GENETICS OF ENDOSPERM PROTEINS AND AGRONOMIC TRAITS IN MAIZE (*Zea mays* L.*)*

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DECLARATION

I declare that the work in this Thesis entitled GENETICS OF ENDOSPERM PROTEINS AND AGRONOMIC TRAITS IN MAIZE (*Zea mays* L.) has been carried out by me in the Department of Plant Science. The information derived from the literature has been duly acknowledged in the text and a list of references provided. No part of this thesis was previously presented for another degree or diploma at this or any other Institution.

Rekiya Otuchu, ABDULMALIK ---------- ----------
Signature Date

CERTIFICATION

The thesis entitled "GENETICS OF ENDOSPERM PROTEINS AND AGRONOMIC TRAITS IN MAIZE *(Zea mays* L.*)"* by Rekiya Otuchu, ABDULMALIK meets the regulations governing the award of the degree of Master of Science of Ahmadu Bello University and is approved for its contribution to knowledge and literary presentation.

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DEDICATION

This work is dedicated to my parents Alhaji and Hajiya Rufai Abdulmalik

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ABSTRACT

The study examined genetics of endosperm proteins and agronomic traits in maize genotypes. Maize genotypes of varying levels of endosperm protein fractions were grouped into four female and two male parents and mated using North Carolina mating design II in 2011. The resultant 8 F_1 hybrids and six parents were evaluated in 2011/2012, using Randomized Complete Block Design, replicated three times during two seasons: wet and dry seasons at Samaru. Protein quality assessment was carried out using Bradford protein assay method. Ten agronomic traits and protein quality of parents and F_1's were studied to determine their heterotic response and genetic analysis (general combining ability (GCA), specific combining abilities (SCA) and heritability) of the maize genotypes. From the analysis of variance, significant differences were observed among the genotypes for the following agronomic traits: days to 50% seedling emergence, days to 50% flowering, days to 50% silking, plant height, ear height, number of cobs per plant, number of kernel rows, ear length, ear weight, grain yield and for protein quality traits (albumins/globulins, zeins, glutelins). Sammaz 20 was the best parent, having better GCA values in terms of grain yield and other agronomic traits during the wet and dry seasons, Sammaz 17 was the best parent, having better GCA values for grain yield and most traits for the two seasons and Sammaz 37 was the best parent with better GCA values for protein quality. The crosses with better SCA values in terms of grain yield and most agronomic traits for the wet season was Sammaz 20 x Sammaz 14 and Sammaz 17 x Oba 98 for the dry season. Sammaz 20 x Sammaz 14 was the best cross with better SCA values in terms of grain yield and most agronomic traits for the two seasons, while Sammaz 18 x Sammaz 14 was the best combiner for protein quality. Narrow sense

heritability (h^2ns) estimates ranged from 0.21 for days to 50% seedling emergence to 0.80 for ear length in the wet season, 0.55 for days to 50% flowering and days to 50% silking to 0.96 for ear weight in the dry season and 0.11 for number of kernel rows to 0.99 for ear weight. Protein quality traits had negative heritability estimates, for albumins/globulins but positive for glutelins 0.51. The $\sigma^2_{GCA}/\sigma^2_{SCA}$ variance ratios for most of the agronomic traits in the wet season and dry season were predominantly governed by non – additive gene action, while across season was governed by additive gene action. The σ2GCA/σ^2_{SCA} variance ratios for protein quality traits were all governed by non-additive gene action. High percentage heterotic response was observed for both agronomic and quality traits. Sammaz 20 x Sammaz 14, Sammaz 37 x Sammaz 14 and Sammaz 17 x Sammaz 14 had the highest heterotic response for agronomic traits (days to 50% seedling emergence, days to 50% flowering, days to 50% silking, plant height, ear height and grain yield) while Sammaz 37 x Oba 98, Sammaz 18 x Oba98 and Sammaz 20 x Oba 98 had the highest heterotic response for quality traits (albumins/globulins and glutelins).

TABLE OF CONTENTS

Title page …….. ii

Declaration ……... iii

Certification …….. iv

Dedication ……..... v

Acknowledgements …….. vi

Abstract …… viii

Table of contents …….. x

List of tables …… xii

List of figures ……..... xiv

Abbreviations …… xv

1.0 INTRODUCTION …….. 1
1.2 Justification ……. 3
1.3 Objectives of the study ……... 4

2.0 LITERATURE REVIEW
2.1 Importance of maize …… 5
2.2 Maize proteins ……. 5
2.3 Distribution of maize proteins in different anatomical parts of Maize …… 10
2.4 Nutritional value of maize …….. 11

2.5 Quality protein maize (QPM) …… 12
2.5.1 Protein quality …….. 14
2.5.2 Importance of lysine and tryptophan …… 17
2.5.3 Consumption of maize ……. 18

2.6 Agronomic performance of maize genotypes ……... 22
2.7 Genetics of maize genotypes …….. 25

3.0 MATERIALS AND METHODS
3.1 Experimental site 28
3.2 Description of materials 28
3.3 Population development 29
3.4 Experimental procedure 29
3.5 Endosperm flour preparation 30

3.6 Protein extraction 30
3.6.1 Extraction of albumin/globulin 30
3.6.2 Extraction of zein 31
3.6.3 Extraction of glutelin 31

3.7 Data collection and observations 32
3.8 Statistical analysis 33
3.8.1 Analysis of variance for randomized complete block design 33
3.8.2 Analysis of variance for design II experiment 35

3.9 Estimation of GCA and SCA effects 39
3.10 Estimation of heritability 41
3.11 Estimation of heterosis 42

4.0 RESULTS
4.1 Analysis of variance for Samaru wet season 43
4.2 Analysis of variance for Samaru dry season 47
4.3 Analysis of variance across seasons 51
4.4 Analysis of variance of endosperm proteins 55
4.5 Analysis of variance for Design II 58
4.6 Combining ability effects for Samaru wet season 65
4.7 Combining ability effects for Samaru dry season 68
4.8 Combining ability effects for Samaru across seasons 72
4.9 Combining ability effects at Samaru for endosperm proteins 75
4.10 Narrow sense heritability estimates 79
4.11 Heterosis estimates for Samaru wet season 85
4.12 Heterosis estimates for Samaru dry season 87
4.13 Heterosis estimates for Samaru across seasons 89
4.14 Heterosis estimates at Samaru for endosperm proteins 91

5.0 DISCUSSION
5.1 Population variability 93
5.2 Combining ability 96

5.3 Heritability ……... 99
5.4 Heterosis …….. 104

6.0 SUMMARY, CONCLUSION AND RECOMMENDATIONS
6.1 Summary ……... 107
6.2 Conclusion …… 110
6.3 Recommendations …… 111
REFERENCES …… 112

LIST OF TABLES

Table Page

2.1: Major classes of maize proteins …… 7

2.2: Major classes of zein proteins …….. 9

2.3: Distribution of different protein fractions in the different anatomical parts of Maize (% total Protein) …… 10

3.1: Description of experimental materials ……. 29

3.2: Analysis of variance for randomized complete block design for one season .. 33

3.3: Analysis of variance for randomized complete block design across seasons …… 34

3.4: Analysis of variance for completely randomized design for endosperm Proteins ……. 35

3.5: Analysis of variance for design II experiment in one season ……. 36

3.6: Analysis of variance for design II experiment across seasons …… 38

4.1: Mean squares for agronomic traits evaluated at Samaru in 2011wet season .. 44

4.2: Mean performance for agronomic traits evaluated at Samaru in 2011 wet season …… 45

4.3: Mean squares for agronomic traits evaluated at Samaru in 2011/2012 dry season ……. 48

4.4: Mean performance for agronomic traits evaluated at Samaru in 2011/2012 dry season …….. 49

4.5: Mean squares for agronomic traits evaluated at Samaru across seasons …….. 52

4.6: Mean performance for agronomic traits evaluated at Samaru across seasons …….. 53

4.7: Mean squares for endosperm proteins at Samaru in 2011……. 56

4.8: Mean performance of endosperm proteins at Samaru in 2011 ……. 57

4.9: Mean squares for design II for agronomic traits at Samaru in 2011 wet season …….. 59

4.10: Mean squares for design II for agronomic traits at Samaru in 2011/2012 dry season …….. 60

4.11: Mean squares for design II for agronomic traits at Samaru across seasons …… 61

4.12: Mean squares for design II for endosperm proteins at Samaru in 2011.. 64

4.13: Estimates of GCA effects for agronomic traits at Samaru in 2011wet season ……. 66

4.14: Estimates of SCA effects for agronomic traits at Samaru in 2011wet season …… 67

4.15: Estimates of GCA effects for agronomic traits at Samaru in 2011/2012 dry season ……. 70

4.16: Estimates of SCA effects for agronomic traits at Samaru in 2011/2012 dry season ……. 71

4.17: Estimates of GCA effects for agronomic traits at Samaru across season .. 73

4.18: Estimates of SCA effects for agronomic traits at Samaru in across seasons .. 74

4.19: Estimates of GCA effects for endosperm proteins at Samaru in 2011…. 77

4.20: Estimates of SCA effects for endosperm proteins at Samaru in 201……. 78

4.21: Estimates of narrow sense heritability for agronomic traits evaluated at samaru 2011wet season, 2011/2012 dry season, across seasons and endosperm proteins …… 80

4.22: Estimate of GCA and SCA variances for agronomic traits at Samaru in 2011 2011 wet season, 2011/2012 dry season and across seasons ……. 82

4.23: Estimate of GCA and SCA variances for endosperm proteins at Samaru in 2011…… 84

4.24: Estimates of percent heterosis for agronomic traits evaluated at Samaru in 2011 wet season …….. 86

4.25: Estimates of percent heterosis for agronomic traits evaluated at Samaru in 2011/2012 dry season …….. 88

4.26: Estimates of percent heterosis for agronomic traits evaluated at Samaru across seasons …… 90

4.27: Estimates of percent heterosis for endosperm proteins at Samaru in 2011.. 92

LIST OF FIGURES

Figure Page

1: Structure of maize kernel 6

ABBREVIATIONS

ABU: Ahmadu Bello University

ANOVA: Analysis of variance

BSA: Bovine serum albumin

CIMMYT: International Maize and Wheat Improvement Center

CRD: Completely randomized design

DAS: Days after sowing

DE: Days to 50% seedling emergence

df: Degrees of freedom

DF: Days to 50% flowering

DS: Days to 50% silking

EAA: Essential amino acid

EH: Ear height (cm)

EL: Ear length (cm)

EMS: Error mean squares

EW: Ear weight (g)

FAO: Food and Agriculture Organization

FAOSTAT: Food and Agriculture Organization production statistics

$F_{1:}$ First filal generation

GCA: General combining ability

GY: Grain yield (kg/ha)

IAR: Institute for Agricultural Research

kDa: Kilo dalton

KJ: Kilo joules

KRW: Number of kernel rows

L/T: Lysine/ tryptophan ratio

MSS: Mean sum of squares

NaCl: Sodium chloride

NC: Number of cobs

OPV: Open pollinated variety

PH: Plant height (cm)

QPM: Quality protein maize

RCBD: Randomized complete block design

SCA: Specific combining ability

SDS- PAGE: Sodium diodecyl sulphate- Polyacrylamide gel electrophoresis

S.E: Standard error

UNICEF: United Nations Children's Fund

WAS: Weeks after sowing

CHAPTER ONE

1.0 INTRODUCTION

Maize *(Zea mays* L.) also known as corn, is a member of the grass family called Poaceae. It is perhaps the most completely domesticated of all cereals (Benz, 1994) and essentially a crop of warm countries with adequate soil moisture (Adeyemi, 1969). It originated from South America where it was taken to all parts of the world (Galinat, 1992; Gonzalez, 2001). Modern maize is considered to have evolved from Teosinte (God's corn) than from early Mesoamerican maize called Chapalote or a Tripsacum species (Doebley *et al.,* 1990; Brenneman, 2001). It has a variety of uses as food, livestock feed and as raw material for industries. Worldwide, more than 60% of maize produced is used for poultry, pigs and ruminant animals. Industrial use of maize includes the manufacture of tortillas, which is produced from wet milling, and oil production from the germ. Maize also found its way in the bio-ethanol industry and its residues have important uses including animal feeds, a source for furfural and xylose extracts from the cob.

Maize is the basic staple cereal grain for large groups of people in Latin America, Africa, and Asia. It provides significant amounts of calories and protein for these people (Mertz, 1992). However, maize is relatively low in protein content and has limiting amounts of two essential amino acids, lysine and tryptophan (Bressani, 1991). Increased lysine and tryptophan content was observed in the protein composition of the endosperm of opaque-2 (*o2*) mutant of maize. The homozygous recessive *o2* gene restricts synthesis of zein that contains little lysine and tryptophan and a pleiotropic increase of the non-zein proteins that contain high lysine and tryptophan levels in endosperm (Habben *et al.,*

1993). Agricultural utilization of the *o2* maize has been limited due to reduced yield and undesirable seed characteristics such as soft, chalky kernels that retain moisture and are slow drying at harvest (Lambert *et al.,* 1969, Loesch *et al.,* 1976). This contributes to greater insect, disease, and aflatoxin susceptibility and mechanical damage during grain harvesting and handling.

Cereals supply more than one half of the energy consumed by the people in the world and nearly one half of the protein. Maize is a cereal of major importance in the developing world and has the highest genetic yield potential of all the cereal grains (CIMMYT, 2001). In the year 2002, corn was the leading cereal crop of the world cereal production followed by rice and wheat (FAO, 2008). World population has risen at a rate of 1.9% per year since 1960, but food production has grown at 2.8% per year due to the application of better crop production techniques (Bynes and Bumb, 1997). However, starvation and malnutrition is still a problem.

According to FAO (2009a), world hunger has reached a record height of 1.02 billion and 100 million of which is caused by the global financial crisis. Thus, an increase in food quantity and quality and better distribution is of main concern. Maize is the third most important food crop in the world, surpassed only by two other grains, wheat and rice. Its economic importance is due to its trade as food, feed, and industrial crop. Demand for maize has been projected to increase by 50% globally and by 93% in Sub-Saharan Africa in the next decade (Pingali and Pandey, 2001). To compensate for the increasing demand for maize, the total harvested area increased to 140,182,000ha from 1997-1999 with a growth rate of 0.7% annually worldwide (CIMMYT, 2000). In 2007,

cereal production increased by 4.3% with its bulk coming from maize (FAO, 2007). By 1988, maize was grown on 156 million hectares in nearly 100 countries within 40˚S and 58˚N latitudes and all longitudes (Brown and Peter, 2008; FAO, 2009a). Developing countries account for 64% of the world's maize area and 43% of global maize production (CIMMYT, 2000). In Nigeria, maize ranks third in importance after sorghum and millet among the cereal crops. It is cultivated both as rain fed and under irrigation on more than 5 million hectares, spread through the six agro-ecological zones and maize production is put at about 26 million tons from 3,845,000 hectares (FAO, 2009b).

1.2 JUSTIFICATION

Maize which makes up a large part of the diet in developing countries, have a low protein concentration and the protein quality is limited by deficiencies in some essential amino acids, mainly lysine and tryptophan, hence, has poor nutritional value (Balinat, 1970; Bressani, 1992). The conversion of low to high protein quality maize in terms of albumin/globulin and glutelin, offers the potential to augment healthy growth and protein metabolism in the rural poor who consume maize on daily basis. Thus, helps to reduce nutrition related diseases, deaths and significantly improve nutritional status of individuals who depend primarily on maize for sustenance (Thielebein, 1969; Vasal, 1974; Ado, 1999). Development of maize with unique grain quality traits, however, has not received the same emphasis in genetics, breeding, and economics as higher yield and agronomic performance (Hallauer, 2001; Scott *et al*., 2006). Breeding for grain quality traits can both diversify and add economic value to a crop. Therefore, the knowledge of heritable variation for breeding purposes is not only important for grain yield and other agronomic characteristics, but also for nutritional purpose (Alexander, 1988; Pollak and

Scott, 2005). The development of biochemical assays that allow efficient characterization of endosperm components among a large number of progeny promises to help breeders better explore existing genetic variation within crop species, thus providing essential information for development of new genotypes from breeding populations (Goodman and Brown, 1988; Mohammadi and Prasanna, 2003). It was in this context that maize varieties with better protein quality were evaluated under local conditions to obtain genetic information on endosperm proteins and agronomic traits. The paucity of information on genetics of endosperm proteins in maize necessitated the use of lysine and tryptophan as a reference for quality in terms of albumin/globulin and glutelin.

1.3 OBJECTIVES OF THE STUDY

1. To estimate the general combining ability for the parents and specific combining ability of their crosses for endosperm proteins and agronomic traits.
2. To estimate heritability of the endosperm proteins and agronomic traits.
3. To estimate the heterosis of endosperm proteins and agronomic traits.
4. To suggest breeding procedures to adopt in improving maize endosperm proteins and agronomic traits.

CHAPTER TWO

LITERATURE REVIEW

2.1 IMPORTANCE OF MAIZE

Corn originated in central Mexico about 7000 years ago, starting from teosinte (*Zea mays parviglumis*) which was domesticated. Maize (*Zea mays*) was essential in Mayan and Aztec civilizations. The oldest maize was found in Teotihuacan, a valley near Mexico City (FAO, 1992). The three principal uses of corn are: as food, as feed for livestock and as raw material for industry. The forms of maize consumed around the world vary, ranging from cooked immature grain to processed shelled kernels (Bressani, 1991). A crop of maize is harvested somewhere around the world every month of the year (Mangelsdorf and Reeves, 1939). In the year 2002, corn was the leading cereal crop with 29.7% of the world cereal production followed by rice (28.5%) and wheat (27.9%) (FAOSTAT, 2003). The maize production leader in 2002 was United States with 39% of world production, followed by China with 18.6%. Specialty corns such as popcorn, sweet corn, high-protein corn, waxy corn, high oil corn, and others, account for less than 5% of the total U.S. corn production; individually each has less than 1% (Boyer and Hannah, 2001).

2.2 MAIZE PROTEINS

The maize grain largely consists of endosperm that is rich in starch (71%) (Fig.1), both the embryo and endosperm contain proteins but the germ proteins are superior in quality as well as quantity. The maize endosperm consists of two distinct regions having different physical properties; the aleurone layer is the outer most layer rich in hydrolytic

enzymes secreted by specialized cells. Within the aleurone layer is the starch rich endosperm having vitreous and starchy regions. The zein proteins found in vitreous region form insoluble accretions called protein bodies in the lumen of rough endoplasmic reticulum and towards maturation are densely packed between starch grains (Gibbon and Larkin, 2005).

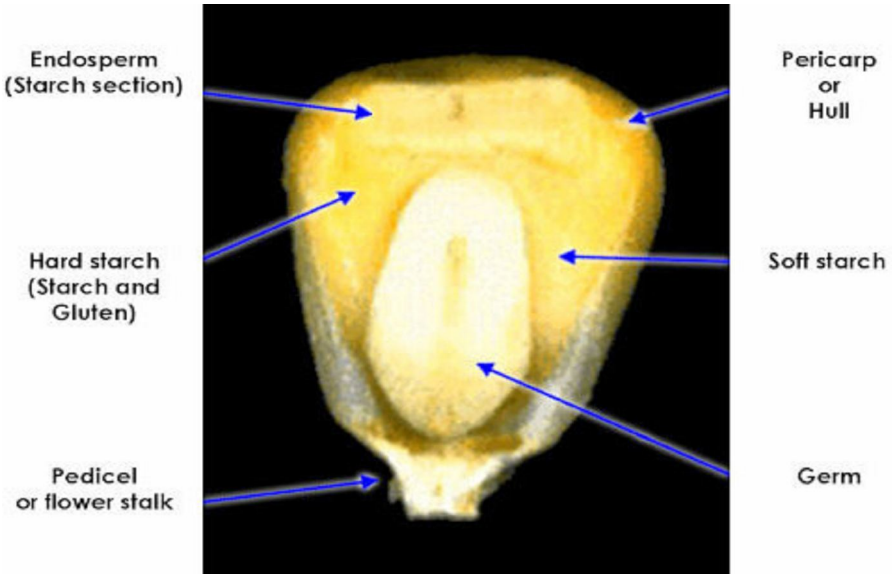


Figure 1: Structure of maize kernel (www.fao.org, 1992)

The relative proportion of different seed protein in the kernel influences the nutritive value of maize protein. Maize kernel protein is divided into four major classes based on their solubility properties (Table 1.1), albumin/globulin, prolamin (zein) and glutelin. The albumin proteins are soluble in water or low salt aqueous solution and globulins are soluble in high salt aqueous solution. Although they are relatively high in lysine (5-7%), these two protein fractions combined represents only 6-12% of the total kernel protein. Glutelins are seed proteins soluble in dilute alkali solution and they contain about 3- 3.4% lysine. Glutelins are the second most abundant class of maize seed

proteins which accounts for about 35- 45% total kernel proteins. The third class of proteins in the maize kernels is the prolamin (zein) fraction which is alcohol soluble (Shewry and Halford, 2002), the zein account for approximately 50- 60% of the total kernel protein.

Table 2.1: Major classes of maize proteins

Protein class	Solubility properties	Relative abundance	Nutritive value
Albumin	Water or low salt aqueous solution	Low	High
Globulin	High salt aqueous solution	Low	High
Glutelin	Dilute alkali solution	High	Intermediate
Zein	Alcohol	High	Low

Zeins are a class of alcohol soluble proteins that are specific to endosperm of maize (Prassana *et al*., 2001) and are not detected in any other plant part. Other proteins such as albumins/globulins (3-7%) and glutelins (30-40%) are collectively called non-zeins.The prolamins of maize grain are called zeins and consist of one major class (α-zein) and three minor classes (β, γ and δ). The zein fraction α is rich in cysteine while band-fractions are rich in methionine. These four types of zeins :α, β, γ and δ constitute about 50-70% of maize endosperm and are essentially rich in glutamine, leucine and proline and poor in lysine and tryptophan. The zein fraction in common maize normally contains higher proportion of leucine (18.7%), phenylalanine (5.2%), isoleucine (3.8%), valine (3.6%) and tyrosine (3.5%), but smaller amounts of other essential amino acids such as threonine (3%), histidine and cysteine (1%), methionine (0.9%), lysine (0.1%) and is essentially devoid of tryptophan as it is absent from the major prolamin fraction (α

-zein) of maize kernel. The non-zein protein fraction is balanced and rich in lysine and tryptophan (Vasal, 2000).

A widely accepted nomenclature system was developed that classified these proteins on the basis of their solubility and structural relationships and molecular mass following SDS-PAGE as β-, α-, γ-, and δ-zeins (Esen, 1987; Coleman and Larkins, 1998). The α- zeins class consists of 19- and 22-kDa proteins and accounts for the majority of zein proteins in common genetic background. Both 19- and 22-kDa α- zein proteins are mixtures of related polypeptides encoded by large gene families (Table 1.2). The α- zein contains no lysine and low levels of methionine, the β-, γ-, and δ-zeins are soluble in alcohol in the presence of a reducing agent. The β-zein is 14kDa protein containing no lysine and approximately 11% methionine. The γ- zein, including 16- and 27-kDa protein is also devoid of lysine and has less than 2% methionine. The δ-zein has very high methionine content. The 10-kDa δ-zein is 20% methionine and the 18-kDa δ-zein is 27%. Additionally, the 18-kDa δ-zein contains one lysine and two tryptophan codons. (Philips and Olsen, 2001). Up-regulation of 27kDa γ- zein are associated with increased kernel hardness in QPM and as a promoter for high expression of transgenes in maize endosperm (Holding and Larking, 2006; Wu *et al.,* 2010), so better understanding of the 27kDa γ- zein and other seed storage proteins may allow for improvement of protein quality in maize without reduction of yield or agronomic qualities.

Table 2.2: Major classes of zein proteins

Zein class	Molecular mass	Lysine and methionine content
α-	19-kDa, 22-kDa	Low levels of methionine, no lysine
β-	14-kDa	Intermediate levels of methionine; no lysine
γ-	16-kDa, 27-kDa	Low levels of methionine; no lysine
δ-	10-kDa, 18-kDa	High levels of methionine; the 18-kDa structural gene also contains one lysine codons.

(Philips and Olsen, 2001)

Zeins play an important role in total protein and amino acid content in maize. For example, in the Illinois long term selection experiment, the high protein lines had increased zein while the low protein lines had decreased zeins (Bhattramakki *et al.,* 1996). Zeins accumulate as accretions, called protein bodies, which form within the lumen of the rough endoplasmic reticulum (RER) (Lending and Larkins, 1989). The smallest zein-containing protein bodies, which are observed in sub-aleurone cells, consist primarily of β- and γ-zeins. Larger protein bodies found in sub-aleurone and starchy endosperm cells contain, in addition to β- and γ-zein, mainly α-, and some δ-zeins. It appears that as storage protein synthesis progresses, the α- and δ-zein proteins penetrate the matrix of β- and γ-zeins, expanding the protein body into a spherical structure that reaches a diameter of 1 to 2μm. Some evidence suggests the β- and γ-zeins proteins play a role in α- and δ-zein retention in the RER (Coleman *et al*., 1996; Bagga *et al*., 1997), although the mechanisms by which this occurs have not been investigated. Additional evidence supporting the large size and complexity of the gene families encoding these proteins came from the heterogeneity observed among zeins after separation by iso-electric focusing and SDS-PAGE.

2.3 DISTRIBUTION OF DIFFERENT PROTEIN FRACTIONS IN THE DIFFERENT ANATOMICAL PARTS OF MAIZE GRAIN

Albumins and globulins together make up 19% of the total protein whole grain flour (Laundry and Moureaux, 1970). However the proportions of these proteins are lower in the endosperm flour, about 3.5- 6% in maize (Yau *et al.,* 1999). This is so, because the albumin and globulin proteins are abundant in the germ (Taylor and Schussler, 1986; Wilson, 1987), which is removed during the decortication and degerming process to produce endosperm flour (Table 1.3). Zeins make up about 50-60% of the total protein whole grain flour (Hamaker *et al.,*, 1995), while a higher proportion of these proteins are found in the endosperm flour about 52-62% (Yau *et al.,* 1999). This is so, because the removal of the germ entails loss of protein material mostly albumin and globulins, but not prolamins which as stated earlier, are located in protein bodies in the starchy endosperm (Taylor *et al.,* 1984b; Lending and Larkins, 1989). Glutelins have been quantified as the amount of proteins remaining after sequential extraction with salt and aqueous alcohol. They account for about 30-40% of endosperm flour (Laundry and Moureaux, 1970).

Table 2.3: Distribution of different protein fractions in the different anatomical parts of normal maize (% total protein)

Protein fractions	Whole grain	Endosperm	Germ
Albumins/Globulins	12	6	52
Zeins	52	60	5
Glutelins	25	26	18

Wilson, 1987 (% total N)

2.4 NUTRITIONAL VALUE OF MAIZE

The importance of cereal grains to the nutrition of millions of people around the world is widely recognized. About 17% of the total maize produced is dedicated for human consumption. Because they make up such a large part of diets in developing countries, cereal grains cannot be considered only as a source of energy, as they provide significant amounts of protein as well. It is also recognized that cereal grains have a low protein concentration and that protein quality is limited by deficiencies in some essential amino acids, mainly lysine. Much less appreciated, however, is the fact that some cereal grains contain an excess of certain essential amino acids that influence the efficiency of protein utilization. The classic example is maize. Other cereal grains have the same constraints but less obvious.

Maize is the basic staple cereal grain for large groups of people in Latin America, Africa, and Asia. Corn provides significant amounts of calories and protein for these people (Mertz, 1992). The mature kernel is composed of 70-75% starch, 9-12% protein, 4.5% oil, 1.3% minerals and vitamins. The endosperm, which makes up 80% of the kernel, is composed of 70% starch while the germ is approximately 30% oil and 18% protein. Endosperm protein is largely made up of zein fractions (60%) which are deficient in lysine and tryptophan in contrast to the germ protein which is composed of albumin, glutelin, and globulin that are rich in lysine and tryptophan. Friedman (1996) pointed out that proteins are an essential component of the diet needed for survival of animals and humans. Protein's basic function is to provide adequate supply of amino acids. The protein quality depends on its amino acid content and on the physiological utilization of the specific amino acids after digestion, absorption and minimal obligatory rates of

oxidation. Availability of amino acids varies with protein source, processing treatment and interaction with other components of the diet.

Maize accounts for between 50% and 60% of dietary protein in human diet. Protein in normal maize has poor nutritive value due to high concentration of zein and low concentration of two essential amino acids: lysine and tryptophan (Balint, 1970; Bressani, 1992). The maize kernel is divided into three parts: the pericarp, endosperm, and the germ. The pericarp is characterized by a high crude fibre content of about 87%, which is constituted mainly of hemicelluloses, 67%; cellulose, 23%; and lignin, 0.1% (Burge and Duensing, 1989). The endosperm, which constitutes 80% of the kernel, is about 87.6% starch and 9% protein. The germ contains 33% crude fat, 18.4% protein and 8.3% starch. Due to the figures mentioned above for the endosperm, maize is of poor nutritional value because of low levels of lysine and tryptophan (FAO, 1992). The protein quality of common maize is similar to that of the other cereals except rice. Both opaque-2 maize and the hard-endosperm QPM have a protein quality not only higher than that of common maize, but also significantly higher than that of other cereal grains.

2.5 QUALITY PROTEIN MAIZE (QPM)

Under-nutrition can stem from one or many nutrient deficiencies. Supplementation and fortification programs targeted at improving vitamin A, zinc, or folic acid status are some examples of current nutritional ameliorating efforts (MI/UNICEF, 2004). Protein deficiency, on the other hand, has been in and out of the international nutrition limelight since the early 1900s. Researchers at the International Maize and Wheat Improvement Centre (CIMMYT) realized the potential for ameliorating

protein malnutrition in maize-dependent populations by using traditional agriculture and nutritionally improved maize cultivars. In the early 1960s, a mutant maize cultivar with similar total protein content but twice the amount of Lysine and Tryptophan (Villegas *et al*., 1980, Mertz *et al*., 1964) and 90% bioavailable protein (Bressani, 1991) was discovered. This nutritionally superior maize was named opaque-2 maize, after the "opaque-2" single gene mutation responsible for its improved protein quality. Thereafter, efficacy testing in humans and animals was enthusiastically undertaken (Bressani, 1992; Knabe *et al*., 1992). Subsequent conventional breeding efforts generated numerous cultivars with improved agronomic characteristics, and these were referred to as QPM (Vivek *et al*., 2008; Bjarnason and Vasal, 1992).

Like its opaque-2 counterpart, QPM is considered a bio-fortified food, because its nutritional profile has been improved using conventional breeding techniques. The basic component of both of these maize cultivars is the opaque-2 (sometimes abbreviated *o2*) mutation. This mutation causes a shift in the synthesis of certain protein types in the endosperm compartment of the maize kernel. Common maize contains nearly 60% endosperm protein as zein, a lysine and tryptophan-poor protein body. The opaque-2 mutation suppresses zein synthesis while simultaneously increasing production of other non-zein proteins that are richer sources of lysine and tryptophan (Gibbon and Larkin, 2005; Geetha *et al*., 1991). Some studies suggest that QPM can provide nutritional benefits in addition to its protein profile, such as higher niacin bioavailability. Other bio-fortification efforts to improve the protein profile include high-methionine varieties (Lai and Messing, 2002).

Furthermore, some QPM hybrids contain as much as 13.5% protein (CIMMYT, 2001). Search for better genes has continued and additional mutants are known that improve protein quality of corn endosperm (opaque-7, opaque-6, floury-3, and opaque-11) but no other mutant has been found to offer any additional advantages over opaque-2 gene (Vasal, 2001). Paiva *et al*., (1991) found changes in the major zein components of QPM. Regular maize had up to seven times more zein than QPM. On the contrary for the "zein-like" fraction, opaque-2, floury-2 and QPM showed twice as much protein than the regular maize. QPM had more δ-zein at the periphery of the protein bodies, compared to opaque-2 and regular maize. δ- zein could be involved in disulphide interactions that influence kernel hardness in QPM genotypes (Paiva *et al*., 1991; Lasztity, 1996). QPMs and opaque-2 showed a stronger reduction of a-zein in going from hard to soft endosperm regions and the δ-zein content was greater in QPM than in regular genotypes regardless of the endosperm region (Paiva *et al*., 1991). QPM traits are caused by recessive genes, thus in open pollinated environment, and pollen from normal maize could decrease protein quality. According to CIMMYT (2001), pollen contamination of QPM from other varieties has been significantly less than originally projected. Open-pollinated varieties (OPVs) can be harvested and sown the following season without yield or quality penalty.

2.5.1 Protein Quality

Protein quality in corn depends on the amount and balance of the essential amino acids (Bressani, 1991). Proteins with high biological value have a lysine: tryptophan (L/T) ratio of 5-8 by weight (Flodin, 1997). Protein quality of maize is similar to wheat or sorghum but lower than opaque-2 maize and quality protein maize. Researchers have agreed that the simultaneous addition of both lysine and tryptophan improves the protein

quality of maize significantly (Ufaz and Ghalili, 2008). This has been demonstrated in experimental work with animals. The improvement in quality obtained after the addition of lysine and tryptophan has been small in some studies and higher in others when other amino acids have been added. The total protein content of maize grain is highly elastic; the most well-known experiment that altered total protein content in maize is the Illinois long term selection experiment. Starting with a single open pollinated variety, selection for high and low protein has been conducted since 1896 (Moose *et al*., 2004). Typical maize lines consist of 9-12% protein, but selection has resulted in a high protein line with over 32% protein and a low protein line with 4% protein (Lucas, 2010). The high protein maize varieties were found to have increased levels of zein while the low protein line had decreased zeins (Bhattaramakki *et al*., 1996). The observed increase in protein content is highly correlated with zein, or the alcohol-soluble protein, which is low in lysine and tryptophan and contains excessive amounts of leucine. Protein quality remains unaltered due to an increase in total zein content, which is deficient in lysine and tryptophan (Bhatnagar, 2001), which means, the improvement is in protein quantity and not protein quality. There is a strong negative correlation between protein content and grain yield (Dudley *et al*., 1977; Glover, 1992).

Even though high protein is possible in maize, selection for yield has increased starch and decreased total protein (Scott *et al*., 2006). The decrease in total protein is not associated with a change in ratios of the essential amino acids lysine, methionine, and tryptophan (Scott *et al*., 2006), but the low content of these amino acids in maize has contributed to nutritional deficiency in regions where maize is the staple food, such as in Africa and Central America, particularly in cases where maize makes up more than 50%

of the diet (Nuss *et al*., 2011). These amino acids are also important when maize is used as an animal feed, such that maize must be combined with other grains or with synthetic amino acids to provide a complete protein source. While there is little variation in amino acid content in modern inbred lines, some mutations such as opaque-2 significantly alter maize amino acid composition. Zarkadas *et al.,* 1995, examined amino acid content of quality protein maize (QPM) line, which contains the opaque-2 mutation, alongside flint and dent inbreds. They showed that the QPM line had approximately twice as much lysine as the flint and dent inbred lines. Using estimates of lysine content in QPM and normal maize, Nuss *et al.,* 2011 showed that 40% less QPM maize was needed to meet daily requirements for lysine compared to non-QPM maize, at 500g per day for adults and 100g per day for children (Nuss *et al*., 2011). Lysine, along with methionine and tryptophan, are important targets for improvement of maize protein quality.

Maize is deficient in two essential amino acids: lysine and tryptophan, making it a poor protein food. The protein concentration is highest in the germ, but the quality is better in the endosperm. The germ proteins contribute significantly to essential amino acids, so maize food products without the germ, including quality protein maize endosperm, are lower in protein quality compared to the whole kernel. The germ contributes most of the oil, sugar, vitamins**,** and minerals of the kernel. The germ also has a lower leucine to isoleucine ratio, giving it a higher biological value. Biological value is defined as the amount of absorbed nitrogen needed to provide the necessary amino acids for the different metabolic functions in the body (Latham, 1997).

The high consumption of maize by the human population and the well-established lysine and tryptophan deficiencies in maize protein motivated researchers to develop the QPM to increase concentrations of these essential amino acids in its protein. Newer varieties provide higher protein content (18%) by increasing the prolamin (zein) fraction in maize endosperm, an example of QPM is opaque-2 maize. QPM varieties have almost double the percentages of lysine and tryptophan compared to normal maize, but is similar in overall protein content (Latham, 1997). However, the QPM varieties have a greatly reduced amount of the major storage protein, zein. The biological value of common maize is 45% whereas the QPM is about 80%. Hence the production and consumption of QPM in countries that use maize as their chief grain crop would have a beneficial effect on the nutritional state of the people and significant economic implications from the better use of what is produced and consumed (Okoruwa, 1996). Compared to normal maize, production of QPM varieties have been found to be more susceptible to storage insects due to their softer, floury endosperms, providing a slightly lower yield. Furthermore, QPM varieties have lower zein content, which is associated with lysine deficiency and a higher balance of essential amino acids (Okoruwa, 1996).

2.5.2 Importance of Lysine and Tryptophan

Lysine and tryptophan are essential amino acids for humans and monogastric animals and have to be supplied by the diet. Of all the essential amino acids, lysine is the most strongly conserved in humans (Flodin, 1997). L-lysine has a positive effect on Ca metabolism in humans. Studies in animals and humans have shown that dietary supplements with L-lysine can increase intestinal calcium absorption and prevents an increase in Ca excretion in the urine after Ca load (Civitelli *et al*., 1992). It is also

involved in the cross-linking process of bone collagen and in the biosynthesis of carnitine and elastin (Flodin, 1997). Therefore the addition of lysine into a lysine deficient diet will improve bone health in children and post-menopausal woman. Tryptophan is required for the production of niacin thus helping to combat pellagra. It is used by the human body to produce serotonin, a major neurotransmitter that is important for normal nerve and brain function. Serotonin is involved in the control of mood, aggression, pain, anxiety, sleep, memory, eating behaviour, addictive behaviour, temperature control, endocrine regulation, and motor behaviour (Sandik, 1992). As mentioned earlier, germ proteins do contribute significantly to essential amino acids (EAA), so maize food products without the germ, including QPM endosperm, are always lower in protein quality than the whole kernel. Similarly, maize with high zein content is of a lower quality than maize with lower prolamin content, because of a higher relative lysine deficiency and a higher imbalance of essential amino acids such as leucine relative to isoleucine.

2.5.3 Consumption of Maize

The high consumption of maize by the human population in a number of countries in Latin America and Africa and the well-established lysine and tryptophan deficiencies in maize protein motivated the search for a maize kernel with higher concentrations of these essential amino acids in its protein. The possibility of finding better varieties of maize appeared feasible on the basis of three facts. One was that by selection, oil content in the maize kernel could be increased from about 4 -15% (Dudley and Lambert, 1992). This increase was obtained by increasing the size of the germ, the part of the kernel where the oil is concentrated. The same researchers showed that it was possible to increase total protein content from about 6 – 18% by increasing the prolamin (zein) fraction in maize

endosperm. The third finding was the wide variability in lysine content reported among varieties and selections of maize. The search for a high quality protein maize succeeded when Mertz, Bates and Nelson (1964) announced their discovery that the opaque-2 gene used as a marker in maize breeding significantly increased lysine and tryptophan in the cereal protein. Results from initial alkaline processing studies of opaque-2 maize (cultivated in Indiana, United States, in 1965) showed that the process did not induce significant nutritional changes in the dough or in the tortillas, as concluded from chemical data and biological trials with rats.

The protein quality of alkali-processed opaque-2 maize was evaluated in children using the nitrogen balance index (the relationship between nitrogen absorption and retention). Six healthy children were used in two studies. The average nitrogen balances, at protein intake levels of 1.8 and 1.5g per kg body weight per day (Bressani *et al.*, 1969). As can be observed, there were no significant differences in nitrogen retention among the children fed the diets based on milk and on alkali-processed opaque-2 maize when the level of protein intake was 1.8g per kg per day. The difference between opaque-2, common maize can be attributed to the better essential amino acid pattern found in opaque-2 maize, since the digestibility of the two is essentially the same. QPM maize also has lower leucine content, implicated in the low nutritional value of maize. The information presented clearly indicates the superiority of opaque-2 maize protein to that of common maize, a fact that is of great importance for populations consuming large quantities of maize as part of their habitual diet. Graham *et al*. (1989) stated: "To anyone familiar with the nutritional problems of weaned infants and small children in the developing countries of the world, and with the fact that millions of them depend on

maize for most of their dietary energy, nitrogen and essential amino acids, the potential advantages of quality protein maize are enormous. To assume that these children will always be given a complementary source of nitrogen and amino acids is a cruel delusion."

Unfortunately no studies have been done on adult human subjects comparing opaque-2 and common maize in the same study. The protein quality of common maize has, however, been evaluated in human adults by Kies *et al.* (1965). In one study ten subjects were fed degermed maize to provide nitrogen intakes of 4, 6 and 8g per day. The results clearly indicated that when the degermed maize provided 4 and 6g of nitrogen, the average nitrogen balance was negative. Furthermore, the amino acid intake pattern is unbalanced, which may be an additional reason for the poor biological value of the common maize protein. The evidence presented from studies in both children and adults clearly indicates the superiority of opaque-2 maize over common maize. In spite of this, of the maize-consuming countries only Colombia and Guatemala have made efforts during the last few years to introduce this superior maize into agricultural production systems. The reasons are not clear, since agronomic studies conducted in a number of locations have shown that there are no differences between QPM and common maize in cultural practices yield per unit of land and physical quality of grain. Furthermore, the plants look alike; QPM kernels are crystalline and grain yields are comparable to those of common maize. These factors are perhaps more important to growers than the nutritional advantages offered by QPM.

Energy content is alike in both types of maize, but the protein content of QPM is higher and is better utilized because of its better essential amino acid balance. The protein

value of opaque-2 maize, however, can be analysed from other points as well. It has been established that the intake of both types of maize as well as their nitrogen content (protein) are alike, but their digestibility percentages are very different: of 48g of nitrogen intake from common maize, only 39.4g are absorbed and 8.6g are lost in the faeces. In the opaque-2 maize, of the 48g of nitrogen intake, 44.2g are absorbed and 3.8g are lost in faeces. The factor that should be considered, then, is the biological value, which is defined as the amount of absorbed nitrogen needed to provide the necessary amino acids for the different metabolic functions. The biological value of common maize is 45%; from the 39.4g absorbed, 17.7g are retained and 21.7g are excreted. In opaque-2 maize the biological value of the protein is 80%; of the 44.2g of absorbed nitrogen, 35.4g are retained and 8.8g are excreted. The total amount of nitrogen lost when common maize is consumed equals 30.3g, while only 12.6g are lost when the same amount of opaque-2 maize protein is consumed. In other words, only 37% of the common maize intake is utilized, compared to 74% from opaque-2 maize.

Nitrogen balance remains a traditional method for estimating protein metabolism and is calculated as the difference between nitrogen lost in faeces and urine from the nitrogen ingested as food. When the value is positive, protein deposition is occurring in the body and an individual is categorized as being protein adequate (WHO, 2007). From Bressani's calculations, an estimated 23.6g normal maize/kg body weight (BW) was required to achieve nitrogen equilibrium, whereas only 8.2g/kg was needed from opaque-2 maize (Bressani, 1992). If a child weighed 15kg, he or she would therefore require approximately 120g/d opaque-2 maize to maintain protein adequacy. This corresponds to 440kcal (1kcal = 4.18kJ), which is much less than daily energy requirements. If this same

child were to consume common maize, he or she would require ~3 times more maize, an amount that far exceeds intake levels in African countries with even the highest adult per capita intakes. The production and consumption of quality maize in maize-eating countries would therefore have a significant beneficial effect on the nutritional state of populations, with important economic implications from the better use of what is produced and consumed.

2.6 AGRONOMIC PERFORMANCE OF MAIZE GENOTYPES

Several studies were conducted on the agronomic potential of high protein quality maize varieties and were found to be as competitive as low protein maize hybrids and in the study of Pixley and Bjarnason (1993) the best protein quality maize materials were found to yield at least 14% better than low protein quality endosperm maize checks on average. Although Pixley and Bjarnason (1993) reported that quality protein maize (QPM) yield level potentials were now of the same level as normal maize, in a later study, using different germplasm and different test environments Bhatnagar *et al.* (2004) found normal maize checks yielding higher than QPM materials but the yield differences were not significant. Krivanek *et al*. (2007) reported the occurrence of QPM varieties yielding 5% less than normal maize varieties in some genetic backgrounds and encouraged the need to investigate the cause.

In the studies of Pixley and Bjarnason (1993), Jompuk *et al.* (2007) and Bhatnagar *et al.* (2004) normal endosperm check varieties were included and it was only in Pixley and Bjarnason (1993) study where QPM hybrids clearly outperformed normal endosperm hybrids for grain yield potential by at least 14% on average. In the study of Bhatnagar *et*

al. (2004) the contrast of normal endosperm check varieties against QPM F_1 hybrids was not significant ($p > 0.05$) but the mean of normal endosperm checks was at least 0.5t ha^{-1} higher than that for the QPM F_1 hybrids. Similarly, in Jompuk *et al.* (2007) study there were no significant differences for grain yield between the normal endosperm hybrid check varieties and the QPM F_1 hybrids. However, Jompuk *et al.* (2007) report was based on one environment. There were differences in genetic backgrounds between the QPM materials and the normal endosperm maize checks that were used in the studies of both Jompuk *et al*. (2007) and Bhatnagar *et al*. (2004) with the normal endosperm check entries being well adapted to the test locations better than the QPM F_1 hybrids. In the study of Pixley and Bjarnason (1993) where the QPM entries performed better than normal endosperm maize entries, the normal endosperm checks used were supposedly adapted to the environments. The reason for implementation of such a seemingly unfair comparison between QPM hybrids and normal endosperm check entries is because in most environments globally, the development of well adapted QPM germplasm is still in its infancy. The lack of overwhelming yield superiority of QPM cultivars over normal endosperm cultivars was also reported in the review by Krivanek *et al.* (2007) who proposed that more research effort was needed for some QPM genetic backgrounds. Arguably much less effort has been devoted to the improvement of QPM germplasm and varieties compared to the effort spent on normal endosperm maize varieties. This has been the trend despite that at least 20% of the children under five in Zimbabwe suffer from protein energy malnutrition (UNICEF, 2006) a situation which can potentially be alleviated with the growing and consumption of QPM grain among other measures.

Therefore, it is prudent to investigate the agronomic potential of QPM cultivars under local conditions.

Vasal *et al.* (1984) reported that the development of QPM germplasm required the manipulation of two genetic systems. This information however did not make it easier for ordinary maize breeders to develop QPM cultivars because maize breeders continued to experience frustrating in consistencies in their attempts to develop QPM versions of elite adapted normal endosperm maize varieties (Gevers, personal communication, 2005). This is in agreement with the experience at CIMMYT where although previous work had indicated that kernel endosperm modification was mainly controlled by additive components of variance , Vasal *et al.* (1984) and Vasal (2002) referred to the inheritance of kernel endosperm modification as complex. Vasal (2002) advocated for the elucidation of mechanism(s) controlling kernel endosperm modification, and the role of gamma zein in kernel endosperm modification. Thus it is important to understand the role of additive and non-additive variance components or the role of GCA and SCA effects in the breeding of kernel modification so that more QPM varieties can be produced easily.

The other frustrating experience included the differential decline in the protein quality with some genetic backgrounds despite the presence of the opaque-2 gene (Vasal, 2002). Earlier on, the experience with kernel endosperm modifiers had shown that endosperm modifiers were difficult to find and accumulate in dent maize generally (Vasal *et al.,* 1980). The low levels of enthusiasm and success in breeding QPM varieties is probably due to this reason. Most breeding programmes in sub-Saharan Africa use dent germplasm. However most of the unimproved landraces maintained by the communities

tend to be of the flint type. This flint types could present advantages in attempts to combine the QPM trait with other agronomic and quality traits that are already preferred by the farmers. Thus despite several studies on the inheritance and role of kernel endosperm modifiers in the expression of the QPM trait, Vasal (2002) lamented the need for more research to be conducted on the genetics of endosperm modifiers in QPM. This was before the discovery of the third genetic system of amino acid modifiers (Vivek *et al.,* 2008). The fact that certain genotypes possessing both the opaque-2 gene and a good level of endosperm modifiers could test poor for protein quality (tryptophan levels) could be one of the reasons why there was confounding in the expression of the QPM phenotype and hence Vasal (2002) encouraged more research to be done on the genetics of kernel endosperm modifiers.

2.7 GENETICS OF MAIZE GENOTYPES

Literature on the determination of combining abilities in QPM has been limited to a few publications. The earliest reported work on combining abilities of QPM germplasm was by Vasal *et al*. (1993a and 1993b). This was immediately followed by the report of Pixley and Bjarnason (1993); the two studies by Vasal *et al.* (1993a and 1993b) were on CIMMYT QPM populations. The experiments in the first study were all grown in Mexico whilst those for the second study were grown at locations in both Mexico and United States of America (Tennessee, Mississippi, and Indiana States). In the study of Pixley and Bjarnason (1993) QPM inbred lines were studied in four different diallel experiments. The experiments were grown at locations in Colombia, Honduras, Costa Rica and Mexico. The parents involved were the first generation of inbred lines from the CIMMYT

QPM breeding programme. Fan *et al.* (2004) reported the combining abilities among five yellow endosperm tropical and subtropical QPM lines from CIMMYT, and five yellow endosperm Chinese QPM lines.

Combining abilities of two separate experiments on QPM inbred lines were also reported by Bhatnagar *et al.* (2004). The inbred lines were from three different programmes, Texas A&M University (TAMU), CIMMYT, and South Africa (Hans Gevers' breeding programme). The environments for the study were all in the southern part of USA, Texas. The study of Jompuk *et al.* (2007) was based on inbred lines extracted from three CIMMYT populations. Hohls *et al.* (1996) found that both kernel vitreousness and kernel hardness were determined by partially dominant genes whilst additive gene action was responsible for kernel modification. Combining abilities tend to be influenced by the environment and the germplasm used in the study (Falconer and Mackay, 1996). The existence of significant SCA effects for grain yield in QPM maize would allow the development of high yielding QPM hybrids from inbred lines. The currently acknowledged high yields in normal endosperm maize are a result of the existence of significant SCA effects in the sets of germplasm used by the different hybrid maize breeding programmes. For QPM maize to be able to compete with normal endosperm maize cultivars for grain yield and other agronomic traits it would be important for the available QPM germplasm in any region to exhibit significant SCA effects that can be exploited in the form of heterosis.

In Bhatnagar *et al.* (2004) study, SCA effects across environments were not significant for all quality traits except test weight whilst in Vasal (1993a and 1993b) and

Pixley and Bjarnason (1993) studies, SCA for all quality traits across environments were also non-significant. In the study of Vasal *et al.* (1993b), yield potential was found to be influenced by the type of endosperms involved in a cross, with both dent x dent, and dent x flint crosses yielding higher than flint x flint crosses. However the kernel endosperm modification for flint x flint was the most desirable followed by dent x flint and then dent x dent.

Heterosis is usually described as the superiority of hybrids (F_1s) over some measure of performance of the average means of parents (mid parent heterosis) or of superior parent (high parent heterosis). Among other means of productivity, the exploitation of heterosis holds a good promise, has increased the production of maize crop and has been one of the major reason for the success of the commercial seed industry in many crops, especially maize (Stuber, 1994). Heterotic response among germplasm is critical for determining the best method of assimilating germplasm with desirable traits into agronomically acceptable populations. Yusuf *et al.* (2009) reported high level of better parent heterosis for desirable agronomic traits and grain quality in quality protein maize.

CHAPTER THREE

MATERIALS AND METHODS

3.1 EXPERIMENTAL SITE

The research was conducted at Institute for Agricultural Research farm located at Samaru, during the 2011 wet and 2011/2012 dry season. Samaru is located at an altitude of 686m above sea level, $11^0$11'N, $07^0$38'E in the Northern guinea savannah zone of Nigeria. Samaru weather is characterized by two seasons, the dry and wet season. The dry season lasts up to seven months (October - May) cool period is usually experienced between November and February. This emanates from the influence of the North-easterly winds (Harmattan) which controls the tropical continental air mass coming from the Sahara and the temperature varies between 10^oC to 35^oC. A brief period of hot but dry weather occurs in March and April with a temperature between 38^oC to 42^oC. The wet season lasts from May to September/October with long- term annual rainfall of 1040mm (A.B.U., 2012).

3.2 DESCRIPTION OF MATERIALS

The plant materials used in the study comprised maize varieties of varying levels of endosperm protein fractions (albumin/globulin, zein and glutelin). Four of the maize varieties were used as female parents viz: Sammaz 17, Sammaz 18, Sammaz 20 and Sammaz 37 and two as male parents; Sammaz 14 and Oba 98. Five genotypes were obtained from IAR and one from Premier Seeds Ltd (Table 3.1). The variety, source, type and description of the genotypes are presented in Table 3.1.

Table 3.1: Description of experimental materials

S/n	Variety	Source	Parent	Type
1	Oba 98	Premier Seed Co.	Male	Hybrid
2	Sammaz 14	IAR	Male	OPV
3	Sammaz 37	IAR	Female	OPV
4	Sammaz 17	IAR	Female	OPV
5	Sammaz 18	IAR	Female	OPV
6	Sammaz 20	IAR	Female	OPV

3.3 POPULATION DEVELOPMENT

Maize is a cross pollinated plant by nature; thus, pollen was generally controlled to ensure progeny of known parentage. The tassels of the male varieties were covered with bags at their emergence to collect the pollens. The cobs of the female parents were also covered with silk bags at emergence from the nodes to prevent contamination of foreign pollen. Thus, were pollinated with the pollens from the male varieties to produce crosses using a North Carolina mating design II resulting in 8 F_1 hybrids and six parents (14 entries) which were evaluated on IAR field at Samaru.

3.4 EXPERIMENTAL PROCEDURE

The evaluation trial was laid out in a randomized complete block design (RCBD) consisting of three replications. Each plot was a single row 5m long spaced 0.75m apart. Sowing was done manually in the wet season on September 7th, 2011 and dry season November 19th, 2011. Three to four seeds were sown per hill, 50cm apart at two weeks after sowing (WAS), and the seedlings were thinned to two plants per hill. Fertilizers

were applied at the recommended rates of 120 kg N ha^{-1}, 60 kg P_2O_5 ha^{-1}, and 60 kg K_20 ha^{-1} at two, four and six weeks after sowing. Weeding was done at 2, 4 and 6 WAS.

3.5 ENDOSPERM FLOUR PREPARATION

Dry seeds of each of the materials (six parents and 8 F_1) after harvest were bulked and 40 seeds from each were taken for the endosperm preparation. The seeds were soaked in distilled water for 1-2 hours; this was done to soften the seeds. The germs and pericarps were removed by hand and the endosperm dried at room temperature for 24 hours. The dried endosperm of each of the materials was grounded into fine powder by hand using mortar and pestle. The fine powder was then defatted by reflux in hexane solution for 4 hours.

3.6 PROTEIN EXTRACTION

Two hundred and fifty milligram (250mg) of dried endosperm flour of each of the materials was weighed into test tubes. Proteins were sequentially extracted from endosperm flour (1:6, flour - to - extraction buffer, w/v) as: 1) Albumin/globulin, 2) Zein and 3) glutelin. Extraction buffers for the three fractions were: 1) 0.5M NaCl solution for albumin/globulin. 2) 70% ethanol and 2% 2- mercapto ethanol (ME) for zein and 3) 1% SDS and 2% 2- mercapto ethanol for glutelin.

3.6.1 Extraction of Albumin/Globulin

1.25ml of the first extraction buffer was pipetted into each of the test tubes containing the samples. Protein was extracted by shaking the samples and buffer in an oscillatory incubator for 1hour at 4^oC. Mixtures of the sample and extraction buffer were

centrifuged at 10,000 x g for 10mins. Each supernatant (extract) was carefully decanted into empty test tubes. It was repeated again and the supernatants from same sample were pooled together, leaving the residues in the test tubes.

3.6.2 Extraction of Zein

Again, 1.25ml of the second extraction buffer was pipetted into the test tubes containing the residue. Protein was extracted by shaking the samples and buffer in an oscillatory incubator for 1hour at 22^{o}C. Mixtures of sample and extraction buffer were centrifuged at 10,000 x g for 10mins. Each supernatant was carefully decanted into empty test tubes. It was repeated again and the supernatants from same sample were pooled together, leaving the residues in the test tubes.

3.6.3 Extraction of Glutelin

Lastly, 1.25ml of the second extraction buffer was pipetted into the test tubes containing the residue. Protein was extracted by shaking the samples and buffer in an oscillatory incubator for 1hour at 22^{o}C. Mixtures of sample and extraction buffer were centrifuged at 10,000 x g for 10mins. Each supernatant was carefully decanted into empty test tubes. It was repeated again and the supernatants from same sample were pooled together, leaving the residues in the test tubes.

The proteins concentrations were measured by dye - binding method using Bradford protein assay (Bradford, 1976) and Bovine Serum Albumin (BSA) as reference in a spectrophotometer at wavelength of 595nm. The whole process of protein extraction was repeated again, which gave two repetitions.

3.7 DATA COLLECTION AND OBSERVATIONS

Data were collected on the following traits:

1. Days to 50 % seedling emergence (DE): The number of days from sowing to when half of the plants in a plot emerged.
2. Days to 50% flowering (DF): The number of days after sowing (DAS) to when 50% of the plants in a plot shed pollen.
3. Days to 50% silking (DS): The number of days after sowing (DAS) to when 50% of the plants in a plot produced silk.
4. Plant height (cm) (PH): The height from soil level to the flag leaf of five random plants/ plot using measuring tape.
5. Ear height (cm) (EH): The height from the soil level to the node bearing the top most ear using measuring tape.
6. Ear length (cm) (EL): The distance between the base and the tip of the cob from five random plants/plot using measuring tape.
7. Number of kernel rows (KRW): The total number of rows of kernel from five random plants/plot.
8. Number of cobs (NC): The total number of dry ears harvested from each plot.
9. Ear weight (g) (EW): The weight of the dry ears, from each plot.
10. Grain yield (kg/ha) (GY): The total weight of grains harvested in each plot measured in grams and converted to kg/ha based on the land area of each plot.
11. Endosperm protein distribution using Bradford protein assays (Bradford, 1976).

3.8 STATISTICAL ANALYSIS

3.8.1. Analysis of Variance (ANOVA) for Randomized Complete Block Design

Statistical analysis was done using statistical analysis system (SAS, 2008). The form of the ANOVA for one season is given in Table 3.2.

Table 3.2: Analysis of variance of randomized complete block design for one season

Source of variation	df	MSS	Cal F
Replication	(r - 1)	RMSS	RMSS/EMS
Genotype	(g - 1)	GMSS	GMSS/EMS
Error	(r - 1)(g - 1)	EMS	
Total	(rg - 1)		

Where:

df = degrees of freedom

r = number of replications

g = genotypes

RMSS = replication mean sum of squares

GMSS = genotype mean sum of squares

MSS = mean sum of squares

EMS = error mean square

CAL = calculate F value

F = variance ratio of genetic to environmental ratio

The form of the ANOVA for the two seasons combined is given in Table 3.3.

Table 3.3: Analysis of variance of randomized complete block design for across seasons

Source of variation	df	MSS	Cal. F
Replication (Season)	s(r - 1)	RMSS	RMSS/EMS
Genotype	(g - 1)	GMSS	GMSS/EMS
Season	(s - 1)	SMSS	SMSS/EMS
G × S	(g - 1)(s - 1)	GSMSS	GSMSS/EMS
Error	s(g - 1)(r - 1)	EMS	
Total	(rsg - 1)		

Where:

df = degrees of freedom

r = number of replications

s = season

g = genotypes

RMSS = replication mean sum of squares

GMSS = genotype mean sum of squares

SMSS = season mean sum of squares

MSS = mean sum of squares

EMS = error mean squares

CAL = calculate F value

F = variance ratio of genetic to environmental ratio

The form of ANOVA for endosperm protein is given in Table 3.4.

Table 3.4: Analysis of variance of completely randomized design for endosperm proteins

Source of variation	df	MSS	EMS
Genotype	g – 1	M_2	$\sigma^2_{e+} r\,\sigma^2_g$
Error	g(r - 1)	M_1	σ^2_e
Total	gr – 1		

Where,

df = degrees of freedom

r = repetition

g = genotype

σ^2_g = genotypic variance $\quad \sigma^2_g = \frac{M_2 - M_1}{R}$

σ^2_e = error variance $\quad \sigma^2_e = M_1$

3.8.2. Analysis of Variance for Design II Experiment

The model for the ANOVA for one season used according to Singh and Chaudary (1985) is:

$X_{ijk} = \mu + m_i + f_j + (fm)_{ij} + e_{ijk.}$

X_{ijk} = k^{th} observation on the i x j^{th} progeny

μ = general mean

f_j = effect of the j^{th} female

m_i = effect of the i male

$(fm)_{ij}$ = interaction effect and

e_{ijk} = error associated with each observation

The form of ANOVA for Design II is shown in Table 3.5.

Table 3.5 Analysis of variance for design II experiment in one season

Source	df	MSS	EMS
Replication	r - 1		
Females	f - 1	M_5	$\sigma^2_e + r\sigma^2_{fm} + mr\sigma^2_f$
Males	m - 1	M_4	$\sigma^2_e + r\sigma^2_{fm} + fr\sigma^2_m$
Female x Males	(f - 1)(m - 1)	M_3	$\sigma^2_e + r\sigma^2_{fm}$
Error	(r - 1)(mf - 1)	M_2	σ^2_e
Total	rmf - 1	M_1	

Where:

df = degrees of freedom

MSS = mean sum of squares

EMS = error mean squares

σ^2_e = error variance

σ^2_{fm} = variance of female x male

σ^2_f = variance of females

σ^2_m = variance of males

f = number of females

m = number of males

r = number of replications

The model of ANOVA for across seasons according to Kang (1994) is as follows:

$$X_{ijk} = \mu + r_k + f_j + m_i + fm_{ij} + b_k + f_{jk} + m_{ik} + fm_{ijk} + e_{ijk}$$

Where;

X_{ijk} = k^{th} observation on the i x j^{th} progeny

μ = general mean

f_j = effect of the j^{th} female

m_i = effect of i^{th} male

mf_{ij} = the interaction effect

b_k = effect of the k^{th} season

f_{jk} = effect of the j^{th} female in the k^{th} season

m_{ik} = effect of the i^{th} male in the k^{th} season

fm_{ijk} = effect of the j^{th} female and i^{th} male in k^{th} season

e_{ijk} = error associated with each observation.

The form of the ANOVA for Design II across seasons is given in Table 3.6.

Table 3.6: Analysis of variance for design II experiment for across seasons

Source	df	MSS	EMS
Season	(s - 1)		
Replication (season)	s(r - 1)		
Females	(f - 1)	M_7	$\sigma^2_e + r\sigma^2_{fms} + rs\sigma^2_{fm} + rsm\sigma^2_f$
Males	(m - 1)	M_6	$\sigma^2_e + r\sigma^2_{fms} + rs\sigma^2_{fm} + rsf\sigma^2_m$
Females x Males	(f - 1)(m - 1)	M_5	$\sigma^2_e + r\sigma^2_{fms} + rs\sigma^2_{fm}$
Males x Season	(m - 1)(s - 1)	M_4	$\sigma^2_e + r\sigma^2_{fms} + rf\sigma^2_{ms}$
Female x Season	(f - 1) (s - 1)	M_3	$\sigma^2_e + r\sigma^2_{fms} + rm\sigma^2_{fs}$
Female x Male x Season	(f - 1)(m - 1)(s - 1)	M_2	$\sigma^2_e + r\sigma^2_{fms}$
Error	(m - 1)(fm - 1)	M_1	σ^2_e
Total	s(rfm - 1)		

Where

Df = degrees of freedom

S = Season

r = Replication

F = female parent

m = male parent

MSS = mean sum of squares

EMS = error mean squares

σ^2 = error variance

σ^2_{fms} = variance female x male x season

σ^2_{fm} = variance female x male

σ^2_f = variance female

σ^2_m = variance male

σ^2_{fs} = variance female x season

σ^2_{ms} = variance male x season

From the anova, components of variance and their interactions with season were calculated from the following formulae:

$$\sigma^2_{fms} = \frac{M_2 - M_1}{r}$$

$$\sigma^2_{ms} = \frac{M_4 - M_2}{fr}$$

$$\sigma^2_{fs} = \frac{M_3 - M_2}{mr}$$

$$\sigma^2_{fm} = \frac{M_5 - M_2}{rs}$$

$$\sigma^2_{f} = \frac{M_7 - M_5}{rm}$$

$$\sigma^2_{m} = \frac{M_6 - M_5}{rf}$$

3.9 ESTIMATION OF GCA AND SCA EFFECTS

The GCA and SCA effects were estimated using the formula suggested by Singh and Chaudhary (1985).

GCA effects of females:

$$g_j = \frac{x_{i\bullet}}{mr} - \frac{\boldsymbol{x}_{...}}{fmr}$$

Where;

g_j = general combining ability

$x_{i.}$ = total of all the hybrids containing an i^{th} males

$x_{...}$ = grand total of crosses

f = number of females

m = number of males

r = number of replications

GCA effects of males;

$$g_i = \frac{x_{.j}}{fr} - \frac{x...}{fmr}$$

Where,

g_i = general combining ability

$x_{.j}$ = total of all hybrids containing the j^{th} female

$x...$ = grand total of crosses

f = number of females

m = number of males

r = number of replications

SCA effects;

$$S_{ij} = \frac{x_{ij}}{r} - \frac{x_i}{mr} - \frac{x_j}{fr} - \frac{x...}{fmr}$$

Where;

S_{ij} = specific combining ability effects

x_{ij} = total of all the hybrids containing j^{th} females with i^{th} males,

x_i = total of all hybrids containing the i^{th} males,

$x_{.j}$ = total of all hybrids containing the j^{th} females

$x..$ = grand total crosses,

f = number of females,

m = number of males

r = number of replications.

i. S.E (GCA for female) = $(M_e/rm)^{1/2}$

ii. S.E (GCA for male) = $(M_e/rf)^{1/2}$

iii. S.E (SCA effect) = $(M_e/r)^{1/2}$ (Singh and Chaudhary 1985)

Where,

Me = error mean squares

r = number of replications

f = number of female parents

m = number of male parents

3.10 ESTIMATION OF HERITABILITY

Narrow-sense heritability (h^2_n) were estimated using Grafius *et al*. (1952) formula

$$h^2ns = \frac{\sigma^2 m + \sigma^2 f}{\sigma^2 m + \sigma^2 f + \sigma^2 fm + \sigma^2 e/r}$$

Where,

r = number of replications

σ^2_f = variance of females

σ^2_m = variance of males

σ^2_{fm} = variance of females x males

σ^2_e = error variance

The Variance estimates were computed using Cockerham (1956).

$\sigma^2_m = \sigma^2_f = \text{Cov HS} = (1/4)\ \sigma^2_A = \sigma^2_{GCA}$

$\sigma^2_{mf} = \text{Cov FS} - \text{Cov HS}_m - \text{Cov HS}_f = (1/4)\ \sigma^2_D = \sigma^2_{SCA}$

Where,

σ^2_f = variance of females

σ^2_m = variance of males

σ^2_{fm} = variance of females x males

σ^2_{GCA}= general combining ability variance

σ^2_{SCA}= specific combining ability variance

σ^2_A= additive variance

σ^2_D= dominance variance

3.11 ESTIMATE OF HETEROSIS

Estimates of heterosis were obtained following Fonesca and Patterson (1968),

$$\text{High parent (Hp)} = 100 \times \frac{(F1 - Hp)}{Hp}$$

Where

F_1 = mean performance of hybrid

Hp = mean performance of high parent or better parent

CHAPTER FOUR

RESULTS

4.1 ANALYSIS OF VARIANCE FOR SAMARU WET SEASON

The maize hybrids derived through crosses, along with their parents were evaluated regarding agronomic parameters under field conditions in two seasons and endosperm proteins were determined in the laboratory. The result revealed for the wet season in Samaru that the genotypes were highly significant ($P<0.01$) for the traits studied except for number of kernel rows, ear length and grain yield which showed no significant differences (Table 4.1). To compare the means for the traits recorded, Duncan multiple range test at 5% level was applied. The results of the mean performance of the parents and crosses are presented in Table 4.2. The mean of days to 50% seedling emergence (DE) showed significant differences among the parental genotypes as well as among the crosses. The DE ranged from 5 to 8 days for Sammaz 18, Sammaz 20, Oba 98, Sammaz 37 x Oba 98, Sammaz 17 x Oba 98, Sammaz 17 x Sammaz 14, Sammaz 18 x Sammaz 14, Sammaz 20 x Sammaz 14 and Sammaz 14, respectively (Table 4.2). The DE was earliest in Sammaz 18, Sammaz 20, Oba 98, Sammaz 37 x Oba 98, Sammaz 17 x Oba 98, Sammaz 17 x Sammaz 14, Sammaz 18 x Sammaz 14 and Sammaz 20 x Sammaz 14 which were not statistically different from Sammaz 37, Sammaz 17, Sammaz 37 x Sammaz 14 and Sammaz 20 x Oba 98. The genotypes Sammaz 37, Sammaz 17, Sammaz 18 x Oba 98 and Sammaz 20 x Oba 98 had moderate number of days to 50% seedling emergence.

Table 4.1 Mean squares for agronomic traits evaluated at Samaru in 2011 wet season

Source	df	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Replication	2	0.17	1.79	1.24	5.53	9.19	23.74	0.30	2.15	141.60	2654391.53
Genotypes	13	1.65**	12.39**	11.38**	353.24**	264.16**	58.73**	1.80	1.97	1217.65**	2068994.71
Error	26	0.55	2.94	2.67	5.61	6.07	19.12	1.09	1.76	572.34	1189776.15
Total	41										

*, ** Significant at 0.05 and 0.01 probability levels, respectively

df = Degrees of freedom
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield

Table 4.2 Mean performance for agronomic traits evaluated at Samaru in 2011wet season

Parents/Crosses	DE	DF	DS	PH(cm)	EH(cm)	NC	KRW	EL(cm)	EW(g)	GY(kg/ha)
PARENTS										
Sammaz 37	6^{bc}	62^{a}	64^{a}	152.13^{c}	65.27^{cd}	9^{d}	13	14.80	115.13^{a}	1956
Sammaz 17	6^{bc}	58^{bc}	61^{abc}	147.60^{d}	65.93^{cd}	9^{d}	13	14.80	107.87^{a}	1867
Sammaz 18	5^{c}	58^{bc}	61^{abc}	137.27^{e}	52.87^{e}	16^{abcd}	15	14.93	107.27^{a}	2444
Sammaz 20	5^{c}	55^{cd}	58de	131.67^{f}	56.87^{e}	14^{bcd}	14	13.60	97.07^{a}	2089
Oba 98	5^{c}	56^{bcd}	58de	158.47^{ab}	76.53^{a}	21^{ab}	14	14.40	129.00^{a}	3378
Sammaz 14	8^{a}	59^{ab}	61^{abc}	132.67^{f}	45.87^{f}	10^{d}	13	13.93	46.53^{b}	667
CROSSES										
Sammaz 37 X Oba 98	5^{c}	59^{ab}	62^{ab}	136.73^{e}	62.93^{d}	11^{cd}	14	15.40	107.93^{a}	2178
Sammaz 37 X Sammaz 14	6^{bc}	58^{bc}	61^{abc}	140.73^{e}	57.00^{e}	15^{abcd}	13	15.53	128.60^{a}	3067
Sammaz 17 X Oba 98	5^{c}	58^{bc}	60^{bcd}	155.80^{bc}	71.07^{b}	21^{ab}	14	15.13	108.60^{a}	3200
Sammaz 17 X Sammaz 14	5^{c}	59^{ab}	61^{abc}	155.93^{bc}	67.60^{bc}	18^{abc}	16	14.94	118.13^{a}	2667
Sammaz 18 X Oba 98	7^{ab}	58^{bc}	60^{bcd}	159.00^{ab}	65.20^{cd}	18^{abc}	14	15.73	120.13^{a}	3244
Sammaz 18 X Sammaz 14	5^{c}	58^{bc}	60^{bcd}	162.00^{a}	67.20^{bcd}	15^{abcd}	15	14.53	112.73^{a}	2089
Sammaz 20 X Oba 98	6^{bc}	56^{bcd}	58^{cde}	136.93^{e}	43.93^{f}	16^{abcd}	14	13.93	102.67^{a}	3200
Sammaz 20 X Sammaz 14	5^{c}	54^{d}	56^{e}	155.13^{bc}	67.87^{bc}	22^{a}	13	12.80	121.00^{a}	3867
Mean	5.74	57.79	60.05	147.29	61.87	15.41	13.85	14.60	108.76	2565.08
C.V%	12.93	2.97	2.72	1.61	3.98	28.39	7.54	9.08	22.00	42.52

Means followed by same letters in a column show that the difference is not significant using DMRT at 5% level of probability

DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield

The days to 50% seedling emergence was later in Sammaz 14 and was not significantly different from Sammaz 18 x Oba 98. The days to 50% flowering (DF) showed significant differences among the genotypes (Table 4.2). It ranged from 54 to 62 days after sowing for Sammaz 20 x Sammaz 14 and Sammaz 37, respectively. The DF was earliest in Sammaz 20 x Sammaz 14, which was not statistically different from Sammaz 20, Oba 98 and Sammaz 20 x Oba 98. The highest number of days to 50% flowering was Sammaz 37, which was not statistically different from Sammaz 37 x Oba 98 and Sammaz 17 x Sammaz 14. Similarly, days to 50% silking (DS) showed significant differences among the genotypes (Table 4.2). It ranged from 56 to 64 days for Sammaz 20 x Sammaz 14 and Sammaz 37, respectively. The earliest days to 50% silking was Sammaz 20 x Sammaz 14 which was not statistically different from Sammaz 20, Oba 98 and Sammaz 20 x Oba 98. Sammaz 37 was late to silk and was not significantly different from Sammaz 14, Sammaz 37 x Oba 98 and Sammaz 17 x Sammaz 14.

Statistically significant differences existed for plant height which ranged from 131.67 to 162.00cm for Sammaz 20 and Sammaz 18 x Sammaz 14, respectively. The shortest was Sammaz 20 which was not significantly different from Sammaz 14, while the tallest was Sammaz 18 x Sammaz 14 and this was not significantly different from Oba 98. Ear height was also statistically different among the genotypes (Table 4.2). The heights ranged from 43.93 to 76.53cm for Sammaz 20 x Oba 98 and Oba 98, respectively. The lowest ear height was observed for Sammaz 20 x Oba 98, which was not significantly different from Sammaz 14. The highest ear height was observed for Oba 98 which was statistically different from all others. Number of cobs per plot showed significant differences which ranged from 9 to 22 for Sammaz 37, Sammaz 17 and Sammaz 20 x Sammaz 14, respectively. Sammaz 37 and Sammaz 17 were not statistically different from Sammaz 18, Sammaz 20, Sammaz 37 x Oba 98, Sammaz 37 x

Sammaz 14, Sammaz 17 x Sammaz 14, Sammaz 18 x Sammaz 14 and Sammaz 20 x Oba98. Sammaz 20 x Sammaz 14which was not significantly different from Sammaz 18, Oba 98, Sammaz 37 x Sammaz 14, Sammaz 17 x Sammaz 14, Sammaz 18 x Sammaz 14 and Sammaz 20 x Oba 98. Number of kernel rows showed no statistical difference among the genotypes (Table 4.2). The rows ranged from 13 for Sammaz 37, Sammaz 17, Sammaz 14, Sammaz 37 x Sammaz 14 and Sammaz 20 x Sammaz 14 to 16 for Sammaz 17 x Sammaz 14. Ear length also showed no statistical difference among the genotypes. It ranged from 12.80cm for Sammaz 20 x Sammaz 14 to 15.73cm for Sammaz 18 x Oba 98. Ear weight showed significant difference among the genotypes and ranged from 46.53 to 129.00g for Sammaz 14 and Oba 98. Sammaz 14 which was significantly different from the rest, while Oba 98 which was statistically the same with all except Sammaz 14 (Table 4.2). Statistical significant differences did not exist for grain yield. However, the genotype with the most yield was Sammaz 20 x Sammaz 14 (3867kg/ha), while the least was Sammaz 14 (667kg/ha).

4.2 ANALYSIS OF VARIANCE FOR SAMARU DRY SEASON

The analysis of variance for the dry season in Samaru showed significant difference ($P<0.01$ and 0.05) for all traits except number of cobs per plot, number of kernel rows and grain yield (Table 4.3). The results of the mean performance of the parents and crosses are presented in Table 4.4. The days to 50% seedling emergence (DE) showed significant difference among the genotypes. It ranged from 11 to 15 days for Sammaz 37 x Oba 98 and Sammaz 14. Sammaz 37 x Oba 98 was statistically same with the rest except Sammaz 17,Sammaz 20, Oba 98, Sammaz 14 and Sammaz 17 x Oba 98 (Table 4.4). Sammaz 14 was statistically different from the rest.

Table 4.3: Mean squares for agronomic traits evaluated at Samaru in 2011/2012 dry season

Source	df	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Replication	2	5.81	0.45	0.17	14.51	9.86	57.45	0.58	0.45	490.27	1131901.84
Genotypes	13	2.21**	27.42**	26.40**	633.83**	206.03**	21.52	2.01	4.14**	1471.67*	1108303.42
Error	26	0.66	0.50	0.71	6.23	5.28	20.30	1.05	0.84	601.08	769453.81
Total	41										

*, ** Significant at 0.05 and 0.01 probability level, respectively

df = Degrees of freedom
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield

Table 4.4: Mean performance for agronomic traits evaluated at Samaru in 2011/2012 dry season

Parents/Crosses	DE	DF	DS	PH(cm)	EH(cm)	NC	KRW	EL(cm)	EW(g)	GY(kg/ha)
Parents										
Sammaz 37	12^{bc}	69^{a}	70^{a}	106.33^{f}	55.33^{cde}	3	13	13.80^{cde}	83.80^{ab}	320
Sammaz 17	13^{b}	64^{c}	66^{cd}	148.00^{a}	51.67^{e}	7	13	14.13^{bcd}	92.47^{a}	1067
Sammaz 18	12^{bc}	63^{cd}	65de	135.80^{c}	60.53^{b}	11	14	13.93^{cd}	127.67^{a}	2000
Sammaz 20	13^{b}	60^{e}	63^{fg}	113.73^{e}	46.60^{f}	7	14	13.67^{cde}	96.13^{a}	1067
Oba 98	13^{b}	61^{e}	63^{fg}	125.27^{d}	66.40^{a}	12	14	14.07^{cd}	126.20^{a}	1778
Sammaz 14	15^{a}	66^{b}	68^{b}	97.40^{g}	35.80^{g}	8	12	12.20^{e}	44.87^{b}	231
Crosses										
Sammaz 37X Oba 98	11^{c}	63^{cd}	65de	126.67^{d}	51.53^{e}	7	14	14.00^{bc}	90.00^{a}	1111
Sammaz 37 X Sammaz 14	12^{bc}	64^{c}	66^{cd}	125.00^{d}	58.27^{bc}	9	13	14.40^{bc}	109.50^{a}	1156
Sammaz 17 X Oba 98	13^{b}	61^{e}	63^{fg}	140.47^{b}	56.80^{bcd}	12	13	16.73^{a}	91.60^{a}	2133
Sammaz 17 X Sammaz 14	12^{bc}	65^{b}	68^{b}	141.60^{b}	54.67^{cde}	13	16	14.20^{bcd}	116.47^{a}	2044
Sammaz 18 X Oba 98	12^{bc}	60^{e}	63^{fg}	135.47^{c}	53.33^{de}	9	13	15.80^{ab}	93.13^{a}	1289
Sammaz 18 X Sammaz 14	12^{bc}	66^{b}	68^{b}	143.80^{b}	66.27^{a}	10	14	14.00^{cd}	124.33^{a}	1333
Sammaz 20 X Oba 98	12^{bc}	59^{f}	61^{hi}	131.53^{c}	43.40^{f}	7	13	12.93^{cde}	79.40^{ab}	533
Sammaz 20 X Sammaz 14	12^{bc}	58^{f}	60^{i}	126.53^{d}	51.07^{e}	12	13	12.47^{de}	99.53^{a}	1422
Mean	12.33	62.81	65.05	128.40	53.69	9.12	13.44	14.05	98.22	1248.89
C.V%	6.57	1.13	1.29	1.94	4.28	49.41	7.61	6.54	24.96	70.24

Means followed by same letters in a column show that the difference is not significant using DMRT at 5% level or probability

PH= Plant height EH = Ear height EL= Ear length NC= Number of cobs
KRW= Number of kernel rows DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking
EW= Ear weight GY= Grain yield.

The days to 50% flowering (DF) showed significant differences among the genotypes (Table 4.4). It ranged from 58 to 69 days after sowing for Sammaz 20 x Sammaz 14 and Sammaz 37, respectively. The Sammaz 20 x Sammaz 14 was not statistically different from Sammaz 20 x Oba 98. Sammaz 37 was significantly different from the rest (Table 4.4). Days to 50% silking (DS) showed significant differences among the genotypes (Table 4.4). It ranged from 60 to 70 days for Sammaz 20 x Sammaz 14 and Sammaz 37, respectively. Sammaz 20 x Sammaz 14 was not statistically different from Sammaz 20 x Oba 98. Sammaz 37 was significantly different from the rest.

Statistically significant difference existed for plant height. It ranged from 97.40 to 148.00cm for Sammaz 14 and Sammaz 17, respectively. Sammaz 14 which was significantly different from the rest, while the tallest, Sammaz 17 was significantly different from the rest. Ear height was statistically different among the genotypes (Table 4.4). The ear heights ranged from 35.80 to 66.40cm for Sammaz 14 and Oba 98, respectively. The lowest ear was Sammaz 14, which was significantly different from the rest. The highest ear placement was observed for Oba 98 and was not statistically different from Sammaz 18 x Sammaz 14. Number of cobs per plot showed no statistical difference among the genotypes. It ranged from 3 for Sammaz 37 to 12 for Oba 98, Sammaz 17 x Oba 98 and Sammaz 20 x Sammaz 14. Number of kernel rows also showed no statistical difference among the genotypes (Table 4.2). The rows ranged from 12 for Sammaz 14 to 16 for Sammaz 17 x Sammaz 14. Ear length showed significant difference among the genotypes and ranged from 12.20 to 15.80cm for Sammaz 14 and Sammaz 18 x Oba 98. The shortest ear was observed for Sammaz 14 and was not significantly different from Sammaz 37, Sammaz 20, Sammaz 20 x Oba 98 and Sammaz 20 x Sammaz 14. Sammaz 18 x Oba 98 was not statistically different from Sammaz 17, Sammaz 37 x Oba 98,

Sammaz 37 x Sammaz 14 and Sammaz 17 x Sammaz 14. Ear weight showed significant difference among the genotypes, which ranged from 46.53 to 129.00g for Sammaz 14 and Oba 98. Sammaz 14 was statistically same but same with Sammaz 37and Sammaz 20 x Oba 98. Oba 98 was statistically same with all except Sammaz 14 (Table 4.4). Grain yield showed no significant differences among the genotypes. It ranged from 231kg/ha for Sammaz 14 as the genotype with the least yield to 2133kg/ha for Sammaz 17 x Oba 98 as the genotype with the highest yield.

4.3 ANALYSIS OF VARIANCE FOR SAMARU ACROSS SEASONS

The analysis of variance for across seasons in Samaru showed highly significant differences for genotypes for days to 50% seedling emergence, days to 50% flowering, days to 50% silking, plant height and ear height, number of kernel rows, ear length, ear weight and grain yield. Number of cobs per plot showed no significant difference. Seasons showed significant difference for all traits except number of kernel rows. The genotype by season interaction showed highly significant differences for days to 50% flowering, days to 50% silking, plant height and ear height (Table 4.5). The results of the mean performance of the parents and crosses across seasons are presented in Table 4.6. The days to 50% seedling emergence (DE) ranged from 8 to 11 days for Sammaz 37 x Oba 98, Sammaz 17 x Sammaz 14 and Sammaz 14. The genotype with the shortest days to DE were Sammaz 37 x Oba 98 and Sammaz 17 x Sammaz 14 were statistically same with the rest of the genotypes except Sammaz 17, Sammaz 14 and Sammaz 18 x Oba 98 (Table 4.6). The days to 50% flowering (DF) ranged from 56 to 65 days after sowing for Sammaz 20 x Sammaz 14 and Sammaz 37, respectively.

Table 4.5: Mean squares for agronomic traits evaluated at Samaru across seasons

Source	df	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Replication(Season)	4	93.96	0.58	0.73	11.47	15.69	74.08	0.80	2.14	119.36	2352616.06
Season	1	913.44**	530.01*	525.00**	7493.85*	1403.85**	829.71**	3.52	6.41*	2333.13*	36379399.47**
Genotypes	13	3.11**	35.31**	33.16**	722.47**	393.91**	68.79	3.58**	5.18**	2350.66**	2386827.45**
Season x Genotypes	13	0.75	4.50**	4.62**	264.60**	76.28**	11.46	0.23	0.93	338.66	790472.43
Error	52	0.66	1.72	1.65	6.02	5.59	19.24	1.03	1.27	583.96	996433.60
Total	83										

*, ** Significant at 0.05 and 0.01 probability levels, respectively

df = Degrees of freedom
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield

Table 4.6: Mean performance for agronomic traits evaluated at Samaru across seasons

Parents/Crosses	DE	DF	DS	PH(cm)	EH(cm)	NC	KRW	EL(cm)	EW(g)	GY(kg/ha)
Parent										
Sammaz 37	9^{bc}	65^{a}	67^{a}	129.33^{f}	60.30^{de}	6	13^{bcd}	14.30^{bcd}	99.47^{ab}	1138^{bc}
Sammaz 17	10^{b}	62^{b}	64^{bc}	147.80^{b}	58.80^{def}	8	13^{bcd}	14.47^{abcd}	100.17^{ab}	1467^{abc}
Sammaz 18	9^{bc}	61^{bc}	63^{c}	136.53^{d}	56.70^{f}	14	14^{bc}	14.43^{bcd}	117.47^{ab}	2222^{ab}
Sammaz 20	9^{bc}	58^{de}	60^{de}	122.70^{g}	51.73^{g}	10	14^{bc}	13.63^{cde}	96.60^{ab}	1578^{abc}
Oba 98	9^{bc}	59^{de}	61^{de}	141.87^{c}	71.47^{a}	16	14^{bc}	14.23^{cd}	127.60^{a}	2578^{a}
Sammaz 14	11^{a}	62^{b}	65^{b}	115.03^{h}	40.83^{i}	9	13^{bcd}	13.07^{de}	45.70^{c}	449^{c}
Crosses										
Sammaz 37 X Oba 98	8^{c}	61^{b}	63^{bc}	131.70^{f}	57.23^{ef}	9	14^{bc}	14.90^{abc}	98.97^{ab}	1644^{abc}
Sammaz 37 X Sammaz 14	9^{bc}	62^{b}	64^{bc}	132.87^{e}	57.63^{ef}	12	13^{bcd}	14.97^{abc}	119.05^{ab}	2111^{ab}
Sammaz 17 X Oba 98	9^{bc}	59^{cd}	62^{d}	148.13^{b}	63.93^{c}	16	13^{bcd}	15.93^{a}	100.10^{ab}	2667^{a}
Sammaz 17 X Sammaz 14	8^{c}	62^{b}	65^{bc}	148.77^{b}	61.13^{d}	15	16^{a}	14.57^{abcd}	117.30^{ab}	2356^{ab}
Sammaz 18 X Oba 98	10^{b}	59^{d}	61^{de}	147.23^{b}	59.27^{def}	14	13^{bcd}	15.77^{ab}	106.63^{ab}	2267^{ab}
Sammaz 18 X Sammaz 14	9^{bc}	62^{b}	64^{bc}	152.90^{a}	66.73^{b}	13	14^{bc}	14.27^{bcd}	118.53^{ab}	1711^{abc}
Sammaz 20 X Oba 98	9^{bc}	60^{e}	60^{e}	134.23^{de}	43.67^{h}	12	14^{bc}	13.43^{cde}	91.03^{b}	1867^{ab}
Sammaz 20 X Sammaz 14	9^{bc}	56^{f}	58^{f}	140.83^{c}	59.27^{def}	17	13^{bcd}	12.63^{e}	110.27^{ab}	2644^{a}
Mean	9.04	60.30	62.55	137.85	57.78	12.26	13.64	14.33	103.49	1906.99
C.V%	8.96	2.17	2.05	1.78	4.09	35.78	7.44	7.87	23.35	52.35

Means followed by same letters in a column show that the difference is not significant using DMRT at 5% level or probability

PH= Plant height EH = Ear height EL= Ear length
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking GY=Grain yield

Sammaz 20 x Sammaz 14 was statistically different from the rest. Sammaz 37 was significantly different from the rest (Table 4.6). Days to 50% silking (DS) ranged from 58 to 67 days for Sammaz 20 x Sammaz 14 and Sammaz 37, respectively. Statistically significant differences existed for plant height which ranged from 115.03 to 152.90cm for Sammaz 14 and Sammaz 18 x Sammaz 14, respectively. Sammaz 14 was significantly different from the rest, while Sammaz 18 x Sammaz 14 was also significantly different from the rest. Ear height was statistically different among the genotypes compared (Table 4.6). Ear heights ranged from 40.83 to 71.47cm for Sammaz 14 and Oba 98 respectively. Sammaz 14 was significantly different from the rest. Oba 98 was also different from the rest. Number of cobs per plot showed no statistical difference among the genotypes. It ranged from 6 cobs for Sammaz 37 to 17 cobs for Sammaz 20 x Sammaz 14. Number of kernel rows was significant for genotypes and the means ranged from 13 to 16 for Sammaz 37, Sammaz 17, Sammaz 14, Sammaz 37 x Sammaz 14, Sammaz 17 x Oba 98, Sammaz 18 x Oba 98, Sammaz 20 x Sammaz 14 and Sammaz 17 x Sammaz 14. The genotype that had cobs with few number of rows was Sammaz 37, Sammaz 17, Sammaz 14, Sammaz 37 x Sammaz 14, Sammaz 17 x Oba 98, Sammaz 18 x Oba 98, Sammaz 20 x Sammaz 14 and was statistically same with the rest except Sammaz 17 x Sammaz 14. Ear length showed significant difference among the genotypes and ranged from 12.63 to 15.93cm for Sammaz 20 x Sammaz 14 and Sammaz 17 x Oba 98. Sammaz 20 x Sammaz 14 was not significantly different from Sammaz 20, Sammaz 14 and Sammaz 20 x Oba 98. Sammaz 18 x Oba 98 was not statistically different from Sammaz 17, Sammaz 37 x Oba 98, Sammaz 37 x Sammaz 14, Sammaz 17 x Sammaz 14 and Sammaz 18 x Oba 98 (Table 4.6). Ear weight showed significant difference for genotypes and ranged from 45.70 to 127.60g for Sammaz 14 and Oba 98, respectively. The heaviest ear was obtained in the genotype Oba

98 which was statistically similar to all except Sammaz 14 and Sammaz 20 x Oba 98 (Table 4.6). Grain yield ranged from 449 to 2667kg/ha for Sammaz 14 and Sammaz 17 x Oba 98, respectively. The least yield was recorded for Sammaz 14, which was not statistically different from Sammaz 37, Sammaz 17, Sammaz 20, Sammaz 37 x Oba 98 and Sammaz 18 x Sammaz 14. Sammaz 17 x Oba 98 was not significantly different from the rest in grain yield except Sammaz 37 and Sammaz 14.

4.4 ANALYSIS OF VARIANCE FOR ENDOSPERM PROTEINS

Analysis of variance for endosperm proteins revealed highly significant difference for the genotypes (Table 4.7). The results of the mean performance of the parents and crosses are presented in Table 4.8. The mean for albumin/globulin ranged from 27.76 to 46.46mg/g for Sammaz 14 and Sammaz 37 x Sammaz 14, respectively. The genotype with the least amount of albumin/globulin was Sammaz 14, which was statistically similar to Sammaz 17, Sammaz 20 and Sammaz 20 x Sammaz 14. Sammaz 37 x Sammaz 14 was statistically same with the rest except Sammaz 17, Sammaz 18, Sammaz 20, Oba 98, Sammaz 14, Sammaz 17 x Oba 98 and Sammaz 20 x Sammaz 14 (Table 4.8). Zein protein ranged from 12.39 to 39.95mg/g for Oba 98 and Sammaz 17. The genotype with the least zein was Oba 98, which was statistically same with Sammaz 14 and different from the rest. Lastly, glutelin ranged from 6.78 to 43.04mg/g for Sammaz 18 x Sammaz 14 and Sammaz 37 x Oba 98. Sammaz 18 x Sammaz 14 followed by Sammaz 17 x Oba 98, Sammaz 20, Sammaz 18, Sammaz 17 and Sammaz 37 were not significantly different from one another.

Table 4.7 Mean squares for endosperm proteins at Samaru in 2011

Source	df	Albumin/globulin	Zein	Glutelin
Genotype	13	84.10**	142.47**	314.22**
Error	14	9.89	4.45	3.03
Total	27			

*, ** Significant at 0.05 and 0.01 probability levels, respectively
df = Degrees of freedom

Table 4.8: Mean performance of endosperm proteins at Samaru in 2011

Parents/Crosses	Albumin/globulin (mg/g)	Zein (mg/g)	Glutelin (mg/g)
Parents			
Sammaz 37	41.08^{abc}	28.51^{cde}	9.32^{f}
Sammaz 17	30.21^{de}	39.95^{a}	9.06^{f}
Sammaz 18	38.30^{bc}	32.35^{bc}	8.27^{f}
Sammaz 20	30.21^{de}	38.35^{a}	7.91^{f}
Oba 98	34.07^{cd}	12.39^{i}	23.67^{d}
Sammaz 14	27.76^{e}	13.96^{hi}	37.15^{b}
Crosses			
Sammaz 37 x Oba 98	43.24^{ab}	21.63^{gf}	43.04^{a}
Sammaz 37 x Sammaz 14	46.46^{a}	22.46^{gf}	33.17^{c}
Sammaz 17 x Oba 98	36.78^{bcd}	25.55^{def}	7.74^{f}
Sammaz 17 x Sammaz 14	46.15^{a}	17.923^{gh}	14.94^{e}
Sammaz 18 x Oba 98	41.49^{ab}	35.34^{ab}	30.85^{c}
Sammaz 18 x Sammaz 14	42.47^{ab}	23.67^{ef}	6.780^{f}
Sammaz 20 x Oba 98	42.73^{ab}	24.31^{def}	25.99^{d}
Sammaz 20 x Sammaz 14	29.39^{de}	29.15^{cd}	22.99^{d}
Mean	37.88	26.11	20.06
C.V%	8.30	8.08	8.67

Means followed by same letters in a column show that the difference is not significant using DMRT at 5% level or probability

4.5 ANALYSIS OF VARIANCE FOR DESIGN II

The analysis of variance for design II is presented in Tables 4.9, 4.10 and 4.11 for the wet and dry seasons and across seasons in Samaru, respectively. The result for ten traits measured during the wet season at Samaru (Table 4.9) indicated that the female source of variation showed significant differences only for plant height, ear height and ear length. The male source of variation showed significant differences for plant height and ear height. The female x male interaction showed significant differences for days to 50% silking and ear height. Grain yield showed no significant difference for all the sources of variation.

The dry season analysis is shown in Table 4.10. The female source of variation showed highly significant differences for Days to 50% flowering, days to 50% silking, plant height, ear height and ear length. The male source of variation showed significant differences for Days to 50% flowering, days to 50% silking, ear height and ear length. The female x male interaction were highly significant for days to 50% flowering, days to 50% silking, plant height, ear height and ear length. Grain yield showed no significant difference for all the sources of variation.

The analysis of variance across seasons is presented in Table 4.11. Highly significant differences for days to 50% flowering, days to 50% silking, plant height and ear height were observed for female source of variance. The male source of variance was highly significant for days to 50% silking, plant height, ear height ear length and significant for days to 50% flowering and ear weight. Female x male interaction indicated highly significant difference for days to 50% silking, plant height and ear height. Female x season interaction was highly significant for days to 50% silking, plant height, ear height and significant for days to 50% flowering.

Table 4.9 Mean squares for design II for agronomic traits at Samaru in 2011 wet season

Source of variation	df	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Replication	2	0.29	2.38	0.54	4.37	2.66	0.22	457.24	5.24	0.04	343854.17
Female	3	0.72	14.04	0.44	574.04**	219.74**	2.15	50.84	5.31*	48.49	148437.50
Male	1	1.50	0.38	0.67	240.67**	102.51**	1.71	634.48	2.16	7.04	937.50
Female x Male	3	0.72	3.82	0.67*	97.91	277.84**	2.72	242.94	0.67	40.38	200381.94
Error	14	0.39	5.71	0.16	5.12	6.06	1.20	465.99	1.45	19.95	223020.83
Total	23										

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

df = Degrees of freedom
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield

Table 4.10 Mean squares for design II for agronomic traits at Samaru in 2011/2012 dry season

Source of variation	df	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Replication	2	2.54	1.04	0.54	15.80	4.21	52.17	0.70	1.41	639.17	534072.82
Female	3	0.15	32.04**	31.93**	345.02**	165.10**	19.39	1.49	8.55**	405.14	1559757.28
Male	1	0.04	40.04**	45.38**	2.94	238.14**	28.17	1.40	8.64**	3434.43	296294.82
Female x Male	3	1.26	13.15**	13.71**	48.27**	58.59**	3.39	2.86	2.06**	43.88	302220.89
Error	14	0.68	0.38	0.54	6.26	5.53	33.50	1.11	0.51	823.54	1238410.76
Total	23										

*, ** Significant at 0.05 and 0.01 probability levels, respectively

df = Degrees of freedom
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield

Table 4.11 Mean squares for design II for agronomic traits at Samaru across seasons

Source	df	DE	DF	DS	PH	EH
Season	1	487.69**	5764.08**	46066.02**	3227.52**	853.45**
Rep (Season)	4	1.42*	1.71	0.54	10.09	3.54
Female	3	0.30	36.22**	16.30**	884.04**	342.62**
Male	1	1.02	16.33*	28.52**	148.40**	326.56**
Female x Male	3	1.58	2.00	9.13**	27.97**	204.54**
Female x Season	3	0.58	9.86*	16.08**	35.02**	42.22**
Male x Season	1	0.52	24.08**	17.52**	95.20**	14.08
Female x Male x Season	3	0.41	14.97**	5.24**	118.21**	131.90**
Pooled error	28	0.54	3.04	0.35	5.69	5.79
Total	47					

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

df = Degrees of freedom
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield

Table 4.11 continued

Source	df	NC	KRW	EL	EW	GY
Season	1	193.60**	123464.65**	1.76	83575.18**	912098.31
Rep (Season)	4	26.19	228.97	3.32*	319.61	438963.49
Female	3	15.97	23.73	12.62**	199.430	694468.49
Male	1	21.87	347.76	9.72**	1867.25*	131949.53
Female x Male	3	0.61	112.40	1.52	6.210	374635.18
Female x Season	3	5.50	28.60	1.24	254.19	913726.16
Male x Season	1	8.00	288.12	1.08	1565.23	165282.78
Female x Male x Season	3	5.50	133.40	1.21	78.05	127967.65
Pooled error	28	17.35	233.55	0.98	421.74	730715.80
Total	47					

*, ** Significant at 0.05 and 0.01 probability levels, respectively.

df = Degrees of freedom
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield

Male x season interaction showed no significant difference for seven traits except for days to 50% flowering, days to 50% silking and plant height which was highly significant. Female x male x season interaction showed highly significant differences for days to 50% flowering, days to 50% silking, plant height and ear height. Grain yield showed no significant difference for all the sources of variation.

The analysis of variance for the protein fractions is presented in Table 4.12. The female source of variation revealed highly significant differences for albumin/globulin and zein while glutelin was not significant. The male source was highly significant for albumin/globulin and zein, while the female x male interaction was highly significant for zein and glutelin.

Table 4.12: Mean squares for design II for endosperm proteins at Samaru in 2011

Source of variation	df	Albumin/globulin	Zein	Glutelin
Rep	1	2.15**	9.40	2.15**
Female	3	53.89**	56.86**	511.63
Male	1	0.01**	46.40**	220.96
Female x Male	3	92.39	57.32**	172.13**
Error	16	8.52	3.31	2.52

*, ** Significant at 0.05 and 0.01 probability levels, respectively

4.6 COMBINING ABILITY EFFECTS FOR SAMARU WET SEASON

The estimates of general combining ability (GCA) effects of parents for the traits measured during the wet season in Samaru are presented in Table 4.13. From the result, Sammaz 20 was the best general combiner as it has high negative GCA for days to 50% seedling emergence (-0.42), high negative value for days to 50% flowering (-1.04) and days to 50% silking (-1.04), positive GCA for plant height (5.25), ear height (4.88), number of cobs per plot (2.96), number of kernel rows (0.33), ear weight (4.59) and grain yield (122.92). This is followed by Sammaz 18 being the best general combiner with negative GCA for days to 50% flowering (-0.56), and days to 50% silking (-0.04), which are good for earliness, plant height (-3.92) and ear height (5.36), number of cobs per plot (1.29) and grain yield (97.92). Sammaz 17 had a negative GCA for days to 50% seedling emergence, positive GCA for ear weight (5.69) and negative grain yield (-135.42). Sammaz 37 was the worst general combiner for plant height (0.42) and had negative GCA effects for number of cobs per plant (-2.38), number of kernel rows (-0.27), ear weight per plot (-0.94) and grain yield (-85.42). Sammaz 14 was the best general combiner for ear length (0.48) and number of kernel rows (0.81).

The estimates of specific combining ability (SCA) effects for the wet season trial in Samaru are presented in Table 4.14. Four hybrids had negative SCA effects for days to 50% seedling emergence, with Sammaz 18 x Sammaz 14 and Sammaz 37 x Oba 98 (-0.42) being the least, while others exhibited positive SCA effect for the trait. Four hybrids had negative SCA effects for days to 50% flowering, with Sammaz 20 x Sammaz 14 (-1.63) being the least, while four others exhibited positive SCA effects. For days to 50% silking, four hybrids also had negative SCA effect with Sammaz 20 x Sammaz 14 (-1.46) being the least, while four others

Table 4.13: Estimates of GCA effects for agronomic traits at Samaru in 2011wet season

Parents	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Females										
Sammaz 37	0.42	1.13	1.13	-2.42	1.22	-2.38	-0.27	1.22	-0.94	-85.42
Sammaz 17	-0.08	0.46	0.46	1.08	-0.75	-1.88	0.20	-0.75	5.69	-135.42
Sammaz 18	0.08	-0.56	-0.56	-3.92	-5.35	1.29	-0.27	-5.35	-9.34	97.92
Sammaz 20	-0.42	-1.04	-1.04	5.25	4.88	2.96	0.33	4.88	4.59	122.92
Males										
Oba 98	-0.25	1.21	1.21	-2.98	1.8	-0.79	0.13	1.8	0.84	-60.42
Sammaz 14	0.25	-1.21	-1.21	2.98	-1.8	0.79	-0.13	-1.8	-0.84	60.42

PH= Plant height EH = Ear height EL= Ear length
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking GY=Grain yield

Table 4.14: Estimates of SCA effects for agronomic traits at Samaru in 2011wet season

Crosses	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Sammaz 37 X Oba 98	-0.42	-0.54	-0.38	-8.15	-2.93	-2.88	-0.07	-2.93	-6.94	-139.58
Sammaz 37 X Sammaz 14	0.42	-0.88	-0.71	-7.65	-6.90	0.96	-0.93	-6.90	7.09	243.75
Sammaz 17 X Oba 98	-0.08	-0.21	-0.38	12.42	11.77	3.46	-0.20	11.77	2.13	60.42
Sammaz 17 X Sammaz 14	0.08	1.63	1.46	3.38	-1.93	-1.54	1.20	-1.93	-2.28	-164.58
Sammaz 18 X Oba 98	0.42	0.54	0.38	8.15	2.93	2.88	0.07	2.93	6.94	139.58
Sammaz 18 X Sammaz 14	-0.42	0.88	0.71	7.65	6.90	-0.96	0.93	6.90	-7.09	-243.75
Sammaz 20 X Oba 98	0.08	0.21	0.38	-12.42	-11.77	-3.46	0.20	-11.77	-2.13	-60.42
Sammaz 20 X Sammaz 14	-0.08	-1.63	-1.46	-3.38	1.93	1.54	-1.20	1.93	2.28	164.58

PH= Plant height EH = Ear height EL= Ear length
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking GY=Grain yield

exhibited positive SCA effects for the trait. For plant height, four hybrids exhibited positive SCA effects with Sammaz 17 x Oba 98 being the highest (912.41), while four others exhibited negative SCA effects. Four hybrids had positive SCA effect for ear height, with Sammaz 17 x Oba 98 being the highest (11.77), while the four others exhibited negative SCA effects.

For number of cobs per plot, four hybrids also had positive SCA effects, with Sammaz 17 x Oba 98 (3.46) being the highest, while the four others exhibited negative SCA effects for the trait. Four hybrids had positive SCA effects for number of kernel rows, with Sammaz 17 x Sammaz 14 (1.20) being the highest, while the other four exhibited negative SCA effect for the trait. Four hybrids had positive SCA effects for ear length, with Sammaz 17 x Oba 98 (11.77) being the highest, while the other four exhibited negative SCA effects for the trait. Four hybrids had positive SCA effects for ear weight per plot, with Sammaz 37 x Sammaz 14 (7.09) being the highest, while the other four had negative SCA effects for the trait. For grain yield, four hybrids had positive SCA effects, with Sammaz 37 x Sammaz 14 (243.75) being the highest, while four others exhibited negative SCA effects for the trait.

4.7 COMBINING ABILITY EFFECTS FOR SAMARU DRY SEASON

The result from the dry season trial (Table 4.15) showed that Sammaz 20 was the most influential parent with the highest negative GCA effects for number of days to 50% seedling emergence (-0.13), highest GCA effects for number of cobs per plot (2.42), number of kernel rows (0.73) and grain yield (355.56). With respect to days to 50%

flowering and days to 50% silking, the best parent with the highest negative GCA effects (-2.13), is Sammaz 18. Sammaz 18 also had the highest GCA effects for plant height (2.13) while Sammaz 37 had the highest negative GCA effects for plant height (-2.82) which induces dwarfism in plants. Sammaz 17 had the highest GCA effects (7.85) with respect to ear height. Sammaz 37 had the highest positive GCA effects for ear length (0.73) while Sammaz 17 (16.42) was the highest for ear weight per plot.

The estimates of specific combining ability (SCA) effects for dry season trial are presented in Table 4.16. Four hybrids had negative SCA effects for days to emergence of which Sammaz 37 x Oba 98 (-0.54) was the highest. The remaining four hybrids had positive SCA effects for the trait. Four crosses had negative SCA effects for days to 50% flowering of which Sammaz 20 x Sammaz 14 (-2.46) was the highest. With respect to days to 50% silking, four hybrids had negative SCA effects, with Sammaz 20 x Sammaz 14 (-2.46) being the highest. The remaining four had positive SCA effects. Sammaz 18 x Sammaz 14 had the highest SCA effects for plant height (8.95), while Sammaz 37 x Sammaz 14 had the highest negative SCA effects for the trait. Sammaz 17 x Oba 98 had the highest SCA effects for ear height (5.80), while Sammaz 37 x Sammaz 14 had the highest negative SCA effects for the trait. With respect to number of cobs per plot, four hybrids had positive SCA effects with Sammaz 17 x Oba 98 (1.92) being the highest. Four hybrids had positive SCA effects for number of kernel rows with Sammaz 17 x Sammaz 14 (0.99) being the highest, Sammaz 20 x Sammaz 14 having the highest negative SCA effect for the trait.

Table 4.15: Estimates of GCA effects for agronomic traits at Samaru in 2011/2012 dry season

Parents	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Females										
Sammaz 37	-0.13	-0.46	-0.46	-2.82	-1.98	-1.75	-0.14	0.73	-8.92	-177.78
Sammaz 17	0.04	2.88	2.88	0.52	7.85	-0.25	-0.24	-0.17	16.42	-133.38
Sammaz 18	0.21	-2.13	-2.13	2.13	-4.32	-0.42	-0.34	0.47	-15.00	-44.44
Sammaz 20	-0.13	-0.29	-0.29	0.18	-1.55	2.42	0.73	-1.03	7.50	355.56
Males										
Oba 98	0.04	1.21	1.21	-0.45	0.90	0.25	0.21	0.57	1.40	233.33
Sammaz 14	-0.04	-1.21	-1.21	0.45	-0.90	-0.25	-0.21	-0.57	-1.40	-233.33

PH= Plant height EH = Ear height EL= Ear length
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking GY=Grain yield

Table 4.16: Estimates of SCA effects for agronomic traits at Samaru in 201/2012 dry season

Crosses	DE	DF	DS	PH	EH	NCB	KRW	EL	EW	GY
Sammaz 37 X Oba 98	-0.54	-0.04	-0.04	-3.95	-1.80	-1.42	-0.01	-1.27	-2.96	-322.22
Sammaz 37 X Sammaz 14	0.29	-2.04	-2.04	-8.95	-4.90	-0.92	-0.64	-0.37	-8.81	-322.22
Sammaz 17 X Oba 98	0.46	-0.38	-0.38	4.92	5.80	1.92	-0.34	1.33	4.70	566.67
Sammaz 17 X Sammaz 14	-0.21	2.46	2.46	7.98	0.90	0.42	0.99	0.30	7.07	77.78
Sammaz 18 X Oba 98	0.54	0.04	0.04	3.95	1.80	1.42	0.01	1.27	2.96	322.22
Sammaz 18 X Sammaz 14	-0.29	2.04	2.04	8.95	4.90	0.92	0.64	0.37	8.81	322.22
Sammaz 20 X Oba 98	-0.46	0.38	0.38	-4.92	-5.80	-0.92	0.34	-1.33	-4.70	-566.67
Sammaz 20 X Sammaz 14	0.21	-2.46	-2.46	-7.98	-0.90	-0.42	-0.99	-0.30	-7.07	-77.78

PH= Plant height EH = Ear height EL= Ear length
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking GY=Grain yield

Four hybrids had positive SCA for ear length with Sammaz 18 x Oba 98 being the highest (1.27) and Sammaz 20 x Oba 98 being the lowest (-1.33). Sammaz 18 x Sammaz 14 had the highest positive SCA effects for ear weight per plot (8.81) while Sammaz 37 x Sammaz 14 had the highest negative SCA effects (-8.81) for the trait. With respect to grain yield, Sammaz 17 x Oba 98 had the highest SCA effects (566.67), while Sammaz 20 x Oba 98 had the highest negative SCA effects (-566.67) for the trait.

4.8 COMBINING ABILITY EFFECTS FOR SAMARU ACROSS SEASONS

The estimates of general combining ability (GCA) effects for across seasons are presented in Table 4.17. Sammaz 14 was the most influential parent for earliness of seedling emergence with highest negative GCA effects (-0.05). The most influential parent for earliness to flowering and silking across the seasons was Sammaz 20 (-0.83) and (-0.58). With respect to plant height (2.66) and ear height (1.46), Sammaz 18 had the highest positive GCA effects for tallness and Sammaz 37 (-3.27) and Sammaz 20 (-2.35) with respect to dwarfism. For number of cobs per plot and ear length, Sammaz 17 had the highest GCA effects. Sammaz 14 had the highest GCA effect across seasons for number of kernel rows (0.90). The estimates of specific combining ability (SCA) effects for across seasons are presented in Table 4.18. Four hybrids had negative SCA effects for days to 50% seedling emergence of which Sammaz 37 x Oba 98 (-0.16) had the highest. Four hybrids had positive SCA effects for the same trait of which Sammaz 37 x Sammaz 14 (0.16) was the highest. Four hybrids also had negative SCA effects for days to 50% flowering of which Sammaz 18 x Oba 98 (-0.17) was the highest, the remaining four had positive SCA effects for the trait of which Sammaz 18 x Sammaz 14 had the highest value (0.17).

Table 4.17: Estimates of GCA effects for agronomic traits at Samaru across seasons

Parents	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Females										
Sammaz 37	-0.04	0.05	0.20	-3.27	-0.40	-0.39	0.50	0.13	-0.77	-60.54
Sammaz 17	-0.04	0.33	0.12	2.12	1.30	0.51	-0.15	0.23	0.97	118.17
Sammaz 18	0.08	0.44	0.26	2.66	1.46	0.04	0.23	0.15	1.31	-28.13
Sammaz 20	-0.01	-0.83	-0.58	-1.52	-2.35	-0.17	-0.58	-0.51	-1.51	-29.51
Males										
Oba 98	0.05	-0.19	-0.26	-0.59	-0.87	-0.23	-0.90	0.15	-2.09	-17.48
Sammaz 14	-0.05	0.19	0.26	0.59	0.87	0.23	0.90	-0.15	2.09	17.48

Table 4.18: Estimates of SCA effects for agronomic traits at Samaru across seasons

Crosses	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Sammaz 37 X Oba 98	-0.16	0.11	0.12	0.39	0.80	0.09	-0.76	-0.16	0.10	-14.01
Sammaz 37 X Sammaz 14	0.16	-0.11	-0.12	-0.39	-0.80	-0.09	0.76	0.16	-0.10	14.01
Sammaz 17 X Oba 98	0.06	-0.06	-0.13	0.48	1.34	-0.05	-0.10	0.08	0.29	41.55
Sammaz 17 X Sammaz 14	-0.06	0.06	0.13	-0.48	-1.34	0.05	0.10	-0.08	-0.29	-41.55
Sammaz 18 X Oba 98	0.12	-0.17	-0.33	-0.36	-0.37	0.03	1.47	0.10	-0.24	49.89
Sammaz 18 X Sammaz 14	-0.12	0.17	0.33	0.36	0.37	-0.03	-1.47	-0.10	0.24	-49.89
Sammaz 20 X Oba 98	-0.02	0.11	0.34	-0.51	-1.76	-0.07	-0.61	-0.02	-0.15	-77.43
Sammaz 20 X Sammaz 14	0.02	-0.11	-0.34	0.51	1.76	0.07	0.61	0.02	0.15	77.43

PH= Plant height EH = Ear height EL= Ear length
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking GY=Grain yield

For days to 50% silking, four hybrids had negative SCA effects, Sammaz 20 x Sammaz 14 was the best specific combination with highest negative SCA effects (-0.34), reducing the number of days to silking. Four hybrids had positive SCA effects for plant height, with Sammaz 20 x Sammaz 14 (0.51) being the highest. Four hybrids also had negative SCA effects for the trait with Sammaz 20 x Oba 98 (-0.51) being the highest. For ear height, four hybrids had positive SCA effects with Sammaz 20 x Sammaz 14 (1.76) being the highest, while the remaining four hybrids had negative SCA effects for the trait with Sammaz 20 x Oba 98 (-1.76) as the highest.

Four hybrids had positive SCA effects for number of cobs per plot, Sammaz 37 x Oba 98 (0.09) was the highest and four others had negative SCA effects, Sammaz 37 x Sammaz 14 (-0.09) being the highest. Four hybrids had positive SCA effects for number of kernel rows with Sammaz 18 x Oba 98 (1.47) being the highest, the remaining four hybrids have negative SCA effects for the trait with Sammaz 18 x Sammaz 14 (-1.47) as the highest. Sammaz 37 x Sammaz 14 had the highest positive SCA effects (0.16) for ear length and Sammaz 37 x Oba 98 (-0.16) has the highest negative SCA effects for the trait. With respect to ear weight per plot, four crosses had positive SCA effects and four had negative SCA effects for the trait, with Sammaz 17 x Oba 98 (0.29) as the highest. Sammaz 20 x Sammaz 14 (77.43) had the highest positive SCA effect for grain yield while Sammaz 20 x Oba 98 (-77.43) showed the highest negative SCA effects for grain yield.

4.9 COMBINING ABILITY EFFECTS FOR ENDOSPERM PROTEINS AT SAMARU

The GCA effects for endosperm proteins are presented in Table 4.19. Sammaz 37 was the best parent for albumin/globulin and the worst was Sammaz 20 with -5.03, indicating lower

quality of protein. Sammaz 18 was the best parent for zein with GCA effects of 4.50 and Sammaz 17 was worst with -3.27. Sammaz 37 was the best parent for glutelin with GCA effects (14.92) while Sammaz 20 was the worst parent in terms of protein quality.

The SCA effects for endosperm proteins are presented in Table 4.20. Four hybrids had positive SCA effects for albumin/globulin, with Sammaz 17 x Sammaz 14 being the best cross with the highest SCA value (6.62). For zein, four hybrids had positive and four hybrids had negative SCA effects, Sammaz 17 x Oba 98 was the highest with (4.13) and Sammaz 20 x Oba 98 had the highest negative value (-4.13). For glutelin, Sammaz 17 x Oba 98 was the best with highest positive SCA value of 8.32, while Sammaz 20 x Oba 98 had the highest negative SCA value -8.32.

Table 4.19: Estimates of GCA effects for endosperm proteins at Samaru in 2011

Parents	Albumin/globulin	Zein	Glutelin
Females			
Sammaz 37	3.76	-2.96	14.92
Sammaz 17	0.38	-3.27	-11.85
Sammaz 18	0.89	4.50	-4.37
Sammaz 20	-5.03	1.73	1.31
Males			
Oba 98	-0.03	1.70	3.72
Sammaz 14	0.03	-1.70	-3.72

Table 4.20: Estimates of SCA effects for endosperm proteins at Samaru in 2011

CROSSES	Albumin/globulin	Zein	Glutelin
Sammaz 37 X Oba 98	-1.58	-2.12	1.22
Sammaz 37 X Sammaz 14	-4.66	2.11	-7.32
Sammaz 17 X Oba 98	-0.46	4.13	8.32
Sammaz 17 X Sammaz 14	6.70	-4.12	-2.22
Sammaz 18 X Oba 98	1.58	2.12	-1.22
Sammaz 18 X Sammaz 14	4.66	-2.11	7.32
Sammaz 20 X Oba 98	0.46	-4.13	-8.32
Sammaz 20 X Sammaz 14	-6.70	4.12	2.22

4.10 NARROW SENSE HERITABILITY ESTIMATES

Narrow sense heritability estimates for the ten characters studied during wet season, dry season and across seasons at Samaru is presented in Table 4.21. Heritability estimates for days to 50% silking, ear height, number of cobs per plot, number of kernel rows, ear weight and grain yield were negative, days to 50% seedling emergence was low (0.21), moderate for days to 50% flowering (0.52) and high for plant height (0.74) and ear length (0.82) in the wet season.

The dry season heritability estimates for days to 50% seedling emergence and number of kernel rows were negative for the traits. The values for days to 50% flowering, days to 50% silking, ear height and grain yield were moderate. The values were high for plant height, ear height, number of cobs per plot, ear length and ear weight. The values were as high as 0.62 for ear height to 0.96 for ear weight. Across the two seasons, heritability estimate was negative only for days to 50% seedling emergence. It was low for ear height (0.33), number of kernel rows (0.11) and grain yield (0.21). It was moderate for days to 50% silking (0.48) and high for days to 50% flowering, plant height, number of cobs per plot, ear length and ear weight. The values were as high as 0.87 for ear length to 0.99 for ear weight.

For protein content, the narrow sense heritability estimates are presented in Table 4.22. The heritability estimates were negative for albumin/globulin and zein but medium for glutelin (0.51).

Table 4.21: Estimates of narrow sense heritability for agronomic traits at Samaru in 2011 wet season, 2011/2012 dry season, across seasons and endosperm proteins in 2011

	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY	GLU
Wet season	0.21	0.52	-	0.74	-	-	-	0.80	-	-	0.51
Dry season	-	0.55	0.55	0.74	0.62	0.81	-	0.70	0.96	0.67	-
Across seasons	-	0.91	0.48	0.94	0.33	0.96	0.11	0.83	0.99	0.21	-

DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking PH= Plant height EH = Ear height
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows EL= Ear length GY=Grain yield
GLU= Glutelin h^2ns= Narrow sense heritability

The GCA and SCA variance estimates and ratios for wet season, dry season and across season are presented in Table 4.22. The $\sigma^2_{GCA/}\ \sigma^2_{SCA}$ ratio estimates was zero for days to 50% silking and negative for ear height, number of cobs per plot, number of kernel rows, ear length and ear weight (Table 4.22). The estimates was less than one for days to 50% seedling emergence, days to 50% flowering, plant height and more than one for grain yield. Also, the ratio of GCA: SCA variances showed that SCA variances were greater than GCA variances for days to 50% seedling emergence, days to 50% silking, plant, ear height, number of cobs per plot, ear weight and grain yield for the wet season.

During the dry season, the $\sigma^2_{GCA/}\ \sigma^2_{SCA}$ ratio estimates was negative for days to 50% seedling emergence, plant height, number of cobs per plot, number of kernel rows and ear weight. The estimates was less than one for days to 50% flowering, days to 50% silking, ear height, grain yield and more than one for ear length. Also, the ratio of GCA: SCA variances showed that SCA variances were greater than GCA variances for days to 50% seedling emergence, days to 50% flowering, days to 50% silking, plant height, ear height, number of kernel rows and grain yield.

Across season, the $\sigma^2_{GCA/}\ \sigma^2_{SCA}$ ratio estimates was negative for days to 50% seedling emergence, days to 50% flowering, number of cobs per plot, number of kernel rows and ear weight. The estimates was less than one for days to 50% silking, ear height, grain yield and more than one for ear length and plant height. Also, the ratio of GCA: SCA variances showed that SCA variances were greater than GCA variances for days to 50% seedling emergence, days to 50% silking and ear height.

Table 4.22: Estimate of GCA and SCA variances for agronomic traits at Samaru in 2011 wet season, 2011/2012 dry season, across seasons

	σ^2_{GCA}	σ^2_{SCA}	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_{GCA}	σ^2_{SCA}	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_{GCA}	σ^2_{SCA}	$\sigma^2_{GCA}/\sigma^2_{SCA}$
		WET			DRY			ACROSS	
DE	0.07	0.11	0.64	-0.10	0.19	-	-0.05	0.35	-
DF	-0.29	-0.63	0.46	2.24	4.26	0.53	1.19	-0.35	-
DS	0	0.17	0	2.64	4.39	0.60	1.62	2.93	0.55
PH	11.90	30.93	0.38	-3.78	14.00	-	10.04	7.43	1.35
EH	-14.61	90.59	-	14.96	17.69	0.85	10.17	66.25	0.15
NC	-0.08	0.51	-	2.07	-10.04	-	1.77	-5.58	-
KRW	32.63	-74.35	-	-0.12	0.58	-	19.61	-40.38	-
EL	0.12	-0.26	-	0.55	0.52	1.06	0.68	0.18	3.78
EW	-2.78	6.81	-	282.55	-259.89	-	155.09	-138.51	-
GY	-16620.40	7546.30	2.20	-493.84	-312063.29	0.001	-20223.80	-118694.54	0.17

The GCA and SCA variance estimates and ratios for endosperm proteins are presented in Table 4.23. The $\sigma^2_{GCA}/\sigma^2_{SCA}$ variance ratio for endosperm proteins was negative for albumin/globulin, zein and less than one for the glutelin protein fraction. Also, all the ratio of GCA: SCA variances showed that the SCA variances were greater than the GCA variance.

Table 4.23: Estimate of GCA and SCA variances for endosperm proteins at Samaru in 2011

	Albumin/globulin	Zein	Glutelin
σ^2_{GCA}	-11.55	-1.37	6.10
σ^2_{SCA}	41.94	27.01	84.81
$\sigma^2_{GCA}/\sigma^2_{SCA}$	-	-	0.07

4.11 HETEROSIS ESTIMATES FOR SAMARU WET SEASON

This is the performance of the hybrids over the mid or high parent. The estimate of high parent heterosis at Samaru wet season is presented in Table 4.24. The heterosis over better parent ranged from -30.45 to 0.00% for days to 50% seedling emergence. All the hybrids exhibited negative heterosis except Sammaz 18 x Oba 98 which had zero heterotic value. With respect to days to 50% flowering, the heterotic value ranged from -8.52 to 5.95%. All except Sammaz 20 x Oba 98 exhibited negative heterotic values. For days to 50% silking, the heterotic values ranged from -8.70 to 5.14%. All except Sammaz 20 x Oba 98 exhibited negative heterotic values. Heterosis for plant height ranged from -13.71 to 16.93%, only three out of five had positive heterotic values. Sammaz 20 x Sammaz 14 gave the highest positive heterotic value.

Ear height had its heterotic values ranging from -25.52 to 19.34% and only two hybrids had positive heterotic values. Sammaz 20 x Sammaz 14 gave the highest positive heterotic value. With respect to number of cobs per plot, the heterotic values ranged from -47.62 to 87.66%. Four hybrids had positive values and Sammaz 37 x Sammaz 14 had the highest positive value. For number of kernel rows, the heterotic values ranged from -7.62 to 11.44%. Sammaz 17 x Sammaz 14 gave the highest positive value over the better parent. Ear length values ranged from -25.52 to 19.34% with Sammaz 20 x Sammaz 14 having the highest positive heterotic value. Heterosis for ear weight per plot ranged from

Table 4.24: Estimates of percent heterosis for agronomic traits evaluated at Samaru in 2011 wet season

Crosses	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Sammaz 37 x Oba 98	-15.79	-4.30	-3.65	-13.71	-17.77	-47.62	-4.19	-17.77	-16.33	-35.33
Sammaz 37 x Sammaz 14	-13.04	-6.45	-6.25	4.51	-0.10	89.66	1.49	0.10	4.34	65.91
Sammaz 17 x Oba 98	-5.56	0.00	0.00	-11.19	-25.52	-26.98	-6.98	-25.52	-0.31	-9.21
Sammaz 17 x Sammaz 14	-30.43	-1.70	-2.72	9.76	1.92	55.17	11.44	1.92	4.51	11.90
Sammaz 18 x Oba 98	0.00	-0.57	-1.10	-1.68	-7.14	0.00	-6.42	-7.14	-15.81	-5.26
Sammaz 18 x Sammaz 14	-21.74	-4.55	-4.89	-0.24	-16.90	-4.08	-5.50	-16.90	-4.29	30.91
Sammaz 20 x Oba 98	-6.25	5.95	5.14	-1.60	-11.67	-15.87	8.84	-11.67	-8.42	-21.05
Sammaz 20 x Sammaz 14	-30.45	-8.52	-8.70	16.93	19.34	63.41	7.62	19.34	24.66	85.11

PH= Plant height EH = Ear height EL= Ear length
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking GY=Grain yield

-16.33 to 24.66%. Only three gave positive heterotic values. The hybrid Sammaz 20 x Sammaz 14 gave the highest positive value over the better parent. The grain yield heterotic values ranged from -35.33 to 85.11%. Sammaz 20 x Sammaz 14 had the highest positive value.

4.12 HETEROSIS ESTIMATES FOR SAMARU DRY SEASON

The estimate of heterosis at Samaru dry season is presented in Table 4.25. The heterotic values ranged from -20.45 to 15.91% for days to 50% seedling emergence, with Sammaz 18 x Oba 98 having zero heterotic value. With respect to days to 50% flowering and days to 50% silking, the heterotic values ranged from -12.14 to 6.52%. Sammaz 37 x Sammaz 14 had negative heterotic values. Heterosis for plant height ranged from -15.04 to 29.26%, with three out of eight crosses having negative heterotic values. Sammaz 37 x Sammaz 14 gave the highest positive heterotic value.

Ear height had its heterotic values ranging from -29.92 to 28.59% and only two crosses had positive values. Sammaz 17 x Sammaz 14 gave the highest positive heterotic value. With respect to number of cobs per plot, the heterotic values ranged from -32.26 to 52.17%. Five hybrids had positive values and Sammaz 20 x Sammaz 14 had the highest positive value. For number of kernel rows, the heterotic values ranged from -9.20 to 14.29%. Sammaz 20 x Oba 98 gave the highest positive value over the better parent. Ear length values ranged from -9.66 to 19.10% with Sammaz 37 x Sammaz 14 having the highest positive heterotic value. Heterosis for ear weight per plot ranged from -32.57 to 53.75%.

Table 4.25: Estimates of percent heterosis for agronomic traits evaluated at Samaru in 2011/2012 dry season

Crosses	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Sammaz 37 x Oba 98	-10.53	-8.74	-8.74	1.71	21.44	-32.26	0.49	-0.92	-32.57	-37.50
Sammaz 37 x Sammaz 14	15.91	-12.14	-12.14	29.26	-3.61	21.74	4.76	19.10	14.23	245.24
Sammaz 17 x Oba 98	-7.50	-0.52	-0.52	-15.04	-11.18	-12.90	-4.93	-0.92	-17.96	-35.00
Sammaz 17 x Sammaz 14	-20.45	0.51	0.51	-2.27	28.59	34.78	10.75	6.60	53.75	180.00
Sammaz 18 x Oba 98	0.00	-4.21	-4.21	2.73	-13.41	12.90	-9.20	15.14	-31.71	20.00
Sammaz 18 x Sammaz 14	-20.45	-9.69	-9.69	-3.80	-29.92	-29.03	-7.41	-7.62	-40.81	-70.00
Sammaz 20 x Oba 98	-7.89	6.52	6.52	13.70	-16.67	25.81	14.29	-2.29	-12.74	15.00
Sammaz 20 x Sammaz 14	-18.18	-11.22	-11.22	12.91	9.74	52.17	-1.51	-9.66	9.70	113.33

PH= Plant height EH = Ear height EL= Ear length GY = Grain yield
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking

Only three hybrids had positive heterotic values. The hybrid Sammaz 17 x Sammaz 14 gave the highest positive value over better the parent. The grain yield heterotic values ranged from -70.00 to 245.24%. Sammaz 37 x Sammaz 14 had the highest positive heterosis for grain yield.

4.13 HETEROSIS ESTIMATES FOR SAMARU ACROSS SEASONS

The percentage high parent heterosis expressed in the F_1 for different traits at Samaru across seasons is presented in Table 4.26. The level of heterosis varied widely among the crosses. The heterosis over better parent ranged from -23.88 to -1.82% for days to 50% seedling. With respect to days to 50% flowering, the heterotic values ranged from -10.43 to 6.25% for Sammaz 20 x Oba 98 and -10.28 to 6.03% for days to 50% silking. Heterosis for plant height ranged from -10.10 to 14.78%, five out of eight had positive heterotic values. Sammaz 20 x Sammaz 14 gave the highest positive heterotic value.

Ear height had its heterotic values ranging from -22.99 to 14.95% and two out of eight crosses had positive heterotic values. Sammaz 20 x Sammaz 14 gave the highest positive heterotic value. With respect to number of cobs per plot, the heterotic values ranged from -44.90 to 64.52%. Four crosses had positive values and Sammaz 20 x Sammaz 14 had the highest positive value. For number of kernel rows, the heterotic values ranged from -7.96 to 12.27%. Sammaz 17 x Sammaz 14 gave the highest positive value over the better parent. Ear length values ranged from -7.33 to 10.39% with Sammaz 18 x Oba 98 which gave the highest positive heterotic value.

Table 4.26: Estimates of percent heterosis for agronomic traits evaluated at Samaru across seasons

Crosses	DE	DF	DS	PH	EH	NC	KRW	EL	EW	GY
Sammaz 37 x Oba 98	-9.09	-6.63	-5.96	-7.17	-19.92	-44.90	-3.98	4.20	-22.44	-36.21
Sammaz 37 x Sammaz 14	-14.93	-9.44	-8.68	13.93	-1.71	53.70	1.26	10.26	7.21	99.22
Sammaz 17 x Oba 98	-5.26	0.00	0.00	-10.10	-19.36	-25.51	-7.96	3.46	-6.70	-18.10
Sammaz 17 x Sammaz 14	-23.88	-1.07	-1.29	3.45	13.49	40.74	12.27	-1.38	18.34	16.67
Sammaz 18 x Oba 98	-1.82	-2.47	-2.38	4.42	-10.54	0.00	-7.41	10.39	-21.55	3.45
Sammaz 18 x Sammaz 14	-20.90	-7.75	-7.71	-1.68	-22.99	-16.87	-6.02	-6.93	-22.50	-16.00
Sammaz 20 x Oba 98	-9.09	6.25	6.03	4.86	-14.46	-6.12	9.13	2.34	-8.07	-8.62
Sammaz 20 x Sammaz 14	-22.39	-10.43	-10.28	14.78	14.95	64.52	-5.80	-7.33	14.15	67.61

PH= Plant height EH = Ear height EL= Ear length
EW= Ear weight NC= Number of cobs KRW= Number of kernel rows
DE= Days to 50% seedling emergence DF= Days to 50% flowering DS= Days to 50% silking GY=Grain yield

The heterosis for ear weight per plot ranged from -7.33 to 10.39% with Sammaz 18 x Oba 98 which gave the highest positive heterotic value. The heterosis for ear weight per plot ranged from -22.50 to 18.34%. Only three crosses gave positive heterotic values. The cross Sammaz 17 x Sammaz 14 gave the highest positive value over the better parent. The grain yield heterotic values ranged from -36.21 to 99.22%. Sammaz 37 x Sammaz 14 had the highest positive value.

4.14 HETEROSIS ESTIMATES FOR ENDOSPERM PROTEINS

Estimates of high parent heterosis for the protein fractions are presented in Table 4.27. The range of heterosis varied from -2.73 to 52.77% for albumin/globulin, all crosses exhibited positive heterotic values except Sammaz 20 x Sammaz 14. With respect to zein, all the crosses had negative heterotic values except Sammaz 18 x Oba 98. The heterotic values ranged from -55.13 to 9.23%. Hybrids had their heterotic values of glutelin ranging from -81.74 to 81.81%, Sammaz 37 x Oba 98 had the highest positive value. Among the $8F_1$ positive heterosis for both albumin/globulin and glutelin (quality traits) was shown by three crosses: Sammaz 37 x Oba 98, Sammaz 18 x Oba 98 and Sammaz 20 x Oba 98.

Table 4.27 Estimates of percent heterosis for endosperm proteins at Samaru 2011

Crosses	Albumin/globulin	Zein	Glutelin
Sammaz 37 x Oba 98	5.27	-24.12	81.81
Sammaz 37 x Sammaz 14	13.10	-21.23	-10.70
Sammaz 17 x Oba 98	7.94	-36.04	-67.31
Sammaz 17 x Sammaz 14	52.77	-55.13	-57.79
Sammaz 18 x Oba 98	8.34	9.23	30.32
Sammaz 18 x Sammaz 14	10.90	-26.83	-81.74
Sammaz 20 x Oba 98	25.40	-36.60	9.81
Sammaz 20 x Sammaz 14	-2.73	-23.98	-38.09

CHAPTER FIVE

DISCUSSION

5.1 POPULATION VARIABILITY

In this study, there were significant differences among the genotypes during the wet season for all traits measured except number of kernel rows, ear length and grain yield. During the dry season, only number of cobs per plot, number of kernel rows and grain yield were not significantly different among the genotypes. The significant differences observed among the genotypes indicate presence of genetic variability in them, while the non-significant ones indicates that they may be conditioned by same genes and are genetically related for these characters. It might be possible that the genotypes are related through some remote ancestors. According to Falconer and Mackey (1996), the amount of genetic improvement that can be achieved among a given set of genotypes depends on the amount of genetic diversity that is present within the population. The significant genotype x season interaction indicated that some traits (number of cobs per plot, number of kernel rows, ear length, ear weight and grain yield) were influenced by the different seasons. For that reason, suitable hybrids could be developed for specific seasons. In other words, some specific hybrids could be better in the wet season, while some hybrids will be better in dry season. This was in agreement with the findings of Showemimo *et al.* (2000a and 2000b) who reported performance or expression of genes controlling maize characters to be strongly influenced by environmental variation.

The significant difference observed for the endosperm proteins would have a significant effect on the quality of the maize proteins. This was in accordance to the findings of Dudley *et al.* (1977), indicating that breeding could improve the quality of maize genotypes.

The mean performance of the hybrids during the wet season showed that the parents from diverse genetic background can combine well to produce good crosses. Among the varieties, Sammaz 14 had the longest days to seedling emergence (8 days), while Sammaz 18, Sammaz 20, Oba 98, Sammaz 37 x Oba 98, Sammaz 17 x Oba 98, Sammaz 17 x Sammaz 14, Sammaz 18 x Sammaz 14 and Sammaz 20 x Sammaz 14 had the shortest days (5days). For days to 50% flowering and 50% silking, Sammaz 20 x Sammaz 14 had the shortest days (54 and 56), while Sammaz 37 had the longest days (62 and 64). Oba 98 was the tallest genotype amongst the parents (158.47cm), while Sammaz 18 x Sammaz 14 was the tallest cross (162.00cm) suggesting overdominance of the hybrid for the character in the cross. Oba 98 had the highest performance for ear placement (76.53cm) suggesting dominance of the parent for the trait. . Sammaz 20 x Sammaz 14 had the highest performance for number of cobs per plot (22.33) and grain yield (3867kg/ha). The result revealed that number of cobs per plot was positively associated with grain yield (the more the number, the higher the yield). Sammaz 17 x Sammaz 14 had the highest performance for number of kernel rows (15.60), while Sammaz 18 x Oba 98 had the longest ears (15.73cm) revealing the importance of the parents in genetic improvement for these traits. Oba 98 had the highest performance for ear weight (129.00g) suggesting dominance gene action. and positive association with

plant height and ear height. The taller the plant, the better the yield. Though, it had the second best performance for grain yield (3378kg/ha).

During the dry season, Sammaz 14 had the longest days to 50% seedling emergence (15 days). The result revealed that the days to emergence was affected by the dry harmattan season, which delays seed emergence. Sammaz 37 had the highest performance for days to 50% flowering and silking (69 and 70days), while Sammaz 20 x Sammaz 14 had the shortest days to flowering and silking (58 and 60days). Sammaz 14 had the lowest performance for plant height (97.40cm), ear height (35.80cm), number of kernel rows (12), ear length (12.20cm), ear weight (44.87g) and grain yield (231kg/ha).

The mean performance during the wet season was better and higher than the dry season, especially the yield. This finding supported that of Redden and Hemdge (1999), though contradicted Hudak and Patterson (1995) who reported the mean performance of traits in the dry season to be better than the wet season in soybean. This might be due to irrigation during the dry season where sufficient water might have been applied during the grain filling period. Fredrick *et al.* (2001) found that water stress had no impact on yield of soybean. This was supported by Panahyan-e-kivi *et al.* (2012).

The mean performance across seasons revealed that Sammaz 37 x Oba 98 and Sammaz 17 x Sammaz 14 had the shortest days to seedling emergence (8days). The results also revealed that the cross Sammaz 20 x Sammaz 14 had the lowest performance for days to 50% flowering and 50% silking (56 and 58days), Sammaz 18 x Sammaz 14 was the tallest plants (152.9cm), Sammaz 17 x Oba 98 was the longest ear (15.93cm), Sammaz 20 x Sammaz 14 had the highest number of cobs per plot (17), Sammaz 17 x

Sammaz 14 had the highest number of kernel rows (16), Sammaz 37 x Sammaz 14 was highest for ear weight (119.05g) and Sammaz 17 x Oba 98 for grain yield (2667kg/ha), indicating that Oba 98 and Sammaz 14 could be selected for extraction of inbred lines for commercial hybrid development for such traits.

The mean performance of endosperm proteins for quality traits revealed that Sammaz 37 was the highest in albumin/globulin (41.08mg/g), while Sammaz 37 x Sammaz 14 was the highest cross (46.46mg/g) for the trait. The result showed dominance effect of the higher parent for protein. Oba 98 had the lowest performance for zein (12.39mg/g), while Sammaz 17 had the highest amount of zein protein (39.95mg/g). Oba 98 could be used to produce improved maize genotypes with low amount of zein, which signifies more quality and low amount of leucine in the diet. Bhattaramakki *et al.* (1996) found positive correlation between low amount of zein and increase protein quality in maize. Zein was found to contain more leucine contents which block the absorption of niacin and vitamins (Knapp, 1975). Sammaz 14 had the highest amount of glutelin (37.15mg/g), while Sammaz 37 x Oba 98 was the highest cross (43.04mg/g). There was additive effect of the protein from both parents. The higher amount of albumin/globulin, glutelin and lower amount of zein indicates more protein availability, digestibility, absorption with minimal obligatory rates of oxidation and an increased biological value of the maize grain. This was supported by Friedman (1996).

5.2 COMBINING ABILITY

Combining ability refers to the ability of a parent to transmit desirable traits or performance through series of specific crosses to its progeny. It serves as a useful tool to

plant breeders since breeding methodologies depend upon the nature of gene action that controls a particular character within a population. Combining ability analysis is of special importance in cross pollinated crops like maize as it helps to know the genetic architecture of various traits and enables the breeder to design effective breeding plan. The GCA effects during the wet season trial revealed that Sammaz 20 was the best general combiner for grain yield traits and other desirable agronomic traits like earliness in seedling emergence, earliness in flowering, silking and plant height which influence the grain yield. The taller the plant, the better the yield. Sammaz 14 shows the same earliness in flowering and silking, tall plant with good yield. These parents can be selected due to their ability to combine well for these traits **to** produce good yield. Similar results were observed by Roy *et al.* (1998) who reported positive GCA values for these traits. Specific combining ability (SCA) effects revealed that Sammaz 20 x Sammaz 14 followed by Sammaz 37 x Sammaz 14 had the best cross combinations for earliness in flowering and silking, with an advantage of short plant height and grain yield. It was observed either that one or both of parents were good combiners (Sammaz 20 and Sammaz 14) for desirable agronomic traits including grain yield. The above crosses involved high x high and low x high combining parents. This was supported by Xingming *et al.* (2002), who reported the involvement of good parents in high yielding crosses.

In the dry season at Samaru, Sammaz 20 followed by Oba 98 were the best general combiners for grain yield and desirable agronomic traits like earliness in seedling emergence, earliness in flowering, silking and plant height which influence the grain yield. Sammaz 17 × Oba 98 had the best cross combination for SCA effect followed

by Sammaz 18 x Sammaz 14. This was in accordance to the findings by of Uddin *et al.* (2006) who observed high and positive SCA effects for grain yields in maize.

The GCA effects across seasons showed Sammaz 17 followed by Sammaz 14 were the best general combiners for grain yield. The SCA effect revealed Sammaz 20 x Sammaz 14 and Sammaz 18 x Oba 98 as the best specific cross combinations. This indicated that performance of genotypes was influenced by the season. This was in support of Falconer and Mackey (1996) who reported that performance of genotypes in an environment tends to be influenced by the environment and the type of germplasm used in the study.

In case of the protein quality traits, Sammaz 17, Sammaz 18 and Sammaz 14 were good general combiners for albumin/globulin fraction while Sammaz 20 and Oba 98 were good general combiners for glutelin showing positive GCA effects. Sammaz 37 had the best combination for quality traits showing high GCA effects for both albumin/globulin and glutelin. The GCA effect suggested that Sammaz 20 was the best general combiner for grain yield along with two major yield components. On the other hand, Sammaz 37 was the best combiner for quality traits showing positive GCA effects both for albumin/globulin and glutelin. These parents could be used in hybridization to improve yield as well as quality with desirable traits as donor parents for the accumulation of favorable genes. The SCA effects showed only one cross: Sammaz 18 x Sammaz 14 as superior combination for albumin/globulin and glutelins. This was similar to Yau *et al*. (1999) who reported that maize genotypes with more albumin/globulin and glutelin fractions indicate better quality (higher lysine and tryptophan) and Amiruzzaman *et al.*

(2011) who reported hybrid cross with superior protein quality in terms of lysine and tryptophan. The results generally showed that GCA effects of the parents were not reflected in their SCA effect for all the traits as reported by Ivy and Howlader (2000). Moreover, Amiruzzaman *et al*. (2011) also pointed out that the SCA is a result of the interaction of GCA effects of the parents and that it can improve or deteriorate the hybrid expression compared to the expected effect based on GCA only. The SCA effects of the crosses did not show any specific trend in cross combinations between parents possessing high, medium and low GCA except that the crosses that showed high SCA effects involved at least one good combiner. Aguiar *et al*. (2003) pointed out that in the diallel analyses, one must select hybrids of highest specific combining ability in which one of the parental lines presents high general combining ability.

5.3 HERITABILITY

Narrow-sense heritability measures the proportion of phenotypic variance among individual in a population that is due to heritable genetic effects while broad sense heritability measures the proportion of phenotypic variance that is attributable to an effect for the whole genotype, comprising sum of additive, dominance and epistatic effects (Nyquist 1991; Falconer and Mackey, 1996). Heritability is a key parameter in quantitative genetics because it determines the response to selection (Piepho and Mo¨hring, 2007). A high value for narrow-sense heritability therefore, indicates that additive gene action is important for controlling the character, while a low value signifies non-additive gene influence. Moderate narrow-sense heritability value would mean that both additive and non-additive actions are important in influencing the expression of the character, and that an appreciable amount of additive effect exists for improvement.

Similar results have been reported in maize (Robinson *et al*., 1949; Marquez and Hallauer, 1970; Verdosrem, 1982) and in sorghum (Showemimo and Nwasike, 1996). In general, it is believed that if a character is governed by non-additive gene action that may give higher heritability but low genetic advance, whereas if the character is governed by additive gene action, both heritability and genetic advance would be high. High genetic advance are based on narrow sense heritability which uses additive portion from the total genotypic variance (Khan *et al*., 2008).

The estimate for narrow sense heritability during the wet season was low for days to 50% seedling emergence (0.21), moderate for days to 50% flowering (0.52) and high for plant height (0.74) and ear length (0.80). The other traits including yield were all negative, which could be due to an inadequate model (genetic design), inadequate sampling (small numbers) or inadequate experimental techniques (competition among progenies). Negative heritability values indicate that the traits cannot be inherited and this therefore gives no room for selection. This was in accordance to Sabal *et al.* (2001) who reported that traits with high heritability are easier to be improved than those with low heritability. During the dry season, only plant height, number of cobs per plot, ear length and ear weight had high heritability values, others were moderate (days to 50% flowering, days to 50% silking, ear height and grain yield) and the rest were negative. Across seasons, low heritability estimates were observed for ear height, number of kernel rows and grain yield, while days to 50% seedling emergence was negative. Moderate heritability values was observed for days to 50% silking and high heritability value was observed for days to 50% flowering, plant height, number of cobs per plot, ear length and ear weight, which shows little influence of environment on the trait. Contrary result was

observed by Ali *et al.* (2012) who reported low heritability value for days to 50% flowering. Heritability value (0.48) for days to 50% silking was moderate. High heritability (0.85) for the trait in testcross of BSK (HI) C8 was recorded by Mulamba *et al*. (1983). Mihaljevic *et al*. (2005) obtained high heritability values (0.90) for plant height. The greater the heritability of a particular trait, the lesser will be the environmental effect on its expression. The heritability of the traits is largely affected by the environment. Similar results were also observed by Malik and Wright (1995) who reported that heritability of traits is largely affected by the environment where the plants are grown.

The estimates of narrow sense heritability for endosperm proteins was negative for albumin/globulin, zein and positively moderate (0.51) for glutelin fraction. The negative values could be due to an inadequate model (genetic designs), inadequate sampling (small numbers) or inadequate experimental techniques (competition among progenies). The moderate heritability value shows the trait is not easily heritable and is largely affected by environment.

A relatively large $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio suggests the importance of additive gene effects while a low ratio implies the presence of dominant or epistatic gene effects (Griffing, 1956). Additivity shows that the performance of heterozygote is intermediate to that of homozygote, therefore, an intermediate heterozygote reflect no-dominance of one allele over the other. The departure of the heterozygote (Aa) from the mean of two homozygote (AA or aa) at a locus reflects the extent of dominance. The result of the wet season revealed that, the magnitudes of the SCA variance were much higher than the

GCA variance for days to 50% seedling emergence, days to 50% silking, plant height, ear height, number of cobs per plot, ear weight and grain yield, indicating the predominance of non- additive gene action controlling the traits. It also denotes that non-additive genetic effects were largely influencing the expression of these traits; hence, heterosis and use of hybrid vigor could be applied for improving them. These results were in agreement with reports of other researchers about predominance of non-additive genetic effects for days to silking, plant height (Akbar *et al*., 2008: Alam *et al.*, 2008), ear height (Rezaei and Roohi, 2004; Alam *et al.*, 2008) and grain yield (Rezaei and Roohi, 2004; Srdic *et al.*, 2007; Bhatnagar *et al.,* 2004). The $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio could not be computed for ear height, number of cobs per plot, number of kernel rows, ear length and ear weight, this was because the σ^2_A ($4* \sigma^2_{GCA}$) or σ^2_D (σ^2_{SCA}) values were negative for the traits. When the estimate of σ^2_A or σ^2_D was reported as a negative value, it was consequently not possible to determine the ratio of σ^2_A / σ^2_D ($\sigma^2_{GCA}/\sigma^2_{SCA)}$. If estimates of σ^2_A or σ^2_D are in reality either very small positive values or zero, negative experimental estimates are not unexpected. Hence the average of the ratio σ^2_A / σ^2_D would be biased upward or downward because the ratios in individual studies that had negative estimates of σ^2_A or σ^2_D were not available (Hallauer *et al.*, 2010).

In the dry season, the ratio of GCA: SCA variances showed that SCA variances were also greater than GCA variances, indicating the predominance of the non – additive effects for days to 50% seedling emergence, days to 50% flowering, days to 50% silking, plant height, ear height, number of kernel rows and grain yield. Comparatively higher estimates of non-additive genetic variance over additive genetic variance were observed for the characters studied. Grain yield was predominantly controlled by non - additive

gene action. This is corroborated with the earlier findings of Khotyleva *et al.* (1986) who reported that grain yield was more influenced by dominant than additive gene effects. Later on similar results were also obtained by Mathur and Bhatnagar (1995) and Zelleke (2000). Predominance of non - additive gene action for grain yield in maize was also reported by Dass *et al.* (1997). Olakojo and Olaoye (2005) also reported non – additive gene action for plant height and ear height. The $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio could not be computed for ear height, number of cobs per plot, number of kernel rows, ear length and ear weight, this was because the σ^2_A ($4* \sigma^2_{GCA}$) or σ^2_D (σ^2_{SCA}) values were negative for the traits.

Across season, the GCA: SCA variance ratio revealed that the GCA variances were greater than SCA variances, indicating the predominance of the additive effects for the magnitudes of the GCA variance were much higher than the SCA variance for days to 50% flowering, plant height, number of cobs per plot, number of kernel rows, ear length, ear weight and grain yield. Similar results in maize have been reported for grain yield and yield component traits by Dodiya and Joshi (2002) and Kumar *et al.* (2005). This hybrid breeding can be an efficient breeding strategy for improvement of grain yield in maize. The $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio could not be computed for ear height, number of cobs per plot, number of kernel rows, ear length and ear weight, this was because the σ^2_A ($4* \sigma^2_{GCA}$) or σ^2_D (σ^2_{SCA}) values were negative for the traits.

The result of the endosperm protein fractions revealed that, the magnitudes of SCA components for all the traits were much higher than the GCA components, indicating the predominance of non- additive gene action controlling the traits. The $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio could not be computed for albumin/globulin and zein, while it was less

than one for the glutelin fraction, this was because the σ^2_A ($4* \sigma^2_{GCA}$) values were negative for the proteins. When the estimate of σ^2_A was reported as a negative value, it was consequently not possible to determine the ratio of σ^2_A / σ^2_D ($\sigma^2_{GCA}/\sigma^2_{SCA}$).

Normally, GCA effects are supposed to be higher than SCA for grain quality traits (Alika and Ojomo, 1996; Reif et al., 2005: Rodrigues and Chaves, 2002) but, it was not so in this case. For the quality of proteins to be improved in hybrids, the gene action needs to be additive, meaning it should be able to be transferred or inherited by the hybrids from the parents. This was, however, in partial agreement with Amiruzzaman *et al*. (2011) who reported protein quality in maize to be controlled by additive and non-additive gene action. The disagreement on the result might be caused by the difference in the genotypes used and also the environments where the evaluations were conducted. The predominance of non-additive gene action for yield-related and protein quality characters was also reported by Hossain and Prasanna (2008) in maize. Earlier research findings on kernel endosperm–modifying factors also reported that the additive variance was more important than non-additive variance (Bjarnason *et al*., 1976; Hohls *et al*., 1996; Vasal, 1975; Vasal *et al.*, 1980).

5.4 HETEROSIS

Heterosis is the vigor manifested in hybrids and represents the superiority in performance of hybrid individuals compared to their parents. Hybrid vigor in maize is manifested in the offspring of inbred lines with high specific combining ability (SCA) (Hallauer *et al.,* 2010). The manifestation of heterosis usually depends on genetic divergence of the two parental varieties. Genetic divergence among varieties usually is

unknown, and the only recourse is to determine level of genetic divergence empirically by means of variety crosses. Genetic divergence of the parental varieties is inferred from the heterotic patterns manifested in the series of variety crosses. If heterosis manifested from the cross of two parental varieties is relatively large, it is concluded that the two parental varieties are more genetically diverse than two varieties that manifest little or no heterosis in their variety crosses (Hallauer *et al.,* 2010). The success of plant breeding aimed at evolution of high yielding maize hybrids depends upon the selection of suitable parents to be utilized in hybridization program. This requires information on the combining ability and heterotic patterns of the germplasm in selection process (Fan *et al.,* 2001).

Among all the crosses, three hybrids: Sammaz 37 x Sammaz 14, Sammaz 17 x Sammaz 14 and Sammaz 20 x Sammaz 14 exhibited the highest positive heterosis for number of cobs per plant, number of kernel rows, ear length, ear weight and grain yield during the wet season trial. These hybrids may be selected and improved for the traits, since they also show negative values for early maturity, flowering and silking. The heterosis exhibited by these hybrids during the wet season was also observed in dry season and across seasons. . Similar reports have been presented on heterosis breeding in maize by Gama *et al.* (1995) and Ojo *et al. (*2007). Yusuf *et al.* (2009) also reported high level of better parent heterosis for desirable agronomic traits and grain quality in maize. Hence these parents are best for improvement of grain yield through recurrent selection. The high heterosis observed in the current work is consistent with previous results of Moll *et al*. (1962), Kim and Ajala (1996); Kim *et al*. (1984 and 1985); and Efron (1985). It is however, not consistent with the low yield advantage of 16.2% and 13% previously reported by Ogunbodede *et al.* (2000) and Vasal *et al.* (1992), respectively. The

inconsistency of the present work compared to the previous ones (Ogunbodede *et al.*, 2000; Vasal *et al.*, 1992) could be attributed to greater genetic diversity due to geographical distance in the origin of the inbred lines used in their studies. Lowest heterosis for desirable agronomic traits including grain yield was observed in Sammaz17 x Oba 98; Sammaz 20 x Oba 98 for wet season, Sammaz 17 x Oba 98; Sammaz 18 x Sammaz 14 for dry season and Sammaz 17 x Oba 98; Sammaz 18 x Sammaz 14 and Sammaz 37 x Oba 98 for the two seasons. Low heterosis of these crosses might be due to the fact that the parents have the same origin. This result is in conformity with Saxena *et al.* (1998) who reported that hybrids produced from inbred lines having different origin tend to have greater consistent yield levels than hybrids of parental lines originating from different source population.

Heterosis in case of protein quality was highest for Sammaz 37 x Oba 98, Sammaz 18 x Oba98 and Sammaz 20 x Oba 98 in terms of albumin/globulin and glutelin. These hybrids may be selected for further improvement on these traits for high protein quality. Similar finding was reported by Amiruzzaman *et al*. (2011) where high positive heterotic values were obtained for quality traits of lysine and tryptophan among some F_1s in maize. It was observed that the crosses with high heterotic value for protein quality possessed low heterotic values for yield related traits and grain yield. This may be due to the fact that maize varieties with high and better protein quality tend to perform badly in terms of grain yield since they have the tendency to be susceptible to damage by insect pests. Similar result was reported by Amiruzzaman *et al*. (2011) and Bhatnagar *et al.* (2004) that maize varieties with better quality fractions performed less in terms of yield.

CHAPTER SIX

SUMMARY, CONCLUSION AND RECOMMENDATIONS

6.1 SUMMARY

The study was conducted to estimate the combining ability, heritability and heterosis for endosperm proteins and agronomic traits in maize varieties. The parental materials used comprised eight genotypes varying in different levels of endosperm protein fractions, which were crossed using North Carolina design II. Fourteen genotypes comprising the crosses and parents were evaluated at Samaru in the wet and dry seasons.

The results of the study indicated significant differences among genotypes during the wet season for all traits studied except number of kernel rows, ear length and grain yield, indicating variability of the parental materials used. In the dry season, number of cobs per plot, number of kernel rows and grain yield were not significant. A significant genotype x season interaction was observed, indicating that suitable hybrids could be produced for specific season. Sammaz 17 x Oba 98, Sammaz 20 x Sammaz 14, Sammaz 17 x Sammaz 14 and Oba 98 are better in terms of plant height, number of cobs per plot, grain yield, number of kernel rows and ear weight in the wet season than in the dry season. Sammaz 37 x Oba 98, Sammaz 37 x Sammaz 14 and Sammaz 18 x Oba 98 were better in terms of albumin/globulin and glutelin.

Sammaz 20 and Sammaz 14 were the best general combiners for grain yield and also some desirable agronomic traits like earliness in seedling emergence, earliness in flowering, silking and plant height which had an influence on the grain yield during the wet season, indicating that the parents could be useful in hybrid breeding programme with a view to increase yield. Sammaz 20 x Sammaz 14 and Sammaz 37 x Sammaz 14

were the best cross combinations for earliness in flowering and silking, with an advantage of short plant height and high grain yield. It was observed that one or both of their parents were good combiners (Sammaz 20 and Sammaz 14) for desirable agronomic traits including grain yield. In the dry season at Samaru, Sammaz 20 and Oba 98 were the best general combiners for grain yield and desirable agronomic traits like earliness in seedling emergence, earliness in flowering, silking and plant height. Sammaz 17 × Oba 98 had the best cross combination for SCA effect followed by Sammaz 18 x Sammaz 14. The GCA effects across seasons showed Sammaz 17 and Sammaz 14 were the best general combiners for grain yield. The SCA effect revealed Sammaz 20 x Sammaz 14 and Sammaz 18 x Oba 98 as the best specific cross combination. Sammaz 37 had the best combination for quality traits showing high GCA effects for both albumin/globulin and glutelin. The GCA effect suggested that Sammaz 20 was the best general combiner for grain yield along with two major yield components. On the other hand, Sammaz 37 was the best combiner for quality traits showing positive GCA effects both for albumin/globulin and glutelin. These parents could be used in hybridization to improve yield as well as quality with desirable traits as donor parents for the accumulation of favorable genes. The SCA effects showed only one cross: Sammaz 18 x Sammaz 14 as superior combination for albumin/globulin and glutelins.

Estimates for narrow sense heritability during the wet season, was low for days to 50% seedling emergence, moderate for days to 50% flowering and high for plant height and ear length. The other traits including yield were all negative. Negative heritability values indicate that the traits cannot be inherited and this therefore gives no room for selection. During the dry season, only plant height, number of cobs per plot, ear length and ear weight had high heritability values, others were moderate (days to

50% flowering, days to 50% silking, ear height and grain yield) and the rest were negative. Across seasons, low heritability estimates were observed for ear height, number of kernel rows and grain yield, while days to 50% seedling emergence was negative. Moderate heritability values was observed for days to 50% silking and high heritability value were observed for days to 50% flowering, plant height, number of cobs per plot, ear length and ear weight, which shows little influence of environment on the trait. The estimates for endosperm proteins were negative for albumin/globulin, zein but positive and low (0.30) for glutelin fraction. The negative values could be due to an inadequate model (genetic designs), inadequate sampling (small numbers) or improper experimental techniques (competition among progenies). The low heritability values show the traits are not easily heritable and are largely affected by environment.

The result of the wet season revealed that, the magnitudes of the SCA variance were much higher than the GCA variance for days to 50% seedling emergence, days to 50% silking, plant height, ear height, number of cobs per plot, ear weight and grain yield, indicating the predominance of non- additive gene action controlling the traits. In the dry season, the ratio of GCA: SCA variances showed that SCA variances were also greater than GCA variances, indicating the predominance of the non – additive gene action for days to 50% seedling emergence, days to 50% flowering, days to 50% silking, plant height, ear height, number of kernel rows and grain yield. Across season, the GCA: SCA variance ratio revealed that the GCA variances were greater than SCA variances, indicating the predominance of the additive gene effect for the magnitudes of the GCA variance were much higher than the SCA variance for days to 50% flowering, plant height, number of cobs per plot, number of kernel rows, ear length, ear weight and grain yield.

The result of the endosperm protein fractions revealed that, the magnitudes of SCA components for all the traits were much higher than the GCA components, indicating the predominance of non- additive gene action controlling the traits.

Sammaz 37 x Sammaz 14, Sammaz 17 x Sammaz 14 and Sammaz 20 x Sammaz 14 exhibited the highest positive heterotic response for number of cobs per plant, number of kernel rows, ear length, ear weight and grain yield during the wet season, in the dry season and across the seasons. These hybrids may be selected and improved for their traits. They also show negative values for days to 50% seedling emergence, days to 50% flowering and days to 50% silking. The heterosis for both seasons and across seasons indicated a unidirectional dominance, this crosses could be tested in multi-locations and if found to be suitable released directly for production. In the case of protein quality, Sammaz 37 x Oba 98, Sammaz 18 x Oba 98 and Sammaz 20 x Oba 98 had higher heterotic values.

6.2 CONCLUSION

In conclusion, the study revealed a high influence of season on the combing ability of parent varieties and crosses. Although the general combiners for the two seasons were the same (Sammaz 20), the specific combiners were not the same for the two seasons (Sammaz 20 x Sammaz 14 and Sammaz 17 x Oba 98). This shows the need to select different parental varieties that would combine well for hybrid production for specific seasons for yield traits. Sammaz 37 was the best combiner for quality traits showing positive GCA effects both for albumin/globulin and glutelin, while Sammaz 20 was the best general combiner for yield trait. These parents could be used in hybridization to improve yield as well as quality with desirable traits as donor parents for the accumulation of favorable genes. The SCA effects showed only one cross:

Sammaz 18 x Sammaz 14 as superior combination for albumin/globulin and glutelins. Heritability of agronomic traits for both wet and dry season showed non – additive gene action, while across seasons was governed by additive gene action. Endosperm proteins showed non-additive gene action, which could be due to environmental influence. Protein results obtained might have been better or different if seeds for the analysis were taken from specific plants of each variety, instead of bulking before sampling.

6.3 RECOMMENDATIONS

Based on the results of this study, it was recommended that Sammaz 20, Sammaz 14, Oba 98 and Sammaz 37 are the best combiners for yield and quality traits. They are recommended for extraction of inbreds lines for hybrid development. There was need to select different parental varieties for hybrid production in different seasons, while specific crosses should be produced during specific season.

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