PATH COEFFICIENT ANALYSIS AND COMBINING ABILITY BETWEEN QUALITY PROTEIN AND PRO-VITAMIN-A MAIZE LINES FOR YIELD AND SECONDARY TRAITS

by

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GENERAL ABSTRACT

In most countries, white maize varieties are more preferred than the yellow/orange maize. Unfortunately, normal yellow and white maize lacks vitamin A which is crucial mainly for sight as well as growth and immunity. Sub-Saharan African (SSA) countries are largely dependent on maize as their meals are predominantly made from maize, and vitamin A deficiency (VAD) is a progressing problem in these countries. In the biofortified orange maize, vitamin A occurs in the form of pro-vitamin A (PVA) carotenoids. This pro-vitamin A maize is being used to alleviate the problem of VAD. Normal maize is also deficient in two essential amino acids, namely lysine and tryptophan that cannot be synthesised by the body. Quality protein maize (QPM) was developed from a mutant maize type that is rich in the essential amino acids, tryptophan and lysine. These two essential amino acids are required in the body for the formation of proteins which reduces the occurrence of protein deficiencies such as kwashiorkor in children. In addition to the nutritional insecurity that is being faced in SSA countries, maize that is being produced remains insufficient to sustain the populations as they are increasing tremendously.

Development of high yielding and adaptable maize hybrids with better nutritional quality in terms of vitamin A and quality protein traits by stacking genes for vitamin A and quality protein in single cross maize hybrids will help alleviate this problem. This study was conducted to establish the combining ability of exotic PVA with locally adapted QPM lines, combining ability of the locally adapted PVA maize with QPM lines and contribution of secondary traits to yield in PVA and QPM hybrids. Line by tester analysis was conducted for two experiments. The maize inbred lines used in this study were developed by a shuttle breeding programme at University of KwaZulu-Natal. In the first experiment, 26 lines were crossed to four testers and 70 selected hybrids, including one check which was repeated twice, were evaluated in another trial. The hybrids were planted at Ukulinga in the summer season of 2015/2016. A 10 X 7 row by column design was used. In the second experiment, 12 lines were crossed to four testers and 44 selected hybrids, including one check, were evaluated in a trial. The hybrids were planted at two sites, Cedara and Ukulinga in summer season of 2015/2016. A 4 X 11 row by column design was used. Recommended agronomic practices were implemented for all the sites. Data was collected using a CIMMYT

protocol and subjected to statistical analyses using Breeding Management System which is linked to Breeding View package, ANOVA and REML packages in GENSTAT 17th edition.

The experimental hybrids performed competitively against the check that was used. The outstanding performance of the hybrids was also displayed by the high genetic gains that were realized for the selected hybrids in both the trials. In the first experiment, hybrid 16XH49 was ranked as the highest yielding. In the second experiment, hybrids 16XP11 and 16XP33 were ranked the highest yielding for Ukulinga and Cedara, respectively. The general combining ability effects of lines were significant for grain yield and shelling percentage for both sites. Cultivar Superiority Analysis revealed that hybrids 16XP33, 16XP11 and 16XP29 were the most stable. Path coefficient analysis revealed significant association of secondary traits with grain yield. Traits such as ear height, plant height, field weight, number of ears per plot, shelling percentage, 100-grain weight and plant stand exhibited positive direct effects on grain yield. Selection of these traits would effectively cause an increase in grain yield. Field weight was found to be the most important trait contributing towards grain yield.
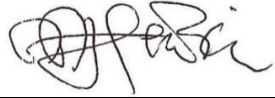
DECLARATION

I, Patience Kumbula, declare that:

1. The research reported in this dissertation, except where otherwise indicated, is my original research.
2. This dissertation has not been submitted for any degree or examination at any other university.
3. This dissertation does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.
4. This dissertation does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:

   i. their words have been re-written but the general information attributed to them has been referenced;

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Signed:

As the candidate's supervisors we agree to the submission of this dissertation

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Professor J. Derera (Supervisor)

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DEDICATION

To God the Almighty who is my pillar of strength in all times.

To my son Jediel, my mother Faith Kumbula, father Aaron Kumbula, siblings (Tecla, Leadison, Isaac and Aaron) and my friend Sharon Migeri.

To my friends, who have stood by me and gave their support.

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LIST OF ACRONYMS AND ABBREVIATION

AD: Anthesis date (days)

ANOVA: Analysis of Variance

ASI: Anthesis-Silking Interval

BMS: Breeding Management System

CIMMYT: International Maize and Wheat Improvement Centre

CV: Coefficient of Variation

D.F: Degrees of Freedom

E: East

EH: Ear height

EPO: Ear position

FAO: Food and Agriculture Organization of the United Nations

FAOSTAT: Food and Agriculture Organization Statistics

FW: Field weight

GCA: General Combining Ability

GCV: Genotypic Coefficient of Variation

GRN: Number of kernel rows per ear

GW100: 100-grain weight

GY: Grain yield

LAN: Limestone Ammonium Nitrate

LSD: Least Significant Difference

m: Metres (distance)

MC: Mean of commercial hybrids

mm: Millimeters

MOI: Grain moisture content

MP: Population mean

MS: Mean of selected hybrids

MSE: Mean square error

NE: Number of ears per plot

NPK: Nitrogen: Phosphorous: Potassium

OPV: Open pollinated varieties

P: Probability significance level

PCV: Phenotypic Coefficient of Variation

PG: Predicted gain

PH: Plant height

PS: Plant stand

PVA: Pro-vitamin A

QPM: Quality protein maize

RG: Realised gains

RL: Root lodging

S: South

SCA: Specific Combining Ability

sd: Standard Deviation

SD: Silking date (days)

SE: Standard Error

SH: Shelling percentage

SL: Stem lodging

SOV: Source of Variation

TEX: Grain texture

TL: Total lodging

t/ha: Tonnes per hectare

VA: Additive variance

VD: Dominance variance

VE: Environmental variance

UKZN: University of KwaZulu-Natal

USA: United States of America

1   INTRODUCTION

Maize (*Zea Mays* L.) is a staple food crop in most Sub-Saharan countries. It is widely grown by subsistence and small scale farmers. Among the mostly grown cereals, maize has the largest annual productivity of above 870 million metric tonnes (Cairns et al., 2013). Maize is also largely utilized for livestock feed and raw material for industrial products. According to Bello et al. (2012), human food and nutrition is a major crisis that is mainly affecting developing countries such as South Africa and Zimbabwe. Pro-vitamin A (PVA) and quality protein maize (QPM) have been adopted in some countries as a way of mitigating the health problems arising due to vitamin A and protein deficiencies.

Vitamin A is a group of C20 carotenoid derivatives (retinal, retinol and its esters, and retinoic acid). Alpha-carotene, beta-carotene and beta-cryptoxanthin are the most abundant carotenoids that have been found in food. They are also called pro-vitamin A carotenoids as they are precursors of vitamin A that can be converted into retinol by the body when required (Pillay, 2011). As stated by Ortiz-Monasterio et al. (2007), beta-carotene and beta-cryptoxanthin are found in higher levels in pro-vitamin A maize than alpha-carotene. Nevertheless, beta-carotene is the most important precursor of vitamin A as one molecule of beta-carotene is converted to two molecules of vitamin A in the body when required. Pro-vitamin A maize refers to maize that has enhanced quantities of beta-carotene which gives rise to the yellow to dark orange grain colour. High total carotenoids are associated with darker orange colour in maize whereas the dark orange colour does not always result in higher pro-vitamin A concentrations. On the other hand QPM is rich in two essential amino acids; namely lysine and tryptophan, which cannot be synthesised by the body. In most east and southern African countries, white maize varieties are more preferred than the yellow maize. Nevertheless, normal yellow and white maize are deficient in these essential amino acids and beta-carotene.

Dietary improvements for the uptake of micronutrients amongst human beings include improvement of different diets taken up by human beings in the form of maize meal or animals. These improvements also include food fortification, supplementation and dietary diversification which used to be the main approaches to eliminate micronutrient malnutrition. Biofortification is a process that involves breeding nutrients into food crops. Biofortification of maize with nutrients such as pro-vitamin A (PVA) and quality protein by conventional breeding has emerged as a possible long-term sustainable approach to improve nutrition status in

humans. It involves the enhancement of crops or animals with nutrients such as vitamin A (Kinfe et al., 2015).

Breeding vitamin A in maize has been successful, leading to the release of yellow maize varieties (Reddy et al., 2013). Yellow maize has been used as a source of food and feed in Africa and the rest of the world (Sudika et al., 2015). Pro-vitamin A maize is usually preferred as a livestock feed due to its contribution towards the yellow colour of the poultry meat, egg yolk and animal fat (Pavlov et al., 2015). Success in developing QPM varieties, with increased levels of essential amino acids (lysine and tryptophan), through biofortification by International Maize and Wheat Improvement Centre (CIMMYT) has been widely reported (Vasal et al., 1980). Nzuve et al. (2014) reported that many commercial QPM varieties have been released in a number of countries including those in parts of Africa, Asia and Central America.

Vitamin A deficiency is a problem affecting many people worldwide, especially the developing countries. This deficiency results in blindness in children (Hefny, 2011). An estimate of 140 million children under the age of five years have been reported to have low serum retinol level and the majority of these children live in sub-Saharan Africa and South Asia (Mason et al., 2001). Infants and pregnant women are the most vulnerable to vitamin A deficiency due to their high requirements of vitamin A. This deficiency causes stunted growth in infants, loss of appetite, cardiovascular diseases and compromised immune system, which lowers resistance to infections. In extreme cases of vitamin A deficiency, death can occur. In 2000, 519 maternal deaths were reported in South Africa and these deaths were due to vitamin A deficiency (Steyn et al., 2006).

Vitamin A deficiency can also cause a medical condition called xerophthalmia. If untreated, it leads to blindness in children. Vitamin A can help prevent cancer as it acts as a scavenger for free radicals (cancer causing) in the body (Serna-Saldivar, 2012). Foods of animal origin such as liver, egg yolk and dairy products contain preformed vitamin A which is the most bio-available. This means that it is directly utilized by the body. However, these animal sourced foods are not affordable by many people in the developing countries (Kang and Ahmad, 2014). The vitamin A found in maize and other plants is in the form of pro-vitamin carotenoids. The most important pro-vitamin carotenoid is β-carotene because one molecule is converted into two of the most active form of vitamin A or retinol in human beings (Serna-Saldivar, 2012).

Protein deficiency remains a problem regardless of the development of QPM varieties. Severe protein malnutrition may cause kwashiorkor, which manifests from chronic protein and energy imbalance, and increases susceptibility to diseases, such as tuberculosis and gastroenteritis (Rolfes et al., 2009). Kwashiorkor mainly affects rural children in Africa as they are mainly fed maize-based porridges (Onofiok and Nnanyelugo, 1998). This is because many poor households particularly those residing in rural areas have limited access to high quality protein sources such as legumes, eggs, dairy products and meat (Begum et al., 2016).

Maize varieties which meet all the farmer requirements from field to fork in different areas are still to be developed. Gene stacking can be done in one variety to meet different farmer requirements such as agronomic performance, adaptation and nutritional value (Sesay et al., 2016).

1.1   Problem statement

There are no adapted maize varieties containing both vitamin A and quality protein traits. Breeding maize hybrids with high levels of nutrients such as quality proteins (QPM) and pro-vitamin A (PVA) would contribute towards alleviation of malnutrition in sub-Saharan Africa. However, development of such hybrids requires knowledge of the combining ability between QPM and PVA maize lines. A survey of the literature indicates that there is no work that has been done to establish combining ability of vitamin A and QPM traits. Most studies have looked at these traits in isolation. Combining ability information is crucial for designing hybrids and devising the breeding strategies.

1.2   Significance of study

This study aimed at identifying the genetic information that is needed in breeding adapted varieties that combine quality protein and high pro-vitamin A traits. Kumar et al. (2006), pointed out the importance of developing maize varieties containing both quality protein and pro-vitamin A, which result in yellow/orange QPM maize. This maize would be having high levels of carotenoids and essential amino acids. The maize varieties would have an even greater impact on health and nutrition for target countries in Africa (Kumar et al., 2006). Combining genes for pro-vitamin A, quality protein traits and adaptability in maize takes the advantage that it is a staple food which predominates part of diets of poor households who are at the risk of vitamin A and protein deficiencies.

1.3   Main objective

The main objective of the study was to develop adaptable and high yielding maize hybrids with better nutritional quality traits in terms of vitamin A and QPM by stacking genes for vitamin A and quality protein in single cross maize hybrids.

1.4   Specific objectives

The following objectives were pursued:

a)   To determine combining ability of exotic PVA with locally adapted QPM inbred lines for grain yield and yield components.
b)   To determine the combining ability of the locally adapted PVA maize with QPM inbred lines for grain yield and yield components.
c)   To determine contribution of secondary traits to yield in PVA and QPM hybrids.

1.5   Research hypotheses

The following hypotheses were tested:

a)   There is high combining ability between foreign PVA and locally adapted QPM inbred lines for grain yield and yield components
b)   There is high combining ability between adapted PVA and QPM inbred lines for grain yield and yield components
c)   There is a significant relationship between grain yield and secondary traits.

1.6   Structure of Dissertation

The dissertation is structured as follows:

Chapter One: Introduction

Chapter Two: Literature review

This chapter presents the importance, production of maize globally, regionally and nationally, as well as progress in breeding maize for different traits. The use of secondary traits in breeding for grain yield and methods that are used to evaluate their relationship with yield are

also reviewed in this chapter. This chapter also looks into the progress in breeding maize for nutritional density specifically for pro-vitamin A and QPM.

Chapter Three: General materials and methods

The materials, procedures and data analysis methods for this study are outlined in this chapter.

Chapter Four: Hybrids derived from Mexican PVA maize inbred lines

This chapter outlines the germplasm development, specific methods for this trial, results which are presented in tables, detailed discussion of the results and conclusions made based on the findings.

Chapter Five: Hybrids derived from South African PVA maize inbred lines

This chapter outlines the germplasm development, specific methods for this trial, results which are presented in tables, detailed discussion of the results and conclusions made based on the findings.

Chapter Six: Conclusion and Recommendations

Conclusions from the completed research are summarized with respect to the study objectives. Recommendations and implications for the future study and plant breeding are emphasized.

2   LITERATURE REVIEW

2.1   Background

This chapter reviews the importance of maize and the combining ability of pro-vitamin A (PVA) and quality protein maize (QPM) lines for grain yield. It also reviews literature on general progress that has been made in maize breeding, importance of secondary traits on grain yield through use of correlation and path coefficient analysis, breeding methods for combining genes and heritability of the traits. The chapter provides the basis for the study of combining ability of PVA and QPM inbred lines.

2.2   Importance of maize

Maize is a major crop in sub-Saharan Africa including South Africa. The maize grain is the principal food security crop for millions who live on the continent. It is widely grown in a range of agro-ecologies, from the sea level at the coastal Dar es Salaam, Mombasa and Mozambique on the east coast and at medium altitude in Zimbabwe, Zambia and Malawi and above 1800 m altitude in the highlands of Kenya and Ethiopia, among many countries that grow maize in Africa. It plays an important role in farming systems and is grown in rotations with legumes such as common beans and soya bean throughout the region. It is an important source of energy, lipids, minerals, protein and vitamins (Menkir et al., 2008). Maize has many uses, and these include making of bread, tortillas, snacks, porridge, *sadza* (thick porridge), home brews and breakfast cereals. In the eastern and southern African region, yellow maize is manly used as an industrial raw material and for feeding animals due to the high levels of protein and at times carotenoids. However, people in this part of Africa prefer the white maize grain which is basically tasteless. Yellow maize is not liked and is therefore fed to animals. This is because during cooking of the yellow maize, the degradation of carotenoids produces a strong aroma that is not desired by the consumers in the region (Pillay et al., 2011)

Production of maize varies between countries. This is explained by differences in area and yield. The data in Tables 2.1 and 2.2 show maize production in South Africa compared to the rest of Africa and other global players in the maize industry.

Table 2.1   Maize production data from the 19 twenty maize producers in the world

Country	Area harvested (hectares)	yield (hg ha-1)	Production(tonnes)
USA	35,478,012	99,695	353,699,441
China, mainland	36,318,400	60,159	218,489,000
Brazil	15,279,652	52,536	80,273,172
Argentina	4,863,801	66,037	32,119,211
Ukraine	4,826,900	64,119	30,949,550
India	9,500,000	24,516	23,290,000
Mexico	7,095,630	31,941	22,663,953
Indonesia	3,821,504	48,441	18,511,853
France	1,849,600	81,385	15,053,000
Canada	1,480,400	95,878	14,193,800
South Africa	3,250,000	38,418	12,486,000
Russian Federation	2,321,860	50,110	11,634,943
Romania	2,523,455	44,969	11,347,633
Nigeria	5,200,000	20,000	10,400,000
Italy	908,114	86,989	7,899,617
Philippines	2,563,635	28,776	7,377,076
Hungary	1,254,000	53,627	6,724,800
Ethiopia	2,069,267	32,253	6,674,048
Turkey	660,000	89,394	5,900,000

Source: (FAOSTAT, 2013)

Table 2.2   Maize production data from the top 20 maize producers in Africa

Country	Area harvested (Ha)	Yield (Hg/Ha)	Production (tonnes)
South Africa	3,250,000	38,418	12,486,000
Nigeria	5,200,000	20,000	10,400,000
Ethiopia	2,069,267	32,253	6,674,048
Egypt	750,000	77,333	5,800,000
United Republic of Tanzania	4,120,269	13,000	5,356,350
Malawi	1,676,758	21,708	3,639,866
Kenya	2,028,202	16,719	3,390,941
Uganda	1,000,000	27,480	2,748,000
Zambia	997,880	25,382	2,532,800
Ghana	1,023,459	17,240	1,764,477
Cameroon	832,400	19,787	1,647,036
Mozambique	1,700,000	9,594	1,631,000
Burkina Faso	913,630	17,353	1,585,418
Angola	1,635,980	9,467	1,548,750
Mali	640,526	23,461	1,502,717
Democratic Republic of the Congo	1,750,000	7,846	1,373,000
Benin	973,453	13,825	1,345,820
Zimbabwe	900,000	8,878	799,000
Togo	550,000	12,593	692,610
Guinea	500000	13440	672000

Source: (FAOSTAT, 2013)

Production of adequate maize grain remains a challenge in Africa. As shown in Tables 2.1 and 2.2, the only sub-Saharan countries that are in the top 19 of world maize producers are South Africa, Nigeria and Ethiopia. Nevertheless, South Africa is still facing maize shortage. Recently it has been reported that South Africa is being forced to import more maize due to the drought it has been facing (BFAP, 2016). Cultivation areas have also been increased over the years in an attempt to meet growing demand due to population increase. The yields in Africa are considerably low due to the negative effect of drought and low soil fertility (FAO, 2010). Among other factors, soil nutrient depletion and soil degradation have been commonly recognized as the main reasons for persistent low grain yields (Folberth et al., 2013). The development of new, stable maize hybrids is one of the major ways that is being used to increase grain yield and food supply in Africa. Most countries do not produce adequate grain for home consumption. For example, the gaps in maize production and consumption in Zimbabwe is explained by imports of grain, during 2005 to 2012 (Figure 2.1).

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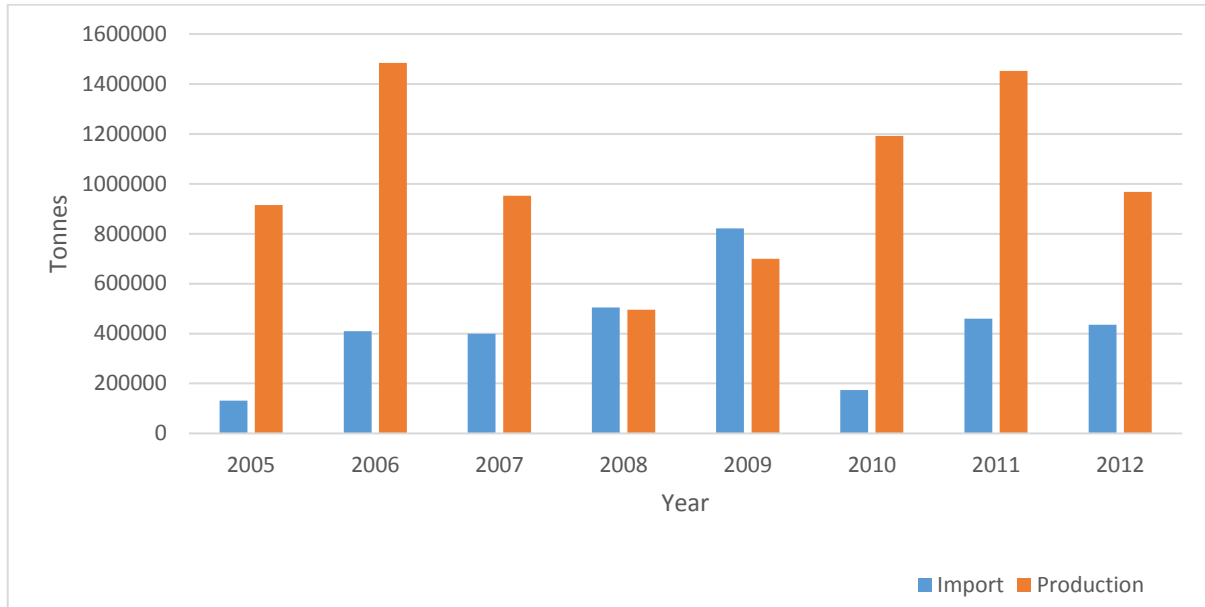
Figure 2.1 Maize production and imports for Zimbabwe
Source: (FAOSTAT, 2015)

As can be clearly seen from Figure 2.1, year 2006 characterises the highest maize production output of 1,484,830 tonnes while 2008 had the lowest output of 496,000 tonnes and imports exceeded the domestic demand. In the year 2009, the imports were also higher than the total production but the yields had picked up from 2008. Figure 2.1 shows evidence that Zimbabwe cannot produce enough maize to meet the demands; it is always relying on grain imports over the years. Given the importance of maize in poultry and pig industry as an input, this maize deficit poses a significant negative effect on the industry. The same can be said for South Africa as its main source of maize imports is Zambia. The local poultry producers are forced to raise their prices depending on the price of imported maize.

2.3 Enhancing nutritional density in maize

The nutritional value of maize is a major constraint in its use for consumption by humans and animals hence the necessity to enhance nutritional density in maize. Biofortification provides a cost-effective, long-term and sustainable way of delivering more micronutrients (Saltzman et al., 2013). Since raw material for pig and poultry feed include vitamins, lysine and other proteins, it is important to breed for high yielding maize with quality protein and pro-vitamin A as this will largely reduce the cost of inputs for the feed. Biofortified foods do not contain all required nutrients per day as supplements but they assist by increasing the daily sufficiency of micronutrient uptake among individuals throughout the lives of humans (Bouis et al., 2011).

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It is crucial to improve both quantity and quality of mineral nutrition in maize grain. In normal maize (both yellow and white) the protein constitutes less than 10% of the kernel. In normal maize, approximately 50 – 70% of the endosperm proteins are of prolamin type. These types of proteins lack the essential amino acids, lysine and tryptophan (Vasal, 2000). The discovery of the recessive opaque-2 (*o2*) (Mertz et al., 1964) led to development of QPM varieties with enhanced levels of lysine and tryptophan. This gene has been thoroughly investigated and exploited in breeding and genetic analysis since its discovery. The problem that was being faced in the early development was due to the negative pleiotropic effects of the *o2* gene on many traits of agronomic importance. Some of the undesirable effects included soft texture, low kernel density, *o2* reduced grain weight, slow dry down and high susceptibility to insects (Lambert et al., 1969;Yau et al., 1999). It was later demonstrated, that the adverse effects of the gene could be overcome through selection for favourable polygenes (modifier genes) (Vasal et al., 1980). The genotypes with modified *o2* gene were then given the name, quality protein maize (QPM) (Vasal, 2000). These genotypes have been introduced into production systems in many tropical and sub-tropical countries. Accumulated evidence has shown that modification of the endosperm in *o2* maize is complex with many genetic factors playing roles in amino acid levels and endosperm texture (Gutiérrez-Rojas et al., 2010). Genetic variation is therefore, one of the most important variables contributing to the variation observed so far.

Breeding for maize with improved pro-vitamin A concentrations is necessary because, although all yellow maize have carotenoids, the proportion of pro-vitamin A (β-cryptoxanthin, α- and β-carotene) is very small (Lozano-Alejo et al., 2007). Maize kernels exhibit considerable phenotypic variation for carotenoid profile (Burt et al., 2011). Classification of the maize endosperm colour mutants led to the discovery of the recessive gene, *Phytoene synthase* (y1), which is responsible for the white endosperm grain. According to Pavlov et al. (2015), white endosperm kernels resulting from the recessive y1 gene provides very insignificant quantities of carotenoids compared to orange and yellow endosperm grain. High pro-vitamin A levels resulted from lycopene ε-cyclase (*lcyE*) and *β-carotene hydroxylase 1* (*crtRB1*) alleles (Harjes et al., 2008). Variation of carotenoid content in maize is therefore attributed to the many genes that control the trait.

2.4   General progress in maize breeding

Maize was first domesticated by farmers and they have developed many landraces which are adapted to multiple environments (Grobman et al., 1961;Goodman and Brown, 1988). In the

19th century, farmers managed to develop open pollinated varieties (OPVs) for U.S Corn Belt states within a few decades of settlement of the region (Hallauer and Miranda, 1988). The grain yield of maize has been increasing progressively since the beginning of its domestication (Russell, 1991). The change from open pollinated maize varieties to double – cross hybrids in early 1920s, and their replacement by the single cross hybrids in the 1960s, gave rise to considerable gains in yield (Crow, 1998). The open-pollinated maize varieties had lower grain yield compared to the hybrid maize. The word heterosis was first introduced by Shull (1914) as cited by Crow (1998) which means "stimulation of heterozygosis". The current study focus is on developing superior single cross maize hybrids which are characterised as high yielding, rich in pro-vitamin A and quality protein traits.

2.5 The role of secondary traits in breeding

Plant breeders aim at developing adaptable and high yielding maize hybrids that are also preferred by the farmers. Grain yield is therefore the most important objective in any breeding programme and it is essential to know association with other traits (Malik et al., 2005). Grain yield is a complex quantitative trait that is controlled by many genes and it is associated with various agronomic, morphological and physiological traits (Stevanović´ et al., 2012). Its inheritance is highly influenced by the environment and therefore its heritability is variable. It is important to have knowledge of the secondary traits that have significant association with grain yield because indirect selection of these traits can help improve the yield potential of maize hybrids (Ojo et al., 2006). This would help the breeder to know which trait to improve or compromise depending on the nature of its association with grain yield. Even though the inheritance of these economically important traits is complex and they are sensitive to environment, their heritability is high and this makes them easy to select. Traits such as anthesis date, silking date, anthesis-silking interval, cob weight, plant height and ear height have been reported to have high heritability (Shanthi et al., 2011;Begum et al., 2016;Mani and Deshpande, 2016). Secondary traits that have been targeted in maize breeding programmes include short anthesis-silking interval, ear prolificacy, tassel branches, plant height (Bekavac et al., 2007), ear height, ear length and grain weight. These traits can either directly or indirectly influence grain yield.

2.5.1   Correlation Analysis

Genotypic and phenotypic correlation coefficients between different plant traits gives information that can be used to determine the degree of their associations in determining

genetic advance (Yousuf and Saleem, 2001). Hallauer and Miranda (1988) reported that ear length and kernel traits are crucial components of maize yield because they showed positive correlation with grain yield.

Kebede (1989) reported positive and significant correlations of grain yield with number of kernels and thousand kernel weights. Positive and significant correlations of grain yield with ear diameter, number of kernels per row and plant height were also found by Dass et al. (1990), Hadji (2004) and Dagne et al. (2008) found positive and significant correlations of grain yield with thousand kernel weight, ear length, ear height, ear diameter, plant height and number of kernels per row. Similar results were reported by Pixley et al. (2011). They found positive and significant correlation of ear height with grain yield. Tulu (2014), also found positive and significant phenotypic associations of grain yield with ear length (r=0.45), plant height (r=0.58) and ear height (r=0.46). Tiwari et al. (2012) observed a significant correlation (r = 0.49) between the kernel colour and total carotenoid concentration. The results mentioned above show overall significant positive correlations between kernel traits and other traits with grain yield and this shows that indirect selections for grain yield can be achieved through these secondary traits.

In contrast, Betran et al. (2003) reported a negative and significant phenotypic correlation between anthesis date and grain yield. A negative and significant correlation between grain yield and silking date was also observed (Hadji, 2004). Tulu (2014) also found negative and significant correlation of grain yield with silking date (r=-0.29), anthesis date (r=-0.27) and anthesis-silking interval (ASI) (r=-0.18). This shows that synchronisation of pollen shed and silking is important in attaining high grain yield. Bekavac et al. (2007) emphasised on the importance of shorter ASI because longer ASI may result in low grain fill resulting in lower yields.

2.5.2 Path coefficient analysis

The concept of path coefficient analysis was first developed by Wright in 1921. Path coefficient, which is a standard partial regression coefficient, measures the direct and indirect effects of one trait on another trait. It allows the partitioning of a correlation coefficient into direct and indirect effects components (Dewey and Lu, 1959). Dewey and Lu (1959) also highlighted that it describes the relative significance of each trait involved in contributing to the ultimate trait which is, yield.

The purpose of this method is to partition a correlation coefficient into components of indirect and direct effects. Breeders make use of this method when dealing with a complex trait like yield which is difficult to improve directly but rather, through an indirect selection for the component traits involved in the pathway leading to the formation of the complex trait. Dewey and Lu (1959), as cited by Rauf et al. (2004) stated that selection criteria for complex traits in many crop species, have been developed using path coefficient analysis. It has been widely applied in many crops like maize (Adesoji et al., 2015; Maphumulo et al., 2015), wheat (Okuyama et al., 2004) and several others. Presence of positive and significant correlations between grain yield and its component traits has been reported by many researchers. Adesoji et al. (2015), Sharifai et al. (2006) and Tulu (2014) reported that grain yield was positively and significantly associated with cob weight, kernel rows per cob, cob diameter, cob length, 100-grain weight and plant height. Maphumulo et al. (2015) conducted research that involved path analysis of 16 traits on yield grain. Of the 16 traits, ear prolificacy had the highest direct and positive effect on grain yield, anthesis date had the highest direct negative effect on grain yield and silking date had the highest indirect negative effect on grain yield through anthesis date. Amini et al. (2013), reported a high and positive direct effect of plant height on grain yield. Tulu (2014) reported positive direct effects of plant height (0.22), thousand kernel weight (0.15) ear height (0.03) and ear length (0.02), on grain yield. Similar results were reported by Hadji (2004) that emphasised positive and direct effects of ear length, ear height and thousand kernel weights on grain yield.

2.5.3 Heritability

Heritability is the proportion of observed variability which is due to genetic causes. It is used to measure quantitative traits and is mainly used to estimate the expected response to selection in a population (Zavala, 2008). It can be expressed as a fraction or as a percentage. If heritability is 100%, phenotypic value is a good estimator of genotypic value and response to selection would be high. Heritability of zero means that the observed variation is mainly due to the environment and the genotype by environment interaction. There are two types of heritability estimates, namely, broad and narrow sense. The ratio of genetic variation to the total phenotypic variation is referred to as broad sense heritability [H^2 = (VA +VD) / (VA +VD + VE)] (Kearsey and Pooni, 1996). Sesardic (2005), defined it as the proportion of phenotypic variation that is attributed to genetic variation and is important in breeding programmes. The second type of heritability is called narrow sense heritability (h^2 = (VA) / (VA +VD + VE), which measures the proportion of observed variability due to the additive effects of genes to

the total phenotypic variance (Mani and Deshpande, 2016). This type is more important because it tells the extent to which a trait is passed from parent to offspring. Narrow sense heritability is always smaller than broad sense heritability because it excludes dominance variance. Heritability helps plant breeders in the choice of selection procedures (Falconer and Mackay, 1996). It allows breeders to allocate resources for effective, cost-effective selection of the desired characteristics, as well as to achieve maximum genetic gain in a small period of time.

Variance components from the analysis of variance (Cortés-Olmos et al., 2015) can be used to estimate heritability. The magnitude of estimated heritability depends on, a) the population being studied, which determines the genetic variation, the more diverse the parents are the more the genetic variation; b) the environment at which the study is being carried out; c) the experimental design, which determines the number of replications and management practices; d) a large sample size which is able to capture all genotypes. The choice of mating design and random model to be used is also useful in obtaining proper estimates of variation. The estimates of variance depend on the mating design that is used.

Tiwari et al. (2012) reported high broad sense heritability (96.6% and 95.6%) of total carotenoids for two different sites. This showed that genetic factors play an important role in determining the carotenoid concentration in maize. Similarly, Chander et al. (2008), reported a high broad sense heritability of 85% for total carotenoid content in maize. High heritability for pro-vitamin A has been accredited to the involvement of a few major genes in the carotenoid biosynthetic pathway (Menkir and Maziya-Dixon., 2004; Pfeiffer and McClafferty, 2007). Bello et al. (2012) reported high heritability estimates (>50%) for grain yield, plant height, number of ears, ear height, silking date, anthesis date, ear prolificacy and ear position. Shanthi et al. (2011) found low heritability estimates (<50%) for grain moisture content, ASI, ear length and number of plants and high heritability of over 85% for tryptophan content, ear length, plant height and 100-grain weight. In a study carried out by Prakash et al. (2006), high heritabilities were observed for grain yield per plot (98.8%), plant height (98.7%), protein content (98.4%), protein yield (98.4%) and days to 50% tasseling (86.9%).

The breeding process depends on genetic variation, which is in the population, as well as many other factors. A more diverse population gives higher heritability. If environmental variation is very low, heritability is increased because most of the phenotypic variation will be

due to genetic factors. In case of high environmental variation, the heritability of a trait will be low (Rao and Gu, 2008).

2.6   Genotypic and phenotypic coefficients of variation

Heritability cannot be used as the only selection criteria. Most secondary traits for grain yield are complex in inheritance since they are controlled by many genes interacting with the environment. The study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is helpful in determining the relative amount of phenotypic and genotypic variations, respectively. The magnitude of the coefficients of variation of a parameter to be selected for breeding programme is very important, especially the GCV. High value of CV illustrates high variability among the tested sample whereas low CV depicts low variation. Environmental effect can also be indicated by the differences between GCV and PCV. Even though GCV indicates the presence of genetic variation, heritability and genetic advance helps to determine the amount of the heritable portion (Rao and Rao, 2015).

2.7   Adaptability of maize hybrids

Adaptability studies provide a detailed description about how a genotype can perform under different environmental conditions and this helps breeders to identify genotypes with phenotypic stability (Cruz et al., 2004). The adaptability of maize landraces to different environments is mainly attributed to their wide genetic variability Ceccarelli (1994). The description of a genotype's performance under different environmental conditions can be used to identify genotypes with superiority in adaptation. According to Tolenaar et al. (1994), maize breeding programmes over time have made it possible to improve stability since the modern varieties have better tolerance to diseases and stress than the older ones. Nevertheless, the climate is always changing and resistance to certain diseases has a short-lived period due to mutation in the pathogen that breaks the resistance. There is still inadequate knowledge on the environmental genotype responses of plant components or on quality or yield. Sprague and Federer (1951), presented evidence that double cross hybrids exhibit better stability of performance than single cross hybrids. It is also possible for the single cross to be more phenotypically stable than the double and the three-way cross hybrids.

2.8   Line by tester analysis

Line by tester is a mating design that was designed by Kempthorne in 1957, and is defined as the mating between a line and a common pollen parent such as, an inbred line or a single cross. Full-sib progenies and half-sibs are produced from crossing of all the lines to each of the testers. It gives us information on GCA, of the lines and SCA of each cross effects as well as their hybrid combination (Sharma et al., 2004;Sharma, 2006;Farhan et al., 2012)

Line x tester analysis is the interaction between the lines and testers for dependant variables in statistical model (Packer, 2007). If line x tester interaction is significant, it shows that the tester determines the ranking of the experimental lines, therefore choice of a suitable tester is important when evaluating new germplasm lines (Aly et al., 2011). The testers can have a narrow or wide genetic based background and they may be related or not to the lines under evaluation. Line x tester can be used to obtain desirable genes from exotic lines, which are lines from other countries and have adaptability to local conditions (Nduwumuremyi et al., 2013). It can also be used to estimate different types of gene action in the expression of quantitative traits (Rashid et al., 2007). According to Sharma et al. (2004), line x tester design has been and continues to be widely used in quantitative genetic studies in maize.

2.9   Combining ability analyses

The main aims of breeding programmes are to distinguish the lines that can be used in future crosses as parents and to determine the best performing lines for commercial use. Combining ability is defined as the ability of an inbred line to transfer desirable characteristics to the hybrid. According to, Allard (1960), combining ability is an estimation of the value of the genotype based on their offspring performance in a certain mating design. Therefore it is measured through progeny testing. As stated by, Sprague and Tatum (1942), general combining ability (GCA) of a line is defined as the deviation of mean performance of a line from the mean of all crosses. General combining ability evaluates the additive effects of a line which determines whether it is a good line or not. They also defined specific combining ability (SCA) as the deviation of each cross from the expected value to greater or lesser extent.

SCA evaluates the non-additive gene action and is used in the identification of superior hybrids. GCA is more important than SCA, but they are still used together (Hallauer et al., 2010). GCA is considered as the main effect while, SCA is an interaction effect (Kulembeka et al., 2012). Parental choice based on SCA effects has limited value in breeding programmes.

GCA is more effective and is used in selection of parents based on their progeny performance, commonly in the F1 generation though it can be used in later generations. Low GCA value (positive or negative) shows that the mean of a particular inbred line in crossing with all the parents vary, to a less extent, from the grand mean of all the crosses that would have been made. On the other hand, a high GCA value (negative or positive) tells the breeder that the mean of the parent is superior or inferior to the grand mean which, shows evidence of a high intensity gene flow from the parents to the offspring (Franco et al., 2001).

Combining ability analyses are usually used in maize breeding programmes to determine GCA and SCA information from a population for genetic diversity evaluation, hybrid development, heterosis estimation, inbred line selection and heterotic pattern classification (Fan et al., 2008). Significant GCA and SCA effects for β-carotene were reported by (Pavlov et al., 2015). (Suwarno et al., 2013), found non-significant SCA effects and the GCA effects were predominant. This indicated that additive gene action mainly accountable for determining β-carotene concentration. Machida (2008), found highly significant SCA effects for grain yield and anthesis date and the GCA effects were highly significant for protein content, tryptophan content, anthesis days and kernel modification. The study also reported that SCA effects prevailed more than GCA effects, which showed that non-additive gene action was more important for grain yield. In their study with QPM inbred lines, Bhatnagar et al. (2004) also found that SCA effects were significant and more essential than GCA effects in the genetic control of grain yield. Likewise, Long et al. (2004), reported that SCA effects were more important than GCA effects although they were both significant. These findings imply that pro-vitamin A and quality protein traits are highly heritable. This helps breeders to improve maize lines containing QPM and PVA for other traits, such as grain yield.

2.10 Conclusion

A lot of effort has been put into the improvement of maize quality and yield. The literature review showed that there has been success in breeding high yielding maize hybrids with high QPM and PVA. These two traits are controlled by a different number genes; QPM is controlled by a recessive gene whereas PVA is controlled by many genes. The literature review also indicated high correlation between secondary traits and yield. Most of these traits have been reported to be highly heritable and this is attributed to the considerable genetic variability in various maize germplasm. These traits can therefore be exploited in the improvement of grain yield in these hybrids. Both QPM and PVA have been shown to have

high heritabilities and genetic gains have been attained for both QPM and PVA, which makes it easy to breed for them. This was also supported by literature that showed that additive gene action was mainly accountable for determining β-carotene concentration and protein content. No literature on combining QPM and PVA maize lines is available in literature. This study will determine the best PVA and QPM inbred lines that combine well for grain yield and its secondary characteristics. The following chapter outlines the steps that were taken to conduct this research.

3   GENERAL MATERIALS AND METHODS

3.1 Introduction

Singe cross hybrids were developed at the University of KwaZulu-Natal. Quality protein and pro-vitamin A maize lines were used to develop the hybrids. This chapter outlines all the procedures that were done during the study. Development of germplasm and experimental designs for each trial are outlined in chapters 4 and 5.

3.2 Crop husbandry

Weeds and pests were controlled through the use of chemical sprays. Pre – and post – emergence herbicides were used namely, basagran, gramoxone and troopers, to control broad leaves and annual grasses. Manual weeding was also carried out when it was required. Basal fertilizer NPK (2:3:4) was applied at the rate of 250 kg/ha. It was applied before planting, was done and covered to avoid damage to the seed from direct contact. At four weeks, top dressing was applied in the form of limestone ammonium nitrate (LAN) (28% nitrogen). The trials were rain fed and supplemented by irrigation especially during planting at Ukulinga as there was little rain at the beginning of the season.

3.2.1   Data collection

Standard procedures of CIMMYT were used to measure the maize traits (Magorokosho, 2009).The description of the traits is listed below. Harvesting was done at Cedara on 16 May 2016. At Ukulinga harvesting was done on 17 and 18 May 2016. No disease rating and scoring was done because diseases did not occur.

i)   **Anthesis date (AD):** measured through visual assessment, from planting date to the date when 50% of the plants in a plot would have shed pollen.

ii)   **Silking date (SD)**: measured through visual assessment from planting date to the date when 50% of the plants have produced 2-3 cm long silk.

iii)   **Anthesis -silking interval (ASI)** = date of silking - date of anthesis.

iv)   **Ear height (EH)**: measured from the ground level to the insertion of the highest ear in the stem.

v)   **Number of kernel rows per ear (GRN)**: counted from three randomly taken ears and the average value was used as kernel rows per ear.

vi) **100-grain weight (GW100)**: measured by randomly taking 100 kernels from each plot which was weighed using sensitive balance.

vii) **Grain moisture content (MOI)**: measured using grain moisture meter.

viii) **Plant height (PH)**: measured by averaging height of five randomly selected plants. The height of each plant was measured in cm from base of the plant to the first tassel branch.

ix) **Grain yield (tons/ha) (GY):** determined from field weight and adjusted to 12.5% grain moisture content, shelling percentage and plot size.

x) **Plant stand (PS)**: plants per plot were recorded at harvest.

xi) **Field weight (FW):** was determined by weighing all the cobs per plot.

xii) **Number of ears per plot (NE):** ears were counted at harvest.

xiii) **Root and stem lodging (RL and SL):** were determined by counting the number of plant that had lodged.

xiv) **Shelling percentage (SH) :** (grain weight-cob weight)/cob weight x 100

xv) **Grain texture (TEX):** a scale of 1 to 5 was used (1= flint, 5=dent)

xvi) **Total lodging percentage (TL %):** was recorded.

3.3 Data Analysis

Data for grain yield and other agronomic traits from individual sites were analysed for variance. Line by tester and correlation analyses were performed using Genstat 17th edition. Descriptive statistics for the data was analysed in BMS. SAS 9.3 (SAS Institute Inc.) was then used for path coefficient analysis.

3.3.1 Mean performance

Mean performance for each hybrid was estimated by analyzing the performance of all the hybrids for every trait.

3.3.2 Grain yield

Grain yield was calculated from field weight which was measured as cob weight, adjusted to 12.50 % grain moisture content and shelling percentage which was determined from the average of shelling percentage of five randomly taken cobs.

$$\text{GYG} = \frac{\text{Field weight (kg)} * 10000 \text{ (m}^2) * (100 - \text{MOI}) * \text{Shelling \%}}{1000 \text{ (kg) Plot area (m}^2) * (100 - 12.5)\%}$$

GYG = Calculated grain yield per ha

MOI = measured grain moisture content at harvest

Shelling % = average shelling % determined from five randomly taken cobs from each plot: (grain weight of 5 cob/ cob weight of five cobs)/ 5

3.3.3   Analysis of Variance

Table 3.1 is showing the interaction of the hybrids by the environment.

Table 3.1   ANOVA table for genotype by environment interaction

Source of variation	Degrees of freedom	Mean sum of squares
Site	s -1	$\sigma^2 e + \sigma^2 b(r*l) + g\sigma^2 r(l) + rg\sigma^2 l$
Rep/site	s(r-1)	$\sigma^2 e + \sigma^2 b(r*l) + g\sigma^2 r(l)$
Block/rep/site	rl(b − 1)	$\sigma^2 e + \sigma^2 b(r*l)$
Genotype	g -1	$\sigma^2 e + r\sigma^2 gl + rl\ \sigma^2 g$
Genotype × site	(g-1)(s-1)	$\sigma^2 e + r\sigma^2 gl$
Error	s(g-1)(r-1)	$\sigma^2 e$

3.3.4   Line by tester analysis

3.3.4.1   ANOVA at single site

$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$

$Y_{ijkl} = \mu + a_l + r_{kl} + b_{mkl} + g_i + g_j + s_{ij} + \varepsilon_{ijklm}$

Y_{ijkl} is the observed value from each experimental unit

μ is the mean of the population

r_{kl} is the effect of replication within a site, k = 1 ...2, l = 1…5;

b_{mkl} is block effect within each replication within each site, m = 10

g_i is general combining ability (GCA) for the ith parental line, i = 1 … 12 in Exp1, i = 1 … 26 in Exp2;

g_j is the GCA effect of jth tester, j = 1… 4;

s_{ij} is the specific combining ability (SCA) for the ij^{th} F1 hybrid

ε_{ijklm} the environmental error associated with each observation

3.3.4.2   ANOVA across sites

Line by tester analysis was done in Genstat using the model:

$$Y_{ijkl} = \mu + a_l + r_{kl} + b_{mkl} + g_i + g_j + s_{ij} + (ag)_{il} + (ag)_{jl} + (as)_{ijl} + \varepsilon_{ijklm}$$

Y_{ijkl} is the observed value from each experimental unit

μ is the mean of the population

a_l is the location effect, l = 1 … 5;

r_{kl} is the effect of replication within a site, k = 1 ...2, l = 1…5;

b_{mkl} is block effect within each replication within each site, m = 10

g_i is general combining ability (GCA) for the ith parental line, i = 1 … 12 in Exp1, i = 1 … 26 in Exp2;

g_j is the GCA effect of jth tester, j = 1… 4;

s_{ij} is the specific combining ability (SCA) for the ij^{th} F1 hybrid

$(ag)_{il}$ is the interaction effect of ith line and l^{th} site

$(ag)_{jl}$ is the interaction effect of jth tester and l^{th} site

$(as)_{ijl}$ is the interaction effect of the ith hybrid and l^{th} the site

3.3.5   Estimation of GCA and SCA effects

The estimation of GCA and SCA was done as follows (Singh and Chaudhary., 1985).

$GCA_L = (Y_L/rl) - \mu$

$GCA_T = (Y_T/rt) - \mu$

Predicted yield $= \mu + GCA_L + GCA_T$

Where

GCA_L = General combining ability effects of lines

GCA_T = General combining ability effects of tester

Y_L = the grand total of all the lines mated with all testers

Y_T = the grand total of all the testers mated with all lines

μ = grand mean

r = the number of replication

l = the number of lines

t = the number of testers

GCA can be used to predict yield with reference to the population under study and the calculation is done as:

Predicted yield $= \mu + GCA_L + GCA_L$

Predicted yield can be under estimated because dominance gene may be present

SCA = observed – predicted yield

3.3.6   Appropriate t test

The significance of the GCA and SCA effects was determined using two-tailed t-tests which were calculated as follows

t_{calc} for GCA effects= $\frac{GCA\ effects}{SE\ of\ GCA}$

SE of GCA for testers = (MSE/r x t)$^{1/2}$

SE of GCA for lines = (MSE/r x l)$^{1/2}$

t_{calc} for SCA effects = $\frac{SCA\ effects}{SE\ of\ SCA}$

SE of SCA effects = (MSE/r)$^{1/2}$

MSE = mean square error from the analysis of variance table.

3.3.7   Heritability

Heritability between environments was calculated as follows: (Hallauer and Miranda, 1988)

H^2 = {$\sigma^2 g$/ ($\sigma^2 e$/re) + ($\sigma^2 ge$/e) + $\sigma^2 g$] × 100

Heritability within an environment was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage (Darbeshwar, 2000)

H^2 = $\sigma^2 g$/ ($\sigma^2 e$/r) × 100

Where $\sigma^2 g$ = genotypic variance, σ = environmental variance, $\sigma^2 ge$ = genotype by environment interaction variance, $\sigma^2 p$ = phenotypic variance = $\sigma^2 g$ + σ^2+ $\sigma^2 g$ e, r = number of replications, e = number of site.

3.3.8   Coefficients of variation

The phenotypic (PCV), environmental (ECV) and genotypic coefficients of variation (GCV) were calculated based on the formula in Singh and Chaudhary (2004)

$$PCV = \left[\frac{\sqrt{\sigma_p^2}}{\chi} \right] * 100$$

$$GCV = \left[\frac{\sqrt{\sigma_p^2}}{\chi} \right] * 100$$

Where σ_g^2=genotypic variance

σ_p^2=phenotypic variance

χ=overall mean

3.3.9   Genetic advance

Genetic advance was calculated using the following formula (Singh and Chaudhary, 2004)

$$GA = i * \sqrt{\delta_p^2 * H^2}$$

Where i = selection intensity, σ_p = phenotypic standard deviation and h^2 = heritability in a broad sense

Estimation of genetic advance as a percentage of mean was calculated as described by (Souza et al., 2009) as follows:

GA (%) = $\frac{GA}{\chi}$ x 100, where GA = genetic advance and χ= grand mean.

3.3.10   Estimation of Realised Genetic Gains

Realised gains were calculated according to the equations adapted from Singh and Chaudhary (1979):

- Realized gains (RG1): genetic gains relative to population mean.

$$RG1 = \left(\frac{MS - MP}{MP}\right) * 100$$

- Realized gains (RG2): genetic gains relative to the check.

$$RG2 = \left(\frac{MS - MC}{MC}\right) * 100$$

3.3.11   Genotypic and phenotypic coefficient of variation

Genotypic (GCV) and phenotypic (PCV) coefficient of variation were calculated for all the quantitative traits using the following formula (Singh and Chaudhary, 2004)

GCV (%) = $(\sqrt{\sigma^2 g}/\chi) \times 100$

PCV (%) = $(\sqrt{\sigma^2 p}/\chi) \times 100$

Where $\sigma^2 g$ = genotypic variance, $\sigma^2 p$= phenotypic variance and χ = grand mean of the character.

3.3.12   Path coefficient analysis

Path coefficient analysis was calculated to determine the direct and indirect effects using the PATHSAS (Cramer, 2000) in SAS version 9.3 (SAS Institute Inc., 2013).

4 PATH COEFFICIENT ANALYSIS AND COMBINING ABILITY BETWEEN PRO-VITAMIN-A MAIZE LINES FROM MEXICO AND ADAPTED QUALITY PROTEIN MAIZE LINES FOR YIELD AND SECONDARY TRAITS

4.1 Introduction

Exotic maize germplasm has been used to increase genetic diversity in breeding programmes. Exotic germplasm refers to maize inbred lines that are not adapted to a breeder's environment (Holland, 2004). The use, importance and potential of exotic lines has been emphasised over the years (Hallauer, 1978; Duvick, 1984). The introduction of genetic material from foreign sources into locally adapted elite crop gene pools whilst preserving their productivity is not easy. On the other hand, for example, the tropical germplasm being introduced may be carrying some genes for adaptation in the temperate environment.

The current study was carried out to determine the combining ability between tropical Pro-vitamin A maize lines and adapted quality protein maize inbred lines. Relationship of grain yield with its secondary traits was also evaluated.

4.2 Materials and methods

Chapter 3 gives a full description of how the study was executed. This section outlines the materials used for this specific trial, the site and the experimental design used.

4.2.1 Germplasm development

4.2.1.1 Parent material

The germplasm comprised of 26 exotic lines, one PVA tester and four QPM testers. QPM lines were obtained from Quality Seeds (Pty) Ltd. The exotic lines were obtained from the CIMMYT breeding programme in Mexico. The lines are listed in Tables 4.1 and 4.2.

Table 4.1   Exotic parental lines used in the formation of the experimental hybrids

Entry	Stock	Name
1	PVAF8-14	DPVAL14
2	PVAF8-15	DPVAL15
3	PVAF8-16	DPVAL16
4	PVAF8-17	DPVAL17
5	PVAF8-18-	DPVAL18
6	PVAF8-19	DPVAL19
7	PVAF8-20	DPVAL20
8	PVAF8-21	DPVAL21
9	PVAF8-22	DPVAL22
10	PVAF8-23	DPVAL23
11	PVAF8-24	DPVAL24
12	PVAF8-25	DPVAL25
13	PVAF8-26	DPVAL26
14	PVAF8-27	DPVAL27
15	PVAF8-28-	DPVAL28
16	PVAF8-29	DPVAL29
17	PVAF8-30	DPVAL30
18	PVAF8-31	DPVAL31
19	PVAF8-32	DPVAL32
20	PVAF8-33	DPVAL33
21	PVAF8-34	DPVAL34
22	PVAF8-35	DPVAL35
23	PVAF8-36	DPVAL36
24	PVAF8-37	DPVAL37
25	PVAF8-38-	DPVAL38
26	PVAF8-39	DPVAL39

Table 4.2   List of PVA and QPM Lines used as testers

Entry	Type
PVAF8-14	QPM-1
PVAF8-15	QPM-2
PVAF8-16	QPM-3
PVAF8-20	QPM-4

4.2.2   Crossing exotic lines with QPM testers

Line by tester mating design was used. Twenty-six exotic lines were crossed to four testers resulting in 104 hybrids but only 68 hybrids had enough seed for the experiment. The 4 testers consisted of four QPM testers. The crosses were done at Ukulinga Research Station, in the KwaZulu-Natal province, South Africa, as shown in Table 4.3.

Table 4.3   Crossing between 26 exotic lines and 4 QPM testers

	Testers			
	QPM1	QPM2	QPM3	QPM4
Lines				
1	×	×	×	×
2	×	×	×	×
3	×	×	×	×
4	×	×	×	×
5	×	×	×	×
6	×	×	×	×
7	×	×	×	×
8	×	×	×	×
9	×	×	×	×
10	×	×	×	×
11	×	×	×	×
12	×	×	×	×
13	×	×	×	×
14	×	×	×	×
15	×	×	×	×
16	×	×	×	×
17	×	×	×	×
18	×	×	×	×
19	×	×	×	×
20	×	×	×	×
21	×	×	×	×
22	×	×	×	×
23	×	×	×	×
24	×	×	×	×
25	×	×	×	×
26	×	×	×	×

4.2.3   Site of study

The field trial was set up at Ukulinga research farm, South Africa (29° 24'E longitude, 30°24' S latitude and altitude of 809 m above sea level). The soils at Ukulinga are loamy clay, fertile and friable with good drainage. Below are figures showing total rainfall and average temperatures that were recorded during the study.
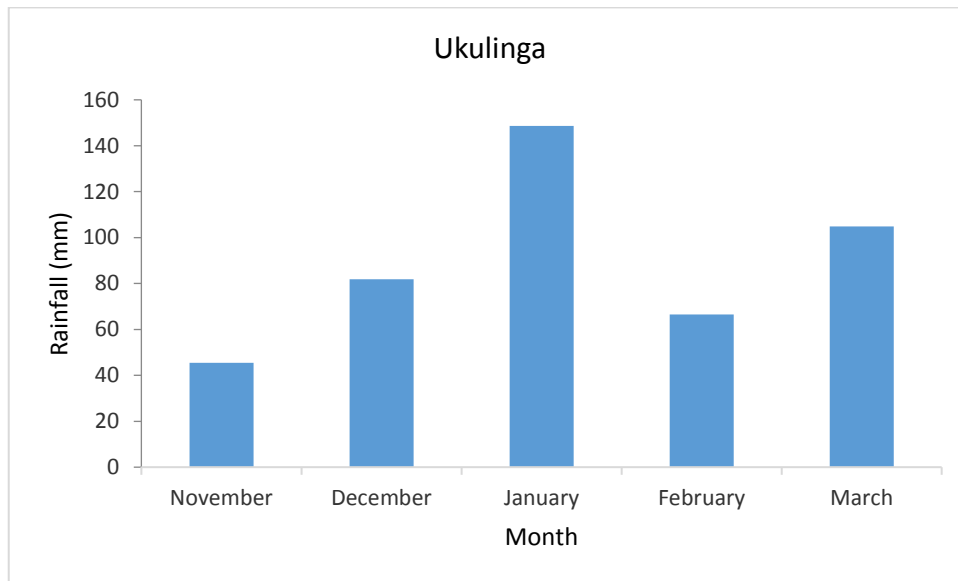
Figure 4.1   Total rainfall for Ukulinga for the duration of the study.
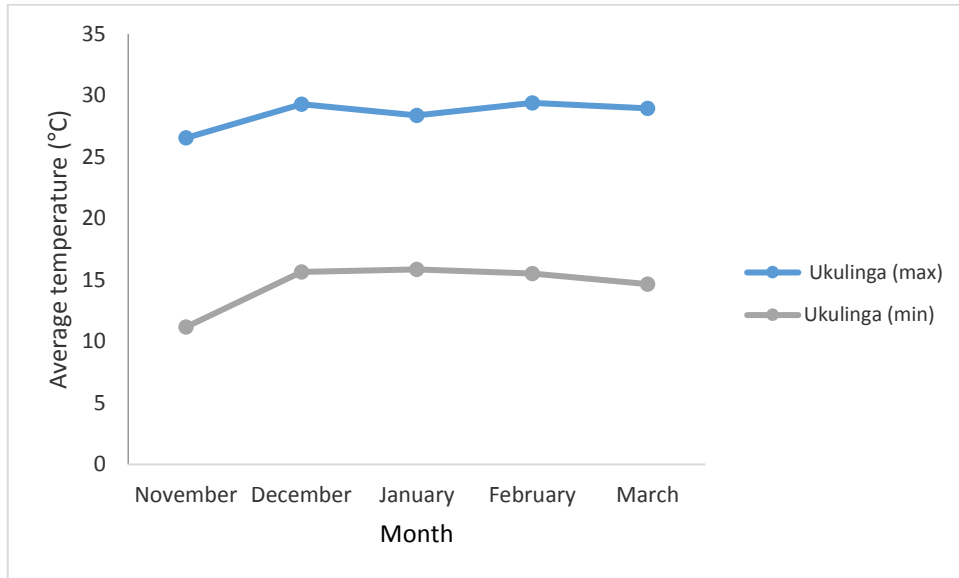
Figure 4.2   Average temperture of Ukulinga the duration of the study.

4.2.4   Experimental design and crop management

There were 70 hybrids which comprised of 1 check (repeated twice) and selected 68 hybrids. The hybrids were evaluated using 7 × 10 row by column design with two replicates at Ukulinga. The plot was 1 row and 5 m long, with inter-row and intra-row spacing of 0.75 m and 0.3 m respectively. Two seeds were planted per station. The planting depth was within the range 3- 5 cm. Thinning was done after the seedlings were fully established leaving only one plant per hill.

4.2.5   Data analysis

Full details of data analyses are given in chapter 3. This section gives information that is specific for this trial.

4.2.6   Line by tester analysis

Analysis of variance was only done for the one site.

4.2.7   Genetic advance

Selection intensity of 1.709 at 11% selection, was used for grain yield and secondary traits to estimate genetic advance

4.3 Results

This section outlines the results of the study acquired through following the procedures described in the previous chapter and preceding sections of this Chapter. The results are presented in the form of tables, and they are described briefly. Statistical estimation such as cultivar superiority is not presented in this chapter.

4.3.1 Genetic variation

Table 4.4 shows that genotype main effects for grain yield, ear position, grain moisture content and shelling percentage were significantly different ($p \leq 0.01$) at Ukulinga. Mean squares for other secondary traits were significantly different ($p \leq 0.001$). Other traits like total lodging percentage, stem lodging, root lodging and plant stand showed non-significant mean squares among the entries. Anthesis-silking interval, root lodging, stem lodging and texture had very high coefficients of variation.

The summary of the descriptive statistics for Ukulinga indicated that the data was significant ($p \leq 0.001$) for the entries for all traits except stem lodging (Table 4.5). Grain yield and plant stand had minimum values of 0.41 t/ha and 4 plants, with maximum of 11.25 t/ha and 22 plants, respectively. Number of ears per plot ranged from 5 to 32 ears. The 100-grain weight had a large range from 3 g to 50 g. Plant and ear height ranged from 1.58 to 3.05 m and from 5.1 to 1.54 m, respectively. Heritability was high ($H^2 > 0.50$) for all the traits except plant stand, stem lodging and total lodging percentage.

Table 4.4   Mean squares for yield and secondary traits for Ukulinga

Source of variation	DF	GY	ASI	AD	SD	EH	EPO	FW	GRN	GW100	MOI	NE	PH	SH	TEX
Replication	1	25.89**	1.21	96.11***	75.78***	9.8	0.00	8.16***	0.03	118.86	0.10	78.75**	1604.80***	4.19	0.11
Rep/Row/Column	18	14.89***	1.98***	10.41***	13.26***	664.40***	0.00*	2.96***	2.00***	91.54**	0.67	41.08***	1678.10***	9.73	4.19**
Genotype	69	7.55**	2.77***	22.0***	29.72***	546.40***	0.00**	1.40***	2.87***	50.7*	1.23**	32.12***	1097.60***	14.29**	4.10***
Residual	51	3.68	0.61	3.39	3.55	133.40	0.00	0.44	0.43	32.35	0.47	9.65	128.60	6.46	1.68
Mean		6.65	-0.49	83.36	82.86	113.95	0.45	3.20	13.09	38.46	16.46	18.28	253.54	82.12	2.11
LSD0.05		3.85	1.57	3.69	3.78	23.19	0.08	1.34	1.31	11.42	1.37	6.24	22.76	5.10	2.60
CV %		28.84	-158.7	2.21	2.27	10.14	8.46	20.81	5.00	14.79	4.15	16.99	4.47	3.09	61.24
SE		1.92	0.78	1.84	1.89	11.55	0.04	0.67	0.65	5.69	0.68	3.11	11.34	2.54	1.30[1]

GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH=Ear height, EPO=Ear position, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=Grain moisture content, NE=Number of ears per plot, PH= Plant height, SL= Stem lodging, SH=shelling percentage, TEX= grain texture
 * p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

Table 4.5   Descriptive statistics of yield and secondary traits for Ukulinga

Trait	SD	Minimum	Maximum	Range	SED of mean	LSD	CV %	Heritability	P value	Sign P
Anthesis silking interval	1.37	-1.00	6.00	7.00	0.12	1.53	-276.96	0.81	0.00	***
Anthesis date	3.77	76.00	97.00	21.00	0.32	3.71	4.53	0.88	0.00	***
Silking date	4.28	75.00	102.00	27.00	0.36	3.91	5.17	0.90	0.00	***
Ear height	20.16	51.00	154.00	103.00	1.70	22.72	17.69	0.81	0.00	***
Ear position	0.05	0.29	0.57	0.28	0.00	0.08	11.04	0.54	0.00	***
Field weight	1.14	0.20	5.60	5.40	0.10	1.36	35.68	0.73	0.00	***
Grain rows	1.36	10.00	16.67	6.67	0.11	1.35	10.37	0.86	0.00	***
GW100	7.05	3.00	50.00	47.00	0.60	11.77	18.34	0.41	0.02	*
Grain yield	2.37	0.41	11.25	10.84	0.20	2.75	36.04	0.75	0.00	***
Lodging %	12.34	0.00	56.25	56.25	1.04	20.98	114.31	0.21	0.14	NS
Grain moisture content	0.93	13.80	19.70	5.90	0.08	1.45	5.67	0.57	0.00	***
Ear number	5.04	5.00	32.00	27.00	0.43	6.70	27.55	0.71	0.00	***
Plant height	28.65	158.00	305.00	147.00	2.42	23.44	11.30	0.90	0.00	***
Plant stand	2.72	4.00	22.00	18.00	0.23	4.48	18.06	0.34	0.04	*
Stem Lodging	1.25	0.00	7.00	7.00	0.11	2.31	148.08	0.15	0.25	NS
Shelling %	3.28	70.68	97.70	27.02	0.28	5.22	3.99	0.56	0.00	***
Grain texture	1.79	1.00	5.00	4.00	0.15	2.65	84.55	0.61	0.00	***2

SD=Standard deviation, LSD=Least significant difference, CV=Coefficient of variation, P=Probability

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %), ns=not significant

4.3.2 Mean Performance of the Hybrids

The hybrids were ranked according to grain yield and the top ten and bottom ten yielding hybrids are shown in Table 4.6. The hybrid that scored the highest was 16XH49. The check, 11C1579, was in the top ten highest yielding hybrids. Hybrids, 16XH49, 16XH45 and 16XH15 performed better than the check, 11C1579.

4.3.1 Line X Tester Analysis

The general ANOVA shown in Table 4.7 shows that the tester main effects were significant ($p \leq 0.01$) for number of ears, ear height and 100-grain weight. However, the line main effects were not significant ($p > 0.05$) for all the traits.

Table 4.6   Top 10 and bottom 10 yielding hybrids at Ukulinga

Rank	Entry	Genotypes	GY	ASI	AD	SD	EH	EPO	FW	GRN	GW100	MOI	NE	PH	PS	SL	SH	TEX
Top yielding hybrids																		
1	49	16XH49	12.98	-1.00	80.66	80.07	126.93	0.47	3.21	12.95	45.28	16.35	14.82	264.19	13.97	0.22	81.05	2.93
2	45	16XH45	11.64	-1.12	80.73	80.09	131.70	0.47	4.34	13.98	42.02	17.08	20.77	272.61	16.72	0.40	82.93	0.55
3	15	16XH15	10.41	-1.00	85.75	84.54	121.75	0.43	4.99	12.95	40.71	16.53	27.16	284.16	15.89	0.56	82.10	1.12
4	69	11C1579	10.37	-0.04	79.12	79.36	108.83	0.41	4.75	13.09	26.28	15.50	20.89	268.90	18.44	2.37	85.31	3.01
5	28	16XH28	10.30	-1.20	86.74	85.76	109.20	0.39	5.01	15.07	40.54	17.61	19.16	278.52	17.27	0.65	82.76	1.13
6	56	16XH56	9.31	-1.07	80.59	79.24	128.75	0.49	4.36	10.97	41.60	15.23	30.30	257.52	19.49	-0.02	83.65	2.84
7	65	16XH65	8.90	-1.05	79.31	78.34	109.64	0.43	4.00	12.76	39.65	16.48	18.26	252.80	16.01	0.12	89.48	5.10
8	27	16XH27	8.89	-0.88	85.59	84.77	141.87	0.47	4.62	15.87	43.56	18.24	17.68	299.68	16.28	0.11	79.49	1.16
10	13	16XH13	8.70	-1.11	81.50	80.65	134.25	0.47	4.30	14.06	36.52	17.58	29.96	277.93	16.58	0.45	84.17	0.78
11	62	16XH62	8.34	-0.82	80.03	79.79	122.94	0.46	3.91	12.73	45.54	15.79	17.27	265.43	16.03	0.51	84.20	5.07
Bottom yielding hybrids																		
61	17	16XH17	4.61	-0.99	88.78	87.47	130.57	0.46	2.49	13.41	39.41	18.69	13.26	286.80	11.01	3.59	77.07	1.07
62	37	16XH37	4.34	-0.87	83.60	82.93	100.04	0.43	2.23	13.17	40.22	16.04	12.81	230.64	13.13	0.99	82.12	3.00
63	20	16XH20	4.25	-0.96	88.90	87.83	118.60	0.45	2.29	11.77	36.60	18.32	14.81	271.58	11.01	0.87	80.10	1.00
64	42	16XH42	4.07	-0.99	85.96	84.70	96.63	0.42	1.95	12.31	41.95	16.05	12.51	230.04	10.87	0.89	81.74	1.06
65	39	16XH39	3.94	-0.88	78.60	77.16	90.69	0.38	2.21	10.57	42.92	16.69	18.75	235.90	15.23	1.02	76.76	2.92
66	68	16XH68	2.03	1.83	81.70	83.97	64.95	0.39	0.23	10.00	24.77	14.33	10.29	164.95	15.42	-0.06	78.82	3.16
67	14	16XH14	1.81	-1.24	86.77	86.01	85.99	0.42	1.30	13.28	25.19	16.11	18.38	200.72	13.35	2.06	80.72	1.20
68	21	16XH21	1.60	4.40	96.06	100.52	70.03	0.38	0.92	12.96	31.53	16.86	8.71	191.70	11.86	-0.41	78.61	0.70
69	30	16XH30	1.23	4.96	93.76	98.42	60.16	0.33	0.81	13.43	19.59	15.64	11.87	181.93	12.46	3.14	73.10	1.20
70	67	16XH67	0.88	5.04	82.09	86.81	58.95	0.35	0.42	10.00	24.16	14.56	9.71	171.69	12.72	0.99	81.47	3.65
LSD			3.78	1.53	3.74	4.01	22.98	0.08	1.37	1.36	11.48	1.46	6.65	23.68	4.41	2.31	5.24	2.68
CV%			40.36	-276.96	4.53	5.17	17.69	11.04	35.68	10.37	18.34	5.67	27.55	11.30	18.06	148.08	3.99	84.55[a]

GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH=Ear height, EPO=Ear position, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=Grain moisture content, NE=Number of ears per plot, PH= Plant height, PS=Plant stand, SL=Stem lodging, SH=shelling percentage, TEX= grain texture, LSD=Least significant difference, CV=Coefficient of variation

Table 4.7   Mean squares for line by tester and their significance for grain yield and related traits at Ukulinga

Source of variation	DF	GY	NE	ASI	AD	SD	EH	FW	GRN	GW100	MOI	PH	PS	SH
Rep	1	0.19	4.08	0	25.52	25.52	65.3	0.85	1.82	56.33	0.11	111.00	30.08*	3.35
Line	11	8.82	21.20	0.24	3.93	3.48	217.40	0.47	1.28	18.91	0.11	516.10	5.92	8.89
Tester	1	5.15	225.33**	0.33	11.02	7.52	1083.00**	0.40	0.15	208.33**	0.00	414.20	16.33	0.15
Line X Tester	11	5.80	24.24	0.33	3.93	3.88	183.20	0.58	1.52	11.24	0.61	165.80	6.11	4.31
Residual	23	6.95	18.43	0.35	7.56	7.74	128.60	0.59	2.53	22.42	0.89	298.30	6.04	5.54
Mean		7.22	19.88	0.83	82.98	82.15	122.90	3.40	13.44	39.00	16.46	261.10	15.42	82.15
LSD		5.45	8.88	1.22	5.69	5.76	23.46	1.59	3.29	9.80	1.95	35.73	5.08	4.87
SE		2.64	4.29	0.59	2.75	2.78	11.34	0.77	1.59	4.74	0.94	17.27	2.46	2.35
CV%		36.51	21.60	-70.77	3.31	3.39	9.23	22.55	11.83	12.14	5.73	6.62	15.94	2.86[b]

GY=Grain yield, NE=Number of ears per plot, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH= Ear height, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=Grain moisture content, , PH= Plant height, PS=Plant stand, SH=shelling percentage, LSD=Least significant difference, SE=Standard error, CV=Coefficient of variation

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %)

4.3.2 Combining ability

4.3.2.1 General combining ability

General combing ability data are presented in Table 4.8. Positive and significant GCA effects were observed for silking date and anthesis for line DPVAL16. Line DPAVL29 showed negative and significant GCA effects for ear position. Significant and negative GCA effects were also observed for grain moisture content and plant height for line DPVAL23. Five lines, DPVAL15, DPVAL31, DPVAL32, DPVAL35 and DPVAL37 showed positive and non-significant GCA effects for grain yield, field weight while one of these lines showed negative and non-significant (p>0.05) GCA effects for number of ears per plot. Lines DPVAL23, DPVAL24, DPVAL28, DPVAL29 and DPVAL35 showed desirable negative GCA effects for plant height and ear height. Lines, DPVAL28, DPVAL32, DPVAL35, DPVAL36 and DPVAL37 exhibited desirable negative GCA affects for anthesis and silking dates. Lines DPVAL24 and DPVAL29 showed negative GCA effects for silking date and anthesis respectively. However, the GCA effects were not significant (p>0.05).

4.3.3 Specific combining ability

Table 4.9 is showing the specific combing ability (SCA) effects for the hybrids at Ukulinga. All SCA effects for grain yield for all traits were non-significant (p>0.05). Lines DPVAL15, DPVAL21, DPVAL23, DPVAL29, DPVAL36 and DPVAL37 showed positive SCA effects for grain yield with tester DQPL19. Lines DPVAL16, DPVAL24, DPVAL28, DPVAL31, DPVAL32 and DPVAL35 exhibited positive SCA effects with tester DQPL23. DPVAL29 had the highest SCA effects with tester DQPL19 whereas line DPVAL16 had the highest SCA effects with tester DQPL23.

Table 4.8   GCA effects for grain yield and secondary traits at Ukulinga

Line	GY	ASI	AD	SD	FW	EH	EPO	GRN	GW100	TL%	MOI	NE	PH	PS	RL	SH	SL	TEX
DPVAL15	0.34	-0.17	2.28	1.66	0.12	4.9	0	-1.02	0.8	-0.01	0.06	1.7	9.18	-0.07	-0.08	1.27	0	-0.65
DPVAL16	-0.39	0.33	2.10*	3.33*	-0.13	8.17	0.02	-1.68	-0.08	-3.83	-0.07	-0.22	4.97	-1.96	-0.83	-1.9	0.25	-0.65
DPVAL21	-0.05	-0.17	0.63	0.36	-0.13	11.88	0.04	-1.42	-0.18	-2.04	-0.59	2.58	2.02	-0.41	-0.08	1.95	-0.25	1.35
DPVAL23	-1.62	0.33	0.25	0.36	-0.83	-8.62	0.01	0.7	-3.58	9.22	-1.02*	-3.7	-22.92*	-0.6	1.17	0.11	0.25	0.35
DPVAL24	-0.3	-0.17	0.24	-0.68	-0.1	-4.66	0.01	1.04	0.76	0.98	0.54	-1.62	-14.81	-0.03	0.17	-0.65	0	1.35
DPVAL28	-0.41	-0.17	-1.87	-1.35	-0.1	-5.17	0	-0.34	-3.39	1.9	0.07	0.58	-11.66	1.6	-0.08	-2.24	0.5	-0.65
DPVAL29	-1.16	0.33	-0.86	0.45	-0.63	-20.95	-0.054*	-0.55	0.84	-2.24	-0.47	-2.37	-15.18	-2.16	-0.58	0.73	0.25	-0.65
DPVAL31	0.37	-0.17	0.91	0.01	0.13	0.51	-0.01	-0.04	-2.69	4.43	0.2	0.19	4.99	0.89	0.92	1.47	-0.25	0.35
DPVAL32	1.35	-0.17	-0.48	-0.86	0.73	9.35	0.01	1.39	1.66	-6.83	0.66	-0.31	12.85	1.14	-0.83	-0.83	-0.25	-0.65
DPVAL35	1.11	-0.17	-1.83	-1.76	0.55	-4.59	-0.01	1.15	1.04	-1.02	0.22	1.82	-5.34	1.64	0.42	0.13	-0.5	0.1
DPVAL36	-0.25	0.33	-1.37	-0.33	-0.1	0.21	-0.01	0.07	1.3	1.6	-0.14	-1.65	9.31	0.4	-0.08	-0.74	0.25	-0.65
DPVAL37	1	-0.17	-0.4	-0.85	0.48	6.49	0	0.07	2.09	-2.15	0.5	2.81	9.88	-0.03	-0.08	0.7	-0.25	0.35
SE	0.85	0.24	1.22	1.24	0.43	8.2	0.02	0.91	1.87	3.96	0.47	1.94	10.44	1.07	0.59	1.26	0.29	0.74

GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, FW=field weight, EH=Ear height, EPO=Ear position, GRN=Grain row number, GW100=100-grain weight, TL%= Total lodging percent, MOI=Grain moisture content, NE=Number of ears per plot, PH= Plant height, PS=Plant stand, RL=Root lodging, SH=shelling percentage, SL= Stem lodging, TEX= grain texture, SE=Standard error

* $p \leq 0.05$ (significant at 5 %)

Table 4.9   SCA effects for grain yield and secondary traits for crosses at Ukulinga

Tester	Line	GY	ASI	AD	SD	FW	EH	EPO	GRN	GW100	TL%	MOI	NE	PH	PS	RL	SH	SL	TEX
DQPL19	DPVAL15	0.26	-0.08	1.54	1.15	0.19	-1.65	-0.01	-0.81	1.48	5.99	-0.1	1.8	4.39	-1.15	0.42	-1.6	0.38	0.65
DQPL19	DPVAL16	-1.12	0.42	2.49*	2.40*	-0.51	6.83	0.03	-0.46	-2.77	1.53	0.42	-3.11	-0.71	-0.82	0.17	-0.69	0.13	0.65
DQPL19	DPVAL21	0.25	-0.08	-1.1	-0.68	0.14	-1.97	0	-0.97	1.72	-2.48	0.11	2.52	-5.82	-0.38	-0.58	-0.53	0.13	-1.35
DQPL19	DPVAL23	0.25	0.42	-1.4	-1.12	0.09	12.92*	0.05	0.51	-2.14	-8.26	-0.77	0.84	4.83	1.05	-0.83	0.19	-0.38	-0.35
DQPL19	DPVAL24	-1.11	-0.08	0.13	0.24	-0.54	-3.1	-0.02	0.74	-0.24	-2.59	-0.23	-3.89	5.48	-2.46*	-0.83	-0.4	0.38	-1.35
DQPL19	DPVAL28	-0.1	-0.08	2.07	1.3	-0.14	4.1	0.01	-0.28	0.16	10.83	-0.1	-0.56	4.72	-0.73	0.92	2.05	0.87	0.65
DQPL19	DPVAL29	1.51	0.42	-2.41	-1.99	0.69	0.58	-0.01	0.07	0	0.45	-0.27	3.52	6	2.75*9	0.42	1.14	-0.38	0.65
DQPL19	DPVAL31	-0.05	-0.08	0.83	0.63	-0.06	-15.63	-0.04	0.26	0.14	2.65	-0.12	0.15	-8.26	0.61	0.42	0.85	0.12	-0.35
DQPL19	DPVAL32	-0.99	-0.08	-1.96	-1.02	-0.41	-2.82	0	0.12	0.53	-1.03	-0.11	-3.42	-4.18	-0.35	0.17	-1.7	-0.38	0.65
DQPL19	DPVAL35	-0.24	-0.08	-1.63	-1.16	-0.04	-3.75	-0.02	1.36*	1.11	-1.28	0.47	-3.69	0.33	-0.2	-0.08	-1.14	-0.13	-0.1
DQPL19	DPVAL36	0.73	-0.58	2.22	0.98	0.36	5.1	0.01	-0.01	3.09*	-9.46	0.31	1.45	7.48	0.49	-0.58	0.08	-0.88	0.65
DQPL19	DPVAL37	0.62	-0.08	-1.2	-1.06	0.24	1.87	0	0.11	-1.65	3.66	0.4	4.57	2.45	0.79	0.42	1.75	0.13	-0.35
DQPL23	DPVAL15	-0.26	0.08	-1.61	-1.21	-0.19	2.07	0.01	0.92	-1.24	-5.99	0.1	-1.77	-1.61	1.09	-0.42	1.6	-0.38	-0.65
DQPL23	DPVAL16	1.12	-0.42	-2.56*	-2.45*	0.51	-6.42	-0.03	0.56	3.01	-1.53	-0.42	3.14	3.49	0.75	-0.17	0.69	-0.13	-0.65
DQPL23	DPVAL21	-0.25	0.08	1.03	0.63	-0.14	2.39	0	1.08	-1.48	2.48	-0.11	-2.49	8.61*	0.31	0.58	0.53	-0.13	1.35
DQPL23	DPVAL23	-0.25	-0.42	1.33	1.07	-0.09	-12.51	-0.05*	-0.41	2.37	8.26	0.77*	-0.81	-2.05	-1.12	0.83	-0.19	0.38	0.35
DQPL23	DPVAL24	1.11	0.08	-0.21	-0.3	0.54	3.51	0.02	-0.64	0.48	2.59	0.23	3.92	-2.69	2.4	0.83	0.4	-0.38	1.35
DQPL23	DPVAL28	0.1	0.08	-2.14	-1.35	0.14	-3.69	-0.01	0.38	0.08	-10.8	0.11	0.59	-1.94	0.66	-0.92	-2.05	-0.87	-0.65
DQPL23	DPVAL29	-1.51	-0.42	2.34	1.93	-0.69	-0.16	0.01	0.03	0.24	-0.45	0.28	-3.49	-3.21	-2.81*	-0.42	-1.14	0.38	-0.65
DQPL23	DPVAL31	0.05	0.08	-0.9	-0.69	0.06	16.05*	0.04	-0.15	0.1	-2.65	0.12	-0.12	11.04*	-0.67	-0.42	-0.85	-0.12	0.35
DQPL23	DPVAL32	0.99	0.08	1.89	0.97	0.41	3.24	0	-0.01	-0.29	1.03	0.11	3.45	6.97	0.28	-0.17	1.7	0.38	-0.65
DQPL23	DPVAL35	0.24	0.08	1.56	1.1	0.04	4.17	0.02	-1.25*	-0.87	1.28	-0.46	3.72	2.45	0.13	0.08	1.14	0.13	0.1
DQPL23	DPVAL36	-0.73	0.58	-2.29	-1.04	-0.36	-4.69	-0.01	0.12	-2.86	9.46	-0.31	-1.42	-4.7	-0.56	0.58	-0.08	0.88	-0.65
DQPL23	DPVAL37	-0.62	0.08	1.13	1.01	-0.24	-1.46	0	0	1.89	-3.66	-0.4	-4.54	0.34	-0.86	-0.42	-1.75	-0.13	0.35
SE		0.76	-0.08	1.19	0.99	0.35	6.22	0.02	13.44	1.52	5.4	0.34	2.76	4.26	1.21	0.55	1.19	0.44	0.741

GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, FW=field weight, EH=Ear height, EPO=Ear position, GRN=Grain row number, GW100=100-grain weight, TL%= Total lodging percent, MOI=Grain moisture content, NE=Number of ears per plot, PH= Plant height, PS=Plant stand, RL=Root lodging, SL= Stem lodging, SH=shelling percentage, TEX= grain texture, SE=Standard error, * p≤0.05 (significant at 5 %)

4.3.4 Genetic parameters for yield and associated traits

The means for the population, the check and the best six selected hybrids are presented in Table 4.10. The results for the estimation of genetic parameters of the quantitative traits under study are furnished in Table 4.11. Grain yield was used as the main trait for selection. Grain yield had high heritability (64.36%). The genetic variance, genotypic coefficient of variation and phenotypic coefficient of variation were also high for grain yield. Heritability estimates were found to be high ($H^2 > 50\%$) for all the traits except for 100-grain weight (43.41%), plant stand (36.05%) and total lodging (22.24%). There was a small discrepancy between PCV and GCV (0.3 - 15) for all the traits with the exception of stem lodging, root lodging, anthesis-silking interval, grain texture and total lodging (26 - 101). Positive genetic gain of 35% over the mean of population was observed for grain yield. High positive gains (55.4%) were realised over the population mean whereas low positive gains were realised over the check.

Table 4.10   Means of selected hybrids and control hybrid for Ukulinga

Traits	GY	ASI	AD	SD	EH	EPO	FW	GRN	GW100	MOI	NE	PH	PS	RL	SH	SL	TEX	TL %
MP	6.65	-0.49	83.35	82.86	113.95	0.45	3.20	13.09	38.46	16.46	18.28	253.54	15.06	0.75	82.12	0.84	2.11	10.67
MC	9.53	-0.50	80.50	80.00	107.50	0.46	4.50	13.33	33.75	15.57	20.25	264.00	15.75	0.75	83.86	1.75	3.00	15.80
MS	10.35	-0.92	82.31	81.52	122.33	0.45	4.41	13.46	39.96	16.63	21.13	272.30	16.76	0.50	83.35	0.55	2.23	51.68[6]

GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH=Ear height, EPO=Ear position, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=Grain moisture content, NE=Number of ears per plot, PH= Plant height, PS=Plant stand, RL=Root lodging, SH=shelling percentage, SL= Stem lodging, TEX= grain texture, TL%= Total lodging percent, MP=Mean of population, MC=Mean of check, MS=Mean of selected hybrids

Table 4.11   Estimates of variance components, heritability and genetic gains of selected hybrids at 11% selection intensity at Ukulinga

Traits	δ^2g	δ^2p	H^2 (%)	GCV (%)	PCV (%)	PG	PG%	RG1	RG2
Grain Yield	2.93	4.55	64.36	25.73	32.07	234.73	35.28	55.54	8.59
Anthesis-silking Interval	1.28	1.58	80.88	-229.42	-255.10	173.83	-352.59	2.25	84.00
Anthesis date	9.65	11.53	83.71	3.73	4.07	485.75	5.83	-1.25	2.25
Silking date	13.95	15.89	87.82	4.51	4.81	598.26	7.22	-1.62	1.90
Ear height	267.90	328.90	81.45	14.36	15.92	2524.54	22.15	7.36	13.80
Ear Position	0.00	0.00	54.52	6.61	8.95	3.73	8.34	-0.54	-4.09
Field Weight	0.63	0.84	75.57	24.84	28.57	118.02	36.90	37.87	-2.00
Grain Row Number	1.38	1.60	86.31	8.97	9.65	186.38	14.24	2.78	0.94
100-grain Weight	11.88	27.37	43.41	8.96	13.60	388.12	10.09	3.87	18.39
Grain Moisture Content	0.34	0.61	56.02	3.55	4.74	74.72	4.54	1.00	6.79
Number of Ears per Plot	12.89	17.66	72.98	19.64	22.99	524.13	28.68	15.61	4.35
Plant Height	591.70	652.90	90.63	9.59	10.08	3957.49	15.61	7.40	3.14
Plant Stand	1.25	3.46	36.05	7.42	12.36	114.63	7.61	11.30	6.40
Root Lodging	-0.06	0.59	-10.09		101.58	-13.18	-17.51	-33.60	-33.33
Shelling Percentage	3.98	7.42	53.67	2.43	3.32	249.79	3.04	1.50	-0.61
Stem Lodging	0.12	0.74	15.57	40.22	101.92	22.87	27.12	-34.62	-68.50
Grain Texture	1.40	2.23	62.74	55.98	70.68	160.23	75.78	5.47	-25.67
Total Lodging	14.70	66.10	22.24	35.94	76.21	309.00	28.97	384.46	227.09[7]

δ^2g=Genotypic variance, δ^2p= Phenotypic variance, H^2 (%)= Broad sense heritability, GCV (%)=Genotypic coefficient of variation, PCV (%)=Phenotypic coefficient of variation, PG=Predicted gain, RG1= realised gain relative to population mean, RG2= realised gain relative to check mean

4.3.5 Correlations between traits

4.3.5.1 Correlations

The phenotypic correlations between traits measured at Ukulinga are presented in Table 4.12. Grain yield had positive correlations with plant height, plant stand, ear height, field weight, grain row number, 100-grain weight and shelling percentage. The correlations were all significant ($p \leq 0.001$). These correlations were strong except for grain row number whose correlation was below 30%. Ear position was positive and significantly ($p \leq 0.05$) correlated with grain yield. Silking date, anthesis date, anthesis-silking interval and total lodging percentage were negatively and significantly ($p \leq 0.001$) correlated with grain yield; whereas root lodging and stem lodging were negatively and significantly ($p \leq 0.05$) correlated with grain yield. The correlations were strong except for anthesis date, root lodging and stem lodging whose correlation was below 30%. Field weight was positively and significantly ($p \leq 0.001$) correlated with plant height, plant stand, ear height and number of ears per plot while it was positively and significantly ($p \leq 0.01$) correlated with ear position. Silking date and anthesis-silking interval had a negative and significant ($p \leq 0.001$) correlation with field weight. Number of ears per plot showed a positive and significant ($p \leq 0.001$) correlation with plant height, plant stand and ear height. Ear height and plant height were positively and significantly ($p \leq 0.001$) correlated. Number of ears per plot, plant height, ear height and 100-grain weight had strong negative and significant correlations with anthesis-silking interval. Plant height and shelling percentage had strong negative and significant ($p \leq 0.001$) correlations with silking date and anthesis date respectively. Plant height was negatively correlated with root lodging, stem lodging and total lodging percentage.

Table 4.12   Correlations between grain yield and secondary traits at Ukulinga

	GY	SD	AD	ASI	PH	PS	EH	EPO	NE	FW	GR	GW100	MOI	SH	RL	SL	TL %	TEX
GY	-																	
DS	-0.41***	-																
DA	-0.28***	0.95***	-															
ASI	-0.49***	0.51***	0.22**	-														
PH	0.65***	-0.23**	-0.03	-0.62***	-													
PS	0.49***	-0.50***	-0.48***	-0.21**	0.21**	-												
EH	0.50***	-0.25**	-0.08	-0.56***	0.83***	0.23**	-											
EPO	0.20*	-0.24**	-0.15	-0.36***	0.39***	0.19*	0.83***	-										
NE	0.64***	-0.33***	-0.22**	-0.44***	0.52***	0.58***	0.45***	0.23**	-									
FW	0.87***	-0.39***	-0.23**	-0.57***	0.76***	0.53***	0.57***	0.22**	0.77***	-								
GRN	0.28***	-0.02	0.04	-0.18*	0.34***	0.12	0.27**	0.12	0.09	0.33***	-							
GW100	0.43***	-0.31***	-0.19*	-0.47***	0.44***	0.02	0.36***	0.18*	0.16*	0.44***	0.00	-						
MOI	0.10	0.15	0.27**	-0.26**	0.39***	-0.08	0.35***	0.21*	0.03	0.19*	0.38***	0.13	-					
SH	0.30***	-0.46	-0.43***	-0.25**	0.08	0.18*	0.11	0.15	0.20*	0.24**	-0.01	0.16*	-0.05	-				
RL	-0.20*	-0.10	-0.13	0.03	-0.24**	0.03	-0.13	0.04	-0.11	-0.24**	-0.04	-0.12	0.01	0.07	-			
SL	-0.19*	0.11	0.08	0.13	-0.08	0.04	-0.10	-0.08	-0.12	-0.18*	0.10	-0.34***	0.08	-0.07	0.12	-		
TL %	-0.33***	0.09	0.05	0.15	-0.24**	-0.08	-0.18*	-0.05	-0.22**	-0.36***	0.01	-0.31***	0.08	-0.05	0.73***	0.73***	-	
TEX	0.10	-0.34***	-0.37***	-0.02	-0.08	0.11	-0.11	-0.09	-0.01	0.08	-0.21**	0.18*	-0.24**	0.27**	0.08	-0.12	-0.06	-[8]

GY=Grain yield, SD=Silking date, AD=Anthesis date, ASI=Anthesis-silking interval, PH=Plant height, PS=Plant stand, EH=Ear height, EPO=Ear position, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=Grain moisture content, SH=shelling percentage, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, TEX= grain texture

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %),

4.3.5.2   Path coefficient analysis

Path coefficient analysis of data for Ukulinga is presented in Table 4.13 and Table 4.14. Grain row number, 100-grain weight, number of ears per plot and shelling percentage showed significant (P<0.0001) direct effects on grain yield (Table 4.13). Significant (P<0.01) positive direct effects were observed on plant stand and plant height. Grain texture also showed significant (P<0.05) direct effects on grain yield.

Plant height had the highest (0.84) positive direct effects on grain yield (Table 4.14). It also had the highest positive indirect effects on grain yield via the number of ears per plot. Number of ears per plot had the second highest (0.43) positive direct effects on grain yield. Ear height had the highest (-0.77) negative direct effects on grain yield. Plant height had the highest (0.44) positive indirect effects on grain yield via number of ears per plot. Ear height illustrated the highest (-0.64) indirect effects via plant and ear position. Ear position (0.35), plant stand (0.18), shelling percentage (0.16), grain row number (0.16) and 100-grain weight (0.17) showed moderate positive direct effects on grain yield.

Table 4.13 Parameter estimates for direct effects based on regression

Variable	Parameter Estimate	Standard Error	t Value	Pr > |t|
ASI	0.010	0.050	0.200	0.84ns
EH	-0.772	0.424	-1.820	0.07ns
GRN	0.157	0.036	4.310	<.0001***
MOI	-0.032	0.039	-0.830	0.41ns
SD	0.053	0.050	1.050	0.30ns
PS	0.180	0.048	3.760	0.0003**
GW100	0.174	0.041	4.290	<.0001***
PH	0.843	0.268	3.140	0.002*
EPO	0.350	0.259	1.350	0.18ns
RL	-0.035	0.112	-0.310	0.80ns
SL	0.008	0.112	0.070	0.94ns
TL	-0.077	0.162	-0.480	0.64ns
NE	0.426	0.048	8.930	<.0001***
TEX	0.081	0.036	2.260	0.0255*
SH	0.161	0.037	4.370	<.0001***.

ASI=Anthesis-silking interval, EH=Ear height, GRN=Grain row number, MOI=Grain moisture content, SD=Silking date, PS=Plant stand, GW100=100-grain weight, PH= Plant height, EPO=Ear position, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, NE=Number of ears per plot, TEX= grain texture, SH=shelling percentage, Pr=Probability

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %), ns=not significant

Table 4.14   Direct and indirect effects of secondary traits on grain yield of maize hybrids at Ukulinga (R^2=0.88)

	ASI	EH	GRN	MOI	SD	PS	GW100	PH	EPO	RL	SL	TL	NE	AD	TEX	SH	GY	FW
ASI	**0.01ns**	0.43	-0.03	0.01	0.03	-0.04	-0.08	-0.52	-0.12	0.00	0.00	-0.01	-0.19	0.00	0.00	-0.04	-0.56	-0.56
EH	-0.01	**-0.77ns**	0.04	-0.01	-0.01	0.04	0.06	0.70	0.29	0.00	0.00	0.01	0.19	0.00	-0.01	0.02	0.55	0.55
GRN	0.00	-0.21	**0.16*****	-0.01	0.00	0.02	0.00	0.29	0.04	0.00	0.00	0.00	0.04	0.00	-0.02	0.00	0.31	0.31
MOI	0.00	-0.27	0.06	**-0.03ns**	0.01	-0.01	0.02	0.32	0.07	0.00	0.00	-0.01	0.01	0.00	-0.02	-0.01	0.15	0.15
SD	0.01	0.19	0.00	0.00	**0.05ns**	-0.09	-0.05	-0.19	-0.09	0.00	0.00	-0.01	-0.14	0.00	-0.03	-0.07	-0.42	-0.42
PS	0.00	-0.18	0.02	0.00	-0.03	**0.18****	0.00	0.18	0.07	0.00	0.00	0.01	0.25	0.00	0.01	0.03	0.53	0.53
GW100	0.00	-0.27	0.00	0.00	-0.02	0.00	**0.17*****	0.37	0.06	0.00	0.00	0.02	0.07	0.00	0.01	0.03	0.44	0.44
PH	-0.01	-0.64	0.05	-0.01	-0.01	0.04	0.08	**0.84****	0.14	0.01	0.00	0.02	0.22	0.00	-0.01	0.01	0.73	0.72
EPO	0.00	-0.64	0.02	-0.01	-0.01	0.03	0.03	0.33	**0.35ns**	0.00	0.00	0.00	0.10	0.00	-0.01	0.02	0.21	0.21
RL	0.00	0.10	-0.01	0.00	-0.01	0.00	-0.02	-0.20	0.01	**-0.03ns**	0.00	-0.06	-0.05	0.00	0.01	0.01	-0.23	-0.23
SL	0.00	0.08	0.02	0.00	0.01	0.01	-0.06	-0.07	-0.03	0.00	**0.01ns**	-0.06	-0.05	0.00	-0.01	-0.01	-0.18	-0.18
TL	0.00	0.14	0.00	0.00	0.00	-0.01	-0.05	-0.20	-0.02	-0.03	0.01	**-0.08ns**	-0.09	0.00	0.00	-0.01	-0.35	-0.35
NE	0.00	-0.35	0.01	0.00	-0.02	0.10	0.03	0.44	0.08	0.00	0.00	0.02	**0.43*****	0.00	0.00	0.03	0.78	0.77
AD	0.00	0.06	0.01	-0.01	0.05	-0.09	-0.03	-0.02	-0.05	0.00	0.00	0.00	-0.09	**0.00**	-0.03	-0.07	-0.27	-0.27
TEX	0.00	0.09	-0.03	0.01	-0.02	0.02	0.03	-0.07	-0.03	0.00	0.00	0.00	0.00	0.00	**0.08***	0.04	0.11	0.11
SH	0.00	-0.09	0.00	0.00	-0.02	0.03	0.03	0.06	0.05	0.00	0.00	0.00	0.09	0.00	0.02	**0.16*****	0.33	0.33[9]

ASI=Anthesis-silking interval, EH= Ear height, GRN=Grain row number, MOI=Grain moisture content, SD=Silking date, PS=Plant stand, GW100=100-grain weight, PH= Plant height, EPO=Ear position, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, NE=Number of ears per plot, AD=Anthesis date, TEX= grain texture, SH=shelling percentage GY=Grain yield, FW=field weight, R^2=coefficient of determination, * p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %), ns=not significant

4.4 Discussion

4.4.1 Genetic variation

The genotype main effects were significant (p<0.05) for grain yield and the majority of other traits. These findings are in line with Reddy and Jabeen (2016) who also found significant genotype effects for all the traits in their study. This is an indication that the hybrids explained the main contribution to these traits than the environmental effect, showing the presence of the genetic variability of hybrids for these traits. This shows that genetic variation attained in this study can be exploited for improvement of hybrids for traits of economic importance.

4.4.2 Mean performance

The hybrids were ranked with respect to their performance in a descending order. The top 3, experimental hybrids (16XH49, 16XH45 and 16XH15) performed better than the check 11C1579 which performs very well in South Africa. The LSD was 3.78 and this shows that there was significant difference among the hybrids in terms of grain yield performance. The hybrid 16XH49 stood out against the rest and was ranked the highest. This qualifies the hybrid for advancement in hybrid trials. Its yield was 12.98 t/ha and this indicated good adaptability as it was a cross between exotic PVA and adapted QPM lines. Hybrids 16XH45 and 16XH15 should also be recommended for advancement in the following season.

4.4.3 General combining ability effects

The line main effects were not significant for all the traits in this study. The results therefore indicate that the lines played a non-significant role in determining the expression of all the traits in hybrids. The tester main effects were only significant for number of ears, ear height and 100-grain weight. All GCA effects for grain yield were not significant, indicating that the lines are not good general combiners for grain yield. Nevertheless, line DPVAL32 had the largest positive GCA effects for grain yield hence the best general combiner for grain yield. These lines had desirable negative GCA effects for anthesis and silking days, and root and stem lodging as well as desirable positive GCA effects for field weight and kernel row number. It needs to be improved on traits like number of ears per plot, shelling percentage, ear height and ear position. Lines DPVAL35 and DPVAL37 also had high positive GCA for grain yield. Line DPVAL 35 needs to be improved on root lodging whereas DPVAL37 need to be fixed in

traits like ear height, plant height and plant stand. These lines can be recommended for further testing for combing ability to see if the positive GCA effects can be repeated.

4.4.4 Specific combining ability

The SCA effects were not significant for grain yield for all the lines. This shows that the SCA was not important in determining the grain yield in all the hybrids. However, line DPVAL29 had the highest SCA effects for grain yield when it was crossed to tester DQPL19. This cross needs to be improved by crossing it to a line which has negative SCA for total, root and stem lodging ear height and plant height. Line DPVAL16 and DPVAL24 had the highest positive SCA effects when it was crossed with DQPL23. DPVAL16, DPVAL24 and DQPL23 had negative GCA effects. This showed that grain yield was conditioned by genes with non-additive effects. The best hybrid in this experiment was obtained when DPVAL16 was crossed with DQPL23. This hybrid had desirable significant negative SCA effects for shorter flowering days, non-significant negative SCA effects for ear height, ear position, total lodging, grain moisture content, root and stem lodging. It also had desirable positive SCA effects for field weight, grain row number, 100-grain weight, number of ears and shelling percentage.

4.4.5 Genetic parameters for yield and associated traits

Grain yield had high heritability. This is in line with the study carried out by, Begum et al. (2016) and Kumar et al. (2014). High heritability of secondary traits indicated that the effect of environment on the traits was low. This therefore means that genotypic variation was high for these traits. Phenotypic selections of these traits can be successful during breeding by implementation of simple selection methods. This can also form the basis of possible genetic improvement of the lines and hybrids. Low heritability was observed for 100-grain weight, plant stand, root, stem and total lodging. Similar results were reported for 100-grain weight (Poudel and Poudel, 2016), stem and root lodging (Nzuve et al., 2014). Kumar et al. (2014) and Anshuman et al. (2013) reported heritability of 88.83% and 90.80%, respectively, for 100-grain weight which was in contrast to the present study. Low heritabilities exhibited by these traits shows that these traits were highly influenced by the environment such as prevailing winds, storms or poor soil structure that was not uniform across the experimental blocks, rows and columns.

Heritability coupled with genetic advance gives a more reliable conclusion rather than using heritability alone (Johnson et al., 1995). Traits with high heritability may not have high genetic

advance as well. Traits that had high heritability, GCV and genetic advance were grain yield ear height, field weight and number of ears per plot. This was in agreement with reports made by Hefny (2011), Panda et al. (2012) and Rajesh et al. (2013). These traits are likely to have been controlled by additive gene action and early generation selection for these traits may be effective. On the other hand, anthesis date, silking date, grain row number and plant height had high heritabilities with low to moderate GCV and genetic advance. Kumar et al. (2014) also found the same result for anthesis date, silking date and grain row number. This reveals non-additive gene action and this limits the scope for improvement of traits through selection.

4.4.6   Relationship between grain yield and secondary traits

Grain yield had highly significant (p ≤ 0.001) correlations with all traits except ear position, grain moisture content, grain texture, root and stem lodging. These findings are consistent with previous studies. It was reported that grain yield had significant positive correlations with field weight and plant height (Aminu et al., 2014; Kinfe et al., 2015; Pavlov et al., 2015), number of ears per plot, ear height (Aminu et al., 2014; Sudika et al., 2015), 100-grain weight (Kumar et al., 2006;Prakash et al., 2006), plant stand, shelling percentage and grain row number. In line with the current study, Tulu (2014) also found positive and significant correlations with plant height and ear height. Ear position had a positive significant (p ≤ 0.05) correlation with grain yield. This shows that grain yield increases as these traits increase, for instance, the higher the field weight the higher the grain yield. Kinfe et al. (2015), found that grain yield had significant (p ≤ 0.05) negative correlations with anthesis-silking interval. Silking date and anthesis date were also negatively correlated to grain yield, which was in line with what Reddy and Jabeen (2016) reported but contrary to what Kinfe et al. (2015) found. This showed that, the earlier the days to flowering, anthesis-silking interval and the lower the total lodging, the higher the grain yield. The results also showed that the earlier the days to flowering the higher the shelling percentage, field weight and the number of ears per pot. This means early flowering days promote prolificacy. Number of ears had a significant positive correlation with plant height. This implied that selection for ear prolificacy might have caused an increase in plant height.

4.4.7   Path coefficient analysis

Path coefficient analysis was done to determine direct and indirect effects of secondary traits on grain yield. For interpretation of results from the current study, indirect effects were ranked similar to those of Lenka and Mishra (1973). In this regard, the path coefficients

were ranked as follows: 0.00 to 0.09 = negligible, 0.10 to 0.19 = low, 0.20 to 0.29 = moderate and >0.30 = high. Path coefficient analysis helps a plant breeder to determine the nature and extent of the relationships between yield and secondary traits.

Plant height had the highest significant (p>0.01) direct effects on grain yield. This is in accordance with the report of Amini et al. (2013), Kang and Ahmad (2014) and Kinfe et al. (2015). Plant height had the highest indirect and positive effects on grain yield through ear height and number of ears per plot. On the other hand, it had the highest indirect and negative effects on grain yield through anthesis-silking interval and Silking date. Ear height had the highest negative direct effects on grain yield. This is in agreement with what Pavlov et al. (2015) reported. When selecting for ear height a compromise had to be reached as it also showed indirect positive effects on grain yield via plant height. Therefore there is a limit to which plant height can be selected for. Number of ears also had high direct effect on grain yield. Results showed that indirect selection of shorter days to flowering, higher plant density and increased plant height via number of ears will increase the grain yield. Plant stand and 100-grain weight had positive but low direct effects on grain yield.

4.5 Conclusion

The following conclusions were drawn from the study

- There were no significant GCA effects for all the traits. This showed that the lines were not significantly different in terms of their performance although the yields were quite high. Line DPVAL32 had the highest GCA effects for grain yield which makes it potentially useful in grain yield improvement although it still needs to be improved in other traits. SCA effects were not significant for grain yield. This showed that non-additive gene action was negligible for grain yield and its secondary traits.
- Hybrid 16XH49 was ranked the highest yielding. It was developed from line DPVAL37. This line is a good line to consider for grain yield as it also had high GCA effects for grain yield.
- Grain yield and other traits were highly heritable. This showed that genetic variation exceeded environmental variation. Genetic gains were therefore made in grain yield and some of the traits. The selected hybrids exhibited 56% genetic gain for grain yield. These hybrids can be recommended for further evaluation in the following

season. There was substantial genetic variability among the hybrid for grain yield, which can be exploited for further improvement of breeding gains.

- Grain yield had strong and significant correlations with field weight, number of ears per plot and plant height, indicating that selection of these traits would result in increasing grain yield.

- Field weight was found to be most important trait contributing to grain yield. Direct selection for this trait would effectively increase yield.

- Most indirect effects were negligible although there were a few which were quite moderate to high and these need to be considered as they would make contribution to grain yield. The high indirect contribution of plant height and number of ears per plot via ear height can be used to deduce the importance of position and growth of the ear on grain yield.

5   PATH COEFFICIENT ANALYSIS AND COMBINING ABILITY BETWEEN SOUTH AFRICAN PRO-VITAMIN-A AND QUALITY PROTEIN MAIZE LINES FOR YIELD AND SECONDARY TRAITS

5.1   Introduction

This study was aimed at determining the combining ability effects of pro-vitamin A (PVA) and quality protein (QPM) maize inbred lines and the association of secondary traits with grain yield. The PVA maize inbred lines and the testers used in this study were developed in South Africa and are adapted to the South African environment. Line x tester analysis was done to identify suitable and adapted parents for the development of high yielding hybrids with both PVA and QPM traits. Kruvadi (1991) as cited by Seyoum et al. (2016) emphasised the importance of the knowledge of general combing ability and specific combining ability effects in the choice of suitable germplasm for inbred line and hybrid development.

5.2   Materials and methods

Chapter 3 gives a full description of how the study was executed. This section outlines the materials used for this specific trial, the site and the experimental design used.

5.2.1   Parental material and germplasm development

The germplasm comprised of 12 local lines, one PVA tester and four QPM testers. The local lines were developed at the Ukulinga Research Station, in South Africa. QPM lines were obtained from Quality Seeds (Pty) Ltd. The lines are listed in Tables 5.1 and 5.2.

Table 5.1   List of local adapted PVA lines

Entry	Stock	Name
1	PVAF8-1	DPVAL01
2	PVAF8-2	DPVAL02
3	PVAF8-3	DPVAL03
4	PVAF8-4	DPVAL04
5	PVAF8-5	DPVAL05
6	PVAF8-6	DPVAL06
7	PVAF8-7	DPVAL07
8	PVAF8-8	DPVAL08
9	PVAF8-9	DPVAL09
10	PVAF8-10	DPVAL10
11	PVAF8-12	DPVAL12
12	PVAF8-13	DPVAL13

Table 5.2   List of PVA and QPM Lines used as testers

Entry	Type
PVAF8-11	PVA-11
PVAF8-14	QPM-1
PVAF8-15	QPM-2
PVAF8-20	QPM-4

5.2.2   Crossing local lines with PVA and QPM testers

A line by tester mating design was used. Twelve local lines were crossed to four testers resulting in 48 hybrids. The 4 testers consisted of 3 QPM testers and 1 pro-vitamin A tester. Of the 48 hybrids that were generated, 43 hybrids (plus one check) that had enough seeds for the experiment were evaluated. The crosses were done at the Makhathini Research Station (27_380S; 32_100E) in KwaZulu-Natal, South Africa. The crossing scheme is shown in Table 5.3.

Table 5.3   Crossing between 12 local lines with 1 PVA and 3 QPM testers

	Testers			
	PVA-11	**QPM1**	**QPM2**	**QPM4**
Lines				
1	×	×	×	×
2	×	×	×	×
3	×	×	×	×
4	×	×	×	×
5	×	×	×	×
6	×	×	×	×
7	×	×	×	×
8	×	×	×	×
9	×	×	×	×
10	×	×	×	×
11	×	×	×	×
12	×	×	×	×

5.2.3   Sites of study

The field trials were set up at Ukulinga and Cedara on 24 November and 8 December 2015 respectively.

Table 5.4 shows the two sites where the field evaluation of the hybrids was done.

Table 5.4   Sites of study

Site	Location	Longitude	Latitude	Altitude	Soil type
Cedara Research Station	South Africa	30° 15'E	29° 32'S	1054 m	loamy clay
Ukulinga Research Station	South Africa	29° 24'E	30°24' S	809 m	sandy clay
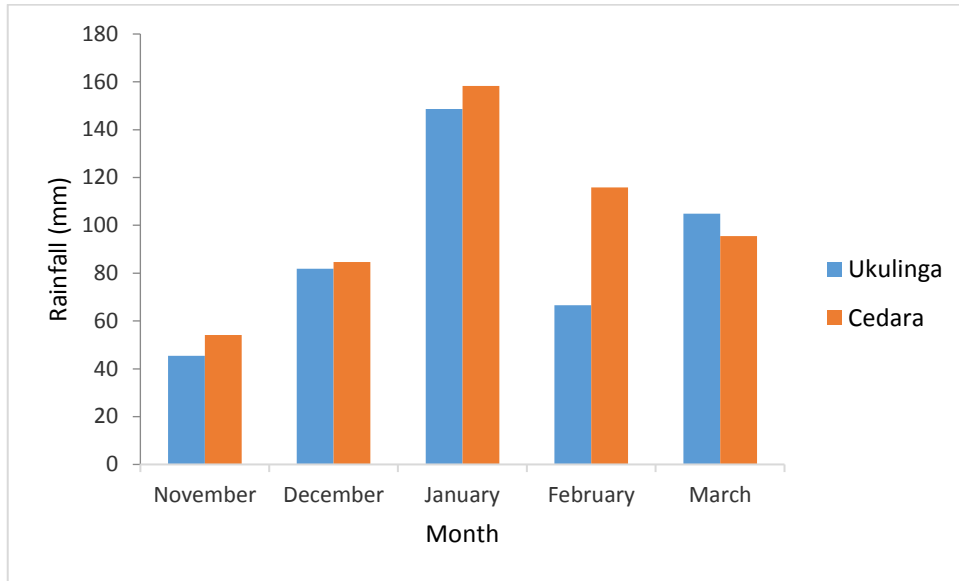
Figure 5.1   Total rainfall for Ukulinga and Cedara for the duration of the study.
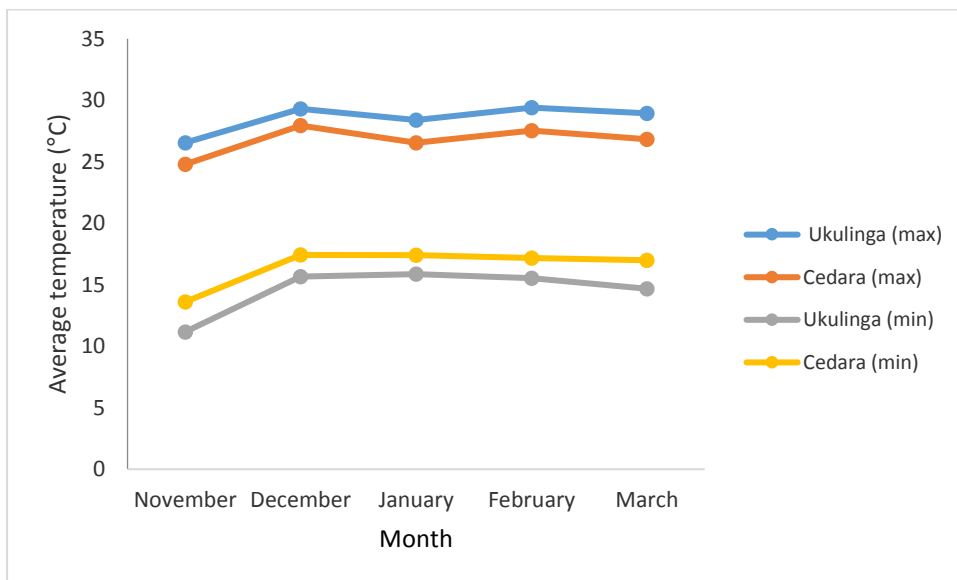
Figure 5.2   Average temperture of Ukulinga and Cedara for the duration of the study.

5.2.4   Experimental design and crop management

Forty-four hybrids (42 hybrids and 1 check repeated twice) were evaluated using 4 × 11 row by column design with two replications at the two sites. The plot was one row of 5 m length, with inter-row and intra-row spacing of 0.75 m and 0.3 m respectively. Two seeds were

planted per hill and planting depth was within the range 3- 5 cm. Thinning was done later after the seedlings had fully established leaving only one plant per hill.

5.2.5   Data analysis

5.2.5.1   Genetic advance

At Ukulinga, selection intensity of 1.6273 at 13% selection and at Cedara selection intensity of 1.8043 at 9% selection were used.

5.2.5.2   Cultivar Superiority Index

The stability of hybrids across environments was analysed in Breeding Management System (BMS) according to the model (Lin and Binns, 1988):

Stability of the hybrids across the environments were estimated by cultivar superiority index

$$P_i = \sum_{j=1}^{n} \frac{\left(X_{ij} - M_j\right)^2}{2n}$$

P_i=mean square between the cultivar's yield and maximum yield in each environment.

X_{ij}=the yield of i_{th} genotype in the j_{th} environment

M_j=the maximum yield in the j_{th} environment

n=number of environments

5.3   Results

5.3.1   Genetic variation

Ukulinga

Table 5.5 shows that entry main effects for grain yield, field weight, stem lodging and texture were significantly different (p≤0.001). Mean squares for anthesis days, silking days and number of ears were significantly different (p≤0.01). Plant height, ear height shelling percentage and total lodging percentage showed non-significant mean squares. The

coefficients of variation were generally low except for total lodging percentage, stem lodging and root lodging.

Cedara

Mean squares for grain yield, silking days, anthesis days, field weight, grain moisture content and texture were significantly different (p≤0.001) as shown in Table 5.6. Other traits like plant height, ear height and shelling percentage showed non-significant mean squares. The coefficients of variation for all traits were low except for root lodging.

Across sites

The site main effects for all traits were significant (p≤0.001) for the hybrids. Only grain yield, field weight, shelling percentage and number of ears showed significant site X hybrid interaction main effects (Table 5.7). Across the two sites genotype main effects were significant (p≤0.05) for all traits except anthesis-silking interval and root lodging. The coefficients of variation across Ukulinga and Cedara were low for all traits except for root lodging, stem lodging and total lodging percentage.

Table 5.5   Mean squares for yield and secondary traits for Ukulinga

Source of variation	D.F	GY	SD	AD	ASI	PH	PS	EH	EPO	NE	FW	GRN	GW100	MOI	SH	RL	SL	TL %	TEX
Replication	1	28.61***	26.18*	29.56**	0.10	27.3	0.41	332.30	0.00	31.92*	7.39***	0.13	147.68**	0.02	2.37	8.91	58.91***	761.00	0.18
Rep/Row/Column	20	2.89***	12.84***	14.39***	0.15	632.90***	6.973***	402.30*	0.00	21.89***	0.72***	0.65	37.61*	0.86	7.69	11.07***	14.07***	895.20.***	2.77***
Genotype	43	2.25***	10.07**	10.15**	0.18	320.70*	2.79	389.80*	0.00	15.05**	0.54***	1.20	31.07	1.11	10.60*	3.66	10.40***	432.8*	3.95***
Residual	23	0.65	3.11	3.18	0.15	155.80	2.46	192.60	0.00	4.99	0.15	0.64	16.48	0.63	4.19	2.44	2.73	184.90	0.12
Mean		6.58	81.23	82.15	-0.92	275.78	15.87	138.51	0.50	19.33	3.28	13.80	39.11	16.39	80.24	1.34	3.36	29.08	2.00
LSD0.05		1.66	3.65	3.69	0.79	25.82	3.24	28.71	0.08	4.62	0.81	1.65	8.40	1.64	4.23	3.23	3.42	28.13	0.72
CV %		12.22	2.17	2.17	-41.37	4.53	9.88	10.02	7.79	11.56	11.94	5.78	10.38	4.82	2.55	116.56	49.12	46.76	17.44
SE		0.80	1.76	1.78	0.38	12.48	1.57	13.88	0.04	2.23	0.39	0.80	4.06	0.79	2.05	1.56	1.65	13.60	0.35[10]

D.F=Degrees of freedom, GY=Grain yield, SD=Silking date, AD=Anthesis date, ASI=Anthesis-silking interval, PH= Plant height, PS=Plant stand, EH=Ear height, EPO=Ear position, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, SH=shelling percentage, RL=Root lodging, SL= Stem lodging, TL%=Total lodging percentage, TEX= grain texture, LSD=Least significant difference, CV=Coefficient of variation, SE=Standard error

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %), ns=not significant

Table 5.6   Mean squares for yield and secondary traits for Cedara

Source of variation	D.F	GY	SD	AD	ASI	PH	PS	EH	EPO	NE	FW	GR	GW100	MOI	SH	RL	SL	TL %	TEX
Replication	1	0.05	0.41	12.38*	8.28***	2662.00***	0.01	125.3	0.00	7.10	0.09	12.13	72.73	0.19	2.37	0.05	96.18**	4080.40***	0.41
Rep/Row/Column	20	1.04*	13.10***	11.89***	0.48***	669.00**	0.55	431.50**	0.00	6.01	0.21	16.5	32.18	1.68**	7.69	0.19	39.56***	1627.30**	2.75***
Genotype	43	1.16***	15.29***	15.46***	0.01	327.40	0.88	241.6	0.00*	6.46	0.32***	14.13	47.89*	2.58***	9.93	0.24*	17.97	614.50	4.00***
Residual	23	0.45	2.46	2.47	0.01	189.60	0.87	129.60	0.00	5.06	0.12	12.49	21.52	0.57	5.44	0.12	12.06	474.90	0.45
Mean		5.06	78.80	79.49	-0.69	258.30	16.31	119.65	0.46	18.33	2.73	14.45	29.14	18.33	80.24	0.11	10.78	66.91	1.95
LSD0.05		1.39	3.24	3.25	0.22	28.49	1.93	23.55	0.07	4.65	0.73	7.31	9.60	1.57	4.83	0.71	7.18	45.08	1.39
CV %		13.32	1.99	1.98	-15.12	5.33	5.73	9.51	7.25	12.28	12.91	24.46	15.92	4.13	2.91	300.79	32.24	32.57	34.30
SE		0.67	1.57	1.57	0.10	13.77	0.93	11.38	0.03	2.25	0.35	3.53	4.64	0.76	2.33	0.34	3.47	21.79	0.67[11]

D.F=Degrees of freedom, GY=Grain yield, AD=Anthesis date, SD=Silking date, ASI=Anthesis-silking interval, PH= Plant height, PS=Plant stand, EH=Ear height, EPO=Ear position, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, SH=shelling percentage, RL=Root lodging, SL= Stem lodging, TL%=Total lodging percentage, TEX= grain texture, LSD=Least significant difference, CV=Coefficient of variation, SE=Standard error

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %), ns=not significant

Table 5.7   Mean squares for yield and secondary traits across sites

Source of variation	D.F	GY	SD	AD	ASI	PH	EH	EPO	NE	FW	GW100	MOI	SH	RL	SL	TL %
Site	1	98.04***	260.21***	311.11***	2.27***	13457.50***	15656.80***	0.07***	44.00**	13.37***	4380.02***	165.37***	695.95***	66.27***	2415.36***	62961.70***
Site/Rep	2	14.36***	13.30*	21.00**	4.19***	1344.60***	228.80	0.00	19.51*	3.74***	110.20**	0.11	4.27	4.48*	77.55***	2420.70**
Site/Rep/Row	40	1.94***	13.42***	13.14***	0.32***	651.00***	416.90***	0.00	13.95***	0.47***	34.90*	1.27**	11.95***	5.63***	26.82***	1261.30**
Genotype	43	2.09***	23.73***	24.05***	0.10	455.00***	473.80***	0.00***	12.91***	0.54***	51.38***	2.79***	17.87***	1.98	16.90**	629.60*
Site X Genotype	43	1.27**	1.64	1.56	0.09	193.10	157.60	0.00	8.60*	0.32**	27.57	0.89	5.51*	1.92	11.47	417.70
Residual	46	0.54	2.78	2.83	0.08	172.70	161.10	0.00	5.03	0.14	19.00	0.60	3.04	1.28	7.40	329.90
Mean		5.83	80.01	80.82	-0.81	267.04	129.08	0.48	18.83	3.01	34.13	17.36	78.25	0.73	7.07	48.00
LSD0.05		1.04	2.37	2.39	0.40	18.70	18.07	0.05	3.19	0.53	6.20	1.10	2.48	1.61	3.87	25.85
CV %		12.56	2.08	2.08	-34.61	4.92	9.83	7.55	11.91	12.40	12.77	4.46	2.23	155.56	38.48	37.84
SE		0.73	1.67	1.68	0.28	13.14	12.69	0.04	2.24	0.37	4.36	0.77	1.74	1.13	2.72	18.16[12]

D.F=Degrees of freedom, GY=Grain yield, AD=Anthesis date, SD=Silking date, ASI=Anthesis-silking interval, PH= Plant height, PS=Plant stand, EH=Ear height, EPO=Ear position, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, SH=shelling percentage, RL=Root lodging, SL= Stem lodging, TL%=Total lodging percentage, TEX= grain texture, LSD=Least significant difference, CV=Coefficient of variation, SE=Standard error

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

5.3.2   Summary statistics

Ukulinga

The descriptive statistics for Ukulinga are shown in Table 5.8. The data was significant (p≤0.05) for all the hybrids for all traits. Heritability was generally high (H^2>0.50) for most traits except for ear position, 100-grain weight, root lodging and plant stand which were below 0.5. Coefficient of variation (CV) was low for all traits except for total lodging percent, root lodging and stem lodging. Grain yield ranged from 3.31 t/ha to 13.45 t/ha. Number of ears and field weight ranged from 12 to 31 ears.

Cedara

The descriptive statistics for Cedara are shown in Table 5.9. The data was significant for all entries for all traits except for grain row number. Grain yield ranged from 2.71 to 7.55 t/ha. Number of ears and field weight had a minimum of 12 ears and 1.5 kg and maximum values of 26 ears and 4.1 kg respectively. Anthesis-silking interval had the least range -1.0 – 0. Plant height and ear height showed large variations within each trait. Coefficients of variation were low for most traits except for root lodging which had a CV of 331.35. Heritability for yield was quite high (0.69). Heritability estimates for all traits ranged from low (0.11%) to high (0.87%) for grain row number and silking days.

Table 5.8   Descriptive statistics of yield and secondary traits for Ukulinga

Trait	SD	Minimum	Maximum	Median	SED	LSD	CV	Heritability	P value
Anthesis date	3.08	75.00	87.00	83.00	1.74	3.51	2.09	0.80	***
Silking days	3.01	75.00	86.00	82.00	1.66	3.34	2.06	0.82	***
Ear height	18.44	89.00	194.00	140.00	14.28	28.80	9.50	0.51	***
Ear position	0.05	0.37	0.63	0.51	0.04	0.08	8.18	0.35	**
Field weight	0.75	1.60	6.70	3.20	0.51	1.02	13.85	0.61	***
Grain rows	0.96	11.33	16.67	14.00	0.76	1.53	5.50	0.54	***
GW100	5.48	24.00	56.00	40.00	4.40	8.88	10.65	0.48	***
Grain yield	1.51	3.31	13.45	6.55	1.03	2.07	13.85	0.62	***
Total Lodging %	21.85	0.00	75.00	26.79	15.74	31.75	45.94	0.52	***
Grain moisture content	0.95	13.80	18.20	16.60	0.75	1.51	4.46	0.56	***
Ear number	3.76	12.00	31.00	19.00	2.40	4.84	10.87	0.71	***
Plant height	18.59	229.00	321.00	277.00	13.62	27.46	4.24	0.54	***
Plant stand	1.91	9.00	19.00	16.00	1.62	3.43	9.26	0.27	*
Root Lodging	2.26	0.00	11.00	0.00	1.69	3.42	110.10	0.46	***
Stem Lodging	3.13	0.00	11.00	3.00	1.91	3.85	49.43	0.72	***
Shelling %	2.85	70.40	92.15	79.98	1.90	4.03	2.50	0.70	***.

·SD=Standard deviation, SED=Standard error of difference, LSD=Least significant difference, CV=Coefficient of variation, P=Probability

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant

Table 5.9   Descriptive statistics of yield and secondary traits for Cedara

Trait	SD	Min	Max	Median	SED	LSD	CV	Heritability	P value
Anthesis date	3.34	72.00	85.00	79.00	1.66	3.35	2.07	0.86	***
Silking days	3.38	71.00	84.00	79.00	1.65	3.33	2.03	0.87	***
Ear height	15.95	79.00	159.00	120.00	12.30	24.80	9.37	0.53	***
Ear position	0.04	0.37	0.57	0.46	0.03	0.07	7.13	0.62	***
Field weight	0.49	1.50	4.10	2.70	0.35	0.71	12.81	0.66	***
Grain rows	3.77	12.00	48.00	14.00	3.67	7.40	25.04	0.11	NS
GW100	6.13	18.00	48.00	28.00	5.20	10.48	18.02	0.43	***
Grain yield	0.96	2.71	7.55	5.09	0.66	1.34	12.66	0.69	***
Total Lodging %	29.16	0.00	121.43	70.59	21.80	43.96	29.14	0.47	***
Grain moisture content	1.35	15.20	20.90	18.35	0.72	1.46	3.61	0.84	***
Ear number	2.45	12.00	26.00	18.00	2.15	4.33	11.86	0.37	**
Plant height	19.91	191.00	295.00	263.00	15.51	31.28	5.40	0.44	***
Root Lodging	0.44	0.00	3.00	0.00	0.37	0.75	331.35	0.45	***
Stem Lodging	4.72	0.00	17.00	12.00	3.40	7.26	29.16	0.54	***
Shelling %	2.85	70.40	92.15	79.98	2.46	5.18	3.20	0.38	***.

SD=Standard deviation, SED=Standard error of difference, LSD=Least significant difference, CV=Coefficient of variation, P=Probability

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %), ns=not significant

5.3.3   Mean performance of the hybrids

The hybrid data for Ukulinga are presented in Table 5.10. All the top 15 selected hybrids outperformed the control hybrid. Hybrid 16XP11 was ranked the highest. It had also the highest field weight, ear position and ear height. The control hybrid, 11C1579, was ranked number 33. The results for Cedara are presented in Table 5.11. The hybrid 16XP33 was ranked the highest with grain yield of 7.07 t/ha which was lower than the highest at Ukulinga. The control hybrid, 11C1579, was ranked number 20.

Table 5.10   Top 10 and bottom 10 yielding hybrids at Ukulinga

Top yielding hybrids

Rank	Entry	Genotype	GY	AD	SD	EH	EPO	FW	GRN	GW100	TL %	MOI	NE	PH	PS	SL	SH
1	11	16XP11	10.03	86.40	85.50	165.93	0.57	5.01	15.30	48.16	20.56	17.18	22.60	296.28	17.39	3.48	82.02
2	33	16XP33	8.71	84.92	84.00	136.48	0.48	4.33	14.38	49.74	16.90	16.49	18.91	280.72	15.55	2.97	81.05
3	17	16XP17	8.57	81.45	80.50	139.19	0.52	4.40	13.67	41.47	15.74	17.02	21.76	277.08	16.29	2.24	78.52
4	29	16XP29	8.16	82.56	81.50	123.75	0.45	3.87	14.37	35.99	30.40	17.10	21.38	271.98	17.08	3.86	84.10
5	21	16XP21	7.93	84.61	83.50	162.11	0.55	3.83	14.66	44.43	23.87	17.09	19.14	290.05	16.76	3.59	82.69
6	9	16XP09	7.90	86.11	85.00	146.94	0.52	4.03	14.63	36.40	55.58	16.57	21.91	284.37	17.30	9.05	78.62
7	18	16XP18	7.50	81.49	81.50	153.04	0.55	3.63	14.99	33.87	11.56	16.96	24.55	285.19	16.32	2.12	83.04
8	25	16XP25	7.30	83.03	82.00	149.74	0.54	3.68	14.65	41.72	29.36	16.68	18.80	273.37	17.27	4.58	79.39
9	15	16XP15	7.26	82.60	81.50	145.91	0.52	3.70	13.68	38.31	19.62	16.74	21.73	277.65	16.18	0.45	80.84
10	24	16XP24	7.22	85.00	84.00	139.63	0.52	3.59	13.37	39.86	29.04	16.01	22.94	268.95	16.40	2.46	80.36
								Bottom yielding hybrids									
35	26	16XP26	5.88	85.79	84.99	131.08	0.46	2.88	13.65	34.74	14.38	16.50	17.30	286.40	13.62	0.79	81.63
36	23	16XP23	5.73	83.00	82.00	140.28	0.51	2.94	13.97	44.08	25.29	17.22	16.38	272.84	15.60	3.27	79.10
37	6	16XP06	5.59	83.10	82.00	160.03	0.53	3.04	13.97	40.77	41.16	17.29	17.48	292.93	15.08	5.18	74.78
38	32	16XP32	5.31	86.47	85.50	132.62	0.49	2.73	12.96	39.63	9.27	16.62	16.63	265.22	14.45	0.78	78.12
39	20	16XP20	5.30	80.97	80.00	146.02	0.54	2.77	13.98	39.70	10.73	17.03	19.26	268.60	16.83	0.77	78.88
40	16	16XP16	5.25	80.91	80.00	141.12	0.52	2.54	13.68	34.36	11.01	14.88	17.96	274.49	13.81	1.30	79.30
41	36	16XP36	4.60	78.50	77.50	132.24	0.51	2.18	12.04	39.05	30.34	13.91	16.76	256.52	15.58	3.05	82.97
42	37	16XP37	4.54	78.47	78.50	130.28	0.50	2.18	14.01	36.11	41.59	15.83	15.49	263.86	11.88	-0.27	80.83
43	4	16XP04	4.46	80.65	79.50	137.06	0.47	2.25	14.01	37.75	33.80	15.97	14.03	292.08	13.49	4.79	79.74
44	10	16XP10	4.10	84.48	83.50	145.90	0.54	2.10	14.01	37.30	22.14	16.96	12.44	270.79	12.42	1.86	76.68
LSD			2.07	3.51	3.34	28.80	0.08	1.02	1.53	8.88	31.75	1.51	4.84	27.46	3.43	3.85	4.03
CV%			13.85	2.09	2.06	9.50	8.18	13.85	5.50	10.65	45.94	4.46	10.87	4.24	9.26	49.43	2.50[13]

GY=Grain yield, AD=Anthesis date, SD=Silking date, EH=Ear height, EPO=Ear position, FW=field weight, GRN=Grain row number, GW100=100-grain weight, TL%=Total lodging percentage, MOI=grain moisture content, NE=Number of ears per plot, PH= Plant height, PS=Plant stand, SL= Stem lodging, SH=shelling percentage, LSD=Least significant difference, CV=Coefficient of variation

Table 5.11 Top 10 and bottom 10 yielding hybrids at Cedara

Top yielding hybrids

Rank	Entry	Hybrid	GY	ASI	AD	SD	EH	EPO	FW	GRN	GW100	TL %	MOI	NE	PH	RL	SL	SH
1	33	16XP33	7.07	-0.85	82.00	81.01	123.53	0.48	3.83	14.17	38.00	70.47	19.50	20.00	261.79	0.00	11.84	79.98
2	29	16XP29	6.69	-0.67	81.98	81.42	118.09	0.46	3.62	13.98	28.99	57.60	19.01	23.00	258.28	0.00	10.34	80.29
3	27	16XP27	6.23	-0.69	80.91	79.90	119.60	0.44	3.47	13.66	31.04	43.26	18.39	17.50	275.51	0.00	6.95	81.18
4	24	16XP24	6.09	-0.66	80.96	80.40	124.15	0.49	3.21	14.06	28.96	75.15	18.51	22.00	252.21	0.00	11.22	79.56
5	6	16XP06	6.03	-0.66	83.02	82.58	107.66	0.43	3.31	13.69	33.00	73.30	19.29	20.50	253.01	0.00	12.28	78.48
6	28	16XP28	6.01	-0.70	82.10	81.78	112.02	0.47	3.30	13.64	31.00	86.07	19.93	18.50	246.31	0.00	13.20	79.24
7	36	16XP36	5.88	-0.73	73.92	72.89	107.43	0.45	2.89	13.03	27.00	31.43	15.47	23.50	236.39	0.00	5.19	80.18
8	39	16XP39	5.86	-0.65	74.94	73.85	116.12	0.46	2.92	14.31	24.03	36.06	17.17	17.50	250.02	0.50	5.39	78.90
9	42	16XP42	5.85	-0.65	73.59	72.67	111.28	0.46	2.90	12.68	28.02	28.71	16.17	17.50	242.57	0.00	5.81	83.23
10	43	16XP43	5.77	-0.53	76.11	75.75	108.76	0.43	2.96	12.81	34.98	56.33	17.58	17.50	250.82	1.00	8.31	76.40
							Bottom yielding hybrids											
35	17	16XP17	4.42	-0.71	81.90	80.84	134.43	0.49	2.52	13.68	28.01	78.30	19.93	16.00	274.26	0.00	12.77	80.51
36	14	16XP14	4.30	-0.82	77.05	76.60	117.76	0.45	2.40	13.49	23.01	78.88	17.34	18.50	265.35	0.00	12.28	80.58
37	19	16XP19	4.29	-0.64	83.00	82.53	135.92	0.51	2.40	14.31	26.01	86.78	19.44	19.00	266.80	0.00	15.86	78.72
38	25	16XP25	4.18	-0.72	80.52	80.07	118.81	0.48	2.32	13.99	31.02	96.79	18.64	15.00	253.01	0.50	16.27	76.49
39	15	16XP15	3.91	-0.72	79.10	78.75	129.49	0.49	2.23	16.01	28.00	86.79	18.86	17.50	261.60	0.00	14.46	75.53
40	12	16XP12	3.82	-0.66	82.05	81.64	120.24	0.44	2.14	13.97	24.98	91.79	18.02	16.00	278.98	0.00	15.50	81.27
41	1	16XP01	3.77	-0.74	77.08	76.26	108.48	0.41	2.04	16.35	27.00	76.59	17.51	18.50	269.30	0.00	12.31	77.20
42	3	16XP03	3.72	-0.67	83.37	82.69	107.59	0.43	2.25	14.32	19.01	84.13	17.50	18.00	243.20	0.00	14.44	78.22
43	22	16XP22	3.69	-0.71	79.08	78.61	120.94	0.45	2.04	14.02	27.98	102.18	18.56	17.00	266.77	0.00	16.06	80.31
44	9	16XP09	3.55	-0.68	82.94	81.95	133.63	0.53	2.01	14.99	27.00	84.78	19.82	15.00	247.30	0.00	13.10	78.75
LSD			1.34	0.27	3.35	3.33	24.80	0.07	0.71	7.40	10.48	43.96	1.46	4.33	31.28	0.75	7.26	5.18
CV %			12.66	-15.57	2.07	2.03	9.37	7.13	12.81	25.04	18.02	29.14	3.61	11.86	5.40	331.35	29.16	3.20[14]

GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH=Ear height, EPO=Ear position, FW=field weight, GRN=Grain row number, GW100=100-grain weight, TL%=Total lodging percentage, MOI=grain moisture content, NE=Number of ears per plot, PH= Plant height, RL=Root lodging, SL= Stem lodging, SH=shelling percentage, LSD=Least significant difference, CV=Coefficient of variation

5.3.4 Line by tester analysis

The general ANOVA (Table 5.12) showed that the line main effects were significant (p>0.05) for grain yield, number of ears per plot, field weight, shelling percentage, grain row number, 100-grain weight, plant height an plant stand at Ukulinga. The line main effects for the rest of the traits were not significant (p>0.05) (Table 5.12). Significant differences were observed for GCA_t for anthesis date, silking date, grain row number, plant height and shelling percentage. The SCA only showed significant differences (p>0.05) only for plant height and shelling percentage. Coefficient of variation was only high for shelling percentage (Table 5.12).

Analysis of variance showed that significant differences (p>0.05) were observed among GCA_l for grain yield, ear height, field weight, 100-grain weight, grain moisture content and shelling percentage (Table 5.13). Among the GCA_t, significant differences (p>0.05 were observed for field weight and 100-grain weight (Table 5.13). SCA showed significant differences (p>0.05) only for 100-grain weight (Table 5.13).

The ANOVA in Table 5.14 shows that the line main effects (GCA_l) were significant (p≤0.05) for grain yield, field weight, root lodging and stem lodging. Significant differences were observed between the testers (GCA_t) for grain yield, field weight, 100-grain weight and grain moisture content. Lines x tester interaction (SCA) effects were non-significant for all traits (Table 5.14). The sites were significant as anticipated. Line x site interaction effects were significant (p≤0.05) for grain yield, root lodging and field weight as shown by the general ANOVA in Table 5.14. Site x tester interaction effects only showed significant differences (p≤0.05) for 100-grain weight and shelling percentage. Site x line x tester interaction effects were only significant (p≤0.05) for root lodging.

Table 5.12   Mean squares for line by tester and their significance for grain yield and related traits at Ukulinga

SOV	DF	GY	ASI	AD	SD	EH	NE	FW	GRN	GW100	MOI	PH	PS	SH
Rep	1	14.64**	0.02	12	11.02	24.1	22.69	4.0252**	0.15	48	0.1	14.1	0.75	0.19
Line	11	5.56**	0.02	6.61	6.75	456.3	29.20**	1.2861**	1.20*	53.36*	0.73	537.5*	6.52*	7.20**
Tester	1	3.13	0.02	18.75*	17.52*	990.1	2.52	0.39	7.26***	56.33	0.16	1587*	0.08	13.02*
Line X Tester	11	1.52	0.02	3.89	3.98	423	10.16	0.35	0.31	18.7	0.61	548.9*	1.45	4.79*
Residual	23	1.59	0.02	3.87	3.89	242.7	7.95	0.39	0.53	22.43	0.68	204.2	2.62	2.14
Mean		6.66	-1.02	83.87	82.85	140.5	19.02	3.37	13.94	38.75	16.69	278.9	15.83	1.1
LSD		2.61	0.3	4.07	4.08	32.23	5.83	1.29	1.51	9.8	1.71	29.56	3.35	3.03
SE		1.26	0.14	1.97	1.97	15.58	2.82	0.62	0.73	4.74	0.83	14.29	1.62	1.46
CV%		18.92	-14.44	2.35	2.38	11.09	14.82	18.5	5.24	12.21	4.96	14.29	10.22	132.61[15]

SOV=Source of variation, DF=Degrees of freedom, Rep=Replication, GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH=Ear height, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, PH= Plant height, PA=Plant stand, SH=shelling percentage, LSD=Least significant difference, SE=Standard error, CV=Coefficient of variation

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

Table 5.13   Mean squares for line by tester and their significance for grain yield and related traits at Cedara

Source of variation	DF	GY	ASI	AD	SD	EH	NE	FW	GRN	GW100	MOI	PH	PS	SH
Rep	1	0.02	5.33	8.33	0.33	10.08	20.02	0.03	23.15	75.00*	0.01	1083	0.52	10.17
Line	11	2.35**	0.11	3.42	3.61	321.98*	10.14	0.65**	23.65	43.24*	1.49**	393.92	1.05	17.20*
Tester	1	13.73	0	8.33	8.33	444.08	7.52	3.00***	7.26	481.33****	10.55	1.33	0.19	3.05
Line X Tester	11	0.27	0.14	5.33	6.15	85.13	9.2	0.08	28.19	50.06**	0.67	259.11	1.01	6.37
Residual	23	0.56	0.12	3.12	3.16	144.13	6.24	0.17	24.62	14.3	0.34	279.61	0.74	5.59
Mean		5.13	-0.67	81.33	80.67	119.1	18.44	2.84	14.92	29.58	18.81	260.8	16.31	80.24
LSD		1.54	0.7	3.65	3.68	24.83	5.17	0.85	10.26	7.82	1.21	34.59	1.78	4.89
SE		0.75	0.34	1.77	1.78	12.01	2.5	0.41	4.96	3.78	0.59	16.72	0.86	2.37
CV%		14.55	-51.08	2.17	2.2	10.08	13.55	14.47	33.26	12.78	3.12	6.41	5.27	2.95[16]

SOV=Source of variation, DF=Degrees of freedom, Rep=Replication, GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH=Ear height, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, PH= Plant height, PS=Plant stand, SH=shelling percentage, LSD=Least significant difference, SE=Standard error, CV=Coefficient of variation

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

Table 5.14   Mean squares for line by tester and their significance across two sites

Source of variation	DF	GY	AD	SD	EH	FW	GRN	GW100	MOI	NE	PH	RL	SL	SH
Site	1	56.33***	155.04***	114.84**	10965.40***	6.88***	22.69	2016.67***	107.74***	8.17	7848.20**	24.00**	1560.09***	25.93*
Site/Rep	2	7.33***	10.17	5.68	17.10	2.03**	11.65	61.5	0.05	21.35	548.50	0.19	92.34***	6.07
Site/Rep/Row	38	2.62**	4.87	5.23	314.00	0.64*	11.20	35.11	0.54	10.65	411.80	2.70**	13.56	7.84
Line	11	2.61**	7.8	7.73	255.80	0.62*	15.48	38.42	1.10	17.82	442.50	2.67**	19.95*	9.73
Tester	1	9.57***	11.78	10.48	70.20	1.62**	9.11	380.32***	7.18*	0.17	278.80	0.07	12.06	13.82
Site X Line	11	1.72*	2.31	2.32	235.50	0.47*	14.75	14.35	0.67	12.11	183.30	4.43***	12.13	9.48
Site X Tester	1	0.58	1.2	1.08	364.30	0.27	0.01	164.85**	3.75	0.15	392.80	0.23	0.35	39.34**
Line X Tester	11	0.29	2.05	2.02	361.20	0.06	14.48	32.50	0.89	11.62	258.60	0.31	1.71	10.39
Site X Line X Tester	11	0.83	1.88	1.88	117.90	0.19	15.91	23.22	0.52	4.61	261.20	1.57*	9.96	3.50
Residual	8	0.40	5.91	6.21	180.40	0.14	9.80	16.09	0.83	8.70	366.00	0.35	5.64	3.87
Mean		5.91	82.60	81.76	129.90	3.11	14.42	34.19	17.76	18.71	269.75	0.66	7.93	79.78
LSD		1.48	5.65	5.79	31.21	0.88	7.28	9.32	2.12	6.85	44.46	1.38	5.52	4.57
SE		0.63	2.43	2.49	13.43	0.38	3.13	4.01	0.91	2.95	19.13	0.59	2.37	1.97
CV%	2.47[17.]	10.76	2.94	3.05	10.35	12.25	21.70	11.74	5.14	15.75	7.09	98.20	29.56	2.47[17.]

DF=Degrees of freedom, Rep=Replication, GY=Grain yield, AD=Anthesis date, SD=Silking date, EH=Ear height, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, NE=Number of ears per plot, PH= Plant height, RL=Root lodging, SL=Stem lodging, SH=shelling percentage, LSD=Least significant difference, SE=Standard error, CV=Coefficient of variation

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

5.3.5   Combining ability analysis

5.3.5.1   General combining ability effects

Ukulinga

General combining ability effects for Ukulinga are presented in Table 5.15. Positive GCA effects were significant (p≤0.05) for grain yield, field weight and 100-grain weights for line DPVAL12. Positive and non-significant GCA effects were also observed for grain yield for lines DPVAL02, DPVAL03, DPVAL07, DPVAL08, DPAVAL, 09 and DPVAL13. Positive GCA effects were also observed for grain texture for lines DPVAL04 and DPVAL12. Significant (p≤0.05) and negative (undesirable) GCA effects were observed for root lodging and stem lodging for lines DPVAL03 and DPVAL09, respectively. The same was also observed for grain yield and field weight for line DPVAL10 making it the worst general combiner for yield. General combining ability effects for grain moisture content were negative and significant for line DPVAL02. Most lines had positive and non-significant GCA effects for anthesis-silking interval except for DPVAL08.

Cedara

Table 5.16 is showing GCA effects for Cedara. GCA effects for grain yield for all lines were not significant. Six lines, DPVAL03, DPVAL03, DPVAL04, DPVAL09, DPVAL10 and DPVAL13, showed negative GCA effects for grain yield. DPVAL07 showed significant (p≤0.05) positive GCA effects for anthesis-silking interval whereas DPVAL10 and DPVAL 12 had significant (p≤0.05) negative GCA effects for anthesis-silking interval. Positive GCA effects were significant for ear height and ear position for line DPVAL09. Shelling percentage GCA effects were positive and significant (p≤0.05) for line DPVAL05. Grain row number and root lodging GCA effects were positive and significant (p≤0.05) for DPVAL10 and DPVAL01, respectively.

5.3.5.2   Specific combining ability effects

Ukulinga

Results for SCA effects at Ukulinga are presented in Table 5.17. There was no line that had significant (p≤0.05) positive effects with both testers. Line DPVAL06 had the highest SCA effects for grain yield with tester DQPL22. DPVAL01 had the second highest

positive SCA effects for grain yield with tester DPVAL11.. Unfavourable significant (p≤0.05) SCA effects for grain yield were observed for line DPVAL06 with tester DPVAL11.

Cedara

Specific combining ability effects for Cedara are presented in Table 5.18. Line DPVAL06 had the largest significant (p≤0.05) positive SCA effects for grain yield with tester DPVAL11. Lines DPVAL03, DPVAL04, DPVAL06, DPVAL08 and DPVAL10 had positive SCA effects for grain yield with tester DPVAL11. Worst SCA effects were observed for lines, DPAVL02, DPVAL07, DPVAL09 and DPVAL12 with tester DPVAL11. Lines DPVAL03, DPVAL04, DPVAL06, DPVAL08 and DPVAL10 showed large negative SCA effects for grain yield with tester DQPL22. Lines DPVAL01, DPVAL02, DPVAL05, DPVAL07, DPVAL09, DPVAL12 and DPVAL13 had positive SCA effects for grain yield with tester DQPL22. Nevertheless, the SCA effects were not significant (p>0.05).

Table 5.15   GCA effects for grain yield and secondary traits for Ukulinga

Lines	Grain yield	Anthesis silking interval	Anthesis days	Silking days	Field weight	Shelling percentage	Ear height	Ear position	Number ears/plot	Grain row number	100-grain weight	Grain moisture content	Plant height	Plant stand	Root lodging	Stem lodging	Texture
DPVAL01	-0.01	0.02	-1.37	-1.35	-0.04	0.08	1.94	0.01	1.07	0.56	1.21	-0.19	-0.17	0.92	-0.85	-1.20	-0.09
DPVAL02	0.61	0.02	-0.38	-0.35	0.27	-0.08	-16.72	-0.05	2.89	-0.28	0.40	-1.00*	-6.67	1.17	-0.10	0.49	-0.46
DPVAL03	0.31	0.02	0.12	0.15	0.23	-1.49	7.22	0.03	-0.93	0.39	-2.84	0.30	-3.92	0.67	3.15*	-2.27	0.24
DPVAL04	-1.29	0.02	-0.63	-0.60	-0.72	0.90	-4.29	-0.04	-3.52	-0.11	-2.48	-0.56	12.83	-2.33	-0.35	-1.89	1.31*
DPVAL05	-0.08	0.02	-0.38	-0.35	0.04	-1.94	11.90	0.02	-2.24	-0.61	1.96	0.30	14.08	0.92	-0.35	0.42	-0.46
DPVAL06	-0.31	0.02	-0.13	-0.10	-0.12	-0.92	5.78	0.03	-1.35	-0.78	0.22	0.56	1.08	-0.33	-0.60	0.28	-0.16
DPVAL07	0.78	0.02	-2.13	-2.10	0.22	3.02	-16.63	-0.03	1.71	0.72	-2.04	0.32	-17.42	0.17	-0.35	0.45	-0.48
DPVAL08	0.00	-0.23	-0.63	-0.85	0.08	-2.29	-16.22	-0.03	-1.73	-0.44	-0.29	0.09	-19.17	-0.58	-0.85	-3.09	-0.54
DPVAL09	1.47	0.02	2.12	2.15	0.66	1.87	8.47	0.03	4.00	0.22	-1.10	0.16	4.33	1.17	-0.85	5.35**	-0.25
DPVAL10	-1.92*	0.02	1.62	1.65	-1.00*	-1.60	-1.94	0.01	-4.59	-0.44	-0.01	0.13	-8.42	-2.58	-0.10	-2.82	-0.44
DPVAL12	1.95*	0.02	1.87	1.90	1.05*	2.21	8.71	0.01	1.19	0.89	10.13**	0.14	8.58	0.67	-1.10	-1.40	1.40*
DPVAL13	0.26	0.02	-0.13	-0.10	0.08	0.25	8.62	0.01	2.81	-0.11	-4.32	-0.37	14.83	0.17	2.40	3.73	-0.08
SE	0.79	0.07	1.23	1.24	0.38	1.66	9.80	0.02	2.36	0.52	3.35	0.40	11.10	1.22	1.28	1.82	0.60[1]

SE=Standard error

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %)

Table 5.16   GCA effects for grain yield and secondary traits for Cedara

Lines	Grain yield	Anthesis silking interval	Anthesis days	Silking days	Field weight	Shelling percentage	Ear height	Ear position	Number ears/plot	Grain row number	100-grain weight	Grain moisture content	Plant height	Plant stand	Root lodging	Stem lodging	Grain texture
DPVAL01	-0.78	-0.06	-1.37	-1.44	-0.49	-2.60	-9.03	-0.03	-0.19	0.23	-0.58	-0.45	-6.83	-0.31	0.90**	-1.81	-0.31
DPVAL02	0.26	0.02	-1.33	-1.17	0.06	-1.17	-1.77	-0.02	2.31	-0.42	-2.58	-0.34	0.92	0.19	-0.10	0.19	-0.33
DPVAL03	-1.14	0.00	0.58	0.72	-0.54	-1.90	-7.77	-0.02	-1.94	-0.74	-4.58	-0.71	-16.08	0.69	0.15	3.19	0.42
DPVAL04	-0.22	-0.01	0.03	-0.04	-0.14	-0.21	-0.84	-0.01	-1.44	-1.53	-1.58	-0.74	5.42	-0.06	-0.10	-3.06	0.67
DPVAL05	0.60	-0.03	-0.19	-0.28	0.39	4.45*	-1.45	0.00	-1.69	-1.08	1.42	-0.26	15.67	-0.06	-0.10	-3.06	-0.37
DPVAL06	0.86	0.03	1.34	1.53	0.46	-2.32	-10.80	-0.02	1.06	-1.21	2.42	0.81	-13.08	-0.56	-0.10	0.94	-0.34
DPVAL07	0.69	0.14*	-0.88	-0.73	0.31	0.86	-6.44	-0.01	2.81	0.56	-3.08	-0.27	-10.83	0.94	-0.10	-0.56	-0.33
DPVAL08	0.09	0.01	-0.29	-0.37	0.11	2.10	-4.73	-0.02	0.56	-1.71	5.92	0.39	0.92	-0.31	-0.10	0.19	-0.35
DPVAL09	-0.86	-0.04	1.69	1.61	-0.46	-1.00	19.77*	0.08**	-0.19	-0.49	-3.58	1.09	-0.33	0.69	-0.10	1.69	-0.31
DPVAL10	-0.09	-0.20**	-0.09	-0.20	0.01	0.07	10.69	0.03	-0.69	7.46**	-0.08	-0.32	5.42	-0.31	-0.10	-0.81	-0.32
DPVAL12	1.27	-0.20***	-0.05	-0.37	0.64	-0.45	3.96	0.00	1.06	-0.25	4.42	0.22	7.67	-0.31	-0.10	-0.56	1.66*
DPVAL13	-0.69	-0.07	0.78	0.93	-0.36	0.72	-0.24	-0.03	-1.69	-1.42	1.92	0.56	11.17	-0.56	-0.10	3.69	-0.08
SE	0.73	0.06	0.90	0.92	0.38	1.56	6.91	0.02	1.52	2.21	3.15	0.54	9.50	0.49	0.28	2.06	0.59

SE=Standard error

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

Table 5.17   SCA for grain yield and secondary traits for crosses at Ukulinga

Tester	Line	Grain yield	Anthesis silking interval	Anthesis days	Silking days	Field weight	Shelling percentage	Ear height	Ear position	Number ears/plot	Grain row number	100-grain weight	Grain Moisture content	Plant height	Plant stand	Root lodging	Stem lodging	Texture
DPVAL11	DPVAL01	0.42	-0.02	0.13	0.10	0.14	1.61	-2.61	-0.01	3.18*	1.38	-3.05	-0.53	-2.00	0.79	-0.77	0.02	0.18
DPVAL11	DPVAL02	-0.04	-0.02	-0.88	-0.90	0.01	0.65	-22.6*	-0.07**	-0.96	-1.28	0.11	-0.02	-11.00	0.54	-1.02	2.24*	0.47
DPVAL11	DPVAL03	-0.58	-0.02	1.62	1.60	-0.23	-0.89	-4.39	-0.02	-1.19	0.69	-4.47*	0.51	-3.75	-0.46	2.73*	-3.15**	-0.18
DPVAL11	DPVAL04	-0.69	-0.02	-2.13*	-2.15*	-0.35*	-0.03	2.26	0.01	-1.39	-0.59	2.65	-0.17	1.00	0.54	-0.27	1.55	-1.4**
DPVAL11	DPVAL05	0.32	-0.02	-0.38	-0.40	0.11	0.55	7.42	-0.01	-0.08	0.43	-0.82	-0.43	17.75	-0.71	-0.77	1.35	0.31
DPVAL11	DPVAL06	-1.0**	-0.02	-0.13	-0.15	-0.33*	-2.71*	7.23	0.02	-0.86	-0.33	2.81	0.01	7.75	-0.46	-0.02	0.48	-0.08
DPVAL11	DPVAL07	-0.69	-0.02	-0.13	-0.15	-0.28	-1.32	-4.57	0.01	0.36	-0.38	1.47	0.13	-18.75	-0.46	-0.27	0.82	0.33
DPVAL11	DPVAL08	0.36	0.23**	0.37	0.60	0.20	1.23	19.02	0.04	1.93	0.48	0.39	0.76*	23.50*	0.79	-0.77	1.05	0.51
DPVAL11	DPVAL09	0.29	-0.02	0.62	0.60	0.20	-1.02	-4.27	-0.01	-0.43	0.44	-0.92	-0.17	-4.00	0.04	-0.27	-1.12	0.26
DPVAL11	DPVAL10	-0.52	-0.02	-0.38	-0.40	-0.29	0.88	0.06	0.01	-2.08	-0.34	-0.18	0.22	-8.25	-0.71	0.48	0.65	0.36
DPVAL11	DPVAL12	0.29	-0.02	1.37	1.35	0.12	0.97	10.47	0.03	1.98	0.31	0.38	0.32	0.25	0.54	-0.52	0.36	-1.33*
DPVAL11	DPVAL13	0.10	-0.02	-0.13	-0.15	-0.05	0.09	-4.90	-0.01	0.21	-0.21	0.78	-0.48	-2.50	-0.46	1.48	-2.33*	0.60
DQPL22	DPVAL01	-0.71	0.02	-0.13	-0.10	-0.27	-1.61	3.14	0.01	-3.06*	1.84	2.91	0.56	2.00	-0.79	0.77	0.30	-0.18
DQPL22	DPVAL02	-0.25	0.02	0.88	0.90	-0.14	-0.65	23.08*	0.07	1.07	-1.74	-0.25	0.05	11.00	-0.54	1.02	-1.92	-0.46
DQPL22	DPVAL03	0.29	0.02	-1.62	-1.60	0.11	0.89	4.92	0.02	1.30	1.11	4.33*	-0.49	3.75	0.46	-2.73*	3.47**	0.18
DQPL22	DPVAL04	0.40	0.02	2.13*	2.15*	0.22	0.03	-1.74	-0.01	1.51	-1.01	-2.79	0.20	-1.00	-0.54	0.27	-1.23	1.41**
DQPL22	DPVAL05	-0.61	0.02	0.38	0.40	-0.23	-0.55	-6.89	0.01	0.19	0.78	0.68	0.46	-17.75	0.71	0.77	-1.03	-0.31
DQPL22	DPVAL06	0.72	0.02	0.13	0.15	0.20	2.71*	-6.70	-0.02	0.97	-0.68	-2.95	0.02	-7.75	0.46	0.02	-0.15	0.09
DQPL22	DPVAL07	0.40	0.02	0.13	0.15	0.16	1.32	5.09	-0.01	-0.24	-8.38**	-1.62	-0.11	18.75	0.46	0.27	-0.50	-0.33
DQPL22	DPVAL08	-0.66	-0.23**	-0.37	-0.60	-0.33*	-1.23	-18.49	-0.03	-1.82	8.48**	-0.53	-0.74	-23.5*	-0.79	0.77	-0.73	-0.51
DQPL22	DPVAL09	-0.58	0.02	-0.62	-0.60	-0.32*	1.02	4.79	0.01	0.54	1.64	0.78	0.19	4.00	-0.04	0.27	1.44	-0.26
DQPL22	DPVAL10	0.23	0.02	0.38	0.40	0.16	-0.88	0.47	-0.01	2.19	-1.54	0.03	-0.19	8.25	0.71	-0.48	-0.33	-0.36
DQPL22	DPVAL12	-0.59	0.02	-1.37	-1.35	-0.24	-0.97	-9.94	-0.03	-1.87	0.74	-0.52	-0.30	-0.25	-0.54	0.52	-0.04	1.33*
DQPL22	DPVAL13	-0.40	0.02	0.13	0.15	-0.08	-0.09	5.43	0.01	-0.10	-0.64	-0.92	0.50	2.50	0.46	-1.48	2.65**	-0.59
	SE	**0.37**	**0.07**	**0.94**	**0.95**	**0.16**	**1.21**	**9.60**	**0.02**	**1.37**	**2.42**	**1.91**	**0.37**	**11.22**	**0.58**	**1.05**	**1.00**	**0.53**

SE=Standard error

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %)

Table 5.18   SCA for grain yield and secondary traits for crosses at Cedara

Tester	Line	Grain yield	Anthesis-silking interval	Anthesis days	Silking days	Field weight	Shelling percentage	Ear height	Ear position	Number ears/plot	Grain row number	100-grain weight	Grain Moisture content	Plant height	Plant stand	Root lodging	Stem lodging	Texture
DPVAL11	DPVAL01	-0.02	-0.08	-2.48*	-2.70*	-0.05	-1.07	2.06	0.01	0.65	1.38	1.17	-0.50	17.83	0.94	-0.90**	1.15	0.36
DPVAL11	DPVAL02	-0.14	0.00	-0.55	-0.53	-0.05	-0.76	-7.22*	-0.04**	-0.85	0.69	1.17	0.21	1.58	0.44	0.10	0.15	0.34
DPVAL11	DPVAL03	0.26	0.02	1.83	1.82	0.20	-0.15	-2.75	-0.01	1.90	0.43	-2.83	-0.08	-11.42	-0.56	-0.15	-0.85	-0.41
DPVAL11	DPVAL04	0.13	0.00	-0.44	-0.68	0.10	1.94	1.03	-0.01	0.90	-0.38	0.17	0.24	-1.92	0.69	0.10	-2.10	-0.66
DPVAL11	DPVAL05	-0.08	0.06	0.69	0.91	-0.03	2.51*	2.58	0.02	-0.35	0.44	3.17	0.51	-5.17	-0.31	0.10	2.40	0.33
DPVAL11	DPVAL06	0.54*	0.00	0.89	0.88	0.25	-1.53	1.37	0.01	1.40	0.31	4.17	0.13	2.08	0.19	0.10	-0.60	0.30
DPVAL11	DPVAL07	-0.45	0.18**	-1.11	-1.10	-0.25	0.54	0.49	0.02	-1.35	1.84	0.67	-0.06	-10.17	-0.31	0.10	1.40	0.34
DPVAL11	DPVAL08	0.14	-0.08	0.88	1.10	0.05	1.59	8.21**	0.05***	2.40	1.11	-8.33*	-0.72	-0.92	-0.56	0.10	1.65	0.32
DPVAL11	DPVAL09	-0.23	-0.04	0.28	0.05	-0.13	-1.10	-3.10	0.02	-2.85	0.78	4.17	0.58	-6.67	-0.06	0.10	-0.85	0.31
DPVAL11	DPVAL10	0.12	0.21**	-0.35	-0.12	0.10	-0.48	2.96	0.01	-1.35	-8.38**	0.67	0.16	3.58	-0.06	0.10	-1.85	0.36
DPVAL11	DPVAL12	-0.21	0.04	-0.23	-0.22	-0.13	0.04	1.96	-0.01	-0.10	1.64	-0.83	0.29	6.83	-0.56	0.10	-0.10	-1.66**
DPVAL11	DPVAL13	-0.07	0.10	0.38	0.40	-0.08	-0.09	1.05	-0.02	-0.35	0.74	-3.33	-0.74	4.33	0.19	0.10	-0.35	0.09
DQPL22	DPVAL01	0.02	0.15*	2.44*	2.67*	0.05	1.32	-0.62	0.00	-0.65	-1.28	-1.17	0.50	-17.83	-0.94	0.90**	-1.15	-0.36
DQPL22	DPVAL02	0.14	0.07	0.51	0.50	0.05	1.00	8.66**	0.05***	0.85	-0.59	-1.17	-0.21	-1.58	-0.44	-0.10	-0.15	-0.34
DQPL22	DPVAL03	-0.26	0.05	-1.86	-1.86	-0.20	0.39	4.19	0.02	-1.90	-0.33	2.83	0.08	11.42	0.56	0.15	0.85	0.41
DQPL22	DPVAL04	-0.13	0.07	0.41	0.65	-0.10	-1.69	0.41	0.01	-0.90	0.48	-0.17	-0.23	1.92	-0.69	-0.10	2.10	0.66
DQPL22	DPVAL05	0.08	0.01	-0.72	-0.94	0.03	-2.27*	-1.14	-0.02	0.35	-0.34	-3.17	-0.51	5.17	0.31	-0.10	-2.40	-0.33
DQPL22	DPVAL06	-0.54*	0.07	-0.92	-0.91	-0.25	1.77	0.07	0.00	-1.40	-0.21	-4.17	-0.13	-2.08	-0.19	-0.10	0.60	-0.29
DQPL22	DPVAL07	0.45	-0.11	1.08	1.07	0.25	-0.30	0.95	-0.01	1.35	-1.74	-0.67	0.06	10.17	0.31	-0.10	-1.40	-0.34
DQPL22	DPVAL08	-0.14	0.15*	-0.92	-1.13	-0.05	-1.35	-6.77*	-0.05***	-2.40	-1.01	8.33*	0.73	0.92	0.56	-0.10	-1.65	-0.32
DQPL22	DPVAL09	0.23	0.11	-0.32	-0.08	0.13	1.34	4.54	-0.01	2.85	-0.68	-4.17	-0.58	6.67	0.06	-0.10	0.85	-0.31
DQPL22	DPVAL10	-0.12	-0.14*	0.32	0.08	-0.10	0.72	-1.52	0.00	1.35	8.48**	-0.67	-0.15	-3.58	0.06	-0.10	1.85	-0.36
DQPL22	DPVAL12	0.21	0.03	0.19	0.19	0.13	0.20	-0.52	0.02	0.10	-1.54	0.83	-0.28	-6.83	0.56	-0.10	0.10	1.66**
DQPL22	DPVAL13	0.07	-0.03	-0.42	-0.43	0.07	0.33	0.39	0.03*	0.35	-0.64	3.33	0.74	-4.33	-0.19	-0.10	0.35	-0.09
	SE	0.25	0.06	1.00	1.07	0.14	1.08	2.88	0.01	1.45	2.42	3.39	0.38	7.71	0.48	0.28	1.34	0.58·

SE= Standard error

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

5.3.6   Genetic parameters for yield and associated traits

Ukulinga

Table 5.19 is showing the means of the best six selected hybrids, mean of the population and of the hybrid check at Ukulinga. Grain yield had a high heritability of 80.88% (Table 5.20). High genotypic (44.55%) and phenotypic (69.22%) coefficients of variations and genetic advance (33.97%) were observed. Positive gains were realised over the mean population and the hybrid check for all the traits except for root lodging, grain texture and total lodging. Realised gains over the hybrid check were higher than the predicted gains. High heritability estimates were observed for field weight (75.57%), grain row number (86.31%) and number of ears per plot (72.98%). Number of ears per plot and field weight had high genetic advance, 34.23% and 25.83%, respectively. Higher positive genetic gains were realised over the hybrid check. Most of the secondary traits had heritability greater than 50% except grain row number, plant stand, stem, root and total lodging.

Cedara

The means of the best four selected hybrids, population and control hybrid at Cedara are presented in Table 5.21. High heritability estimates were observed for grain yield (71.20%). Low heritability estimates were recorded for grain row number (11.30), 100-grain weight (43.08%), number of ears per plot (37.11%), plant height (48.56%), root lodging (44.97%), and shelling percentage (34.51%). Most of these traits had high differences between their genotypic and phenotypic coefficients of variation. High genetic advance were observed for grain yield (21.08%), root lodging (253.84), stem lodging (32.31%), grain texture (130.72) and total lodging (28.13) (Table 5.22).

Table 5.19   Means of selected hybrids and control hybrid for Ukulinga

Traits	GY	ASI	AD	SD	EH	EPO	FW	GRN	GW100	MOI	NE	PH	PS	RL	SH	SL	TEX	TL%
MP	6.58	-0.92	82.15	81.23	138.50	0.50	3.28	13.80	39.11	16.39	19.33	275.80	15.86	1.34	80.23	3.36	2.00	29.08
MC	6.31	0.00	80.50	80.50	115.00	0.46	3.00	13.00	53.00	15.75	14.00	270.00	14.00	0.00	83.03	4.50	5.00	32.14
MS	8.55	-1.00	84.34	83.33	145.73	0.52	4.25	14.50	42.70	16.91	20.95	283.41	16.73	0.67	81.17	4.20	1.58	27.18[19]

MP=Mean of population, MC=Mean of check, MS=Mean of selected hybrids, GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH=Ear height, EPO=Ear position, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, NE=Number of ears per plot, PH= Plant height, PS=Plant stand, RL=Root lodging, SH=shelling percentage, SL= Stem lodging, TL%=Total lodging percentage

Table 5.20   Estimates of variance components, heritability and genetic gains of selected hybrids at 13% selection intensity at Ukulinga

Traits	$\delta^2 g$	$\delta^2 p$	H^2 (%)	GCV (%)	PCV (%)	PG	PG%	RG1	RG2
Grain Yield	2.93	4.55	64.36	44.55	69.22	2.24	33.97	29.96	35.41
Anthesis-silking Interval	1.28	1.58	80.88	-139.04	-171.92	1.66	-179.91	8.70	
Anthesis date	9.65	11.53	83.71	11.75	14.03	4.63	5.63	2.67	4.77
Silking date	13.95	15.89	87.82	17.18	19.56	5.70	7.01	2.59	3.52
Ear height	267.90	328.90	81.45	193.43	237.47	24.04	17.36	5.22	26.72
Ear Position	0.00	0.00	54.52	0.17	0.32	0.04	7.09	2.79	11.96
Field Weight	0.63	0.84	75.57	19.22	25.44	1.12	34.23	29.30	41.50
Grain Row Number	1.38	1.60	86.31	9.99	11.57	1.77	12.86	5.08	11.55
100-grain Weight	11.88	27.37	43.41	30.38	69.97	3.70	9.45	9.17	-19.44
Grain Moisture Content	0.34	0.61	56.02	2.08	3.72	0.71	4.34	3.16	7.35
Number of Ears per Plot	12.89	17.66	72.98	66.67	91.36	4.99	25.82	8.38	49.64
Plant Height	591.70	652.90	90.63	214.54	236.73	37.68	13.66	2.76	4.97
Plant Stand	1.25	3.46	36.05	7.87	21.83	1.09	6.88	5.47	19.49
Root Lodging	-0.06	0.59	-10.09	-4.40	43.62	-0.13	-9.36	-50.29	
Shelling Percentage	3.98	7.42	53.67	4.96	9.24	2.38	2.96	1.17	-2.24
Stem Lodging	0.12	0.74	15.57	3.42	21.95	0.22	6.47	24.80	-6.70
Grain Texture	1.40	2.23	62.74	70.05	111.65	1.53	76.28	-20.83	-68.33
Total Lodging	14.70	66.10	22.24	50.55	227.30	2.94	10.12	-6.55	-15.45[20]

$\delta^2 g$=Genotypic variance, $\delta^2 p$=Phenotypic variance, H^2=Broad sense heritability, GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation, PG=Predicted gain, RG1= realised gain relative to population mean, RG2= realised gain relative to check mean

Table 5.21   Means of selected hybrids and control hybrid for Cedara

Traits	GY	ASI	AD	SD	EH	EPO	FW	GRN	GW100	MOI	NE	PH	PS	RL	SH	SL	TEX	TL%
MP	5.06	-0.69	79.49	78.80	119.60	0.46	2.73	14.45	29.14	18.33	18.33	258.30	16.31	0.11	80.23	10.77	1.96	66.91
MC	5.09	-1.00	79.50	78.50	126.00	0.47	2.65	14.00	28.00	17.80	18.00	269.50	16.00	0.00	82.50	2.00	5.00	12.94
MS	6.52	-0.72	81.46	80.68	121.34	0.47	3.53	13.97	31.75	18.85	20.63	261.95	16.63	0.00	80.25	10.09	2.00	61.62[21]

MP=Mean of population, MC=Mean of check, MS=Mean of selected hybrids, GY=Grain yield, ASI=Anthesis-silking interval, AD=Anthesis date, SD=Silking date, EH=Ear height, EPO=Ear position, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, NE=Number of ears per plot, PH= Plant height, PS=Plant stand, RL=Root lodging, SH=shelling percentage, SL= Stem lodging, TL%=Total lodging percentage

Table 5.22   Estimates of variance components, heritability and genetic gains of selected hybrids at 13% selection intensity at Cedara

Traits	δ^2g	δ^2p	H^2 (%)	GCV (%)	PCV (%)	PG	PG%	RG1	RG2
Grain Yield	0.49	0.69	71.20	9.70	13.63	1.07	21.08	28.88	28.14
Anthesis-silking Interval	0.00	0.01	0.00	0.00	-0.82	0.00	0.00	3.54	-28.25
Anthesis date	8.40	9.74	86.30	10.57	12.25	4.86	6.11	2.48	2.47
Silking date	8.77	10.02	87.53	11.13	12.71	5.00	6.34	2.39	2.78
Ear height	83.30	145.30	57.33	69.65	121.49	12.47	10.43	1.46	-3.70
Ear Position	0.00	0.00	60.80	0.18	0.30	0.04	8.87	0.97	-0.11
Field Weight	0.12	0.18	66.50	4.32	6.50	0.51	18.51	29.30	33.30
Grain Row Number	0.81	7.17	11.30	5.61	49.58	0.55	3.78	-3.34	-0.23
100-grain Weight	10.19	23.66	43.08	34.97	81.18	3.78	12.97	8.95	13.38
Grain Moisture Content	1.26	1.52	82.86	6.88	8.31	1.84	10.06	2.85	5.91
Number of Ears per Plot	1.38	3.71	37.11	7.50	20.22	1.29	7.03	12.52	14.58
Plant Height	89.90	185.15	48.56	34.80	71.68	11.92	4.62	1.41	-2.80
Plant Stand	-0.02	0.43	-3.56	-0.09	2.63	-0.04	-0.26	1.93	3.91
Root Lodging	0.06	0.13	44.97	50.18	111.58	0.29	253.84	-100.00	
Shelling Percentage	1.76	5.09	34.51	2.19	6.34	1.40	1.75	0.03	-2.72
Stem Lodging	6.57	11.61	56.61	61.00	107.75	3.48	32.31	-6.34	404.38
Grain Texture	2.24	2.50	89.63	114.49	127.74	2.56	130.72	2.30	-60.00
Total Lodging	209.10	401.80	52.04	312.51	600.51	18.82	28.13	-7.91	376.20.

δ^2g=Genotypic variance, δ^2p=Phenotypic variance, H^2=Broad sense heritability, GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation, PG=Predicted gain, RG1= realised gain relative to population mean, RG2= realised gain relative to check mean

5.3.7 Correlations between grain yield and secondary traits

Ukulinga

Ukulinga results are presented in Table 5.23. Plant height and 100-grain weight had a significant (p≤0.01) and positive correlation with grain yield. Number of ears per plot, field weight and plant stand were significant (p≤0.001) and positively correlated with grain yield. The correlations were all strong because they were all more than 30%. Anthesis-silking interval (ASI), root lodging, total lodging percentage and grain texture were negatively correlated to yield but were not significant (p>0.05). Number of ears per plot showed positive correlation with all traits and significant correlation was with anthesis-silking interval, plant height, plant stand and ear height. Other positive and highly significant (p≤0.001) correlations occurred between anthesis days and silking days, ear height and flowering (anthesis and silking) days, ear height and plant height, ear position and plant height, number of ears and plant stand, field weight with plant stand, grain moisture content and flowering days, stem lodging and plant height, stem lodging and plant height, grain texture and flowering days, grain texture and grain moisture content, grain texture and shelling percentage. Negative and significant correlations (p>0.05) occurred between anthesis-silking interval and anthesis days, number of ears and root lodging, number of ears and ASI, shelling percentage and anthesis days, root lodging and flowering days. Grain texture was negatively correlated with most traits except with ASI, 100-grain weight and root lodging.

Table 5.23   Correlations between grain yield and secondary traits at Ukulinga

	GY	SD	AD	ASI	PH	PS	EH	EPO	NE	FW	GRN	GW100	MOI	SH	RL	SL	TL %	TEX
GY	-																	
DS	0.01	-																
DA	0.10	0.10***	-															
ASI	-0.05	-0.12	-0.25*	-														
PH	0.31**	0.25*	0.24*	-0.00	-													
PS	0.43***	-0.02	-0.02	0.04	0.2	-												
EH	0.18	0.38***	0.37***	0.05	0.72***	0.2	-											
EPO	0.01	0.36***	0.34**	0.08	0.30***	0.13	0.88***	-										
NE	0.62***	0.04	0.03	0.07*	0.29**	0.50***	0.30**	0.21	-									
FW	0.99***	0.15	0.16	-0.07	0.32**	0.43***	0.2	0.03	0.60***	-								
GRN	0.14	0.16	0.14	0.14	0.11	0.04	0.14	0.11	0.22*	0.17	-							
GW100	0.34**	-0.03	-0.05	0.11	0.05	0.11	-0.05	-0.11	-0.12	0.33**	-0.09	-						
MOI	0.14	0.51***	0.49***	0.04	0.23*	0.2	0.37***	0.33**	0.1	0.21	0.25*	-0.06	-					
SH	0.19	-0.23	-0.24*	0.13	-0.03	0.13	-0.03	-0.02	0.16	0.04	-0.12	0.065	-0.17	-				
RL	-0.20	-0.25*	-0.26*	0.16	-0.09	0.03	-0.11	-0.09	-0.07*	-0.2	-0.02	-0.24*	-0.11	-0.07	-			
SL	0.00	0.31**	0.30**	0.01	0.35***	0.36***	0.36***	0.25*	0.22*	0	0.08	-0.06	0.19	0.07	-0.13	-		
TL %	-0.18	0.10	0.076	0.14	0.22*	0.22*	0.21*	0.14	0.09	-0.18	0.07	-0.21*	0.09	0	0.55***	0.75***	-	
TEX	-0.15	-0.38***	-0.39***	0.16	-0.19	-0.19	-0.28**	-0.23*	-0.27**	-0.23*	-0.33**	0.174	-0.47***	0.42***	0.11	-0.22	-0.1	-[22]

GY=Grain yield, SD=Silking date, AD=Anthesis date, ASI=Anthesis-silking interval, PH= Plant height, PS=Plant stand, EH=Ear height, EPO=Ear position, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, SH=shelling percentage, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, TEX= grain texture
* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

5.3.8   Correlations between grain yield and secondary traits

Cedara

Results for Cedara are presented in Table 5.24. Ear position and number of ears per plot were positively and significantly (p≤0.001) correlated with grain yield. Stem lodging and total lodging percentage were negatively and significantly (p≤0.001) correlated with grain yield. 100-kernels weight was positively and significantly (p≤0.01) correlated with grain yield. Grain texture was positively and significantly (p≤0.05) correlated with grain yield.

Grain moisture content had positive and significant (p≤0.001) correlation with flowering days, 100-grain weight, stem and total lodging percentage. Flowering days also had positive and significant (p≤0.001) correlations with stem lodging and total lodging percentage. Ear height had positive and significant (p≤0.001) correlations with plant height and ear position. Positive and significant correlations were also observed between total lodging percentage and stem lodging as well as field weight and number of ears per plot. Significant (p≤0.01) and positive correlations were observed between plant height and silking days, ear height and anthesis days, grain moisture content and ear height, 100-grain weight and field weight. Positive and significant correlations (p≤0.05) were also observed between grain moisture content and plant height, total lodging and grain row number, ear position and plant height. Grain texture had negative and significant (p≤0.001) correlation with flowering days, grain texture, grain moisture content, stem lodging and total lodging percentage. Field weight was negatively and significantly (p≤0.05) correlated with stem lodging and total lodging percent, grain texture with plant height.

Across sites

Correlation results across the two sites are presented in Table 5.25. Grain yield (main primary trait) was positively and significantly (p≤0.05) correlated with all secondary traits except for anthesis-silking interval, grain moisture content, stem lodging and total lodging percentage whose correlation was significant and negative. There was no significant correlation between yield and grain row number, root lodging and grain texture. Field weight exhibited significant positive correlations with flowering days, ear position, plant height, plant stand, ear height, number of ears per plot, shelling percentage and 100-kernels weight. Number of ears per plot had significant positive correlations with ear position, plant height shelling percentage, ear

height, and plant stand. The 100-kernels weight also had significant correlations with shelling percentage, flowering days, ear position, plant height and ear height.

Table 5.24   Correlations between grain yield and secondary traits at Cedara

	GY	DS	DA	ASI	PH	PS	EH	EPO	NE	FW	GRN	GW100	MOI	SH	RL	SL	TL %	TEX
GY	-																	
DS	-0.09	-																
DA	-0.08	0.99***	-															
ASI	-0.12	0.15	0.01	-														
PH	-0.01	0.32**	0.31	0.12	-													
PS	-0.05	0.05	0.05	0.05	0.09	-												
EH	0.02	0.32	0.33**	-0.04	0.71***	0.09	-											
EPO	0.02***	0.2	0.22	-0.14	0.21*	0.05	0.83***	-										
NE	0.51***	0.01	0.02	-0.07	-0.09	-0.03	0.06	0.15	-									
FW	0.96	0.1	0.12	-0.11	0.09	-0.04	0.08	0.04	0.49***	-								
GRN	0.03	0.12	0.13	-0.06	0.03	-0.15	0.1	0.12	0.17	0.07	-							
GW100	0.31**	-0.06	-0.08	0.14	0.06	-0.05	-0.11	-0.2	-0.16	0.34**	-0.05	-						
MOI	-0.08	0.62***	0.61***	0.1	0.25*	0.04	0.27**	0.18	-0.06	0.12	0.07	0.36***	-					
SH	0.09	-0.07	-0.07	0	0.03	0.01	-0.06	-0.11	-0.06	0.08	0.03	0.01	-0.1	-				
RL	0.06	-0.02	-0.02	0	-0.12	-0.18	-0.04	0.04	-0.06	0.01	-0.06	-0.07	-0.07	-0.19	-			
SL	-0.4***	0.47***	0.46***	0.11	0.04	0.06	0.11	0.12	-0.11	-0.26*	0.21	-0.06	0.45***	-0.07	-0.11	-		
TL %	-0.39***	0.47***	0.46***	0.1	0.01	-0.1	0.09	0.11	-0.11	-0.25*	0.23*	-0.05	0.45***	-0.09	-0.01	0.98***	-	
TEX	0.25*	-0.44***	-0.43***	-0.1	-0.24*	0.02	-0.19	-0.08	0.01	0.07	-0.15	0.07	-0.47***	0.07	0.09	-0.49***	-0.49***	-[23]

GY=Grain yield, AD=Anthesis date, SD=Silking date, ASI=Anthesis-silking interval, PH= Plant height, PS=Plant stand, EH=Ear height, EPO=Ear position, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, SH=shelling percentage, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, TEX= grain texture
* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

Table 5.25   Correlations between grain yield and secondary traits across two sites

	GY	DS	DA	ASI	PH	PS	EH	EPO	NE	FW	GR	GW100	MOI	SH	RL	SL	TL %	TEX
GY	-																	
DS	0.20**	-																
DA	0.23**	0.99***	-															
ASI	-0.20***	-0.06	-0.19*	-														
PH	0.35***	0.39***	0.39***	-0.05	-													
PS	0.20**	-0.05	-0.06	0.08	0.08	-												
EH	0.34***	0.46***	0.46***	-0.12	0.77***	0.07	-											
EPO	0.21**	0.38***	0.39***	-0.13	0.38***	0.03	0.88***	-										
NE	0.58***	0.08	0.08	-0.03	0.18*	0.34***	0.26***	0.23**	-									
FW	0.98***	0.25***	0.27***	-0.18*	0.35***	0.23**	0.32***	0.18*	0.58***	-								
GRN	-0.02	0.06	0.06	0.01	-0.01	-0.03	0.02	0.04	0.11	0.02	-							
GW100	0.54***	0.2**	0.21**	-0.07	0.31***	-0.06	0.26***	0.15*	0	0.49***	-0.12	-						
MOI	-0.31***	0.18*	0.15*	0.22**	-0.1	0.18*	-0.1	-0.08	-0.08	-0.15*	0.15*	-0.31***	-					
SH	0.45***	-0.1	-0.09	-0.1	0.07	-0.02	0.18*	0.20**	0.22**	0.26***	-0.15*	0.39***	-0.58***	-				
RL	0.05	-0.02	-0.02	0	0.08	-0.04	0.1	0.09	-0.01	0.00	-0.06	0.12	-0.28***	0.17*	-			
SL	-0.46***	0.03	0	0.23**	-0.18*	0.25***	-0.19**	-0.15*	-0.07	-0.35***	0.21**	-0.48***	0.64***	-0.54***	-0.30***	-		
TL %	-0.48***	0.03	-0.01	0.24**	-0.18*	0.16*	-0.19*	-0.14	-0.1	-0.38***	0.22**	-0.46***	0.58***	-0.51***	0.03	0.94***	-	
TEX	0.01	-0.38***	-0.38***	0.01	-0.19*	-0.12	-0.2**	-0.14	-0.15*	-0.09	-0.16*	0.1	-0.36***	0.44***	0.09	-0.29***	-0.27***	-[24]

GY=Grain yield, AD=Anthesis date, SD=Silking date, ASI=Anthesis-silking interval, PH= Plant height, PS=Plant stand, EH=Ear height, EPO=Ear position, NE=Number of ears per plot, FW=field weight, GRN=Grain row number, GW100=100-grain weight, MOI=grain moisture content, SH=shelling percentage, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, TEX= grain texture

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %)

5.3.9   Path coefficient analysis

Ukulinga

Significant (P<0.0001) direct effects were obtained at Ukulinga for number of ears per plot and 100 grain weight Table 5.26. Ear height had the highest non-significant positive direct effects on grain yield (Table 5.28). High direct effects were also observed for number of ears per plot (0.57) and 100-grain weight (0.36). Moderate positive direct effects were observed for silking date (0.16), plant stand (0.15), total lodging percent (0.12) and shelling percentage (0.15). Ear height illustrated positive indirect effects via most of the traits except for grain texture, root lodging, 100 kernels weight and shelling percentage whose indirect effects were negative.

Cedara

At Cedara, significant direct effects were observed for number of ears per plant and 100-grain weight (Table 5.27). At both Cedara and Ukulinga, grain row number, shelling percentage and plant stand did not show significant direct effects. Ear height had the highest positive direct effects on grain yield and it also illustrated high positive indirect effects via; grain moisture content (0.46), silking date (0.55), anthesis date (0.56), plant height (1.23) and ear position (1.44) (Table 5.29). High positive direct effects of secondary traits on grain yield were also observed for total lodging (1.06) and number of ears (0.54). Moderate positive direct effects were observed for plant stand (0.16), silking date (0.22) and shelling percentage (0.12). Although number of ears had significant direct effects on grain yield, it had negligible positive and negative indirect effects via all the other traits. A negligible indirect effects of 100-grain weight on yield was observed on all the traits except for moderate indirect effects illustrated via grain moisture content (0.18) (Table 5.29).

Table 5.26   Parameter estimates for direct effects based on regression at Ukulinga

Variable	Parameter Estimate	Standard Error	t Value	Pr > |t|
ASI	-0.13	0.08	-1.70	0.09ns
EH	2.11	1.40	1.51	0.13ns
GRN	0.05	0.07	0.72	0.47ns
MOI	0.03	0.09	0.35	0.73ns
SD	0.16	0.09	1.69	0.10ns
PS	0.16	0.14	1.14	0.26ns
TEX	-0.01	0.10	-0.05	0.96ns
PH	-0.88	0.70	-1.26	0.21ns
EPO	-1.67	1.01	-1.65	0.10ns
RL	-0.12	0.55	-0.21	0.83ns
SL	-0.36	0.73	-0.49	0.63ns
TL	0.12	0.82	0.14	0.89ns
NE	0.57	0.09	6.44	<.0001***
GW100	0.36	0.08	4.70	<.0001***
SH	0.15	0.08	1.80	0.08ns.

ASI=Anthesis-silking interval, EH= Ear height, GRN=Grain row number, MOI=grain moisture content, SD=Silking date, PS=Plant stand, TEX= grain texture, PH= Plant height, EPO=Ear position, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, NE=Number of ears per plot, GW100=100-grain weight, SH=shelling percentage, Pr=Probability

*** p≤0.0001 (significant at 0.01 %), ns=not significant

Table 5.27   Parameter estimates for direct effects based on regression at Cedara

Variable	Parameter Estimate	Standard Error	t Value	Pr > |t|
Intercept	0.00	0.08	0.00	1.00ns
ASI	-0.12	0.08	-1.44	0.15 ns
EH	1.73	1.66	1.04	0.30 ns
GRN	0.01	0.08	0.12	0.90 ns
MOI	-0.20	0.13	-1.56	0.12 ns
SD	0.22	0.11	1.90	0.06 ns
PS	0.16	0.22	0.72	0.47 ns
TEX	0.05	0.10	0.48	0.63 ns
PH	-0.94	0.94	-1.00	0.32 ns
EPO	-1.17	1.18	-0.99	0.33 ns
RL	0.02	0.15	0.13	0.90 ns
SL	-1.35	1.48	-0.91	0.37 ns
TL	1.06	1.49	0.71	0.48 ns
NE	0.535	0.083	6.43	<.0001***
GW100	0.495	0.097	5.09	<.0001***
SH	0.124	0.078	1.58	0.12 ns

ASI=Anthesis-silking interval, EH= Ear height, GRN=Grain row number, MOI=grain moisture content, SD=Silking date, PS=Plant stand, TEX= grain texture, PH= Plant height, EPO=Ear position, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, NE=Number of ears per plot, GW100=100-grain weight, SH=shelling percentage, Pr=Probability

*** p≤0.0001 (significant at 0.01 %), ns=not significant

Table 5.28   Direct (underlined) and indirect effects of secondary traits on grain yield at Ukulinga (R^2=0.68)

	ASI	EH	GRN	MOI	SD	PS	TEX	AD	PH	EPO	RL	SL	TL	NE	GW100	SH	GY	FW
ASI	**_-0.1ns_**	0.11	0.01	0	-0.02	0.01	0	0.00	0.00	-0.13	-0.02	0	0.02	0.04	0.04	0.02	-0.05	-0.05
EH	-0.01	**_2.11ns_**	0.01	0.01	0.06	0.03	0	0	-0.64	-1.46	0.01	-0.13	0.02	0.17	-0.02	0	0.18	0.17
GRN	-0.02	0.29	**_0.05ns_**	0.01	0.02	0	0	0	-0.1	-0.17	0.00	-0.03	0.01	0.12	-0.03	-0.02	0.14	0.14
MOI	-0.01	0.78	0.01	**_0.03ns_**	0.08	0.03	0	0	-0.21	-0.56	0.01	-0.07	0.01	0.06	-0.02	-0.02	0.14	0.14
SD	0.01	0.81	0.01	0.02	**_0.16ns_**	0	0	0	-0.22	-0.6	0.03	-0.11	0.01	0.02	-0.01	-0.03	0.1	0.1
PS	-0.01	0.43	0.00	0.01	0.00	**_0.15ns_**	0	0	-0.18	-0.21	0.00	-0.13	0.03	0.28	0.04	0.02	0.43	0.43
TEX	-0.02	-0.58	-0.02	-0.02	-0.06	-0.03	**_-0.0ns_**	0	0.17	0.38	-0.01	0.08	-0.01	-0.15	0.06	0.06	-0.15	-0.15
AD	0.03	0.77	0.01	0.02	0.15	0	0	**_0ns_**	-0.21	-0.57	0.03	-0.11	0.01	0.02	-0.02	-0.03	0.1	0.1
PH	0.00	1.52	0.01	0.01	0.04	0.03	0	0	**_-0.9ns_**	-0.51	0.01	-0.12	0.02	0.16	0.02	0.00	0.31	0.3
EPO	-0.01	1.85	0.01	0.01	0.06	0.02	0	0	-0.27	**_-1.7ns_**	0.01	-0.09	0.02	0.12	-0.04	0.00	0.01	0.01
RL	-0.02	-0.23	0.00	0.00	-0.04	0	0	0	0.08	0.15	**_-0.1ns_**	0.05	0.06	-0.04	-0.09	-0.01	-0.2	-0.2
SL	0.00	0.75	0.00	0.01	0.05	0.06	0	0	-0.31	-0.41	0.02	**_-0.4ns_**	0.09	0.12	-0.02	0.01	0	0
TL	-0.02	0.44	0.00	0	0.02	0.03	0	0	-0.19	-0.23	-0.06	-0.27	**_0.12ns_**	0.05	-0.08	0.00	-0.18	-0.18
NE	-0.01	0.63	0.01	0	0.01	0.08	0	0	-0.26	-0.34	0.01	-0.08	0.01	**_0.57***_**	-0.04	0.02	0.61	0.61
GW100	-0.01	-0.11	0.00	0	0	0.02	0	0	-0.04	0.18	0.03	0.02	-0.02	-0.07	**_0.36***_**	0.01	0.34	0.34
SH	-0.02	-0.07	-0.01	-0.01	-0.04	0.02	0	0	0.03	0.03	0.01	-0.03	0	0.09	0.02	**_0.15ns_**	0.19	0.19[25]

ASI=Anthesis-silking interval, EH= Ear height, GRN=Grain row number, MOI=grain moisture content, SD=Silking date, PS=Plant stand, GW100=100-grain weight, PH= Plant height, EPO=Ear position, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, NE=Number of ears per plot, AD=Anthesis date, TEX= grain texture, SH=shelling percentage GY=Grain yield, FW=field weight

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %), ns=not significant

Table 5.29   Direct (underlined) and indirect effects of secondary traits on grain yield at Cedara (R^2=0.59)

	ASI	EH	GRN	MOI	SD	Plant	TEX	AD	PH	EPO	RL	SL	TL	NE	GW100	SH	GY	FW
ASI	**-0.11ns**	-0.07	0	-0.02	0.03	0.01	0	0	-0.11	0.17	0	-0.15	0.11	-0.04	0.07	0	-0.12	-0.11
EH	0	**1.73ns**	0	-0.05	0.07	0.02	-0.01	0	-0.67	-0.98	0	-0.15	0.09	0.03	-0.05	-0.01	0.02	0.02
GRN	0.01	0.18	**0.01ns**	-0.01	0.03	-0.02	-0.01	0	-0.03	-0.14	0	-0.28	0.24	0.09	-0.03	0	0.03	0.03
MOI	-0.01	0.46	0	**-0.2ns**	0.13	0.01	-0.02	0	-0.24	-0.21	0	-0.6	0.47	-0.03	0.18	-0.01	-0.08	-0.07
SD	-0.02	0.55	0	-0.12	**0.22ns**	0.01	-0.02	0	-0.3	-0.23	0	-0.63	0.49	0.01	-0.03	-0.01	-0.09	-0.09
PS	-0.01	0.16	0	-0.01	0.01	**0.16ns**	0	0	-0.09	-0.06	0	-0.08	-0.1	-0.01	-0.03	0	-0.05	-0.05
TEX	0.01	-0.32	0	0.09	-0.1	0	**0.05ns**	0	0.23	0.09	0	0.67	-0.52	0.01	0.03	0.01	0.25	0.24
AD	0	0.56	0	-0.12	0.21	0.01	-0.02	**0ns**	-0.29	-0.26	0	-0.62	0.48	0.01	-0.04	-0.01	-0.08	-0.08
PH	-0.01	1.23	0	-0.05	0.07	0.02	-0.01	0	**-0.94ns**	-0.25	0	-0.05	0.01	-0.05	0.03	0	-0.01	-0.01
EPO	0.02	1.44	0	-0.04	0.04	0.01	0	0	-0.2	**-1.17ns**	0	-0.17	0.12	0.08	-0.1	-0.01	0.02	0.02
RL	0	-0.07	0	0.01	0	-0.03	0	0	0.11	-0.04	**0.02ns**	0.15	-0.01	-0.03	-0.03	-0.02	0.06	0.06
SL	-0.01	0.19	0	-0.09	0.1	0.01	-0.02	0	-0.04	-0.15	0	**-1.35ns**	1.04	-0.06	-0.03	-0.01	-0.4	-0.38
TL	-0.01	0.15	0	-0.09	0.1	-0.02	-0.02	0	-0.01	-0.13	0	-1.32	**1.06ns**	-0.06	-0.03	-0.01	-0.39	-0.38
NE	0.01	0.11	0	0.01	0	0	0	0	0.09	-0.18	0	0.15	-0.12	**0.54ns**	-0.08	-0.01	0.51	0.49
GW100	-0.02	-0.18	0	-0.07	-0.01	-0.01	0	0	-0.06	0.23	0	0.08	-0.06	-0.08	**0.5ns**	0	0.31	0.3
SH	0	-0.1	0	0.02	-0.02	0	0	0	-0.03	0.13	0	0.09	-0.09	-0.03	0	**0.12ns**	0.09	0.09[26]

ASI=Anthesis-silking interval, EH= Ear height, GRN=Grain row number, MOI=grain moisture content, SD=Silking date, PS=Plant stand, GW100=100-grain weight, PH= Plant height, EPO=Ear position, RL=Root lodging, SL= Stem lodging, TL%= Total lodging percent, NE=Number of ears per plot, AD=Anthesis date, TEX= grain texture, SH=shelling percentage GY=Grain yield, FW=field weight

* p≤0.05 (significant at 5 %), ** p≤0.01 (significant at 1 %), *** p≤0.0001 (significant at 0.01 %), ns=not significant

5.3.10   Stability and cultivar superiority analysis

The hybrids were ranked according to their mean grain yield across the two sites. The top and bottom 10 are presented in Table 5.30. Cultivar superiority index ranged between 0.212 and 3.998. Hybrid 16XP33, 16XP11, 16XP29, 16XP21 and 16XP24 had the lowest superiority index values, respectively and were placed at the top of the stability table. Highest superiority indices were observed for the hybrids, 16XP10, 16XP04, 16XP36, 16XP37 and 16XP20.

Table 5.30   Yield superiority of hybrids averaged for the two different sites

Hybrid Name	Cultivar superiority index	Means (tonnes/hectare)
Top 10		
16XP33	0.212	7.111
16XP11	0.269	7.053
16XP29	0.285	6.927
16XP21	0.563	6.515
16XP24	0.723	6.451
16XP28	0.877	6.348
16XP27	1.064	6.295
16XP18	1.066	6.115
16XP31	1.126	6.076
16XP17	1.127	6.128
Bottom 10		
16XP32	2.36	5.575
16XP12	2.519	5.327
16XP01	2.709	5.244
16XP16	2.797	5.314
16XP03	2.943	5.147
16XP20	2.981	5.201
16XP37	3.063	5.29
16XP36	3.079	5.457
16XP04	3.647	4.992
16XP10	3.998	4.922

5.4 Discussion

5.4.1 Genetic variation

At Ukulinga, substantial variation was observed among hybrids for grain yield, field weight, stem lodging, grain texture, silking date, anthesis date and number of ears per plot. Hybrids showed significant variability for grain yield, field weight, silking and anthesis date at Cedara. Wegary et al. (2014) reported similar results for grain yield, anthesis date and silking date. Analysis of variance across the two sites showed significant site main effects for all the traits. This was in agreement with what Maphumulo (2014) reported. This shows the effect of environmental variation on hybrid performance. The different environmental conditions at each site had significant effects on the growth of the plants. Since G X E compromises heritability, environmental influence on economic traits may slow down the breeding progress. Site x genotype interaction was significant for grain yield, number of ears per plot, field weight and shelling percentage. This shows that the hybrids performed differently at the two sites and there is ample genetic variability which allows valuable improvement from selection of the traits. There is therefore need to evaluate the hybrids at more sites. This is in line with previous studies (Martin, 2004; Sesay et al., 2016).

5.4.2 Mean performance

The variation in performance of hybrids at different sites could have been caused by the different weather conditions and agronomic practices at the sites. The difference in the grain yield for the two sites may also have been attributed by the difference in planting dates for the two sites. The trial at Cedara was planted two weeks later than at Ukulinga. According to Tsimba et al. (2013) as cited by Mathew (2015), delayed planting usually overlap with deterioration in the environmental conditions for example temperature and grain moisture content at grain filling stage resulting in reduced yields. In the present study, only three hybrids were ranked in the top ten of high yielding hybrids at both Ukulinga and Cedara. 16XP33 was the best hybrid in the experiment, and it should be considered for improvement of grain yield in breeding programmes. It can be speculated that this hybrid is adapted at both sites. This is desirable for small holder farming conditions where agronomic practices are not consistent. Hybrid 16XP11 was the best at Ukulinga with grain yield of 10.03 t/ha. Other common high performing hybrids (16XP24 and 16XP29) at Ukulinga and Cedara are also considered to respond positively to improved agronomic practices and environment. These

hybrids can be recommended for trial advancement. They should be tested for disease resistance at disease hotspots to check whether they also carry genes for disease resistance.

5.4.3   General combining ability effects

The results from Ukulinga showed genetic variation among the maize inbred lines which can be utilised in the development of new hybrids with better nutritional qualities. The line main (GCA_L) effects were significant ($p<0.05$) for grain yield, number of ears, field weight, 100-grain weight, plant height and plant stand. Tester main (GCA_T) effects were significant for anthesis date, silking date, grain row number and plant stand. A conclusion can be made that these traits were under additive gene action for the specific lines and testers.

Line DPVAL12 had the largest significant positive GCA effects for grain yield which means it is the best general combiner for grain yield. It has the capability of producing above average grain yield when crossed with different testers. This line also had desirable positive GCA effects for field weight, shelling percentage, grain row number, plant stand and 100-grain weight. However, this line has the tendency of increasing flowering days, grain moisture content and plant height as shown by the positive GCA effects for these traits. Line DPVAL09 had high positive GCA effects for grain yield, field weight; shelling percentage, number of ears per plot, although they were not significant. This implied that this line can be utilised in a maize breeding programme to improve grain yield. Nevertheless, it has undesirable tendency of increasing number of flowering days, ear height, grain moisture content and plant height. Line DPVAL10 exhibited undesirable significant and negative GCA effects and should be excluded from breeding programmes where the main objective is to increase grain yield. It can either be discarded or crossed to different populations. It can also be evaluated for other agronomic traits.

At Cedara, the line DPVAL12 also had the highest GCA effects for grain yield, number of ears per plot and 100-grain weight, qualifying it as a high potential line for use in developing productive hybrids. On the other hand, it should be improved for higher shelling percentage, grain row number and for shorter plants as well as lower grain moisture content. This line had desirable negative GCA effects for number flowering days, which means that it can also be used in a breeding programme where early maturity is a main objective. DPVAL06 had the second highest positive GCA effects for grain yield but it needs to be improved for higher

shelling percentage, grain row number, and lower grain moisture content. At this environment, unlike at Ukulinga, DPVAL09 had the highest negative GCA effects for grain yield. This line should be excluded from breeding programmes where grain yield is the main objective.

5.4.4 Specific combining ability effects

Tester DPVAL11 produced hybrids with non-significant positive SCA effects for grain yield with lines DPVAL03, DPVAL04, DPVAL06, DPVAL08 and DPVAL10. Line DPVAL06 showed significant SCA effects for grain yield when it was crossed with tester DPVAL11. Both DPVAL06 and DPVAL11 had negative GCA effects but had positive SCA effects, and this was controlled by non-additive gene action. This was the best hybrid in this experiment and should be considered for a breeding programme whose main objective is   grain   yield improvement. It also had desirable positive SCA effects for field weight, number of ears per plot, grain row number and 100-grain weight. However this cross had undesirable non-significant positive SCA effects for number of flowering days, ear height, grain moisture content, plant height, root lodging and negative SCA effects for shelling percentage.

Tester DPQL22 produced all non-significant positive SCA effects with lines DPVAL01, DPVAL02, DPVAL05, DPVAL07, DPVAL09, DPVAL12 and DPVAL13. Hybrid (DPQL22 x DPVAL07) had highest SCA effects for grain yield. However this cross needs to be improved in other traits such flowering days, shelling percentage, ear height, grain row number, 100-grain weight, grain moisture content and plant height. Line DPVAL06 exhibited undesirable significant negative SCA effects when it was crossed to DPQL22. DPVAL06 had a negative GCA value while DPQL22 had a positive GCA value hence; these parents were not the good specific combiners for grain yield. This cross should be excluded in breeding programmes for improving grain yield.

5.5 Genetic parameters for yield and associated traits

High heritability estimates for both Ukulinga and Cedara were observed for grain yield, anthesis date, silking date, ear position, field weight and grain texture. Grain yield, silking date and field weight had higher GCV and genetic advance at Ukulinga. This means these traits are predominantly influenced by additive gene action and genetic improvement can be made through selection. High heritability and strong and significant positive correlation of field weight with grain yield helped the hybrids to have higher yield. The 100-grain weight had low heritability at both sites and this was in agreement with (Reddy et al., 2013). It had high GCV

but low genetic advance and this indicated that non-additive gene action was important in controlling the traits in hybrids.

Number of ears per plot had high heritability, GCV and genetic advance at Ukulinga, while it had low heritability at Cedara. This trend is in agreement with previous investigations (Muchie and Fentie, 2016). On the other hand, number of ears had low heritability, GCV and genetic advance at Cedara. This could be due to the masking of genetic effects by the large environmental variance. Since number of ears had a strong correlation with yield, this could have contributed to the lower yield at Cedara.

Estimates of GCV and PCV give the magnitude of genotypic and phenotypic variations among traits, respectively. It is also useful in determining the scope of improving a certain trait in a line or hybrid. The 100-grain number, plant height, ear height, grain texture and total lodging had high GCV and PCV estimates at both sites. Bello et al. (2012), reported the same observations for plant and ear height. In contrast to the present study, Sesay et al. (2016) reported moderate GCV and PCV for 100-grain weight. High GCV and PCV estimates indicated the existence of large variability. This gives enough scope for the improvement of the traits through selection.

Most traits had large difference between GCV and PCV at Cedara. This indicated higher environmental effects although the GCV measures the variability in the trait (Akinwale et al., 2011). These traits include ear height, root lodging, stem lodging and total lodging. Lower differences between the GCV and PCV for most traits at Ukulinga indicated low effect of the environment on the hybrids.

High values of GCV and PCV for root lodging, stem lodging, total lodging and grain texture are inconsistent due to the storm that was experienced during the season. Influence of the environment was higher at Cedara and this is also reflected by the lower grain yields at the site than at Ukulinga.

5.6 Relationship between grain yield and secondary traits

Results at Ukulinga revealed significant positive and negative correlations among the traits. Grain yield had positive significant correlation with plant height, plant stand, number of ears, field weight and 100-grain weight. This means that indirect selection of these secondary traits would result in grain yield increase. Field weight had a significant positive correlation with

number of ears, 100-grain weight and plant stand. This implied that selection of these plant aspects would result in the increase of field weight. Indirect selection of traits that showed positive correlation between each other can result in their parallel improvement. Eventually this would help in increasing the grain yield potential of the hybrids. Negative correlations were also observed between traits. This implied that there was an inverse relationship between the traits. Selection for one trait would cause a decline in another trait. If both traits are being selected for, there is need to compromise so that there is a balance.

At Cedara, significant positive and negative correlations were also observed. Grain yield had significant positive correlations with ear position, number of ears per plot and 100-grain weight. Selection for these traits would result in a parallel increase in grain yield. Field weight had a positive correlation with number of ears per plot and 100-grain. Indirect selection of these traits would increase the grain yield potential because there was a strong correlation between field weight and grain yield. These findings were similar to those reported in the first experiment of this study.

The behaviour of traits should be taken into account when designing new hybrids. This is because when selecting for other traits, there is need to compromise, for example, even though plant height, ear height and ear position had positive correlation with grain yield in both experiments; there is a limit to which they can reach. If plant height keeps increasing it might have an undesirable effect on grain yield through lodging.

5.6.1   Path coefficient analysis

At Ukulinga, ear height, number of ears per plot and 100-grain weight had significant high direct effects on grain yield. This in agreement with previous investigations by other researchers (Akinwale et al., 2011). Number of ears also had indirect positive effects on grain yield via ear height, grain row number, silking date, plant stand, root lodging, total lodging percentage and shelling percentage. Indirect selection of these traits would improve the yield of the hybrids. 100-grain weight had positive indirect effects via plant stand, ear position, root lodging, stem lodging and shelling percentage. Therefore, when selecting for 100-grain weight, one would also be selecting for these traits. Allard and Bradshaw (1964) reported similar results as in the current study for the following traits; plant height, ear height, grain row number and 100-grain weight. Plant height and anthesis-silking interval had negative direct effects on grain yield. This is in agreement with reports of Allard (1960). All traits had negative indirect effects on grain yield except for shelling percentage and anthesis-silking interval.

These results revealed that number of ears and 100-grain weight should be given priority during breeding. Although ear height had high positive and direct effects on grain yield, there should be a limit of selecting for it, because if it exceeds a certain height it can cause a risk of stem lodging.

In line with the results from Ukulinga, results from Cedara also showed that number of ears per plot and 100-grain weight are the most important traits to consider for grain improvement. Therefore, selecting for these traits would help improve grain yield. At Ukulinga, grain moisture content had positive direct effects on grain yield whereas negative effects were observed at Cedara. Although direct effects of root lodging were negligible at both sites, negative effects were observed at Ukulinga but positive effects were observed at Cedara. This showed that target traits for yield improvement were dependent on the environment.

5.7 Stability and cultivar superiority analysis

According to Lin and Binns (1988), superior genotypes have smaller indices. Stability analysis showed that hybrid 16XP33 was the most stable hybrid since it had the highest mean yield and lowest superiority index. Hybrid 16XP10 was the least stable since it had the lowest mean yield and the highest superiority index. Selection of hybrids across environments should be based on their high stability and yield superiority over the given experimental environments. Data from the two environments used in this study is not sufficient to make conclusions regarding the stability of the hybrids. Data from many sites would be required to make conclusions regarding the stability of hybrids.

5.8 Conclusions

The findings from this study are as follows

- Genotype X environment across the two sites was significant for grain yields and a few other traits. This showed that the sites were discriminating of the hybrids and this allows useful advancement of the hybrid through selecting for the measure traits.
- Stability and cultivar superiority analysis revealed 16XP33, 16XP11 and 16PX29 to be the most stable hybrids.
- GCA effects were significant for grain yield and other traits. Inbred line DPVAL12 should be maintained as it had the highest positive GCA for grain yield at both sites.

- Inbred lines DPVAL09 and DPVAL10 had the highest negative GCA effects for grain and should therefore be discarded or used in other breeding programme whose main objective is not grain yield.

- SCA effects were high and significant for 16XP06. This hybrid should be considered for advancement in the breeding programme.

- Grain and other secondary traits were highly heritable and had high predicted gains. These traits showed great potential for grain yield enhancement through selection.

- Strong positive correlations, direct and indirect effects of secondary traits and grain yield shows that these traits can be exploited for grain yield improvement, especially field weight as it was found to be the most important trait contributing towards grain yield.

6   CONCLUSION AND RECOMMENDATIONS

This chapter gives an overall summary of the major findings from literature and the completed research. It also gives recommendations based on the findings, to fulfil the objectives. This Chapter is based on the findings outlined in Chapters 4 and 5.

The specific objectives of this study were

a) To determine combining ability of foreign PVA maize with locally adapted QPM inbred lines.

b) To determine the combining ability of the locally adapted PVA maize with QPM inbred lines.

c) To determine contribution of secondary traits to grain yield in PVA and QPM hybrids.

6.1   Summary of main findings

6.2   Combining ability effects

- Inbred lines had different strengths in terms of general combining ability (GCA) for the different traits. The lines should be used in breeding programmes where the main o focus is on the traits that exhibited high GCA values.

- Inbred lines DPVAL12, DPVAL32, DPVAL37 should be maintained for breeding programmes that focus on enhancing yield

- SCA effects were not significant for most traits. This showed that additive gene action was more important than non-additive gene action for these traits. Nonetheless, hybrids 16XH49 and 16XP06 had the highest positive SCA effects on gain yield and other traits. These hybrids should be advanced in the breeding programme.

6.3   Genetic variability, heritability, genetic gain of grain yield and Inter-relationships among phenotypic traits

- High genetic gains for grain yield were displayed by the selected hybrids in all the trials. Substantial genetic variation for traits was observed among the hybrids.

- Traits such as grain yield, anthesis date, silking date, ear height, ear position, field weight and grain moisture content exhibited high heritability and they showed moderate to high genetic advance. These traits can therefore be effectively selected

for in the improvement of grain yield. For some traits, heritability varied in direction and magnitude according to the environment.

- The realised genetic gain exceeded the predicted gain implying that the strategy implemented for selecting the high performing hybrids was effective.

- Grain yield was positively correlated to plant height, plant stand, ear height, number of ears per plant, grain row number, shelling percentage and other traits. Breeding towards increasing these traits would cause a parallel increase in grain yield.

- Traits revealed different pathways in their effects toward grain yield. These direct and indirect effects are important when selecting for grain yield.

6.4 Conclusion and recommendations

- The hypothesis that there is high combining ability between the exotic lines and the locally adapted QPM lines can be accepted. This is because the hybrids produced performed competitively with the check. There is still room for grain yield improvement in this germplasm as it revealed high genetic variability.

- The hypothesis that there is high combining ability between adapted PVA and QPM lines can be accepted because there were high realised genetic gains for grain yield and other traits. The hybrids developed were quite competitive against the check.

- The hypothesis that there is significant association of secondary traits with grain yield can be accepted. This is because significant relationships of secondary traits with grain yield were observed and these traits can be effectively exploited in the improvement of grain yield.

Since genetic gains were realised, this breeding programme should continue at UKZN. It is recommended that these hybrids be tested at more sites for different seasons. They should also be planted in sites that are disease hot spots so as to test their response towards diseases. These superior hybrids can also be assessed for tolerance to abiotic stresses such as drought, low soil nitrogen and low soil pH before recommending them to famers. This could help improve the stability of performance of the varieties when grown in diverse agro-ecologies. More lines can be crossed to the tester to increase the genetic variability among the hybrids so as to increase the scope for selection.

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