# INHERITANCE STUDIES OFPRO-VITAMIN A ANDSOMEAGRONOMIC TRAITS INFIVE SORGHUM [*SORGHUM BICOLOR* (L.) MOENCH] GENOTYPES

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**NIGERIA**

**AUGUST, 2016**

# INHERITANCE STUDIES OFPRO-VITAMIN AAND SOMEAGRONOMIC TRAITS IN FIVESORGHUM [*SORGHUM BICOLOR* (L.) MOENCH] GENOTYPES

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**AUGUST, 2016**

## Declaration

I declare that the work in this Dissertationentitled INHERITANCEOF PRO-VITAMIN A AND SOME AGRONOMIC TRAITS IN FIVE SORGHUM [*SORGHUM BICOLOR* (L.) MOENCH] GENOTYPES has been performed by me in the Department of Plant Science. The information derived from literature have been duly acknowledged in the text and a list of references provided. No part of this Dissertation was previously presented for another degree or diploma at this or any other Institution.

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Signature Date

## Certification

This dissertation entitledINHERITANCEOF PRO-VITAMIN A AND SOME AGRONOMIC TRAITS IN FIVE SORGHUM [*SORGHUM BICOLOR* (L.) MOENCH] GENOTYPESbyGlory Enoette ONONOKPONO meets the regulations governing the award of the Degree of Master of Science Plant Breeding of Ahmadu Bello University and is approved for its contribution to knowledge and literary presentation.

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## Dedication

This Dissertation is dedicated to God Almighty who by His Grace sustained and enabled me to complete the work successfully.

**Acknowledgements**

I sincerely appreciate my major supervisor, Prof. D.A. Aba whose guidance, contributions made this Dissertation a success. I also wish to express my gratitude to members of my supervisory team, Prof. S.G. Ado and Dr. S.M. Bugaje for giving me their time and advice, which contributed to the success of this work. My profound gratitude also goes to all the academic and technicalstaff of the Department of Plant Science, Institute for Agricultural Research(IAR) especially Mr. Ibrahim Jumarewho assisted me at every stage in the course of this work, may God reward them all.My profound gratitude also goes to Prof. B.O. Solomon, former Director General of National Biotechnology Development Agency (NABDA). Thank you for your permission to come for this program and the present Director General Prof. Mrs. Lucy J. Ogbadufor extending my study leave period to enable me complete the program. To all staff of NABDA, I say thank you all for your prayers. To my friendsand colleagues Habu Hamisu, Afolabi Samsom Oluwaseum, Kabiru D. Dawaki, Garba Alhassan (Class Rep), Victor Musa, Alhamdu Joseph, Hauwa O. Ahmad, Zainab Miko, Ronke, Esther, Chinenye, Aafa, Keny, Naomi GraceandFatima to mention a few,thank youforyour support, encouragement and companionship, your presence and support made the work load easier, God bless youall.I wish to extend my heartfelt thanks to my parents, Mr. and Mrs. Enoette Ononokpono, my siblings and family members for their prayers, financial and moral support, which helped me in the accomplishment of this work. Above all, I thank God Almighty for granting me the grace to complete this work, may His name alone be glorified.

**Abstract**

Sorghum [*Sorghum bicolor* (L.) Moench] is a cereal belonging to the family *Poaceae*.Sorghum is an important staple food crop in northern Nigeria. Most Sorghum, varieties especially white endosperm colouredvarietieshave low pro-vitamin A (PVA) content compared to some yellow endosperm varieties leading to PVAmalnutrition on populations who depend on them as dietary source.Understanding the inheritance of PVA andother agronomic traits will assist in providing a useful tool for developing efficient breeding strategies for selecting PVAtrait in new sorghum varieties so as to combat malnutrition in Nigeria. This study was conducted to determine the gene action controlling PVAand other agronomic traitsand then their heritability in six Sorghum crosses and to compute the correlations between PVA and every other agronomic trait. Six crosses of Sorghum were developed from five sorghum genotypes comprising of two genotypes with relatively high PVA content and three genotypes relatively low PVAcontent. Field evaluation was conducted at Research Trial site of the Institute for Agricultural Research (IAR), Samaru.The trial was laid in a Randomized Complete Block Design (RCBD) with three replications. Observations were recorded on days to 50% flowering, plant height, panicle length, panicle weight, grain weight per plant, 1000-grain weight, grain yield andPVA.Analysis of variance revealed highly significant differences ($P < 0.01$) among the six generations indicating existence of genetic variation.The grain yields were highest in $F_1$generations which ranged from997.5 to 1252kgha$^{-1}$ for SAMSORG 43 × SAMSORG44 andSAMSORG 17 × SAMSORG 14 respectively. In the case of SAMSORG 17 × SAMSORG 44, the $P_1$recorded higher yield (1229.47kgha$^{-1}$) than$F_1$(1208.81kgha$^{-1}$). The $F_1$ generationsin PVAwere midway between theparental values, 7.87 mg/l, 5.76 mg/l,

9.71mg/l, 6.48 mg/l, 6.49 mg/l and 6.92 mg/l for SAMSORG 17 × SAMSORG 44, SAMSORG 17 × SAMSORG 14, SAMSORG 17 × CSR01,SAMSORG 43 × SAMSORG 44, SAMSORG 43 × SAMSORG 14, SAMSORG 43 × CSR01 studiedindicating preponderance of additive gene action.Significant differences for two or more individual scaling tests A, B and Cin all crosses were recorded forPVAand other traits, indicating the presence of non-allelic gene interactions. Hayman six-parameter genetic modelsuggested that additive, dominance and epistasis effects were important for PVAand othertraits,althoughthe dominance effect was significant inPVA in all the crosses but in negative direction indicating thatduplicate type of epistasis for dominant decreasing alleles was exhibited.PVA contentexhibited significance in SAMSORG 43 × SAMSORG 44, for mean7.87** ± 0.42, additive9.46** ± 2.99,dominance-5.70** ±0.66,additive × additive-8.13**±2.98, additive × dominance2.93**±0.66anddominance × dominance13.36**±4.32suggesting the presence of linkage or higher order epistatic interactions.Furthermore,PVAshowed high heritability (98.00%) coupled with high genetic advance of mean (66.86%) for SAMSORG 17 × SAMSORG 44 which was the pattern in most of the crosses confirming that PVA is under the influence of additive gene action in its inheritance and expression.PVAshowed significant positive genotypiccorrelationwithpanicle weight;(r=0.606)and grain yield;(r=0.591),in SAMSORG 17 ×CSR01this indicates that opportunities exist to increase PVA without lowering grain yield and other desirable agronomic traits. Generation mean analysis indicated that non allelic gene interactions is the integral part of genetic architecture of the present materials used in this study and that selection of PVA in early generation is sufficient.

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## List of Abbreviations

ACC/SCN Administrative Committee on Coordination/ Subcommittee onNutrition (United Nations)

ANOVA Analysis of variance

$BC_1P_1$ First backcross to parent one

$BC_1P_2$ First backcross to parent two

CV Coefficient of Variation

df Degrees of Freedom

EMS Error Mean Square

$F_1$First filial generation

$F_2$ Second filial generation

FAO Food and Agriculture Organization of the United Nations

GA Genetic Advance

GIEWS Global Information and Early Warning System

GLM General Linear Model

GMA Generation Mean Analysis

IAR Institute for Agricultural Research Samaru

MS Mean Square

NARICT National Research Institute for Chemical Technology.

NB Nigerian Brewery

PVA Pro-Vitamin A

$P_1$ Parent one

$P_2$ Parent two

$P_3$ Parent three

$P_4$ Parent four

$P_5$ Parent five

RCBD Randomized Complete Block Design

SAS Statistical Analysis System

SAT Semi-Arid Tropics

SE Standard Error

SD Standard Deviation

SSA Sub-saharan Africa

UV Ultra Violet

VADVitamin A Deficiency

W H O World Health Organization

$\chi^2$ Chi- square

$H_B$ Broad sense heritability

$H_N$ Narrow sense heritability

QTL Quantitative trait loci

# CHAPTER ONE

# 1.0 INTRODUCTION

## 1.1 Background of Study

Sorghum [*Sorghum bicolor* (L.) Moench] is a cereal of the family *Poaceae* with remarkable genetic variability. It is called *milo, jowar, kafir, cholam, dawa, oka baba* in some Nigerian languages and Guinea corn in English language. Sorghum originated in equatorial Africa i.e. East Africa (likely from Ethiopia (Ecoport, 2010) and is distributed throughout the tropical, semi-tropical, and arid regions of the world. It is the fifth major cereal crop of the world following wheat, rice, maize and barley in terms of production and utilization. In terms of tonnage, sorghum is Africa's second most important cereal. It is also the second cheapest source of energy and micronutrients (after pearl millet); because a vast majority of the populations in Africa and central India depend on sorghum for their dietary energy and micronutrient requirements (Parthasarathy Rao *et al.*, 2006).

Sorghum has unique tolerance to drought and adaptation to dry tropical and subtropical ecosystems throughout the world. Africa produces about 20 million tons of sorghum per annum. Sorghum production in Nigeria is increasing at a very rapid rate 8.5 million tons in 2008, 9.32 million tons in 2009, 11.5 million tons in 2011 and63.7 million tons in 2014, making the country the largest producer in the world (Obilana, 2011). Sorghum grain is a small, hard caryopsis covered by glumes. In grain sorghum, panicles are compact and bear 25,000 to 60,000 seeds $kg^{-1}$ (Ecoport, 2009). Sorghum in its processed form is food to more than 65 million Nigerians daily. The whole grain can be boiled, roasted, popped or ground to make flour for bakery (flat breads) and pastry or indigenously consumed as solid foods (*Tuwo*), thin porridges (*Kamu, Ogi*), which is used as weaning food for infants and gruels

(*Kunu*) as breakfast food drinks, boiled grain (*pate*) (Obilana, 2011). Sorghum is extensively used worldwide in food production systems, and in food aid programs, the emphasis is on grain sorghum (Rooney and Waniska, 2000).

Sorghum grain is also used for the production of alcoholic and non-alcoholic beverages, including beer and liquors. Some sorghum varieties are used for dyeing textiles or leathers. However, it has a wide range of applications that are being explored with worldwide interest in renewable resources. The crop is a gluten-free cereal and recent research has begun to evaluate it for flour characteristics that would make it more amenable to baking and other processing technologies. New technologies are allowing sorghum germplasm to be screened for high levels of anti-oxidants that show promise in cancer research and glycemic control (Jeff *et al* 2011). Recently, various forage accessions have been evaluated for their potential for renewable fuel production. Given its genetic variability, new utilization of sorghum within the health food market, local utilization markets and the bioenergy arena makes sorghum an attractive renewable resource for future generations (Jeff *et al* 2011).

In animal nutrition, grain sorghum is mostly used as an energy source and is a good feedstuff for poultry, pigs and ruminants. The remaining stalks can be grazed after harvest as some varieties stay green for a long time. Sorghum can also be grown for fodder, as a pasture or cut green to make silage and hay (Balole and Legwaila *2*006). The importance of sorghum in Africa can be adjudged from the fact that there is an almost bewildering variety of African traditional sorghum foods and beverages. These include: whole grain rice-type products, breads and pancakes, dumplings and couscous, porridges, gruels, opaque and cloudy beers, and non-alcoholic fermented beverages (Waniska, 2000). Vitamin A is made

up of a family of compounds called the retinoid. The retinoid designation resulted from finding that vitamin A had the biologic activity of retinol, which was originally isolated from retina. There are essentially three forms of vitamin A: retinols, beta carotenes, and carotenoids. Retinol is the most active form and is mostly found in animal sources of food. Beta carotene, also known as PVA, is the plant source of retinol from which mammals make two-thirds of their vitamin A (George *et al*, 2014) Carotenoids, the largest group of the three, contain multiple conjugated double bonds and exist in a free alcohol or in a fatty acyl-ester form (George *et al*, 2014)

**1.2 Statement of Problem**

Malnutrition hinders the attainment of human potential and the nation's social and economic development.VAD, affecting approximately 250 million poor people in the semiarid region of Africa and Asia, is the primary cause of blindness, increased mortality in children and pregnant women, and susceptibility to malaria and diarrheal disease (Horton, 2001). Sorghum is a critical food cereal crop in those extremely drought-prone and poor regions, where other crops such as maize cannot be grown (FAO/GIEWS, 1998; FAO, 1995). In Africa, direct per capita food use of sorghum reaches levels as high as 100 kg a year and 74% of the sorghum produced is consumed by the farmer and his family (FAO, 1995). In Nigeria, a study published in 2001 showed the national prevalence of night blindness as 1.1%, the national prevalence of marginal VAD as 28.1% and severe retinol deficiency as 7.0%. No fewer than 80,000 Nigerian children die annually from VAD related ailments; study found that the distribution of VAD in children less than five years was 25.6% in the rural areas, 32.6% in semi urban areas and 25.9% in the urban areas, (Busie *et al*, 2006).Two micronutrients namely iron (Fe) and zinc (Zn) and PVA are

recognized by the World Health Organization (WHO) of the United Nations as limiting. Deficiency for Fe, Zn and β-carotene is highest in South and South-east Asia and sub-Saharan Africa (SSA). These are also the regions [typified as semi-arid tropics (SAT)] where sorghum is cultivated and consumed as a staple food by millions of people.Dicko (2006) reported that sorghum grain is low in protein and ash and rich in fibre component but lacks vitamin A. There are over 3,000 accessions of sorghum in Nigeria; some of them the *kaura* with yellow endosperm screened by Dicko (2006) have relatively low PVA content. Therefore, increasing the carotenoid content of sorghum might have a great impact on the health of poor people in the world who depend on sorghum as staple food.

### 1.3 Justification

Nutrition disorders can be caused by insufficient intake of food or of certain nutrients or by inability of the body to absorb and use nutrients. VAD is a micronutrient deficiency and the leading cause of preventable blindness in children. It increases the risk of disease and death from severe infections. Mehlo, (2013) explained that sorghum is "ripe'' for further improvement, especially for a continent that is plagued by malnutrition, which remains a leading, direct cause of the rise in many non-communicable diseases especially in Africa. Therefore developing vitamin-enriched staple plant food is a powerful intervention tool that targets the most vulnerable people, resource-poor women, infant and children (Combs Jr. *et al*. 1996; Bouis, 2000), who cannot afford commercially marketed fortified foods. Furthermore, it is a sustainable intervention, unlike interventions that depend on the supplementation and fortification programs that have not proved to be sustainable in many developing nations (Subbulakshmi and Naik, 1999). Nutritionally improved crop varieties will continue to be grown and consumed year after year, even if government attention and

international funding for micronutrient and vitamin A issues fade. Once the investment is made in developing nutritionally improved crop varieties, seeds can be adapted to similar growing conditions in numerous countries (Howarth, 2002).

There are several interacting factors affecting the color and overall appearance of sorghum caryopses. Endosperm color affects appearance, especially in caryopses with a thin pericarp and without a pigmented testa. Caryopses appear yellow when the pericarp is thin and colorless, the testa is absent and the endosperm is yellow (Rooney and Miller 1982). This is of great importance since the yellow endosperm cultivars contain relatively higher levels of carotenoid pigments which are precursors for vitamin A. The understanding of the inheritance of this trait will assist in providing useful information for developing efficient breeding strategies for inheritance of yellow endosperm trait (PVA) in sorghum so as to combat malnutrition in Nigeria (Rooney and Miller 1982). Therefore crop varieties bred for increased PVA contents through conventional breeding approach will complement the existing approaches (such as transgenic crops and food supplementation while processing) to combat malnutrition.

### 1.4 Objectives

The general objective of this work is to develop sorghum genotypes with improved PVA content.Specific objectives of the study are:

1. To determine the gene action involved in the inheritance of PVA and other agronomic traits in five genotypes of sorghum.
2. To estimate the heritability of PVA and other agronomic traits in sorghum.
3. To determine the genotypic and phenotypic correlations of PVA with other agronomic traits in sorghum.

# CHAPER TWO

# 2.0 LITERATURE REVIEW

## 2.1 Origin

Domestication probably took place in sub-Saharan Africa. This is suggested by the fact that the last wild relatives of commercial sorghum are currently confined to Africa south of the Sahara although Zohary and Hopf (2000) add "perhaps" Yemen and Sudan. However, Zohary and Hopf (2000), "the archaeological exploration of sub-Saharan Africa is yet in its early stages, and we still lack critical information for determining where and when sorghum could have been taken into cultivation." Although *S. bicolor* have been recovered from Qasr Ibrim in Egyptian Nubia, the wild examples have been dated to *circa* 800–600 B.C.E. and the domesticated ones no earlier than CE 100. The earliest archeological evidence comes from sites dated to the second millennium B.C.E. in India and Pakistan where *S. bicolor* is not native. These incongruous finds have been interpreted, according again to Zohary and Hopf (2000), as indicating: (i) An even earlier domestication in Africa, and (ii) an early migration of domestic sorghum, from East Africa into the Indian subcontinent.

The Food and Agricultural Organization of the United Nations (FAO) notes that sorghum likely was taken from eastern Africa to India during the first millennium B.C.E. and that it existed there around 1000 B.C.E. (FAO 1995).The FAO reports that cultivated sorghum likely arose from a wild form belonging to the subspecies *verticilliflorum* (FAO 1995).Most cultivated varieties of sorghum can be traced back to Africa, where they grow on savanna lands. During the Muslim Agricultural Revolution, sorghum was sown extensively in parts of the Middle East, North Africa, and Europe (Watson 1983). The name "sorghum" comes from Italian "sorgo," in turn from Latin "Syricum (granum)" meaning "grain of

Syria."Despite the antiquity of sorghum, it arrived late to the Near East. It was unknown in the Mediterranean area into Roman times. Tenth century records indicate that it was widely grown in Iraq, and became the principal food of Kirman in Persia.In addition to the eastern parts of the Muslim world, the crop was also grown in Egypt and later in Islamic Spain. From Islamic Spain it was introduced to Christian Spain and then France (by the twelfth century). In the Muslim world, sorghum was grown usually in areas where the soil was poor or the weather too hot and dry to grow other crops (Watson 1983).Grain sorghum likely arrived in America from West Africa as "guinea corn" around the middle of the nineteenth century with slave traders (FAO 1995).

**2.2 Taxonomy of Sorghum**

Sorghum (*Sorghum bicolor* L. Moench) is a tropical grass grown primarily in semiarid parts of the world, particularly in Africa, India, and Asia, where it is an important staple food crop.

Sorghum is classified as,

Kingdom *Plantae* – Plants

Sub-kingdom *Tracheobionta* – Vascular plants

Super-division *Spermatophyta* – Seed plants

Division *Magnoliophyta* – Flowering plants

Class *Liliopsida* – Monocotyledons

Sub-class *Commelinidae*

Order *Cyperales*

Family *Poaceae*– Grass family

Genus *Sorghum Moench*– sorghum

Species *Sorghum bicolor* USDA, NRCS. (2006).

It is a member of the tribe *Andropogoneae*, of which are three species:

1. *S. bicolor* - diploid (2n=20) all annual and domesticated types, including stabilized weedy derivatives such as Sudan grass. Widely distributed.
2. *S. halepense* – Johnson grass, tetraploid, native perennial of southern Eurasia, east to India.
3. *S. propinquum* - Diploid, native perennial of Sri Lanka and southern India.

*Sorghum bicolor* is divided into three subspecies:

1. *bicolor* - cultivated sorghum
2. *arundinaceum* - wild sorghum (e.g. Sudan grass)
3. *drummondii* - hybrids between the above two subspecies ICRISAT, (2006)

Cultivated sorghums are divided into seven basic races (agronomic types) Kafir (S. Africa) - short plants, Milo-Caudatums (E. Africa), Feterita-Guineas (Sudan), Durra (East Africa, Middle East and India), Sballu (India), Koaliang (China), Hegari (Sudan) ICRISAT, (2006).

**2.3Production**

The FAO reports that 440,000 square kilometers were devoted worldwide to sorghum production in 2004. The United States is the world's largest producer, followed by India and Nigeria (FAO 1995).In the United States, sorghum mainly is produced for animal feed. In India, it is produced as an important food for people. The top exporters are the United

States, Australia, and Argentina (FAO 1995). The United States has held a share of seventy percent or more of the world trade throughout the last decade, with exports mainly to Mexico (FAO 1995). As a continent, Africa is the largest producer with about 21.6 million metric tons (850.6 million bushels) annually (FAO 1995).It is the leading cereal grain produced in Africa(FAO 1995).

**2.4Morphology and Genetics of GrainSorghum**

Sorghum is a rich source of B-complex vitamins. Some yellow-endosperm varieties of sorghum contain ß-carotene which can be converted to vitamin A by the human body. Detectable amounts of other fat-soluble vitamins, namely D, E and K, have also been found in sorghum grain (FAO, 2011).

Several interacting factors affect the color and overall appearance of sorghum caryopses. Appearance is mainly affected by pericarp color and thickness, presence of pigmented testa, and endosperm color (Rooney and Miller, 1982; Waniska, 2000) Secondary plant and glume colors, as well as, deterioration due to the environment, insects and molds, complicate the evaluation of pericarp color and other properties. Immature pericarp tissues, when damaged, respond with antimicrobial phenolic compounds, which form pigments that stain the pericarp and endosperm. Insect and mold damage of the pericarp commonly occurs together when caryopses mature in hot, humid environments. Pericarp color is genetically controlled by the R and Y genes. The combination of these genes can produce white or colorless (R_yy or rryy), lemon yellow (rrY_), or red (R_Y_) color. The intensifier (I) gene increases the brightness of the pericarp color; this is especially prominent in red pericarp sorghums. The Z gene controls pericarp thickness (Waniska, 2000). Sorghum with homozygous recessive (zz) genes possess a thick mesocarp. A thick pericarp contains small

starch granules, which causes a chalky appearance that masks the color of the testa and endosperm (Earp and Rooney, 1982; Rooney and Miller, 1982; Waniska, 2000). A pigmented seed coat or testa is present when both B1_ and B2_ genes are dominant. The tptp genes control testa color, which can be brown or purple. Caryopses with a pigmented testa (B1_B2_) and a recessive spreader gene (ss; type II) or dominant spreader gene (S_; type III) contain condensed tannins and are called brown or tannin sorghums (Hahn and Rooney, 1986; Waniska, 2000). Type III sorghums have more tannins than type II sorghums, whereas type I sorghums do not contain tannins or proanthocyanidins. A black sorghum from Sudan, Shawaya, has very high levels of flavonoids that oxidize in the pericarp during caryopsis development and mask pericarp color. The black pigmentation is a recessive trait. Some sorghum have dominant trait for intense pigmentation or blotching in the pericarp and peripheral endosperm when damaged. Blotching detracts from appearance and food utilization.

Darker secondary plant and glume colors are dominant and increase the pigmentation of milling and food products. Each secondary plant color (tan, red, and purple) has a range of glume colors (from very light to very dark). The lighter glume colors yield products that are less pigmented and are preferred in most foods. Yellow endosperm cultivars contain high levels of carotenoid pigments. Endosperm color affects appearance, especially in caryopses with a thin pericarp and without a pigmented testa. Caryopses appear yellow when the pericarp is thin and colorless, the testa is absent, and the endosperm is yellow. A thick mesocarp and colorless pericarp cause white or chalky appearance. Heteroyellow endosperm sorghum results when sorghum with yellow and non- yellow endosperm colors are hybridized (Rooney and Miller, 1982; Waniska, 2000). Bronze sorghums contain a

thin, red pericarp with yellow endosperm color, while cream sorghums contain a thin, white pericarp with yellow endosperm. Waxy endosperm cultivars contain three genes (wx) in the recessive form. Heterowaxy genotypes contain one or two of these genes in the dominant form whereas normal or non-waxy endosperm sorghums contain all three genes in the dominant form.

The environmental conditions during caryopsis development and maturation greatly affect the appearance of sorghum because the panicle or head is readily exposed to biotic and abiotic agents (Castor and Frederiksen, 1980; Glueck and Rooney, 1980; Waniska, 2000). An environment that is hot and humid during maturation negatively affects quality. Deterioration results from insects, molds, moisture, and sunshine. Physical damage resulting from insect attack activates a phenolic defense mechanism that produces discolored spots in the pericarp and the endosperm. Mold colonization discolors the pericarp surface initially, breaks down the endosperm composition and structure, and adversely affects processing quality (Waniska, 2000). Sorghums that have an open panicle structure and caryopses with thin pericarp, condensed tannins, corneous endosperm, and large, tight glumes are generally considered to be more resistant to grain molding and weathering (Waniska, 2000).

### 2.5 Genetics of Carotenoid Content of Sorghum Grain

Sorghum grains exhibit a wide variety of colours, ranging from red or purple to white. This colour is determined by the allelic constitution of genes affecting pericarp colour, mesocarp thickness, pigmented testa, and endosperm colour. Endosperm colour in sorghum is either yellow or white with a range of variation between the two. Carotenoids are a group of lipophilic pigments with diverse biological functions. In plants, they are part of light

harvesting complexes, involved in photo-oxidative protection, serve as precursors of the hormone abscisic acid and provide color in flowers and fruits to attract pollinators helping to disperse pollen and seeds (Hirschberg, 2001; DellaPenna and Pogson, 2006). In humans, carotenoids have been associated with a reduced risk of cancer, decreased cardiovascular diseases, reduced risk of cataract and age-related mascular degeneration, and increased levels of iron absorption (Garcia-Casal, 2006; Van den Berg *et al.*, 2000; Mares-Perlman *et al*., 2002). The best known activity of carotenoids, however, is as precursors of vitamin A (retinol).

Although there is limited genetic information about carotenoid biosynthesis in sorghum, the pathway has been thoroughly studied in other species such as maize, tomato, and *Arabidopsis (*Hirschberg, 2001; Thorup *et al.*, 2000; DellaPenna and Pogson, 2006). Understanding the genetic mechanisms involved in the synthesis and regulation of carotenoids in sorghum endosperm is a necessary step to breed high-carotenoid sorghum. Phytoene synthase (PSY) is the enzyme responsible for the first committed step of the pathway in which two molecules of geranyl geranyl diphosphate (GGDP) are condensed to form phytoene. PSY catalyzes a rate-limiting step and has been found to be associated with major QTL in several species (Thorup *et al*., 2000; Palaisa *et al.*, 2003; Wurtzel *et al*., 2004; Gallagher *et al.*,2004; Pozniak *et al*.,2007). In maize, the phytoene synthase family includes PSY1, mainly expressed in leaves, embryo, and in the endosperm, if it is yellow, PSY2, expressed in all tissues and endosperm irrespective of the color, (Gallagher *et al*., (2004); and a recently identified PSY3, highly expressed in embryo and roots particularly in response to abiotic stress (Li *et al*., 2007; Maria*et al.*, 2008).

## 2.6 Heritability of Pro-Vitamin A and other agronomic traits

Heritability is an important parameter in breeding program. It indicates how much of the phenotypic variability can be transmitted to the next generation (falconer, 1981; Akhshi *et al*. (2014). The magnitude of such estimates also suggests the extent to which improvement is possible through selection. An analogous research on beans was reported by Nechifor *et al.* (2011) that numbers of pod per plant and numbers of seed per pod have medium heritability values and high genetic advance.

High broad sense heritability for total carotenoids was reported by Chander *et al.* (2008) wherein 85% broad sense heritability for total carotenoids in a maize recombinant inbred lines population. Moderate to high heritability estimates for carotenoids have also been reported in the past for maize Wurtzel *et al.* (2004). High heritability of pro-vitamin A could be due to the involvement of a few major genes in the carotenoid biosynthetic pathway Pfeiffer and McClafferty (2007). Biradar *et al.* (1996) stated that high heritability was associated with high genetic advance. Khanure, (1993); Biradar *et al*. (1996); Rao and Patil (1996); Reddy *et al*. (1996); Tiwari *et al*. (2003); and Veerabadhiran and Kennedy (2001) reported high heritability for panicle length. Umakanth *et al*. (2004) and Umakanth and Kuriakose (2005) reported that estimates of variance indicated predominance of non-additive gene action for panicle length. Khanure (1993); Biradar *et al*. (1996); Rao and Patil (1996); Reddy *et al*. (1996); Nguyen *et al.* (1997); Tiwari *et al*. (2003); and Veerabadhiran and Kennedy (2001) reported high heritability for 100 grain weight. High heritability coupled with high genetic advance for 100 grain weight was reported by Khanure (1993); Biradar *et al*. (1996); Reddy *et al*.(1996); Nguyen *et al*. (1997); Prabhakar (2001); Veerabadhiran and Kennedy (2001); Umakanth *et al*.(2004); and Deepalakshmi and

Ganesamurthy (2007) reported that high heritability combined with low genetic advance was recorded for test weight. Khanure (1993); Biradar *et al*. (1996); Rao and Patil (1996); Reddy *et al*. (1996); Tiwari *et al*. (2003); and Veerabadhiran and Kennedy (2001) reported high heritability for days to 50% flowering. Deepalakshmi and Ganesamurthy (2007); and Jain and Patel (2012) in their studies on genetic variability in sorghum reported high heritability accompanied with high genetic advance as per cent of mean for days to 50 per cent flowering in sorghum suggesting that the character was under additive gene action and thus gives wider scope for selection.

Tiwari *et al*. (2003); Kishor and Singh (2005)reported high genetic advance for days to 50 per cent flowering in sorghum. Khanure (1993); Biradar *et al*. (1996); Rao and Patil (1996); Reddy *etal*. (1996); Tiwari *et al*. (2003); and Veerabadhiran and Kennedy (2001) reported high heritability for plant height. Deepalakshmi and Ganesamurthy (2007) and Jain and Patel (2012) revealed high heritability accompanied with high genetic advance as per cent of mean for plant height suggesting that the character was under additive gene action and thus gives better scope for selection.

**2.7 Correlation Coefficient**

Before placing strong emphasis on breeding for nutritional quality characters, knowledge of the association between yield and yield attributes and also interrelations between yield and nutritional quality traits will enable the breeder to carry out simultaneous improvement of yield and nutritional traits. The correlation coefficient helps to identify characters that are associated positively and negatively. The existence of correlation may be attributed to presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or a combination of all.

Egesel *et al*. (2003) reported highly significant difference and positive correlation between grain yield and total carotenoids (pro-vitamin A). This result indicates that opportunities exist to increase β carotene in yellow endosperm in maize without lowering grain yield and other desirable agronomic traits.Also, Willy*et al.* (2014) reported grain yield was not significantly correlated with pro-vitamin A concentration in maize, indicating that both traits could be improved simultaneously.

Godbharle *et al.* (2010) found that the trait, test weight, had positive and non-significant association with grain yield per plant. Potdukhe *et al*. (1994); Sankarapandiyan *et al*. (1996); Veerabadhiran and Kennedy (2001); Ezeaku and Mohammed (2006); Sharma *et a*l. (2006); Elangovan *et al.* (2007); Warkad *et al*. (2010); Mahajan *et al*. (2011); and Ali *et al*. (2012) studied correlations in sorghum genotypes and revealed that the grain yield was positively and significantly correlated with 100-grain weight. Iyanar *et al*. (2001) also reported direct contribution of 100- seed weight on grain yield. Sharma, *et al*. (2006); and Mahajan *et al*. (2011) reported significant positive association of grain yield with days to 50 per cent flowering. Potdukhe *et al*. (1994) reported weak correlations between grains yield/plant and days to 50% flowering. Godbharle *et al*. (2010); and Ali *et al*. (2012) reported that the correlation between grain yield/plant and days to 50% flowering was negative and weak. Jeyaprakash *et al*. (1997); Iyanar *et al*. (2001); Veerabadhiran and Kennedy (2001); Ezeaku and Mohammed (2006); Mahajan *et al.* (2011); Ali *et al*. (2012); and Vijaya Kumar *et al*. (2012) revealed that grain yield was significantly positively correlated with plant height. Potdukhe *et al*. (1994) reported weak correlation between grain yield/plant and plant height. Potdukhe *et al*. (1994); Jeyaprakash *et al.*(1997); Iyanar *et al*. (2001); Tiwari *et al*. (2003); Umakanth *et al*. (2004); Aruna and Audilakshmi (2008);

Makanda *et al*. (2010); Chavan *et al*. (2011); and Mahajan *et al*. (2011) reported that grain yield showed significant positive correlation with panicle length. However, Panicle length recorded non-significant association with grain yield in sorghum (Potdukhe *et al*. 1994; Jayprakash *et al.* 1997; Chavan *et al*. 2011).

Highly significant positive correlation coefficient between grain yield and panicle weight were observed in sorghum (Raut *et al*., 1994; Potdukhe *et al.,* 1994; Jeyaprakash *et al*., 1997; Iyanar *et al*., 2001; Ezeaku and Mohammed 2006; Deepalakshmi and Ganesamurthy, 2007). Mallinath *et al*. (2004); Ambekar *et al*. (2000); and Mahajan *et al*. (2011) reported that panicle length had non-significant association with days to 50% flowering. Vijaya Kumar *et al*. (2012) reported that panicle length showed positive significant association with panicle weight. Aruna and Audilakshmi (2008) reported that panicle weight was significantly positively correlated with panicle length. Ezeaku and Mohammed (2006); Aruna and Audilakshmi (2008); Vijaya Kumar *et al*. (2012) noticed that panicle weight was highly correlated with 100-grain weight. Iyanar *et al*. (2001); Veerabadhiran and Kennedy (2001); and Aruna and Audilakshmi (2008) reported that panicle weight was highly correlated with plant height. Sharma *et al*. (2006) reported that days to 50% flowering showed highest positive correlation with 100 seed weight. Non-significant positive association was observed between days to 50% flowering and plant height in sorghum by Warkad *et al*. (2010).

### 2.8 Gene Action of Pro Vitamin A

Generation mean analysis provides information on the relative importance of additive and dominance effects in populations created from two inbreds. It involves measuring the means of different generations ($P_1$, $P_2$, $F_1$, $F_2$, $BC_1P_1$, $BC_1P_2$, etc.) derived from two inbreds

and interpreting the means in terms of the different genetic effects because the actual means of single loci are unobservable (Bernardo, 2002). Generation means also estimate the pooled genetic effects across loci. Generation mean analysis is most useful when the two parents differ greatly in favorable alleles; that is when one parent has most, if not all, of the favorable alleles and the other parent has few, if any, favorable alleles. The pooled estimates of effects are summed across all loci for which $P_1$and $P_2$ differ. Generation mean analysis has been commonly used to study disease resistance, where one parent has high resistance and the other has high susceptibility (Bernardo, 2002).

Egesel, *et al.* (2003) showed the number of maize alleles for yellow maize endosperm colour was directly related to the amount of PVA pigments but the number of alleles did not affect the proportion of the different pigments. Mangelsdorf and Fraps (1931); Johnson and Miller (1938); Randolph and Hand (1940) showed PVA levels in $F_1$ seed tended to be a little lower than mid parents value indicating some dominance for low pro-vitamin A. Total carotenoid levels tended to be higher than expected, indicating partial dominance gene action for total carotenoid concentration. Brunson and Quackenbush (1962); Egesel *et al.* (2003) found considerable genetic variation among a group of 10 yellow endosperm inbred for five carotenoid compounds.

# CHAPTER THREE

# 3.0 MATERIALS AND METHODS

## 3.1 Materials

### 3.1.1 Description of experimental site

The research was conducted at the Field Trial site of the Institute for Agricultural Research (IAR), Samaru in Ahmadu Bello University, Zaria, Kaduna State, Nigeria. Samaru is located on latitude $11^0$ 11'N, longitude $7^0$ 38'E, and 686 m above sea level in the Northern Guinea savannah ecological zone of Nigeria. The average annual rainfall of the area is about 1,058 mm which is distributed within 160 days (May – September). The temperature distribution is fairly uniform with a mean daily temperature of $27^0$C. The soil is mostly sandy loam (Hamma *et al.* 2012)

### 3.1.2 Description of experimental materials

The plant materials used in this study comprised of five (5) IAR sorghum genotypes: SAMSORG 17, SAMSORG 43, SAMSORG 44, SAMSORG 14 and CSR01 (Table 3.1). The first four were obtained from the Institute for Agricultural Research (IAR) Cereal Research Program, while CSR01 was obtained from Nigerian Brewery. These varieties were chosen because of the fact that they constitute part of the most commonly grown cultivars by the farmers within the sorghum ecological zones. SAMSORG 17 and SAMSORG 43 were also chosen because of their improved level of PVA so as to bring unique alleles to the gene pool.

**Table 3.1 Morphological Description of Sorghum Genotypes Used In This Study**

| Cultivar | Origin | Description | Brix Content (Pro-vitamin A) mg/l |
|---|---|---|---|
| SAMSORG 17 | IAR | Semi-dwarf, semi-compact elliptic ear head; medium sized yellow seed. Late maturing 160-180 days. Plant height: 140-150 cm. potential yield 1,800- 3,000 kg/ha. | 19.695 |
| SAMSORG 43 | IAR | Yellow Medium size seeds. Medium maturing at 105-120 days. Plant height: 160-170 cm. potential yield 2,500-3,000 kg/ha. Type of variety: pure line (open pollinated). | 10.572 |
| SAMSORG 44 | IAR | Type of variety: pure line (open pollinated). Matures between 95-100 days. Plant height 110-120 cm potential yield 2,000-2,500 kg/ha. Medium white seeds. | 5.038 |
| SAMSORG 14 | IAR | Pure line selection by modified bulk method. Tall fairly long, elliptical and semi compact ear head, tan coloured glumes white seed. Medium maturing (140-150 days). Plant height: 150-160 cm. Potential yield 1,500- 3000 kg/ha. | 3.981 |
| CSR01 | NB | Tall plant with medium white seeds. Medium maturing at 120-130 days. Plant height 170-180 cm. Potential yield 2,000- 3,000 kg/ha. | 3.718 |

Sources: IAR: Institute for Agricultural Research, NB: Nigerian Brewery

## 3.2 Methods

### 3.2.1 Population development

#### *3.2.1.1 The $F_1$ hybrids*

In the 2013 main season (June to September), the parents seeds ($P_1$, $P_2$, $P_3$, $P_4$ and $P_5$,) were sown in order to make crosses between the yellow endosperm varieties (male) and the white endosperm varieties (female) using North Carolina Design II (factorial mating design). Staggered planting of the genotypes was adopted in order to synchronize the flowering period and subsequent pollination. SAMSORG 17, SAMSORG 43, SAMSORG 44, SAMSORG 14 and CSR01, were sown in 15 row plots each measuring 5 m long, with a spacing of 0.75 m between rows and 0.30 m between plants within a row. All agronomic practices such as land preparation, ridging, fertilizer application, weeding were done. SAMSORG 44, SAMSORG 14 and CSR01 designated as female parents were hand emasculated using cellophane bags to abort their pollen because they are not male sterile cultivars and used as females and were pollinated with the male parent SAMSORG 17, SAMSORG 43 to produce $F_1$ seeds.

#### *3.2.1.2 The $F_2$ populations*

In the 2014 dry season (January to June), the $F_1$ hybrids developed from the crosses in 2013, together with the parental lines were sown in the Institute for Agricultural Research (IAR) Samaru irrigation field. Standard agronomic practices were carried out to maintain field. At heading, $F_1$ plants were selected at random in each cross and their panicles covered

with paper bags to ensure complete selfing. Seeds from the selfed plants in each cross were harvested at maturity, threshed and kept in clearly labeled bags as $F_2$ seeds.

*3.2.1.3 The backcross population*

From the same plot used to produce the $F_2$ seeds, 10 plants for each replication were randomlyselected and the heads were covered with paper bags. 10 plants for each replication were also selected from the parental lines and emasculated. The $F_1$ of each cross were backcrossed to the parental ($P_1$, $P_2$, $P_3$, $P_4$ and $P_5$) to generate $BC_1P_1$, $BC_1P_2$, $BC_1P_3$, $BC_1P_4$ and $BC_1P_5$ by hand pollination. At maturity, seeds developed from the plants were harvested and kept in labeled bags as backcrossed seeds.

3.2.2 Evaluation of populations

The five parental lines, six each of $F_1$, $F_2$, and the backcross populations were evaluated in the 2014 main season at the IAR Research farm. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications.Plot size for non-segregating populations ($P_1$, $P_2$ and $F_1$) was 2 rows of 4 m long and 0.75 m apart and the segregating populations ($F_2$, $BC_1P_1$and $BC_1P_2$) were 5 rows of 4 m length and 0.75 m apart, the inter – row spacing was 0.30 m with two plants per hill in every plot. All the agronomic practices such as land preparation, ridging, fertilizer application, weeding were observed.

3.2.3 Compositional analysis for vitamin A

Compositional analysis for Vitamin A was carried out at the National Research Institute for Chemical Technology (NARICT).

At the onset of this research work the parents were analyzed to determine the PVA concentration while at the end of the evaluation period the $F_1$s and the segregating populations ($F_2$s, and the backcrosses) were also analyzed.

3.2.4 Data collection

The following agronomic data were collected:

Days to Fifty Per Cent (50%) Flowering: The numbers of days from the day of sowing to the days 50% of plants have floweredwere recorded as days to 50% flowering.

Plant Height (cm): Plant height recorded on 10 randomly selected plants per plot for non-segregating generations and 50 plants per plot for segregating generations from ground level to the tip of the ear head of the plant at physiological maturity.

Panicle length (cm): Panicle length was measured from base of the Panicle using a meter rule.

Panicle Weight (g): Mean weight of fully dried panicles was taken randomly from 10 plants per plot for 3 replications for non-segregating generations and 50 plants per plot for segregating generations were recorded as grams per plant.

Grain Weight per panicle (g):Grains separated from the panicle of each plant were weighed and the weight of the grains recorded in grams.

One Thousand Grain Weight (g): The weights of 1000-grains from each of the selected plants were recorded in grams.

$$\text{Grain yield per panicle (g ha}^{-1}) = \frac{\text{Grain Weight per panicle (g)}}{\text{Plot area (m)}} \times 10{,}000$$

Composition analysis for PVA (mg/l)

0.5 g of each sample was weighed and placed in test tubes, then 5 ml of methanol solvent was added and allowed to stand for 10 minutes so as to extract properly, after which the sample was filtered. One ml of the filtrate was removed and poured in a cuvette and then run in the UV-Visible Spectrometer. The concentration and wavelength readings at absorption were taken. Rutkowski and Grezegorczy (2007)

### 3.3 Statistical Analysis

3.3.1 Analysis of variance (ANOVA)

Analysis of Variance was conducted using the General Linear Model (GLM) procedure of the Statistical Analysis System (SAS) version 9.0 Software (2002). Least Significant Difference Test Fisher, (1935) was used to separate the means where significant differences exist.

The standard linear model for an RCBD (Layman and Michael, 2010) is as follows:

$$y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}\ i = 1.....a,\ j = 1.....b$$

Where: $y_{ij}$ = An observation in treatment i and block j

$\mu$ = The overall mean $\alpha_i$ = the effect of treatment

$\beta_j$ = The effect of block j $e_{ij}$ = Random error with mean 0 and variance $\sigma^2$

$a$ = The number of treatments; b = the number of blocks.

**Table 3.2 Form of ANOVA for RCBD**

| Source of variation | df | *MS* | *EMS* |
|---|---|---|---|
| Replication | $(r-1)$ | | |
| Genotypes | $(g-1)$ | $MS_g$ | $\sigma_e^2 + r\sigma_g^2$ |
| Error | $(r-1)(g-1)$ | $MS_e$ | $\sigma_e^2$ |

Where: $\sigma_g^2$ = genotypic variance $\sigma_e^2$ = error variance

$r$ = Number of replications g = Number of genotypes

$MS_g$ = Mean square due to genotype $MS_e$ = Error mean square

3.3.2 Coefficients of Variation

The coefficient of variation was calculated to measure the relative variability of given populations. Variance estimates have units attached to them. A common application of variance is the test to find out if one biological sample is more variable for one trait than for another. The coefficient of variation facilitates the comparison because it is unit free. The coefficient of variation (CV) is calculated as: CV = $(S/\overline{X}) \times 100$

Where S = Standard deviation, and $\overline{X}$ = mean

3.3.3 Estimation of heritability

Broad and narrow sense heritability estimates were obtained using the variance component methods. The $F_2$ variances were used to compute the broad sense heritability according to Roham *et al.* (2011) as given below.

$$H_{(B)} = \frac{\sigma^2 F_2 - \sqrt{\sigma^2 P_1 X \sigma^2 P_2}}{\sigma^2 F_2} X100$$

Where: $\sigma^2 F_2 = \sigma^2 G + \sigma^2 E$, $\sigma^2 P_1 = \sigma^2 E_1$, $\sigma^2 P_2 = \sigma^2 E_2$

In these relationships

$H_{(B)}$ = Broad sense heritability

$\sigma^2 F_2$ = Phenotypic variance of $F_2$ population of a cross

$\sigma^2 G$ = Genotypic variance of the $F_2$ population of a cross

$\sigma^2 E$ = Environmental variance of $F_2$ population of a cross

Narrow sense heritability estimates was computed using the formulae described by Roham *et al.* (2011).

$$H_{(N)} = \frac{2\sigma^2 F_2 - \left(\sigma^2 B_1 + \sigma^2 B_2\right)}{\sigma^2 F_2}$$

Where $H_{(N)}$ = narrow sense heritability

$$\sigma^2 F_2 = 1/2 A + 1/4 D + E$$

$$\sigma^2 B_1 + \sigma^2 B_2 = \tfrac{1}{2} A + \tfrac{1}{2} D + E$$

$$2\sigma^2 F_2 - \sigma^2 B_1 - \sigma^2 B_2 = A + \tfrac{1}{2} D + 2E - \left(\tfrac{1}{2} A + \tfrac{1}{2} D + 2E\right) = \tfrac{1}{2} A$$

A = additive variance

D = dominance variance

E = environmental variance

$B_1$ = backcross to parent $P_1$

$B_2$ = backcross to parent $P_2$

$F_2$ = second filial generation

The heritability percentage was categorized as low, moderate and high (Robinson *et al.*, 1949, Feyissa *et al.* 2014).

0-30% = low

30-60 % =moderate

60-100%=high

3.3.4 Correlation analysis

Correlation coefficients were estimated using the formula given bySingh and Chaudhary (1985) and Bozokalfa et al. (2010) $r_{xy} = \frac{\text{cov}(xy)}{\sqrt{\text{var}(y)\,\text{var}(x)}}$

Where: $\text{cov}(xy)$ = covariance of traits x and y

Var(y) =variance of y Var(x) = variance of x

3.3.5 Scaling Tests

The following Mather's scaling tests (Mather, 1949) were applied to detect presence or absence of epistasis (gene interactions) and their type (Akhshi *et al*. 2014).

$A = 2BC_1P_1 – P_1 – F_1$

$B = 2BC_1P_2 – P_2 – F_1$

$C = 4F_2 – 2F_1 – P_1 – P_2$

$D = 2F_2– BC_1P_1 – BC_1P_2$; where, $P_1$, $P_2$, $F_1$, $F_2$, $BC_1P_1$ and $BC_1P_2$ are the mean values of the respective generations. The variances of A, B, C and D were calculated as follows:

$VA = 4VBC_1P_1 + VP_1 + VF_1$

$VB = 4VBC_1P_2 + VP_2 + VF_1$

$VC = 16VF_2 + 4VF_1 + VP_1 + VP_2$

$VD = VF_2 + VBC_1P_1 + VBC_1P_2$; Where, VA, VB, VC and VD are variances of A, B, C and D, respectively, while $VP_1$, $VP_2$, $VF_1$, $VF_2$, $VBC_1P_1$ and $VBC_1P_2$ are the variances of means of the respective generations. The standard errors of A, B, C and D were worked out by taking square root of the respective variances and 't' values calculated by dividing the effects of A, B, C and D by their respective standard errors. The calculated 't' values were compared against 1.96 which is the table value of 't' at 5% level of significance. The values of A, B, C and D should be equal to zero within the limits of their standard error. The significance of any one of these scales is taken to indicate the presence of non- allelic interactions (Singh and Chaudary 1985).

3.3.6 Generation Mean Analysis (GMA)

To estimate the mode of gene interaction, GMA was used following the procedure described by Hayman (1958), and revised by Gamble (1962), Weerapun *et al.* (2010).

*3.3.6.1Three Parameter Model*

The model described by Cavalli (1952) using the weighted least square (Q) technique was employed using three parameters viz.,m (mean), d (additive) and h (dominance) to test the adequacy of additive-dominance model. However, the calculated chi-square ($\chi^2$) value at 3 degrees of freedom was used to test the goodness of fit of the model if and only if more than three families are available.

$$\bar{p}_1 = m - a$$

$$\bar{p}_2 = m + a$$

$$\bar{F}_1 = m + d$$

$$\bar{F}_2 = m + 1/2(d)$$

$$\overline{BCP}_1 = m - (1/2)a + (1/2)d$$

$$\overline{BCP}_2 = m + (1/2)a + (1/2)d$$

Where; m = mean

a = value of additive gene effects

d = value of dominance gene effects

*3.3.6.2 Hayman's Six Parameter Model*

To obtain information on the nature of gene effects governing the traits under study, all the six components of generation means were computed.

This analysis allows the estimation of the following genetic parameters:

Mean = m

Additive = d

Dominance = h

Additive × additive = i

Additive × dominance = j

Dominance × dominance = l

Means of six generations *viz.*, $P_1$, $P_2$, $F_1$, $F_2$, $BC_1P_1$ and $BC_1P_2$ were used to estimate the six parameters by following the equation given by Hayman (1958), Weerapun *et al.* (2010).

$$m = \overline{F_2}$$

$$d = \overline{BC_1P_1} - \overline{BC_1P_2}$$

$$h = \overline{2BC_1P_1} + \overline{2BC_1P_2} + \overline{F_1} - \overline{4F_2} - \overline{\tfrac{1}{2}P_1} - \overline{\tfrac{1}{2}P_2}$$

$$i = \overline{2BC_1P_1} + \overline{2BC_1P_2} - \overline{\tfrac{1}{2}P_1} + \overline{\tfrac{1}{2}P_2}$$

$$j = \overline{BC_1P_1} - \overline{BC_1P_2} - \overline{\tfrac{1}{2}P_1} + \overline{\tfrac{1}{2}P_2}$$

$l = \overline{P_1} - \overline{P_2} + \overline{\frac{1}{2}F_1} + \overline{4F_2} + \overline{4BC_1P_1} - \overline{4BC_1P_1}$

The variances of the estimates of gene effects were obtained as follows.

V (m) = $VF_2$

V (d) = $VBC_1P_1 + VBC_1P_2$

V (h) = $4(BC_1P_1 + BC_1P_2) + VF_1 + 16VF_2 + ½ (VP_1 + VP_2)$

V (i) = $4V (BC_1P_1 + BC_1P_2) + 16V F_2$

V (j) = $VBC_1P_1 + VBC_1P_2 + ¼ (VBC_1P_1 + VP_2)$

V (l) = $VP_1 + VP_2 + 4VF_1 + 16(VF_2 + VBC_1P_1 + VBC_1P_2)$

Where, V(m), V(d), V(h), V(i), V(j) and V(l) are the variances of m, d, h, i, j and l, respectively. $VP_1$, $VP_2$, $VF_1$, $VF_2$, $VBC_1P_1$ and $VBC_1P_2$ are the variances of the mean. To test the significance of the estimates, the 't' values calculated for each component were obtained by dividing the gene effect of respective components by their respective standard error (SE) as given below:

$$t(m) = \frac{m,}{SE(m)}, \quad t(d) = \frac{d,}{SE(d)}, \quad t(h) = \frac{h,}{SE(h)}, \quad t(i) = \frac{i,}{SE(i)}, \quad t(j) = \frac{j,}{SE(j)}, \quad t(l) = \frac{l}{SE(l)}$$

3.3.7 Genetic Advance (GA)

Genetic Advance (GA) was calculated in accordance with the method described by Allard (1960), Wolie *et al.* (2013) as: GA= $h_n^2\sqrt{\sigma_P^2}$ × K at 10 % selection intensity**,** Where, K is the standardized selection differential, at 10 % selection intensity, K=1.755and GA (as % of the mean) = $\left[\frac{(GA)}{\overline{X}}\right]X100$ Where, k = selection differential (at 10% selection intensity), $\sigma_p$ = phenotypic standard deviation, $h_n^2$ = Narrow sense heritability and $\overline{X}$ = grand mean. Falconer and Mackay (1996) classified genetic advance as percent of mean as low (0-10%), medium (10 - 20%) and high (20% and above).

# CHAPTER FOUR

# 4.0 RESULTS

## 4.1 Analysis of Variance for PVA and other Agronomic traits

The variances among the six generations for each cross were highly significant ($P < 0.01$) for all measured traits (Table 4.1).

## 4.2 Mean Performance

Pro-Vitamin A in the cross SAMSORG 17 × SAMSORG 44 across the six generations recorded amean of 7.87 mg/lfor the $F_1$ generation and a mean of 19.70 mg/lfor $P_1$ and5.04 mg/lfor $P_2$(Table 4.2).The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for PVA of 8.93 mg/l, 6.41 mg/l and 8.76 mg/l respectively. $F_1$ (7.872) mg/l was significantly ($P < 0.05$) different from $P_1$ (19.70) mg/l but not significantly different ($P < 0.05$) from $P_2$ (5.04) mg/l. $F_1$ generation 1208.81 kg $ha^{-1}$ was the top performing generation with regards to yield for this cross.

A mean of 112.0 days was recorded for days to 50% flowering in the same cross for $F_1$ generation. The parent generations had mean of 110.0 days for $P_1$ and76.0 daysfor $P_2$ generation.The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for days to 50% flowering of 107.0 days, 83.0 days and 90.0 days respectively. The mean for this trait among the six generations for this cross are significantly different except $F_1$ which was not significantly($P < 0.05$) differentfrom $P_1$ and $BCP_1$.

Table 4.1 Mean squares for pro-vitamin A concentration and other agronomic traits involving SAMSORG 17, SAMSORG 44, SAMSORG 43, SAMSORG 14 and CSR01

| Source of Variation | Degrees of Freedom | Days to 50% flowering | Plant Height (cm) | Panicle Length (cm) | Panicle Weigh (g) | Grain Weight (g) | 1000–Grain Weight (g) | Pro-vitamin A (mg/l) | Grain Yield (kg/ha) |
|---|---|---|---|---|---|---|---|---|---|
| **CROSS 1 (SAMSORG 17 × SAMSORG 44)** | | | | | | | | | |
| Generation | 5 | 14512.9** | 40348.7** | 95.6** | 136818.7** | 134930.1** | 2325.4** | 964.3** | 2665286.0** |
| Replication | 2 | 1.9 | 520.8 | 0.0 | 123.2 | 102.7 | 45.0 | 0.2 | 2034.0 |
| Error | 10 | 80.3 | 381.3 | 4.1 | 825.2 | 825.7 | 57.1 | 6.8 | 16309.9 |
| **CROSS 2 (SAMSORG 17 × SAMSORG 14)** | | | | | | | | | |
| Generation | 5 | 9048.5** | 116250.3** | 81.9** | 101452.0** | 102779.3** | 1032.0** | 1984.0** | 2030209.0** |
| Replication | 2 | 1.1 | 29.3 | 2.8 | 324.5 | 180.1 | 27.2 | 0.1 | 3557.5 |
| Error | 10 | 44.7 | 688.7 | 4.2 | 1184.2 | 1368.8 | 43.9 | 5.3 | 27037.3 |
| **CROSS 3 (SAMSORG 17 × CSR01)** | | | | | | | | | |
| Generation | 5 | 5279.6** | 154653.4** | 103.3** | 223022.9** | 219491.9** | 2108.1** | 2098.1** | 4335643.0** |
| Replication | 2 | 10.3 | 119.3 | 3.0 | 124.5 | 125.8 | 31.7 | 1.6 | 2484.6 |
| Error | 10 | 25.8 | 761.3 | 3.8 | 1153.5 | 1209.1 | 49.0 | 4.5 | 23883.3 |
| **CROSS 4 (SAMSORG 43 × SAMSORG 44)** | | | | | | | | | |
| Generation | 5 | 2946.1** | 76852.8** | 727.3** | 11939.2** | 14762.8** | 4092.9** | 679.5** | 291610.8** |
| Replication | 2 | 120.3 | 774.6 | 4.5 | 5.2 | 232.9 | 48.0 | 17.6 | 4601.0 |
| Error | 10 | 57.5 | 461.0 | 17.1 | 508.6 | 701.5 | 63.2 | 5.8 | 13856.8 |
| **CROSS 5 (SAMSORG 43 × SAMSORG 14)** | | | | | | | | | |
| Generation | 5 | 1169.4** | 69457.5** | 701.8** | 37556.3** | 40838.3** | 2813.5** | 861.2** | 806682.4** |
| Replication | 2 | 21.3 | 1835.2 | 36.3 | 90.2 | 55.4 | 38.5 | 1.2 | 1095.1 |
| Error | 10 | 26.9 | 1052.0 | 32.7 | 463.3 | 524.4 | 88.0 | 4.2 | 10357.6 |
| **CROSS 6 (SAMSORG 43 × CSR01)** | | | | | | | | | |
| Generation | 5 | 1583.7** | 128003.9** | 547.7** | 93041.9** | 88612.8** | 2178.9** | 735.7** | 1750375.9** |
| Replication | 2 | 19.4 | 293.5 | 11.6 | 2288.0 | 679.0 | 24.6 | 0.0 | 13412.4 |
| Error | 10 | 27.5 | 1046.8 | 13.4 | 2875.4 | 2519.0 | 51.3 | 5.7 | 49757.2 |

Table 4.2 Mean performance of pro-vitamin A and other traits of six generations of sorghum cross SAMSORG 17 × SAMSORG 44 evaluated at Samaru in 2014

| Generations | Days to 50% flowering | Plant Height (cm) | Panicle Length (cm) | Panicle Weight (g) | 1000 Grain Weight (g) | Pro-vitamin A (mg/l) | Grain Yield (kg/ha) |
|---|---|---|---|---|---|---|---|
| $P_1$ (SAM 17) | 110.27 | 180.63 | 37.86 | 293.00 | 14.67 | 19.70 | 1229.47 |
| $P_2$ (SAM 44) | 75.70 | 116.33 | 36.33 | 195.90 | 24.00 | 5.04 | 791.85 |
| $F_1$ | 112.20 | 189.00 | 39.30 | 292.67 | 33.00 | 7.87 | 1208.81 |
| $F_2$ | 90.12 | 178.89 | 38.33 | 252.77 | 25.73 | 8.76 | 1042.70 |
| $BCP_1$ | 106.46 | 175.39 | 36.82 | 279.10 | 16.73 | 8.93 | 1161.66 |
| $BCP_2$ | 82.71 | 144.81 | 36.38 | 200.80 | 21.40 | 6.41 | 815.17 |
| Mean | 94.15 | 165.63 | 37.28 | 246.94 | 21.72 | 8.50 | 1018.21 |
| LSD (0.05) | 10.35 | 22.55 | 2.34 | 33.17 | 8.73 | 3.00 | 147.47 |
| CV (%) | 9.52 | 11.79 | 5.43 | 11.63 | 34.79 | 30.56 | 12.54 |

Plant height in SAMSORG 17 × SAMSORG 44 recorded a mean of 189.0 cmfor the $F_1$ generation and a mean of 180.63 and 116.33 cm were recorded for $P_1$ and$P_2$ respectively(Table 4.2).The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for plant height of 175.4 cm, 144.8 cm and 178.9 cm respectively.There were significant differences among the populations for plant height in this cross. The $F_1$ were the tallest and yielded more but were not significantly ($P < 0.05$) differentfrom the $F_2$.In the same cross panicle length had a mean of 39.30 cmfor the $F_1$ generation, 37.86 cm for $P_1$ and 36.33 cmfor $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean panicle length of 36.82 cm, 36.38 cm and 38.33 cm respectively. $F_1$ was the top performing generation with respect to yield and also recorded the longest length which was not significantly($P < 0.05$)differentfrom $P_1$ and $F_2$.

SAMSORG 17 × SAMSORG 44 for panicle weight recorded a mean of 292.67 g for $F_1$ generation, 293.0 g for $P_1$ and195.9 gfor $P_2$ (Table 4.2). The $F_1$ generation recorded the heaviest while $P_2$ was the lightest.The mean for this trait among the six generations for this cross were significantly($P < 0.05$) different. One thousand Grain weight in the cross SAMSORG 17 × SAMSORG 44 had a mean of 14.67 g for $P_1$ generation and a mean of 24.0 gfor $P_2$. The $F_1$generation recorded mean of 33.0 g. The segregating generations $F_2$, $BC_1P_1$ and$BC_1P_2$, recorded a mean of 25.73 g, 16.73 g and 21.40 g respectively. $F_1$ was significantly ($P < 0.05$) differentthe parent generations.

PVA in the cross SAMSORG 17 × SAMSORG 14 a mean of 5.76 mg/l was recorded for the $F_1$ generation while for parent generationsmean of 19.70 mg/l was recorded for $P_1$ and3.98 mg/l for $P_2$(Table 4.3). The segregating generations $BC_1P_1$, $BC_1P_2$, and $F_2$ recorded mean values for PVA, 9.01 mg/l, 1.65 mg/l and 6.78 mg/l respectively.$F_1$ 5.762 mg/l was significantly ($P < 0.05$) different from $P_1$ and the backcrosses and the top performing for PVA in this cross also days to 50% flowering had a mean of 112.0 days for the $F_1$ generation, 110.0 days for $P_1$ and86.0 days for $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for days to 50% flowering of 105.86 days, 86.34 days and 94.86 days respectively. The means for this trait for the six generations are significantly($P < 0.05$)differentexcept $F_1$ which was not significantly($P < 0.05$) differentfrom $P_1$.

In SAMSORG 17 × SAMSORG 14plant height produced a mean of 280.8 cm for the $F_1$ generation, 180.6cm for $P_1$ and 274.97cmfor $P_2$(Table 4.3). There were significant ($P < 0.05$) differences among the generations for plant height in this cross with $F_1$ as the tallest generation with the highest yield. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for plant heights of 188.75 cm, 222.50 cm and 214.01 cm respectively. The $F_1$ generation for panicle length in the cross SAMSORG 17 × SAMSORG 14 was longest and yielded more even though it was not significantly($P < 0.05$) differentfrom the other generationsand recorded a mean value of 38.63 cm for the $F_1$ generation, 37.86 cm for $P_1$ and 36.76 cm for $P_2$. The Segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for panicle length of 37.52 cm, 36.35 cm and 38.51 cm respectively.

Table 4.3 Mean performance of pro-vitamin A and other traits of six generations of sorghum cross SAMSORG 17 × SAMSORG 14 evaluated at Samaru in 2014

| Generations | Days to 50% Flowering | Plant Height (cm) | PanicleLength (cm) | PanicleWeight (g) | 1000-Grain Weight (cm) | Pro-vitamin A (mg/l) | Grain Yield ($kgha^{-1}$) |
|---|---|---|---|---|---|---|---|
| $P_1$ (SAM 17) | 110.27 | 180.63 | 37.86 | 293.00 | 14.67 | 19.70 | 1229.47 |
| $P_2$ (SAM 14) | 85.73 | 274.97 | 36.76 | 194.33 | 17.33 | 3.98 | 786.55 |
| $F_1$ | 111.90 | 280.80 | 38.63 | 295.00 | 23.00 | 5.76 | 1252.00 |
| $F_2$ | 94.86 | 214.01 | 38.51 | 244.59 | 25.33 | 6.78 | 1013.72 |
| $BCP_1$ | 105.86 | 188.75 | 37.52 | 258.10 | 18.93 | 9.01 | 1059.31 |
| $BCP_2$ | 86.34 | 255.50 | 36.35 | 201.90 | 21.13 | 1.65 | 819.96 |
| Mean | 96.84 | 223.76 | 37.51 | 239.18 | 21.22 | 6.48 | 985.16 |
| LSD (0.05) | 7.72 | 30.30 | 2.38 | 39.74 | 7.66 | 2.65 | 189.87 |
| CV (%) | 6.90 | 11.73 | 5.49 | 14.39 | 31.24 | 35.41 | 16.69 |

Panicle weight in the cross SAMSORG 17 × SAMSORG 14 recorded a mean of 295.0 g for the $F_1$ generation, 293.0 g for $P_1$ and194.33 g for $P_2$(Table 4.3). The mean for this trait among the six generations for this cross are significantly different. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for panicle weight of 258.1 g, 201.9 g and 244.6 g respectively. The $F_1$ generation was the heaviest and top performing generation with regards to yield while the $P_2$ was the lightest. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for 1000 grain weight in the cross SAMSORG 17 × SAMSORG 14 18.93 g, 21.13 g and 25.33 g respectively.$F_2$ recorded the highest mean grain weight 25.3 g which was significantly different from the parents, but was not significantly ($P < 0.05$) differentfrom the $F_1$ and the backcross populations.The $F_1$ generation recorded mean of 23.0 gwhile $P_1$ had a mean 14.67 g and $P_2$ had a mean 17.33g.

A mean of 9.71 mg/l was recorded for the $F_1$ generation for PVA in the cross SAMSORG 17 × CSR01 and for the parent generations, amean 19.70 mg/l for $P_1$ and a mean 3.72 mg/l for $P_2$(Table 4.4).The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for Pro-vitamin A as 8.55 mg/l, 1.28 mg/l and 6.01 mg/l respectively. Days to 50% flowering in the cross SAMSORG 17 × CSR01 had a mean of 111.0 days for the $F_1$ generation, 110.0 days for $P_1$ and88.0 daysfor $P_2$. The mean values for this trait among the six generations for this cross are significantly($P < 0.05$) differentexcept the $F_1$ for which was not significantly($P < 0.05$) differentfrom $P_1$ and $BC_1P_1$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for days to 50% flowering as 107.0 days, 93.0 days and 102.0 days, respectively.

Table 4.4 Mean performance of pro-vitamin A and other traits of six generations of sorghum cross SAMSORG 17 × CSR01 evaluated at Samaru in 2014

| Generations | Days to 50% flowering | Plant Height (cm) | Panicle Length (cm) | Panicle Weight (g) | 1000–Grain Weight (g) | Pro-vitamin A (mg/l) | Grain Yield $kgha^{-1}$ |
|---|---|---|---|---|---|---|---|
| $P_1$ (SAM 17) | 110.27 | 180.63 | 37.86 | 293 | 14.67 | 19.7 | 1229.47 |
| $P_2$ CSR01 | 87.67 | 295 | 36.16 | 147.33 | 22.67 | 3.72 | 591.05 |
| $F_1$ | 111 | 295 | 40.27 | 294.83 | 26.67 | 9.71 | 1239.13 |
| $F_2$ | 102.39 | 218.84 | 39.04 | 241.47 | 26.13 | 6.01 | 988.35 |
| $BCP_1$ | 106.5 | 184.72 | 37.47 | 263.33 | 15.8 | 8.55 | 1093.38 |
| $BCP_2$ | 92.57 | 258.96 | 37.39 | 173.5 | 22.67 | 1.28 | 695.74 |
| Mean | 100.9 | 226.85 | 37.99 | 229.26 | 21.5 | 6.24 | 941.5 |
| LSD (0.05) | 5.86 | 31.86 | 2.24 | 39.22 | 8.09 | 2.45 | 178.45 |
| CV (%) | 5.03 | 12.16 | 5.1 | 14.81 | 32.57 | 33.96 | 16.41 |

Plant height in the cross SAMSORG 17 × CSR01 recorded a mean of 295.0 cmfor $F_1$ generation, 295.0 cm for $P_1$ and295.0 cmfor $P_2$ (Table 4.4). The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for plant height as 184.7 cm, 258.9 cm and 218.84 cm respectively. In the cross SAMSORG 17 × CSR01 also panicle length recorded a mean of 40.27 cm for the $F_1$ generation, 37.86 cm for $P_1$ and 36.16 cm for $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for panicle length of 37.5 cm, 37.4 cm and 90.1 cm respectively. The mean for this trait among the six generations for this cross are significantly($P < 0.05$) differentexcept for $F_1$ which was not significantly($P < 0.05$)differentfrom $F_2$. In the same cross panicle weight had a mean of 294.8 g for the $F_1$ generation, 293.0 gfor $P_1$ and 147.3 gfor $P_2$. The $F_1$ generation was the heaviest while $P_2$ was the lightest. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ also recorded mean values for panicle weight as mean 263.3 g, 173.5 g and 241.5 g respectively. The mean for this trait among the six generations for this cross are significantly($P < 0.05$) different.

One thousand grain weight in the cross SAMSORG 17 × CSR01 recorded a mean of 26.67gfor the $F_1$ generation, 14.67 g for $P_1$ and22.67g for $P_2$(Table 4.4).The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values as 15.80g, 22.60 g and 26.13g, respectively. The $F_1$ were the top performing generation with regards to yield andwas significantly ($P < 0.05$) differentfrom $P_1$ and $BC_1P_1$ but not significantly ($P < 0.05$) different from the $F_2$, $P_2$ and $BC_1P_2$. PVA in the cross SAMSORG 43 × SAMSORG 44 recorded a mean of 6.48 mg/lfor $F_1$ the generation which was not significantly different from all other generation. The parent generationrecorded a mean of 10.57 mg/lfor $P_1$

and5.04 mg/l for $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean as 8.68 mg/l, 2.98 mg/l and 7.87 mg/l respectively.

Days to 50% flowering in the same cross had a mean of 99.03 daysfor the $F_1$ generation which was not significantly($P < 0.05$) differentfrom $P_1$(Table 4.5).$P_1$ recorded a mean of 92.97 days and 75.7days for $P_2$.The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for days to 50% flowering of 84.85 days, 80.21 days and 87.41 days respectively.Plant height in the cross SAMSORG 43 × SAMSORG 44, segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for plant height of 168.4 cm, 123.3 cm and 180.9 cm respectively while non-segregation generationsrecorded mean of 200.67cmfor the $F_1$ generationbeen the tallest generation which was not significantly($P < 0.05$) different from $F_2$, 166.5 cm for $P_1$ and116.3 cmfor $P_2$.

In the same cross panicle length recorded a mean of 36 cmfor the $F_1$ generation, 37.51 cm for $P_1$ and 36.33 cm for $P_2$(Table 4.5).The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for panicle length of 29.32 cm, 31.06 cm and 29.68 cm respectively. The mean values for this trait among the six generations for this cross are significantly different except for $F_1$ which was the longest and was not significantly($P < 0.05$) differentfrom $P_1$ and $P_2$. Also in panicle weight $F_1$ generation was the heaviest and recorded a mean of 241.7 g while $P_2$ generation was the lightest with a mean of 195.90 g and $P_1$ had a mean 221.17 g. The Segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values of 213.5 g, 201.14 g and 217.8 g respectively.

Table 4.5 Mean performance of pro-vitamin A and other traits of six generations of sorghum cross SAMSORG 43 × SAMSORG 44 evaluated at Samaru in 2014

| Generations | Days to 50% flowering | Plant Height(cm) | Panicle Length (cm) | Panicle Weight (g) | 1000-Grain Weight (g) | Pro-vitamin A (mg/l) | Grain Yield (kg $ha^{-1}$) |
|---|---|---|---|---|---|---|---|
| $P_1$ (SAM 43) | 92.97 | 166.5 | 37.51 | 221.17 | 19.33 | 10.57 | 901.79 |
| $P_2$ (SAM 44) | 75.7 | 116.33 | 36.33 | 195.9 | 24 | 5.04 | 791.85 |
| $F_1$ | 99.03 | 200.67 | 36.28 | 241.67 | 23 | 6.48 | 997.59 |
| $F_2$ | 87.41 | 180.85 | 29.68 | 217.77 | 21.07 | 7.87 | 873.67 |
| $BCP_1$ | 84.85 | 168.41 | 29.32 | 213.53 | 19.93 | 8.68 | 854.42 |
| $BCP_2$ | 80.21 | 123.28 | 31.06 | 201.14 | 34.4 | 2.98 | 790.21 |
| Mean | 85 | 158.12 | 31.14 | 212.28 | 24.63 | 6.65 | 849.04 |
| LSD (0.05) | 8.76 | 24.79 | 4.77 | 26.04 | 1.99 | 2.78 | 135.93 |
| CV (%) | 8.92 | 13.58 | 13.27 | 10.62 | 32.3 | 36.18 | 13.87 |

One thousand (1000) grain weight in the cross SAMSORG 43 × SAMSORG 44 recorded a mean of 23.0 gfor the $F_1$ generation which was not statistically different from $F_2$ and $P_2$(Table 4.5).$P_1$ had a mean of 19.33 g while $P_2$ recorded a mean 24.00 g.The Segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean for 1000-grain weight of 19.93 g, 34.40 g and 21.07 g respectively.$BC_1P_2$ recorded the highest mean 1000-grain weight 34.40 g which was significantly different from all the other generations.Grain yield in the same cross recorded a mean of 997.59 kg/ha for the $F_1$ generation which was significantly different from $P_2$ and $BC_1P_2$.$P_1$recorded a mean of 901.79 kg/ha and791.85 kg/ha for $P_2$.

PVA in the cross SAMSORG 43 × SAMSORG 14, the segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values of 9.10 mg/l, 2.95 mg/l and 8.87 mg/l, respectively while for the non-segregating generations(Table 4.6). $F_1$ generation had a mean of 6.49 mg/l and was significantly ($P < 0.05$) different from $P_1$, $P_2$, $F_2$ and $BC_1P_1$ and the parent generation recorded a mean of 10.57 mg/l for $P_1$ and a mean of5.04mg/l for $P_2$, while for days to 50% flowering in the same cross $F_1$ generation which was not significantly different from the $F_2$recorded a mean of 100.23 days, 92 days of for $P_1$ and85.73 days for $P_2$.The mean for plant height in the cross SAMSORG 43 × SAMSORG 14 among the six generations are significantly different except the $F_1$ which was not significantly($P < 0.05$) differentfrom $BC_1P_1$.The $F_1$ generation recorded a mean of 264.5 cmwhile $P_1$had mean of 166.5 and 274.9 cmfor $P_2$. The Segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ also recorded mean values for plant height of mean 197.1 cm, 209.1 cm and 189.1 cm respectively.

Table 4.6 Mean performance of pro-vitamin A and other traits of six generations of sorghum cross SAMSORG 43 × SAMSORG 14 evaluated at Samaru in 2014

| Generations | Days to 50% flowering | Plant Height (cm) | Panicle Length (cm) | Panicle Weight (g) | 1000–Grain Weight (g) | Pro-vitamin A (mg/l) | Grain Yield (kg $ha^{-1}$) |
|---|---|---|---|---|---|---|---|
| $P_1$ (SAM 43) | 92.97 | 166.5 | 37.51 | 221.17 | 19.33 | 10.57 | 901.79 |
| $P_2$ (SAM 14) | 85.73 | 274.97 | 36.76 | 194.33 | 17.33 | 3.98 | 786.55 |
| $F_1$ | 100.23 | 264.5 | 41.37 | 249.5 | 18.33 | 6.49 | 1032.93 |
| $F_2$ | 95.79 | 189.12 | 33.06 | 208.4 | 19.67 | 8.87 | 849.08 |
| $BCP_1$ | 94.03 | 197.06 | 31.58 | 234.02 | 29.93 | 9.1 | 963.44 |
| $BCP_2$ | 89.95 | 209.13 | 32.11 | 192.03 | 17.87 | 2.95 | 765.88 |
| Mean | 93.21 | 204.59 | 33.3 | 213.18 | 21.8 | 6.98 | 867.55 |
| LSD (0.05) | 5.99 | 37.45 | 6.6 | 24.85 | 10.83 | 2.38 | 117.52 |
| CV (%) | 5.57 | 15.85 | 17.16 | 10.1 | 43.04 | 29.51 | 11.74 |

Panicle length in the cross SAMSORG 43 × SAMSORG 14 recorded a mean of 41.37 cmfor the $F_1$ generation, of 37.51 cm for $P_1$ and36.76 cm for $P_2$ and $F_1$ which was the longest and was not significantly different($P < 0.05$) from $P_1$ and $P_2$(Table 4.6). The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for panicle length of 31.58 cm, 32.11cm and 33.06 cm respectively.Panicle weight in the same cross recorded a mean of 249.5 g for the $F_1$ generation which was the heaviest while $P_2$ generation was the lightest, and the parent generations recorded a mean of 221.17 g for $P_1$ and194.33 g for $P_2$. The segregating generations, $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for panicle weight of 234.0 g, 192.0 g and 208.4 g respectively.

One thousand (1000) grain weight in the cross SAMSORG 43 × SAMSORG 14 had a mean of 18.33 gfor the $F_1$ generation which was not significantly different ($P < 0.05$) from $F_2$, $P_1$, $BC_1P_2$, and $P_2$(Table 4.6). $P_1$ had a mean of 19.33 g and17.33 g for $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for 1000 grain weight of 29.93 g, 17.87 g and 19.64 g respectively.$BC_1P_1$ recorded the highest mean grain weight for one seeds per panicle as 29.93 g which was significantly different ($P < 0.05$) from $P_2$, $F_1$ and $BC_1P_2$ also grain yield recorded a mean of 10032.93 kg $ha^{-1}$for $F_1$ generation which was the highest yield 1032.933 kg $ha^{-1}$ and was significantly different from $P_1$, $F_2$, $P_2$ and $BCP_2$ while a mean 901.79 kg $ha^{-}1$ was recorded for $P_1$ and75.7 kg $ha^{-1}$ for $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for grain yield of 963.44 kg $ha^{-1}$, 765.88 kg $ha^{-1}$ and 849.08 kg $ha^{-1}$respectively.

PVA in the cross SAMSORG 43 × CSR01 recorded a mean of 6.92 for the $F_1$ generation which was significantly different from the parents and $BC_1P_2$. $P_1$ recorded mean of 10.57 mg/l and3.72 mg/l for $P_2$(Table 4.7).The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for PVA of 8.84 mg/l, 3.07 mg/l and 8.11 mg/l respectively.Days to 50% flowering in the same cross had a mean of 97.87 daysfor the $F_1$ generation while $P_1$ recorded mean of 92.97 days and 87.67 days for $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for days to 50% flowering of 94.32 days, 86.74 days and 95.00 days respectively. The mean for this trait among the six generations for this cross are significantly($P < 0.05$) differentexcept for $P_1$ which was not significantly($P < 0.05$) different from $P_2$, $F_2$ and $BC_1P_1$.

The Segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ for plant height in the cross SAMSORG 43 × CSR01 recorded mean values as 192.8 cm, 248.0 cm and 220.9 cm respectively and a mean of 296.4 cm for $F_1$ generation which was not significantly($P < 0.05$) different from $P_2$(Table 4.7). $P_1$ recorded a mean 166.5 cm and295.7 cm for $P_2$.Panicle length in the same cross recorded a mean of 38.50 cmfor the $F_1$ generation a mean 37.51 cm for $P_1$ and36.16 cm for $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for panicle length of 37.24 cm, 34.42 cm and 32.02 cm respectively. The mean values for this trait among the six generations for this cross are significantly($P < 0.05$) differentexcept the $F_1$ for which was not significantly($P < 0.05$) differentfrom $P_1$, $P_2$, $BCP_1$ and $BCP_2$.

Table 4.7 Mean performance of pro-vitamin A and other traits of six generations of sorghum cross SAMSORG 43 × SAMSORG 44 evaluated at Samaru in 2014

| Generations | Days to 50% flowering | Plant Height (cm) | Panicle Length (cm) | Panicle Weight (g) | 1000-Grain Weight (g) | Pro-vitamin A (mg/l) | Grain Yield (kg $ha^{-1}$) |
|---|---|---|---|---|---|---|---|
| $P_1$ (SAM 43) | 92.97 | 166.5 | 37.51 | 221.17 | 19.33 | 10.57 | 901.79 |
| $P_2$ (CSR01) | 87.67 | 295 | 36.16 | 147.33 | 22.67 | 3.72 | 591.05 |
| $F_1$ | 97.87 | 296.4 | 38.5 | 247.17 | 32.67 | 6.92 | 1030.64 |
| $F_2$ | 95 | 220.9 | 32.02 | 159.2 | 27.87 | 8.11 | 627.97 |
| $BCP_1$ | 94.32 | 192.75 | 37.24 | 215.36 | 17.73 | 8.84 | 875.68 |
| $BCP_2$ | 86.74 | 248 | 34.42 | 211.9 | 23.13 | 3.07 | 842.6 |
| Mean | 92.16 | 225.9 | 35.03 | 197.11 | 23.24 | 6.74 | 791.93 |
| LSD (0.05) | 6.06 | 37.36 | 4.23 | 61.92 | 8.27 | 2.75 | 257.57 |
| CV (%) | 5.69 | 14.32 | 10.45 | 27.21 | 30.81 | 35.29 | 28.17 |

The mean for panicle weight among the six generations for SAMSORG 43 × CSR01 are significantly different, the $F_1$ generation was the heaviest with a mean of 247.17gwhile $P_2$ generation was the lightest with a mean of 147.33 g and 221.17g for $P_1$(Table 4.7). The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for panicle weight of 215.4 g, 211.9 g and 159.2 g respectively alsoone thousand grain weight in the same cross recorded a mean of 32.67gfor the $F_1$ generation which was the highest mean weight 34.40 g and was significantly ($P < 0.05$) differentfrom all other generations except $F_2$, a mean of 19.33g was recorded for $P_1$ and22.67g for $P_2$. The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean values for 1000 grain weight of 17.73 g, 23.13 g and 27.87 g respectively.

Grain yield in the cross SAMSORG 43 × CSR01 recorded a mean of 1030.64 kg ha$^{-}$1for $F_1$ generation, 901.79 kg ha$^{-1}$ for $P_1$ and591.05 kg ha$^{-1}$ for $P_2$(Table 4.7). The segregating generations $BC_1P_2$, $BC_1P_1$ and $F_2$ recorded mean and for grain yield of 875.68 kg ha$^{-}_1$, 842.60 kg ha$^{-1}$ and 627.97 kg ha$^{-1}$ respectively. The $F_1$ recorded the highest yield 1030.64kg ha$^{-1}$which is significantly($P < 0.05$) differentfrom $P_2$ and $F_2$.

## 4.3 Scaling Test

In the six crosses studied either one or more of the scaling tests A, B or C was highly significant for all traits(Table 4.8 and 4.9). Scaling tests A, B and C was highly ($P<0.01$)significant in SAMSORG 17 × SAMSORG 44 and SAMSORG 17 × CSR01 for PVA, days to 50% flowering, plant height panicle weight, grain weight and grain yield. Scaling tests B and C were also highly ($P<0.01$)significant in SAMSORG 43 × SAMSORG 44 and SAMSORG 43 × SAMSORG 14 for PVA.

## 4.4 Generation Mean Analysis

### 4.4.1 Estimates of the three parameter model

Mean data on various traits recorded on different generation viz., parents, $F_1$, $F_2$, $BC_1$ and $BC_2$ for the six cross combinations of sorghum were subjected to Three Parameter Model(Table 4.10and 411).However, the calculated chi-square ($\chi^2$) value at 3 degrees of freedom was highly significant for PVA, days to 50% flowering, plant height, panicle weight, grain weight, 1000-grain weight and grain yield in SAMSORG 17 × SAMSORG 44, SAMSORG 17 × SAMSORG 14, SAMSORG 17 × CSR01, SAMSORG 43 × SAMSORG 44, SAMSORG 43 × SAMSORG 14 and SAMSORG 43 × CSR01.

Table 4.8 Scaling Test for pro-vitamin A and other traits of six generations of sorghum involving SAMSORG 17, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Scaling Test | A | B | C |
|---|---|---|---|
| Trait | | | |
| | **SAMSORG 17 × SAMSORG 44** | | |
| Days to 50% flowering | -9.55**±0.81 | -22.47**±1.37 | -49.89**±4.63 |
| Plant Height (cm) | -18.85 **±2.50 | -15.72**±4.60 | 40.58**±8.54 |
| Panicle Length (cm) | -3.52 **±0.39 | -2.88**±0.43 | 0.52±0.78 |
| Panicle Weight (g) | -27.47**±3.04 | -86.97**±4.97 | -63.17**±14.17 |
| Grain Weight (g) | -25.87**±3.67 | -83.32**±5.78 | -60.33**±13.77 |
| 1000-Grain Weight (g) | -14.20**±1.66 | -14.20**±1.70 | -1.73±3.87 |
| Pro-vitamin A(mg/l) | -9.73**±0.55 | 0.40**±0.08 | -5.45**±0.88 |
| Grain Yield(kg/ha) | -114.96**±16.32 | -370.32**±25.69 | -268.14**±61.18 |
| | **SAMSORG 17 × SAMSORG 14** | | |
| Days to 50% flowering | -10.45**±0.85 | -24.95**±0.55 | -40.36**±3.70 |
| Plant Height (cm) | -83.93**±5.70 | -44.77**±6.72 | -161.15**±15.77 |
| Panicle Length (cm) | -1.45**±0.29 | -2.69**±0.64 | 2.15**±0.77 |
| Panicle Weight (g) | -71.80**±6.60 | -85.53**±4.68 | -98.99**±14.83 |
| Grain Weight (g) | -81.64**±7.20 | -89.69**±5.37 | -104.65**±15.85 |
| 1000-Grain Weight (g) | 0.20±1.70 | 1.93±1.85 | 23.33**±3.08 |
| Pro-vitamin A(mg/l) | -7.43**±0.42 | -6.45**±0.22 | -8.10**±1.11 |
| Grain Yield(kg/ha) | -362.85**±32.01 | -398.64**±23.87 | -465.14**±70.45 |
| **SAMSORG 17 × CSR01** | | | |
| Days to 50% flowering | -8.27**±0.79 | -13.53**±0.95 | -10.39**±2.24 |
| Plant Height (cm) | -106.19**±2.00 | -72.08**±4.83 | -190.27**±13.88 |
| Panicle Length (cm) | -3.19**±0.33 | -1.65**±0.46 | 1.59±0.89 |
| Panicle Weight (g) | -61.17**±5.52 | -95.17**±4.83 | -64.13**±15.48 |
| Grain Weight (g) | -63.41**±5.74 | -98.71**±4.97 | -77.71**±16.25 |
| 1000-Grain Weight (g) | -9.73**±1.72 | -4.00*±1.72 | 13.87**±3.62 |
| Pro-vitamin A(mg/l) | -12.30**±0.45 | -10.88**±0.24 | -18.81**±0.81 |
| Grain Yield(kg/ha) | -281.86**±25.50 | -438.70**±22.10 | -345.40**±72.22 |

* Significant at 5% level; ** Significant at 1% level

Table 4.9 Scaling Test for pro-vitamin A and other traits of six generations of sorghum involving SAMSORG 43, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Scaling Test | A | B | C |
|---|---|---|---|
| Trait | **SAMSORG 43 × SAMSORG 44** | | |
| Days to 50% flowering | -22.31**± 1.87 | -14.32** ± 1.18 | -17.08** ± 3.11 |
| Plant Height (cm) | -30.35** ± 4.25 | -70.44** ± 3.86 | 39.25** ± 9.95 |
| Panicle Length (cm) | -15.15** ± 0.70 | -10.50**± 0.75 | -27.69** ± 1.68 |
| Panicle Weight (g) | -35.77** ± 6.46 | -35.29** ± 3.73 | -29.32** ± 9.05 |
| Grain Weight (g) | -42.87** ± 6.75 | -47.03**± 4.62 | -43.68**±11.04 |
| 1000-Grain Weight (g) | -2.47 ± 2.03 | 21.80** ± 2.03 | -5.07 ± 3.79 |
| Pro-vitamin A(mg/l) | 0.32± 0.47 | -5.55**± 0.29 | 2.90**± 1.01 |
| Grain Yield(kg/ha) | -190.55**±30.01 | -209.02**±20.51 | -194.15**±49.07 |
| | **SAMSORG 43 × SAMSORG 14** | | |
| Days to 50% flowering | -5.13 **± 1.50 | -6.06 **±0.87 | 3.98 ±2.28 |
| Plant Height (cm) | -36.88 **±6.04 | -121.2 **±6.12 | -213.98**±11.27 |
| Panicle Length (cm) | -15.72**± 1.03 | -13.9 ** ± 1.31 | -24.76** ± 2.00 |
| Panicle Weight (g) | -2.63±5.94 | -59.76 **±2.88 | -80.9 **± 10.80 |
| Grain Weight (g) | -1.76 ± 5.99 | -64.73**±3.38 | -80.52**±11.40 |
| 1000-Grain Weight (g) | 22.2**± 2.83 | 0.07 ± 2.13 | 5.33 ± 4.03 |
| Pro-vitamin A(mg/l) | 1.15 ±0.47 | -4.56 **±0.27 | 7.94**±0.65 |
| Grain Yield(kg/ha) | -7.84 ± 26.64 | -287.72**±15.05 | -357.86**±50.68 |
| **SAMSORG 43 × CSR01** | | | |
| Days to 50% flowering | -2.19±1.50 | -12.05 **±0.59 | 3.63±2.82 |
| Plant Height (cm) | -77.39 **±4.12 | -95.40**±6.61 | -170.70**±13.06 |
| Panicle Length (cm) | -1.52±**0.40 | -5.82**±0.69 | -22.61**±1.72 |
| Panicle Weight (g) | -37.61**±7.30 | 29.30*±13.70 | -226.03**±15.36 |
| Grain Weight (g) | -40.73**±7.65 | 14.28 ±12.44 | -234.50**±14.64 |
| 1000-Grain Weight (g) | -16.53**± 1.73 | -9.07**± 1.59 | 4.13 ± 3.74 |
| Pro-vitamin A(mg/l) | 0.19± 0.49 | -4.50**±0.42 | 4.30**±0.82 |
| Grain Yield(kg/ha) | -181.06**±34.01 | 63.49±55.32 | -1042.25**±65.07 |

*Significant at 5% level; ** Significant at 1% level

Table 4.10 Three Parameter Model for pro-vitamin A and other traits of six generations of sorghum involving SAMSORG 17, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Trait | m | d | h | $\chi^2$ |
|---|---|---|---|---|
| | **SAMSORG 17 × SAMSORG 44** | | | |
| Days to 50% flowering | 9.20**±0.11 | 0.57±0.42 | 36.99**±0.54 | 496.03** |
| Plant Height (cm) | 110.07**±3.24 | 110.46**±1.47 | 76.45**±0. 11 | 119.77** |
| Panicle Length (cm) | 35.08**±0.45 | -3.94**±2.36 | -11.10**±5.61 | 68.47** |
| Panicle Weight (g) | 184.19**±5.47 | -143.27**±14.56 | -341.37**±0.86 | 2139.30** |
| 1000-Grain Weight (g) | 127.31**±0.45 | -77.54**±1.35 | -149.25**±5.67 | 77.00** |
| Pro-vitamin A (mg/l) | 2.58**±0.011 | 5.63**±0.036 | 8.437**±0.083 | 724170.83** |
| Grain Yield (kg/ha) | 190.53**±4.56 | -134.01**±3.76 | -48.07**±14.86 | 12738.08* |
| | **SAMSORG 17 × SAMSORG 14** | | | |
| Days to 50% flowering | 111.36**±0.20 | 86.55**±1.95 | 9.58**±0.35 | 107.58** |
| Plant Height (cm) | 276.22**±1.48 | 45.05±5.46 | 389.13**±10.46 | 1374.65** |
| Panicle Length (cm) | 35.08**±0.45 | -3.94**±2.36 | -11.10**±5.61 | 68.47** |
| Panicle Weight (g) | 82.43**±6.77 | 62.83**±2.56 | -158.38**±5.64 | 1158.42** |
| 1000-Grain Weight (g) | 89.71**±0.86 | -59.47**±0.54 | 72.87**±0.56 | 87.00** |
| Pro-vitamin A (mg/l) | 0.64**±0.016 | -2.27**±0.016 | 0.002±0.001 | 5858.1984** |
| Grain Yield (kg/ha) | 97.91**± 3.67 | -46.28**±5.88 | 376.80**±10.43 | 984518.00** |
| | **SAMSORG 17 × CSR01** | | | |
| Days to 50% flowering | 15.45**±0.35 | 0.33±0.87 | 6.78**±0.78 | 68.04** |
| Plant Height (cm) | 173.74**±5.88 | 82.33**±6.33 | -19.24**±.0.45 | 286.35** |
| Panicle Length (cm) | 6.67**±0.27** | -10.30**±3.56 | 27.54**±2.63 | 141.42** |
| Panicle Weight (g) | 269.52**±3.92 | -232.73**±0.45 | -211.66**±7.85 | 3425.92** |
| 1000-Grain Weight (g) | 66.00**±0.78 | 83.11**±4.67 | 51.77**±4.52 | 129.10** |
| Pro-vitamin A (mg/l) | -1.86**±0.001 | -1.87**±0.001 | 0.003±0.029 | 6911.4938** |
| Grain Yield (kg/ha) | 262.26**±2.65 | -181.79*±6.44 | -382.16**±0.53 | 45632.49** |

* Significant at 5% level ** Significant at 1% level

Table 4.11 Three Parameter Model Scaling Test for pro-vitamin A and other traits of six generations of sorghum involving SAMSORG 43, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Trait | m | d | h | $\chi^2$ |
|---|---|---|---|---|
| **SAMSORG 43 × SAMSORG 44** | | | | |
| Days to 50% flowering | 100.45**±0.45 | 43.67**±3.29 | 7.56**±0.56 | 1547.68** |
| Plant Height (cm) | 214.70**±9.74 | 103.86**±10.56 | -0. 06.±0.23 | 328.12** |
| Panicle Length (cm) | 31.25**±1.44 | -0.65±0.48 | -15.84**±4.03 | 78.60** |
| Panicle Weight (g) | 165.83**±10.63 | -37.86*±14.32 | 24.18**±4.53 | 684.60** |
| 1000-Grain Weight (g) | 189.87**±3.45 | -126.26**±15.82 | -32.49**±7.23 | 95.12** |
| Pro-vitamin A (mg/l) | 1.48**±0.010 | 3.342**±0.010 | 5.513**±0.013 | 375547.18** |
| Grain Yield (kg/ha) | 483.15**±1.66 | -66.71**±8.55 | 115.8**±0.45 | 1384.00** |
| **SAMSORG 43 × SAMSORG 14** | | | | |
| Days to 50% flowering | 96.54**±0.38 | 183.57**±5.63 | 47.6**±3.72 | 113.54** |
| Plant Height (cm) | 209.04**±3.29 | 227.43±4.78 | -244.61**±0.68 | 1455.26** |
| Panicle Length (cm) | 4.20**±0.33 | -1.05*±0.99 | -33.47**±0.06 | 25.40** |
| Panicle Weight (g) | 167.34**±17.35 | -110.80**±7.65 | 367.35**±2.13 | 313.11** |
| 1000-Grain Weight (g) | 59.18**±4.82 | 197.73**±6.36 | 11.26**±8.54 | 151.80** |
| Pro-vitamin A (mg/l) | -2.001**±0.010 | -2.01**±0.002 | 0.007±0.004 | 308676.97** |
| Grain Yield (kg/ha) | 91.96**±0.78 | 210.22**±2.33 | 55.97**±1.76 | 1532.9** |
| **SAMSORG 43 × CSR01** | | | | |
| Days to 50% flowering | 96.99**±1.36 | 18.17**±3.29 | 46.83**±1.35 | 392.95** |
| Plant Height (cm) | 146.62**±1.06 | -1.03±2.38 | -337.12*±8.75 | 1883.48 ** |
| Panicle Length (cm) | 24.32**±0.78 | -32.54**±0.45 | -20.11**±3.25 | 151.43** |
| Panicle Weight (g) | 262.56**±7.69 | -55.85**±8.74 | 344.05**±3.76 | 514.04** |
| 1000-Grain Weight (g) | 83.46**±5.38 | -63.51*±8.77 | 132.09**±4.21 | 82.00** |
| Pro-vitamin A (mg/l) | -2.243**±0.016 | -2.242**±0.001 | 8.303**±0.116 | 689.85316** |
| Grain Yield (kg/ha) | 159.56**±0.45 | -312.87**±4.31 | -213.73**±0.56 | 16399.50** |

* Significant at 5% level ** Significant at 1% level

4.4.2 Estimates of the six parameter model

The means (m) for the PVA were highly (P<0.01) significantfor SAMSORG 17 × SAMSORG 44 (8.76mg/l), SAMSORG 17 × SAMSORG 14 (6.77 mg/l) and SAMSORG 17 × CSR01 (6.01mg/l)(Table 4.12).The Additive x dominance (j) and dominance x dominance (l) interactions were highly (P<0.01) significant for SAMSORG 17 × SAMSORG 44whiledominance x dominance interaction was highly significant for SAMSORG 17 × SAMSORG 14 and SAMSORG 17 × CSR01. Opposite signs of dominance (h) and dominance x dominance (l) gene effects were observed for SAMSORG 17 × SAMSORG 44, SAMSORG 17 × SAMSORG 14 and SAMSORG 17 × CSR01 indicating duplicate epistasis.

The means (m) for days to 50% flowering were highly (P<0.01)significantfor SAMSORG 17 × SAMSORG 44 (90.12 days), SAMSORG 17 × SAMSORG 14 (94.86 days) and SAMSORG 17 × CSR01 (102.39 days)(Table 4.12).Among the various interactions, additive × dominance effect (j) was highly (P<0.01)significant for this trait in cross SAMSORG 17 × SAMSORG 44,SAMSORG 17 × SAMSORG 14 and SAMSORG 17 × CSR01. Dominance x dominance (l) was significant and highly (P<0.01) significant in cross SAMSORG 17 × SAMSORG 14 and SAMSORG 17 × CSR01. Similar signs of dominance (h) and dominance x dominance (l) gene effects were observed for SAMORG 17 × SAMSORG 44, SAMSORG 17 × SAMSORG 14 and SAMSORG 17 × CSR01 indicating complementary type of epistasis. Highly (P<0.01) significant means (m) were observed for plant height in SAMSORG 17 × SAMSORG 44 (178.89 cm), SAMSORG 17 × SAMSORG 14 (214.01 cm) and SAMSORG 17 × CSR01 (218.84 cm).

Table 4.12 Gene Effect for pro-vitamin A and other traits of six generations of sorghum involving SAMSORG 17, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Gene Effects | Days to 50% flowering | Plant Height (cm) | Panicle Length (cm) | Panicle Weight (g) | Grain Weight (g) | 1000-Grain Weight (g) | Pro-vitamin A (mg/l) | Grain Yield (kg/ha) |
|---|---|---|---|---|---|---|---|---|
| | | | | **SAMSORG 17 × SAMSORG 44** | | | | |
| m | 90.12**±2.00 | 178.89**±3.47 | 38.33**±0.31 | 252.77**±6.07 | 234.61**±5.70 | 25.73**±1.40 | 8.76**±0.38 | 1042.70**±25.33 |
| d | 37.08**±12.34 | 30.59**±5.20 | 2.45**±0.62 | 78.30**±6.36 | 77.96**±6.89 | -4.67*±1.94 | 8.86**±3.30 | 346.49**±30.60 |
| h | 23.75**±1.87 | 34.63±28.25 | -4.72**±1.48 | -3.05±40.71 | -4.27±42.47 | -13.00**±2.58 | -2.51**±0.82 | -18.98±188.75 |
| i | 17.87±11.62 | -75.15**±24.30 | -6.92**±2.47 | -51.27±36.99 | -48.85±36.57 | -26.67**±9.46 | -4.37±3.14 | -217.10±162.53 |
| j | 6.46**±2.25 | -1.56±7.85 | -0.32±0.83 | 29.75**±8.33 | 28.73**±9.70 | 0.00±3.56 | -4.82**±0.82 | 127.68**±43.10 |
| l | 14.15±16.67 | 109.71*±42.61 | 13.32**±4.63 | 165.7**±57.16 | 158.04*±62.14 | 55.07**±19.58 | 14.18**±5.10 | 702.41*±276.17 |
| | 4 (m d h j) | 4 (m d i l) | 5 (m d h i l) | 4 (m d j l) | 4 (m d j l) | 4 (m d i l) | 5 (m d h j l) | 4 (m d j l) |
| | | | | **SAMSORG 17 × SAMSORG 14** | | | | |
| m | 94.86**±1.60 | 214.01**±5.25 | 38.51**±0.26 | 244.59**±6.32 | 228.09**±6.69 | 25.33**±0.91 | 6.77**±0.48 | 1013.70**±29.74 |
| d | 19.52**±1.11 | -66.75**±5.96 | 2.17**±0.62 | -7.01**±2.52 | 53.85**±10.07 | 14.20±10.97 | 11.85**±3.15 | 239.35**±44.74 |
| h | 18.86*±9.29 | 85.45±43.30 | -4.97**±1.80 | 56.20**±9.24 | -11.78±52.33 | -3.20**±0.09 | -7.36**±0.52 | -52.36±232.56 |
| i | 4.96±8.61 | 32.45*±12.9 | -6.29**±2.28 | -58.35±43.75 | -66.68*±26.9 | -21.20**±7.62 | -5.78±2.95 | -296.40*±118.43 |
| j | 7.25**±1.51 | -19.58**±7.26 | 0.62±0.93 | 6.87*±2.71 | 4.03±13.43 | -0.87±3.81 | -0.49±0.52 | 17.89±59.69 |
| l | 30.44*±12.18 | 96.24±65.61 | 10.43*±4.56 | 215.68**±69.76 | 238.01**±77.89 | 19.07*±8.30 | 19.66**±4.40 | 1057.80**±346.18 |
| | 5 (m d h j l) | 4 (m d i j) | 5 (m d h i l) | 5 (m d h j l) | 4 (m d i l) | 4(m d i l) | 4 (m d h l) | 4 (m d i l) |
| | | | | **SAMSORG 17 × CSR01** | | | | |
| m | 102.39**±0.93 | 218.84**±5.98 | 39.04**±0.32 | 241.47**±6.67 | 222.38**±6.94 | 26.13**±1.19 | 6.01**±0.35 | 988.35**±30.84 |
| d | 13.93**±1.38 | 69.18±37.72 | 1.08*±0.53 | -17.53±47.32 | 89.47**±8.77 | -6.87**±1.9 | 7.28**±0.61 | 397.63**±38.97 |
| h | 0.62±7.33 | -74.24**±5.54 | -3.17**±0.95 | 89.83**±8.75 | -10.41±49.89 | -19.60±11.72 | -6.37*±2.65 | -46.29±221.71 |
| i | -11.41±6.50 | 12.00±35.02 | -6.43**±2.36 | -92.20*±44.21 | -84.41±45.29 | -27.60**±8.57 | -4.37±2.62 | -375.20±201.28 |
| j | 2.63**±0.91 | -17.06*±6.9 | -0.77±0.77 | 17.00±10.49 | 17.65**±6.11 | -2.87±3.42 | -0.71±0.61 | 78.43**±19.33 |
| l | 33.21**±10.91 | 166.27**±51.5 | 11.27*±4.59 | 248.53**±67.95 | 246.53**±72.02 | 41.33*±18.67 | 27.55**±3.89 | 1095.7**±320.08 |
| | 4 (m d j l) | 4 (m d j l) | 5 (m d h i l) | 4 (m d i l) | 4 (m d j l) | 4 (m d i l) | 4 (m d h l) | 4(m d j l) |

* Significant at 5% level;** Significant at 1% level

Among the non-allelic gene interactions, additive × additive (i) and dominance × dominance gene effects (l) were significant in SAMSORG 17 × SAMSORG 44 (Table 4.12). In the cross SAMSORG 17 × SAMSORG 14 additive x additive (i) was significant, additive x dominance (j) was highly (P<0.01)significant while in SAMSORG 17 × CSR01 additive × dominance (j) and dominance × dominance (l) was highly (P<0.01)significant. Opposite signs of dominance (h) and dominance × dominance (l) gene effects were observed for plant height in SAMSORG 17 × SAMSORG 44 indicating duplicate epistasis while dominance (h) and dominance × dominance (l) were both in positive direction indicating complementary epistasis for plant height in SAMSORG 17 × SAMSORG 14 and SAMSORG 17 × CSR01.

The means (m) of panicle length for SAMSORG 17 × SAMORG 44 (38.33cm), SAMSORG 17 × SAMSORG 14 (38.51cm) and SAMSORG 17 × CSR01 (39.04cm) were highly (P<0.01) significant(Table 4.12).Among the various gene interactions, additive x additive (i) was highly significant in the three crosses considered while dominance x dominance effect (l) was significant but highly (P<0.01) significant for SAMSORG 17 × CSR01. The opposite signs of dominance (h) and dominance x dominance (l) gene effects were observed for SAMSORG 17 × SAMSORG 44, SAMSORG 17 × SAMSORG 14 and SAMSORG 17 × CSR01 indicating duplicate epistasis. Highly significant means (m) were observed for panicle weight for SAMSORG 17 × SAMORG 44 (252.77g), SAMSORG 17 × SAMSORG 14 (244.59g) and SAMSORG 17 × CSR01 (241.47g). Among the interaction effects, dominance x additive (j) and dominance x dominance (l) was highly (P<0.01)significant for SAMSORG 17 × SAMSORG 44, dominance x additive (j) was

significant butdominance x dominance (l) was highly significant for SAMSORG 17 × SAMSORG 14.

Opposite signs of dominance (h) and dominance x dominance (l) gene effects were observed for SAMSORG 17 × SAMSORG 44, SAMSORG 17 × SAMSORG 14 and SAMSORG 17 × CSR01 indicating duplicate epistasis.

The means (m) for the grain weight were highly (P<0.01)significant for SAMSORG 17 × SAMORG 44 (234.6g), SAMSORG 17 × SAMSORG 14 (228.09g) and SAMSORG 17 × CSR01 (222.38g) (Table 4.12).Among the interaction effects, additive x dominance (j) was highly significant and dominance x dominance (l) was significant for SAMSORG 17 × SAMSORG 44. Additive x additive (i) was significant and dominance x dominance (l) was highly (P<0.01) significant in cross SAMSORG 17 × SAMSORG 14. In the cross SAMSORG 17 × CSR01, additive x dominance (j) and dominance x dominance (l) was highly (P<0.01) significant. Further, opposite signs of dominance (h) and dominance x dominance (l) gene interactions indicate the expression of this trait was under the control of duplicate epistasis.Highly (P<0.01)significant means (m) were observed for SAMSORG 17 × SAMSORG 44 (25.73 g), SAMSORG 17 × SAMSORG 14 (25.33 g) and SAMSORG 17 × CSR01 (26.13 g) for 1000 grain weight. The opposite signs of dominance (h) and dominance x dominance (l) gene effects indicated the expression of this trait under the control of duplicate epistasis for the three crosses considered. The means (m) for the grain yield were highly (P<0.01) significant for SAMSORG 17 × SAMSORG 44 (1042.7 kg/ha), SAMSORG 17 × SAMSORG 14 (1013.7 kg/ha) and SAMSORG 17 × CSR01 (988.4 kg/ha) for grain yield. Further, opposite signs of dominance (h) and dominance x dominance (l) gene effects indicated the expression of this trait under the control of duplicate epistasis.

The means (m) for the PVAwere highly (P<0.01) significant for SAMSORG 43 × SAMSORG 44 (7.87mg/l), SAMSORG 43 × SAMSORG 14 (8.87mg/l) and SAMSORG 43 × CSR01 (8.10mg/l)(Table 4.13). The gene interaction and non-allelic interactions were all significant in SAMSORG 43 × SAMSORG 44, SAMSORG 43 × SAMSORG 14 and SAMSORG 43 × CSR01. Opposite signs of dominance (h) and dominance x dominance (l) gene effects were observed for SAMSORG 43 × SAMSORG 44, SAMSORG 43 × SAMSORG 14 and SAMSORG 43 × CSR01 indicating duplicate epistasis The means (m) for days to 50% flowering were highly (P<0.01) significant for SAMSORG 43 × SAMSORG 44 (87.41 days), SAMSORG 43 × SAMSORG 14 (95.79 days) and SAMSORG 43 × CSR01 (95.00 days) (Table 4.13).

Among the various gene effects, additive x additive effect (i) was significant for this trait and dominance x dominance (l) were highly (P<0.01)significant for SAMSORG 43 × SAMSORG 44, additive x additive effect (i) and dominance x dominance (l) was significant for SAMSORG 43 × SAMSORG 14 while in SAMSORG 43 × CSR01 additive x additive was highly (P<0.01)significant, additive x dominance (j) and dominance x dominance (l) were significant. Opposite signs of dominance (h) and dominance x dominance (l) gene effects were observed for SAMSORG 43 × 44, SAMSORG 43 × SAMSORG 14 and SAMSORG 43 × CSR01 indicating duplicate epistasis. Highly (P<0.01)significant means (m) were observed for plant height for SAMSORG 43 × SAMSORG 44 (180.85cm) SAMSORG 43 × SAMSORG 14 (189.12cm) and SAMSORG 43 × CSR01 (220.9cm).

Table 4.13 Gene Effect for pro-vitamin A and other traits of six generations of sorghum involving SAMSORG 43, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Gene Effects | Days to 50% flowering | Plant Height (cm) | Panicle Length (cm) | Panicle Weight (g) | Grain Weight (g) | 1000-Grain Weight (g) | Pro-vitamin A (mg/l) | Grain Yield (kg/ha) |
|---|---|---|---|---|---|---|---|---|
| | | | | **SAMSORG 43 × SAMSORG 44** | | | | |
| m | 87.41**±1.16 | 180.85**± 3.94 | 29.68** ± 0.71 | 217.77**±3.21 | 196.57**± 4.14 | 21.07**± 1.15 | 7.87** ± 0.42 | 873.67** ±18.38 |
| d | -4.85± 10.63 | 45.13**± 5.55 | 5.69** ± 1.39 | 12.39** ± 4.78 | 14.45** ± 3.70 | -14.47**± 2.27 | 9.46** ± 2.99 | 64.21** ± 0.73 |
| h | 4.64* ± 2.51 | -80.79**± 21.95 | -3.74**± 1.16 | -8.6 ± 33.59 | -12.3 ± 39.57 | 25.73* ± 12.91 | -5.70** ±0.66 | -54.65± 175.88 |
| i | -19.55*± 8.96 | -140.00** ±26.89 | 2.03 ± 5.17 | -41.73 ± 26.41 | -46.22 ± 31.94 | 24.4* ± 9.13 | -8.13** ± 2.98 | -205.4 ± 141.94 |
| j | -3.99 ± 3.49 | 20.04* ± 8.49 | -2.33 ± 1.42 | -11.77**± 1.24 | 13.01**± 2.08 | -12.13** ± 4.13 | 2.93** ± 0.66 | 57.83**± 9.24 |
| l | 56.17**± 16.6 | 240.8**± 48.11 | 23.62**± 8.54 | 112.8*± 54.32 | 136.1*± 62.61 | -43.73*± 21.23 | 13.36** ± 4.32 | 604.99*±278.25 |
| | 4 (m d i l) | 6 (m d h i j l) | 4 (m d h l) | 4 (m d j l) | 4 (m d j l) | 6 (m d h i j l) | 6 (m d h i j l) | 4 (m d j l) |
| | | | | **SAMSORG 43 × SAMSORG 14** | | | | |
| m | 95.79**±0.82 | 189.12**±4.73 | 33.06**±0.76 | 208.40**±4.12 | 191.04**±4.39 | 19.67**±1.07 | 8.87**±0.28 | 849.08**±19.5 |
| d | 4.08**±1.48 | -55.25**±8.72 | -1.86**±0.53 | 60.25±33.3 | 44.45**±5.33 | 12.07**±2.92 | 12.15**±2.45 | 197.56**±23.86 |
| h | -4.29±7.9 | 63.56±42.74 | -7.76**±0.63 | 41.98**±4.88 | 56.49±36.63 | 16.93±14.61 | -6.15**±0.65 | 251.06±158.37 |
| i | -15.17*±6.23 | 55.91**±6.23 | -4.87±6.71 | 18.5±26.23 | 14.02±28.21 | 16.93**±5.12 | -11.35**±2.42 | 62.29±125.37 |
| j | 0.46±2.78 | 42.16**±2.78 | -0.91±2.19 | 28.57**±10.37 | 31.49**±11.19 | 11.07*±4.97 | 2.85**±0.65 | 139.94**±49.75 |
| l | 26.37*±12.52 | 102.17**±12.52 | 34.49**±12.47 | 50.12**±13.89 | 52.49**±13.71 | -39.20±24.94 | 14.77**±3.78 | 233.28**±38.73 |
| | 4 (m d i l) | 5 (m h i j l) | 4 (m d h l) | 4 (m d j l) | 4 (m d j l) | 4 (m d i j) | 6 (m d h i j l) | 4 (m d j l) |
| | | | | **SAMSORG 43 × CSR01** | | | | |
| m | 95.00**±1.06 | 220.9**±5.58 | 32.02**±0.70 | 159.2**±6.14 | 141.29**±5.75 | 27.87**±1.32 | 8.10**±0.34 | 627.97**±25.56 |
| d | 7.58**±1.03 | 99.67*±49.93 | 16.93**±5.00 | 280.64**±62.23 | 272.00**±59.98 | -18.07±12.09 | -5.77**±0.76 | 1208.9**±266.60 |
| h | -10.33±8.2 | -12.07±10.14 | 2.82**±0.85 | 3.46**±15.55 | 7.44±14.93 | -5.40**±1.79 | 8.83**±3.12 | 33.09±66.37 |
| i | -17.88**±6.29 | -2.09±39.74 | 15.26**±4.51 | 217.72**±55.67 | 208.05**±52.98 | -29.73**±8.88 | -8.60**±2.88 | 924.69**±234.99 |
| j | 4.93*±2.45 | 9.00*±4.37 | 2.15±1.14 | -33.46±20.30 | -27.51±19.77 | -3.73±3.54 | 2.35**±0.76 | -122.3±87.85 |
| l | 32.13*±12.17 | 174.89**±63.17 | -7.91±7.19 | -209.4*±99.87 | -181.6**±26.96 | 55.33**±18.89 | 12.90**±4.88 | -807.2**±43.94 |
| | 5(m d i j l) | 4 (m d j l) | 4 (m d h i) | 4 (m h i l) | 4 (m h i l) | 4 (m d i l) | 6 (m d h i j l) | 4 (m d i l) |

* Significant at 5% level; ** Significant at 1% level

Among the non-allelic gene interactions, additive × additive (i) and dominance × dominance gene effects (l) were highly (P<0.01) significant while additive x dominance was significant in the cross SAMSORG 43 × SAMSORG 44; additive x dominance (j), dominance x dominance (l) were significant in cross SAMSORG 43 × SAMSORG 14 and SAMSORG 43 × CSR01 (Table 4.13). Opposite signs were observed for dominance (h) and dominance × dominance gene effects (l) in SAMSORG 43 × SAMSORG 44 while similar signs were observed for dominance (h) and dominance × dominance gene effects (l) in SAMSORG 43 × SAMSORG 14 and SAMSORG 43 × CSR01.The means (m) for panicle length were highly (P<0.01) significant, and for SAMSORG 43 ×SAMSORG 44 (29.68 cm), SAMSORG 43 × SAMSORG 14 (33.06 cm) and SAMSORG 43 × CSR01 (32.02 cm). Among the various gene interactions, dominance x dominance effect (l) was highly significant for this trait in cross SAMSORG 43 × SAMSORG 44 and SAMSORG 43 × SAMSORG 14 while additive x additive was highly significant in SAMSORG 43 × CSR01.

Highly significant means (m) were observed for panicle weight for SAMSORG 43 × SAMSORG 44 (217.77 g), SAMSORG 43 × SAMSORG 14 (208.40 g) and SAMSORG 43 × CSR01 (159.20 g)(Table 4.13). Among the interaction effects, dominance x dominance (l) type of epistasis was significant for SAMSORG 43 × SAMSORG 44, additive x dominance was highly (P<0.01) significant for SAMSORG 43 × SAMORG 14 and additive x additive was highly significant while dominance x dominance was significant in SAMSORG 43 × CSR01. The opposite signs observed for dominance (h) and dominance × dominance (l) gene effects for SAMSORG 43 × SAMSORG 44, and SAMSORG 43 × CSR01 indicates the presence of duplicate type of epistasis.

The means (m) for the grain weight were highly significant, and for SAMSORG 43 × SAMSORG 44 (196.57 g), SAMSORG 43 × SAMSORG 14 (191.04 g) and SAMSORG 43 × CSR01 (141.29 g)(Table 4.13). Dominance x dominance type of gene interactions was significant for SAMSORG 43 × SAMSORG 44, additive x dominance was highly ($P<0.01$) significant for SAMSORG 43 × SAMSORG14 and additive x additive was also highly ($P<0.01$) significant in SAMSORG 43 × CSR01.

Highly ($P<0.01$) significant means (m) were observed for 1000-grain weight for SAMSORG 43 × SAMSORG 44 (21.07 g), SAMSORG 43 × SAMSORG 14 (14 19.67 g) and SAMSORG 43 × CSR01 (27.87 g) (Table 4.13). Additive x dominance was highly ($P<0.01$) significant while additive x additive and dominance x dominance (l) were significant for SAMSORG 43 × SAMSORG 44, additive x dominance (j) was significant for SAMSORG 43 × SAMSORG 14, additive x additive (i) and dominance x dominance were highly significant in the cross between SAMSORG 43 × CSR01. Further, the opposite signs of dominance (h) and dominance x dominance (l) gene interactions indicate the expression of the trait was under the control of duplicate epistasis. The means (m) for the grain yield were highly ($P<0.01$) significant for SAMSORG 43 × SAMSORG 44 (873.67 kg/ha), SAMSORG 43 × SAMSORG 14 (849.08 kg/ha) and SAMSORG 43 × CSR01 (627.97 kg/ha). Dominance x dominance (l) type of gene interaction effects was significant for SAMSORG 43 × SAMSORG 44, additive x dominance (j) was highly ($P<0.01$) significant for SAMSORG 43 × SAMSORG14.

### 4.5 Genetic Variability, Heritability and Genetic Advance

Phenotypic variances $\sigma_P^2$ were large for all the traits compared to genotypic variances $\sigma_G^2$ in all the crosses (Tables 4.14 and 4.15).Positive values were obtained for genotypic variance. For most of the traits in all the crosses studied, genotypic variances were greater than environmental variances. Genotypic variance was then partitioned into additive and dominance variances. It was observed also that additive variances were higher than the dominance variances in all crosses.

The broad sense heritability estimates were high for all the measured traits in the six crosses except for 1000-grain weight (47%) which was moderate in SAMSORG 43 × SAMSORG 14 (Tables 4.14 and 4.15). 1000-grain weight (15%) and panicle length (17%) recorded low narrow sense heritability in SAMSORG 17 × SAMSORG14. PVA however, recorded high genetic advance as percent of mean in the six crosses according to Falconer and Mackay's (1996) classification.

Table 4.14 Variance Components, Heritability and Genetic Advance for pro- vitamin A and other traits of six generations of sorghum involving SAMSORG 17, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Trait | $\sigma_P^2$ | $\sigma_E^2$ | $\sigma_G^2$ | $\sigma_A^2$ | $\sigma_D^2$ | Broad Sense Heritability | Narrow Sense Heritability | GA (10%) | GAM% |
|---|---|---|---|---|---|---|---|---|---|
| **SAMSORG 17 × SAMSORG 44** | | | | | | | | | |
| Days to 50% flowering | 100.27 | 21.42 | 78.85 | 43.30 | 35.55 | 0.78 | 0.43 | 75.67 | 80.37 |
| Plant Height (cm) | 103.34 | 60.67 | 42.67 | 23.10 | 19.57 | 0.41 | 0.22 | 39.90 | 24.09 |
| Panicle Length (cm) | 4.71 | 0.25 | 4.46 | 2.17 | 2.29 | 0.94 | 0.46 | 3.80 | 10.20 |
| panicle weight (g) | 147.40 | 62.40 | 85.00 | 47.30 | 37.70 | 0.57 | 0.32 | 82.78 | 33.52 |
| 1000-Grain Weight ( g) | 97.74 | 24.44 | 73.30 | 27.82 | 45.48 | 0.75 | 0.28 | 48.03 | 221.13 |
| Pro-Vitamin A (mg/l) | 7.04 | 0.12 | 6.92 | 3.68 | 3.24 | 0.98 | 0.52 | 6.42 | 75.58 |
| Grain Yield (kg/ha) | 214.00 | 82.00 | 132.00 | 122.40 | 9.60 | 0.61 | 0.57 | 214.07 | 21.02 |
| **SAMSORG 17 × SAMSORG 14** | | | | | | | | | |
| Days to 50% flowering | 127.88 | 31.20 | 96.67 | 64.12 | 50.55 | 0.75 | 0.36 | 80.79 | 83.43 |
| Plant Height (cm) | 176.50 | 51.70 | 124.80 | 88.12 | 36.68 | 0.70 | 0.49 | 151.78 | 67.83 |
| Panicle Length (cm) | 29.11 | 3.49 | 25.62 | 5.12 | 20.50 | 0.88 | 0.17 | 8.68 | 23.15 |
| panicle weight (g) | 197.50 | 51.02 | 146.48 | 55.74 | 85.74 | 0.74 | 0.28 | 97.05 | 40.58 |
| 1000-Grain Weight ( g) | 41.39 | 12.68 | 28.70 | 6.30 | 22.40 | 0.69 | 0.15 | 10.90 | 51.35 |
| Pro-Vitamin A (mg/l) | 11.30 | 3.21 | 8.09 | 5.75 | 2.34 | 0.71 | 0.51 | 10.11 | 156.08 |
| Grain Yield (kg/ha) | 221.90 | 51.90 | 170.00 | 146.50 | 23.50 | 0.76 | 0.60 | 233.66 | 23.72 |
| **SAMSORG 17 × CSR01** | | | | | | | | | |
| Days to 50% flowering | 43.72 | 2.02 | 41.70 | 39.81 | 1.89 | 0.95 | 0.91 | 69.82 | 69.20 |
| Plant Height (cm) | 171.20 | 39.80 | 131.40 | 52.00 | 79.40 | 0.76 | 0.30 | 90.14 | 39.73 |
| Panicle Length (cm) | 5.61 | 0.91 | 4.70 | 3.89 | 0.82 | 0.84 | 0.69 | 6.79 | 17.88 |
| panicle weight (g) | 129.80 | 25.10 | 104.70 | 33.40 | 71.30 | 0.80 | 0.25 | 56.95 | 24.84 |
| 1000-Grain Weight ( g) | 71.13 | 25.74 | 45.39 | 41.55 | 3.84 | 0.64 | 0.58 | 72.40 | 336.76 |
| Pro-Vitamin A (mg/l) | 6.13 | 1.09 | 5.04 | 2.68 | 2.18 | 0.82 | 0.44 | 4.73 | 75.86 |
| Grain Yield (kg/ha) | 203.60 | 127.30 | 110.60 | 106.70 | 3.90 | 0.62 | 0.52 | 185.81 | 19.74 |

$\sigma_P^2$ = Phenotypic variance, $\sigma_G^2$ = Genotypic Variance, $\sigma_E^2$ = Environmental Variance, $\sigma_D^2$ = Dominance variance, $\sigma_A^2$ =Additive variance.

Table 4.15 Variance Components, Heritability and Genetic Advance for pro-vitamin A and other traits of six generations of sorghum involving SAMSORG 43, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Trait | $\sigma_P^2$ | $\sigma_E^2$ | $\sigma_G^2$ | $\sigma_A^2$ | $\sigma_D^2$ | Broad Sense Heritability | Narrow Sense Heritability | GA (10%) | GAM % |
|---|---|---|---|---|---|---|---|---|---|
| | | | | **SAMSORG 43 × SAMSORG 44** | | | | | |
| Days to 50% flowering | 68.49 | 12.79 | 55.71 | 10.69 | 45.02 | 0.81 | 0.15 | 18.03 | 21.21 |
| Plant Height (cm) | 191.21 | 82.54 | 108.67 | 42.22 | 66.45 | 0.89 | 0.22 | 73.83 | 46.69 |
| Panicle Length (cm) | 25.38 | 0.68 | 24.70 | 16.40 | 8.30 | 0.97 | 0.65 | 28.95 | 92.97 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| panicle weight (g) | 117.63 | 45.63 | 72.00 | 46.30 | 25.70 | 0.63 | 0.39 | 80.51 | 37.93 |
| 1000-Grain Weight ( g) | 67.67 | 36.11 | 31.56 | 2.16 | 29.40 | 0.47 | 0.03 | 3.56 | 14.47 |
| Pro-Vitamin A (mg/l) | 8.91 | 1.65 | 7.26 | 6.41 | 2.51 | 0.81 | 0.71 | 11.10 | 166.95 |
| Grain Yield (kg/ha) | 147.00 | 2.30 | 144.70 | 122.60 | 22.1 | 0.76 | 0.83 | 214.13 | 25.22 |
| | | | | **SAMSORG 43 × SAMSORG 14** | | | | | |
| Days to 50% flowering | 33.51 | 12.69 | 20.81 | 12.29 | 8.53 | 0.62 | 0.37 | 21.76 | 23.34 |
| Plant Height (cm) | 132.68 | 37.28 | 95.4 | 50.1 | 45.3 | 0.97 | 0.38 | 65.20 | 31.87 |
| Panicle Length (cm) | 29.11 | 3.49 | 25.62 | 5.12 | 20.5 | 0.88 | 0.17 | 8.68 | 26.08 |
| panicle weight (g) | 148.57 | 25.07 | 123.50 | 20.70 | 102.8 | 0.76 | 0.13 | 33.90 | 15.90 |
| 1000-Grain Weight ( g) | 57.46 | 51.11 | 6.34 | 5.32 | 1.02 | 0.11 | 0.09 | 9.08 | 41.63 |
| Pro-Vitamin A (mg/l) | 3.96 | 1.58 | 2.38 | 1.37 | 1.01 | 0.60 | 0.34 | 2.36 | 33.85 |
| Grain Yield (kg/ha) | 124.4 | 44.00 | 80.40 | 53.2 | 27.2 | 0.64 | 0.42 | 91.70 | 10.57 |
| | | | | **SAMSORG 43 × CSR01** | | | | | |
| Days to 50% flowering | 43.72 | 2.02 | 41.70 | 39.81 | 1.89 | 0.95 | 0.91 | 69.82 | 75.76 |
| Plant Height (cm) | 150.1 | 24.13 | 125.97 | 108.5 | 17.47 | 0.83 | 0.75 | 197.57 | 87.46 |
| Panicle Length (cm) | 27.01 | 0.62 | 26.39 | 18.30 | 8.09 | 0.97 | 0.67 | 31.76 | 90.66 |
| panicle weight (g) | 68.4 | 21.83 | 46.57 | 26.57 | 20.00 | 0.68 | 0.38 | 45.62 | 23.14 |
| 1000-Grain Weight ( g) | 87.81 | 26.67 | 61.14 | 10.21 | 50.93 | 0.69 | 0.11 | 16.95 | 72.94 |
| Pro-Vitamin A (mg/l) | 5.80 | 0.28 | 5.53 | 3.52 | 2.01 | 0.95 | 0.60 | 6.10 | 90.61 |
| Grain Yield (kg/ha) | 158.00 | 76.00 | 82.00 | 56.30 | 25.7 | 0.89 | 0.35 | 97.05 | 12.26 |

$\sigma_P^2$ = Phenotypic variance, $\sigma_G^2$ = Genotypic Variance, $\sigma_E^2$ = Environmental Variance, $\sigma_D^2$ = Dominance variance, $\sigma_A^2$ =Additive variance.

### 4.6 Correlation Analysis

Among the six crosses, SAMSORG 17 × CSR01 (r=0.591), SAMSORG 43 × SAMSORG 14 (0.584), SAMSORG 43 × CSR01 (r=0.543) PVA showed positive and significantly genotypic correlation with grain yield (Table 4.16-4.17).Grain yield showed positive significant genotypic correlation with panicle weight (r=0.985), plant height (r=0.626) and 1000-grain weight (r=0.561) and showed positive and significant phenotypic correlation plant height (r= 0.533), panicle weight (0.928) in SAMSORG 17 × SAMSORG 44. In the same cross, grain yield was negatively and significantly correlated with panicle length.

In three out of the six crosses, PVA showed positive and significantly genotypic correlation with plant height (r=0.591, 0.584, 0.543) in SAMSORG 17 × CSR01, SAMSORG 43 × SAMSORG 14 and SAMSORG 43 × CSR01 respectively (Table 4.16-4.17). PVA inSAMSORG 17 × CSR01 (r=0.606) also showed positive and significant genotypic correlation with panicle weight.

Table 4.16 Phenotypic (lower diagonal) and genotypic (upper diagonal) correlations between pro–vitamin A and agronomic traits of six generations of sorghum involving SAMSORG 17, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014.

| Trait | Days to 50% flowering | Grain Yield (kg ha$^{-1}$) | Plant Height (cm) | Panicle Length (cm) | Panicle Weight (g) | Pro-Vitamin A (mg/l) | 1000-Grain Weight (g) |
|---|---|---|---|---|---|---|---|
| **SAMSORG 17 × SAMSORG 44** | | | | | | | |
| Days to 50% flowering | | 0.029 | -0.082 | -0.027 | 0.004 | 0.088 | -0.218 |
| Grain Yield (kg/ha) | -0.037 | | 0.626** | -0.026 | 0.985** | -0.066 | 0.561* |
| Plant Height (cm) | -0.131 | 0.533* | | 0.188 | 0.132 | 0.128 | 0.005 |
| Panicle Length (cm) | -0.059 | -0.428* | 0.132 | | 0.047 | 0.269 | -0.067 |
| Panicle Weight (g) | 0.082 | 0.928** | 0.533* | 0.003 | | -0.073 | 0.129 |
| Pro-Vitamin A (mg/l) | 0.081 | -0.014 | 0.106 | 0.279 | 0.027 | | -0.112 |
| 1000-Grain Weight (g) | -0.078 | 0.512* | 0.445* | 0.007 | 0.090 | -0.241 | |
| **SAMSORG 17 × SAMSORG 14** | | | | | | | |
| Days to 50% flowering | | 0.605** | 0.129 | -0.083 | 0.557* | 1.000 | 0.181 |
| Grain Yield (kg/ha) | 0.076 | | 0.469* | 0.579* | 0.987** | 0.211 | 0.074 |
| Plant Height (cm) | 0.128 | 0.434* | | -0.033 | 0.178 | 0.077 | 0.095 |
| Panicle Length (cm) | -0.127 | 0.508* | -0.120 | | 0.184 | -0.212 | 0.015 |
| Panicle Weight (g) | 0.177 | 0.600** | 0.489* | -0.024 | | 0.183 | 0.166 |
| Pro-Vitamin A (mg/l) | 0.097 | 0.014 | 0.274 | 0.099 | 0.091 | | 0.181 |
| 1000-Grain Weight (g) | 0.049 | 0.588** | 0.024 | 0.231 | 0.182 | 0.105 | |
| **SAMSORG 17 × CSR01** | | | | | | | |
| Days to 50% flowering | | 0.003 | -0.182 | -0.027 | 0.002 | 0.018 | -0.183 |
| Grain Yield (kg/ha) | -0.07 | | 0.036 | 0.675** | 0.930** | 0.591** | 0.581* |
| Plant Height (cm) | -0.096 | 0.490* | | 0.001 | 0.179 | 0.245 | 0.064 |
| Panicle Length (cm) | 0.041 | 0.527* | -0.07 | | 0.133 | 0.041 | 0.045 |
| Panicle Weight (g) | -0.018 | 0.897** | 0.295 | -0.054 | | 0.606** | 0.005 |
| Pro-Vitamin A (mg/l) | -0.098 | 0.027 | 0.044 | -0.031 | 0.722 | | 0.066 |
| 1000-Grain Weight (g) | 0.027 | 0.523* | 0.111 | -0.022 | -0.13 | -0.116 | |

* Significant at 5% level, ** Significant at 1% level.

Table 4.17 Phenotypic (lower diagonal) and genotypic (upper diagonal) correlations between pro–vitamin A and agronomic traits of six generations of sorghum involving SAMSORG 43, SAMSORG 44, SAMSORG 14 and CSR01 evaluated at Samaru in 2014

| Trait | Days to 50% flowering | Grain Yield (kg ha $^{-1}$) | Plant Height (cm) | Panicle Length (cm) | Panicle Weight (g) | Pro-Vitamin A (mg/l) | 1000-Grain Weight (g) |
|---|---|---|---|---|---|---|---|
| **SAMSORG 43 × SAMSORG 44** | | | | | | | |
| Days to 50% flowering | | 0.241 | 1.000** | -0.159 | 0.026 | 0.003 | 0.082 |
| Grain Yield (kg/ha) | 0.119 | | 0.746** | 0.498* | 1.000** | 0.141 | 0.302 |
| Plant Height (cm) | 0.199 | 0.719** | | -0.001 | 0.294 | 0.196 | 0.064 |
| Panicle Length (cm) | -0.112 | 0.614** | -0.006 | | 0.044 | -0.223 | 0.199 |
| Panicle Weight (g) | 0.033 | 0.768** | 0.870** | -0.017 | | 0.057 | 0.056 |
| Pro-Vitamin A (mg/l) | 0.036 | 0.186 | 0.094 | -0.290 | 0.193 | | 0.185 |
| 1000-Grain Weight (g) | 0.924** | 0.691** | 0.870** | 0.054 | 0.253 | 0.015 | |
| **SAMSORG 43 × SAMSORG 14** | | | | | | | |
| Days to 50% flowering | | 0.038 | -0.030 | 0.191 | 0.005 | 0.305 | -0.004 |
| Grain Yield (kg/ha) | 0.054 | | 0.449* | 0.688** | 0.993** | 0.584* | 0.655** |
| Plant Height (cm) | 0.155 | 0.558* | | -0.045 | -0.054 | -0.266 | -0.131 |
| Panicle Length (cm) | 0.279 | 0.542* | -0.895 | | 0.105 | 0.299 | -0.245 |
| Panicle Weight (g) | 0.081 | 1.085** | -0.542* | 0.069 | | 0.603** | 0.292 |
| Pro-Vitamin A (mg/l) | 0.054 | -0.014 | -0.036 | 0.255 | -0.093 | | -0.038 |
| 1000-Grain Weight (g) | -0.454 | 0.503* | -0.455* | 0.715 | 0.267 | -0.272 | |
| **SAMSORG 43 × CSR01** | | | | | | | |
| Days to 50% flowering | | 0.072 | 1.000** | 0.441 | -0.119 | 0.123 | 0.003 |
| Grain Yield (kg/ha) | 0.089 | | 1.000** | -0.167 | 0.939** | 0.543* | 0.514* |
| Plant Height (cm) | -0.001 | 1.017* | | 1.000** | 1.000** | 0.044 | 0.060 |
| Panicle Length (cm) | 0.286 | -0.539* | 0.082 | | -0.217 | 0.224 | 0.002 |
| Panicle Weight (g) | -0.163 | 0.979** | 1.029** | -0.375 | | 0.516* | 0.103 |
| Pro-Vitamin A (mg/l) | 0.272 | -0.023 | -1.152 | 0.122 | -0.335 | | 0.165 |
| 1000-Grain Weight (g) | -0.065 | -0.569* | -0.819** | 0.063 | -0.119 | -0.012 | |

* Significant at 5% level, ** Significant at 1% level

# CHAPTER FIVE

## 5.0 DISCUSSIONS

The highly ($P < 0.01$) significant differences among the generations for days to 50% flowering, plant height, panicle length, panicle weight, grain weight per panicle, 1000-grain weight, PVA and grain yield in each of the six crosses indicates the existence of genetic variation.These results are in conformity with findings of Muhammad *et al.* (2007) who reported significant differences among genotypes of sorghum for agronomic traits.Wolie *et al.* (2013) also reported similar results in millet.Therefore, generation means for the six crosses could be analyzed to estimate the genetic parameters for the traitsthereby offering scope for selection for the development of desirable sorghum genotypes.

A wide range of variability was observed for plant height, days to 50% flowering, panicle length, panicle weight, 1000 grain weight, grain weight per panicle and PVA in the six generations this is in agreement with the findings of Wolie *et al.* (2013) and Zinaw *et al.*, (2014) who reported that finger millet and soybean genotypes respectively showed wide range of variability for, plant height, seed yield per plant, hundred seed weight, days to 50% flowering. The mean performance of these generations also indicates that they have diverse genetic backgrounds and could serve as sources of desirable genes for improvement in sorghum. The $F_1$ hybrids for PVA in the six crosses were midway between the parental values indicating preponderance of additive gene action. $F_1$ hybrids matured later than the parent generations similar pattern is seen for plant height, panicle length, panicle weight, 1000 grain weight, grain weight per panicle and grain yieldacross the six crosses. The mean values for the backcrosses ($BC_1P_1$ and $BC_1P_2$) were skewed towards their respective recurrent parents. The $F_2$ generation for Pro-vitamin A showed continuous distribution,

suggesting the involvement of more than one gene controlling the inheritance of PVA trait and it also suggests that the gene controlling PVA trait are dispersed among the parents. The wide range for $F_2$ generations was these observations clearly demonstrate that the PVA concentration is under polygenic control, and the large variance in $F_2$ generation could be due to segregation and recombination among the favorable genes/alleles contributed by both the parental lines. Interestingly, the mean values for PVA and agronomic traits for $BC_1P_1$ generation was similar to $P_1$ parents, while the mean for $BC_1P_2$ was towards $P_2$ parent this suggested that the $P_1$ parent contributed more favorable genes/allelic combinations for the target trait, while it got diluted in $BC_1P_2$ generation due to unfavorable alleles contributed by the $P_2$ parent this corroborates with the findings of Anshuman*et al.* (2012) in maize inbred lines.

One or more Individual scale tests, A, B and C were significantly different from zero for the generation means of each trait in the six crosses. The results corroborate with the findings of Akhshi *et al.* (2014), Fekadu *et al.* (2009). This indicates the insufficiency of the simple additive-dominance model to explain the inheritance of plant height, days to 50% flowering, panicle length, panicle weight, 1000 grain weight, grain weight,grain yield and PVA in each of the crosses and suggest a major role of epistasis in controlling the inheritance of these studied traits (Akhshi *et al*., 2014).

In addition to testing in A, B and C scales, data were further subjected to joint scaling test Cavalli, (1952). The goodness of fit test of the model estimated for plant height, days to 50% flowering, panicle length, panicle weight, 1000 grain weight, grain weight,grain yield and PVA in the six crosses revealed thesignificance chi-square ($\chi^2$)for these traitsthis corroborates with the findings of Akhshi *et al* (2014) who reported significance of chi-

square values for agronomic traits in sorghum. Thisalso shows that the additive-dominance model was inadequate to explain the genetic differences observed for these traits in all the crossesindicating the presence of non-allelic interactions also suggesting possible involvement of digenic interaction of the traits. Thus, it is difficult to estimate the genetic mechanism of these traits by this simple model. Hence six parameters model was needed to explain the genetic variation, due to inadequacy of the three-parameter genetic model and significance of scaling tests, six parameter model suggested by Hayman, (1958) was used to estimate the genetic components and when all the components were significant in the model, no further analysis was carried out. In the event of non-significance of any one of the components, the same was deleted. This procedure was followed until all the components were significant in the model. Where four or five genetic components were significant this indicates the presence of digenic non allelic interaction.

Additive gene effect played a predominant role in the inheritance of days to 50% flowering and epistasis was also evidenced for this trait in most of the crosses indicating that selection in the early generation will be effective (Akhshi *et al*., 2014). Dominance and non-allelic gene interactions played a predominant role in the inheritance of days to 50 % flowering in SAMSORG 43 × SAMSORG 44 indicating that selection in the early generation will not be effective for this trait in this cross. The non-significantAdditive × dominance (j) in SAMSORG 43 × SAMSORG 44 and SAMSORG 43 × SAMSORG 14 indicates that selection under selfing can be effective for the breeding of days to 50% flowering in this crosses as suggested by (Akhshi *et al*., 2014). Additive and epistasis is more important than dominance to a breeder of self-pollinating species, because dominance will be broken by segregation following hybridization (Akhshi *et al*; 2014). Generally the significance of

additive × dominance (j) for days to 50% flowering, panicle weight, grain weight and PVA and grain yield in most of therevealed that selection through selfing is not effective for improving these traits as observed by Farshadfar *et al*. (2001) and Sharifi (2005) because among the digenic interactions, additive × dominance interraction is more fixable and more useful for plant breeders (Sunil-Kumar,2005).Additive component played a predominant role in the control of plant height. Epistasis was evident for the control of plant height in all the crosses except in SAMSORG 43 × SAMSORG 14. This result is not in agreement with the findings ofAkhshi *et al*. (2014) who suggested predominant role of dominance in the control of plant height. Reason for differences in findings could be that favourable genes in both parents contributed to the expression of plant height in six crosses. The predominance of additive component for plant height in the present study is indicating that selection in early generation will be effective and that there is a good potential for the improvement of these traits as selection can be done in the early segregating generation.

The prevalence of epitasis in the inheritance of panicle length in all the crosses indicates greater genetic diversity in the parental lines and selection may not be possible Akhshi *et al*. (2014) except in SAMSORG 43 × CSR01 where Additive and dominance were significant but dominance was predominant in the genetic control of this trait. Additive component played a predominant role in the control of panicle weight for panicle weight, grain weight and 1000 grain weight in most of the crosses indicating that selection in early generation will be effective.

Additive effect also played predominant role in the control of PVA trait in addition, the dominance effect was significant but with undesirable direction (negative) indicating that there is duplicate interaction between dominant decreasing alleles across all the crosses for PVA. The degree of association and dispersion genes is determined by the sign of (i) (additive x additive) when (i) additive x additive is positive it is an indication that the genes are in association but when (i) additive x additive is negative the genes are in dispersion. For PVA, the genes are in dispersion for the six crosses because the component (i) additive x additive is negative. From the six parameter model it was deciphered that PVA and1000 grain weightexhibited significance for all the tested six genetic components in most crosses suggesting the presence of linkage or higher order epistatic interactions.

The development of effective breeding program depends on existence of genetic variability. Genetic variability within a given population is very important as it indicates the presence of heritable characters, most especially additive genetic variance which could be exploited in crop improvement programs. Genetic variability is a prerequisite for measuring the effectiveness of selection in any breeding program.Sufficient genetic variability present in the material used for this study will facilitate improvement through selection for days to 50% flowering, plant height, panicle length, panicle weight, grain weight, 1000-grain weight, grain yield and PVA traits.

The separation of total genetic variance into its components revealed presence of variability due to additive (a) and dominance (d) gene effects for PVA and agronomic traits studied.High broad sense heritability for PVA was estimated in the six crosses these estimates indicate that genetic factors play a major role in determining the PVA concentration. These observations are in congruence with report from Chander *et al.*,

(2008) who reported 85% broad sense heritability for PVA estimated in a maize RIL population. Moderate to high heritability estimates for carotenoids have also been reported in the past for maize (Wurtzel *et al.*,2004). High heritability of PVA could be due to the involvement of a few major genes in the carotenoid biosynthetic pathway (Pfeiffer *et al.*,2007). Therefore, expressions for PVA and most of the agronomic traits were genetic which can be exploited in breeding programs. This finding is in agreement with the findings of Basu (1981)and Abu-Gasim and Kambal (1985) and Bello, *et al.* (2001) who reported that the expressions for several quantitative characters in sorghum genotypes were genetic. Zaveri *et al.*,(1989) also reported similar results in pearl millet. Bello *et al.*, (2001) observed that high environmental variance estimate for some characters similar to what was obtained in this study for plant height in SAMSORG 17 × SAMSORG 44 could be attributable to large sample size.

The greater the genetic variability the higher would be the heritability hence the better the chances of success to be achieved through selection. In this study days to 50% flowering, plant height, panicle length, panicle weight, grain weight, 1000-grain weight, grain yield and pro-vitamin A showed high broad sense heritability indicating the possibility of a positive response to selection. This is because there is a likelihood of transferring the heritable components from parents to offspring during breeding. Robinson *et al*. (1949) and Dergicho *et al.* (2015) classified heritability values as high (>60%), moderate (30-60%) and low (0-30%). High broad sense heritability estimate also indicates low influence of the environment and that the variation observed was mainly under genetic control this may also be attributed to uniform environmental conditions during the conduct of the experiment (Fekadu *et al*., 2003).The high heritability obtained from days to 50% flowering, plant

height, panicle length, panicle weight, grain weight, 1000-grain weight, and grain yieldagreed with the findings of Eckebil *et al*. (1977); Totok (1997); Aba *et al.* (2001) and Biswas *et al.* (2001). High narrow sense heritability observed for panicle length, grain yield in most crosses indicates the importance of additive genetic variation. However, low narrow sense heritability versus high broad sense heritability as in the case of days to 50% flowering in SAMSORG 43 × SAMSORG 44 signify the importance of dominance and inability of additive genetic components to induce earliness for days to 50% flowering in this cross.

Estimates of genetic advance help in understanding the type of gene action involved in the expression of polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993). Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al.*, 1955). High heritability associated with high genetic advance of mean was observed for days to 50% flowering in the six crosses this corroborates the report of Deepalakshmi and Ganesamurthy (2007).

Plant height, panicle weight, 1000 grain weight and grain yield showed high heritability associated with high genetic advance of mean in most of the crosses, this corroborates with the report of Deepalakshmi and Ganesamurthy (2007) and Jain and Patel (2012) who revealed high heritability accompanied with high genetic advance (GA) as per cent of mean for plant height, panicle weight, 1000 grain weight and grain yield indicating that these traits are under the influence of additive gene action in their expression and selection of genotypes based on phenotypic performance would be useful in a breeding program and

selection may be effective in early generations for these traits, hence, selection in the segregating generation would be fairly effective for them.In the present study, panicle length showed high heritability combined with low genetic advance in SAMSORG 43 × SAMSORG 14,this is in corroboration with the report of Umakanth *et al*, (2004) and Umakanth and Kuriakose (2005) who reported that estimates of variance indicated predominance of non-additive gene action for panicle length may indicate that the trait is governed by non-additive genes hence heterosis breeding would be recommended for improvement of this trait.

Correlation coefficient is a statistical measure, which denotes the degree and magnitude of association between any two casually related variables. This association is due to pleiotropic gene action or linkage or more likely both. In plant breeding correlation measures the mutual relationship between two characters and it determines character association for yieldimprovementand other economic characters. Since the association pattern among yield components help to select the superior genotypes from divergent population based on more than one interrelated characters. Thus information on the degree and magnitude of association between characters is of prime important for the breeder to initiate any selection plan (Kumar, 2013).The positive association between possible pair of traits suggested the possibility of correlated response to selection so that with the improvement of one trait, there will be an improvement in the other positively correlated trait. The positive genotypic correlation allows simultaneous genetic improvement for grain yield. This is because a positive genetic correlation between two desirable traits makes the job of plant breeder easy for improving both traits simultaneously. PVA content showed non-significant genotypic and phenotypic correlation with grain yield in SAMSORG 17 ×

SAMSORG 44, SAMSORG 17 × SAMSORG 14 and SAMSORG 43 × SAMSORG 44 this result corroborates with the findings of Willy*et al.* (2014) who reported grain yield was not significantly correlated with PVA concentration in maize, indicating that both traits could be improved simultaneously but in SAMSORG 17 × CSR01, PVA content showed significant genotypic correlation with grain yield in most of the crosses this also agrees with the result of Egesel *et al*., (2003) who reported highly significant difference and positive correlation between grain yield and total carotenoids in maize. This result indicates that opportunities exist to increase β carotene (PVA) without lowering grain yield and other desirable agronomic traits.

Grain yield showed significant positive phenotypic correlations with plant height, panicle length, grain weight, 1000-grain weight and panicle weight in the six crosses this is in conformity with Ezeaku and Mohammed (2006) who found high positive phenotypic correlation coefficients of grain yield with plant height. From the result obtained in this study there is possibility of simultaneous improvement of grain yield through indirect selection of these positively correlated traits. Days to 50% flowering showed significant positive correlation with 1000-grain which corroborates with Sharma *et al*., (2006) who reported that the days to 50% flowering showed highest and positive correlation with 1000 grain weight in sorghum. There was no significant association between panicle length and days to 50% flowering in the six crosses studied which corroborates with Mahajan *et al*., (2011) who reported that panicle length had non-significant association with days to 50% flowering and this indicates that these traits could be improved independently. Grain yield also showed significant negative correlation with and panicle length in SAMSORG 17 × SAMSORG 44 and SAMSORG 43 × CSR01 which corroborates with Goud and Asawa

(1978) who reported negative correlation between panicle length and grain yield. Positive correlation of pairs of traits indicates the possibility of correlated response to selection. Contrary to this, the negative correlation prevents or impedes the simultaneous improvement of those traits along with each other. Generally, the existence of strong positive correlation betweenPVA,grain yieldand agronomic traits helps in identifying traits that could be used for indirect selection for improvement. Therefore, to facilitate selection in breeding for PVA, high yield and other desirable traits, it is logical to examine various components and give more attention to those having the greatest influence.

# CHAPTER SIX

## 6.0 SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

The existence of genetic variations were observed in the materials used in this study.

Estimates of the six parameters for the various gene effects showed that additive, dominance and epistatic gene effects contribute significantly to the inheritance of the traits studied, with preponderance of additive gene effects in most of the crosses.

Additive effect played predominant role in the genetic control of PVA trait. In addition, dominance effect was significant but with undesirable direction the result indicates that there is duplicate interaction between dominant decreasing alleles across all the crosses for this trait. Generally both additive and non-additive gene actions are essential for yield improvement in sorghum.

Days to 50% flowering, plant height, panicle weight, 1000-grain weight, grain yield and Pro- vitamin A in most of the crosses showed high heritability coupled with high genetic advance. This indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits hence selection in the segregating generation would be fairly effective for them.

Grain yield showed positive phenotypic associations with plant height, panicle weight per plant, 1000-grain weight across the six studied crosses. Generally, the values of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for most of the traits suggesting.

## CONCLUSION

Generally, five of the $F_1$ generations were the top performing for grain yields. Analysis of variance revealed significant difference among the genotypes in respect to all the characters studied indicating high degree of variability and diversity among the genotypes. PVA concentration was controlled primarily by additive gene action. In addition, dominance effect was significant, but in an undesirable direction. The result indicates that there is duplicate interaction between dominant decreasing alleles for the six crosses for this trait. Also, additive effect played predominant role in the genetic control of most of the other agronomic traits studied. PVA content and 1000 grain weight of three crosses in this study exhibited significance for all the six parameters tested, suggesting the presence of linkage or higher order epistatic interactions. Generation mean analysis indicated that epistasis is the integral part of genetic architecture of the materials used in the investigation which the breeder cannot ignore it.

## RECOMMENDATIONS

Since genotypic variation and high heritability for PVA trait has been observed in sorghum genotypes from this study, it is recommended that:

1. National and international research institutions should collaborate to exploit this genotypic variation to ensure increased production of PVA content in sorghum because nutritionally improved varieties will continue to be grown and consumed year after year, even if government attention and international funding for micronutrient and vitamin A issues fade.

2. The new hybrids developed with increased PVA as well as high yield such as; $F_1$ in SAMSORG 17 × SAMSORG 44 (8.6mg/l), $BC_1P_1$ in SAMSORG 17 × CSR01 (11.60mg/l), $BC_1P_1$ inSAMSORG 17 × SAMSORG 14 (12.70mg/l), $BC_1P_1$ in SAMSORG 43 × SAMSORG 14 (13.10mg/l) and $BC_1P_1$ SAMSORG 43 × SAMSORG 44 (19.90mg/l) should be tested, released made available to indigenous sorghum farmers via registered seed companies and other seed agencies.

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