m altitude; 29°20'S, 30°46'E) research stations which are characterised by a high altitude and climates with shorter summers and long and cold winters. Bruyns Hill is located on humic soils with 5% organic matter, 18 to 36% clay, 3% N mineralisation, 60 to 80 cm rooting depth compared to sandy soils at Glenside with 2% organic matter, 10 to 15% clay, 1.2 to 1.8% N mineralisation and a rooting depth of 40 to 60 cm.

Table 3.2 The number of female and male genotypes used to make families (crosses) planted in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated trials

Populations	Year planted	Females	Males	Crosses
Humic soil	2010	38	22	102
Humic soil	2011	47	31	113
Humic soil	2012	35	32	111
Humic soil	2013	40	26	127
Sandy soil	2010	38	23	121
Sandy soil	2011	92	45	163
Sandy soil	2012	36	34	112
Sandy soil	2013	31	19	111
Sandy soil	2015	47	40	85
CLCHP	2011	93	71	217
CLCHP	2012	59	50	217
CLCHP	2013	59	52	217
CLCHP	2014	51	24	93
CLCHP	2015	78	38	167
CLCAP	2011	53	42	127
CLCAP	2012	39	31	128
CLCAP	2013	43	28	119
CLCAP	2014	60	33	109
CLCAP	2015	48	36	97
CSCHP	2011	65	44	198
CSCHP	2012	69	46	199
CSCHP	2013	61	29	141
CSCHP	2014	93	54	183
CSCHP	2015	86	41	166
CSCAP	2011	60	43	120
CSCAP	2012	52	31	147
CSCAP	2013	35	25	118
CSCAP	2014	63	31	118
CSCAP	2015	60	32	119
Irrigated	2011	95	44	241
Irrigated	2012	79	35	166
Irrigated	2013	93	37	253
Irrigated	2014	115	57	290
Irrigated	2015	78	22	138

Coastal long cycle high potential trials were planted at Kearsney research station (241 m altitude; 29°17'S, 31°16'E) while coastal long and short cycle average potential trials were established at Gingindlovu research station (93 m altitude; 29°1'S, 31°36'E). The coastal short cycle high potential trials were planted at Empangeni research station (102 m altitude; 28°43'S, 31°53'E) and the irrigated trials at Pongola research station (308 m altitude; 27°24'S, 31°35'E).

3.3.4 Data collection

Stalk number, stalk height and stalk diameter per family plot were measured from the first 20 individual genotypes. The number of millable stalks was counted per genotype plot. Stalk height (m) was measured from the ground level to the topmost visible dewlap of the stalk. Stalk diameter (cm) was measured using a digital calliper at the centre of each of three stalks. Cane yield (kg) was calculated from stalk number, stalk height and stalk diameter using the formula described by Chang and Milligan (1992a):

Cane yield = $ndr^2\pi h$ …..……..……Equation 3.1

Where n = number of stalks, d = the density considered equal to 1 g cm^{-3}, r = radius of stalk in centimetres, π = 3.14159265, and h = stalk height in metres. The calculation assumed the stalk was a perfect cylinder with a density of 1.00 g cm^{-3}.

3.3.5 Data analysis

Data for cane yield, stalk height, stalk number and stalk diameter were analysed using linear mixed models of Statistical Analysis System (SAS Institute 2014). The estimates of variance components, their standard errors and probability tests were calculated using the COVTEST option in the model statement. The following statistical linear mixed model was used for family analysis:

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

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

3.4 RESULTS

3.4.1 Cane yield

Family variance (σ^2_F) for cane yield was highly significant ($P<0.001$) in all except the sandy soils (2010, 2015), CLCAP (2011, 2012, 2015), CSCAP (2014, 2015) and irrigated (2015) trials (Table 3.3). The family variances for humic and sandy soil trials increased in trials of 2011-2013 and 2010 to 2012 seasons, respectively. Fluctuations in family variance was observed in CLCHP, CSCHP and CLCAP populations. The family variances for the CSCAP and irrigated trials decreased in crop year 2013 and from 2012 to 2015, respectively. The humic soil, CLCHP, CSCAP and irrigated trials produced larger family variances than the sandy soil, CLCAP, and CSCHP trials.

The family by replication variance (σ^2_{FR}) was highly significant ($P<0.001$) for all populations. The humic soil, CSCHP and irrigated trials produced fluctuations in family by replication variance. The family by replication variances for sandy soil, CLCHP and CSCAP increased from 2011 to 2015, 2011 to 2013 and 2013 to 2015, respectively. The CLCAP family by replication variance decreased from 2011 to 2014. The sandy soil, humic soil, CLCHP, CSCHP and irrigated trials produced larger family by replication variance than CLCAP and CSCAP. The family residual error variance ($\sigma^2_{G(FR)}$) was highly significant ($P<0.001$) across all populations. The humic soil and sandy soil residual variances increased from 2010 to 2013 and 2010 to 2015, respectively. The residual error variances of CLCHP, CLCAP, CSCHP, CSCAP and irrigated trials varied across the populations. The humic soil, sandy soil, CLCHP, CLCAP and CSCAP trials produced larger residual error variances than the CSCHP and irrigated trials. The residual error was the largest of the three variances across populations.

Table 3.3 Variance components (± standard error) for cane yield (kg) for family (F) and individual genotype selection (G) in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations, planted in 2010, 2011, 2012, 2013, 2014 and 2015

Year planted	Statistic	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
Family								
2010	σ^2_F	2.49±0.52***	0.35±0.26ns					
	σ^2_{FR}	2.09±0.33***	2.35±0.34***					
	$\sigma^2_{G(FR)}$	18.98±0.38***	14.34±0.28***					
2011	σ^2_F	2.41±0.61***	1.38±0.39***	1.89±0.35***	1.46±0.94ns	0.19±0.04***	6.29±1.89***	5.79±0.84***
	σ^2_{FR}	3.32±0.47***	2.33±0.35***	2.04±0.30***	6.98±1.24****	0.28±0.03***	8.17±1.63***	3.41±0.48***
	$\sigma^2_{G(FR)}$	27.47±0.53***	17.36±0.34***	33.81±0.48***	44.05±1.23***	2.30±0.03***	61.01±1.73***	34.06±0.51***
2012	σ^2_F	6.00±1.13***	3.62±1.16***	7.91±1.60***	0.46±0.70ns	2.32±0.46***	4.69±1.58***	9.27±2.95***
	σ^2_{FR}	3.08±0.55***	6.99±1.06***	9.68±1.26***	4.09±0.93***	1.68±0.32***	8.74±1.71***	18. 85±2.95***
	$\sigma^2_{G(FR)}$	40.78±0.80***	37.00±0.78***	101.01±1.54***	24.45±0.80***	19.82±0.37***	41.88±1.33***	104. 90±2.22***
2013	σ^2_F	8.80±2.34***	2.21±0.95**	3.18±1.39**	0.94±0.33**	1.35±0.26***	0.43±0.20**	3.72±0.71***
	σ^2_{FR}	9.82±1.88***	9.25±1.18***	16.47±1.74***	2.62±0.36***	1.48±0.18***	2.10±0.25***	2.51±0.40***
	$\sigma^2_{G(FR)}$	96.94±2.13***	36.54±0.76***	66.48±1.06***	11.58±0.26***	9.24±0.16***	6.38±0.13***	12.88±0.23***
2014	σ^2_F			2.36±0.78***	1.61±0.54***	0.09±0.04*	0.56±0.42ns	3.00±0.69***
	σ^2_{FR}			6.09±0.81***	2.57±0.49***	0.63±0.06***	2.92±0.49***	8.20±0.81***
	$\sigma^2_{G(FR)}$			28.29±0.58***	24.00±0.52***	2.33±0.04***	7.89±0.20***	30.64±0.55***
2015	σ^2_F		2.64±1.89ns	7.72±1.10***	1.26±0.86ns	1.60±0.33***	0.56±0.44ns	0.20±0.39ns
	σ^2_{FR}		11.19±2.11***	2.87±0.45***	8.34±1.19***	2.37±0.26***	4.06±0.58***	4.58±0.59***
	$\sigma^2_{G(FR)}$		46.47±1.22***	42.34±0.69***	36.12±0.82***	13.73±0.22***	19.56±0.40***	15.90±0.32***
Individual								
2010	$\sigma^2_{G(F)}$	2.31±0.37***	0.29±0.26ns					
	$\sigma^2_{G(FR)}$	21.34±0.52***	17.29±0.41***					
2011	$\sigma^2_{G(F)}$	2.21±0.49**	1.13±0.29***	2.33±0.43***	0.54±1.14ns	0.23±0.03***	6.48±1.76***	5.64±0.59***
	$\sigma^2_{G(FR)}$	31.03±0.72***	20.54±0.47***	35.80±0.62***	52.75±1.79***	2.56±0.05***	68.48±2.39***	38.05±0.73***
2012	$\sigma^2_{G(F)}$	4.93±0.80***	4.15±0.83***	7.82±1.41***	0.33±0.85ns	1.85±0.45***	4.53±1.50***	10. 19±2.24***
	$\sigma^2_{G(FR)}$	49.10±1.14***	44.71±1.16***	111.76±2.07***	29.75±1.25***	22.37±0.57***	52.07±2.09***	126. 52±3.27***
2013	$\sigma^2_{G(F)}$	5.80±2.25**	2.32±0.75***	0.00±0.00	0.54±0.26*	1.31±0.17***	0.41±0.15**	3.25±0.48***
	$\sigma^2_{G(FR)}$	111.9±3.18***	45.38±1.14***	96.76±1.50***	14.57±0.40***	10.97±0.22***	8.85±0.23***	16.40±0.48***
2014	$\sigma^2_{G(F)}$			2.79±0.57***	1.11±0.51**	0.00±0.00	0.00±0.00	3.45±0.62***
	$\sigma^2_{G(FR)}$			33.66±0.83***	27.20±0.74***	3.79±0.06***	12.07±0.29***	39.23±0.87***
2015	$\sigma^2_{G(F)}$		1.48±1.35ns	6.49±0.73***	00.00±00.00	0.55±0.22**	0.00±0.00	0.06±0.35ns
	$\sigma^2_{G(FR)}$		59.62±2.01***	48.22±0.96***	35.79±1.22***	18.30±0.35***	26.05±0.52***	21.14±0.54***

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 error variance ***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non significant at P≥0.05

Individual genotype variance ($\sigma^2_{G(F)}$) for cane yield was highly significant (P<0.001) in all conditions except the sandy soil (2010, 2015), CLCAP (2011, 2012) and irrigated (2015) trials (Table 3.3). The humic soil individual genotype variance increased during 2011 to 2013 crop years. The individual genotype variance for the sandy soil, CLCHP, CLCAP, CSCAP, CSCHP and irrigated populations varied across trials and the individual residual error variance ($\sigma^2_{G(FR)}$) was highly significant (P<0.001) across all populations. The humic soil, sandy soil, CLCHP and irrigated trials produced larger individual genotype residual error variance than CSCHP, CSCAP, and CLCAP. Family variances were larger than individual variances across all populations. The individual residual error variance was larger than that for families.

3.4.2 Stalk number

The family variance (σ^2_F) for stalk number was highly significant (P<0.001) for all except the CLCAP (2012) and irrigated (2012, 2013) trials (Table 3.4). The family variances for both the humic soil and sandy soil trials increased during 2010 to 2012 crop season. The family variances for the CLCHP, CLCAP, CSCHP and CSCAP populations varied across trials. The family variance for the irrigated trial decreased during 2012 and 2013 seasons. The humic soil, CLCHP, CSCAP and irrigated trials produced larger family variances than the sandy soil, CLCAP, and CSCHP trials. The family by replication variance (σ^2_{FR}) was highly significant (P<0.001) across all populations and the variance for the humic soil, CLCHP, CLCAP, CSCHP, CSCAP and irrigated populations varied across trials. The family by replication variance for the sandy soil trial increased during three crop seasons (2010-2012). The family by replication variances for the sandy soil, CLCHP, CLCAP, CSCAP and irrigated trials were larger than that for CSCHP.

The residual error variance ($\sigma^2_{G(FR)}$) was highly significant (P<0.001) across all populations and the residual variance for the humic soil, CLCAP, CSCHP, CSCAP, and irrigated trials varied across populations. The residual variance for sandy soil trial increased during crop years 2010-2015. The residual variance for CLCHP decreased during 2012 to 2015. The residual variance for the humic soil, sandy soil, CLCHP, and CLCAP trials was larger than that for the CSCAP, CSCHP, and irrigated trials.

Table 3.4 Variance components (± standard error) for stalk number for family (F) and individual genotype selection (G) in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations, planted in 2010, 2011, 2012, 2013, 2014 and 2015

Year planted	Statistic	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
Family								
2010	σ^2_F	4.31±0.83***	1.41±0.59**					
	σ^2_{FR}	1.96±0.44***	3.72±0.65***					
	$\sigma^2_{G(FR)}$	41.63±0.83***	41.94±0.81***					
2011	σ^2_F	9.16±2.15***	7.02±1.75***	7.45±1.01***	3.10±1.21**	2.88±0.38***	18.89±3.71***	23.88±2.70***
	σ^2_{FR}	8.72±1.44***	5.55±1.06***	3.59±0.53***	6.65±1.38***	1.03±0.16***	8.21±1.72***	9.43±1.11***
	$\sigma^2_{G(FR)}$	103.55±2.01***	69.15±1.37***	58.12±0.82***	60.74±1.69***	17.12±0.26***	62.64±1.78***	32.20±0.48***
2012	σ^2_F	12.64±2.33***	13.26±2.89***	19.49±2.78***	1.70±3.28ns	13.71±2.00***	15.08±3.66***	4.89±3.12ns
	σ^2_{FR}	5.52±1.01***	10.40±1.73***	7.88±1.35***	17.99±4.11***	3.92±0.92***	9.32±2.77***	28.43±4.20***
	$\sigma^2_{G(FR)}$	77.43±1.52***	75.66±1.61***	150.22±2.29***	95.87±3.14***	75.12±1.38***	92.17±2.93***	137.16±2.89***
2013	σ^2_F	10.19±2.16***	2.64±1.14**	13.48±2.43***	4.79±1.30***	6.22±1.03***	3.50±1.07***	1.01±1.35ns
	σ^2_{FR}	10.27±1.57***	9.17±1.40***	13.52±1.83***	8.12±1.21***	4.11±0.53***	8.57±1.09***	11.64±1.55***
	$\sigma^2_{G(FR)}$	99.97±1.92***	70.96±1.47***	127.99±2.04***	52.35±1.15**	33.35±0.56***	33.83±0.71***	18.62±0.34***
2014	σ^2_F			11.53±2.31***	14.26±2.78***	3.76±0.58***	3.94±2.12*	2.85±0.66***
	σ^2_{FR}			7.00±1.20***	7.55±1.42***	3.46±0.36***	12.58±2.28***	7.06±0.77***
	$\sigma^2_{G(FR)}$			77.36±1.57***	70.41±1.52***	19.27±0.30***	40.87±1.01***	36.41±0.66***
2015	σ^2_F		9.12±3.53**	14.90±2.11***	11.56±3.32***	5.07±0.79***	10.83±2.60***	1.55±0.62**
	σ^2_{FR}		16.07±3.36***	5.93±0.85***	20.07±2.91***	2.97±0.40***	13.29±1.95***	4.60±0.73***
	$\sigma^2_{G(FR)}$		120.24±3.15***	70.77±1.15***	81.28±1.84***	32.26±0.51***	59.85±1.23***	36.10±0.72***
Individual								
2010	$\sigma^2_{G(F)}$	4.70±0.74***	1.61±0.71*					
	$\sigma^2_{G(FR)}$	43.23±1.05***	45.55±1.09***					
2011	$\sigma^2_{G(F)}$	7.60±1.77***	1.46±1.07ns	8.51±0.83***	4.97±1.57***	3.40±0.27***	15.84±2.53***	29.42±1.00***
	$\sigma^2_{G(FR)}$	113.22±2.62***	81.44±1.87***	60.69±1.07***	65.98±2.23***	17.92±0.33***	70.15±2.65***	36.30±0.69***
2012	$\sigma^2_{G(F)}$	9.84±1.51***	17.02±1.97***	24.30±2.34***	00.00±00.00	15.12±1.72***	14.42±3.85***	4.56±2.63*
	$\sigma^2_{G(FR)}$	90.91±2.12***	83.55±2.45***	153.01±2.90***	119.8±3.71***	78.62±1.99***	101.99±4.58***	166.31±4.23***
2013	$\sigma^2_{G(F)}$	10.54±1.87***	2.38±1.30*	9.37±2.24***	3.33±1.20**	5.71±0.60***	1.85±0.80**	00.00±00.00
	$\sigma^2_{G(FR)}$	111.70±2.63***	80.73±2.04***	152.19±3.13***	64.81±1.77***	37.91±0.77***	46.22±1.19***	33.24±0.582***
2014	$\sigma^2_{G(F)}$			10.50±1.55***	11.91±1.78***	2.47±0.35***	5.62±1.52***	3.36±0.71***
	$\sigma^2_{G(FR)}$			85.15±2.10***	80.62±2.23***	27.03±0.50***	53.64±1.88***	44.35±0.99***
2015	$\sigma^2_{G(F)}$		11.30±3.35***	15.23±1.30***	7.39±2.24***	3.96±0.53***	6.32±1.62***	2.05±0.70**
	$\sigma^2_{G(FR)}$		135.44±4.59***	78.42±1.57***	116.38±3.27***	37.32±0.73***	78.78±2.13***	40.48±1.02***

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 error variance ***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non significant at P≥0.05

The individual genotype variance ($\sigma^2_{G(F)}$) was highly significant (P<0.001) for all except for the sandy soil (2011) trial (Table 3.4). The individual genotype variance for the humic soil (2010 to 2013), CLCHP (2013 to 2015) and CSCAP (2013 to 2015) populations increased across trials. The individual genotype variance for the sandy soil, CLCAP, CSCHP and irrigated trials varied across populations. The individual genotype variance for the humic soil, CLCHP, CSCAP and CSCHP trials was larger than that for the sandy soil, CLCAP and irrigated trials.

The individual residual error variance ($\sigma^2_{G(FR)}$) for stalk number was highly significant (P<0.001) across all populations. The residual variance for the humic soil, sandy soil, CLCAP, CSCHP, CSCAP and irrigated trials varied across populations. The residual variance for the CLCHP trial decreased during 2012 to 2015 crop seasons. The residual variance for the humic soil, CLCHP and CLCAP trials was larger than for the sandy soil, CSCHP, CSCAP and irrigated trials. Stalk number family variances were larger than individual variances across all trials. The individual residual error variance for stalk number was larger than that for families.

3.4.3 Stalk height

Family variance ($\sigma^2_{F)}$ was highly significant (P<0.001) for all except for the sandy soil (2013), CLCAP (2011) and CSCAP (2015) trials (Table 3.5). The family variances decreased in the humic soil (2010 to 2012), sandy soil (2010 to 2013), CSCHP (2011 to 2014) and irrigated (2012 to 2015) trials. The family variances for the CLCHP, CLCAP and CSCAP populations varied across trials. The family by replication variance (σ^2_{FR}) was highly significant (P<0.001) for all populations and family by replication variance for the humic soil, sandy soil, CLCAP and irrigated trials varied across populations. The CLCHP and CSCHP family by replication variances increased in both the populations during 2011 to 2013 seasons. The CSCAP family by replication variance decreased in 2011, 2012 and 2013. The family residual error variance ($\sigma^2_{G(FR)}$) for stalk height was highly significant (P<0.001) across all populations. The residual variance decreased for the humic soil (2010 to 2012), CLCHP (2012 to 2015), CLCAP (2011 to 2015) and CSCAP (2011 to 2014) trials.

Table 3.5 Variance components (± standard error) for stalk height for family (F) and individual genotype selection (G) in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated breeding populations, planted in 2010, 2011, 2012, 2013, 2014 and 2015

Year planted	Statistic	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
Family								
2010	σ^2_F	0.016±39.270***	0.0098±0.0028***					
	σ^2_{FR}	0.026±31.730***	0.0206±0.0025***					
	$\sigma^2_{G(FR)}$	0.075±15.130***	0.0562±0.0010***					
2011	σ^2_F	0.009±0.002***	0.0087±0.0018***	0.0097±0.0018***	0.007±0.003*	0.0085±0.0011***	0.0253±0.0061***	0.0205±0.0030***
	σ^2_{FR}	0.014±0.002***	0.0072±0.0010***	0.0174±0.0016***	0.029±0.004***	0.0034±0.0004***	0.0275±0.0043***	0.0191±0.0019***
	$\sigma^2_{G(FR)}$	0.054±0.001***	0.0409±0.0008***	0.0558±0.0008***	0.081±0.002***	0.0283±0.0004***	0.0972±0.0028***	0.0418±0.0006***
2012	σ^2_F	0.006±0.001***	0.0068±0.0058***	0.0178±0.0034****	0.0074±0.0022***	0.0058±0.0013***	0.0147±0.0035***	0.0206±0.0058***
	σ^2_{FR}	0.007±0.001***	0.0080±0.0017***	0.0284±0.0027***	0.0073±0.0020***	0.0084±0.0011***	0.0140±0.0029***	0.0449±0.00056***
	$\sigma^2_{G(FR)}$	0.053±0.001***	0.0557±0.0013***	0.0790±0.0012***	0.0623±0.0020***	0.0408±0.0008***	0.0657±0.0021***	0.0601±0.0013***
2013	σ^2_F	0.013±0.002***	0.0011±0.0023ns	0.0116±0.0035***	0.0073±0.0017***	0.0052±0.0013***	0.0061±0.0015***	0.0070±0.0016***
	σ^2_{FR}	0.010±0.001***	0.0315±0.0037***	0.0428±0.0040***	0.0090±0.0013***	0.0120±0.0012***	0.0100±0.0013***	0.0099±0.0014***
	$\sigma^2_{G(FR)}$	0.066±0.001***	0.0686±0.0014***	0.0669±0.0011***	0.0510±0.0011***	0.0313±0.0005***	0.0421±0.0009***	0.0536±0.0010***
2014	σ^2_F			0.0128±0.0035***	0.0096±0.0022***	0.0048±0.0010***	0.0067±0.0021***	0.0059±0.0012***
	σ^2_{FR}			0.0261±0.0031***	0.0077±0.0013***	0.0085±0.0008***	0.0108±0.0018***	0.0144±0.0013***
	$\sigma^2_{G(FR)}$			0.0528±0.0011***	0.0497±0.0011***	0.0329±0.0005***	0.0380±0.0009***	0.0438±0.0008***
2015	σ^2_F		0.0118±0.0032***	0.0215±0.0029***	0.0074±0.0027**	0.0252±0.0033***	0.0017±0.0013ns	0.0033±0.0013**
	σ^2_{FR}		0.0100±0.0020***	0.0090±0.0010***	0.0226±0.0029***	0.0061±0.0009***	0.0138±0.0018***	0.0127±0.0016***
	$\sigma^2_{G(FR)}$		0.0571±0.0015***	0.0460±0.0008***	0.0487±0.0011***	0.0946±0.0015***	0.0443±0.0009***	0.0367±0.0007***
Individual								
2010	$\sigma^2_{G(F)}$	0.013±19.060***	0.0079±0.0015***					
	$\sigma^2_{G(FR)}$	0.106±25.840***	0.0873±0.0022***					
2011	$\sigma^2_{G(F)}$	0.008±0.001***	0.0103±0.0010***	0.0097±0.0010***	0.0050±0.0030*	0.0084±0.0006***	0.0224±0.0037***	0.0172±0.0012***
	$\sigma^2_{G(FR)}$	0.068±0.002***	0.0484±0.0011***	0.0779±0.0014***	0.1120±0.0040***	0.0317±0.0006***	0.1268±0.0045***	0.0638±0.0013***
2012	$\sigma^2_{G(F)}$	0.003±0.001**	0.0073±0.0013***	0.0143±0.0017***	0.0088±0.0024***	0.0034±0.0010***	0.0156±0.0034***	0.0064±0.0024**
	$\sigma^2_{G(FR)}$	0.068±0.002***	0.0658±0.0017***	0.1257±0.0023***	0.0688±0.0030***	0.0532±0.0013***	0.0819±0.0038***	0.1445±0.0037***
2013	$\sigma^2_{G(F)}$	0.011±0.001***	0.0004±0.0015ns	00.00±00.00	0.0070±0.0013***	0.0049±0.0007***	0.0064±0.0010***	0.0085±0.0013***
	$\sigma^2_{G(FR)}$	0.079±0.002***	0.0991±0.0025***	0.1463±0.0023***	0.0620±0.0017***	0.0451±0.0009***	0.0510±0.0013***	0.0648±0.0016***
2014	$\sigma^2_{G(F)}$			0.0095±0.0015***	0.0075±0.0013***	00.00±00.00	0.0024±0.0014*	0.0086±0.0010***
	$\sigma^2_{G(FR)}$			0.0824±0.0020***	0.0622±0.0017***	0.0618±0.0009***	0.0592±0.0020***	0.0588±0.0013***
2015	$\sigma^2_{G(F)}$		0.0106±0.0019**	0.0175±0.0013***	00.00±00.00	0.0266±0.0018***	00.00±00.00	00.00±00.00
	$\sigma^2_{G(FR)}$		0.0682±0.0024***	0.0698±0.0014***	0.1252±0.0028***	0.1006±0.0020***	0.0667±0.0013***	0.0625±0.0012***

σ^2_F = Family variance, σ^2_{FR} = Family by replication variance, σ^2e= Residual variance, $\sigma^2_{G(F)}$ = Genotype nested within family variance, $\sigma^2_{G(FR)}$ = Residual error variance ***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non significant at P≥0.05

The individual genotype variance ($\sigma^2_{G(F)}$) for stalk height was highly significant (P<0.001) across populations except the humic soil (2012) sandy soil (2013, 2015), CLCAP (2011), CSCAP (2014) and irrigated (2012) trials (Table 3.5). Individual genotype variance decreased in the humic soil (2010 to 2012) and CSCAP (2011 to 2015) trials. The individual genotype variance for the sandy soil, CLCAP, CSCHP and irrigated trials varied across populations. The CLCHP individual genotype variance increased during 2013 to 2015 The residual variance ($\sigma^2_{G(FR)}$) was highly significant (P<0.001) across all populations and varied across trials. Family variances were generally larger than individual variances across all populations. Individual residual variance was larger than that for families.

3.4.4 Stalk diameter

Family variance (σ^2_F) was highly significant (P<0.001) for stalk diameter across all except the sandy soil trial for 2010 (Table 3.6). The family variance increased for the humic soil (2010 to 2013), CLCAP (2012 to 2015) and CSCHP (2011 to 2014) trials. The sandy soil and CLCHP variances varied across trials. Family by replication variance (σ^2_{FR}) was highly significant (P<0.001) across all populations. The family by replication variance increased for the humic soil (2011 to 2013), CLCAP (2011 to 2014), CSCHP (2012 to 2015) and irrigated (2013 to 2015) trials. The family by replication variance for the sandy soil, CLCHP and CSCAP trials varied across populations. The residual variance ($\sigma^2_{G(FR)}$) was highly significant (P<0.001) across all populations. The residual variance increased in both humic soil and CSCHP (2011 to 2013), and CSCAP (2012 to 2015) trials.

The individual genotype variance was highly significant (P<0.001) across all populations (Table 3.6). The individual genotype variances increased for the humic soil (2010 to 2013), CLCHP (2013 to 2015), CLCAP (2012 to 2015) and CSCHP (2011 to 2014) trials. The sandy soil individual genotype variance varied across trials. The individual genotype variance decreased for the CSCAP (2013 to 2015) and irrigated (2013 to 2015) trials. The residual variance ($\sigma^2_{G(FR)}$) was highly significant (P<0.001) across all populations. The residual variance increased for both the CLCHP, CSCHP (2011 to 2013) and irrigated (2011 to 2014) trials. The residual variances for the humic soil, sandy soil, CLCAP, and CSCAP populations varied across trials. Family variances were larger than individual variances. The individual residual variance was larger than that for families.

Table 3.6 Variance components (± standard error) for stalk diameter for family (F) and individual genotype selection (G) in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations , planted in 2010, 2011, 2012, 2013, 2014 and 2015

Year planted	Statistic	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
Family								
2010	σ^2_F	0.009±0.002***	0.0086±0.0015*					
	σ^2_{FR}	0.006±0.001***	0.0038±0.0007***					
	$\sigma^2_{G(FR)}$	0.066±0.001***	0.0544±0.0010***					
2011	σ^2_F	0.015±0.002***	0.0080±0.0017***	0.020±0.002***	0.017±0.003***	0.009±0.001***	0.040±0.007***	0.036±0.004***
	σ^2_{FR}	0.003±0.001***	0.0026±0.0011***	0.002±0.0004***	0.006±0.002***	0.003±0.0005***	0.021±0.003***	0.011±0.001***
	$\sigma^2_{G(FR)}$	0.062±0.001***	0.0902±0.0018***	0.057±0.001***	0.086±0.002***	0.050±0.001***	0.080±0.002***	0.079±0.001***
2012	σ^2_F	0.030±0.005***	0.0235±0.0038***	0.041±0.005***	0.011±0.003***	0.013±0.002***	0.009±0.003***	0.028±0.005***
	σ^2_{FR}	0.006±0.001***	0.0040±0.0011***	0.006±0.001***	0.006±0.002***	0.002±0.001***	0.010±0.002***	0.018±0.003***
	$\sigma^2_{G(FR)}$	0.085±0.002***	0.0737±0.0015***	0.108±0.002***	0.062±0.002***	0.057±0.001***	0.056±0.002***	0.096±0.002***
2013	σ^2_F	0.031±0.005***	0.0164±0.0031***	0.030±0.004***	0.024±0.004***	0.020±0.003***	0.023±0.004***	0.038±0.005***
	σ^2_{FR}	0.010±0.002***	0.0092±0.0016***	0.009±0.001***	0.011±0.002***	0.004±0.001***	0.008±0.001***	0.017±0.003***
	$\sigma^2_{G(FR)}$	0.105±0.002***	0.0973±0.0020***	0.104±0.002***	0.071±0.002***	0.088±0.001***	0.075±0.002***	0.103±0.002***
2014	σ^2_F			0.029±0.005***	0.037±0.006***	0.034±0.004***	0.025±0.007***	0.025±0.004***
	σ^2_{FR}			0.003±0.001***	0.012±0.002***	0.007±0.001***	0.023±0.004***	0.029±0.003***
	$\sigma^2_{G(FR)}$			0.081±0.002***	0.069±0.001***	0.068±0.001***	0.079±0.002***	0.107±0.002***
2015	σ^2_F		0.0173±0.0037***	0.040±0.005***	0.039±0.007***	0.010±0.002***	0.022±0.006***	0.009±0.004*
	σ^2_{FR}		0.0071±0.0017***	0.002±0.001***	0.008±0.002***	0.026±0.002***	0.037±0.005***	0.039±0.005***
	$\sigma^2_{G(FR)}$		0.0778±0.0020***	0.089±0.001***	0.086±0.002***	0.037±0.001***	0.091±0.002***	0.079±0.002***
Individual								
2010	$\sigma^2_{G(F)}$	0.008±0.001***	0.0086±0.0011***					
	$\sigma^2_{G(FR)}$	0.072±0.002***	0.0581±0.0014***					
2011	$\sigma^2_{G(F)}$	0.013±0.001***	0.0074±0.0015***	0.020±0.001***	0.014±0.003***	0.011±0.001***	0.034±0.004***	0.031±0.002***
	$\sigma^2_{G(FR)}$	0.066±0.001***	0.0928±0.0022***	0.060±0.001***	0.097±0.003***	0.052±0.001***	0.104±0.004***	0.093±0.002***
2012	$\sigma^2_{G(F)}$	0.029±0.002***	0.0236±0.0021***	0.044±0.002***	0.010±0.002***	0.013±0.001***	0.010±0.002***	0.028±0.003***
	$\sigma^2_{G(FR)}$	0.094±0.002***	0.0776±0.0021***	0.112±0.002***	0.071±0.003***	0.059±0.002***	0.073±0.003***	0.116±0.003***
2013	$\sigma^2_{G(F)}$	0.030±0.002***	0.0175±0.0021***	0.026±0.002***	0.024±0.002***	0.021±0.002***	0.026±0.002***	0.046±0.003***
	$\sigma^2_{G(FR)}$	0.117±0.003***	0.1065±0.0027***	0.119±0.002***	0.086±0.002***	0.091±0.002***	0.083±0.002***	0.120±0.003***
2014	$\sigma^2_{G(F)}$			0.027±0.002***	0.037±0.003***	0.037±0.002***	0.019±0.004***	0.033±0.003***
	$\sigma^2_{G(FR)}$			0.087±0.002***	0.081±0.002***	0.075±0.001***	0.110±0.004***	0.136±0.003***
2015	$\sigma^2_{G(F)}$		0.0183±0.0026***	0.043±0.002***	0.040±0.003***	0.006±0.001***	0.017±0.003***	0.007±0.002***
	$\sigma^2_{G(FR)}$		0.0865±0.0030***	0.090±0.002***	0.097±0.003***	0.071±0.001***	0.130±0.003***	0.124±0.003***

σ^2_F = Family variance, σ^2_{FR} = Family by replication variance, σ^2e= Residual variance, $\sigma^2_{G(F)}$ = Genotype nested within family variance, $\sigma^2_{G(FR)}$ = Residual error variance ***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non significant at P≥0.05

3.5 DISCUSSION

Family variance was consistently larger than individual genotype variance across the populations evaluated in trials during 2010 to 2015. This indicated that family variance provided more accurate selection for cane yield and its components in populations compared to selecting genotypes without reference to family evaluation and selection. Importance of family evaluation and selection was reported by several studies (Kimbeng and Cox 2003; Shanthi et al. 2008; Pedrozo et al. 2011). While acknowledging the value of family evaluation and selection in these studies, due to high cost in data collection of genotypes, only few studies (Zhou 2014a) compared family and genotype selection. The larger family variance compared to individual genotypes provides justification for implementing family evaluation and selection in breeding programmes to achieve genetic gain. The expected higher selection efficiency and the ability to quantify family values would result in subsequent cycles of planting seedlings focusing only on high trait value families. This approach would lower the cost of breeding because only few families will be planted to achieve the same number of genotypes for advancing to later testing stages, thereby lowering the cost of managing smaller fields of selection trials. Another approach based on these results would be to establish a family evaluation stage where a smaller number of seedlings per cross are planted and only families with high trait values are advanced for planting large number of seedlings for a large scale evaluation. The approach will also improve resource use efficiency and increase the ability to achieve higher genetic gains. Genetic gain refers difference in the mean value of the selection criterion between the original generation and the next generation, which is formed from only the selected individuals, when they are compared in the same environment.

Results showed significant family and genotype differences indicating that although family genetic variance was larger than that of genotypes, both levels of genetic variability can be utilised to increase efficiency of selection at this stage. Firstly, families with higher trait values will be selected and then genotypes within these selected families will be selected and advanced for further testing. Family selection focus on elite clones (individual clone selection) in the superior families, thereby increasing the possibility of identifying maximum elite clones at advanced stages of testing within these families. The added advantage of family selection in sugarcane is that family data can be used to address the breeding value of parents based on progeny performance. Implementing family selection followed by individual selection would result in increased in heritability which will ultimately increase genetic gains in sugarcane

breeding. Further, to enhance the value of family evaluation as observed in this study, where measurements were done at the genotype level, within family variability for trait values can be estimated. The within family variability can further be utilized as a statistical parameter to evaluate families. Those families with higher within family variability will be more desirable as they have maximum genotypic variation for the economic traits of selection and potentially superior heterotic recombinants for the traits, making it easier to select superior genotypes. The worthiness of the family is well understood only when it includes superior individuals there by suggesting that combined family selection followed by individual clone selection is superior to either family or individual clone selection alone. As in early stages of selection, G x E effect is high, selection among and within families is an important tool for genetic improvement and this dual approach of family and genotype selection will provide additional benefits of family evaluation in early stages of sugarcane breeding.

The humic soil, CLCAP, CSCHP and CSCAP populations produced larger family variances than genotype variances for cane yield compared to sandy soil, CLCHP and irrigated populations. Breeding programmes with larger positive family variances are known to achieve higher population (Zhou 2013a) and cultivar genetic gains (Zhou 2014b; Zhou and Gwata 2016; Zhou 2017). Therefore, early generation family evaluation results are associated with genotype yields and its performance in advanced variety trials and as well as cultivars released from the breeding programmes. For example, low cane yield genetic gains (Zhou 2013a; Zhou 2017) for the irrigated breeding programme appear to be associated with low genetic variability for cane yield among families. Therefore, to increase genetic gain, interventions including selection of parents of choice, evaluating parents, and crossing diverse parents and identifying divergent and viable families those imparting higher genetic variability for cane yield will be a first step. In the Midlands programmes, higher genetic gains for cane yield have been achieved (Zhou 2013a, 2014b; Zhou and Gwata 2016), from the families with high genetic variability. Similarly in this study, parents from the CSCHP programme could be potential sources for cane yield with higher genetic variability for the irrigated region since they are both 12 month cycle crops. On the other hand, the Midlands humic soil programme could be a source of parents of higher genetic variability for cane yield for sandy soils and CLCHP breeding programmes since they are both long cycle crops (i.e. harvest age is 24 and 18 months, respectively). Therefore, family evaluation and selection provides insights into strengths and weaknesses of breeding programmes as well as potential sources of highly adaptable genetic

material for future breeding to identify varieties optimally adapted to the existing ecological conditions and to mitigate the climate change in future.

The family variances for stalk number and stalk height were larger than those for stalk diameter, indicating the role of stalk number and height on the magnitudes of cane yield. Earlier studies on path coefficient analysis (Kang et al. 1983, 1989; Milligan et al. 1990; De Sousa-Vieira and Milligan 2005) and logistic regression models (Zhou 2004, 2013b) indicated that the yield dependent variables: stalk number and stalk height had larger influence on the magnitude of cane yield than stalk diameter. In our study also family variances for stalk number and stalk height were larger than those for stalk diameter. This influence is particularly strongly addressed in South Africa and subtropical environments where growing conditions are less favourable to sugarcane. Wider adaptability of the clones to varied environments have been shown to be imparted by stalk number and stalk height (Zhou 2018), with important implications for family evaluation for cane yield. The results of the present study suggests that measuring stalk number and height alone will generate a selection index for cane yield that can then be used to evaluate families. The importance of this result is advantageous in resource limited breeding programmes wherein the stalk number and height are measured to evaluate their families and guide their early stage selection.

The residual variance was the largest variance in all trials, indicating that a large proportion of variability was not accounted for by the statistical model. A randomised complete block design is currently used for these trials. Adopting incomplete block designs is expected to reduce residual error by accounting for within block variability. Including covariates to account for spatial variability will also reduce error variance. However, in sugarcane, there is generally very high genotype variability among progenies from a cross because of large segregation that occurs at crossing and in first filial generation. The high residual error also reflects high variability among genotypes which is unaccountable as genotypes are unreplicated at this stage. G x E effects become confounded with the residual error. Studies to determine optimum sample size (Zhou 2014a) as well as optimum replications is to be strengthened to determine appropriate genetic parameters for early stage seedling evaluation in sugarcane.

3.6 CONCLUSIONS

Results from this study demonstrated large genetic variability among SASRI breeding populations that may be exploited for improving breeding and selection. The study highlighted the superiority of family selection compared to individual genotype selection in sugarcane breeding. Combined gains from adopting family selection followed by individual genotype selection will increase the heritability of cane yield and its components and correspondingly the overall genetic gains in sugarcane breeding. The study highlighted the importance of two yield traits *viz.,* stalk number and height as of prime importance to evaluate families for cane yield. The introduction of new divergent genotypes in hybridization programme will pave way for building up new gene pool with new sources of variations and large diversity for base broadening programmes in sandy soils, CLCAP and CSCAP populations and identification of location specific families which will ultimately improve selection efficiency.

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CHAPTER 4

TRENDS IN FAMILY AND INDIVIDUAL GENOTYPE BROAD-SENSE HERITABILITY AMONG SUGARCANE BREEDING POPULATIONS

4.1 ABSTRACT

Heritability is the proportion of genetic variability contributed to a phenotype observed in populations and is used to determine selection efficiency in a breeding programme. The objectives of this study were to determine the magnitude and trends in broad-sense heritability (H) among breeding populations, compare H between family and individual genotypes and evaluate their implications on sugarcane breeding and selection. Data were collected from the Midlands humic, and sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations, respectively, planted from 2010 to 2015. Yield components (stalk number, stalk height and stalk diameter) were measured from a sample of the first 20 mini-lines in each of the three replications per family and used to calculate cane yield. Families produced larger H estimates (21 to 96%) compared to individual genotypes (0 to 31%), indicating that selecting superior families would be more effective than selecting individual genotypes. The humic soil (68%), CLCHP (57%), CSCHP (57%) and irrigated (53%) populations had higher family H estimates for cane yield than sandy soil (42%), CLCAP (37%) and CSCAP (43%) populations, suggesting that a high proportion of the observed variability was heritable and thus provides a bigger scope for improving cane yield through selection in these populations. Lower H estimates in sandy soil, CLCAP and CSCAP populations indicated a low proportion of genetic variability and thus a potentially low selection efficiency among these populations and stress upon the need for identifying new set of populations for the region. More cycles of recurrent breeding for cane yield and its components will improve the genetic background in sandy soil, CSCAP and CLCAP populations, which will increase H estimates and selection efficiency among populations. The CLCAP and CSCAP programmes are located on a site with high prevalence of Eldana borer, resulting in potential in an increased selection pressure for Eldana resistance populations at the expense of cane yield genetic variation. Therefore, research is required to quantify genetic interactions between yield and Eldana damage to guide future breeding for the CLCAP and CSCAP programmes

Key words: Family, individual genotypes, broad-sense heritability, genetic variability, selection efficiency

4.2 INTRODUCTION

Heritability is the ratio of genetic to phenotypic variance and is used in plant and animal breeding to quantify the precision of selection in field trials (Piepho and Mohring 2007). There are two types of heritability, namely broad-sense and narrow-sense heritability. Broad-sense heritability is the proportion of phenotypic variance that is attributed to total genetic variance in a population (Allard 1960; Falconer 1960; Zhou and Joshi 2012). Broad-sense heritability is utilised to determine the proportion of genetic variability for a trait in a population without reference to the actual underlying genetic control. Narrow-sense heritability is the proportion of phenotypic variation that is attributed to additive genetic effects in a population (Falconer and Mackay 1995). It is expressed as the ratio of additive genetic variance to phenotypic variance (Wei and Jackson 2016). Because the additive component of genetic variance determines the response to genetic effects that can be utilised and predicted easily during breeding, the estimation of narrow-sense heritability is more useful to plant breeders where it determines the potential of population for genetic enhancement of trait. However, in breeding clonally propagated crops such as sugarcane and banana, where segregation events are limited to time of pollination and recombination events, subsequent trial testing stages evaluate only broad-sense heritability. The magnitude of narrow-sense heritability is equal to or lower than that of broad-sense heritability estimates (Milligan 1988) for cane yield and sucrose yield.

In clonally propagated crops such as sugarcane, only the first stage of testing is planted from true seeds and subsequent generations are vegetatively propagated. Genetic recombination does not occur after crossing in vegetative crops, therefore, broad-sense heritability is utilised to measure the proportion of genetic variability, which determines the effectiveness of selection of superior genotypes to be advanced to later stages of sugarcane breeding (Zhou and Joshi 2012). Broad-sense heritability estimates are used to determine the accuracy of selecting superior genotypes among populations and can be applied to study changes in genotype selection efficiency across breeding cycles (Hansche and Beres 1966), among breeding populations, among traits and as well as to study the effectiveness of breeding and selection strategies (Zhou and Joshi 2012). Broad-sense heritability is also used to estimate the genetic gain during selection (Allard 1960; Wolie et al. 2013).

SASRI operates seven regional breeding programmes under different agro-ecological regions for variety development (described in Chapter 3, section 3.2). These are broadly divided into irrigated and rainfed breeding programmes (Nuss 1998). The irrigated (12 months harvest cycle) programme is situated in areas where there is erratic and insufficient rainfall for optimal crop growth and, therefore, irrigation is required to attain economic yields. The rainfed programme is further divided into coastal and high altitude programmes. The coastal programmes (12 to 18 months harvest cycle) were established along the coastal areas of the Indian Ocean and are characterised by high temperatures, hilly topography, soil variability and mainly summer rainfall. The Midlands programmes (24 months harvest cycle) are located in the inland and are characterised by high altitudes with long and cold winters.

The origin of breeding populations, age of harvest, age of breeding programmes and the effect of recurrent breeding and selection all have an influence on breeding parameters. Studies on broad-sense heritability among breeding programmes have been limited to the advanced breeding stage for yield and quality traits (Zhou and Joshi 2012), early stages for quality traits (Zhou et al. 2013b) and few studies (Zhou 2014) compared family and individual genotype selection for cane yield.

Considering broad-sense heritability as a parameter for family evaluation and selection, it is possible to identify superior populations for advancing to the evaluation in next breeding stage and changes in selection efficiency across breeding cycles and genetic gains can be evaluated. The objectives of this study were to (i) determine the magnitude and trends in broad-sense heritability among breeding populations, (ii) compare broad-sense heritability between family and individual genotypes and evaluate their implications on sugarcane breeding and selection.

4.3 MATERIALS AND METHODS

4.3.1 Experimental material

Sugarcane families (crosses) included in this study were made at Mount Edgecombe research station (96 m altitude; 29°42', 31°2'E) located in Durban, KwaZulu-Natal province of South Africa. The families included in this study were developed between May and August of 2007 to 2015 seasons. Three mating designs were used to generate families namely, bi-parental, males only and melting pot. Bi-parental mating involves crossing of one pistil parent with one pollen parent. Males' only mating involves inter-crossing of at least two male parents and

collecting seed from all genotypes in which the identity of the pollen donor is unknown. Melting pot is one technique where several male parents pollinate a single female parent. A total of 34 mini-line trials were planted in the field from 2010 to 2015 for the seven regional breeding programmes (described in Chapter 3, Table 3.2). Four humic soil trials were planted in 2010, 2011, 2012 and 2013 and five sandy soil trials were planted in 2010, 2011, 2012, 2013 and 2015. Five trials each for irrigated, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) were planted in 2011, 2012, 2013, 2014 and 2015, respectively.

4.3.2 Experimental sites

Humic trials were established at Bruyns hill (1012 m altitude; 29º25'S, 30º68'E) and sandy soil Glenside (997 m altitude; 29°20'S, 30°46'E) research station a high altitude climate with shorter summers and long cold winters. Coastal long cycle high potential were planted at Kearsney research station (241 m altitude; 29°17'S, 31°16'E). Coastal long cycle average potential were established at Gingindlovu research station (93 m altitude; 29°1'S, 31°36'E). The coastal short cycle high potential trials were planted at Empangeni research station (102 m altitude; 28°43'S, 31°53'E) and irrigated trials at Pongola research station (308 m altitude; 27°24'S, 31°35'E).

4.3.3 Experimental design and data collection

All trials were laid out as randomised block design with three replications (described in Chapter 3, section 3.3.4). The number of families planted in a trial ranged from 85 to 290. Data on stalk number, stalk height and stalk diameter were measured from the first 20 genotypes per family plot and used to estimate cane yield.

4.3.4 Data analysis

The heritability estimates were calculated from the variance components estimated from equation 3.2 and 3.3 in section 3.3.5. The estimate of broad-sense heritability (H) for family was calculated using:

$$H_F = \frac{\sigma_F^2}{(\sigma_F^2 + \sigma_{\frac{FR}{r}}^2 + \sigma_{\frac{G(FR)}{rg}}^2)} \quad \text{Equation 4.1}$$

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

$$H_G = \frac{\sigma^2_{G(F)}}{(\sigma^2_{G(F)} + \sigma^2_{G(FR)})} \text{ ……..…….....Equation 4.2}$$

Where σ^2_F = variance component of the family effects, $\sigma^2_{G(F)}$ = variance component of individual genotype nested with the family, σ^2_{FR} = variance component of the interaction effect of replication by family, $\sigma^2_{G(FR)}$ = 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):

$$SE = \sqrt{\frac{2(1-H)^2\,[1+H(q-1)]^2}{q(q-1)(n-1)}} \text{ ……...…….Equation 4.3}$$

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

4.4 RESULTS

4.4.1 Cane yield

Family H estimates respectively ranged from 59 to 78% for humic soil, 25 to 55% for sandy soil, 33 to 82% for CLCHP, 21 to 56% for CLCAP, 27 to 72% for CSCHP, 25 to 63% for CSCAP, and 10 to 78% for the irrigated populations (Table 4.1). The mean H estimates for humic soil, CLCHP and CSCHP populations were generally higher than that for irrigated, sandy soil, CLCAP and CSCAP populations. Across years, the sandy soil, CSCAP and irrigated H estimates decreased from 55 to 37% (2011 to 2015), 63 to 25% (2011 to 2015) and 78 to 10% (2013 to 2015), respectively. For individual genotypes, the H estimates ranged from 5 to 10% for humic soil, 2 to 9% for sandy soil, 0 to 12% for CLCHP, 0 to 4% for CLCAP, 0 to 11% for CSCHP, 0 to 9% CSCAP and 0 to 17% for the irrigated populations, respectively. The mean H estimates for humic soil and the irrigated populations were higher compared to the rest of the populations. Across years, the H estimates for CLCHP increased from 6 to 16% (2011 to 2015), while the H estimates for CSCAP decreased from 9 to 0% (2011 to 2015). Family H estimates were higher than those for individual genotypes.

Table 4.1 Broad-sense heritability (H) (± standard error), coefficient of determination (R^2) and coefficient of variation (CV) for cane yield (kg) in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations, planted in 2010, 2011, 2012, 2013, 2014 and 2015

Year	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
Family				**H**			
2010	0.70±0.03	0.25±0.03					
2011	0.59±0.11	0.55±0.03	0.60±0.02	0.32±0.02	0.59±0.02	0.63±0.02	0.77±0.02
2012	0.78±0.02	0.54±0.03	0.62±0.02	0.21±0.02	0.72±0.02	0.57±0.03	0.54±0.03
2013	0.64±0.03	0.37±0.04	0.33±0.02	0.47±0.03	0.68±0.02	0.35±0.02	0.78±0.02
2014			0.49±0.04	0.56±0.04	0.27±0.03	0.34±0.02	0.48±0.02
2015		0.37±0.03	0.82±0.02	0.27±0.03	0.61±0.04	0.25±0.04	0.10±0.04
Mean	0.68±0.05	0.42±0.03	0.57±0.02	0.37±0.03	0.57±0.03	0.43±0.03	0.53±0.03
Individual							
2010	0.10±0.02	0.02±0.01					
2011	0.07±0.02	0.05±0.01	0.06±0.01	0.01±0.01	0.08±0.01	0.09±0.01	0.13±0.01
2012	0.09±0.02	0.09±0.02	0.07±0.01	0.01±0.01	0.08±0.01	0.08±0.01	0.08±0.01
2013	0.05±0.01	0.05±0.01	0.00±0.00	0.04±0.01	0.11±0.01	0.04±0.01	0.17±0.02
2014			0.08±0.02	0.04±0.01	0.00±0.01	0.00±0.01	0.08±0.02
2015		0.02±0.01	0.12±0.02	0.00±0.01	0.03±0.01	0.00±0.00	0.00±0.02
Mean	0.08±0.02	0.05±0.01	0.07±0.01	0.02±0.01	0.06±0.01	0.04±0.00	0.09±0.02
Family				**R^2**			
2010	0.24	0.22					
2011	0.22	0.24	0.15	0.26	0.22	0.27	0.26
2012	0.29	0.28	0.20	0.27	0.23	0.34	0.26
2013	0.22	0.28	0.35	0.29	0.29	0.36	0.36
2014			0.27	0.20	0.42	0.38	0.36
2015		0.20	0.27	0.36	0.31	0.29	0.29
Individual							
2010	0.43	0.43					
2011	0.43	0.42	0.44	0.43	0.47	0.48	0.55
2012	0.41	0.49	0.46	0.55	0.60	0.64	0.53
2013	0.43	0.42	0.45	0.45	0.44	0.43	0.69
2014			0.40	0.47	0.32	0.58	0.52
2015		0.49	0.48	0.37	0.40	0.29	0.48
Family				**CV %**			
2010	66.54	62.10					
2011	57.28	44.89	54.56	57.13	45.04	60.99	42.05
2012	42.27	41.17	59.28	61.91	41.90	54.65	53.21
2013	51.60	54.83	56.99	56.32	44.55	56.24	53.47
2014			49.29	50.00	57.24	57.74	42.81
2015		53.87	44.61	55.44	42.17	53.94	48.83
Individual							
2010	71.15	68.31					
2011	60.32	49.08	54.23	62.42	47.67	64.43	43.93
2012	46.37	45.35	62.27	69.92	42.90	66.37	56.07
2013	56.36	61.49	69.14	62.49	48.14	66.25	52.29
2014			53.71	53.39	71.19	74.32	48.77
2015		62.59	47.75	66.48	47.25	63.44	57.21

Family R^2 values ranged from 0.22 to 0.29 for humic soil, 0.20 to 0.28 for sandy soil, 0.15 to 0.35 for CLCHP, 0.20 to 0.36 for CLCAP, 0.22 to 0.42 for CSCHP, 0.27 to 0.38 for CSCAP, and 0.26 to 0.36 for the irrigated populations respectively (Table 4.1). Family R^2 values across populations were similar. Individual genotype R^2 ranged from 0.41 to 0.43 for humic soil, 0.42 to 0.49 for sandy soil, 0.40 to 0.48 for CLCHP, 0.37 to 0.55 for CLCAP, 0.32 to 0.60 for CSCHP, 0.29 to 0.64 for CSCAP, and 0.48 to 0.69 for the irrigated populations respectively. The R^2 values for individual genotypes ranged from 0.29 to 0.69 and were higher than the R^2 values for families (0.15 to 0.42).

Family CV values ranged from 42.27 to 66.54% for humic soil, 41.17 to 62.10% for sandy soil, 44.61 to 59.28% for CLCHP, 50 to 61.91% for CLCAP, 41.90 to 57.24% for CSCHP, 53.94 to 60.99% for CSCAP, and 42.05 to 53.47% for the irrigated populations (Table 4.1). The range of the CV values for CLCAP and CSCAP were higher than other populations. Individual genotype CV values ~~respectively~~ ranged from 46.37 to 71.15% for humic soil, 45.35 to 68.31% for sandy soil, 47.75 to 69.14% for CLCHP, 53.39 to 69.92% for CLCAP, 42.90 to 71.19% for CSCHP, 63.44 to 74.32% for CSCAP, and 43.93 to 57.21% for the irrigated populations. Family CV values across populations were similar. The CV ranged from 41.17 to 66.54% for families and were lower for individual genotypes which ranged from 42.90 to 74.32%.

4.4.2 Stalk number

Family H estimates ranged from 64 to 80% for humic soil, 38 to 73% for sandy soil, 67 to 83% for CLCHP, 18 to 79% for CLCAP, 72 to 84% for CSCHP, 45 to 83% for CSCAP and 19 to 87% for the irrigated populations (Table 4.2). The mean H estimates for the humic soil, CLCHP and CSCHP populations were higher than those for sandy soil, CLCAP, CSCAP and the irrigated populations. Across years, the family H estimates for sandy soil increased from 40 to 73% (2010 to 2012). However, the H estimates for the CSCAP and irrigated populations decreased from 83 to 45% (2011 to 2014) and 87 to 19% (2011 to 2013), respectively. With individual genotypes, the H estimates ranged from 6 to 10% for humic soil, 2 to 19% for sandy soil, 6 to 16% for CLCHP, 0 to 13% for CLCAP, 8 to 16% for CSCHP, 4 to 18% for CSCAP and 0 to 45% for the irrigated populations, respectively. The mean H estimates for CLCHP, CSCHP and the irrigated populations were higher than for the humic soil, sandy soil, CLCAP, and CSCAP populations. Across years, the H estimates for CSCHP, CSCAP and the irrigated populations decreased from 16 to 8% (2011 to 2014), 18 to 4% (2011 to 2013) and 45 to 0%

(2011 to 2013), respectively. In general H estimates for Family were higher than those for individual genotypes.

Family R^2 values ranged from 0.18 to 0.27 for humic soil, 0.15 to 0.28 for sandy soil, 0.20 to 0.28 for CLCHP, 0.23 to 0.38 for CLCAP, 0.24 to 0.38 for CSCHP, 0.29 to 0.36 for CSCAP, and 0.20 to 0.56 for the irrigated populations (Table 4.2). Family R^2 values were similar across the populations. Individual genotype R^2 ranged from 0.43 to 0.44 for humic soil, 0.39 to 0.55 for sandy soil, 0.43 to 0.50 for CLCHP, 0.46 to 0.56 for CLCAP, 0.43 to 0.63 for CSCHP, 0.44 to 0.68 for CSCAP, and 0.51 to 0.71 for the irrigated populations. Individual genotypes in irrigated populations had the highest range of R^2 and the humic soil had the lowest. The R^2 values for individual genotypes ranged from 0.39 to 0.71 and were higher than the R^2 values for families which ranged from 0.15 to 0.56.

Family CV values ranged from 34.97 to 52.26% for humic soil, 31.59 to 48.54% for sandy soil, 34.92 to 42.68% for CLCHP, 34.07 to 42.62% for CLCAP, 31.18 to 35.27% for CSCHP, 30 to 47.75% for CSCAP, and 25.56 to 37.61% for the irrigated populations (Table 4.2). Family CV values were similar across populations. Individual genotype CV values respectively ranged from 37.74 to 53.53% for humic soil, 32.67 to 50.62% for sandy soil, 36.84 to 41.88% for CLCHP, 36.56 to 48.43% for CLCAP, 33.45 to 42.04% for CSCHP, 42.72 to 47.76% for CSCAP, and 30.38 to 42.23% for the irrigated populations respectively. The CV for individual genotypes ranged from 30.38 to 53.53% and were higher than for families which ranged from 30.00 to 52.26%.

Table 4.2 Broad-sense heritability (H) (± standard error), coefficient of determination (R^2) and coefficient of variation (CV) for stalk number in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations, planted in 2010, 2011, 2012, 2013, 2014 and 2015

Year	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
Family				**H**			
2010	0.75±0.03	0.40±0.04					
2011	0.64±0.03	0.69±0.03	0.77±0.02	0.49±0.03	0.82±0.01	0.83±0.01	0.87±0.01
2012	0.80±0.02	0.73±0.03	0.79±0.02	0.18±0.02	0.84±0.01	0.76±0.02	0.29±0.02
2013	0.67±0.03	0.38±0.04	0.67±0.02	0.57±0.03	0.76±0.02	0.51±0.03	0.19±0.02
2014			0.76±0.03	0.79±0.03	0.72±0.03	0.45±0.04	0.49±0.02
2015		0.55±0.04	0.83±0.02	0.59±0.04	0.77±0.03	0.67±0.03	0.42±0.04
Mean	0.72±0.02	0.55±0.04	0.76±0.02	0.52±0.03	0.78±0.02	0.64±0.03	0.45±0.02
Individual							
2010	0.10±0.02	0.03±0.01					
2011	0.06±0.02	0.02±0.01	0.12±0.01	0.07±0.01	0.16±0.02	0.18±0.02	0.45±0.03
2012	0.10±0.02	0.17±0.03	0.14±0.02	0.00±0.00	0.16±0.02	0.12±0.01	0.03±0.01
2013	0.09±0.02	0.19±0.02	0.06±0.01	0.05±0.01	0.13±0.01	0.04±0.01	0.00±0.00
2014			0.11±0.02	0.13±0.02	0.08±0.02	0.09±0.02	0.07±0.00
2015		0.08±0.01	0.16±0.03	0.06±0.02	0.10±0.02	0.07±0.02	0.05±0.02
Mean	0.09±0.02	0.10±0.02	0.12±0.02	0.06±0.01	0.14±0.02	0.10±0.02	0.12±0.01
Family				**R^2**			
2010	0.18	0.15					
2011	0.19	0.21	0.20	0.23	0.24	0.34	0.56
2012	0.27	0.28	0.20	0.29	0.24	0.29	0.25
2013	0.23	0.20	0.25	0.29	0.28	0.34	0.48
2014			0.23	0.28	0.38	0.36	0.32
2015		0.22	0.28	0.38	0.26	0.34	0.20
Individual							
2010	0.43	0.45					
2011	0.43	0.42	0.49	0.47	0.51	0.58	0.71
2012	0.44	0.55	0.50	0.56	0.63	0.68	0.51
2013	0.44	0.39	0.50	0.46	0.45	0.44	0.61
2014			0.43	0.52	0.43	0.64	0.53
2015		0.53	0.49	0.46	0.45	0.52	0.51
Family				**CV %**			
2010	52.26	48.54					
2011	40.88	31.89	42.68	41.71	33.92	47.75	34.33
2012	34.97	31.59	42.53	42.62	33.04	40.05	37.61
2013	38.72	32.68	38.55	38.42	33.43	30.00	25.56
2014			35.44	34.07	35.27	37.97	27.61
2015		38.97	34.92	39.51	31.18	39.54	35.02
Individual							
2010	53.53	50.62					
2011	42.46	34.37	41.88	43.48	35.02	47.76	37.25
2012	37.74	32.67	37.15	48.43	33.72	42.72	42.23
2013	40.77	41.69	36.84	42.79	35.65	44.09	32.65
2014			37.15	36.56	42.04	43.88	30.38
2015		41.73	36.84	47.22	33.45	42.72	37.70

4.4.3 Stalk height

Family H estimates respectively ranged from 61 to 74% for humic soil, 8 to 73% for sandy soil 43 to 85% for CLCHP, 37 to 74% for CLCAP, 53 to 88% for CSCHP, 24 to 72% for CSCAP and 40 to 74% for the irrigated populations (Table 4.3). The mean H estimates for humic soil, CLCHP and CSCHP were higher compared to the rest of the populations. Across years, the humic soil H estimates increased from 61 to 74% (2010 to 2013), while the H estimates for the CSCHP and irrigated populations decreased from 84 to 53% (2011 to 2013) and from 63 to 40% (2013 to 2015), respectively. For individual genotypes, H estimates respectively ranged from 4 to 12% for humic soil, 0 to 18% for sandy soil, 0 to 20% for CLCHP, 0 to 11% for CLCAP, 0 to 21% for CSCHP, 0 to 16% for CSCAP and 0 to 21% for the irrigated populations. The mean H estimates for the CSCHP population was higher than ~~for~~ the other populations. Across years, the H estimates for the humic soil and CLCHP populations decreased respectively from 11 to 4% (2010 to 2012) and 18 to 0% (2011 to 2013). Family H estimates were in general higher than for individual genotypes.

Family R^2 values ~~respectively~~ ranged from 0.30 to 0.40 for humic soil, 0.28 to 0.44 for sandy soil, 0.40 to 0.57 for CLCHP, 0.28 to 0.64 for CLCAP, 0.32 to 0.50 for CSCHP, 0.32 to 0.42 for CSCAP, and 0.32 to 0.63 for the irrigated populations (Table 4.3). Family R^2 values were similar across populations. Individual genotype R^2 respectively ranged from 0.39 to 0.46 for humic soil, 0.41 to 0.56 for sandy soil, 0.43 to 0.52 for CLCHP, 0.32 to 0.61 for CLCAP, 0.33 to 0.59 for CSCHP, 0.44 to 0.70 for CSCAP, and 0.47 to 0.62 for the irrigated populations. The R^2 values for individual genotypes ranged from 0.32 to 0.70 and were higher than the R^2 values for families (ranged from 0.28 to 0.64).

Family CV values ranged from 19.32 to 29.33% for humic soil, 18.71 to 25.55% for sandy soil, 13.55 to 22.10% for CLCHP, 17.91 to 29.56% for CLCAP, 13.20 to 28.13% for CSCHP, 20.47 to 27.01% for CSCAP, and 10.44 to 23.57% for the irrigated populations (Table 4.3). Family CV values were similar across populations. Individual genotype CV values respectively ranged from 21.30 to 33.13% for humic soil, 20.30 to 30.43% for sandy soil, 16.68 to 32.97% for CLCHP, 23.62 to 31.28% for CLCAP, 13.67 to 39.97% for CSCHP, 23.27 to 35.03% for CSCAP, and 12.84 to 27.79% for the irrigated populations. The CV for individual genotypes ranged from 12.84 to 39.97% and were higher than for families which ranged from 10.44 to 29.56%.

Table 4.3 Broad-sense heritability (H) (± standard error), coefficient of determination (R^2) and coefficient of variation (CV) for stalk height in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations, planted in 2010, 2011, 2012, 2013, 2014 and 2015

Year	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
Family				**H**			
2010	0.61±0.04	0.55±0.04					
2011	0.61±0.03	0.73±0.02	0.59±0.02	0.37±0.03	0.84±0.01	0.70±0.02	0.74±0.02
2012	0.66±0.37	0.64±0.03	0.62±0.02	0.68±0.02	0.63±0.02	0.72±0.02	0.56±0.03
2013	0.74±0.03	0.08±0.02	0.43±0.03	0.66±0.02	0.53±0.03	0.60±0.02	0.63±0.02
2014			0.57±0.04	0.74±0.03	0.59±0.04	0.61±0.04	0.51±0.02
2015		0.73±0.03	0.85±0.02	0.47±0.04	0.88±0.02	0.24±0.03	0.40±0.04
Mean	0.66±0.12	0.55±0.03	0.61±0.03	0.58±0.02	0.69±0.02	0.57±0.03	0.57±0.03
Individual							
2010	0.11±0.02	0.08±0.02					
2011	0.10±0.02	0.18±0.02	0.11±0.01	0.04±0.01	0.21±0.02	0.15±0.02	0.21±0.02
2012	0.04±0.01	0.10±0.02	0.10±0.01	0.11±0.01	0.06±0.01	0.16±0.02	0.04±0.01
2013	0.12±0.02	0.00±0.01	0.00±0.00	0.10±0.01	0.10±0.01	0.11±0.01	0.12±0.01
2014			0.10±0.02	0.11±0.02	0.00±0.00	0.04±0.01	0.13±0.01
2015		0.13±0.02	0.20±0.03	0.00±0.01	0.21±0.03	0.00±0.01	0.00±0.02
Mean	0.09±0.02	0.10±0.02	0.10±0.02	0.07±0.01	0.12±0.01	0.09±0.01	0.10±0.01
Family				**R^2**			
2010	0.40	0.44					
2011	0.34	0.34	0.40	0.38	0.33	0.41	0.51
2012	0.30	0.28	0.47	0.28	0.32	0.39	0.63
2013	0.31	0.36	0.57	0.32	0.41	0.32	0.32
2014			0.46	0.33	0.50	0.42	0.42
2015		0.32	0.50	0.64	0.30	0.37	0.44
Individual							
2010	0.44	0.48					
2011	0.45	0.50	0.48	0.45	0.55	0.52	0.59
2012	0.39	0.50	0.48	0.61	0.59	0.70	0.51
2013	0.46	0.41	0.45	0.49	0.43	0.48	0.62
2014			0.43	0.52	0.33	0.60	0.54
2015		0.56	0.52	0.32	0.52	0.44	0.47
Family				**CV %**			
2010	26.64	22.49					
2011	29.33	24.27	14.77	21.25	19.09	20.47	10.44
2012	19.32	18.71	21.15	29.56	16.76	22.31	17.41
2013	19.42	25.34	22.10	23.11	18.75	24.27	23.57
2014			21.52	21.35	28.13	27.01	15.16
2015		25.55	13.55	17.91	13.20	20.73	16.67
Individual							
2010	31.76	27.96					
2011	33.13	26.68	17.38	25.00	20.17	23.27	12.84
2012	22.11	20.30	26.73	31.28	19.12	24.86	27.79
2013	21.30	30.43	32.97	25.44	22.50	26.65	25.71
2014			26.78	23.62	39.97	35.03	18.39
2015		27.99	16.68	31.28	13.67	25.48	22.40

4.4.4 Stalk diameter

Family H estimates respectively ranged from 73 to 90% for humic soil, 75 to 89% for sandy soil, 86 to 95% for CLCHP, 77 to 90% for CLCAP, 51 to 91% for CSCHP, 62 to 85% for CSCAP and 40 to 88% for the irrigated populations (Table 4.4). The mean H estimates for humic soil, CLCHP and CLCAP were higher than for the rest of the populations. Across years, family H estimates for the humic soil, CLCHP and CLCAP populations increased from 73 to 90% (2010 to 2012), 86 to 95% (2013 to 2015) and 77 to 90% (2012 to 2015), respectively. The H estimates decreased from 84 to 40% (2012 to 2015) in irrigated soils and it varied across years in sandy soil, CSCHP and CSCAP H. For individual genotypes, H estimates ranged from 10 to 24% for humic soil, 7 to 23% for sandy soil, 5 to 28% for CLCHP, 12 to 31% for CLCAP, 8 to 33% for CSCHP, 12 to 24% for CSCAP and 5 to 28% for the irrigated populations. The mean H estimates for CLCAP, CSCHP and the irrigated populations were higher than those for humic soil, sandy soil, CLCHP and the CSCAP populations. Across years, the H estimates for the humic soil and CSCHP populations increased from 10 to 24% (2010 to 2012) and 17 to 33% (2011 to 2014), respectively. The H estimates for sandy soil, CLCHP, CLCAP, CSCAP and the irrigated populations varied across years. Family H estimates were in general higher than for individual genotypes.

Family R^2 values ranged from 0.22 to 0.34 for humic soil, 0.15 to 0.31 for sandy soil, 0.32 to 0.37 for CLCHP, 0.31 to 0.44 for CLCAP, 0.25 to 0.55 for CSCHP, 0.35 to 0.48 for CSCAP, and 0.38 to 0.44 for the irrigated populations (Table 4.4). Family R^2 values for CLCHP, CLCAP, CSCAP and irrigated populations were higher than for humic soil, sandy soil and CSCHP populations. Individual genotype R^2 respectively ranged from 0.45 to 0.52 for humic soil, 0.47 to 0.58 for sandy soil, 0.51 to 0.60 for CLCHP, 0.49 to 0.63 for CLCAP, 0.44 to 0.64 for CSCHP, 0.53 to 0.68 for CSCAP, and 0.52 to 0.69 for the irrigated populations. The R^2 values for individual genotypes ranged from 0.44 to 0.69 and were higher than the R^2 values for families which ranged from 0.15 to 0.48.

Family CV values ranged from 10.38 to 12.45% for humic soil, 10.24 to 13.09% for sandy soil, 10.88 to 14.56% for CLCHP, 11.36 to 13.19% for CLCAP, 10.50 to 16.19% for CSCHP, 10.39 to 13.36% for CSCAP, and 11.87 to 14.20% for the irrigated populations (Table 4.4). Family CV values were similar across populations. Individual genotype CV values ranged from 10.71 to 13.18% for humic soil, 10.55 to 13.52% for sandy soil, 11.14 to 15.55% for CLCHP,

12.22 to 14.52% for CLCAP, 11.20 to 22.50% for CSCHP, 12.80 to 15.54% for CSCAP, and 12.98 to 16.04% for the irrigated populations. The CV for individual genotypes ranged from 10.55 to 22.50% and were higher for families which ranged from 10.24 to 14.56%.

4.4.5 Trends for cane yield and its components across populations

Family and individual H estimates for all populations were subjected to ANOVA and their least square mean values presented in Table 4.5. The ANOVA comparisons among the populations showed that for cane yield, the sandy soil, CLCAP and CSCAP populations had significantly ($P<0.05$) lower H estimates than the humic soil populations. The humic soil (68%) had the highest H estimate whereas the lowest was observed for CLCAP (37%). The CSCHP population produced a significantly ($P<0.05$) higher H estimate for stalk number than sandy soil, CLCAP and the irrigated populations. The CSCHP population (78%) had the highest H estimate whereas the irrigated population (45%) had the lowest. All populations produced non-significant ($P>0.05$) H estimates for stalk height. The CSCHP population (69%) had the highest H estimate whereas the sandy soil population (55%) had the lowest. The CLCHP population produced a significantly ($P<0.05$) higher H estimate for stalk diameter than the CSCAP and irrigated populations. The CLCHP population (91%) had the highest H estimate, whereas the irrigated population (72%) had the lowest.

In general, family H estimates were higher for all traits among the humic soil, CLCHP and CSCHP compared to other populations (Table 4.5). Across all populations, the H estimated for stalk diameter was higher than for cane yield.

For individual genotypes, humic soil and irrigated populations produced significantly ($P<0.05$) higher H estimates for cane yield than CLCAP. The irrigated population (9%) had the highest H estimate while the CLCAP population (2%) had the lowest. All populations produced non-significant ($P>0.05$) H estimates for stalk number, stalk height and stalk diameter, respectively. Generally, families produced larger H estimates for all traits compared to individual genotypes.

Table 4.4 Broad-sense heritability (H) (± standard error), coefficient of determination (R^2) and coefficient of variation (CV) for stalk diameter in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations, planted in 2010, 2011, 2012, 2013, 2014 and 2015

Year	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
Family				**H**			
2010	0.73±0.03	0.78±0.02					
2011	0.88±0.02	0.75±0.02	0.92±0.01	0.83±0.01	0.83±0.01	0.83±0.01	0.88±0.01
2012	0.90±0.01	0.89±0.01	0.92±0.01	0.77±0.02	0.89±0.01	0.68±0.02	0.79±0.02
2013	0.86±0.02	0.78±0.02	0.86±0.01	0.83±0.01	0.88±0.01	0.85±0.01	0.84±0.01
2014			0.92±0.01	0.88±0.02	0.91±0.01	0.74±0.03	0.69±0.03
2015		0.82±0.02	0.95±0.01	0.90±0.01	0.51±0.04	0.62±0.04	0.40±0.04
Mean	0.84±0.02	0.80±0.02	0.91±0.01	0.84±0.01	0.80±0.02	0.74±0.02	0.72±0.02
Individual							
2010	0.10±0.02	0.13±0.02					
2011	0.17±0.03	0.07±0.01	0.25±0.02	0.13±0.01	0.17±0.02	0.24±0.02	0.25±0.02
2012	0.24±0.03	0.23±0.03	0.28±0.02	0.12±0.01	0.18±0.02	0.12±0.01	0.19±0.02
2013	0.21±0.03	0.14±0.02	0.28±0.02	0.22±0.02	0.19±0.02	0.24±0.02	0.28±0.02
2014			0.19±0.01	0.31±0.04	0.33±0.04	0.15±0.02	0.19±0.03
2015		0.17±0.02	0.05±0.03	0.29±0.04	0.08±0.02	0.12±0.02	0.05±0.01
Mean	0.18±0.03	0.14±0.02	0.17±0.02	0.21±0.02	0.19±0.02	0.17±0.04	0.19±0.02
Family				**R^2**			
2010	0.22	0.23					
2011	0.27	0.15	0.32	0.31	0.25	0.48	0.40
2012	0.34	0.31	0.34	0.31	0.25	0.40	0.38
2013	0.33	0.27	0.33	0.41	0.26	0.35	0.41
2014			0.33	0.44	0.44	0.42	0.44
2015		0.30	0.37	0.41	0.55	0.42	0.43
Individual							
2010	0.45	0.51					
2011	0.49	0.47	0.55	0.49	0.52	0.58	0.61
2012	0.52	0.58	0.59	0.62	0.64	0.63	0.61
2013	0.51	0.48	0.56	0.56	0.49	0.56	0.69
2014			0.51	0.63	0.58	0.68	0.58
2015		0.58	0.60	0.60	0.44	0.53	0.52
Family				**CV %**			
2010	10.39	10.24					
2011	10.38	13.09	10.88	12.55	10.90	11.49	11.87
2012	11.57	11.72	14.31	11.36	10.50	10.39	12.87
2013	12.45	12.87	14.56	13.19	12.92	13.36	14.20
2014			12.68	12.08	12.43	12.82	14.01
2015		11.11	13.63	12.08	16.19	13.29	12.42
Individual							
2010	10.83	10.55					
2011	10.71	13.00	11.14	13.44	11.20	12.89	12.98
2012	12.12	11.90	14.47	12.22	11.65	12.80	14.20
2013	13.18	13.52	15.55	14.52	13.14	13.97	15.10
2014			13.10	13.05	13.21	14.71	16.04
2015		12.31	13.63	13.82	22.50	15.54	15.70

Table 4.5 Broad-sense heritability least square mean values and their standard errors from ANOVA analysis for cane yield, stalk number, height and diameter in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations

Populations	Cane yield	Stalk number	Stalk height	Stalk diameter
Family				
Humic soil	0.68±0.05a	0.72±0.03abc	0.66±0.13a	0.84±0.02ab
Sandy soil	0.42±0.03b	0.55±0.03bcd	0.55±0.03a	0.80±0.02ab
CLCHP	0.57±0.02ab	0.76±0.02ab	0.61±0.03a	0.91±0.01a
CLCAP	0.37±0.03b	0.52±0.03cd	0.58±0.03a	0.84±0.01ab
CSCHP	0.57±0.03ab	0.78±0.03a	0.69±0.03a	0.80±0.02ab
CSCAP	0.43±0.03b	0.64±0.02abcd	0.57±0.02a	0.74±0.02b
Irrigated	0.53±0.03ab	0.45±0.02d	0.57±0.03a	0.72±0.02b
Individual				
Humic soil	0.08±0.02a	0.09±0.02a	0.09±0.02a	0.18±0.03a
Sandy soil	0.05±0.01ab	0.10±0.02a	0.10±0.02a	0.14±0.02a
CLCHP	0.07±0.01ab	0.12±0.02a	0.10±0.03a	0.17±0.02a
CLCAP	0.02±0.01b	0.06±0.01a	0.07±0.01a	0.21±0.01a
CSCHP	0.06±0.001ab	0.14±0.02a	0.12±0.02a	0.19±0.02a
CSCAP	0.04±0.01ab	0.10±0.02a	0.09±0.01a	0.17±0.02a
Irrigated	0.09±0.02a	0.12±0.01a	0.10±0.01a	0.19±0.09a

4.5 DISCUSSION

Families had higher H estimates than the individual genotypes for cane yield traits and this indicated that a larger proportion of genetic variability is associated within families than individual genotypes. Families are replicated in trials while individual genotypes are not replicated, therefore, genetic variability decreased with an increase inter-plot competition and field variability among genotypes. Replications account for environmental variability and provide accurate estimates of genetic variability within families. Broad-sense heritability is the proportion of genetic variance to the total variance in a population (Zhou and Joshi 2012) and the results of the present study indicated that families exhibited larger genetic variability compared to individual genotypes. The larger proportion of phenotype attributed to genetic variation showed that selection of elite families with higher trait values was more effective than selecting individual genotypes with higher trait values. Similar trend was observed for stalk number, stalk height and stalk diameter, indicating that characterising populations through families was more accurate than through individual genotypes. Results of this study confirms with previous report that proved family evaluation and selection superior to individual genotype selection (Zhou 2014; Zhou and Mokwele 2015).

Traditionally, families with high traits values are identified from which superior individual genotypes are selected for advancement to the next stage. While results have shown the superiority of family selection, individual genotype variances were also significant as highlighted in Chapter 3. Individual genotypes had significant, low H estimates. Before adoption of family evaluation and selection, progress in genetic gain was achieved, through mass selection though at considerably lower levels of efficiency (Skinner 1982). Therefore, adopting the strategy of family evaluation to identify superior families with high trait values and superior performance followed by applying efficient individual genotype selection within the selected families is expected to increase genetic gain in sugarcane breeding. However, applying other approaches to selection for individual genotypes in best populations such as logistic regression models (Zhou et al. 2013a; Zhou 2018) would further increase accuracy of identifying high yielding elite genotypes within selected families.

The humic soil, CLCHP, CSCHP and irrigated populations produced higher mean H estimates (above 0.5) for cane yield compared to sandy soil, CLCAP and CSCAP populations, indicating larger proportions of genetic variability among the families. The breeding programmes with high H estimates are known to be located in areas with uniform soil conditions and family genetic values are measured with lower effect from field variability and true family variability can be determined. The sandy soil, CLCAP and CSCAP populations were established in fields with higher field variability, and therefore, genetic variability among families and genotypes is confounded by large field variability. On an average, the larger coefficient of variation (CV) values associated with individual genotypes in CLCAP (64%), and CSCAP (64%) compared to humic soil (58%), sandy soil (57%), CLCHP (57%), irrigated (51%) and CSCHP (50%) for cane yield suggested large variability in the data and lower experimental precision. Generally, the low R^2 values (0.15 to 0.42 for families and 0.29 to 0.69 for individual genotypes) and large CV % values (41.17 to 66.54% for families and 42.90 to 74.32% for individual genotypes) for cane yield observed in the study was an indication of the larger variability in the data.

The breeding programmes such as humic soil, CLCHP and CSCHP with higher family H estimates have produced higher population genetic gains (Zhou 2013) and cultivar genetic gains (Zhou and Gwata 2016; Zhou 2017) in previous studies. The humic soil and irrigated breeding programmes have been in existence for more than 47 years while the sandy soil, CLCAP and CSCAP were established 21 years ago (Nuss 1998). The longer cycles of breeding

and selection for the humic soil and irrigated populations have resulted in higher genetic improvement and higher accumulation of small additive effects for cane yield compared to the sandy soil, CLCAP and CSCAP populations. A previous study by Lingle et al. (2010) also demonstrated high genetic gains achieved by several cycles of recurrent selection for quality traits, cane yield and sugar yield in sugarcane breeding in Louisiana, USA. Further, when the sandy soil and CSCAP breeding programmes were established, there were no suitable and sufficient sources of parental material to initiate the breeding programmes. Consequently, parents for the sandy soil breeding programme were derived mainly from the humic soil and other SASRI breeding programmes. On the other hand, parents for CSCAP and CLCAP were derived mainly from old SASRI breeding programmes such as coastal (Shakaskraal, Mtunzini, Central field station), irrigated (Pongola) and Midlands breeding programmes. Most of the genetic material used to establish the sandy soil, CLCAP and CSCAP programmes were not adapted and are still being evaluated for suitability. In the Midlands region, sugarcane is grown for 24 months to mature and, therefore, fewer cycles of breeding and selection are realised in a short period of time, which further have an impact on the recurrent selection benefits for the sandy soil programme. Results also suggested that with the adoption of family evaluation and selection in sandy soils, CLCAP and CSCAP breeding programmes, higher selection efficiency and genetic gains for cane yield can be achieved which indicates the high yielding potential associated with these soil types.

The CLCAP and CSCAP programmes are located on a site with high prevalence of Eldana borer, resulting in potential in an increased selection pressure for Eldana resistance populations at the expense of cane yield genetic variation. This high pressure on breeding and selection for Eldana resistance populations interferes with evaluation and selection of parents with high breeding values for cane yield. Hence, there is a need to combine high cane yield with Eldana resistance populations. Therefore, research is required to quantify genetic interactions between yield and Eldana damage to guide future breeding for the CLCAP and CSCAP programmes. Eldana damage will also increase phenotypic variability for yield among the families and genotypes that is not associated with genetic differences. Hence suitable breeding strategy for identifying Eldana resistance combining high yield should be identified for this region. The humic soil, CLCHP and CSCHP had higher family H estimates, for stalk number and height respectively compared to sandy soil, CLCAP, CSCAP and irrigated populations. This highlighted the potential differences in yield components among the breeding programmes.

The larger H estimates among the humic soil, CLCHP and CSCHP for stalk number and height indicated that superior families could be identified and selected with higher precision for these traits. This has implications for SASRI breeding programmes since stalk number is a major component trait for cane yield (Zhou 2004; Kumar and Singh 2005). Therefore, families with high stalk number are most likely to be superior to those with a lower stalk number, particularly in sub-tropical regions of countries such as South Africa (Zhou and Shoko 2012). Stalk number was found important for adaptability and ratooning ability, particularly in sub-tropical breeding programmes such as for South Africa (Zhou and Shoko 2012) and the USA (Milligan et al. 1996). The study emphasis that further selection should be done among families with high stalk number and generally with taller stalks. The results of the present study implies that measuring stalk number and height will constitute an optimal selection index for cane yield that can then be used to evaluate families. The importance of these results is that in breeding programmes with limited resources, stalk number and height alone can be used to assess potential of families in early stages of selection.

Stalk number, stalk height and stalk diameter had higher family H estimates than cane yield for almost all the populations, suggesting that indirect selection for cane yield could be efficient. During selection, genotypes are visually evaluated for stalk number, stalk height and stalk diameter. This is particularly important since estimating cane yield through yield components remains the most viable and practical approach for smaller and resource limited breeding programmes. Zhou (2014) showed that cane yield, estimated from stalk number, stalk height and stalk diameter, was suitable for family evaluation and selection. Further studies on logistic regression models by Zhou et al. (2013a) and Zhou (2018) demonstrated that selection for cane yield, through its components may be more efficient. Path coefficient analysis studies (Kumar and Singh 2005) have also shown that cane yield components such as stalk number, stalk height and stalk diameter can accurately predict cane yield. In contrast with studies done in Australia (Kimbeng et al. 2000; Kimbeng and Cox 2003), family evaluation, based on harvesting whole plots of families using automatic weighing machines (Hogarth and Mullins 1989), has been effective. However, the use of automatic weighing machines may be expensive and unaffordable for smaller breeding programmes where such an investment in equipment is considered uneconomical. Hence, the indirect selection of cane yield through its components will benefit breeding programmes with limited resources and further encourage the adoption of family evaluation in many environments.

4.6 CONCLUSIONS

Family evaluation and selection produced higher broad-sense heritability estimates compared to individual selection and was, therefore, more efficient than individual genotype selection. Combined gains from adopting family selection followed by individual genotype selection will increase overall genetic gains in sugarcane breeding. The higher proportion of genetic variability among humic soil, CLCHP, CSCHP and irrigated populations compared to sandy soil, CLCAP, and CSCAP populations for cane yield indicated the efficacy of family evaluation and the potential to improve genetic gains through identification of location specific families and selection. More cycles of recurrent breeding will improve the genetic background in sandy soil, CSCAP and CLCAP breeding populations which will be useful in enhancing selection efficiency and genetic gains. The study showed that cane yield and its component traits recorded high family H estimates and thereby offers opportunity to increase the selection rate and identifying superior families. In addition, these families will form a new source of population for improvement of yield components through recurrent selection strategy. Visual selection combined with family selection will be more accurate in identifying elite families and superior clones for genetic improvement in sugarcane.

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CHAPTER 5

ESTIMATING BREEDING VALUES OF GENOTYPES FOR SUGARCANE YIELD

5.1 ABSTRACT

Breeding value refers to the ability of a genotype to produce superior progenies when crossed with other genotypes. Breeding values are used to predict the breeding performance of genotypes in sugarcane, which is a complex polyploid crop. The objectives of this study were to estimate the breeding values of genotypes for cane yield, to determine the proportions of elite female and male, and implications for sugarcane breeding. Data were collected from family (cross) evaluation trials planted across the South African Sugarcane Research Institute (SASRI) seven breeding programmes. The trials were planted in a randomised complete block design with three replications per family. Cane yield was estimated from stalk number, stalk height and stalk diameter measured from the first 20 progenies per plot. Best linear unbiased prediction (BLUP) analysis, which provides comparison of genotypes with population means, was done using Statistical Analysis Software (SAS) mixed models. Significant ($P<0.05$) female and male variances indicated that the large variability observed among progenies could be attributed to the variability among genotypes used for crossing. The following genotypes; 82H0397, 85H0428, N52, B74713, 87W0629, 01G1662, 88W1323, 02K1657, 87L0573, 97E0474, N31, 93E0888, 03U1030, 06T3608, 96W0246, WI82498 and 79F0779, with high breeding values when crossed with diverse genotypes, produced progenies with high cane yield. Genotypes with high breeding values can be used as testers for future crossing and to build a core germplasm pool of genotypes known to produce progenies with high cane yield. The proportions of genotypes with high breeding values were higher for the CSCHP (29.4%), CLCHP (28.0%), humic soil (27.8%) and irrigated (26.0%) populations compared to the sandy soil (22.9%), CSCAP (21.0%) and CLCAP (18.4%) populations, probably due to longer cycles of recurrent breeding and selection. Low numbers of genotypes with high breeding values suggested that intensive evaluation and development of genotypes, used for crossing, is required in these populations.

Key words: Breeding values, diverse genotypes, genetic variability, progenies, cane yield

5.2 INTRODUCTION

The breeding value of a genotype refers to the value of genes that the genotype can transmit to its progenies during crossing. It can be used to determine the performance of the genotype when used in making crosses. The choice of parents used in crossing is critical for an efficient breeding programme in order to combine desirable genes in progenies. Parent selection is based on the genotype's potential to produce high proportions of progenies with high trait values. The genetic combination of selected parents determines the genetic variability among progeny populations, which eventually is exploited during selection (Balzarini 2000). Therefore, parent evaluation is critical in any plant breeding programme. Making crosses with complementary genotypes 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 genotypes known to produce progenies with high trait values increases genetic recombination and segregation of genes during crossing (Barbosa et al. 2001; Kimbeng and Cox 2003). Genetic recombination and segregation in sugarcane only occurs at crossing. Thereafter, subsequent selection stages are planted from vegetative material with no further genetic recombination (Zhou and Joshi 2012).

One of the challenges in sugarcane breeding is predicting the genetic potential of genotypes as parents required to produce superior progenies. Modern commercial sugarcane cultivars are complex interspecific hybrids of the genus *Saccharum*. Cultivars are polyploid and highly aneuploid, with an unbalanced number of chromosomes ranging from 100 to 130 (Sreenivasan et al. 1987), resulting in limited control of genetic transmission during crossing. In addition, sugarcane is heterozygous and an outcrossing plant, and the genotypes utilised as commercial cultivars are interspecific hybrids. Intermating between two clones produces large variability among progenies in first generation itself and considering the large genetic variation existing among commercial cultivars due to their interspecific hybrid nature, heterozygosity and high polyploidy, it is difficult to predict progeny performance.

In the early years of sugarcane breeding, the proven parent system was used to identify genotypes to be used as donors in crosses (Heinz and Tew 1987). The proven parent system used the number of seedlings advanced to the next testing stage to determine the performance of parental genotypes (Heinz and Tew 1987; Skinner et al. 1987) and this system was biased towards older parents that had previously produced large number of seedlings, as well as

genotypes producing crosses with higher germination rates. Another disadvantage was lack of a suitable statistic model to objectively compare performance of genotypes in crosses. In South Africa, sugarcane takes 12 to 24 months from planting to harvest. The genetic material advanced 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 proven parent system took several years to determine whether parents were good combiners and productive because of accumulation of advancement data over long period of time and crop cycles (Kimbeng and Cox 2003).

To overcome these challenges, progeny data measured from the first stage of a four-stage sugarcane breeding and selection programme (in South Africa), is used to determine the breeding values of parents. Breeding values were first estimated in animal breeding using the best linear unbiased prediction (BLUP) (Henderson 1977, 1984). The breeding value refers to the ability of a genotype to produce progenies with high trait values when crossed with other genotypes. Breeding values predict additive genetic effects particularly in complex genomes such as sugarcane. In plants, the use of breeding values started with forestry breeding (White and Hodge 1989) and are now used in maize (Vivek et al. 2017), soybean (De Carvalho et al. 2008), peach (De Souza and Byrne 2000) and sugarcane (Chang and Milligan 1992a, 1992b; Atkin et al. 2009; Atkin 2010; Zhou and Mokwele 2015). In sugarcane, breeding values were estimated from family data (Stringer et al. 1996), predicted using pedigree data (Atkin et al. 2009), and used to select parents (Jackson 2016).

The BLUP method is used to accurately predict the breeding values of genotypes in animal and agricultural crops. The main advantage of the BLUP over other statistical methods is that it can accommodate highly unbalanced data sets, such as those generated from routine sugarcane progeny evaluation trials (Stringer et al. 2011; Zhou and Mokwele 2015) which are caused by variable germination. Chang and Milligan (1992a, 1992b) reported the use of BLUP to predict cross performance. BLUP has been applied to identify and select genotypes used in crosses and to design new crosses in Australia (Stringer 1999; Atkin et al. 2009; Atkin 2010; Jackson 2016), South Africa (Zhou 2014; Zhou and Mokwele 2015) and Brazil (Moreira and Peternelli 2015). Others (Piepho et al. 2008; Atkin et al. 2009) have reported BLUP, estimated from pedigree data, was more accurate than estimates from a single trial.

Currently, parent selection at South African Sugarcane Research Institute (SASRI) is largely based on the proven parent system and genetic values (e.g. dominance). Progeny cane yield data collected from the last seven years have been used for family evaluation, however, family evaluation data have been used to evaluate parents in Australia (Atkin et al. 2009; Atkin 2010; Jackson 2016) and other countries. To increase efficiency of parent selection, the use of breeding values are being explored in South Africa. The objectives of this study were to estimate the breeding values of genotypes for cane yield, to determine the proportions of elite genotypes used in making crosses, and to investigate their implications in sugarcane breeding.

5.3 MATERIALS AND METHODS

5.3.1 Experimental material

The number of female and male parents that were used in effecting families (crosses) in this study are presented in Table 5.1. The number of female parents ranged from 31 to 115, whereas the number of male parents ranged from 19 to 71. Crossing was done in cubicles in a glasshouse at Mount Edgecombe to control pollen contamination and included full-sib progenies (derived from bi-parental crosses) and half-sib progenies (derived from polycrosses). Bi-parental crosses are effected between a single female parent with a male parent. The number of female parents used in bi-parental crosses ranged from 14 to 61, whereas that of male parents ranged from 17 to 69. Some of the female and male parents were utilized in more than one cross. Polycrosses were made using only male parents and melting pot crossing systems. Males' only involved inter-crossing of at least two male parents and collecting seed from all the plants. Melting pot involved several male parents pollinating a single female parent. In the males' only and melting pot, the source of pollen is always unknown.

5.3.2 Experimental sites

The data were collected from 34 mini-line trials (Table 5.1), planted in the field from 2010 to 2015 across seven regional breeding programmes (described in Chapter 3, Table 3.2). Humic trials were established at Bruyns hill (1012 m altitude; 29º25'S, 30º68'E) and sandy soil Glenside (997 m altitude; 29°20'S, 30°46'E) research station at a high altitude climate with shorter summers and long cold winters. Coastal long cycle high potential were planted at Kearsney research station (241 m altitude; 29°17'S, 31°16'E). Coastal long cycle average potential were established at Gingindlovu research station (93 m altitude; 29°1'S, 31°36'E). The coastal short cycle high potential trials were planted at Empangeni research station (102

m altitude; 28°43'S, 31°53'E) and irrigated trials at Pongola research station (308 m altitude; 27°24'S, 31°35'E).

5.3.3 Experimental design and data collection

The number of families planted in a trial ranged from 85 to 290. Each family was planted in three replications in a randomised complete block design (RCBD). Data on stalk number, stalk height and stalk diameter were recorded from the first 20 genotypes per family plot. The number of millable stalks was counted for genotype plot. Stalk height (m) was measured from the ground level to the topmost visible dewlap of stalk. Stalk diameter (cm) was measured using a digital calliper at the centre of each of three stalks. Cane yield (kg) was calculated from stalk number, stalk height and stalk diameter using the formula described by Chang and Milligan (1992a), which assumes that sugarcanestalk is a perfect cylinder with a density value of 1.00 g cm^{-3} (Equation 3.1).

5.3.4 Data analysis

Data were analysed using linear mixed model of Statistical Analysis System (SAS Institute 2014). The estimates of variance components, standard errors and probability tests were calculated using the COVTEST in the model statement. BLUP was used to determine the breeding values pf genotype because it can accommodate a highly unbalanced data set. BLUP analysis for the female and male genotype effects was done using the linear model:

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

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

Table 5.1 Populations, number of female and male genotypes used to make crosses (families) for each trial planted in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated mini-line series planted in 2010, 2011, 2012, 2013, 2014 and 2015

Populations	Year planted	Females	Males	Crosses	Females for bi-parental	Males for bi-parental	Bi-parental crosses	MO/MP crosses
Humic soil	2010	38	22	102	25	20	48	54
Humic soil	2011	47	31	113	27	29	53	60
Humic soil	2012	35	32	111	25	30	45	66
Humic soil	2013	40	26	127	22	24	38	89
Sandy soil	2010	38	23	121	24	21	39	82
Sandy soil	2011	92	45	163	45	43	87	76
Sandy soil	2012	36	34	112	27	32	53	59
Sandy soil	2013	31	19	111	14	17	23	88
Sandy soil	2015	47	40	85	33	38	53	32
CLCHP	2011	93	71	217	61	69	119	98
CLCHP	2012	59	50	217	40	48	89	128
CLCHP	2013	59	52	217	38	50	83	134
CLCHP	2014	51	24	93	25	22	30	63
CLCHP	2015	78	38	167	39	36	55	112
CLCAP	2011	53	42	127	34	40	69	58
CLCAP	2012	39	31	128	21	29	46	82
CLCAP	2013	43	28	119	24	26	48	71
CLCAP	2014	60	33	109	34	31	50	59
CLCAP	2015	48	36	97	26	34	44	53
CSCHP	2011	65	44	198	41	42	90	108
CSCHP	2012	69	46	199	39	44	73	126
CSCHP	2013	61	29	141	28	27	41	100
CSCHP	2014	93	54	183	53	52	80	103
CSCHP	2015	86	41	166	35	39	46	120
CSCAP	2011	60	43	120	40	41	71	49
CSCAP	2012	52	31	147	27	29	40	107
CSCAP	2013	35	25	118	17	23	32	86
CSCAP	2014	63	31	118	30	29	39	79
CSCAP	2015	60	32	119	30	30	43	76
Irrigated	2011	95	44	241	18	42	23	218
Irrigated	2012	79	35	166	43	33	68	98
Irrigated	2013	93	37	253	38	35	59	194
Irrigated	2014	115	57	290	50	55	80	210
Irrigated	2015	78	22	138	18	20	23	115

The BLUP refers to the estimates of breeding value relative to the population mean (Zhou 2014). After analysis, the female and male genotypes with high breeding values (i.e. genotypes with the largest significant (P<0.05) and positive BLUP values) and low breeding values (i.e. genotypes with the largest significant (P<0.05) and negative BLUP values) for cane yield were further evaluated in separate populations and subjected to simple analysis of variance (ANOVA) to generate the least square mean yield values of their progenies relative to the population mean yield.

5.4 RESULTS

5.4.1 Covariance parameters within groups of populations for cane yield

The female variances for cane yield were highly significant (P<0.001) in all trials except for the sandy soil [significant (P<0.01) in 2010 and 2012] and CLCAP [significant (P<0.05) in 2012] populations, respectively (Table 5.2). The variances for humic soils and sandy soils increased during 2010 to 2013, and 2010 to 2015, respectively. The female variances observed for the CLCHP, CLCAP, CSCHP, CSCAP and irrigated populations showed variations across trials. The humic soil, irrigated, CLCHP and CSCAP female variances were larger than for the sandy soil, CLCAP and CSCAP populations respectively.

For the humic soil populations, the male variances were highly significant (P<0.001) in 2012 and 2013, and significant (P<0.01) during 2010 and 2011. For the sandy soil populations, the male variances were highly significant (P<0.001) in 2012 and 2015, significant (P<0.01) in 2013 and significant (P<0.05) in 2010 and 2011. For the CLCHP populations, the male variances were highly significant (P<0.001) during 2011, 2012, 2013 and 2015, and significant (P<0.01) in 2014. For the CLCAP populations, the male variances were highly significant (P<0.001) in 2014 and 2015, significant (P<0.01) in 2012 and 2013, and significant (P<0.05) in 2011. The male variances observed for the CSCHP populations were highly significant (P<0.001) during 2011, 2014 and 2015, significant (P<0.01) in 2013, and significant (P<0.05) in 2012. The male variances for the CSCAP populations were significant (P<0.01) during 2013, 2014 and 2015, and significant (P<0.05) in 2011 and 2012. The male variances for the irrigated populations were highly significant (P<0.001) during 2011, 2013 and 2014, significant (P<0.01) in 2015, and significant (P<0.05) in 2012.

Table 5.2 Covariate parameter estimates of cane yield (kg) for female and male effect, residual error and their standard error (S.E.) for the humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations

Year	Covariate parameter	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
2010	Female	1.80±0.52***	0.50±0.18**					
	Male	1.12±0.52**	0.56±0.25*					
	Residual	21.33±0.42***	16.38±0.31***					
2011	Female	1.97±0.52***	1.69±0.43***	1.43±0.33***	10.10±3.44***	0.27±0.06***	9.06±2.36***	7.09±1.19***
	Male	1.36±0.56**	0.88±0.49*	1.04±0.33***	7.17±3.76*	0.21±0.06***	3.23±1.45*	4.52±1.46***
	Residual	30.94±0.59***	19.40±0.38***	38.27±0.53***	195.96±5.25***	2.54±0.04***	66.75±1.83***	38.06±0.56***
2012	Female	4.99±1.46***	2.34±0.79**	5.47±1.33***	0.93±0.46*	2.00±0.54***	6.57±1.84***	20.25±4.34***
	Male	5.71±1.95***	7.37±2.18***	8.69±2.73***	1.63±0.64**	1.31±0.62*	4.20±1.88*	5.96±3.19*
	Residual	44.86±0.86***	42.98±0.89***	109.90±1.64***	26.42±0.84***	21.51±0.44***	48.35±1.48***	134.00±2.78***
2013	Female	8.38±2.45***	1.90±0.66***	5.31±1.24***	1.37±0.38***	1.36±0.29***	0.56±0.17***	3.89±0.76***
	Male	7.16±3.28***	5.58±2.37**	8.13±2.21***	1.18±0.45**	0.86±0.31**	0.81±0.34**	4.52±1.52***
	Residual	106.26±2.28***	44.51±0.90***	80.18±1.25***	14.17±0.30***	10.98±0.18***	8.19±0.17***	16.87±0.30***
2014	Female			2.92±0.71***	2.00±0.51***	0.14±0.03***	1.32±0.36***	4.82±0.85***
	Male			2.60±1.10**	1.37±0.55***	0.29±0.08***	1.91±0.71**	5.56±1.56***
	Residual			33.07±0.66***	25.88±0.55***	3.22±0.05***	10.25±0.25***	37.86±0.66***
2015	Female		8.32±2.30***	4.83±0.95***	3.06±0.95***	1.75±0.33***	2.44±0.62***	1.52±0.33***
	Male		9.75±3.30***	6.94±1.99***	2.87±1.10***	2.03±0.63***	2.65±0.97**	3.70±1.49**
	Residual		52.97±1.37***	46.28±0.74***	48.90±1.09***	16.75±0.26***	22.24±0.45***	18.92±0.37***

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

In general, the humic soil, sandy soil, CLCHP and irrigated male variances were larger than for the CLCAP, CSCAP and CSCHP populations. The females produced larger variances and smaller standard error compared to the males in the humic soil, CLCAP and CSCHP populations. The males produced larger variances and standard error compared to the females in the sandy soil, CLCHP, CSCAP and irrigated populations. The CSCHP population generally produced the least female and male variances across all populations.

The residual error variance was highly significant (P<0.001) across all populations and trials (Table 5.2). The humic soil and sandy soil residual error variances increased from 2010 to 2013 and from 2010 to 2015, respectively. The residual error variance varied across trials for the CLCHP, CLCAP, CSCHP, CSCAP and irrigated populations. The residual error variance was in general larger than both the female and male variances across populations. The overall mean values for cane yield were variable within and across populations (Table 5.3).

Table 5.3 Overall mean values (± standard deviation) for cane yield (kg) in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations

Year planted	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
2010	6.55±4.36	6.10±3.79					
2011	9.16±5.24	9.29±4.17	11.06±6.07	11.62±6.99	3.37±1.59	12.80±8.16	13.98±5.95
2012	15.11±6.39	14.77±6.08	16.95±10.25	8.02±5.26	10.87±4.63	11.89±6.99	20.59±10.45
2013	18.85±9.72	11.02±6.04	14.32±8.96	6.12±3.71	6.87±3.30	4.49±2.86	7.06±3.78
2014			10.79±5.76	9.79±5.08	2.87±1.69	4.86±2.96	12.94±6.15
2015		12.55±6.89	14.59±6.82	11.73±6.49	9.10±3.96	8.21±4.69	8.16±4.35

5.4.2 Female and male genotype BLUPs

Best linear unbiased prediction analysis was used to generate estimates of breeding values for both the female and male genotypes. A sample BLUP output is presented in Table 5.4. BLUP estimates can be significant (P<0.05) positive or negative, indicating that a genotype produced higher or smaller values than the population mean, respectively. The overall population mean values are presented in Table 5.3.

5.4.2.1 Proportions of genotypes with high breeding values

The proportions of female and male genotypes that produced significantly ($P<0.05$) higher BLUP values (genotypes with high breeding values) for cane yield were counted for all populations and are presented in Table 5.5. The numbers of female and male genotypes with high breeding values in each population were divided by the total number of female and male genotypes in the trial to give a percent value of genotypes with high breeding values.

Comparisons across populations

The humic soil (18.8%), CLCHP (18.2%), CSCHP (16.8%) and irrigated (16.3%) populations had higher proportions of female genotypes with high breeding values compared to the CSCAP (15.2%), CLCAP (12.8%) and sandy soil (12.3%) populations (Table 5.5). The humic soil population produced the highest number of female genotypes with high breeding values (18.8%) while the sandy soil population had the lowest (12.3%). The CSCHP (12.6%), sandy soil (10.6%), CLCHP (9.8%), irrigated (9.7%) and humic soil (9.0%) populations had higher proportions of male genotypes with high breeding values compared to the CLCAP (5.9%) and CSCAP (5.6%) populations. The CSCHP had the highest proportions of male genotypes with high breeding values (12.6%) while the CSCAP had the lowest (5.6%).

Least square means for the proportions of genotypes with high breeding values

The proportions of female and male genotypes with high breeding values for cane yield were compared across populations (Table 5.6). The least square means showed that the proportions of females with high breeding values for the humic soil population were non-significantly ($P>0.05$) different from the CLCHP, CSCHP, CSCAP and irrigated populations. The sandy soil female genotypes were non-significantly ($P>0.05$) different from the CLCAP, CSCHP, CSCAP and irrigated populations. The female genotypes for humic soil and CLCHP were significantly ($P<0.05$) different from the sandy soil and CLCAP populations.

Table 5.4 Sample output for female and male best linear unbiased prediction (BLUP), standard error (S.E.) of BLUP, t-stats (t-statistic) and probability of a larger t-statistic (P>t) for the humic soil (BML10) populations

Female	BLUP	S.E.	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 5.5 Proportions of female and male genotypes with high breeding for cane yield (kg) in humic soil, sandy soil, coastal long high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations

Populations	Female			Male		
	Total	Elite	% Elite	Total	Elite	% Elite
Humic soil	160	30	18.8	111	10	9.0
Sandy soil	244	30	12.3	161	17	10.6
CLCHP	340	62	18.2	235	23	9.8
CLCAP	243	31	12.8	170	10	5.9
CSCHP	374	63	16.8	214	27	12.6
CSCAP	270	41	15.2	162	9	5.6
Irrigated	460	75	16.3	195	19	9.7

The proportions of male genotypes with high breeding values for the CSCHP population was non-significantly (P>0.05) different from the humic soils, sandy soil, CLCHP and irrigated populations (Table 5.6), however, the CSCHP population was significantly (P<0.05) different from the CLCAP and CSCAP populations. The CLCAP and CSCAP male genotypes were non-significantly (P>0.05) different from each other as well from the humic soil, sandy soil, CLCHP and irrigated populations. The proportions of female genotypes with high breeding values were 10% higher than for males.

Table 5.6 Least square means for the proportions of female and male genotypes with high breeding values for cane yield (kg) in humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated populations

Populations	Female	Male
Humic soil	19.05a	8.77ab
Sandy soil	12.54b	11.30ab
CLCHP	18.82a	10.00ab
CLCAP	12.78b	5.86b
CSCHP	17.34ab	12.88a
CSCAP	15.42ab	5.70b
Irrigated	16.32ab	9.44ab

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

5.4.2.2 Genotypes with high breeding values in two or more trials (2010-2015)

A summary of genotypes with high breeding values for cane yield in two or more populations is presented as an average per breeding programme (expressed in percentages) in Table 5.7. Genotypes 82H0397, 85H0428, N52, B74713, 87W0629, 01G1662, 88W1323, 02K1657, 87L0573, 97E0474, N31, 93E0888, 03U1030, 06T3608, 96W0246, WI82498 and 79F0779 produced superior progenies with higher cane yield than the population mean yield when crossed with diverse genotypes.

5.4.2.3 Genotypes with low breeding values in two or more trials (2010-2015)

Genotypes 98G1178, 94M0017, 94W0947, N27, N40 and N49, when crossed with diverse genotypes, produced progenies with lower cane yield compared to their mean population yield (Table 5.7). Genotypes 98G1178 and 94M0017 (both from the CLCAP, CSCHP and CSCAP populations), 94W0947 (CSCHP, CSCAP and irrigated), N27 and N40 (both from the CSCHP

and irrigated populations) and N49 (irrigated) produced progenies with low cane yield when crossed with diverse genotypes.

Table 5.7 A summary of parent genotypes with high and low breeding values (BV) when used in two or more populations [humic soil, sandy soil, coastal long cycle high potential (CLCHP), coastal long cycle average potential (CLCAP), coastal short cycle high potential (CSCHP), coastal short cycle average potential (CSCAP) and irrigated] and their progeny least square mean yield relative to a population mean yield. Values are presented as averages per breeding programme (expressed in percentages)

	Humic soil	Sandy soil	CLCHP	CLCAP	CSCHP	CSCAP	Irrigated
High BV				**Progeny % mean**			
82H0397	127	126					
85H0428	127	120					
N52	123	130	138	137	125		
B74713		180	130	129	140	125	133
87W0629			143	132		130	
01G1662			126	122		103	
88W1323				133	135	144	
02K1657			118	122			
87L0573			125			112	
97E0474			150		128		
N31					124	118	
93E0888					138	151	
03U1030					156	117	
06T3608					133		
96W0246					129	124	128
WI82498			124			122	127
79F0779					142		160
Low BV				**Progeny % mean**			
98G1178				70	84	75	
94M0017				77	71	37	
94W0947					81	63	75
N27					72		72
N40					73		76
N49							73

5.5 DISCUSSION

The significant female and male variance components observed across populations indicated that genotypes contributed significantly to the variability among the progeny populations. Generally, the humic soil, CLCHP and irrigated populations had larger variances for both female and male effects compared to sandy soil, CLCAP, CSCAP and CSCHP populations,

which indicated higher genetic variability contributed by parental genotypes among the progenies from these populations. The female effects produced larger variances and smaller standard error than male effects for humic soil, CLCAP and CSCHP populations, which suggested that most of the genetic variability in progenies were attributed to variability among female genotypes. Results indicated the potential existence of dominance or maternal effects among the humic soil, CLCAP and CSCHP compared to other populations. The strong maternal effects compared to paternal effects have been reported earlier among the SASRI populations (Zhou 2015). Milligan (1998) had the same result. He suggested that female parent is always known. Because of outcrossing and selfing, male parent is not always clear, even in a bi-parental cross. He concluded higher breeding value with lower standard error for female compared to male clones.

The results implies the occurrence of high genetic variability among female parents used to make these crosses. The higher female variances compared to male variances also highlights the difficulty in synchronising sugarcane genotype flowering during the time of crossing. Low synchronisation results in more polycrosses where the identity of the male genotype is unknown (Zhou and Mokwele 2015). The male effects for sandy soil, CLCHP, CSCAP and irrigated populations produced larger variances and standard errors compared to the female effects, which suggested that most of the genetic variability observed among the progenies was contributed by the male genotypes. Results suggest higher genetic variability and diversity among the male parents used in these crosses. This could potentially be linked to higher flowering among the males resulting in abundancy of pollen from several males being used during crossing. The humic soil, sandy soil and CLCAP populations showed an increase in both female and male variance effects with advanced breeding cycles, which suggested the presence of additive genetic effects among these populations. This may be largely derived from the selected genotypes that have produced progenies with higher trait values from previous progeny evaluation.

The high residual error variances (higher than both the female and male variances) across populations suggested that a higher proportion of the variability observed in the data was not contributed to the female and male genotypes but their interaction with environment. The high unaccounted variability could be attributed to non-additive genetic effects in this analysis. This suggests a need for future research to investigate the influence and proportion of non-additive genetic effects in sugarcane breeding. The high residual variability could also be attributed to

large spatial variability associated with the large trials, which is characteristic at this stage in plant breeding trials. Further, the large residual error may indicate the need to optimise experimental designs to improve trial efficiency. Currently, the RCBD 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 design can account for within block variability and thus reduce error variance and increasing the efficiency during the comparison of family performance.

Genotypes 82H0397 and 85H0428, when crossed with diverse genotypes, produced progenies with higher cane yield in more than three humic soil and sandy soil populations, which indicated that these genotypes have high breeding values for cane yield specifically for the Midlands breeding programmes. Genotypes 87W0629, 01G1662, 88W1323, 02K1657, 87L0573, 97E0474, N31, 93E0888, 03U1030 and 06T3608, when crossed with diverse genotypes, produced progenies with higher cane yield in CLCHP, CLCAP, CSCHP and CSCAP populations, which indicated that these genotypes had high breeding values for coastal breeding programmes. Genotypes with high breeding values for Midlands and coastal breeding programmes are potential candidates for use as testers and good combiners of new parent genotypes in these breeding programmes. The use of these genotypes as testers needs validation using appropriate statistical designs.

Genotype N52, when crossed with diverse genotypes, produced progenies with higher cane yield in humic soil, sandy soil, CLCHP, CLCAP and CSCHP populations, respectively which indicated that this genotype has high breeding values for coastal and Midlands populations. Genotype N52 can be a universal tester for SASRI breeding programmes because of its high breeding values across several breeding programmes in different locations. Future research is required to validate its potential as a tester. The N52 genotype is the product of the cross including N31 as a parent. Genotype N31 is also known to have produced high trait value progenies in several breeding programmes. Genotype B74713, when crossed with diverse genotypes, produced progenies with higher cane yield in sandy soil, CLCHP, CLCAP, CSCHP, CSCAP and irrigated populations. The study suggest that B74713 with high breeding values can be a suitable donor for the Midlands sandy soil, coastal and irrigated populations. Genotypes 96W0246, WI82498 and 79F0779, when crossed with diverse genotypes, produced progenies with higher cane yield in CLCHP, CSCHP, CSCAP, and irrigated populations which indicated that these genotypes have high breeding values for the coastal and irrigated breeding

programmes. All these genotypes have potential for use as pollen parents in SASRI breeding programmes depending on synchronisation during flowering.

Genotypes 98G1178 and 94M0017, when crossed with diverse genotypes produced progenies with low cane yield in CLCAP, CSCHP and CSCAP populations, which indicated that these genotypes have low breeding values for the coastal breeding programmes. Genotypes 94W0947, N27 and N40 when crossed with diverse genotypes, produced progenies with low cane yield mainly in the CSCHP and irrigated populations, which suggested that these genotypes have low breeding values to coastal and irrigated 12 months harvest cycle programmes. Genotype N49, when crossed with diverse genotypes, produced progenies with low cane yield for the irrigated populations, which indicated that genotype N49 have low breeding values for cane yield specifically in irrigated breeding programme.

Despite the poor performance of genotypes N27, N40 and N49 as parents, these genotypes are SASRI released varieties based on high cane yield, high quality, diseases and pest resistance, and other agronomic traits. Results suggested that genotypes N27, N40 and N49, despite having high genetic values, they have low breeding values. This implies that parent selection, based on genetic values as what is practiced at SASRI before introducing breeding values, is not sustainable. Evaluation of genotypes for breeding values is essential to increase genetic gains. Genotypes that have produced low breeding values can be discarded from the germplasm pool because of their limited contribution to SASRI breeding as parents. It is, therefore, recommended that parent selection for future crossing be focused only on genotypes that have high breeding values. Similar results were reported in South Africa involving selection for Eldana borer resistance (Zhou and Mokwele 2015) and cane yield (Mbuma et al. 2019) using family data. In addition, more genotypes need to be tested for breeding values before they can be used in commercial crossing. Development of testers as well as a focussed testing strategy for genotypes will help to identify genotypes that are more suitable as parents for utilisation in crossing.

The numbers of genotypes with high breeding values in humic soil, CLCHP, CSCHP and irrigated populations were more compared to those in sandy soil, CLCAP and CSCAP populations. This indicated the potential to enhance breeding and crossing efficiency among these populations. This further implied that an increase in superior progenies is expected, and thus higher genetic gains for sugarcane yield are also expected among humic soil, CLCHP,

CSCHP and irrigated populations. The relatively low proportions of genotypes with high breeding values in sandy soil, CLCAP and CSCAP populations could indicate limited efforts in identification of parents and hence efforts to be strengthened to include newer parents for hybridization. This could be explained by the effect of fewer cycles of recurrent selection among sandy soil, CLCAP and CSCAP populations with a narrow genetic base. The sandy soil, CLCAP and CSCAP breeding programmes were established recently with genotypes used for crossing sourced from older SASRI breeding programmes (Nuss 1998). Genotypes used for crossing in the sandy soil breeding programme were derived mainly from the humic soil and other SASRI breeding programmes, while that for CLCAP and CSCAP programmes were derived from older SASRI breeding programmes. Most of the genotypes used for crossing were less adapted and are still being developed for its suitability. Further, because these are relatively new breeding programmes, with fewer recurrent breeding and selection cycles, fewer genotypes have been tested for their breeding potential.

In CLCAP and CSCAP trials, large variability in the data has been frequently observed, probably due to environmental conditions where these breeding programmes are located. The CLCAP and CSCAP breeding programmes were established at Gingindlovu research farm where Eldana damage is most predominant (Lichakane and Zhou 2016), thereby, negatively influencing the potential of detecting the differences among the families and further making it difficult to identify superior genotypes for cane yield (Zhou and Joshi 2012). Thus fewer genotypes with high breeding values are being used for crossing. Furthermore, results could be reflecting the confounding effects of Eldana resistance breeding. The focus is mainly on breeding for Eldana resistance, which improves the quality of sugarcane at the expense of cane yield among CSCAP and CLCAP populations. Therefore, balancing of trait combinations during crossing and breeding may provide the desired increase in genotypes with high breeding values and increase in predicted selection gains for sugarcane yield. Intensive screening of Eldana damage at the early stage of breeding and adoption of genotypes that are highly resistant to Eldana would be ideal in coastal regions. Intensive screening of Eldana damage at early stage of sugarcane breeding will reduce the variability in the data, thereby increasing the variation among the populations for other traits such as cane yield and its components.

5.6 CONCLUSIONS

Significant female and male variance components obtained indicated the effectiveness of using progeny data to estimate breeding values of genotypes that were used in crosses. The significant

female and male genotype's variance effects were also associated with variability for cane yield among progenies, which suggested the existence of genetic variability among genotypes used for crossing. Seventeen genotypes 82H0397, 85H0428, N52, B74713, 87W0629, 01G1662, 88W1323, 02K1657, 87L0573, 97E0474, N31, 93E0888, 03U1030, 06T3608, 96W0246, WI82498 and 79F0779, with high breeding values for cane yield were identified from progeny data across SASRI populations. These genotypes can be used as testers for future crossing and to build a core germplasm pool of genotypes known to produce progenies with high cane yield.

Genotypes with low breeding values can be discarded from crossing programme. Results from this study will encourage breeders to make new crosses using the identified genotypes with high breeding values from where higher genetic gains for sugarcane yield are expected. The study also recommends the balancing of trait combinations (Eldana, sucrose content and cane yield) during breeding and crossing, particularly for the coastal average potential breeding programmes (CLCAP and CSCAP).

Longer cycles of recurrent selection are required for the development and improvement of genotypes with high breeding values in sandy soil, CLCAP and CSCAP breeding programmes. The identification of less number of genotypes with high breeding values suggested that more intensive evaluation and development of genotypes is essential to broaden the genetic base in these populations.

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CHAPTER 6

FAMILY BY ENVIRONMENT INTERACTION FOR SUGARCANE YIELD IN SOUTH AFRICA

6.1 ABSTRACT

In sugarcane breeding, knowledge on progenies and traits controlling their adaptability is expected to increase crossing and selection efficiency. Family evaluation uses progeny data to determine family trait values. In family evaluation, families with high trait values are identified and individual genotypes with high trait values are selected from these families. Families are planted in several locations and over years to evaluate family by environment interactions. The objectives were to determine family by environment interaction breeding parameters, family values across locations and traits controlling adaptability to different locations. Data were collected from plant, first and second ratoon crops of family evaluation trials, planted in randomised complete block design with three replications at five different locations representing the major agro-climatic regions where sugarcane is grown in South Africa. Cane yield was estimated from stalk number, stalk height and stalk diameter, measured from the first 20 plants per family plot and analysed using SAS mixed models. Significant ($P<0.01$) family (F) variance for cane yield traits indicated genetic variability among the families. Significant ($P<0.01$) family by location (FL) variance for cane yield, stalk number and diameter indicated that the magnitude of genetic variability among families was different across locations. The non-significant ($P>0.05$) family by crop year (FC) and family by location by crop year (FLC) variances indicated similar genetic variability across crop years. Therefore, testing families in multi-locations was more important than across ratoons. Best linear unbiased predictors estimates identified families TT1051, UU0332 and UU0312 with significantly higher cane yield across locations, indicating their wide adaptability. Families VV0701 (Pongola), VV0390 (Glenside and Bruyns Hill) and UU0198 (Glenside and Bruyns Hill) produced higher cane yield and showed location specific adaptability. The irrigated, coastal and Midlands populations showed specific adaptability for cane yield and stalk height.

Key words: family by environment interactions, progenies, cane yield traits, adaptability

6.2 INTRODUCTION

Family evaluation involves using progeny data to determine family values (Kimbeng and Cox 2003). In sugarcane, families with high trait values are identified and individual genotypes with high trait values are selected from these families. The advantage is that families can be replicated within and across trials and locations while individual genotypes cannot due to limited planting material. When families are planted across locations, family by environment interactions can be evaluated.

Family by environment interactions were reported in Australia (Hogarth and Bull 1990; Cox and Hogarth 1993; Jackson et al. 1995; McRae and Jackson 1995), Louisiana (Milligan and Legendre 1990; Souza-Vieira and Milligan 1999) and Mauritius (Bissessur et al. 2000). Hogarth and Bull (1990) reported significant family by location interaction for cane and sugar yield from a study of 35 families. Jackson et al. (1995) and Jackson and McRae (1998) proposed multi-location testing of families where significant genotype by environment interactions was present. Jackson et al. (1995) reported significant family by location interaction for cane and sugar yield in the Herbert Region of North Queensland, Australia, where genotype by environment interactions were known to be important (Hogarth and Bull 1990). Studies by McRae and Jackson (1995) reported non-significant family by location interactions for cane yield and sugar content in the Burdekin region of Australia. The study also reported non-significant family by crop year interactions for cane yield and sugar content. In Louisiana, Souza-Vieira and Milligan (1999) reported non-significant family by location interactions for cane yield components and suggested for family evaluation in a single environment in Louisiana. In Mauritius, family by location interactions was significant for cane and sugar yield and non-significant for Brix % in either plant or ratoon crops (Bissessur et al. 2000).

In South Africa, sugarcane is grown in three agro-climatic regions (irrigated, Midlands and coastal). The Midlands (high altitude) and coastal regions are rain-fed. The coastal region is represented by the coastal long high potential, coastal short high potential, coastal long average potential, and coastal short average potential environments. Sugarcane matures at 18 months for the coastal long cycle and 12 months for the coastal short cycle programmes. The Midlands region is represented by the humic and sandy soils where sugarcane matures at 24 months (Nuss 1998). The irrigated region represents areas with low and insufficient annual rainfall for sugarcane growth where high temperatures and irrigation are required to achieve economic yields. The differences in the agro-climatic regions could result in trait values of families

varying from one region to another, resulting in family by environment interaction. Significant genotype by environment interaction has been reported for sugarcane (Zhou et al. 2011; Zhou et al. 2012; Zhou 2015; Zhou and Gwata 2015; Sengwayo et al. 2017) suggesting potential existence of family by environment interaction in South Africa. The objectives of this study were to determine family by environment interaction breeding parameters, family values across locations and their significance to sugarcane breeding.

6.3 MATERIALS AND METHODS

6.3.1 Experimental material

Sugarcane families (crosses) included in this study were made at Mount Edgecombe research station (96 m altitude; 29°42', 31°2'E) located in Durban, KwaZulu-Natal province of South Africa. The families included in this study were developed between May and August in 2007 to 2015. In total, 44 families were developed from crosses between 18 female and 18 male genotypes (Table 6.1). Three mating designs were used to generate the crosses namely bi-parental (generating full-sib families), males only and melting pot (generating half-sib families). Bi-parental families are effected by crossing one female parent with a male parent. Males' only involve inter-crossing of at least two male parents and collecting seed from all genotypes. With male's only families, the identity of the male genotype is unknown when three or more genotypes are inter-crossed. Genotypes with complementary traits are inter-crossed as male parents only. Melting pot families are made when several male parents pollinate a single female parent. The proportion of pollen contributed by each male is unknown. However, males with complementary traits are used. Of the 18 female parents used, nine were used to generate the bi-parental families and crossed with 16 male parents.

One parent (82Z3441) was obtained from the Zimbabwe Sugar Association Experiment Station while the remaining clones were from SASRI. The parents were derived from irrigated (F), coastal short cycle (E), and coastal long cycle (W), Midlands's humic soil (B), Midlands's sandy soil (S), coastal short cycle average potential (U), coastal long cycle average potential (G) and coastal long cycle high potential (K) breeding programmes.

Table 6.1 Families, females, males, breeding programmes and genotypes per family planted in Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside research stations in 2013

Family	Female	Male	Breeding programme	Genotypes
KK0489	82Z3441	MO	Irrigated	160
MM0036	79F0779	MO	Irrigated	140
MM0050	79F0779	MO	Irrigated	215
MM1497	79F0779	MO	Irrigated	210
NN0719	99S1362	99S0106	Midlands	184
NN1223	N25	94H0323	Midlands	380
PP0542	N25	76E0537	Coastal	180
QQ0839	85W0426	MO	Coastal	304
RR0321	85W0426	92W0763	Coastal	160
SS0583	89F1649	MO	Irrigated	335
SS0754	99F1718	MP	Irrigated	212
SS0870	92W0077	MO	Coastal	400
SS1237	N25	MO	Irrigated	120
TT0165	99F1718	MO	Irrigated	160
TT0774	92W0077	92L0429	Coastal	106
TT1051	00K0769	MO	Coastal	300
UU0099	01G1662	94M0382	Coastal	180
UU0163	99B1659	MO	Midlands	190
UU0183	82Z3441	99F2004	Irrigated	140
UU0197	82Z3441	00F0602	Irrigated	180
UU0198	98B0460	95H0517	Midlands	150
UU0231	99S1362	95H0517	Midlands	200
UU0312	98B0460	95H0517	Midlands	210
UU0332	98B0460	99B1889	Midlands	230
UU0333	98B0460	MP	Midlands	180
UU0387	98S0082	MO	Midlands	180
UU0388	95H0130	MO	Midlands	210
UU0466	98S0082	MP	Midlands	160
UU0513	95H0130	MO	Midlands	120
UU0554	95H0130	MO	Midlands	140
UU0669	92W0077	87L0573	Coastal	150
UU0954	99S1362	99S1504	Midlands	180
VV0102	79F0779	MO	Irrigated	237
VV0131	01G1662	01K0433	Coastal	259
VV0390	05U0114	91W1482	Coastal	180
VV0527	82Z3441	MP	Irrigated	204
VV0531	N25	MO	Irrigated	230
VV0701	82Z3441	MP	Irrigated	160
WW0108	96H0289	99B1979	Midlands	400
XX0137	01G1662	05U0696	Coastal	190
XX0311	03S0282	MP	Midlands	400
XX0372	01G1662	MP	Coastal	400
XX0476	01S1681	MO	Midlands	400
XX1149	N25	MP	Irrigated	82

6.3.2 Experimental sites

Data were collected from plant crop, first ratoon crop and second ratoon crop (representing crop years) of Stage I "mini-line" trials planted in the field in 2013 at Bruyns Hill, Glenside, Gingindlovu, Empangeni and Pongola research stations, respectively (Table 6.2). Midlands's trials were established at Bruyns Hill and Glenside research stations that are characterised by a high altitude and a climate with shorter summers and long cold winters. The coastal long cycle average potential trials were established at Gingindlovu research station. The coastal short cycle high potential trials were planted at Empangeni research station and the irrigated trials at Pongola research station.

Table 6.2 Five experimental sites used in the study representing unique growing conditions

Site	Regions	Conditions	Harvest cycle	Altitude (m)	Latitude	Longitude
Pongola	Irrigated	Irrigated	12	308	27°24'S	31°35'E
Empangeni	Coastal	Short cycle high potential	12	102	28°43'S	31°53'E
Gingindlovu	Coastal	Long cycle average potential	18	93	29°1'S	31°36'E
Bruyns Hill	Midlands	Humic soil	24	1012	29º42'S	30º68'E
Glenside	Midlands	Sandy soil	24	997	29°20'S	30°46'E

6.3.3 Experimental design and data collection

A total of 44 families were planted in each trial in 2013 (Table 6.1). A randomised complete block design was used and each family was planted in three replications. Data on stalk number, stalk height and stalk diameter were collected from the first 20 genotypes in each family plot. The number of millable stalks was counted in each genotype plot. Stalk height (m) was measured from the ground level to the topmost visible dewlap. Stalk diameter (cm) was measured using a digital calliper at the centre of each of three stalks. Cane yield (kg) was calculated from stalk number, stalk height and stalk diameter using the formula described by Chang and Milligan (1992), assuming that sugarcane stalk is a perfect cylinder with 1.00 g/ cm^{-3} (Equation 3.1).

6.3.4 Data analysis

Data on cane yield, stalk height, stalk number and stalk diameter were analysed using the linear mixed model of Statistical Analysis System (SAS Institute 2014). The estimates of variance components, their standard errors and probability tests across locations and crop years were

determined using the COVTEST option in the mixed model procedure. The following statistical linear mixed model was used for family by environment interaction analysis:

$Y_{ijklm} = \mu + L_i + R(L)_{ij} + F_k + FL_{ik} + FR(L)_{ijk} + C_l + CL_{il} + CR(L)_{ijl} + FC_{lk} + FLC_{kil} + FRC(L)_{ijkl} + G(FRC(L))_{ijklm}$…….. Equation 6.1

Where Y_{ijklm} = cane yield of the m^{th} genotype in the i^{th} location in l^{th} crop years of the j^{th} replication, and k^{th} family random effects, μ = overall mean, L_i = fixed effect of i^{th} locations, $R(L)_{ij}$ = random effect of the j^{th} replications nested within i^{th} locations and is the experimental error for locations, F_k = fixed effect of families, FL_{ik} = fixed effect of the interaction between the k^{th} families and i^{th} locations, $FR(L)_{ijk}$ = random effects of the interaction of family by replication nested within locations and is the experimental error for family and family by locations fixed effects, C_l = random effect of the l^{th} crop year, CL_{il} = random effect between i^{th} locations and the lth crop year, CR(L) = random effect of the interaction between l^{th} crop years and j^{th} replications within i^{th} locations, FC_{kl} = random effect of the interaction between k^{th} family and l^{th} crop year, FLC_{kil} = random effect between the interaction of the with k^{th} family, with i^{th} location and l^{th} crop year , $FRC(L)_{ijkl}$ = random effect of the interaction j^{th} replications by l^{th} crop years by k^{th} family nested within i^{th} locations, $G(FRC(L))_{ijklm}$ = random effects of m^{th} genotype nested within the interaction effects of k^{th} family by j^{th} replication and by l^{th} crop year nested within i^{th} locations and is also the residual error. Families, locations and crop years were assumed to be random. The families represent a random sample of possible families from Stage I "mini line" trials. Locations represent a random sample of all possible locations representing sugarcane growing environments in South Africa. Crop year represent a random sample of the combined effect of year-to-year variability associated with ratooning of sugarcane.

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

$$H = \frac{\sigma_F^2}{(\sigma_F^2 + \frac{\sigma_{FC}^2}{c} + \frac{\sigma_{FL}^2}{l} + \frac{\sigma_{FLC}^2}{cl} + \frac{\sigma_{FR(L)}^2}{r(l)} + \frac{\sigma_{FRC(L)}^2}{rc(l)} + \frac{\sigma^2 e}{rlcg})}$$ ……Equation 6.2

Where σ^2_F = variance component of the family effects, σ^2_{FC} = variance component of the interaction effect of family by crop year effect, σ^2_{FL} = variance component of the interaction effect of family by location, σ^2_{FLC} = variance component of the interaction effect between

family, location and crop year effect and is also residual variance component, $\sigma^2_{FR\,(L)}$ = variance of the interaction effect family by replication within the location, $\sigma^2_{FRC(L)}$ = variance of the interaction effect family by replication by crop years within the location, σ^2_e = is the variance component for the residual term in the model, g = the number of seedlings sampled per plot, r = the number of replications, l = the number of locations, and c = the number of crop years. The standard error (SE) for H was estimated using Becker (1992):

$$SE = \sqrt{\frac{2(1-H)^2\,[1+H(q-1)]^2}{q(q-1)(n-1)}} \quad \text{Equation 6.3}$$

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):

$$Gs = K\sigma_F H \quad \text{Equation 6.4}$$

Where K = family selection intensity, σ_F = family phenotypic standard deviation and H = broad-sense heritability. Family selection intensity (K) was 30, the expected selection intensity in Stage I.

Best linear unbiased predictors (BLUP) analysis for the family effects used the linear mixed model:

$$Y_{ijk} = \mu + R_i + F_j + G(FR)_{k(ij)} \quad \text{Equation 6.5}$$

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

Grouping of the data, based on the breeding programme source (refers to the origin of genotypes that were used to make crosses) was used to create a new design variable. Families produced from genotypes with the letter F and Z were categorised as irrigated, genotypes with letter B, H and S were categorised as Midlands and genotypes with letter E, W, L, U, G and K were categorised as coastal. The new data created with these categories (irrigated, Midlands and coastal) were subjected to ANOVA to determine family traits for adaptability to different locations. In this study the family categories [breeding programme (B)] were considered as fixed because they were grouped based on the genetic background of genotypes used in making crosses. Locations (L) were treated as fixed because they represent the target environment for sugarcane breeding and cultivar release. Crop years (C) were considered as a fixed variable because of the importance of breeding and selection for ratooning ability (Kang et al. 1987).

The linear mixed model used was:

$$Y_{ijklm} = \mu + L_i + R(L)_{ij} + B_k + BL_{ik} + BR(L)_{ijk} + C_l + CL_{il} + CR(L)_{ijl} + BC_{kl} + BLC_{ikl} + BRC(L)_{ijkl} + G(BRC(L))_{ijklm} \quad \text{Equation 6.6}$$

Where Yijklm = cane yield of the m^{th} genotype in the i^{th} location in lth crop years of the j^{th} replication, and kth breeding programme fixed effects, μ = overall mean, L_i = fixed effect of i^{th} locations, $R(L)_{ij}$ = random effect of the j^{th} replications nested within ith locations and is the experimental error for locations. B_k = fixed effect of breeding programme, BL_{ik} = fixed effect of the interaction between the k^{th} breeding programme and i^{th} locations, $BR(L)_{ijk}$ = random effects of the interaction of k^{th} breeding programme by j^{th} replication nested within i^{th} locations and is the experimental error for breeding programme by location fixed effects, C_l = fixed effect of the l^{th} crop year, CL_{il} = fixed effect between i^{th} locations and the lth crop year, CR(L) = random effect of the interaction between l^{th} crop years and j^{th} replications within i^{th} locations, BC_{kl} = fixed effect of the interaction between k^{th} breeding programme and l^{th} crop year, BLC_{ikl} = fixed effect between the k^{th} breeding programme with i^{th} location and with l^{th} crop year, $BRC(L)_{ijkl}$ = random effect of the j^{th} breeding programme by j^{th} replications by l^{th} crop years nested within i^{th} locations, $G(BRC(L))_{ijklm}$ = random effects of m^{th} genotype nested within the interaction effects of k^{th} breeding programme by j^{th} replication by l^{th} crop year nested within i^{th} location and is also the residual error.

6.4 RESULTS

6.4.1 Breeding parameters

The location (L) and replication nested within location [R(L)] variances were non-significant (P>0.05) for all traits (Table 6.3). The family (F) variance was highly significant (P<0.001) for stalk number, height and diameter and significant (P<0.01) for cane yield. Family by location (FL) variance was highly significant (P<0.001) for cane yield, significant (P<0.01) for stalk number and stalk diameter and non-significant (P>0.05) for stalk height. Family by replication within the location [FR(L)] interaction variance was highly significant (P<0.001) for all traits. The crop year (C) variance was non-significant (P>0.05) for all traits.

Table 6.3 Family by environment interaction variance components (± standard error), broad-sense heritability (H), predicted selection gain (Gs), mean and standard deviation (SD), coefficient of determination (R^2) and coefficient of variation (CV) for cane yield (kg), stalk number, stalk height and stalk diameter

Effect	Cane yield	Stalk number	Stalk height	Stalk diameter
L	32.48±32.49ns	5.46±8.77ns	0.0948±0.0975ns	0.0021±0.0103ns
R(L)	0.00±0.00	0.02±0.57ns	0.0003±0.0018ns	0.0003±0.0005ns
F	3.62±1.33**	17.87±4.56***	0.0079±0.0021***	0.0242±0.0056***
FL	4.28±1.29***	3.94±1.35**	0.0012±0.0012ns	0.0025±0.0011**
FR(L)	10.28±1.26***	11.57±1.45***	0.0124±0.0015***	0.0077±0.0011***
C	0.00±0.00	14.52±21.67ns	0.0000±0.0000	0.0394±0.0513ns
CL	34.12±18.10*	14.89±9.68ns	0.1033±0.0552*	0.0287±0.0166*
CR(L)	1.53±0.61**	0.95±0.60ns	0.0051±0.0022*	0.0008±0.0004*
FC	0.00±0.00	2.51±0.77***	0.0000±0.0000	0.0000±0.0000
FLC	0.79±0.55ns	0.00±0.00	0.0012±0.0007*	0.0012±0.0005*
FRC(L)	1.58±0.87*	0.00±0.00	0.0055±0.0007***	0.0000±0.0000
Residual	91.13±1.44***	119.49±1.84***	0.0657±0.0011***	0.0973±0.0015***
H	0.68±0.05	0.88±0.03	0.86±0.03	0.95±0.01
Gs	7.52	11.22	0.25	0.35
% Gs	45.40	41.90	60.74	15.72
Mean±SD	16.57±9.59	26.78±11.04	1.48±0.26	2.21±0.31
R^2	0.57	0.43	0.81	0.53
CV %	57.85	41.23	17.32	14.22

***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non-significant at P≥0.05, L = location, R(L) = replications within location, F = family, FL = family by location interaction, FR(L) = family by replications within location, C = crop, CL = location by crop year interaction, CR(L) = crop by replications within location, FC = family by crop year interaction, FLC = family by location by crop year interaction, FRC(L) = family by replication by crop year within location

The crop year by location interaction (CL) variance was significant (P<0.05) for all traits except for stalk number (Table 6.3). The replication by crop year interaction within location [RC(L)] variance was significant (P<0.01) for cane yield, significant (P<0.05) for stalk height and stalk diameter, and non-significant (P>0.05) for stalk number. Family by crop year (FC) variance for stalk number was highly significant (P<0.001). Family by location by crop year (FLC) interaction variances for stalk height and stalk diameter were significant (P<0.05). Family by replication by crop year within location [FRC(L)] variance was highly significant (P<0.001) for stalk height and significant (P<0.05) for cane yield. The residual variance was highly significant (P<0.001) and was the largest variance component for all traits. The order of importance was FL>F>FLC>FC for cane yield, F>FL>FC>FCL for stalk number and F>FL>FCL>FC for stalk height and stalk diameter, respectively.

The broad-sense heritability (H) value for cane yield (0.68±0.05) was lower than that for stalk number (0.88±0.03), stalk height (0.86±0.03), and stalk diameter (0.95±0.01) (Table 6.3). The percent predicted selection gain (% Gs) for cane yield (45.40%), stalk number (41.90%) and height (60.74%) were higher than for diameter (15.72%). Stalk height had the highest coefficient of determination (R^2) value, whereas stalk number had the lowest value. Cane yield had the highest coefficient of variation (CV %) value and stalk diameter had the lowest value.

The proportions of combined family by environment interaction (FL + FC + FLC) variances to the variance of the family (F) main effect are shown in Table 6.4. The family by environment interaction (FE) was proportionately higher for cane yield (1.40) than stalk number (0.36), height (0.30) and diameter (0.15). Ranking of the family by environment interaction variance components showed that FL (84%) was the most important source of variation for cane yield followed by FLC (16%) and FC (0%). For stalk number, FL (61%) was the largest followed by FC (39%), and FLC (0%). For stalk height, FL and FLC (50%) were equal and while FC was 0%. For stalk diameter, FL (68%) was the largest, followed by FLC (32%) and FC (0%).

6.4.2 Family BLUPs

BLUP analysis was used to generate family values (Tables 6.5, 6.6, 6.7 and 6.8). BLUP refers to estimates of an individual family value relative to the population mean (Zhou 2014). The BLUP estimates can be significant (P<0.05) positive or negative, indicating that a family produced higher or smaller values than the population mean, respectively. Larger values of the standard error of the BLUP indicated higher within-family variability.

Table 6.4 Variance components as a proportion of the family main effect for estimated cane yield, stalk number, stalk height and stalk diameter. Values are expressed as a ratio (and percentage)

Trait	FE	FE:F	FL:F	FC:F	FLC:F	FE ranking
Cane yield	5.07	1.40 (100)	1.18 (84)	0.00	0.22 (16)	FL>FLC>FC
Stalk number	6.45	0.36 (100)	0.22 (61)	0.14 (39)	0.00	FL>FC>FLC
Height	0.0024	0.30 (100)	0.15 (50)	0.00	0.15 (50)	FL=FLC>FC
Diameter	0.0037	0.15 (100)	0.10 (68)	0.00	0.05 (32)	FL>FLC>FC

F = family, FE = family by environment interaction = total of the three interaction components namely, FL = family by location interaction, FC = family by crop year interaction, FLC = family by location by crop year interaction

Families TT1051 (Empangeni, Gingindlovu, Bruyns Hill and Glenside), UU0332 (Pongola, Empangeni, Bruyns Hill and Glenside) and UU0312 (Pongola, Bruyns Hill and Glenside) produced significantly ($P<0.05$) higher BLUP values for cane yield (Table 6.5). Family VV0701 produced significantly higher BLUP values at Pongola and Empangeni. Families NN1223 (Pongola, Gingindlovu and Bruyns Hill), UU0388 (Pongola, Bruyns Hill and Glenside) and QQ0839 (Pongola, Empangeni and Gingindlovu) produced significantly ($P<0.05$) lower BLUP values. Families VV0390 produced significantly higher BLUP values (Bruyns Hill and Glenside) and significantly lower values at Pongola and Empangeni.

Family UU0198 produced significantly higher BLUP values Bruyns Hill and Glenside and significantly lower values at Gingindlovu. Family UU0954 produced significantly higher BLUP values at Gingindlovu and Glenside and significantly lower values at Bruyns Hill and Pongola. Family UU0333 produced significantly higher BLUP values at Pongola and significantly lower values at Gingindlovu, respectively. Family PP0542 had significantly higher BLUP values at Gingindlovu and significantly lower values at Bruyns Hill. Family XX1149 produced significantly higher BLUP values at Pongola and significantly lower values at Bruyns Hill.

Families TT1051 and UU0332 (Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside), respectively produced significantly higher BLUP values for stalk number (Table 6.6). UU0099 produced significantly higher BLUP values at Pongola, Empangeni, Gingindlovu and Bruyns

Hill, while UU0198 had significantly higher BLUP values at Pongola, Empangeni, Bruyns Hill and Glenside), respectively.

Table 6.5 Family best linear unbiased prediction (BLUP) and their standard errors for cane yield (kg) of populations planted in Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside locations

Family	Pongola	Empangeni	Gingindlovu	Bruyns Hill	Glenside
KK0489	-3.18±2.62ns	0.52±1.13ns	-0.55±2.01ns	-2.08±1.56ns	-3.13±1.79ns
MM0036	-2.32±2.03ns	-1.51±0.87ns	-0.67±1.54ns	-0.50±1.22ns	1.61±1.36ns
MM0050	-5.68±2.84*	-0.74±1.11ns	-1.21±2.01ns	-2.45±1.63ns	1.97±1.85ns
MM1497	0.62±2.24ns	-1.52±0.95ns	-0.94±1.78ns	3.52±1.41*	-0.85±1.45ns
NN0719	-7.12±1.95***	0.55±0.90ns	0.76±1.50ns	-2.42±1.24ns	2.36±1.40ns
NN1223	-3.75±1.48*	-0.88±0.69ns	-3.87±1.20**	-2.74±0.94**	-0.17±1.09ns
PP0542	0.27±2.02ns	0.68±1.05ns	3.99±1.71*	-3.78±1.45**	-0.72±1.36ns
QQ0839	-6.47±1.86***	-1.51±0.70*	-3.51±1.47*	-1.91±1.19ns	-2.11±1.43ns
RR0321	-1.93±2.24ns	0.80±0.91ns	0.15±1.75ns	0.92±1.45ns	-0.51±1.48ns
SS0583	-0.61±1.61ns	-0.63±0.76ns	-3.45±1.29**	-0.78±1.02ns	-2.53±1.27*
SS0754	1.63±1.86ns	-2.25±0.86**	-2.93±1.51ns	-2.86±1.20*	0.26±1.34ns
SS0870	-1.96±1.79ns	0.48±0.77ns	1.04±1.44ns	-3.41±1.14**	-0.11±1.36ns
SS1237	-2.31±2.12ns	-2.89±0.85***	2.17±1.69ns	0.22±1.35ns	-3.42±1.51*
TT0165	-3.55±2.36ns	-2.08±1.16ns	-4.54±1.83*	-2.33±1.33ns	-2.57±1.65ns
TT0774	1.61±2.26ns	0.65±0.99ns	-2.35±1.80ns	-0.22±1.56ns	-0.92±1.58ns
TT1051	0.72±1.54ns	2.16±0.63***	4.86±1.22***	4.41±0.97***	2.92±1.07**
UU0099	0.81±1.48ns	2.49±0.76**	0.87±.1.15ns	-1.77±0.94ns	-1.16±1.08ns
UU0163	-2.42±1.81ns	1.47±0.95ns	-2.08±1.47ns	-0.50±1.22ns	1.17±1.25ns
UU0183	3.24±1.85ns	-1.98±0.80*	2.21±1.42ns	-0.01±1.08ns	-0.76±1.27ns
UU0197	0.62±1.96ns	1.80±0.93ns	2.64±1.58ns	-1.32±1.27ns	-1.74±1.43ns
UU0198	3.36±1.86ns	1.49±0.81ns	-3.00±1.41*	6.12±1.10***	4.55±1.29***
UU0231	-0.93±1.96ns	-2.76±0.85**	-1.04±1.52ns	1.19±1.15ns	2.38±1.27ns
UU0312	10.93±1.54***	1.05±0.72ns	-1.07±1.28ns	7.95±0.97***	4.34±1.16***
UU0332	6.17±1.61***	3.23±0.71***	1.80±1.29ns	9.73±1.03***	4.14±1.09***
UU0333	4.32±1.69*	1.06±0.74ns	-4.03±1.34**	1.69±1.04ns	-2.39±1.30ns
UU0387	1.66±198ns	0.58±0.92ns	-2.95±1.60ns	-0.34±1.39ns	-2.60±1.65ns
UU0388	-6.80±2.51**	-1.38±1.34ns	-2.54±1.97ns	-2.89±1.43*	-4.42±1.85*
UU0466	4.16±1.72*	-0.10±0.73ns	-1.53±1.40ns	3.32±1.11**	0.68±1.25ns
UU0513	-8.88±2.33***	-0.79±1.23ns	2.47±2.21ns	-2.25±1.56ns	-0.77±1.65ns
UU0554	-8.89±3.14**	-1.70±1.25ns	-2.34±1.88ns	-5.25±1.66**	0.47±2.06ns
UU0669	4.03±2.54ns	0.70±1.06ns	5.50±1.97**	-2.10±1.59ns	2.95±1.98ns
UU0954	-4.70±.1.67**	1.07±0.81ns	4.06±1.29**	-4.60±1.07***	2.69±1.16*
VV0102	1.23±2.58ns	0.98±1.03ns	-0.66±1.94ns	3.51±1.59*	1.69±1.65ns
VV0131	0.84±1.69ns	0.33±0.75ns	2.92±1.34*	-0.37±1.07ns	-1.37±1.16ns
VV0390	-6.00±1.86**	-2.51±0.87**	-0.42±1.50ns	2.41±1.16*	3.12±1.43*
VV0527	10.14±2.36***	-1.97±0.91*	1.62±1.78ns	1.59±0.41ns	-3.41±1.54*
VV0531	3.32±1.43*	0.52±0.73ns	1.76±1.12ns	-0.70±95ns	0.34±1.02ns
VV0701	8.80±2.06***	3.09±0.89***	2.01±1.65ns	-0.08±1.37ns	-1.38±1.54ns
WW0108	3.71±1.82*	0.38±0.95ns	-1.32±1.48ns	3.65±1.33**	2.75±1.29ns
XX0137	-3.18±1.68ns	1.33±0.77ns	2.29±1.38ns	1.33±1.11ns	0.68±1.21ns
XX0311	-0.83±1.93ns	0.002±0.84ns	3.24±1.58*	0.18±1.19ns	0.44±1.38ns
XX0372	-0.27±1.38ns	0.06±0.60ns	-0.36±1.08ns	0.19±0.89ns	0.66±1.03ns
XX0476	3.66±1.77*	-0.78±0.81ns	1.23±1.39ns	-0.40±1.08ns	-2.12±1.18ns
XX1149	5.93±2.31*	0.52±1.18ns	-0.24±1.82ns	-3.88±1.63*	-3.01±1.58ns

***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non-significant at P≥0.05

Table 6.6 Family best linear unbiased prediction (BLUP) and their standard errors for stalk number of populations planted in Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside locations

Family	Pongola	Empangeni	Gingindlovu	Bruyns Hill	Glenside
KK0489	-8.34±2.36***	-1.26±2.10ns	-3.27±2.70ns	-3.17±2.46ns	-6.15±3.07*
MM0036	-3.73±1.82*	-3.73±1.59*	-2.58±1.99ns	-0.33±1.91ns	0.74±2.27ns
MM0050	-6.00±2.58*	5.11±2.15*	0.44±2.70ns	-3.83±2.56ns	0.30±3.18ns
MM1497	1.06±2.01ns	-2.85±1.74ns	-0.83±2.33ns	5.90±2.21**	-1.99±2.43ns
NN0719	-4.52±1.74**	2.56±1.62ns	-0.63±1.93ns	-5.05±1.95**	2.15±2.34ns
NN1223	-2.56±1.35ns	-4.16±1.25***	-5.84±1.54***	-5.92±1.48***	-1.98±1.81ns
PP0542	0.24±1.81ns	-0.47±1.93ns	2.40±2.23ns	-4.46±2.29ns	-0.92±2.27ns
QQ0839	-5.64±1.67***	-0.84±1.28ns	-3.76±1.90*	-1.80±1.88ns	-1.08±2.39ns
RR0321	1.90±2.01ns	0.12±1.66ns	1.14±2.30ns	1.19±2.29ns	-0.45±2.48ns
SS0583	-4.02±1.45**	-4.07±1.38**	-5.53±1.66***	-5.39±1.60***	-5.21±2.11*
SS0754	-1.41±1.67ns	-4.38±1.57**	-6.71±1.95***	-3.83±1.90*	-1.95±2.23ns
SS0870	-0.88±1.61ns	-2.02±1.39ns	6.96±1.85***	-4.79±1.80**	-0.69±2.27ns
SS1237	-2.08±1.90ns	-2.28±1.54ns	1.30±2.20ns	-1.03±2.12ns	-3.03±2.54ns
TT0165	-4.90±2.12*	-4.59±2.18*	-9.48±2.41***	-4.66±2.09*	-4.97±2.80ns
TT0774	0.68±2.03ns	0.23±1.81ns	-2.34±2.37ns	2.26±2.46ns	0.10±2.66ns
TT1051	7.69±1.40***	5.88±1.15***	9.04±1.57***	8.23±1.53***	11.12±1.78***
UU0099	6.85±1.35***	7.30±1.37***	9.50±1.49***	4.99±1.49***	2.34±1.78ns
UU0163	-1.99±1.63ns	-2.16±1.74ns	-2.63±1.86ns	-1.75±1.91ns	-0.58±2.08ns
UU0183	-2.96±1.67ns	-5.67±1.46***	-2.97±1.83ns	-4.77±1.73**	-1.36±2.11ns
UU0197	-5.79±1.76**	-1.87±1.70ns	-4.33±2.05*	-7.18±2.00***	-8.18±2.39***
UU0198	6.41±1.67***	3.53±1.47*	-0.46±1.82ns	10.70±1.73***	9.94±2.14***
UU0231	-0.85±1.77ns	-3.46±1.54*	1.01±1.97ns	3.32±1.81ns	6.80±2.11**
UU0312	7.91±1.40***	2.35±1.31ns	-0.25±1.65ns	8.52±1.53***	8.43±1.92***
UU0332	9.39±1.46***	9.69±1.28***	4.94±1.66**	11.06±1.62***	6.15±1.80***
UU0333	3.19±1.53*	2.94±1.34*	-3.42±1.72*	0.77±1.63ns	-3.21±2.17ns
UU0387	-0.99±1.77ns	-0.45±1.67ns	-4.72±2.07*	-2.23±2.19ns	-4.17±2.80ns
UU0388	-9.29±2.26***	-2.75±2.51ns	-5.96±2.59*	-4.11±2.25ns	-8.54±3.18**
UU0466	5.82±1.55***	1.58±1.33ns	-1.66±2.81ns	4.52±1.74**	2.02±2.08ns
UU0513	-10.13±2.10***	-0.32±2.33ns	5.45±3.07ns	-5.98±2.46*	-2.60±2.80ns
UU0554	-6.63±2.88*	-1.90±2.39ns	-3.41±2.49ns	-7.73±2.62**	-2.81±3.62ns
UU0669	3.92±.229ns	-1.21±1.96ns	7.88±2.64**	-0.15±2.51ns	1.13±3.46ns
UU0954	-4.06±1.50**	0.48±1.47ns	2.74±1.67ns	-6.44±1.68***	3.75±1.92ns
VV0102	-1.51±2.23ns	-5.03±1.90**	-3.24±2.59ns	-2.34±2.51ns	-0.66±2.80ns
VV0131	4.22±1.53**	3.84±1.6**	8.34±1.71***	2.37±1.68ns	1.87±1.92ns
VV0390	1.30±1.67ns	2.93±1.59ns	8.55±1.93***	7.99±1.83***	9.07±3.39***
VV0527	1.17±2.10ns	-2.43±1.64ns	-4.12±2.33ns	0.84±2.21ns	-6.54±2.59*
VV0531	0.97±1.31ns	-0.87±1.32ns	1.45±1.45ns	-2.73±1.47ns	-0.66±1.83ns
VV0701	0.56±1.85ns	2.92±1.62ns	-3.59±2.15ns	0.27±2.15ns	-4.79±2.59ns
WW0108	10.33±1.64***	1.38±1.74ns	-0.19±1.91ns	6.59±2.09**	5.40±2.14*
XX0137	1.95±1.52ns	6.03±1.39***	4.93±1.78**	6.69±1.74***	4.83±2.01*
XX0311	4.07±1.74*	2.28±1.53ns	2.92±2.05ns	5.23±1.88ns	2.72±2.30ns
XX0372	1.83±1.26ns	0.67±1.10ns	1.65±1.40ns	2.06±1.40ns	1.45±1.71ns
XX0476	2.39±1.59ns	-2.64±1.48ns	0.44±1.79ns	2.17±1.71*	-2.87±1.96ns
XX1149	4.43±2.07*	-0.41±2.23ns	0.82±2.41ns	-6.00±2.56*	-4.92±2.65ns

***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non-significant at P≥0.05

Families XX0137 (Empangeni, Gingindlovu, Bruyns Hill and Glenside), VV0390 (Gingindlovu, Bruyns Hill and Glenside), UU0312 and WW0108 (Pongola, Bruyns Hill and Glenside), respectively, UU0466 (Pongola and Bruyns Hill), VV0131 (Pongola, Empangeni and Gingindlovu) and UU0333 (Pongola and Empangeni) produced significantly higher BLUP values for stalk number.

Families SS0583 (Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside), TT0165 (Pongola, Empangeni, Gingindlovu and Bruyns Hill), UU0197 (Pongola, Gingindlovu, Bruyns Hill and Glenside), UU0388 (Pongola, Gingindlovu and Glenside), NN1223 and SS0754 (Empangeni, Gingindlovu and Bruyns Hill), respectively, UU0183 (Empangeni and Bruyns Hill), KK0489 (Pongola and Glenside), NN0719, UU0554, UU0513 and UU0954 (Pongola and Bruyns Hill), respectively, MM0036 (Pongola and Empangeni) and QQ0839 (Pongola and Gingindlovu) produced significantly ($P<0.05$) lower BLUP values (Table 6.6). Family SS0870 produced significantly higher values at Gingindlovu and significantly lower values at Bruyns Hill. Family UU0231 produced significantly higher values at Glenside and significantly lower values at Empangeni.

Families TT1051 and WW0108 (Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside), respectively, UU0231 and VV0531 (Pongola, Gingindlovu and Bruyns Hill), respectively, NN0719 (Gingindlovu, Bruyns Hill and Glenside), UU0954 (Empangeni, Gingindlovu and Glenside), VV0102 (Empangeni and Bruyns Hill), XX0372 (Empangeni and Glenside), UU0099 and VV0131 (Pongola, Empangeni and Gingindlovu), respectively, and XX0476 (Pongola and Gingindlovu) produced significantly ($P<0.05$) higher BLUP values for stalk height (Table 6.7). Family UU0332 produced significantly ($P<0.05$) higher values at Bruyns Hill and Glenside. Families QQ0839 at Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside, SS0583 at Gingindlovu and Glenside, TT0165 and UU0388 at Pongola, Empangeni, Bruyns Hill and Glenside, respectively, and UU0554 at Pongola, Gingindlovu and Bruyns Hill produced significantly lower BLUP values. Family UU0197 produced significantly ($P<0.05$) lower values at Bruyns Hill and Glenside.

Family UU0312 produced significantly higher values at Pongola and Bruyns Hill and significantly lower values at Gingindlovu. Family VV0527 produced significantly higher values at Pongola and significantly lower values at Glenside, while family XX1149 produced significantly higher values at Pongola and significantly lower values at Bruyns Hill. Family

PP00542 produced significantly higher values at Gingindlovu and significantly lower values at Bruyns Hill. Family UU0198 produced significantly higher values at Bruyns Hill and significantly lower values at Gingindlovu.

Table 6.7 Family best linear unbiased prediction (BLUP) and their standard errors for stalk height of populations planted in Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside locations

Family	Pongola	Empangeni	Gingindlovu	Bruyns Hill	Glenside
KK0489	-0.119±0.055*	-0.078±0.054ns	-0.056±0.064ns	-0.115±0.060ns	-0.222±0.082**
MM0036	-0.013±0.043ns	-0.032±0.041ns	-0.041±0.047ns	-0.075±0.047ns	0.119±0.061ns
MM0050	-0.174±0.059**	-0.012±0.053ns	-0.066±0.064ns	0.008±0.062ns	0.094±0.085ns
MM1497	-0.017±0.047ns	-0.082±0.045ns	-0.044±0.055ns	0.072±0.054ns	0.002±0.065ns
NN0719	0.060±0.041ns	0.083±0.042ns	0.223±0.047***	0.219±0.048***	0.241±0.063***
NN1223	-0.028±0.031ns	0.056±0.032ns	-0.075±0.037*	0.028±0.036ns	0.017±0.049ns
PP0542	-0.039±0.043ns	-0.018±0.050ns	0.128±0.053*	-0.115±0.056*	-0.064±0.061ns
QQ0839	-0.125±0.039**	-0.093±0.033**	-0.168±0.045***	-0.162±0.046***	-0.197±0.064**
RR0321	-0.080±0.047ns	0.026±0.043ns	-0.120±0.055*	-0.046±0.056ns	-0.009±0.067ns
SS0583	0.013±0.034ns	0.051±0.035ns	-0.091±0.039*	0.043±0.039ns	-0.115±0.057*
SS0754	-0.106±0.039**	-0.146±0.040***	-0.187±0.046***	-0.236±0.046***	-0.030±0.060ns
SS0870	-0.110±0.038**	0.070±0.036ns	-0.011±0.044ns	-0.011±0.044ns	-0.004±0.061ns
SS1237	0.007±0.045ns	-0.048±0.40ns	0.086±0.052ns	0.044±0.052ns	-0.135±0.068*
TT0165	-0.102±0.049*	-0.161±0.056**	-0.109±0.057ns	-0.153±0.051**	-0.221±0.075**
TT0774	0.050±0.048ns	0.004±0.047ns	-0.061±0.056ns	-0.109±0.060ns	-0.053±0.071ns
TT1051	0.096±0.032**	0.151±0.029***	0.197±0.037***	0.194±0.038***	0.104±0.048*
UU0099	0.111±0.031***	0.098±0.035**	0.101±0.035**	-0.037±0.036ns	0.064±0.048ns
UU0163	-0.029±0.038ns	0.062±0.045ns	-0.129±0.045**	-0.033±0.047ns	0.086±0.056ns
UU0183	-0.040±0.039ns	-0.056±0.038ns	0.036±0.044ns	0.007±0.042ns	-0.077±0.057ns
UU0197	-0.070±0.041ns	-0.067±0.044ns	-0.002±0.049ns	-0.206±0.049***	-0.157±0.064*
UU0198	0.038±0.039ns	0.007±0.038ns	-0.118±0.043**	0.128±0.042***	0.076±0.057ns
UU0231	0.112±0.041**	-0.056±0.040ns	0.105±0.047*	0.104±0.044*	0.075±0.057ns
UU0312	0.088±0.032**	-0.029±0.034ns	-0.123±0.039**	0.142±0.037***	-0.021±0.052ns
UU0332	0.038±0.034ns	0.051±0.033ns	0.044±0.039ns	0.296±0.040***	0.128±0.049**
UU0333	0.054±0.036ns	-0.001±0.035ns	-0.145±0.041***	0.076±0.040ns	-0.067±0.058ns
UU0387	0.079±0.042ns	-0.003±0.043ns	-0.095±0.09ns	-0.013±0.053ns	-0.018±0.075ns
UU0388	-0.141±0.053**	-0.129±0.064*	-0.027±0.063ns	-0.214±0.055***	-0.313±0.085***
UU0466	-0.033±0.036ns	-0.065±0.034ns	-0.126±0.043**	0.081±0.043ns	0.006±0.560ns
UU0513	-0.245±0.049***	-0.224±0.060***	0.043±0.073ns	-0.043±0.060ns	0.001±0.075ns
UU0554	-0.147±0.066*	-0.083±0.061ns	-0.154±0.059**	-0.235±0.064***	0.084±0.097ns
UU0669	-0.006±0.053ns	0.053±0.050ns	0.018±0.063ns	-0.155±0.061*	0.159±0.093ns
UU0954	0.004±0.035ns	0.119±0.038**	0.298±0.040***	0.062±0.041ns	0.145±0.052**
VV0102	0.047±0.052ns	0.134±0.049**	-0.016±0.062ns	0.127±0.061*	0.027±0.075ns
VV0131	0.110±0.036**	0.086±0.035*	0.088±0.041*	0.006±0.041 ns	0.033±0.052ns
VV0390	0.026±0.039ns	-0.046±0.041ns	0.016±0.046ns	0.148±0.045***	0.093±0.064ns
VV0527	0.141±0.049**	-0.027±0.042ns	0.088±0.055ns	0.048±0.054 ns	-0.218±0.070**
VV0531	0.063±0.030*	0.065±0.034ns	0.118±0.035***	0.106±0.036**	0.067±0.049ns
VV0701	0.034±0.044ns	0.105±0.042*	-0.033±0.051ns	-0.063±0.052 ns	-0.063±0.070ns
WW0108	0.140±0.038***	0.158±0.045***	0.106±0.045*	0.281±0.051***	0.271±0.057***
XX0137	-0.018±0.035ns	0.026±0.036ns	0.107±0.042*	0.020±0.043ns	0.020±0.054ns
XX0311	0.034±0.041ns	-0.089±0.039*	0.055±0.049ns	-0.059±0.046ns	0.070±0.062ns
XX0372	0.020±0.029ns	0.119±0.028***	0.0003±0.033ns	0.065±0.034ns	0.130±0.046**
XX0476	0.104±0.037**	0.018±0.038ns	0.162±0.043***	-0.081±0.042ns	-0.017±0.053ns
XX1149	0.173±0.049***	0.001±0.057ns	-0.025±0.057ns	-0.145±0.062*	-0.113±0.071ns

***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non-significant at P≥0.05

Families UU0197 and UU0183 (Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside), respectively, SS0583 (Pongola, Empangeni, Bruyns Hill and Glenside), VV0701 (Pongola, Empangeni, Gingindlovu and Glenside), UU0312 and VV0102 (Pongola, Empangeni and Bruyns Hill), respectively, KK0489 (Pongola, Empangeni and Gingindlovu), VV0527 (Pongola and Gingindlovu) and SS0754 (Pongola, Bruyns Hill and Glenside) produced significantly ($P<0.05$) higher BLUP values for stalk diameter (Table 6.8). Families NN0719, TT1051, UU0099, VV0131, VV0390, (Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside), respectively, UU0231 (Pongola, Empangeni, Gingindlovu and Bruyns Hill), WW0108 (Pongola, Gingindlovu, Bruyns Hill and Glenside), XX0137 (Pongola, Empangeni and Bruyns Hill) and XX0372 (Empangeni, Gingindlovu, Bruyns Hill and Glenside) produced significantly ($P<0.05$) lower BLUP values. Family SS1237 produced significantly lower values at Pongola and Empangeni.

6.4.3 Breeding programme by location interactions

Highly significant ($P<0.001$) F-values were observed for location (L) and crop year by location (CL) effects for all traits (Table 6.9). Breeding programme (B) and crop year (C) produced highly significant ($P<0.001$) F-values for all traits except cane yield. Breeding programme by location interaction (BL) produced highly significant ($P<0.001$) F-values for cane yield and stalk number and significant ($P<0.05$) F-values for diameter. Breeding programme by crop year interaction (BC) produced highly significant ($P<0.001$) F-values for stalk number, while breeding programme by location by crop year interaction (BLC) produced significant ($P<0.05$) F-values for cane yield and diameter, respectively.

6.4.4 Mean values for breeding programme by location interaction effects

In this study, only mean values for BL effect were estimated because they were highly significant ($P<0.001$) for all traits, except stalk height, and represented exploitable family by location interaction effects. Results showed smaller differences in cane yield and stalk height of populations across locations while differences for stalk number and stalk diameter were large (Figure 6.1). The coastal populations generally produced higher cane yield and taller stalks at Empangeni and Gingindlovu locations. The irrigated populations produced higher cane yield and taller stalks at Pongola location and the lowest cane yield and shortest stalks at other locations. The Midlands populations produced higher cane yield and taller stalks at Bruyns Hill and Glenside locations. The coastal populations produced the highest stalk populations while the irrigated populations produced the lowest across all locations. The irrigated populations

produced the highest stalk diameter while the coastal populations produced the lowest across all locations.

Table 6.8 Family best linear unbiased prediction (BLUP) and their standard errors for stalk diameter of populations planted in Pongola, Empangeni, Gingindlovu, Bruyns Hill and Glenside locations

Family	Pongola	Empangeni	Gingindlovu	Bruyns Hill	Glenside
KK0489	0.308±0.071***	0.145±0.066*	0.227±0.075**	0.100±0.076ns	0.017±0.092ns
MM0036	0.071±0.055ns	0.038±0.050ns	0.119±0.055*	0.056±0.060ns	0.070±0.068ns
MM0050	-0.043±0.078ns	-0.053±0.065ns	-0.043±0.075ns	0.024±0.080ns	0.118±0.095ns
MM1497	0.046±0.060ns	0.064±0.055ns	-0.014±0.064ns	0.066±0.069ns	-0.005±0.073ns
NN0719	-0.338±0.053***	-0.149±0.051**	-0.239±0.053***	-0.229±0.061***	-0.156±0.070*
NN1223	-0.104±0.042*	0.054±0.040ns	-0.060±0.043ns	0.002±0.048ns	0.088±0.054ns
PP0542	0.055±0.055ns	0.050±0.061ns	0.097±0.062ns	-0.130±0.071ns	0.014±0.068ns
QQ0839	-0.019±0.051ns	-0.028±0.041ns	0.028±0.053ns	0.078±0.059ns	-0.036±0.072ns
RR0321	-0.065±0.060ns	0.074±0.052ns	0.099±0.063ns	0.115±0.071ns	0.072±0.074ns
SS0583	0.138±0.045**	0.119±0.043**	0.002±0.046ns	0.234±0.051***	0.130±0.063*
SS0754	0.188±0.051***	0.052±0.049ns	0.073±0.054ns	0.128±0.059*	0.173±0.067**
SS0870	-0.077±0.049ns	0.053±0.044ns	-0.133±0.051**	-0.170±0.056**	0.066±0.068ns
SS1237	-0.112±0.057*	-0.220±0.048***	-0.074±0.061ns	0.079±0.066ns	-0.111±0.076ns
TT0165	0.051±0.064ns	-0.062±0.069ns	0.059±0.068ns	0.151±0.065*	-0.012±0.084ns
TT0774	0.008±0.061ns	0.090±0.057ns	-0.058±0.066ns	0.009±0.076ns	-0.128±0.080ns
TT1051	-0.270±0.043***	-0.121±0.037**	-0.116±0.044**	-0.155±0.049**	-0.142±0.053**
UU0099	-0.230±0.042***	-0.177±0.043***	-0.296±0.042***	-0.454±0.048***	-0.307±0.054***
UU0163	-0.022±0.050ns	0.253±0.055***	0.053±0.053ns	0.068±0.060ns	-0.009±0.062ns
UU0183	0.296±0.051***	0.154±0.046***	0.301±0.051***	0.277±0.054***	0.124±0.063ns
UU0197	0.372±0.053***	0.379±0.053***	0.428±0.057***	0.629±0.062***	0.480±0.072***
UU0198	-0.052±0.051ns	0.029±0.046ns	-0.105±0.051*	-0.016±0.054ns	-0.090±0.064ns
UU0231	-0.122±0.053*	-0.178±0.048***	-0.195±0.054***	-0.216±0.057***	-0.043±0.063ns
UU0312	0.139±0.043**	0.091±0.042*	0.018±0.046ns	0.103±0.049*	0.106±0.058ns
UU0332	-0.035±0.045ns	-0.070±0.041ns	-0.070±0.046ns	0.036±0.051ns	0.053±0.054ns
UU0333	0.061±0.047ns	-0.030±0.042ns	-0.086±0.048ns	0.099±0.052ns	-0.073±0.065ns
UU0387	0.072±0.054ns	0.094±0.052ns	0.040±0.057ns	0.140±0.068*	-0.103±0.084ns
UU0388	0.089±0.068ns	-0.174±0.084*	0.005±0.074ns	0.009±0.070ns	0.151±0.095ns
UU0466	-0.024±0.047ns	0.020±0.042ns	0.015±0.050ns	0.064±0.055ns	-0.008±0.062ns
UU0513	0.035±0.063ns	0.029±0.075ns	-0.066±0.087ns	0.043±0.076ns	0.022±0.084ns
UU0554	-0.199±0.087*	-0.098±0.077ns	0.024±0.069ns	-0.102±0.082ns	0.189±0.109ns
UU0669	0.052±0.069ns	0.117±0.062ns	0.084±0.074ns	-0.102±0.078ns	0.167±0.104ns
UU0954	-0.131±0.046**	-0.008±0.046ns	-0.066±0.046ns	-0.460±0.053***	-0.097±0.058ns
VV0102	0.266±0.070***	0.226±0.060***	0.125±0.072ns	0.366±0.078***	0.155±0.084ns
VV0131	-0.156±0.047***	-0.140±0.043**	-0.125±0.048**	-0.159±0.057**	-0.217±0.058***
VV0390	-0.396±0.051***	-0.414±0.050***	-0.407±0.053***	-0.240±0.069***	-0.175±0.072*
VV0527	0.210±0.063***	-0.097±0.052ns	0.286±0.064***	0.134±0.047ns	0.065±0.078ns
VV0531	0.108±0.041**	0.049±0.042ns	-0.037±0.041ns	0.013±0.067ns	0.022±0.051ns
VV0701	0.383±0.056***	0.180±0.051***	0.356±0.059***	0.093±0.065ns	0.166±0.078*
WW0108	-0.222±0.050***	-0.094±0.055ns	-0.206±0.053***	-0.199±0.055**	-0.165±0.064*
XX0137	-0.149±0.046**	-0.102±0.044*	-0.084±0.049ns	-0.177±0.059**	-0.116±0.060ns
XX0311	-0.189±0.053***	-0.084±0.048ns	0.089±0.057ns	-0.160±0.059**	-0.133±0.069ns
XX0372	-0.063±0.040ns	-0.159±0.036***	-0.111±0.040**	-0.123±0.045**	-0.109±0.051*
XX0476	0.036±0.049ns	-0.014±0.046ns	-0.020±0.050ns	-0.067±0.054ns	-0.071±0.059ns
XX1149	0.033±0.062ns	0.113±0.07ns	0.082±0.067ns	0.041±0.080ns	-0.140±0.080ns

***Significant at P<0.001, **Significant at P<0.01, *Significant at P<0.05, ns = Non-significant at P≥0.05

Table 6.9 F-values and P-values for cane yield (kg), stalk number, stalk height and stalk diameter for location (L), breeding programme (B), crop year (C) and their interactions

	Cane yield		Stalk number		Height		Diameter	
Effect	F value	P value	F value	P value	F value	P value	F value	P value
L	113.71	<.0001	25.03	<.0001	85.87	<.0001	32.85	<.0001
B	3.37	0.0548	157.52	<.0001	11.55	0.0005	170.81	<.0001
BL	6.97	0.0002	7.03	0.0002	2.07	0.0897	3.09	0.0193
C	2.56	0.0773	308.89	<.0001	188.27	<.0001	699.51	<.0001
CL	377.70	<.0001	72.22	<.0001	1294.01	<.0001	205.76	<.0001
BC	0.91	0.4599	5.30	0.0003	2.30	0.0560	1.77	0.1319
BLC	1.89	0.0415	1.09	0.3622	0.87	0.5637	2.06	0.0244

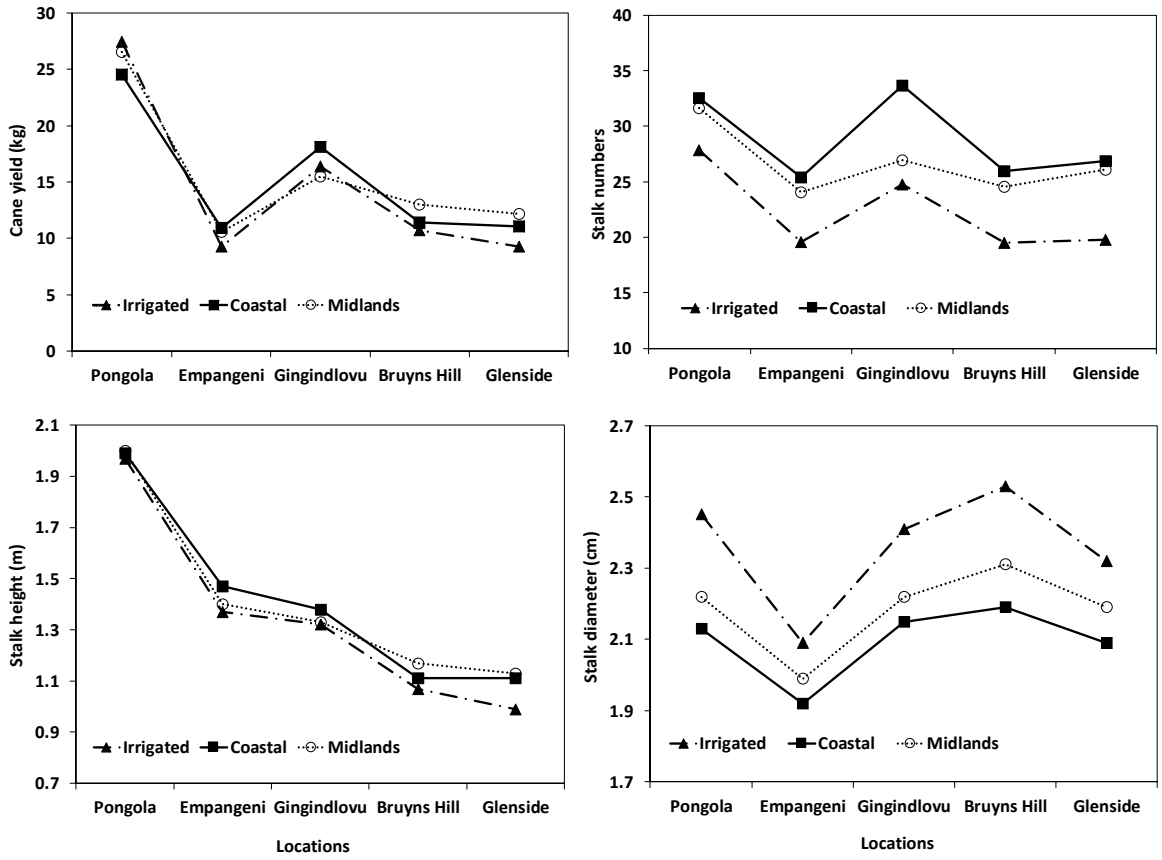

Figure 6.1 Trends in breeding programme by location interaction for cane yield, stalk number, stalk height and stalk diameter

6.5 DISCUSSION

The highly significant family variance components observed for all traits studied indicated large amount of genetic variability among families for sugarcane yield through its components. This suggested that genetic variability among families was present regardless of the test location of the populations. The family effect (F) was the largest for stalk number, stalk height and stalk diameter, which indicated that genetic variability among families, was largest for yield components than for cane yield. This suggested that indirect selection of families for yield using components may be less sensitive to effects of the environment. This result may also suggest that other variables, in addition to yield components, influence variability in cane yield of families. The significant FL variance component for cane yield, stalk number and diameter indicated that genetic variability among families varied across locations. The FL variance was largest for cane yield compared to yield components, indicating that cane yield was more sensitive to family by location interactions. Results suggested location specific evaluation and identification of families. Similar results have been reported in Australia (Hogarth and Bull 1990; Cox and Hogarth 1993; Jackson et al. 1995; McRae and Jackson 1995), Louisiana (Milligan and Legendre 1990; Souza-Vieira and Milligan 1999) and Mauritius (Bissessur et al. 2000). The non-significant FL variance for stalk height indicated that families were not influenced by locations for this trait but were stable for the trait.

The highly significant FC variance for stalk number suggested that there was a large crop year interaction effect on genetic variability for stalk number among families. This also indicated potential effect of seasonal weather variability on stalk number and possibly stalk mortality. However, crop year effect and its interactions are confounded and unpredictable and, therefore, not useful for guiding breeding and selection strategies (Ramburan 2013; Zhou and Shoko 2012).

The FLC variance component was largely non-significant for cane yield and stalk number, which indicated less influence of location specific crop year effects on these traits. Results were similar to findings from a study carried out in Myanmar, Southeast Asia (Lwin et al. 2016). However, these results are in contrast with findings (Zhou et al. 2011; Zhou and Gwata 2015) observed at clonal level where cane yield produced large and significant genotype by location by crop years effect values, indicating the complexity of selection for yield traits. Yields traits are known to be controlled by several quantitative genes that have small additive effects (Kimbeng and Cox 2003; Zhou et al. 2011) and due to several small additive genes, the effect

of the environment is cumulatively large on yield traits, resulting in complex genotype by environment interaction effects which makes selection tedious.

Results from the current study highlighted that families were less influenced by environmental effects compared to genotypes within families and, therefore, family evaluation could be used to improve precision and selection for cane yield at the early stages of breeding. The significant FLC variance components observed for stalk height and diameter highlighted differences in family variability across crop years and locations, which further suggested a possibility of complex environmental effects on these traits.

The proportion of combined FE variance to the variance of the F main effect showed that FLC was higher for cane yield, followed by stalk height, stalk diameter and stalk number. Ranking of variance components indicated that FL variance was the largest source of variance for cane yield, stalk number and diameter, which indicated that breeding populations differed for these traits across locations and possibly location specific variability. The FLC variance was shown to be the second largest source of FE variance for cane yield and stalk diameter, indicating complex FE interaction for improving cane yield and stalk diameter. The FC variance was shown to be the least contributing source of FE variance for cane yield, stalk height and diameter, which suggested that ratooning ability was less important on these traits. Therefore, results suggested that multi-environmental trials were more important than ratoon crops.

The residual variance component was highly significant for all traits and the largest variance compared to other variances. This indicated that there was variability that was not accounted for by the model. To increase the reliability of results, future studies must consider reviewing current trial designs to enhance experimental precision. The current experimental design used was the randomised complete block design. In future, adopting lattice designs that are known for their ability to account for larger within replications and within field variability may potentially reduce the residual variance.

Generally, high broad-sense heritability (above 50%) was observed for all traits, which indicated potential accuracy in selecting higher trait value families. This trends also highlighted high proportion of genetic variability among families for yield components. The higher H for stalk number, height and diameter compared to cane yield, indicated that families would be selected with higher precision for yield components compared to cane yield. This further

suggested the possibility of indirect selection for cane yield through it components. Preliminary studies (Zhou 2014) have shown that yield components could be used to select superior families for cane yield. Results also indicated that the use of traits (i.e. stalk number, height and diameter) with high heritability as a selection criteria could lead to genetic improvement in cane yield. The effectiveness of selection depends not only on heritability but also on predicted selection gain and genetic variability available to exploit through selection (Butterfield and Nuss 2002; Wolie et al. 2013).

The higher % Gs for cane yield, stalk number and height indicated the potential to increase the probability to achieve higher realised genetic gains for cane yield through stalk number and height. The % Gs were highest for stalk height and lowest for stalk diameter, suggesting that during visual selection within elite families, focus should be on stalk height followed by stalk number and least on stalk diameter. Previous studies (Zhou 2004, 2014; Mbuma et al. 2017) showed that stalk number and height had the strongest influence on cane yield. Other studies on path coefficient analysis (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. 2013) showed the strong influence of stalk number on cane yield.

Families such as TT1051, UU0332 and UU0312 (for cane yield), TT1051, UU0332, UU0099, and UU0198 (for stalk number), TT1051, WW0108, UU0231 and VV0531 (for stalk height), and UU0197, UU0183, SS0583, VV0701, UU0312 and VV0102 (for stalk diameter), showed potential broad adaptation of progenies because these families produced high trait values in diverse environments such as irrigated, coastal and high altitude Midlands regions. Irrigated areas represent low rainfall and high temperatures, resulting in the use of irrigation water to achieve economic yield. Coastal environments represents rainfed areas, high Eldana damage prevalence and larger variability in soils (shallow or deep). High altitude Midlands region represents rainfed areas with low temperatures due to long winters and shorter summers. Therefore, the diverse adaptation of families suggested the possibility to use these families for selecting broadly adapted cultivars to meet future demands and to mitigate climate change.

Family VV0701 (for cane yield) showed potentially narrow/specific adaptation to 12 months harvest cycle because their progenies produced significantly higher cane yield only in irrigated and coastal short cycle locations, representing shorter growing conditions. The coastal short

cycle programme is located in an area known to have high Eldana predominance, resulting in sugarcane to be harvested at 12 months as an escape mechanism for Eldana. The irrigated region represents areas with very low and erratic rainfall, and high temperatures. High temperatures result in high heat units and when combined with irrigation, enables the crop to mature at the age of 12 months.

Families VV0390 and UU0198 (for cane yield) and UU0332 (for stalk height) indicated specific adaptation of progenies to Midlands 24 months harvest cycle because these families produced high traits values only in areas that represents slow crop growth caused by the long cold winters and short summers. Families UU0333 and XX1149 (for cane yield), and VV0527 and XX1149 (for stalk height) showed specific adaptation of progenies to the irrigated programme because these families only produced high trait values in irrigated areas, which represent low rainfall and high temperatures.

Families PP0542 and UU0954 produced significantly higher cane yield at Gingindlovu and Glenside and significantly lower cane yield at Bruyns Hill and Pongola, suggesting that these were more adapted to harsh growing conditions than optimal growing conditions. Bruyns Hill with deep soils and Pongola with irrigated crop, provide non-limiting growing conditions compared to sandy soils at Glenside and shallow soils at Gingindlovu.

Generally, results suggested the potential of exploiting niche breeding in sugarcane. Niche breeding by nature allows for the development of varieties with adaptation to specific environments (Zhou 2015). Niche breeding is also acknowledged to increase selection and genetic gains because it reduces genotype by environment interactions.

The significant breeding programme by location effect (BL) for all traits, except for stalk height, indicated that response of the breeding populations varied across environments. Significant BL also indicated that breeding populations, which were not adapted across locations with different climates, had different roles in identification of populations with adaptability. The breeding programme by location by crop year effect (BLC) was significant for cane yield and stalk diameter, which indicated that there was location specific performance of breeding populations across the crop years. This further highlights the complexity of breeding for ratooning ability. Results also suggested that testing in multiple agro-ecological regions (environments and crop years), where sugarcane is grown, would be required to identify and select the most superior

crosses because location effects appeared to influence ratooning ability of the breeding populations for cane yield and stalk diameter.

The least square mean values showed high discriminating ability among the breeding populations for all traits, which suggested that identification of populations that produced high trait values would be accurate. The irrigated, coastal and Midlands populations showed the most specific adaption for cane yield and stalk height because each population produced high trait values in specific environments that represents unique conditions. The coastal populations showed broad adaption for stalk number in diverse environments which represent the major agro-ecological regions of sugarcane production. This has implications for breeding and crossings among SASRI regional breeding programmes. During crossing, parents are selected based on their genetic background to make crosses. For example, genotypes that were originally developed in coastal areas and are known to have high breeding values, are mainly used in making crosses for the coastal breeding programmes. Therefore, the present results could indicate potential opportunity to enhance selection gains through transfer of desirable genes in genotypes that were used in making crosses across programmes. The irrigated populations showed wide adaption for stalk diameter in diverse environments, representing the major agro-ecological regions of sugarcane production. Similar findings have been reported on logistic regression models (Zhou 2018).

6.6 CONCLUSIONS

This study was the first to investigate the nature and magnitude of family by environment interactions in South African sugarcane populations and demonstrated the existence of large and complex family by environment interactions that may be further exploited for improved breeding and selection. The FL effect was more important, indicating the presence of location specific variability among families, which allows exploitation of niche breeding. The FC and FLC effects have shown to be less important on performance of families for cane yield and its components. This study showed that testing of families for cane yield in several environments as plant crop was more important than across ratooning cycles. There was a large proportion of genetic variability among families. Families TT1051, UU0332 and UU0312 showed potential broad adaptation for cane yield. Families VV0701, VV0390 and UU0198 indicated specific adaptation of progenies for cane yield. The irrigated, coastal and Midlands populations for cane yield and stalk height showed the most specific adaption response to environments of the

breeding populations. Knowledge on adaptation of families and traits adaptability will guide crossing and cross allocation for SASRI breeding programmes.

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CHAPTER 7

GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS FOR FUTURE RESEARCH

7.1 GENERAL DISCUSSION

Sugarcane with a complex genome, which is characterised by polyploidy and aneuploidy and the high polyploidy nature contributes to cytogenetic complexity which makes genetical studies difficult. The sugarcane quantitative traits such as cane yield and sucrose content are controlled by quantitative genes and significantly influenced by genotype by environment interactions (Jackson and McRae 1998). The effect of genotype by environment interaction is large, particularly at early stages of sugarcane breeding where genotypes are not replicated and are planted in small plots. Small plots are prone to large competition effects among genotypes, which reduces selection efficiency (Jackson and McRae 2001) in breeding populations. As a result, family evaluation, which involves using progeny data to determine family values, has been adopted as a method to increase selection efficiency and genetic gains at early stages in sugarcane breeding (Hogarth 1971; Hogarth et al. 1990). Family evaluation data is also used to determine the breeding values of genotypes (Kimbeng and Cox 2003). Breeding values refers to the ability of genotypes to produce progenies with high trait values (Jackson 2016). The aim of this study was to evaluate families and estimate the breeding values of genotypes in order to increase crossing and selection efficiency for cane yield in sugarcane breeding. Therefore, four research areas were identified namely; family versus individual genotype selection for variance components (Chapter 3), broad-sense heritability (H) for family and individual genotype selection (Chapter 4), breeding values of genotypes (Chapter 5), and family by environment interaction across populations (Chapter 6).

This study found that family evaluation and selection was superior to individual genotype evaluation, generating larger genetic variability and higher broad-sense heritability. Results indicated that an increase in genetic values for cane yield and its components could be achieved using family selection rather than individual genotype selection.

The humic soil, CLCHP, CSCHP and irrigated populations produced higher H estimates (above 50%) for cane yield compared to sandy soil, CLCAP and CSCAP populations. This indicated

that a large proportion of the total variance is heritable and that selection for cane yield would be effective in these soil types. The high H estimates also indicated high precision in selection from humic soil, CLCHP, CSCHP and irrigated populations compared to sandy soil, CLCAP and CSCAP populations. The sandy soil, CLCAP and CSCAP populations had low H estimates (below 50%), indicating lower precision of selection for families with higher cane yield or the less response of these families under the extreme conditions. These breeding programmes are located on more variable soils that could be suppressing genetic expression of traits because of high variability in data.

During selection, genotypes are visually evaluated for stalk number, height and diameter. Stalk number, stalk height and stalk diameter had higher family H estimates than cane yield for almost all the populations, suggesting that selecting indirectly for cane yield could be efficient. This result is particularly important because it highlights that estimating cane yield through yield components remains the most viable and practical approach for smaller and resource limited breeding programmes.

The significant female and male variance components across the populations indicated that genotypes contributed significantly to the variability among the progeny populations. Generally, the humic soil, CLCHP and irrigated populations had larger variances for both females and males compared to the sandy soil, CLCAP, CSCAP and CSCHP populations, indicating higher genetic variability contributed by genotypes used for crossing. The females produced larger variances and smaller standard error than males for humic soil, CLCAP and CSCHP populations, which suggested that the larger proportion of the genetic variability observed in progenies were attributed to female parents. Results indicated the potential for maternal effects among the humic soil, CLCAP and CSCHP populations compared to other populations. The strong maternal effects compared to paternal effects have been reported earlier among the SASRI populations (Zhou 2015).

The male parents among sandy soil, CLCHP, CSCAP and irrigated populations produced larger variances and standard errors compared to the females, which suggested that most of the genetic variability observed among the progenies was contributed by the male genotypes. Results may also suggest higher genetic variability among the males used in these crosses. This could potentially be linked to higher flowering among the males resulting in abundancy of pollen from the several males that were used during crossing or the dominant expression of male parents.

Genotypes with high breeding values could be used to build a core germplasm pool of genotypes known to produce superior progenies for cane yield and could be used to guide future crossing in sugarcane breeding. Genotype 82H0397 and 85H0428 had high breeding values for cane yield, specifically for the Midlands breeding programmes. Genotypes 87W0629, 01G1662, 88W1323, 02K1657, 87L0573, 97E0474, N31, 93E0888, 03U1030 and 06T3608 had high breeding values specifically for coastal breeding programmes. Genotypes N52, B74713, 96W0246, WI82498 and 79F0779, when crossed with diverse genotypes, produced progenies with higher cane yield, indicating that these genotypes had broad general combing ability. Future research is required to validate their potential for use as testers.

The numbers of female and male genotypes with high breeding values in humic soil, CLCHP, CSCHP and irrigated populations were more than those in sandy soil, CLCAP and CSCAP populations. The low proportions of female and male genotypes with high breeding values for cane yield among sandy soil, CLCAP and CSCAP potential breeding populations could indicate poorer genetic combinations among genotypes and need for introgression and trait breeding to develop genotypes with higher breeding values for use in crossing. The lower proportions of female and male genotypes with high breeding values in sandy soil, CSCAP and CLCAP populations could be attributed to these breeding programmes being more recently established (Nuss 1998), using less adapted genotypes from other breeding programmes during crossing. These new breeding programmes are still in progress developing genotypes suitable for crossing from recurrent breeding and selection cycles. The CLCAP and CSCAP programmes are located on a site with high prevalence of Eldana borer, resulting in increased selection pressure for Eldana resistance populations at the expense of cane yield. This high pressure on breeding and selecting for Eldana resistance could be affecting evaluation of genotypes where the need to combine yield and Eldana resistance reduces the ability to identify genotypes with high breeding values for both traits. Concentrated research is required to quantify genetic interactions between yield and Eldana damage to guide future breeding for CLCAP and CSCAP programmes.

In the study on family by environment interactions, significant family variance indicated more variability among families and greater selection efficiency. Significant family by location interaction variance indicated that selection for location specific families would also allow exploitation of niche breeding in South Africa. Higher H estimates for cane yield indicated

higher proportion of genetic variability among families. Families TT1051, UU0332 and UU0312 with significantly high BLUP values for cane yield across locations, indicated broad adaptation of progenies in diverse agro-climatic regions. Families such as VV0390 and UU0198 showed specific adaptation to Midlands where sugarcane is harvested at 24 months, while VV0701 was adapted to 12 months harvest in coastal short cycle and irrigated environments. The coastal region showed adaptation for progenies with high stalk number, thin stalks while irrigated environments preferred progenies with thicker stalks and less stalk number. The irrigated, coastal and Midlands populations showed the most specific adaptability for cane yield and stalk height.

7.2 CONCLUSIONS

Results from this study demonstrated large genetic variability among SASRI breeding populations that may be exploited for improving breeding and selection and in identification of genotypes with tolerance to drought, water deficit, extreme cool conditions and waterlogging. Family breeding parameters were larger than for individual genotypes, indicating higher selection efficiency for families. Combined gains from adopting family selection, followed by individual genotype selection, will increase overall genetic gains in sugarcane breeding. There was a higher proportion of genetic variability among the humic soil, CLCHP, CSCHP and irrigated populations than the sandy soil, CLCAP and CSCAP populations, indicating the efficacy of family evaluation. Therefore, genotypes from the humic soil, CLCHP, CSCHP and irrigated populations could be used during crossing to diversify and improve the variability and selection efficiency among the sandy soil, CLCAP and CSCAP populations. More cycles of recurrent breeding will improve the genetic background in sandy soil, CSCAP and CLCAP populations, which will then enhance selection efficiency and genetic gains. Selecting families indirectly for cane yield through the yield components was efficient, indicating that visual selection which focuses on the yield components, was more accurate.

The significant female and male variance components indicated the effectiveness of using family data to estimate the breeding values of genotypes that were used in crosses. Genotypes with high breeding values for cane yield were identified using BLUP analysis from progeny data that were collected from SASRI breeding populations. Genotypes with high breeding values for cane yield can be used to build a core germplasm while those with low breeding values can be discarded from germplasm pool. The high breeding values obtained from genotypes in diverse populations was an indication of broad general combining ability. Testing

breeding values of genotypes from diverse populations assisted in determining genotypes with broad general combining ability that can be used as testers in sugarcane breeding. The low proportions of genotypes with high breeding values observed for cane yield across all populations indicated a need for trait breeding.

Testing families in multi-locations was more important than across ratoon crops. BLUP estimates identified families with significantly high values for cane yield across locations, indicating the potential for broad adaptation among progenies. Families with significantly high BLUP values for cane yield in specific locations indicated that narrow adaptation of progenies and these populations could be exploited for niche breeding in sugarcane. The irrigated, coastal and Midlands populations showed specific adaption for cane yield and stalk height.

7.3 RECOMMENDATIONS FOR FUTURE RESEARCH

1. There is a need to quantify the genetic gains that can be achieved from family, followed by individual genotype selection.
2. The effectiveness of simultaneous breeding and selection for yield and Eldana resistance needs to be determined through appropriate breeding strategy.
3. Research that focus on estimating breeding values for other traits such as dry matter, fibre, Brix, purity, sucrose content, ERC, pest and diseases resistance is required and identification of trait specific genetic stocks for future.

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