APPLICATION OF HETEROSIS AND COMBINING ABILITY IN SOME SORGHUM CROSSES (*Sorghum bicolor* (L) MOENCH) FOR AGRONOMIC AND MALTING QUALITY TRAITS

BY

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DECLARATION

I hereby declare that this dissertation titled "Application of Heterosis and Combining ability in some Sorghum crosses [*Sorghum bicolor* (L) Moench] for agronomic and malting quality traits" was written by me and it is a record of my own research work in the Department of Plant Science under the supervision of Prof. Mary Yeye. It has not been presented in any previous application for a higher degree. References made to published literature have been fully acknowledged.

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CERTIFICATION

The dissertation entitled "Application of Heterosis and Combining ability in some Sorghum crosses [*Sorghum bicolor* (L) Moench] for agronomic and malting quality traits" by Badiru, Evilla Olabiyi meets the regulations governing the award of the degree of Master of Science in Plant Breeding of Ahmadu Bello University, Zaria, and is approved for its contribution to scientific knowledge and literary presentation.

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DEDICATION

To God Almighty for wisdom, sound health, favour and life. To Him alone be all the glory in Jesus name, Amen.

To my husband OLABIYI, and sons FEMI and DAMI for their patience and understanding.

To my mother Christiana E. Bassey and mother in-law Mary Badiru for their daily prayers.

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ABSTRACT

A study was carried out to examine the Application of Heterosis and Combining ability in some Sorghum crosses for agronomic and malting quality traits. Line x tester procedure was used to intermate three sterile and five restorer lines to generate fifteen hybrids. Twenty seven entries consisting of fifteen hybrids, eight parents and four checks were evaluated at two locations; Samaru and Kadawa. From the analysis of variance, significant mean squares were observed among the entries and hybrids for all the agronomic(heading date, plant height, panicle length, 1000 grain weight, yield per hectare) and malting quality traits (germination capacity, malting loss, protein, starch, α and β - amylase). Similarly, mean squares of location x entries revealed highly significant differences ($p<0.01$) for all the agronomic and malting quality traits. Combining ability analysis of variance indicated that General Combining Ability (GCA) (Line), GCA (tester) and Specific Combining Ability SCA (line x tester) were significant for all the agronomic and malting quality traits, indicating the importance of additive and non-additive gene actions in the expression of these characters. However, the estimate of variance components showed that SCA variances were higher than the GCA variance revealing the preponderance of non-additive genes. Some parents having significant negative general combing ability for days to heading, malting loss and significantly positive indication for 1000 grain weight, grain yield, alpha and Beta amylase, protein and starch were considered as good combiners. High level of heterosis was observed for all the malting and agronomic characters. However, the level of heterosis varied from one location to another greatly. Across the locations, most of the hybrids showed negative to positive heterosis. . ICSA11 XCF35.5 recorded the highest heterosis value for germination capacity (1.69%). ICSA 731 x KSV14 (Samsorg8) showed a desirable lowest negative and significant heterosis for heading date, lowest value for 1000 grain weight

and yield . ICSA38 x NR71168 recorded the height heterosis value for 1000 grain weight and α- amylase. ICSA731 x Chokwe exhibited the highest value of high parent heterosis for malting loss, starch and protein. ICSA38 X Chokwe showed the highest high parent heterosis for grain yield (44%) and lowest value for β - amylase. Some specific cross combinations gave very high yields with a maximum of 3200 kg/ha. Information on general and specific combining ability and heterosis for those traits could contribute to more efficient breeding programme. All the pollinators proved to be effective restorers on the A1 system of cytoplasmic male sterility. Correlations among the characters in sorghum across locations showed that there was a positive and significant correlation between grain yields with heading date, beta amylase, grain weight, malting loss and starch. Consequently, simultaneous selection for any of those characters could lead to indirect improvement of grain yield and malting quality. The hybrids from the following crosses: ICSA38 X CHOKWE has good potential for grain yield while ICSA38 X CF35.5 and ICSA38 X NR71168 have potential for high yield and malting quality .These could be recommended for use in the food and brewery industries.

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CHAPTER 1

1.0 INTRODUCTION

Sorghum (*Sorghum bicolor* (L.) Moench) belongs to the tribe Andropogonae of the grass family Poaceae. Sorghum is the fifth most important cereal crop in the world, after rice, wheat, maize and barley. (FAO, 2007). It constitutes the main grain food for over 750 million people who live in the semi arid tropics of Africa, Asia and Latin America (FAO, 2007). Sorghum is indigenous to semi arid tropics of Africa (Dewar, 2003). Typically, sorghum is an annual crop, but some varieties are perennial. Sorghum is a very versatile and hardy crop that is adapted to varying locations, from the wet Guinean savanna through to the vast dry sudanian savanna and semi-arid Sahel zones in Nigeria. These cultivated areas in Nigeria lie between latitudes 6˚ 30' N and 13˚ 55' N of the country (Obilana, 1984).Moisture is the agro-climatic limiting factor for sorghum production in most areas. The morphological characteristics of the crop make it one of the most drought tolerant cereal crops currently under cultivation. It has large root to surface area ratio and during drought it rolls its leaves to reduce water loss by transpiration (Haussmann *et al*, 1998).

The total world sorghum production in 2008/2009 was over 64 million tones, out of which 27 million tons were produced in Africa (FAO, 2010). In Nigeria, Sorghum production had raised from 6,197 metric tones in 2002 to 9.318 metric tones in 2008.The area under cultivation also has increased from 6.93 million hectares in 2001 to 7.07 and 7.62 million hectares in 2002 to 2008, respectively. In 2009, sorghum production dropped from 5.271metric tones to 4.784metric tones in 2010(FAO STAT, 2011).In Northern Nigeria, a large area is cropped to late sorghum and it accounts for about 90% of the total area cropped to Sorghum (Azeaku and Aba, 2005). Despite the increase in area under cultivation, the average yield trend is downward. Areas sown to Sorghum in the United

State of America is low but productivity is high, estimated Sorghum yield in USA stands at 3.9t/ha. (FAO, 2010) .The largest group of the producers in Africa is the small-scale subsistence farmers with minimal access to production inputs such as fertilizers, pesticides, improved seeds (hybrids or varieties), good soil, water and improved credit facilities in addition to many socio-economic obstacles. In view of the low input systems, productivity levels are very low throughout the African countries and India, ranging from 1.5 to less than 0.6 ton per ha in Ethiopia and Sudan respectively (FAO, 2010). In general, the most significant change in sorghum productivity has been the development of hybrid sorghum.

The increased uses of Sorghum as food in sub-tropical Africa could alleviate the problem of chronic undernourishment, as the air-dried whole grain Sorghum contains approximately 8-19% moisture, 68-74% carbohydrates, 8-15% protein, 2-5% fats, 1-3% fibre and 1.5-2.0% ash (Dasai*et al.,* 1992). The grain is consumed in the form of paste, porridge and confectionaries. Soft and sweet grains are also used as concentrate feeds while the shoots are used as fodders, silage and hay for livestock. The stalk is used for fencing, making baskets, hats, mats and roofing materials as well as fuel (Dogget, 1988). Appreciable quantities of Sorghum are being used by commercial food industries in the production of flour, alcoholic and malted beverages. Some sorghum varieties are rich in antioxidants and all sorghum varieties are gluten free, an attractive alternative for wheat allergy sufferers. The stems of other types yield sugar, syrup, and even liquid fuels for powering vehicles or cooking meals (Murty and Kumar, 1995; Rooney, 2000, Taylor *et al*., 2000). The living plants are used for windbreaks, for cover crops, and for staking yams and other heavy climbers. Sorghum promises to be a "living factory" as Industrial alcohol, vegetable oil, adhesives, waxes, dyes, sizing for paper and cloth, are just some of the products that could be obtained. Malts of some sorghum varieties display α-amylase

and **β**-amylase activities comparable to those of barley, making them useful for various agro-industrial foods (Palmer, 1991) .Selection of varieties meeting specific local food and industrial requirements from this great biodiversity is of high importance for food security. In developing countries in general and particularly in West Africa, demand for sorghum is increasing. This is due to not only to the growing population, but also to the countries' policy to enhance their processing and industrial utilization (Akintayo and Sedgo, 2001). The ultimate goal is to enhance sorghum production efficiency and make good use of new economic opportunity in the brewing, non alcoholic beverages and weaning foods industries, which are offered today to sorghum growers (USA Grain Council, 2011). Sorghum has the potential to improve nutrition, boost food security and foster rural development.

Local demands for cereals, including grain sorghum is progressively increasing due to Population growth and total production is not sufficient to cover the internal demands (Ali, 2000).The discovery of cytoplasmic male-sterility in sorghum by Stephens and Holland (1954) and Dogget (1969) facilitates the commercial utilization of hybrid vigour. Hybrid cultivars make use of male sterility to enhance the combining ability of the parent lines, resulting in heterosis and significant increases in phenotypic traits such as yield, plant height and days to flowering (Reddy *et al*., 2006).

The utilization of heterosis in various crops throughout the world has tremendously increased the production of human food and livestock feed. In USA, Sorghum production has tripled since the adoption of hybrid Sorghum cultivars and exploitation of hybrid vigour in conjunction with intensive management practices (Quinby, 1974; Doggett, 1988). Another important requirement for increased production is the multiplication and supply of high quality seed to farmers, with the advent of 'hybrid' cultivars, producing good quality seed is essential.

Sorghum production in Africa is widespread with low yields due to low inputs and use of open- pollinated varieties; for lack of commercialized hybrids. This situation has forced most farmers to grow maize hybrids even in areas not suitable resulting in crop failure and food insecurity (Taylor, 2001).

In breeding programmes, information on combining ability of parents and heterosis of crosses are very important. By analyzing combining ability and estimating degree of heterosis, clues about the nature of gene action, desirable parent and important yield traits will emerge, particularly in those crops which are amenable to commercial production of F_1 hybrid seed using cytoplasmic male sterility. Little information is available on the development of hybrid Sorghum using the cytoplasmic male-sterility mechanism and there is currently a paucity of information on the extent and nature of expression of heterosis among hybrids.

Parents that will contribute favourable combination of genes for yield and other agronomic traits are the most sought. As such, studies on heterosis and combining ability involving local germplasm are essential for African breeding programmes in particular and the Sorghum breeding work at large. A more complete understanding of the phenomenon of heterosis is essential to effect continued improvement in Sorghum breeding programme.

Therefore, the objectives of this study are:

1. To generate hybrids using A – lines.
2. To evaluate combining abilities of sorghum lines used as parents
3. To evaluate a comparative expression of heterosis among the F_1 hybrids generated.
4. To determine the proximate and malting quality traits in the hybrids generated.

CHAPTER 2

2.0 LITERATURE REVIEW

2.1 HYBRID DEVELOPMENT IN SORGHUM

Commercial exploitation of F1 hybrids in grain sorghum started in USA by the mid-1950s with the use of the cytoplasmic male sterility system (CMS) A1 (Quinby, 1974).When the cytoplasmic male sterility (CMS) system was implemented in sorghum; it allowed a cost effective way to produce F_1 sorghum hybrids. Once hybrid seed was produced, it was rapidly accepted by sorghum producers and replaced sorghum open pollinated cultivars in a period of less than ten years (Maunder, 1999). Currently, most sorghum hybrid seed production still relies on the A1 CMS system described by Stephens and Holland (1954). Hybrid sorghum predominates the US and world markets, however OP populations still represent a significant component of production. (Havey, 2004).

Cytoplasmic Male Sterility is routinely used to produce hybrid seed of sorghum. Although several sources of CMS have been described (Al through A4), the predominant male-sterile cytoplasm is the Al (milo) cytoplasm (Holland and Stephans, 1954; Pring *et al*., 1995 Schertz *et al*., 1997). Today, in the entire sorghum seed industry, the Sorghum hybrids grown by farmers in the USA were based on Milo (A1) type of cytoplasm. In other few instances are other cytoplasm used to induce male sterility. Different cytoplasmic male sterility systems have been developed. The A_2 cytoplasm was first reported by Schertz (1977). The source of the original A_2 cytoplams is 1S1266C, which is from the Caudatum Nigrican group (Guinea race) from Ethiopia. The source of nuclear genes and the maintainer is 1S5344C, which is in the Roxburghii group (Guinea Race) from India. The designation A3 was given to the male sterility inducing cytoplasm in

1S1112C by Quinby (1980) who proposed that plants with A3 cytoplasm are "ultra females" thus reducing the probability of finding restorers.

Fertility restoration of the Al cytoplasm requires the action of two complementary nuclear male-fertility restorers *(RfI* and *RJ2),* similar to T-cytoplasmic maize. (Havey, 2004).Variation in grain sorghum yield among different sorghum production systems throughout the world is mainly due to the use of hybrids and improved equipment and production techniques in developed countries, compared with the use of land races and subsistence agriculture that predominate in the developing world. However, male sterility in plants caused by the interaction of sterility inducing factors in the cytoplasm with genetic factors in the nucleus is called cytoplasmic genetic male sterility. In sorghum, such system was discovered by Stephens and Holland in 1954 who observed from Milo x Kafir crosses, that cytoplasmic male-sterility (CMS) existed, resulting from an interaction between Milo cytoplasm (A1) and Kafir nuclear genome. The F_2 generation of the cross Milo x Kafir exhibited some male sterile plants, whereas the progenies of the reciprocal cross, Kafir x milo were all fertile. Male sterility was expressed only when milo was used as a female parent thereby indicating the importance of milo cytoplasm. This ability to have 100% male sterility resulting from a cross, quickly stimulated the interest of other agencies and private industries to begin sorghum hybrid breeding programmes.

The product of a cross between generally dissimilar parent (F1 generation) is called a "hybrid". Three types of parental lines are used are for hybrid seed production in sorghum. The R line (pollen parent, homozygous for nuclear restorer genes with normal or male fertile cytoplasm), the A line (female or seed parent, homozygous for nuclear non-restorer gene with male-sterile cytoplasm), and the B line (maintainer of A line, homozygous for nuclear non restorer genes with normal cytoplasm).

Grain Sorghum (*Sorghum bicolor (L)* Moench) has been grown as hybrids for about 40 years starting in the USA (Doggett, 1988). About 48% of grain sorghum plantings in United State of America are now hybrid. (Okiyo*et al.*, 2009). The first hybrid yielded at least 40% more than the local varieties; the advantage was much higher under severe drought stress. Grain Sorghum varieties naturally are quite highly inbred and presumably have low numbers of deleterious recessive genes. Perhaps for this reason, Sorghum hybrids exhibit much less heterosis for yield than is typical for crosses of maize inbred.

One of the many problems breeders and producers of hybrid grain sorghum seed have encountered while trying to develop new hybrids is the crossing of lines differing in flowering time (Trybom *et al*., 1978). Sorghum pollen grains remain viable only for a very short time (in hours) whereas the stigma remains viable for about ten days. However, stigma receptivity increases and reaches its maximum on the fifth day after flowering (Puttarudrappa and Goud 1970, Patil and Goud 1980) and decreases gradually thereafter. Therefore, unless the pollen parent flowers within the range of maximum stigma receptivity of the seed parent, seed production is mostly limited.

2.2 COMBINING ABILITY

Combining ability refers to the potential of a line to produce a superior hybrid. The yields of inbred lines per se are not useful indicators of hybrid yields. The gains in yield could result from a balanced heterotic combination of superior germplasm. Studies on combining ability furnish useful information on the suitability of parents for effective hybridization and the nature and magnitude of different types of gene action involved. In a population of lines unselected for combining ability, genes with additive effects are either preponderant or produce greater effects than genes with dominance or epistatic effects are more important than genes with additive effects (Sprague and Tatum, 1942).

Selection for specific combining ability often means balancing non-heterotic defensive traits as much as or more than balancing dominant gene combinations for yields.

General combining ability (GCA) of a line refers to the average value of a line estimated on the basis of its performance when crossed with other lines (Falconer, 1989). The performance of a particular cross can deviate from the average general combining ability of the two parental lines. This deviation is defined as the specific combining ability (SCA). It is not possible to predict the potential lines in hybrid combinations for many traits; therefore combining ability should be carefully examined when the objectives is to develop superior hybrids for quantitative traits. Beil and Atkins (1967) reported that both general and specific combining ability effects were important in the expression of grain yield in Sorghum. GCA effects were greater than SCA effects for number of panicles per plants, weight of 100 seeds, and the number of seeds per panicle. They concluded from their study that in the selection of lines for use in hybrids combinations, greatest progress could be made by first selecting on the basis of general combining ability of the lines with further selected guided by evaluation for specific effects. Nieshaus and Pickett (1966) noted from a combining ability study of Sorghum grain yield and its components in the F1 and F2 generations that the variance components of GCA were larger than those of SCA, for grain yield, number of panicles per row, height and days to 50% anthesis.

Combining ability for food quality characteristics has been studied as well, Ketala *et al.*, (1976) reported that additive gene effects were significant for grain protein content in all crosses and consistently greater than dominance effects. The preponderance of additive gene action suggests that improvement of grain protein content can be achieved through standard breeding procedures which may result in a superior pure line cultivar. Collins and Picket (1972) observed significant differences in GCA effects for yield, protein and

lysine content in restorer lines and significant differences for yield and protein content in male – sterile lines but, SCA effect were not significant for any of the characters.

However, in another study, Monyo *et al*. (1988) obtained significant differences for male x female crosses (SCA effects) for grain yield. They also reported significant GCA effects for Kernel weight, protein and lysine concentrations. The relatively higher magnitude of GCA variances compared to that of SCA indicated the preponderance of additive genes effects in the genetic control of grain protein content; while on the other hand, a significant SCA variance would indicate the presence of a considerable amount of non-additive variance among this set of parents.

Combining ability of inbred lines is the ultimate factor in determining future usefulness of lines for hybrids (Hallauer and Miranda, 1981). Investigation of the relative magnitude of additive and dominance genetic effects in crosses of unrelated lines of sorghum provides a basis of characterization for combining ability. To establish a sound basis for any breeding programme aimed at achieving higher yield, breeders must have genetic information on the nature of combining ability of parents, their behaviour and performance in the hybrid combination. Such knowledge of combining ability is essential for selection of suitable parents for hybridization and identification of promising hybrids for further exploitation in breeding hybrids of further exploitation in a breeding programme (Alabi *et al.*, 1987).

Beil and Atkins (1967) found significant difference among GCA of all the lines in Sorghum for all the characters measured, while significant difference among SCA were expressed only for 1000 seed weight. Mukuru (1970) also working on Sorghum reported significant GCA mean squares for all characters studied, although SCA mean squares were also significant for 1000 seed weight, days to 50% flowing and percent oil. Crook

and Casady (1974) studied combining ability in Sorghum for 10 characters and found significant GCA and SCA for all the characters. Tadesse *et al* 2008 working on Combining ability of introducedsorghum parentallines reportedthat GCA for plant height, panicle exsertion, panicle length, grain yield and seed weight were significant among male parents indicating the prevalence of additive gene action in determining these traits. The GCA for females was not significant for any of the observed traits except panicle exsertion.

2.3 HETEROSIS

Heterosis is the performance of the hybrid that falls outside the range of the mid-parental value with respect to characters such as growth, flowering and economic yield. It is the difference between the hybrid and means of the two parents (Falconer and Mackey, 1996) .This is called mid parent heterosis. However, high parent heterosis (i.e. the performance of the hybrid over best parent) is important if the goal is to identify the hybrid that is superior to either of the parents. It is thought to result from a combination of allelic and non-allelic genes separately inherited from the parents and is closely related and positively correlated with heterozygosity. If the relationship between heterosis and heterozygosity is linear, dominant gene action is indicated. Falconer (1981) showed that heterosis will be expressed when there is the presence of some level of dominance and relative difference in gene frequency of two parents to determine the magnitude of heterosis expressed in a cross. Heterosis has been observed in many cross-pollinated and self pollinated crops (Gallais, 1988).

The level of heterosis exhibited by a hybrid is a function of genetic divergence between parents. However, commercial exploitation has been possible only in a few crops. This might be attributed to the fact that the magnitude of heterosis in these crops for economic

characters are high enough or consistent across a range of production location to justify the replacement of currently cultivated varieties with hybrids. It might also be attributed to the occurrence of stable and heritage mechanisms (genetic or cytoplasm) in these crops to enable large scale and economic production of hybrid seeds. The heterotic effect is in general, more pronounced in cross-pollinated than in self-pollinated crops (Gallais, 1988). However, significant levels of heterosis have been reported in a number of self-pollinated crops. In Eu-sorghum, a nature of diversity, particularly the cytoplasmic-genic interaction between milo and Kafir group has enabled the development of cytoplasmic-genetic male sterile lines and the commercial exploitation of heterosis.

Heterosis suggests complementary interactions of specific alleles of different genes (Sybenga, 1983). According to Strunnikov (1986), heterosis results from combination of favourable non allelic, totally dominant genes separately inherited from both parents, and the favourable effects of some alleles in the heterozygous state. The level of heterosis is largely determined by the relationship between the effects of useful and harmful genes.

Many studies have been carried out on the existence of hybrid vigour in Sorghum crosses. The most evident expression of heterosis was increased vegetative growth and higher grain production associated with extreme lateness (Bartel, 1949; Karper and Quinby, 1937; Stephens and Quinby, 1952). The absolute increase of grain yield of hybrid over the better parent varied depending upon the individual parental combinations involved and their genetic divergence. Quinby *et al.* (1958) reported that Sorghum hybrid developed for commercial production were characterized by early maturity, slights increases in height and tillering, and substantial increase in grain yield. However, Kambal and Webster (1966) found that tillering in sorghum was not a contributing factor to the yield advantage as hybrids mean performances usually equal that of the parents for a number of panicles per plants. In a study of hybrids produced by crossing 10 male –

sterile lines with 19 fertility restorers, heterosis for yield was due mainly to increase in the number of seeds per panicle (Kambal and Webster, 1966). The number of panicle per plant had the least influence in determining yield. Heterosis for plant height was reported to be a function of stem, peduncle and head length. Considering the relative performance of the hybrids and their parents for days to bloom, leaf number and leaf exertion, it was observed that the ability of the sorghum hybrids to attain a height greater than that of the parents in a shorter time suggested that they were growing at a faster rate. This high rate of growth was interpreted to be a manifestation of heterosis. This is encouraging because early maturing crops are desirable in the drought prone areas of the semi-arid and low input agricultural regions of Africa where hybrids should be developed. In sorghum, one leaf is produced at each node. The stem length is a function of the number and length of the internodes. On the average, the hybrids had taller stems and approximately the same number of nodes as parents. The implication was that heterosis for stem length was manifested as an increase in length rather than in the number of internodes (Kambel and Webster, 1966). Quinby (1963) and Patanothai and Atkins (1971) also reported that heterosis in plants was expressed by early anthesis, increased height, large panicles and panicle exertion of hybrids over parents. In analyzing grain yield data from 391 sorghum trials carried out in four regions of the world with the objective of studying the relationship between the yield of the hybrids and the yield of an adapted high yielding pure line variety, yield was rather constant over a wide range of growing conditions and management levels (Dogget, 1969). Virtually, everywhere those Sorghum hybrids have been compared with improved varieties and land races; there has been a yield advantage commonly in the order of 20 to 60% (House, 1991). As growing conditions become unfavourable, the yield of both declined, but the yield differences between hybrids and varieties became proportionately larger, favouring the hybrids.

Evaluating the performance of hybrid Sorghum under varying drought conditions in Kenya, it was reported that the relative mid-parent heterosis for grain yield was larger under extreme drought stress than under-non stress conditions and the average relative hybrid superiority over the better parent was 32 and 59% under non-stress and stress conditions respectively (Haussmann *et al.,* 1998). In comparing hybrids with local varieties, they also found that hybrids were on the average superior to local varieties for grain yields, harvest index, number of seeds per head and 1000 grain weights, but did not differ significantly in biomass production.

Results on heterosis have been reported form other crops species. In primary hexaploid triticale (*Triticosecale wittmaek*), the average relative heterosis was greater in an unfavourable year than in a favourable year (Oettler *et al*., 1988). Significant heterosis of up to 17% was reported for wheat grain yields under irrigation (Sinolinding and Chowdhry, 1974), while little or negative heterosis occurred under moisture stress (-36% to 7%).

Despite the many studies undertaken on heterosis, it is difficult to predict its occurrence. Few generalizations about the phenomenon can be made because the nature of gene action is known to vary with genetic architecture of the population involved in hybridization and the degree of divergence between the parents and their combining ability. That is to say, the magnitude of heterotic effect is influenced by the performance of both the parents and hybrids. Given that these relative performances will differ between locations, the magnitude of heterosis may also show similar variation.

Measurements of sequential changes in heterosis have not been made for Sorghum in the recent years. Hybrids offer some advantages over open pollinated cultivars in that complementary traits from parental lines can be combined in a single F_1 cross. The

general superiority of hybrids over varieties with respect to performance levels as well as stability has been demonstrated (Rao *et al*., 1981). However, it seems likely that increased yield in grain sorghum hybrids gradually will depend less on heterosis per se but more on other kinds of gene action, particularly for defensive traits that confer high yield stability under all types of expected stresses, as well as on ability to give high yields on highly favourable locations.Estimates of average better parent heterosis for grain yield in grain sorghum ranged from 9.0 to 97%. Lower estimates were obtained with crosses of adapted parent lines (Amir,1999; Abd-El Mottaleb,2004; Hovny *et al*.,2001; Essa, 2009) while high values were most often resulted from studies which involved exotic germplasm (Thawari *et al*.,2000;Abd-El-Halim,2003; Mahmoud, 2007; Mohamed, 2007) or which were conducted under locational stress conditions(Prabhakar,2001; Al-Nagger *et al*., 2000; Honvy *et al.,* 2005; Ali 2000; Mohamed, 2007 and Essa, 2009) stated that F_1 showed range of heterosis with negative and positive value which indicated the potential for developing hybrids superior to their better parent for earliness, plant height, grain yield and 1000grain weight.

Mahdy *et al.,*; (2010) studied effect of location on combining ability and heterosis among 25 F_1 hybrids and their parents and found that, the variance components general combining ability (GCA) for both days to blooming and 1000-grain weight were larger than those of specific combining ability (SCA) under different locations over two years and overall location, while the variances for SCA for grain yield were larger than those of GCA under early and late planting. A comparative component of GCA and SCA were obtained for plant height. Several hybrids had significantly negative days to flowering heterosis. Therefore, a comprehensive evaluation of heterosis would involve the estimation of parent and hybrid differences in a range of locations.

2.4 SORGHUM MALTING QUALITY TRAITS

Malting is the process whereby cereal grains are germinated under controlled conditions of moisture, temperature and aeration in order to produce large complement of enzymes capable of grain modification (Brigss *et al.*, 1981). Malt is therefore a cereal which has been germinated and then dried under defined set of conditions. Barley is traditionally the cereal chosen for malting. However, barleycultivation in tropical areas has not been successful. Thus, the production of malted food requires the importation of barley from temperate regions or utilization of tropicalcereals for germination and malting.

Malting properties of tropical cereals have beeninvestigated (Ilori *et al,* 1991 and Dufour and Melotte, 1992). Sorghum has been malted for centuries and used for the production of baby food and traditional alcoholicand non - alcoholic beverages. Starch degradation in plants is accomplished by α-amylase [α-1, 4-D-glucan 4-glucanohydrolase], β-amylase [α-1, 4-D-glucanmaltohydrolase], amyloglucosidase [α-1, 4-glucan-glucohydrolase], and starchphosphorylase [1, 4-a-D- glucan: phosphate α-D glucosyltransferase], action on α -(1*4)-linkages (Manners, 1974). α- Amylases are hydrolytic enzymes, whichdepolymerize starch according to a classic acid-base mechanism. α- Amylases areendo-enzymes that randomly split a--1*4--linkage in starch with retention ofanomeric configuration of glucose residues. β- Amylase is an exoglucosidase actingfrom the non-reducing end, releasing β- maltose units from starch, hence the name β amylase(Kaplan and Guy, 2004). The β- maltoses released undergo mutarotation intoα- maltose (Dicko *et al.*, 2000). Both α- amylase and β- amylase cannot split α--1* 6--linkage in amylopectin. Therefore, the degradation of starch by these enzymesis incomplete. In addition, plant amylases scarcely hydrolyze raw starch: their action islower than 5% hydrolysis (Dicko *et al.*, 1999). Both α- and β- amylases are needed tohydrolyze starch and produce

fermentable sugar in this process (Trust *et al,* 1995). Sorghum has been identified to replace barley following the ban on the importation ofbarley.

The potential utilization of Sorghum brewing technology may not be realize inview of the acute shortage of the sorghum food crop because of low productivity, highdemand pressure for human consumption and industrial need. Besides, not all Sorghum varieties are suitable to brewing industry. For example, the red Sorghum is not suitablebecause of the tannin content. The Sorghum variety Samsorg 40 (ICSV 400) to date has the best malting quality but because of the small panicle, hence low yield, it is not popular as theSamsorg - 17 (SK5912) with farmers who are primarily concerned with economicreturns.There is therefore an urgent need to increase productivity.The clear polymorphism of α-amylase and β- amylaseactivities in Sorghum varieties may give direction for the selection of Sorghum varietiescontaining these enzymes for specific food utilization.

It is interesting to note that amylase activities could be correlated with food processingof Sorghum. For instance, low α- amylase activity of some varieties is beneficial toobtain a relatively tick porridge (Dicko *et al.,* 2006). For industrial beer preparations,high α-amylase and β-amylase activities are desired. The high amylase activitiesprobably explain the preference for red sorghums for the preparation of "dolo". (Dicko*et al.,* 2005). In industrial brewing, a specific interest exists in high β-amylase-containing Sorghum varieties (Verbruggen *et al.,* 1996). Some malted Sorghum genotypes contain β- amylase activities comparable to that of barley malt. Thesegenotypes can be suggested for industrial brewing. A constraint in the utilization of Sorghum for industrial brewing is the high starch gelatinization temperature (Okafor andAniche, 1987). For couscous preparation varieties displaying low α- amylase activityare required to avoid starch dextrinization during the process. (Dicko *et al*., 2005) Quite a number of parameters

influence malting quality of cereal grain; these include; the number of broken kernel and foreign materials, 1000 –grain weight, germination energy, germination capacity, biochemical test such as starch determination, protein, lipid, ash, cold and hot water extracts, diastatic power, α – and β- amylase activities (Aisien, 1989). Syed *et al*. (2000) reported significant variations in the contents of protein, starch, fat, ash and moisture in various long season sorghum genotypes they studied. They observed that varieties PVK 823 (11.0%) and PVK 801 (10.4%) were statistically superior to others in protein content and maximum percentage of starch (72.33%) was observed in PVK 801. They concluded that some varieties were superior to others and these wide variations may be due to genetic variability among these cultivars. Similar conclusions were also reported by Desai *et al*. (1992) who studied heterosis and combining ability in sorghum.

Although it is not simple to find a group of attributes unequivocally reflex the quality of the grain malting (Savina and Molinacana, 2002) malt extract is undoubtedly, most widely accepted indicator (Valeria *et al*., 2003). As malt extract is an expression of the results of multiple interactions between main components, it is relatively difficult to select for a single malting trait and to achieve an acceptable level of all quality attributes (Anderson and Reinberg, 1985). Malting loss represents the combined losses during steeping (leaching of the preformed matters into the steep liquor and minerals), respiratory losses as carbon dioxide and water, and weight losses of shoot and roots (Haruna, 1991). He opined that genotype with high malting loss were undesirable for malting and attributed these losses to excessive growth during germination. The high malting loss of sorghum (20-30%) compared to barley (9-12%) has been attributed to variations in the solubility patterns of their amylases (Maloma, 1989) as well as the high temperature employed during malting. Demuyakor and Ohta (1992) compared malting characteristics of grain sorghum with commercial barley malt using micro- malting

method. Their result indicated that the optimum germination time of 30^{o}C to produce malt grain of high diastatic power and good malt extract was 4-5 days for barley. Hot water extract of malted sorghum cultivars had higher and sustainable amount of free amino N than the commercial barley malt. Malts with higher dry matter losses were observed in sorghums with higher germination energies, higher α-amylase activities, and lower starch content.

CHAPTER 3

MATERIALS AND METHODS

3.1 GENETIC MATERIALS

Three (3) cytoplasmic male sterile lines (A lines) used as females were Kafir-Milo derivatives with the same cytosterile mechanism and the maintainer counterparts B-lines were obtained from the International Crops Research Institute for Semi-Arid Tropics (ICRISAT) Patancheru, India. The five (5) restorer lines (R lines) were from different origins and they are representatives of elite varieties commonly cultivated in the West and Central African region. Two of the four (4) Checks are hybrids earlier released by IAR and the other two are open-pollinated varieties. (Table 3.1) A lines, commonly referred to as *females*, possess an A cytoplasm [A], lacking a dominant *Rf*(restoration of fertility) allele in the nuclear genome, resulting in a male sterile plant. B lines, commonly referred to as *maintainers,* possess an N cytoplasm [N], and also lack a dominant Rfallele. The sole purpose of the B line was to perpetuate or maintain the A line. The A line and the B line are *isocytoplasmic*, meaning that these two lines are genetically identical, except that the A line plants that are male sterile can be pollinated with pollen from B line plants to produce the next generation of A lines or male sterile plants. The R lines, commonly referred to as *restorer lines,* carry the dominant *Rf*alleles, restoring fertility in the progeny of the A line.

Table 3.1: Genetic Materials used in the Study

No	Designation MALE STERILE LINES	Origin
1	ICSA 11	ICRISAT
2	ICSA 38	ICRISAT
3	ICSA 731	ICRISAT
	MAINTENER LINES	
4	ICSB 11	ICRISAT
5	ICSB 38	ICRISAT
6	ICSB 731	ICRISAT
	RESTORER LINES	
7	NR 711 68	INSTITUTE FOR AGRIC. RESEARCH
8	SAMSORG8 (KSV14)	INSTITUTE FOR AGRIC. RESEARCH
9	CHOKWE	SOUTH AFRICA
10	SPV 422	REGIONAL EXCHANGE FROM MALI
11	CF 35.5	REGIONAL EXCHANGE FROM MALI
	CHECKS	
1	SAMSORG H2	SAMSORG H_2 (IAR HYBRID)
2	SAMSORG H1	SAMSORG H_1 (IAR HYBRID)
3	SAMSORG 41 (ICSV 111)	ICRISAT, NIGERIA
4	SAMSORG 40 (ICSV 400)	ICRISAT, NIGERIA

3.2 DEVELOPMENT OF HYBRIDS

The 3 sterile lines (A lines) and their B counterpart were planted alongside the Restorer (R lines) at the research farm of the Institute for Agriculture Research (IAR), ABU Samaru with in ratio of 4: 2 (4 rows of A-lines and 2 rows of R-lines) at the irrigation location. Each male parent was cross to the three female parents in a Line x Tester mating design to produce 15 hybrids.

3.3 EXPERIMENTAL DESIGN AND PROCEDURES.

Fifteen F_1 hybrids, 8 parents and 4 checks were evaluated at two locations; Samaru and Kadawa. The treatment were organisedas a factorial arrangement in a Randomised Complete Block Design (RCBD) with three replications. Each plot consisted of 2 rows, 5 m long; the intra and inter row spacing was 25cm x 75cm respectively. Five seeds were planted and later thinned to two plants per stand after 3 weeks of planting. Two panicles on each plot were selfed to check fertility restoration. In all locations, standard cultural practices for optimum Sorghum production were carried out. Birds were scared off from flowering time to harvest; weeding was done when necessary. 100 g of sample were milled into flour at IAR Food Science Laboratory and analyzed for their proximate composition according to AOAC (1990) procedure. The malting quality parameters weredetermined as described by Novellie, (1962) and A.S.B.C, (1992).

3.4. DATA COLLECTION

The following data were collected from each of the locations.

1. **Heading date**: - Number of days from planting to when 50 per cent of the plants in the plot have headed

2. Plant height: - The average distance in cm from the ground to the tip of the panicle at maturity from two randomly selected plants/plot.

3. **Panicle length (cm)**: the distance between the base and tip of the panicle measured from two randomly selected plant/plot.

4.**1000 grain weight (gm)**: The weight of 1000 randomly selected seeds/plot were weighed on the Metter Balance and the data was recorded in grams

5. **Grain yield**: - All panicles harvested (at maturity) in the two rows were allowed to dry naturally and were threshed. Weights were recorded in grams for each plot after threshing using an electric balance. Grain yield were converted to kg per hectare based on the plot size.

6. **Fertility Restoration**: Measured by covering the panicles of two plants after full panicle exertion until maturity. Panicles were observed for grain setting. Complete grain setting was scored full fertile (FF), partial grain setting scored partial restoration (PF), and absence of grain scored non-restoring (NF).

3.5 STATISTICAL ANALYSIS

Data were first analyzed on individual location basis, and also combined across 2 locations. Statistical analyses were computed using SAS (2002). Macro Interactive Line x Tester package.

The linear model used for the combined analysis of variance is expressed as:

$Y_{ijk} = \mu + E_i + R_{ij} + G_t + G_l + (G \times G)_{itl} + e_{ijk}$ (Singh and Chaudhary 1985)

Where

Y_{ijk} = observation made

μ = overall mean

E_i = effect of the i^{th} location, I = 1, 2

R_{ij} = effect of the j^{th} rep. In the i^{th} location, j = 1, 2, 3.

G_t = effect of t^{th} (male) genotype, t = 1, 2, 3, 4, 5.

G_l = effect of l^{th} (female) genotype, l = 1, 2, 3.

$(G \times G)_{itl}$ = the interaction effect between t^{th} and l^{th} genotype in the i^{th} location.

$e_{ijk=}$ pooled error.

Table 3.2: Combined ANOVA for Line x Tester analysis including parents and checks

Sources of variation	DF	Expected mean square
Location(Loc)	1	
Replication/Loc	4	
Genotypes	26	σ^2_e + rhcEnvσ^2_p+ rpcEnvσ^2_h+rphEnvσ^2c
Parent	7	σ^2_e+ + rhcEnvσ^2_p
Testers	4	
Lines	2	
Lines x Testers	8	
Hybrid	14	σ^2_e + + rpcEnvσ^2_h
Parents vs Hybrids	1	
Checks	3	σ^2_e + rphEnvσ^2c
Checks vs Hybrids	1	
Loc x Genotype	26	σ^2_e +r $\sigma^2_{(Env\ XEntry)}$
Loc x Parents	7	σ^2_e +rhc $\sigma^2_{(Env\ x\ p)}$
Loc x Testers	4	
Loc x Lines	2	
Loc x Lines x Testers	1	
Loc x Hybrid	14	σ^2_e + rpc $\sigma^2_{(h\ x\ Env)}$
Loc x P vs Hybrid	1	
Loc x checks	3	
Pooled Error	104	σ^2_e

*r=replication, ent=entry, h=hybrid, Loc =Location, p=parents, c=checks

Table 3.3: Form of analysis of variance for combining ability for individual location

Sources of variation	Df	Ms	Expectation of Means Squares
Location(Env)	(L- 1)		
Replication/ Loc	(r - 1)L		
Hybrids	(tl-1)		
Testers(male)	(t-l)		Mt σ^2+ r[cov.(F.S.)-2cov.(H.S.)] +[lrcov.(H.S)
Lines(females)	(l-1)		M1σ^2 + r[cov.(F.S.)-2cov.(H.S.)] + [trcov.H.S)]
Lines x Tester	(l-1)(t-1)		Mlxt σ^2 + r[cov.(F.S.)-2cov.(H.S.)]
Error	E(r-1)(lt-1)	Me	σ^2

H.S. denoting half-sibs and F.S. denoting full-sibs

$Cov(H.S) = \{(M_t-M_{lxt}) + (M_l-M_{lxt})\}/ r(t+l)$

$$Cov(F.S.) = \frac{(Mt-Me) +(Ml+Me)+(Mlxt-Me)}{3r} + \frac{6r\ cov\ H.S.-r(l+t)\ cov\ H.S.}{3r}$$

$\sigma^2 gca = cov(H.S)$

$\sigma^2 sca = cov(F.S.) - 2\ cov\ (H.S.)$

3.5.2 Genetic Analysis

3.5.2.1 Combining Ability Analysis

Plot means in the two locations were used for analysis of combining ability. For each trait, general combining ability (GCA) effect and the specific combining ability (SCA) effect were estimated using the Line x Tester analysis developed by Kempthone (1957)

3.5.2.2 *Estimation of GCA and SCA effects,* using the formula suggested by Singh and Chaudhary (1985).

GCA effects of lines

$$gi = \frac{x_i..}{tr} - \frac{x...}{ltr}$$

Where;

$x_i.$ = total of ith lines over testers

$x....$ = grand total

l = number of lines

t = number of testers

r = number of replications

GCA effects of testers

$$g_t = \frac{x._j}{lr} - \frac{x..}{ltr}$$

Where,

$x._j$ = total of the jth tester over lines

$x...$ = grand total

l = number of lines

t = number of testers

r = number of replication

Estimation of SCA effects

$$S_{ij} = \frac{x_{ij}}{r} - \frac{x_{i.}}{tr} - \frac{x_{j}}{rl} + \frac{x..}{ltr}$$

Where;

x_{ij} = value of the jth lines with ith testers,

x_i = total of ith over all tester,

$x._j$ = total of jth tester over all lines,

$x..$ = grand total crosses,

l = number of lines,

t = number of testers; and

r = number of replication.

3.6 HETEROSIS

Estimate of high-parent heterosis were calculated for each individual hybrid in each location and for combined locations according to Fehr 1987as follows:

High – parent (HP) = 100 X (F_1 - HP)/ HP;

Where F_1 denotes the mean performance of the hybrid averaged over three replications. HP ==the mean of the parent which gave the higher mean value.

Significant differences were determined using the standard error.

S.E of HP = $(2EMS/r)^{1/2}$

The standard error (difference) for high parent heterosis was calculated as $(2EMS/r)^{1/2}$, Where EMS =error mean squares, and r = number of replication.

If the difference between F_1 value and the higher parent were greater than the least significant difference (LSD) value at the desired level of significance, the high –parent estimates were considered significant, otherwise they were not significantly different.

3.7 ESTIMATION OF FOOD AND MALTING QUALITY

At harvest, 100 g of sample from each entry of the Samaru and Kadawa location were dried, dawned and cleaned. Samples were milled into flour at IAR Food Science Laboratory and analyzed for their proximate composition (i.e. moisture, crude fibre, ash, carbohydrates and protein) according to AOAC (1990) procedure. The malting quality parameters: germinationenergy, germination capacity, malting loss, α- and β- amylases activities weredetermined as described by Novellie, (1962) and A.S.B.C, (1992).

3.8 CORRELATION

Genotypic and phenotypic correlations were used to investigate the association between agronomic characters and malting/proximate quality traits of Sorghum genotypes. Correlation coefficients were calculated from component of variance and covariance according to Shivaji and Gritton (1975). The genotypic components were computed by equating the genotypic variances and covariance to the expected mean square and cross products, and hence genotypic correlations were computed by the formula:

$$rg = \frac{\text{COV}_{g12}}{\sqrt{(\sigma^2{}_{g1})(\sigma^2{}_{g2})}}$$ Where

rg = genotypic correlation coefficient

$\text{cov}_{g1.2}$ = the estimates of the genotypic covariance for traits 1 and 2

σ^2_{g1} = estimate of the genotypic variance of trait 1

σ^2_{g2} = estimate of the genotypic variance of trait 2.

Phenotypic correlation was computed using the following formula:

$$rp = \frac{Cov_{ph1}}{\sqrt{(\sigma^3_{ph1})(\sigma^2_{ph2})}}$$ Where:

rp = phenotypic correlation coefficient

$\text{cov}_{ph1.2}$ = estimate of the phenotypic covariance for traits 1 and 2

σ^2_{ph1} = estimate of the phenotypic variance for trait 1,

σ^2_{ph2} = estimate of phenotypic variance for trait 2.

CHAPTER 4

RESULTS

4.1 ANALYSIS OF VARIANCE FOR LOCATION 1: SAMARU

The analyses of variance for Samaru location for agronomic and malting quality traits are presented in Tables 4.1 and 4.2, respectively. In Samaru, (Table 4.1) Means squares due to genotypes were significant for all traits. There were significant variations among the lines, tester for heading date, and plant heights, but no significant yield different were observed neither among the lines nor the tester. Line x tester and hybrids showed highly significant differences ($p< 0.01$) for all characters studied. The variation among parents were highly significant ($p<0.01$) for heading dates, plant height, panicle length, and 1000grain weight. There were no significant different between parents for grain yield. Parent vs hybrids showed highly significant differences for all the traits measured except panicle length and 1000 grain weight. Checks showed highly significant differences for heading dates, plant height, panicle length, 1000grain weight and grain yield. Checks vs (parent, hybrids) showed significant differences for heading dates, plant height, and grain yield.

The analysis of variance for malting and proximate quality traits in Samaru are presented in Table 4.2. Mean squares due to entries were significant for all traits measured. Hybrid parents showed highly significant differences for all traits measured. Partitioning of the variance due to parents revealed that there was no significant variation among the male (testers) for all the traits, while for female parents (lines), significant variation was observed only for beta-amylase. The source of variation due to line × testers, hybrids, and parent vs. hybrid, differed significantly for all traits at ($p<0.01$). The checks differed significantly from the parents and their hybrids for all traits except protein

Table 4.1: Mean Squares from the Analysis of Variance for Agronomic Traits in Samaru 2010

Sources of variation	df	Heading Date	Plant Height(cm)	Panicle Length(cm)	1000GrainWeight(gm)	Grain Yield per Hectare(kg)
Rep	2	9.7901*	15.3981**	2.8394ns	5.23ns	250425ns
Genotypes	26	388.178**	1833.451**	37.7995**	30.625**	38115**
C Vs (P,H)	1	343.962**	5157.515**	9.8334ns	5.1815ns	594026*
Parent VsHybrids	1	0.0947**	18658.511**	3.5357ns	17.7901ns	2795236**
Checks©	3	399.194**	1685.076**	64.0897**	25.1697*	349136*
Parent (P)	7	484.095**	1690.380**	85.7899**	51.8226**	152275ns
Hybrid (H)	14	368.7365**	497.558**	12.6157*	23.9288**	314808**
Line	2	356.6889**	459.072**	7.4202ns	36.9749ns	120099ns
Tester	4	346.1333**	209.064**	6.5109ns	27.6219ns	440099ns
Line x Tester	8	383.0500**	651.4264**	16.9669**	18.8207*	300840*
Error	52	2.867	29.1353	5.5312	7.9069	115953
CV %		2.41	3.91	11.09	10.79	13.53

*, **: Significant at 0.05 and 0.01 probability level respectively. ns: non significant

C Vs(PH) = Checks versus (Parent, Hybrids)

Table 4.2: Mean Squares from the Analysis of Variance for Malting /Proximate Quality Traits of Sorghum at Samaru . 2010

Source of Variation	Df	%Germination Capacity	%Malting Loss	α – amylase µg/100	β – amylase µg/100	% Starch	%Protein
Rep	2	0.1111ns	0.1098ns	0.0005ns	0.3087ns	0.0401ns	0.0037**
Genotypes	26	6.9829**	4.2824*	2.8273**	2.5226**	2.1208**	0.5550**
C vs (PH)	1	4.2041**	10.467**	5.8068**	7.8329**	1.0194**	0.0003ns
Parent vs Hybrids	1	5.6348**	7.7232**	0.1865**	7.9447**	12.4880**	3.2143**
Checks	3	2.7500*	2.5416**	3.7083**	1.6535**	0.2436**	0.0176**
Parents	7	16.6667**	5.2499**	2.5626**	1.2600**	5.1705**	1.3926**
Hybrids	14	3.34**29****	3.4841**	2.7467**	2.5735**	0.3363**	0.1010**
Lines	2	4.2000ns	1.1980ns	2.2551ns	12.0474**	0.3737ns	0.0532ns
Testers	4	4.7000ns	4.5935ns	2.6547ns	1.7764ns	0.1430ns	0.0876ns
Line x Tester	8	2.4500**	3.5009**	2.9156**	0.6036**	0.4237**	0.1197**
Error	52	0.0598	0.0600	0.0600	0.0002	0.1140	0.0007

*,** Significant at 0.05 and 0.01 probability levels, respectively. ns: non significant. α: Alpha, β: Beta. C Vs (PH) = Checks versus (Parent, Hybrids)

4.1.1 Analysis of Variance for Agronomic and Malting traits: Location 2: Kadawa

The mean squares from the analysis of variances in Kadawa for agronomic traits are presented in Table 4.3 and 4.4 Mean squares due to genotype were highly significant ($p<0.01$) for all traits measured. Parents showed highly significant differences for all traits. Partitioning of the variance due to parents revealed that there were significant variations among the male parent (testers) for plant height and 1000 grain weight, while for the female parent (lines), significant variation was observed for all traits. The line x Testers differed significantly for all traits. The variations among hybrids were highly significant for all traits measured. The source of variation due to parent vs hybrid showed significant differences for, plant height, 1000 grain weight, and yield/ha. The checks differed significantly from the hybrid parents and their hybrids for all traits except panicle length.

The analysis of variance for malting and proximate quality traits in Kadawa is presented in table 4.4 Mean squares due to entries was significant for all traits measured. There were no significant variations among the lines and testers for all traits measure. Partitioning of the variances among parents revealed that male and female parents showed significant variation in all the traits except for α-amylase. The mean squares due to line × tester were significant for all traits except β-amylase. There were highly significant differences ($p<0.01$) among hybrids for all the traits measured. The parent's vs hybrid mean squares were highly significant for malting loss, α-amylase, β-amylase, starch and protein, indicating that there was a high heterotic response for these traits. The checks differed significantly from the parents and the hybrids for malting loss, starch and protein.

Table 4.3: Mean Squares From the Analysis of Variance of Parents, Hybrids and Checks for Agronomic Characters grown at Kadawa in 2010

Source of variance	df	Heading Date	Plant Height (cm)	Panicle Length (cm)	1000Grain Weight (gm)	Grain Yield per Hectare(kg)
Replication	2	320.11*	313.15 ns	0.89**	11.02**	66721.54ns
Genotypes	26	358.56**	3265.64**	42.41**	46.42**	564195.42**
C vs (P, H)	1	187.48*	2084.73*	0.01 ns	175.59*	667599.45*
P vs H	1	86.44 ns	38945.87**	0.05 ns	57.23*	395728.39**
Checks	3	958.89**	1970.57**	50.92*	10.91**	266172.84*
Parents	7	601.11*	2545.55**	67.19**	59.72*	758412.7**
Hybrids (H)	14	140.00*	1437.85**	34.25**	37.37*	281453.26**
Line	2	69.00**	1051.49**	4.47**	2.14**	118913.58**
Tester	4	234.09ns	821.68**	71.04 ns	35.65**	372740.74 ns
Line x Tester	8	111.54*	1842.53**	23.31*	47.05*	276444.44*
CV (%)		11.23	7.80	10.71	10.77	7.79

*, **: Significant at 0.05 and 0.01 probability levels, respectivelyns: non significant.

Table 4.4: Mean Squares from the Analysis of Variance for Parents, Hybrids and Checks for Malting Quality Traits at Kadawa in 2010

Source of Variation	df	%Germination Capacity	%Malting Loss	α – amylase µg/100	β-amylase µg/100	% Starch	%Protein
Rep	2	0.2859ns	0.000ns	0.0082ns	1.6816*	0.0221ns	0.0039**
Genotypes	26	1.8600**	6.9490**	5.5555**	1.7182**	0.4704**	0.5553**
C vs (PH)	1	0.2255ns	8.1049**	0.0085ns	1.5106ns	1.2403**	0.0003ns
P vs H	1	0.1566ns	17.7318**	4.4568**	12.7449**	0.1515*	3.2173**
Checks	3	1.3178*	2.2852**	3.1244**	1.9406*	0.9833**	0.0376**
Parents	7	3.3688**	6.2604**	5.5495ns	1.5110**	0.6012**	1.3946**
Hybrids	14	1.4602**	7.4400**	6.5541**	1.0013*	0.2629**	0.2017**
Lines	2	3.6470ns	2.9343ns	0.8356ns	2.1851ns	0.3668ns	0.0532ns
Testers	4	1.0503ns	4.9082ns	4.8986ns	1.1527ns	0.3073ns	0.0874ns
Line x Tester	8	1.1184*	9.8323**	8.8114*	0.6296ns	0. 2147**	0.1199**
Error	52	0.4198	0.0005	0.0138	0.5393	0.0309	0.0013

*, ** Significant at 0.5 and 0.1 probability levels, respectively. ns: non significant α: Alpha, β: Beta. C Vs (PH) = Checks versus (Parent, Hybrids)

4.1.2 Combined Analysis of Variance across the two Locations for Agronomic and Malting Quality Traits

Mean squares for the combined analysis of variances across the two locations for the agronomic and malting quality traits are presented in Tables 4.5 and 4.6, respectively. The source of variation attributable to locations was highly significant for all the agronomic and malting quality traits. There were highly significant ($p<0.01$) differences among entries (genotypes) for all the traits measured. Highly significant variations were obtained among the parents for all traits except 1000 grain weight. Further partitioning of the variances among parents revealed that there were significant differences among the male parents (testers) for all the traits , while amongst the female parents (lines), highly significance difference in four traits were also indicated. The line X tester mean squares varied highly significantly for plant height and yield per hectare and significantly for panicle length and 1000 grain weight.

The variations among hybrids were highly significant for all the traits measured. So also variations due to parents vs hybrids for plant height and yield /ha. There were highly significant differences among the four checks for heading date, plant height and panicle length.

The mean squares for location x entry interaction were significant for heading dates, plant height, 1000 grain weight and grain yield. The male parents (testers) also interacted significantly with the location for heading dates and plant heights. While the performances of female parents (lines) were consistent across the location. The location interacted significantly with the hybrids for heading dates, plant height, 1000 grain weight and grain yield. The checks also indicated highly significant difference with the locations for heading dates and plant height.

Mean squares for the combined analysis of variance for malting /proximate traits across the two locations are presented in Table 4.6. The source of variation attributable to locations was highly significant for all the traits except germination capacity. There were highly significant ($p<0.01$) differences among entries and parents for all the traits measured. Further partitioning of the variances among parents revealed that there were significant difference among the testers for all the traits except starch while amongst the lines there were significant difference for all traits measured. The line × tester mean squares varied significantly for all the traits. The variations among hybrids were also highly significant for all the traits measured.

The variations due to parent vs hybrids were highly significantly for malting loss, β-amylase, starch and protein. There were highly significant differences among the four checks for all the traits measured.

The mean squares for location × entry interaction were significant for all traits, indicating differential responses of the entries in all the locations. The female parent (testers) also interacted significantly with the location for germination capacity, malting loss, α and β-amylase, and protein.

While the male parent (lines) interacted significantly with the location for all the traits measured. The line × tester source of variation interacted significantly with the location for all the traits. The locations interacted significantly with the hybrids for all the traits.

Checks also interacted significantly with the location for all traits measured.

Table 4.5: Mean Squares of Agronomic Traits in Sorghum Hybrids, Parents and Checks Combined across Two Locations–Samaru and Kadawa, 2010.

Sources of variation	Df	Heading Date	Plant Height(cm)	Panicle Length(cm)	1000Grain Weight(g)	Grain Yield per Hectare(kg)
Locations	1	8121. **	16907.5617**	276.386173**	1305.605**	1581234.72**
Rep(locs)	4	169. **	182.2469*	2.619877	9.870741	156278.51
Genotypes	26	560. 87**	4716.8121**	73.306102**	42.959786**	752334.89**
Parents	7	712.08 **	3843.84321**	176.550357**	1918.24988	673876.274**
Testers	4	523.62*	1259.445833**	29.8311667*	51.3661667*	212014.8833*
Lines	2	1258.7**	3564.055556**	50.6538889**	62.1755556*	747390.167**
Lines*Testers	8	372.67ns	17074.22006**	1105.5845**	1.33472222*	2374294.05*
Hybrids	14	375.84**	1094.23016**	37.2961587**	43.8786825**	419496.421**
Parents vs. Hybrids	1	20.17ns	71989.212**	1.02367391ns	1177.493336ns	6872935.867**
Checks	3	1316.67**	3661.31597**	110.365**	10.249ns	281718.6667ns
Checks vs hybrids	1	429.50ns	53843.10009*	0.28821053	82.5442nsns	94113.79883
Loc*GENOTYPE	26	203.18**	512.1419**	5.819634	33.463974**	195234.08**
Loc*parents	7	373.13**	778.7057ns	18.988452	2176.58036ns	237140.845*
Loc*Testers	4	254.22*	332.070833*	3.7195ns	35.9261667ns	54785.206ns
Loc*Lines	2	26.06ns	2.166667	0.6372ns	2.3622ns	119479.056ns
Loc*hybrids	14	151.11**	387.71111**	8.257587ns	14.5356667*	168833.233*
Loc*Checks	3	162.83*	969.89931*	0.8567ns	25.83ns	321817.33ns
Error	104	20.05	62.8559	5.781928	10.478754	79455.17

*, **: Significant at 0.05 and 0.01 probability level respectively. ns=non significant

Table 4.6: Means Squares Analysis for Malting Quality Traits of Sorghum Hybrids, Parents and Checks Combined

Sources of variation:	df	% Germination Capacity	Malting Loss (u/100gm)	α-amylase (ug/100)	β-amylase(ug/100)	%Starch	%Protein
Location	1	0.46ns	1.04**	12.32**	46.65**	7.70**	61.86 **
Rep(Loc)	4	0.19ns	0.05ns	0.00ns	0.99*	0.03ns	0.04ns
Genotypes	26	4.76**	9.49**	4.97**	2.84**	0.92**	1.18**
Parents	7	9.09**	9.45**	3.39**	1.91*	1.50**	1.69**
Testers	4	3.82**	8.18**	1.76**	1.33**	0.02ns	0.29**
Lines	2	5.95**	3.44**	1.85**	7.77**	0.04*	1.06**
Lines*Testers	8	2.26**	10.49**	8.79**	0.83**	0.40**	0.98**
Hybrids	14	3.24**	8.83**	5.79**	1.96**	0.24**	0.79**
Parents vs. Hybrids	1	1.96ns	24.43**	1.41ns	20.41**	4.94**	5.78**
Checks	3	3.23**	4.77**	6.75**	1.51**	0.98**	0.14**
Checks vs hybrids	1	4.39ns	7.86*	1.58ns	2.31ns	0.71ns	0.27ns
Loc*genotype	26	4.08**	1.74**	3.41**	1.39**	1.67**	1.54**
Loc*parents	7	10.95**	2.08**	4.71**	0.8ns5	4.27**	3.54**
Loc*Testers	4	1.93**	1.34**	5.79**	1.60**	0.43**	0.71**
Loc *Lines	2	1.91**	0.69**	1.24**	6.46**	0.70**	1.84**
Loc*hybrids	14	1.58**	2.09**	3.52**	1.61**	0.36**	0.97**
Loc *Checks	3	0.84**	0.06**	0.01**	2.07**	0.24**	0.12**
Error	14	0.24	0.03	0.01	0.33	0.03	0.02

*, **: Significant at 0.05 and 0.01 probability level respectively.ns: non significant.α: Alpha, β: Beta

4.2 MEAN PERFORMANCE OF AGRONOMIC AND MALTING QUALITY TRAITS FOR LOCATION 1: SAMARU

Mean performance for heading date for parental lines ranged from 52 .00 to 86.67 days, hybrids from 41.33 to 80.33 days while the checks ranged from 63.33 to 88.57 days.(Table 4.7) Three hybrids ICSA11 X NR71168, ICSA11 X SAMSORG 8, ICSA 731 X SAMSORG were earlier than the earliest Checks. The hybrids were generally tall, with the heights ranging from 116.2cm to 164cm. The tallest hybrid was ICSA 11 X SPV 422, and the shortest ICSA 11 X CF35.5 .Most of the hybrids was taller than the taller parent. Mean panicle length ranged from 17.20 to26.00 cm for hybrids, 14.63 to 29.33cm for parents and Checks from16.03 to 26.37cm. Hybrids varied in mean for grain weight values ranged from 21.37 to 31.5g, all the checks had a uniform 1000 grain weights of 26.6g, however, the parents ranged from 23.07 to 32.1g. Mean grain yield for hybrids ranged from 2133.kg ha^{-1} to as high as 3156.kg ha^{-1} .The analysis of variance table(Table 4.3)shows highly significant differences ($p<0.01$) between hybrids. The highest yielding hybrids was: ICSA 38 X CHOKWE (3156.kg ha^{-1}), and the least was ICSA 11 X SPV 422(2133 kg ha^{-1}). The first two high yielding hybrids were significantly different from each other, and yielded significantly more than the best Check (ICSA38 X NR71182, 2978kg $ha^{-1)}$. Most of the hybrids were high yielding. Out of the 15 hybrids, more than half had grain yield greater than or equal to that of the best parents. The parental means with respect to grain yield varied from 1733 kg ha-1 to 2444 kg ha-1. The highest yielding parent was SPV422(2444kg), and ICSA 11(1733kg) recorded the lowest yield.

The Mean performance for germination capacity of hybrids ranged from 94 to 98%.(Table 4.8) Twelve hybrids have germination capacity of 98%. Germination capacity of the checks ranged from 96 to 98% while the parents germination capacity varied from 92 to 99%. The mean performance based on malting loss for hybrid revealed that ICSA731 × NR71168 has the highest rate of malting loss of 24.48%. For hybrids,

malting loss ranged from 20.41-24.48%. Malting loss for checks ranged from 22, 4 to 23.32% and parents ranged from 20.27 to 23.47%. With respect to α-amylase, the mean performance for hybrids ranged from 22.1 to 26.03µg/100. Three hybrids had α-amylase activities higher than that of the highest check (24.16µg/1000). The lowest α-amylase activity was recorded by the parent ICSA11 (20.4µg/100).

The checks Samsorg 41(ICSVIII) and ICSA38×NR71182 recorded the highest β-amylase activities more than the hybrids with 24.1µg. Hybrids β-amylase ranged from 20.14 to 22.41µg; while that of parent varied from 20.95 to 22.85µg.

The hybrid means with respect to the percentage of starch varied from 22.43 to 24.86%, parental means ranged from 66 to 68.16%; while checks varied from 21.34 to 76.36%. The check ICSA38 × NR71182 had the highest percentage of starch (76.36%) while the hybrid ICSA38 × chokwe recorded the lowest starch of 21.27%.

The genotypes were not significantly different with respect to percentage protein. Hybrid means ranged from 9.48 to 10.12%, parent varied from 8.42 to 10.12% while checks ranged from 9.6 to 9.8%.

Table 4.7: Mean Performance of agronomic traits at Samaru .2010

Genotypes	Heading Date	Plant Height(cm)	Panicle Length(cm)	1000Grain Weight(gm)	Grain Yield per Hectare(kg)
PARENTS					
ICSA731	83.67[a]	120.67[j]	25.70[b-g]	26.83[edf]	2044.3[j]
ICSA11	51.00[ihg]	77.00[k]	31.07[a]	27.90[c-f]	1422.0[k]
ICSA38	68.33[b]	81.67[k]	29.33[bac]	22.97[f]	2266.3[hij]
Chokwe	49.00[ihg]	124.50[j]	22.33[f-k]	29.40[b-f]	2133.3[ij]
CF.35.5	50.00[ihg]	119.50[j]	16.50[l]	26.83[edf]	2444.3[f-i]
NR71168	44.00[i]	143.33[i]	21.33[g-k]	32.57[a-e]	2933.7[bcd]
SPV422	64.67[cb]	159.67[f-i]	21.33[g-k]	34.30[bac]	2489.0[e-i]
SAMSORG 8	43.33[i]	142.17[i]	22.33[f-k]	36.40[ba]	2978.0[bc]
HYBRIDS					
ICSA731x Chokwe	63.00[b-e]	182.33[bdc]	20.17[i-l]	33.87[a-d]	2800.0[c-f]
ICSA731x CF35.5	64.33[cb]	181.33[b-e]	23.33[d-j]	32.80[a-e]	2977.7[bc]
ICSA731x NR71168	64.00[cbd]	182.67[bdc]	20.50[i-l]	31.67[a-e]	2844.3[b-e]
ICSA731x SPV422	60.00[b-g]	171.00[d-g]	23.50[d-i]	34.13[bac]	2355.3[g-j]
ICSA731x SAMSORG 8	57.00[b-h]	163.83[e-h]	18.67[klj]	26.03[ef]	2578.0[c-h]
ICSA11xChokwe	60.00[b-g]	158.67[f-i]	26.17[b-g]	27.33[c-f]	2978.0[bc]
ICSA11 xCF35.5	52.33[e-i]	126.00[j]	21.33[g-k]	27.90[c--f]	2622.0[c-h]
ICSA11 xNR71168	43.00[i]	197.50[ba]	24.50[d-i]	36.50ba	2578.0[c-h]
ICSA11 xSPV422	53.33[e-i]	175.00[c-f]	20.83[h-l]	34.30[bac]	2934.0[bcd]
ICSA11 xSAMSORG 8	49.33[ihg]	155.33[ihg]	23.00[e-k]	26.80[edf]	2889.0[b-e]
ICSA38xChokwe	46.00[ih]	18417[bdc]	27.50[a-e]	34.00[bac]	3244.3[ba]
ICSA38 x CF35.5	52.33[d-i]	182.50[bdc]	26.67[a-f]	30.47[a-e]	3245.0[ba]
ICSA38 x NR71168	57.67[b-h]	174.50[c-f]	30.33[ba]	33.30[a-d]	3511.3[a]
ICSA38 x SPV422	62.67[b-f]	192.00[bac]	24.67[c-i]	33.23[a-d]	2755.3[c-f]
ICSA38 x AMSORG 8	44.67[i]	192.67[bac]	27.83[a-d]	36.00[ba]	2667.0[c-g]
CHECKS					
SAMSORG41(ICSV111)	51.67[e-i]	145.17[i]	18.33[kl]	36.67[a]	2533.3[d-h]
SAMSORG40(ICSV400)	86.0[a]	195.00[ba]	22.83[e-k]	32.50[a-e]	2889.0[b-e]
SAMSORG H2 (ICSA38 x NR71182)	42.67[i]	204.67[a]	25.50[c-h]	35.67[ba]	2933.3[bcd]
SAMSORG H1 (ICSA38 x NR71176)	53.33[c-i]	146.83[ih]	27.50[a-e]	36.33[ba]	3245.0[ba]
SE±	2.09	4.05	0.85	1.13	70.23

*Means with the same alphabet in the same column are not significantly different according to Duncan multiple range text. (DMRT)

Table 4.8: Mean performance for malting quality traits of parents, hybrid and checks at Samaru 2010.

	Malting					
GENOTYPES	%Germination Capacity	%Malting Loss	α-Amylase **(µg/100)**	β-Amylase **(µg/100)**	%Starch	%Protein
PARENTS						
ICSA731	98.00^{b}	23.15^{cd}	20.74^{f}	22.33^{fgh}	64.59^{j}	8.42^{g}
ICSA11	95.33^{e}	22.15^{f}	20.40^{i}	22.64^{d-h}	66.14^{i}	8.64^{f}
ICSA38	98.00^{b}	24.18^{b}	20.64^{h}	22.70^{d-h}	66.10^{i}	8.69^{e}
Chokwe	98.00^{b}	22.08^{f}	22.18^{c}	22.91c-f	67.13^{h}	9.63^{d}
CF.35.5	96.69^{c}	23.11^{cd}	22.15^{d}	20.94^{i}	68.14^{bcd}	9.67c
NR71168	92.00^{g}	22.70^{de}	20.12^{kl}	22.75^{d-h}	67.84^{edf}	10.12^{a}
SPV422	99.00^{a}	20.11^{h}	20.15^{j}	22.85^{c-f}	68.16^{bc}	10.10^{a}
SAMSORG8	99.00^{a}	20.77^{g}	22.11^{e}	22.11^{h}	68.15^{bc}	9.72^{b}
HYBRIDS						
ICSA731xChokwe	97.00^{c}	26.03^{a}	20.15^{j}	22.93^{c-f}	68.12^{bcd}	9.84^{b}
ICSA731 x CF35.5	98.00^{b}	22.79^{de}	20.15^{j}	23.41^{c}	67.57^{efg}	9.84^{b}
ICSA731 x NR71168	94.00^{f}	23.43^{c}	22.10^{e}	22.82^{c-g}	67.57^{efg}	9.83^{b}
ICSA731 x SPV422	98.00^{b}	22.10^{f}	22.40^{b}	22.58^{e-h}	68.08^{bcd}	9.81^{b}
ICSA731 x SAMSORG8	98.00^{b}	22.19^{f}	22.12^{e}	22.42^{fgh}	68.72^{a}	9.92^{a}
ICSA11xChokwe	98.00^{b}	22.74^{de}	20.63^{h}	23.25^{c}	67.62^{efg}	9.57^{c}
ICSA11xCF35.5	98.00^{b}	24.16^{b}	20.42^{h}	24.86^{a}	67.48^{g}	9.85^{b}
ICSA11xNR71168	98.00b	22.16^{f}	20.10^{l}	24.20^{b}	68.11^{bcd}	9.73^{c}
ICSA11xx SPV422	98.00^{b}	22.10^{f}	20.62^{h}	24.13^{b}	67.64^{efg}	10.8^{a}
ICSA11xSAMSORG8	98.00^{b}	22.74^{de}	22.41^{b}	24.16^{b}	67.86^{cde}	9.80^{b}
ICSA38x Chokwe	98.00^{b}	22.64^{e}	22.10^{e}	21.26^{i}	68.16^{bc}	9.92^{a}
ICSA38 x CF35.5	98.00^{b}	24.18^{b}	20.14^{jk}	22.64^{d-h}	68.14^{bcd}	9.71^{c}
ICSA38 x NR71168	97.00^{c}	22.18^{f}	20.14^{jk}	23.16^{cde}	68.11^{bcd}	10.12^{a}
ICSA38 x SPV422	98.00^{b}	22.64^{e}	20.12^{kl}	22.74^{d-h}	68.02^{bcd}	9.63^{d}
ICSA38 x SAMSORG8	98.00^{b}	22.70^{de}	20.70^{f}	22.18^{gh}	67.66^{efg}	10.10^{a}
CHECKS						
SAMSORG41(ICSV111)	98.00^{b}	24.10^{6b}	22.64^{a}	24.11^{b}	68.20^{b}	9.66^{c}
SAMSORG40(ICSV400)	96.00^{d}	24.00^{4b}	22.10^{e}	24.10^{b}	68.10^{bcd}	9.60^{c}
SAMSORG H2 (ICSA38X NR71182)	96.00^{d}	22.39^{ef}	22.12^{e}	24.14^{b}	67.56^{fg}	9.66^{c}
SAMSORG H1 (ICSA38XNR71176)	97.00^{c}	24.42^{b}	20.12^{kl}	22.63^{d-h}	67.86^{cde}	9.78d
SE±	0.008	0.0003	0.008	0.004	0.01	0.0009

α: Alpha and β: Beta Amylase

* Means with the same alphabet in the same column are not significantly different. (DMRT).

4.2.1 Mean Performance of Agronomic and Malting Quality Traits for Location 2:Kadawa

Mean performance for five agronomic characters evaluated at Kadawa are presented in Tables, 4.9 .The hybrids were early maturity, the mean heading date varied from 43 to 64 days, while the parents' means ranged from 43 to 84 days. The checks ranged from 43 to 86 days. The heights of hybrid ranged from 126 to 198 cm. The tallest being ICSA 11 X NR71168 (197.57cm) followed by ICSA38 X Samsorg 8(192.67cm). The panicle length for hybrid ranged from 18.7 to 37cm. The mean of the hybrids ranged from 18.7 to 30 cm .The 1000 grain weight ranged from 27 to 37g. The mean yield for hybrids ranged from 235kg/ha to 3511kg/ha. The best yielding hybrids were from the following crosses: ICSA38 X NR71168 (3511kg/ha), ICSA 38 X CF35.5 (3244kg/ha), ICSA38 X Chokwe (3244kg/ha), ICSA 11 X SPV 422 (2933kg/ha), ICSA 11 X Chokwe (2978kg/ha), ICSA11 X Samsorg 8 (2889kg/ha), ICSA731 X NR71168 (2844kg/ha), ICSA731 X Chokwe (2800kg/ha). The hybrid ICSA38 X NR71168 out yielded the best checks ICSA38 X NR71176 (3245kg/ha).

The high yielding parents were: Samsorg 8 (2978kg/ha), NR71168 (2933kg/ha). The mean yield of the parent lines ranged from 1422kg/ha to 2978kg/ha.

The Mean performance for germination capacity of hybrids ranged from 96.44 to 98.48. (Tables 4.10) The hybrids with the highest percentage germination capacity was ICSAII × CF35.5 (98.48%) followed by ICSAII × NR7II68 (98.36%) and ICSA731 × Chokwe (98.05%). The malting loss for all hybrids varied from 20.18 to 25.67%, α-amylase for hybrids ranged varied from 20.12 to 26µg/100. β-amylase also ranged from 20.12 to 24.7µg/100, the following hybrids ICSAII × Chokwe and ICSAII × CF35.5 recorded similar β-amylase activities of 24.18µg/100. With respect to starch, the mean performance for all the hybrids ranged from 23.43 to 25.11%.

Protein also varied significantly for hybrids and ranged from 7.15 to 9.74%. The parental means with respect to germination capacity varied from 95.44 to 98.37%. Malting loss ranged from 20.47 to 23.87% parents with high α-amylase activities were: - Chokwe (24.44µg), ICSAII (24.24µg) and ICSA731 (23.67µg). The α-amylase activities of the parents were higher than that of the best checks. For starch mean ranged from 22.4 to 24.44% while mean performance for protein ranged from 7.2% to 9.73%.

The checks recorded the highest percentage of starch ranging from 67.5 to 68.25%.

Table 4.9: Mean performance of parents, hybrids and checks for five agronomic characters in sorghum at Kadawa 2010

Genotypes	Heading Date	Plant Height(cm)	Panicle Length(cm)	1000GrainWeight(gm)	Grain Yield perHectare(kg)
PARENTS					
ICSA731	83.67^{a}	120.67^{j}	25.70^{b-g}	26.83^{edf}	2044.3^{j}
ICSA11	51.00^{ihg}	77.00^{k}	31.07^{a}	27.90^{c-f}	1422.0^{k}
ICSA38	68.33^{b}	81.67^{k}	29.33^{bac}	22.97^{f}	2266.3^{jih}
Chokwe	49.00^{ihg}	124.50^{j}	22.33^{f-k}	29.40^{b-f}	2133.3^{ji}
CF.35.5	50.00^{ihg}	119.50^{j}	16.50^{l}	26.83^{edf}	2444.3^{f-i}
NR71168	44.00^{i}	143.33^{i}	21.33^{g-k}	32.57^{a-e}	2933.7^{bcd}
SPV422	64.67^{cb}	159.67^{f-i}	21.33^{g-k}	34.30^{bac}	2489.0^{e-i}
SAMSORG 8	43.33^{i}	142.17^{i}	22.33^{f-k}	36.40^{ba}	2978.0^{bc}
HYBRIDS					
ICSA731 x Chokwe	63.00^{b-e}	182.33^{bdc}	20.17^{i-l}	33.87^{a-d}	2800.0^{c-f}
ICSA731 x CF35.5	64.33^{cb}	181.33^{b-e}	23.33^{d-j}	32.80^{a-e}	2977.7^{bc}
ICSA731 x NR71168	64.00^{cbd}	182.67^{bdc}	20.50^{i-l}	31.67^{a-e}	2844.3^{b-e}
ICSA731 x SPV422	60.00^{b-g}	171.00^{d-g}	23.50^{d-i}	34.13^{bac}	2355.3^{g-j}
ICSA731 x SAMSORG 8	57.00^{b-h}	163.83^{e-h}	18.67^{klj}	26.03^{ef}	2578.0^{c-h}
ICSA11 x Chokwe	60.00^{b-g}	158.67^{f-i}	26.**17**$^{b-g}$	27.33^{c-f}	2978.0^{bc}
ICSA11 x CF35.5	52.33^{e-i}	126.00^{j}	21.33^{g-k}	27.90^{c-f}	2622.0 $^{c-h}$
ICSA11 x NR71168	43.00^{i}	197.50^{ba}	24.50^{d-i}	36.50^{ba}	2578.0^{c-h}
ICSA11 x SPV422	53.33^{e-i}	175.00^{c-f}	20.83^{h-l}	34.30^{bac}	2934.0^{bcd}
ICSA11 x SAMSORG 8	49.33^{ihg}	155.33^{ihg}	23.00^{e-k}	26.80^{edf}	2889.0^{b-e}
ICSA38 x Chokwe	46.00^{ih}	18417^{bdc}	27.50^{a-e}	34.00^{bac}	3244.3^{ba}
ICSA38 x CF35.5	52.33^{d-i}	182.50^{bdc}	26.67^{a-f}	30.47^{a-e}	3245.0^{ba}
ICSA38 x NR71168	57.67^{b-h}	174.50^{c-f}	30.33^{ba}	33.30^{a-d}	3511.3^{a}
ICSA38 x SPV422	62.67^{b-f}	192.00^{bac}	24.67^{c-i}	33.23^{a-d}	2755.3^{c-f}
ICSA38 x SAMSORG 8	44.67^{i}	192.67^{bac}	27.83^{a-d}	36.00^{ba}	2667.0^{c-g}
CHECKS					
SAMSORG41 (ICSV111)	51.67^{e-i}	145.17^{i}	18.33^{kl}	36.67^{a}	2533.3^{d-h}
SAMSORG40(ICSV400)	86.0^{a}	195.00^{ba}	22.83^{e-k}	32.50^{a-e}	2889.0^{b-e}
SAMSORG H2 (ICSA38 X NR71182)	42.67^{i}	204.67^{a}	25.50^{c-h}	35.67^{ba}	2933.3^{bcd}
SAMSORGH1 (ICSA38 X NR71176)	53.33^{c-i}	146.83^{ih}	27.50^{a-e}	36.33^{ba}	3245.0^{ba}
SE ±	2.09	4.05	0.85	1.13	70.23

* Means with the same alphabet in the same column are not significantly different. (DMRT)

Table 4.10: Mean Performances for Malting Traits of Parents, Hybrids and Checks at `Kadawa.2012

	Malting Quality Traits					
Parents	%Germination Capacity	%Malting Loss	α_Amylase	β_Amylase	%Starch	%Protein
ICSA731	98.26^{ab}	22.14^{p}	24.20^{b}	23.67^{a-f}	67.76^{ac}	7.73^{d}
ICSA11	97.87^{abc}	20.09^{r}	22.08^{d}	24.24^{a-d}	67.45^{cd}	9.15^{c}
ICSA38	98.36^{a}	24.75^{b}	20.26^{h}	22.40^{f}	67.80^{b}	9.10^{b}
Chokwe	97.88^{abc}	22.18^{n}	20.56^{g}	24.43^{abc}	66.95^{ef}	8.76 ^{d}
CF.35.5	95.43^{f}	23.15^{h}	21.79^{e}	23.01^{def}	66.55^{g}	8.28^{e}
NR71168	97.99^{abc}	22.71^{m}	20.64^{g}	23.21^{c-f}	67.47^{bcd}	8.71^{de}
SPV422	97.87^{abc}	22.14^{p}	20.85^{e}	23.70^{a-f}	67.00^{ef}	9.31^{a}
SAMSORG 8	96.23^{ef}	20.63^{q}	20.10^{h}	22.77^{def}	66.90^{f}	8.41^{e}
ICSA731xChokwe	98.00^{abc}	26.12^{a}	20.19^{h}	24.51^{abc}	67.03^{ef}	2.62^{n}
ICSA731 x CF35.5	97.92^{abc}	22.84^{j}	20.20^{g}	24.33^{a-d}	67.28^{de}	2.84^{l}
ICSA731 x NR71168	96.46^{def}	26.14^{a}	24.70^{a}	23.43^{c-f}	66.80^{fg}	2.4 9^{l}
ICSA731 x SPV422	96.57^{def}	20.12^{r}	22.64^{c}	23.54^{b-f}	66.93^{f}	3.10^{i}
ICSA731 x SAMSORG8	96.95b-e	22.80^{k}	22.14^{d}	23.52^{b-f}	66.90^{f}	2.67^{n}
ICSA11xChokwe	97.96^{abc}	22.72^{m}	20.72^{e}	24.51^{abc}	67.45^{d}	3.01^{j}
ICSA11 x CF35.5	98.48^{a}	24.10^{f}	24.18^{b}	25.01^{a}	67.61^{bcd}	3.43^{g}
ICSA11 x NR71168	98.36^{a}	22.10^{o}	20.16^{h}	24.99^{ab}	67.59^{bcd}	3.24^{h}
ICSA11 x SPV422	97.41^{a-e}	22.14^{p}	22.68^{c}	23.72^{a-f}	66.97^{ef}	3.03^{j}
ICSA11 x SAMSORG 8	97.54^{a-d}	22.78^{lk}	20.64^{g}	24.22^{a-d}	66.99^{ef}	2.73^{n}
ICSA38x Chokwe	96.44^{def}	24.17^{e}	22.60^{c}	25.10^{a}	66.83^{fg}	2.58^{o}
ICSA38x CF35.5	97.43^{a-e}	22.74^{ml}	21.73^{e}	24.63^{abc}	67.44^{cd}	3.04^{j}
ICSA38x NR71168	96.52^{def}	22.14^{op}	22.80^{c}	24.24^{a-d}	66.86^{ef}	2.79^{m}
ICSA38x SPV422	97.71^{abc}	24.60^{d}	22.15^{d}	24.97^{ab}	67.54^{bcd}	3.26^{h}
ICSA38x SAMSORG 8	97.02^{b-e}	23.74^{h}	20.65^{g}	24.07^{a-e}	66.95^{ef}	2.87^{k}
SAMSORG41(ICSV111)	98.01^{abc}	24.12^{e}	22.18^{d}	24.92^{ab}	67.50^{bcd}	2.85^{k}
SAMSORG40(ICSV400)	97.59^{a-d}	23.86^{f}	22.10^{d}	24.90^{ab}	68.25^{a}	2.74^{m}
SAMSORG H2 (ICSA38XNR71182)	96.50^{def}	22.60^{n}	22.14^{d}	23.22^{c-f}	66.85^{ef}	2.53^{n}
SAMSORG H1 (ICSA38XNR71176)	97.00^{b-e}	97.00^{b-e}	20.10^{h}	24.56^{abc}	67.49^{bcd}	2.64^{n}
SE	0.09	0.22	0.007	0.12	0.24	0.07

α-Alpha and β- Beta Amylase

* Means with the same alphabet in the same column are not significantly different. (DMRT)

4.2.2Combined Mean Performance of Parents, Hybrids and Checks for Agronomic Traits in Sorghum Evaluated at Samaru and Kadawa in 2010

The mean performance of hybrids, the parents and the checks across the two locations for all traits measured are presented in Table 4.11. Means for heading date for hybrids ranged from 42 to 72 days. Parents headed from 52 to 80 days while checks took 53 to 87 days to head. However, hybrids headed earlier than the earliest checks and parents. The plant height for parents ranged from 78 to 152 cm. The hybrids were significantly taller than their parents. Among the hybrids, ICSA38 X SPV422 was the tallest with a height of 177 cm, although shorter than the tallest check that was 192.2 cm.

Among the parents a wide variation for panicle length was observed. The means ranged from 15.6 (CF35.5) to 30.2 cm (ICSA11). The hybrid ICSA38 X NR71168 produced the longest panicle length. The panicle length of hybrids ranged from 18 to 26.02 cm, while checks ranged from 17.2 to 27 cm.

Grain yield is an important trait to be considered for large scale hybrid production. Highly significant differences were observed among the 15 hybrids for grain yield. The mean grain yield of the hybrids over the two locations ranged from 2333.2kg/ha to 3199.8kg/ha. The best performing hybrids across the two locations were from the following crosses: ICSA38 X Chokwe (3199.8kg/ha), 1CSA38 X NR71168 (3111.3kg/ha) and ICSA38 XCF35.5 (3111.2kg/ha), The high yielding hybrids were significantly different from each other and out yielded the best check ICSA38 X NR71168 (3023kg/ha). The parents also showed wide variation for grain yield per unit area across the two locations. Their mean yield ranged from 1577.7 for 1CSA11 to 2666.7kg/ha for SAMSORG 8. The highest yielding parents across the two locations were: SAMSORG 8 (2666.7kg/ha) and NR71168 (2577.8kg/ha).

The mean performances of hybrids, parents and the checks for malting/proximate traits across location for all traits measured are presented in Table 4.12.

The mean germination capacity of the hybrids over the two locations ranged from 95.23 to 98.24%. All the fifteen hybrids performed well in terms of germination capacity cereal germination capacity of up to 80% were recommended as viable. Malting loss for hybrids ranged from 21.11 to 26.07% ICSA73 × Chokwe and ICSAII × NR7II68 recorded the highest malting loss of 26.07 to 24.73% respectively. Among the hybrids, ICSA731 × NR7II68 recorded the highest α-amylase activities of 23.4 µg/100. With respect to β-amylase, hybrids mean performance range from 22.98 to 24.9.µg/100. ICSAII × CF35.5 recorded the highest β-amylase of 24.93 µg/100 followed by ICSAII × NR7II68 (24.60 µg/100) while ICSA731 × KSV14 recorded the lowest β-amylase of 22.98 µg/100. The means performance of the hybrids with respect to starch were not significantly different from each other. The highest percentage of starch was from ICSAII × NR7II68 (67.85%) while percentage protein of hybrids was low; it ranged from 2.59 to 3.43%.

The germination capacity for parents ranged from 96.05% to 98.44%, parent with the highest germination capacity was SPV 422. Malting loss of parent varied from 20.7 to 24.47% ksv14 recorded the lowest malting loss.

The mean performance of parent with respect to α-amylase ranged from 20.38 to 22.47 µg/100, ICSA731 recorded highest α-amylase. B-amylase for parent ranged from 21.98 to 23.44µg/100. Protein contents was high amongst parent, it ranged from 7.76 to 9.35%. Means performance with respect to starch, ranged from 66.17 to 67.66%.

Among the checks, no wide variation for germination capacity was observed, the mean ranged from 96.43 (ICSVIII) to 98.23 % (ICSA38 × NR7II76). Malting loss varied from 22.12 to 23.02%. α-amylase ranged from 20.23 to 21.04 µg/100 while β-amylase ranged

from 22.68 to 23.12µg/100. Percentage starch ranged from 66.65 to 67.11% and percentage protein was very low. Percentage proteins in hybrids even though was low but were more than that of the best check. Mean performance with respect to protein for checks varied from 2.66 to 2.88%.

Table 4.11: Mean performance of parents, hybrids and checks for agronomic traits of Sorghum genotypes evaluated at Samaru and Kadawa in 2010

GENOTYPES	Heading Date	Plant Height(cm)	Panicle length(cm)	1000Grain Weight(gm)	Grain Yield per Hectare(kg)
PARENTS					
ICSA731	80.33^{b}	121.50^{i}	24.65^{c-f}	28.83^{a-h}	2199.8^{gh}
ICSA11	51.5^{k}	77.50^{k}	30.20^{a}	30.00^{a-g}	1577.7^{i}
ICSA38	68.33^{dce}	81.33^{k}	28.92^{ba}	23.93^{i}	2177.5^{h}
Chokwe	67.83^{dce}	129.08^{hi}	21.08^{h-j}	24.73^{hi}	2222.2^{gh}
CF.35.5	51.50^{k}	111.66^{j}	15.56^{l}	27.10^{d-i}	2288.7^{fgh}
NR71168	58.50^{hji}	127.41^{hi}	20.83^{h-j}	27.82^{c-i}	2577.8^{c-g}
SPV422	73.33^{c}	152.17^{f}	19.25^{ikj}	32.11^{bac}	2466.7^{g-h}
SAMSORG 8	53.66^{kj}	132.50^{gh}	19.95^{h-k}	30.63^{a-f}	2666.7^{b-f}
HYBRIDS					
ICSA731xChokwe	67.17^{de}	163.50^{ced}	20.23^{h-k}	30.23^{a-f}	2666.7^{b-f}
ICSA731 x CF35.5	68.83^{dce}	169.33^{cbd}	22.53^{e-i}	28.30^{b-h}	2666.5^{b-f}
ICSA731 x NR71168	68.83^{dce}	163.83^{ced}	19.60^{ikj}	30.78^{a-e}	2866.5^{a-d}
ICSA731 x SPV422	64.33^{gfe}	159.67^{fed}	21.08^{h-j}	30.60^{a-f}	2333.2^{e-h}
ICSA731 x SAMSORG 8	57.33^{ji}	154.83^{fe}	17.93^{klj}	23.70^{i}	2422.0^{e-h}
ICSA11xChokwe	67.00^{de}	154.83^{fe}	25.88^{dc}	26.50^{f-i}	2866.7^{a-d}
ICSA11 x CF35.5	58.67^{hji}	121.08^{i}	20.71^{ihj}	26.50^{hig}	2866.5^{a-d}
ICSA11 x NR71168	42.17^{l}	173.75^{cb}	22.48^{e-i}	30.47^{a-f}	2555.5^{d-h}
ICSA11 x SPV422	64.00^{hfe}	169.25^{cbd}	20.33^{h-k}	32.90^{a}	2533.5^{d-h}
ICSA11 x SAMSORG 8	51.00^{k}	149.58^{f}	21.60^{f-i}	24.91^{hi}	2888.8^{a-d}
ICSA38xChokwe	60.83^{ghf}	153.00^{f}	25.38^{dce}	28.72^{a-h}	3199.8^{a}
ICSA38 x CF35.5	66.33^{dfe}	169.25^{cbd}	24.03^{c-g}	26.50^{e-i}	3111.2^{a}
ICSA38 x NR71168	69.00^{dce}	163.25^{ced}	26.02^{dc}	30.51^{a-f}	3111.3^{a}
ICSA38 x SPV422	71.50^{dc}	176.58^{b}	23.23^{c-g}	30.10^{a-g}	2555.3^{d-h}
ICSA38 x SAMSORG 8	57.83^{ji}	168.67^{cbd}	25.15^{dce}	31.30^{a-d}	2555.7^{d-h}
CHECKS					
SAMSORG41(ICSV111)	60.00^{ghi}	138.67^{g}	17.18^{kl}	32.60^{ba}	2711.2^{b-e}
SAMSORG40(ICSV400)	87.33^{a}	192.17^{a}	21.87^{f-i}	30.98^{a-e}	2555.5^{d-h}
SAMSORG H2 (ICSA38XNR71182)	53.00^{kj}	178.83^{b}	25.18d^{ce}	29.40^{a-g}	2955.5^{abc}
SAMSORG H1 (ICSA38XNR71176)	67.00^{de}	150.58^{f}	26.93^{bc}	30.91^{a-e}	3022.5^{ab}
SE ±	1.49	2.64	0.8	1.08	93.96

* Means with the same alphabet in the same column are not significantly different. (DMRT)

Table 4.12: Mean Performance of Parents, Hybrids and Checks for Malting Quality Traits Combined Across the Two Locations Samaru and Kadawa In 2010

	Malting					
GENOTYPES	%Germination Capacity	%Malting Loss	α-Amylase (µg/100)	β-Amylase (µg/100)	%Starch	%Protein
PARENTS						
ICSA731	98.13^{a-d}	22.64^{ij}	22.47^{cb}	23.00^{f-i}	66.17^{l}	7.76^{e}
ICSA11	96.61^{kjl}	21.12^{l}	21.24^{j}	23.44^{d-g}	66.79^{k}	9.16^{c}
ICSA38	98.18^{bac}	24.47^{b}	20.45^{n}	22.55^{hij}	66.95^{jk}	9.21^{b}
Chokwe	97.94^{a-e}	22.14^{k}	21.37^{i}	23.68^{d-g}	67.05^{ij}	8.79^{d}
CF.35.5	96.05^{k}	23.13^{h}	21.97^{g}	21.98^{j}	67.35^{ghf}	8.38^{e}
NR71168	94.99^{l}	22.71^{ij}	20.38^{o}	22.98^{ghi}	67.66^{bcd}	8.77^{de}
SPV422	98.43^{a}	21.13^{l}	20.50^{n}	23.28^{e-f}	67.58^{cde}	9.35^{a}
SAMSORG 8	97.62^{b-g}	20.70^{m}	21.12^{k}	22.44^{ij}	67.53^{def}	8.41^{e}
HYBRIDS						
ICSA731xChokwe	97.52^{d-e}	26.07^{a}	20.17^{p}	23.79^{c-f}	67.57^{cde}	2.72^{n}
ICSA731 x CF35.5	97.96^{a-d}	22.82^{i}	20.17^{p}	23.87^{b-e}	67.42^{gef}	2.84^{l}
ICSA731 x NR71168	95.23^{l}	24.79^{b}	23.40^{a}	23.13^{e-i}	67.18^{hi}	2.59^{l}
ICSA731 x SPV422	97.29^{e-h}	21.11^{l}	22.52^{b}	23.06^{f-i}	67.51^{d-f}	3.10^{i}
ICSA731 x SAMSORG8	97.47^{d-g}	22.49^{j}	22.13^{f}	22.97^{ghi}	67.81^{b}	2.68^{n}
ICSA11xChokwe	97.98^{a-d}	22.73^{i}	20.67^{m}	23.88b-e	67.48^{d-f}	3.01^{j}
ICSA11 x CF35.5	98.24^{ba}	24.13^{d}	22.30^{e}	24.94^{a}	67.54^{cde}	3.43^{g}
ICSA11 x NR71168	98.18^{bac}	22.18^{k}	20.15^{p}	24.60^{ab}	67.85^{b}	3.25^{h}
ICSA11 x PV422	97.70^{b-f}	22.12^{k}	21.65^{h}	23.92^{bcd}	67.31^{gh}	3.03^{j}
ICSA11 x SAMSORG 8	97.77^{a-f}	22.76^{i}	21.27^{j}	24.19^{abc}	67.42^{egf}	2.73^{n}
ICSA38x Chokwe	97.22f^{i}	23.41^{fg}	22.35^{ed}	23.19^{e-i}	66.17^{d-e}	2.59^{o}
ICSA38 x CF35.5	97.71^{b-f}	23.46^{ef}	20.94^{l}	23.64^{d-g}	67.79^{bc}	3.04^{j}
ICSA38 x NR71168	96.76^{hji}	22.17^{k}	21.45^{i}	23.79^{d-g}	67.49^{d-f}	2.79^{m}
ICSA38 x SPV422	97.85^{a-f}	23.62^{d}	21.14^{k}	23.86^{b-e}	67.78^{bc}	3.26^{h}
ICSA38 x SAMSORG 8	97.52^{d-g}	23.22gh	20.67^{k}	23.12^{e-i}	67.31^{gh}	2.87^{k}
CHECKS						
SAMSORG41 (ICSV111)	98.00^{a-d}	24.14^{d}	22.40^{cd}	24.52^{abc}	67.85^{b}	2.88^{k}
SAMSORG40(ICSV400)	96.25^{jk}	23.95^{d}	22.10^{f}	24.50^{abc}	68.18^{a}	2.78^{m}
SAMSORG H2 (ICSA38XNR71182)	96.79^{hij}	22.49^{j}	22.13^{f}	23.68^{d-g}	67.21^{hi}	2.66^{n}
SAMSORGH1 (ICSA38XNR71176)	22.49^{jih}	24.54^{c}	22.1^{h}	23.60^{d-g}	67.67^{bcd}	2.67^{n}
SE ±	0.16	0.05	0.03	0.19	0.05	0.05

*Means with the same alphabet in the same column are not significantly different. (DMRT)

4.3 GENETIC ANALYSIS

4.3.1 Combining Ability Analysis and Estimates of Variance Components

The estimates of general combining ability effects, the variance component estimates and proportional contribution to total variance of the parents for different agronomic traits for individual location are presented in Tables 4. 13. The estimates of specific combining ability effects of the crosses for different traits for individual location are presented in Table 4.14.

Location 1 (Samaru)

The estimates of general combining ability (GCA) effect of the parents for agronomic traits are presented in Table 4.13.

The GCA estimates for lines and testers revealed that; ICSA 38 exhibited positive significant GCA effect for heading date, and highest positive value for plant height, panicle length and 100 grain weight (Table 4.13).

ICSA 11 exhibited significant negative GCA effect for heading date, and lowest value for plant height. It was the most desirable combiner for earliness and for dwarf stature hybrid but showed negative effect for grain yield. The ICSA731 was the best combiner for grain yield. The GCA effects of lines did not differ significantly from one another for panicle length.

The GCA effects for the male (testers) indicated that for heading date, Chokwe and Samsorg 8 showed significant positive GCA effect .This lines are good combiner in developing late maturing hybrids. NR71168 and CF35.5 exhibited significant negative GCA effect and were the best pollinator parents for earliness while SPV422 showed significant negative GCA effect for plant height but highly significant positive values for

grain yield, this is a good combiner in developing short- stature and high yielding hybrid. SAMSORG 8 (KSV14) exhibited positive GCA value for panicle length but showed negative value for yield.

Estimates of variance components showed that SCA variance were higher than those of GCA variance for all the characters indicating the predominance of non-additives gene action. The ratio of the variance of GCA to SCA was less than unity for all traits. The contribution of the interaction component of line x tester was more than that of the testers for all traits.

Estimates of specific combining ability (SCA) for five agronomic traits in Samaru are shown in Table 4.14.Thirteen hybrids were significant for heading dates, out of these eight exhibited positive SCA effect while the other five showed negative SCA for heading date. For plant height, nine crosses showed significantly positive SCA effects, seven of these indicated positive SCA with ICSA11 X SPV 422 having the highest value while two exhibited negative SCA with ICSA11 X CHOKWE having the highest value. With respect to panicle length, only two hybrids showed significantly SCA effect, ICAS11 X CHOKWE was positive and ICSA 731 X SAMSORG 8 exhibited negative SCA effect. While for 1000 grain weight only ICSA11X SPV422 showed positive SCA effects. For grain yield, only ICSA11 X CF35.5 showed significant SCA effect value.

Table 4.13: General Combining Ability (GCA) Effects, Variance Component Estimate and Proportional Contribution to Total Variance of Lines x Tester for Agronomic Traits in Sorghum crosses at Samaru 2010

Genotypes	Heading Date	Plant Height(cm)	Panicle length(cm)	1000Grain Weight(gm)	Grain yield per hectare(kg)
LINES					
ICSA731	-1.7556 ns	-5.7556 ns	-0.7022 ns	0.0111 ns	82.963 ns
ICSA11	-3.7556*	0.4778 ns	-0.0022 ns	-1.5756 ns	-94.815 ns
ICSA38	5.5111**	5.2778 ns	0.7044 ns	1.5644 ns	11.8519 ns
TESTERS					
Chokwe	3.3556**	2.2444 ns	-0.6511 ns	1.1911 ns	-35.556 ns
CF.35.5	-2.6444**	1.6333 ns	-0.4067 ns	-1.0422 ns	-183.7 ns
NR71168	-8.6444**	-3.5333 ns	-0.7622 ns	0.9022 ns	-35.556 ns
SPV422	0.1333 ns	-6.2*	0.7267 ns	-2.5756*	379.259*
KSV14(SAMSORG 8)	7.8**	5.8556*	1.0933 ns	1.5244 ns	-124.44 ns
S.E (GCA for line)	0.4372	1.3937	0.6072	0.726	87.9213
S.E (GCA for Tester)	0.5644	1.7992	0.7839	0.9373	113.506
Variance Component Estimate					
σ^2GCA	-1.3183	-21.9342	-0.4169	0.5615	-864.198
σ^2SCA	63.3638	103.72	11.44	1.8188	30814.53
σ^2GCA/σ^2SCA	0.02081	-0.2115	-0.0364	0.3087	-0.02805
Proportional contribution to total variance					
Line	13.82	13.18	8.4	22.07	5.45
Tester	26.82	12.01	14.75	32.98	39.94
Line x Tester	59.36	74.81	76.85	44.94	54.61

*, **: Significant at 0.05 and 0.01 probability level respectively.ns= non significant

Table 4.14: Specific Combining Ability (SCA) Estimates of Hybrids from Line X Tester Analysis of Agronomic Characters in Sorghum Crosses at Samaru.2010

HYBRIDS	Heading Date	Plant height (cm)	Panicle length(cm)	1000Grain Weight(gm)	Grain yield per hectare(kg)
ICSA731 x Chokwe	0.3111 ns	1.4222 ns	0.7578 ns	-0.1778 ns	-142.22 ns
ICSA731 x CF35.5	4.3111**	7.8556*	1.4911 ns	-1.3911 ns	-142.22 ns
ICSA731 x NR71168	-4.6222**	-9.2778*	-2.2489 ns	1.5689 ns	284.444 ns
ICSA731 x SPV422	3.6444**	5.7 ns	-1.12 ns	2.5222 ns	-216.3 ns
ICSA731 x SAMSORG 8	-5.3556**	-3.0333 ns	-3.2867*	-1.5911 ns	-82.963 ns
ICSA11 x Chokwe	1.7111 ns	-2.6667 ns	4.4067*	-0.9311 ns	299.259 ns
ICSA11 x CF35.5	6.3111**	-21.3 ns	0.6689 ns	-2.9889 ns	435.556*
ICSA11 x NR71168	-15.6889**	6.3*	0.3356 ns	-0.4689 ns	35.5556 ns
ICSA11 x SPV422	9.3778**	15.0**	-1.0044 ns	3.4578*	-471.11 ns
ICSA11 x SAMSORG 8	-15.1333**	9.0333*	-0.72 ns	0.0222 ns	-201.48 ns
ICSA38 x Chokwe	9.8667**	19.2**	1.6467 ns	2.0089 ns	242.963 ns
ICSA38 x CF35.5	5.2667**	10.1667**	-0.9267 ns	-2.0311 ns	41.4815 ns
ICSA38 x NR71168	4.8667**	5.1444 ns	0.4133 ns	0.6222 ns	35.5556 ns
ICSA38 x SPV422	6.8667**	8.0778*	-0.1867 ns	1.4422 ns	-53.333 ns
ICSA38 x SAMSORG 8	-11.7333**	-13.222**	-0.2267ns	2.0644 ns	-71.111 ns
SE ±	0.9776	3.1164	1.3578	1.6235	196.598

*, **: Significant at 0.05 and 0.01 probability level respectively.ns: non significant

4.3.2Combining Ability Analysis and Estimates of Variance Componentsfor Malting/Proximate Quality Traits at Samaru

The estimate of general combining ability effects (GCA), the variance component estimates and proportional contribution to total variance of parents for different malting/ proximate quality traits for individual location are presented in Table 4.15.

The estimate of specific combining ability effects (SCA) of the crosses for different traits for individual location are shown in Table 4.16

Location 1 (Samaru)

The GCA estimates for Lines (females) revealed that: ICSA731 exhibited positive significant GCA effect for malting loss, α-amylase activities, starch and protein but showed negative significant GCA for germination capacity and β-amylase. ICSAII exhibited positive significant GCA effect for germination capacity and β-amylase. It is a good general combiner for high malting hybrids. Lines ICSA38 exhibited positive significant GCA effect for germination capacity and starch. ICSAII and ICSA38 are good lines for the development of viable hybrid with good malting quality traits. While ICSA731 is a good general combiner for α-amylase activities, starch and protein. These lines are suitable for malting because they have high germination capacities. The GCA effect for the Testers (males) indicates that CF35.5, SPV422 and SAMSORG 8 showed positive significant GCA effect for germination capacity while NR7II68 exhibited negative GCA effect for germination capacity. These Testers except NR71168 are good general combiner in developing hybrids with good malting quality. Chokwe and CF35.5 exhibited positive significant GCA effect for malting loss while NR7II68, SPV422 and SAMSORG 8 exhibited negative significant GCA effect and are considered as good general combiners in developing good hybrid with less malting loss. SPV 422 and

SAMSORG 8 exhibited positive significant GCA effect for α-amylase while NR71168 and CF35.5 showed negative significant GCA effect for α-amylase.

For β-amylase, CF35.5 and NR71168 exhibited significant positive GCA effect. The GCA effect of Samsorg 8 was positively significant for starch and protein alsoNR71168 indicated positive significant GCA for protein.

The contribution of the testers to the total variance was greater than that of the lines for all the traits except β-amylase and starch while the contribution of the interaction component of line x tester was more than that of testers for all the traits except β-amylase for which the contribution of lines was higher. The estimates of variances due to SCA were higher than those of GCA for all traits except β-amylase. The ratio of GCA to SCA variance was less than unity for all traits except β-amylase.

The estimates for specific combining ability (SCA) are presented in Table 4.14. Nine out of fifteen hybrids showed significant SCA effect for germination capacity. Out of these, five hybrids showed significant positive SCA effect while another four showed significant negative SCA effect for germination capacity. ICSA X NR71168 had the highest positive SCA values .Thirteen out of fifteen hybrids showed significant SCA effect for malting loss. Only five indicated positive significant SCA effect while seven showed negative significant SCA values for malting loss. Fourteen hybrids indicated significant SCA effect for α-amylase, six hybrids showed significant positive and eight indicated negative significant SCA effects for α-amylase. Twelve hybrids had significant SCA effect for β-amylase; six of these exhibited positive significant SCA with ICSA731 × Chokwe showing the highest positive SCA value while eight showed negative significant SCA effect with ICSA11 X NR71168 having the lowest negative value. Six hybrids showed significant SCA effect for Starch, three of these showed positive while

three showed negative significant SCA effects. The highest positive values of SCA for starch was indicated by ICSA731 × KSV14.Twelve hybrids had significant SCA effect for Protein, six of these exhibited positive significant SCA with ICSA38 X SPV 422 showing the highest positive SCA values while six showed negative significant SCA effect with ICSA731 X CF35.5 having the lowest negative value.

Table 4.15: General Combining Ability (GCA) Effects, Variance Component Estimate and Proportional Contribution to Total Variance for Malting Quality Traits of Sorghum at Samaru, 2010

GENOTYPES	Germination Capacity (%)	Malting Loss (%)	α-Amylaseμg/100	βAmylase μg/100	Starch (%)	Protein (%)
LINES						
ICSA731	-0.6**	0.3222**	0.4307**	-0.2831**	0.0884*	0.0667**
ICSA11	0.4**	-0.2058**	-0.1093**	1.0036**	-0.1822**	-0.048**
ICSA38	0.2**	-0.1164*	-0.3213**	-0.7204**	0.0938*	-0.0187**
TESTERS						
Chokwe	0.0667 ns	0.8164**	0.0067	-0.6347**	0.0418 ns	-0.0462**
CF.35.5	0.4**	0.7253**	-0.7178**	0.5187**	-0.1938*	-0.144**
NR71168	-1.2667**	-0.3924**	-0.1733**	0.2809*	0.0084 ns	0.0693**
SPV422	0.4**	-0.7058**	0.0933*	0.0298 ns	-0.0116 ns	0.016 ns
SAMSORG 8	0.4**	-0.4436**	0.7911**	-0.1947 ns	0.1551*	0.1049**
S.E (GCA for Lines)	0.0499	0.05	0.0027	0.0689	0.0317	0.0056
S.E(GCA for Testers)	0.0815	0.0817	0.0044	0.1125	0.0518	0.0091
Variance Component Estimate						
σ^2GCA	0.1667	-0.0504	-0.0384	0.55257	-0.0138	-0.0041
σ^2SCA	0.7967	1.147	0.9718	0.1632	0.1332	0.0397
σ^2GCA/σ^2SCA	0.2092	-0.044	-0.0395	3.2211	-0.1035	-0.1036
Proportional contribution to total variance						
LINES	17.95%	4.91%	11.73%	66.88%	15.87%	7.53%
TESTERS	40.17%	37.67%	27.61%	19.72%	12.15%	24.78%
LINES X TESTERS	41.88%	57.42%	60.66%	13.40%	71.98%	67.70%

***, **:** Significant at 0.05 and 0.01 probability level, respectively, ns:non significant. α: Alpha, β: Beta

Table 4.16: Specific Combining Ability (SCA) effects for Malting Quality Trait evaluated at Samaru, 2010

GENOTYPES	%Germination Capacity	Malting Loss (Log Ug /100g)	α-Amylase (Ug /100g)	β-Amylase (Ug/100g)	%Starch	%Protein
ICSB 731 X CHOKWE	-0.0667 ns	1.9022 ns	-1.2373 ns	0.732 ns	0.0649 ns	0.0756 ns
ICSB731 X CF35.5	0.6**	-1.24**	-0.5196**	0.0587**	-0.2462*	-0.0333*
ICSB 731 X NR71168	-1.7333**	0.5178**	0.8893**	-0.2902**	-0.4484**	0.16**
ICSB 731 X SPV 422	0.6**	-0.5022**	0.9227**	-0.2858**	0.0782 ns	-0.2733**
ICSA731 x SAMSORG 8	0.6**	-0.6778**	-0.0551**	-0.2147**	0.5516**	0.0711**
ICSA 11 X CHOKWE	-0.0667 ns	-0.8564**	-0.224**	-0.2347**	-0.1644 ns	0.1102**
ICSA 11 X CF35.5	-0.4**	0.6547**	0.2938**	0.2187**	-0.0689 ns	-0.152**
ICSA 11 X NR71168	1.2667**	-0.2276 ns	-0.5307**	-0.1969**	0.3622**	-0.012 ns
ICSA 11 X SPV 422	-0.4**	0.0258 ns	-0.3173**	-0.0258 ns	-0.0911 ns	0.0147 ns
ICSA 11 XSAMSORG 8	-0.4**	0.4036**	0.7782**	0.2387**	-0.0378 ns	0.0391*
ICSA 38 X CHOKWE	0.1333 ns	-1.0458**	1.4613**	-0.4973**	0.0996 ns	-0.1858**
ICSA 38 X CF35.5	-0.2 ns	0.5853**	0.2258**	-0.2773**	0.3151**	0.1853**
ICSA38 X NR71168	0.4667*8	-0.2902*	-0.3587**	0.4871**	0.0862 ns	-0.148**
ICSA 38 X SPV 422	-0.2 ns	0.4764**	-0.6053**	0.3116**	0.0129 ns	0.2587**
ICSA38 X SAMSORG 8	-0.2 ns	0.2742 ns	-0.7231**	-0.024 ns	-0.5138**	-0.1102**
SE ±	0.1412	0.1414	0.0076	0.1949	0.0897	0.0158

*, **: Significant at 0.05 and 0.01 probability level respectively, ns: non -significant. α: Alpha, β: Beta.

Location 2: Kadawa

The GCA effects of the parents are presented in Table 4.17. ICSA38 exhibited significant positive GCA effect for heading dates and was the best combiner for late maturing hybrids. ICSA 11 recorded a non significant negative value for heading date. The line ICSA 731 exhibited significant negative GCA effects for plant height; it would be preferred for the production of dwarfs to medium tall hybrids. The GCA effects of lines did not differ significantly from one another for 1000 grain weight, panicle length and yield.

ICSA 38 was the most desirable combiner for grain yield and also best combiner for panicle length.

The testers NR71168 and SPV422 exhibited significant negative GCA value for heading dates and were the best combiners for earliness while chokwe and CF35.5 showed significant positive values and were the best combiners for late maturing hybrid. SAMSORG 8(KSV14) showed significant positive GCA effects for plant height, panicle length and 1000 grain weight. SPV422 showed significant positive GCA effect for panicle length and grain yield. It is a general good combiner for panicle length and grain yield.

The estimates of variance due to SCA were higher than those of GCA variances for all the traits. The ratio of GCA to SCA variance was less than unity for all traits.

The contribution of testers to the total variance was greater than that of the lines for all traits studied while the contribution to total variance by the interaction of line x tester was more than that of testers for all the traits except Heading dates and panicle length.

The estimates for specific combining ability (SCA) showed that nine hybrids out of fifteen showed positive SCA effects for Heading date. ICSA38 X SAMSORG8 was the earliest. Five out of fifteen hybrid showed significant SCA for plant height (Table 4.18) Out of these, three hybrids showed significant positive SCA effects for plant height while two showed significant negative SCA effect.ICSA11 X NR71168 had the highest positive SCA values while ICSA 731X CF35.5 had the lowest negative SCA value for plant height and is the best specific combiner for dwarfism.ICSA731 X SAMSORG 8 showed significant negative SCA value for panicle length. Six hybrids indicated significant SCA effect for 1000grain weight, three of these exhibited positive significant SCA effect with ICSA731 X SPV422 showing the highest positive SCA value and three indicated negative significant SCA for 1000 grain weight.

Two hybrids showed significant SCA effect for grain yield with ICSA38 X NR71168 (539.26kg/ha) exhibiting the highest positive significant SCA value followed by ICSA11X CHOKWE (248.89kg/ha), and ICSA38 X Chokwe (204.44kg/ha).

Table 4.17: General Combining Ability Effects (GCA) Of Lines and Tester for Agronomic Traits at Kadawa.2010

Genotypes	Heading Date	Plant Height(cm)	Panicle length(cm)	1000Grain Weight(gm)	Grain yield per hectare(kg)
LINES					
ICSA731	2ns	-9.1111*	-0.1333ns	-0.0289ns	-5.9259ns
ICSA11	-2.2667ns	1.7556ns	-0.4667ns	-0.3622ns	-85.926ns
ICSA38	4.6*	7.3556ns	0.6ns	-0.0289ns	91.8519ns
TESTERS					
Chokwe	5.2667*	-7.2778ns	-3.1333**	-0.4178ns	-85.926ns
CF.35.5	4.6*	-6.4444ns	-1.0222ns	-2.3956*	-204.44ns
NR71168	-5.2889*	-4.7778ns	-1.5778ns	1.3378ns	-130.37ns
SPV422	-5.1778*	3.0556ns	1.9222*	-1.14ns	284.444*
SAMSORG 8(KSV14)	0.6ns	15.4444**	3.8111**	2.6156*	136.296ns
S.E (GCA for line)	1.6195	3.1369	0.6577	0.8759	54.3969
S.E (GCA for Tester)	2.0908	4.0498	0.849	1.1308	70.2261
Variance component estimates					
σ^2GCA	1.6669	-37.7477	0.6019	-1.1731	-1275.72
σ^2SCA	18.2417	306.41	3.74	7.653	46062.37
σ^2GCA/σ^2SCA	0.09138	-0.1232	0.1609	-0.1533	-0.02769
Proportional contribution to total variance					
Line	7.02	10.45	1.86	0.82	6.04
Tester	47.61	16.33	59.25	27.25	37.84
Line X Tester	45.37	73.23	38.88	71.93	56.13

*, **: Significant at 0.05 and 0.01 probability level respectively.ns :non significant.

σ^2GCA=Variance of General Combining Ability.

σ^2SCA = Variance of Specific Combining Ability

Table 4.18: Specific Combining Ability (SCA) Estimates of Hybrids from Line X Tester Analysis of Agronomic Characters in Sorghum Crosses at Kadawa.2010

HYBRIDS	Heading Date	Plant Height(cm)	Panicle Length(cm)	1000Grain Weight(gm)	Grain Yield per hectare(kg)
ICSA731 x Chokwe	1.3333ns	27.7778**	-0.3667ns	3.0844ns	50.3704ns
ICSA731 x CF35.5	-5.4ns	-39.422**	1.1333ns	-3.2156*	-47.407ns
ICSA731 x NR71168	4.0667ns	11.6444ns	-0.7667ns	0.1311ns	-2.963ns
ICSA731 x SPV422	-1ns	15.6111*	0.8556ns	5.3289*	-275.56ns
ICSA731 x SAMSORG 8	0.2667ns	2.4222ns	-3.6444*	-3.1044ns	26.6667ns
ICSA11 x Chokwe	0.7333ns	-13.189ns	2.7889ns	-2.2244ns	248.889*
ICSA11 x CF35.5	-0.8889ns	-31.056**	0.7556ns	-4.6378*	-82.963ns
ICSA11 x NR71168	-3.8444ns	29.5778**	2.7444ns	3.6289*	-47.407ns
ICSA11 x SPV422	2.9556ns	1.4778ns	-1.9889ns	1.0089ns	130.37ns
ICSA11 x SAMSORG 8	-1.8889ns	-9.5556ns	-2.5889ns	-3.26*	-231.11ns
ICSA38 x Chokwe	-0.9556ns	8.4111ns	2.2444ns	3.6067*	204.444ns
ICSA38 x CF35.5	2.8444ns	1.1444ns	0.3444ns	-0.3467ns	26.6667ns
ICSA38 x N R71168	0.6667ns	-2.7778ns	2.8556ns	-0.5156ns	539.259**
ICSA38 x SPV422	9.9333ns	3.8556ns	-2.4778ns	-0.9156ns	-136.3ns
ICSA38 x SAMSORG 8	-10.6ns	-1.0778ns	-0.3778ns	1.4311ns	-402.96ns
SE ±	3.6213	7.0144	1.4706	1.9586	121.635

*, **: Significant at 0.05 and 0.01 probability level, respectively, ns =non significant

4.3.3 Combining Ability Analysis and Estimates of Variance Componentsfor malting/proximates quality traits at Kadawa

The estimate of general combining ability effects (GCA), the variance component estimates and proportional contribution to total variance of parents for different malting/ proximate quality traits for individual location are presented in Table 4.19. The estimate of specific combining ability effects (SCA) of the crosses for different traits for individual location is shown in Table 4.20.

In Table 4.19, The GCA effects for Lines indicated that ICSA731 showed significant positive GCA value for malting loss and α-amylase but significant negative value for β-amylase, starch and protein. While ICSA II exhibited significant positive GCA effect for germination capacity, starch and protein, but showed highly significant negative GCA effect for α-amylase and malting loss and was the best general combiner for these traits. It would be preferred for the production of high malting hybrids. The Lines ICSA38 showed significant positive GCA effect for malting loss, α-amylase, and protein but showed significant negative GCA effect for germination capacity. The GCA effects of Testers revealed that Chokwe recorded the highest significant positive GCA value for malting loss but significant negative GCA effect for - α amylase. CF35.5 exhibited significant positive GCA effect for germination capacity, α amylase, starch and protein but indicated highly significant negative GCA effect for malting loss. It was the most desirable combiner for malting loss because it recorded the lowest malting loss. Tester NR7II68 recorded significant positive GCA value for malting loss, α-amylase and protein. SPV422 indicated highly significant positive GCA effect for α-amylase and highly significant negative effect for malting loss. SAMSORG 8 exhibited significant negative GCA effect for malting loss, α-amylase, starch and protein.

The estimates of variance due to SCA were higher than those of GCA for all traits measured except β amylase. The ratio of GCA to SCA variance was less than unity for most traits.

The contribution of Testers to the total variance was greater than that of lines for malting loss, α and β amylase and starch while the contribution to total variance by the interaction of lines x testers was more than that of testers for all the traits .

Estimates of specific combining ability (GCA) for malting/proximate quality traits are presented in Table 4.20.

Two hybrids exhibited significant positive SCA effect for germination capacity. All the fifteen hybrids showed significant SCA effect for malting loss. Out of these, seven hybrids showed positive significant SCA while eight hybrids showed negative SCA effect for malting loss. ICSA731 × NR71168 had the highest positive SCA value while ICSA11 x NR71168 had the lowest negative SCA value for malting loss. Fourteen hybrids indicated significant SCA effect for α-amylase. Six hybrids showed positive significant SCA effect for α-amylase while eight hybrids showed significant negative SCA effect. ICSA11 × CF35.5 had the highest positive significant SCA value for α-amylase while ICSA 11 x NR71168 showed negative significant SCA value. ICSA11 × NR71168 and ICSA38 × SPV422 exhibited positive significant SCA effect while ICSA11 X SPV422 and ICSA38 X CHOKWE showed negative significant SCA effect for starch. Ten hybrids indicated significant SCA effects for protein, five of which showed positive SCA with ICSA731 X CHOKWE being the best specific combiner for protein while the other five showed negative significant SCA effect.

Table 4.19: General Combining Ability (GCA) Effects, Variance Component Estimate and Proportional Contribution to TotalVariance for Malting Quality Traits of Sorghum at Samaru, 2010

GENOTYPE	%Germination Capacity	%Malting Loss	α-Amylase(µg/100)	β-Amylase(µg/100)	%Starch	%Protein
LINES						
ICSA731	-0.1969ns	0.3142**	0.1302**	-0.4358**	-0.1498**	-0.4947**
ICSA11	0.5611*	-0.5058**	-0.2724**	0.1609ns	0.1622**	0.3293**
ICSA38	-0.3642*	0.1916**	0.1422**	0.2749ns	-0.0124	0.1653*
TESTERS						
Chokwe	0.0971ns	1.048**	-0.6756**	0.4233ns	-0.068ns	0.0304ns
CF.35.5	0.556*	-0.0609**	0.1933**	0.3267ns	0.3042**	0.326**
NR71168	-0.2718ns	0.1991**	0.7089**	-0.1089ns	-0.0558ns	0.1516*
SPV422	-0.1618ns	-1.0031**	0.6467**	-0.2533ns	0.0098ns	0.0193ns
SAMSORG 8	-0.2196ns	-0.1831**	-0.8733**	-0.3878ns	-0.1902*	-0.5273**
S.E (GCA for line)	0.1323	0.0045	0.024	0.1499	0.0359	0.0439
S.E (GCA for Tester)	0.216	0.0074	0.0391	0.2448	0.0586	0.0718
Variance Component Estimate						
σ^2GCA	0.1025	-0.4929	-0.4954	0.0866	0.0102	0.0125
σ^2SCA	0.2329	3.2742	2.9325	0.0301	0.0613	0.5635
σ^2GCA/σ^2SCA	0.4403	-0.1505	-0.1689	2.8774	0.1664	0.0222
Proportional contribution to total variance						
Lines	35.68%	5.63%	1.82%	31.18%	19.93%	24.52%
Testers	20.55%	18.85	21.35%	32.89%	33.39%	15.80%
LINES X TESTERS	43.77%	75.52%	76.82%	35.93%	46.67%	59.68%

*, **: Significant at 0.05 and 0.01 probability level respectively.ns :non significant. σ^2GCA=Variance of General Combining Ability, σ^2SCA = Variance of Specific Combining Ability

Table 4.20: Specific Combining Ability (SCA) effect for Malting Quality Traits at Kadawa in 2010

GENOTYPES	%Germination Capacity	Malting Loss. (Log Ug/100g)	α-Amylase (Ug/100g)	β-Amylase (Ug/100g)	%Starch	%Protein
ICSA 731 X Chokwe	0.7636*	1.468**	-1.1124**	0.328ns	0.112ns	0.8702**
ICSA731 X CF35.5	0.1747ns	-0.7031**	-1.968**	0.108ns	-0.0136ns	-0.7053**
ICSA 731 X NR71168	-0.4542ns	2.3369**	2.0164**	-0.3531ns	-0.1336ns	0.1358ns
ICSA 731 X SPV 422	-0.4609ns	-2.4809**	0.0187	-0.102ns	-0.0691ns	0.0213ns
ICSA 731 X SAMSORG 8	-0.0231ns	-0.6209**	1.0453**	0.0191ns	0.1042ns	-0.322*
ICSA 11 X CHOKWE	-0.0811ns	-1.112**	-0.1764*	-0.4053ns	0.1133ns	-1.0071**
ICSA 11 X CF35.5	-0.0267ns	1.3769**	2.4147**	0.1913ns	0.0044ns	0.5907**
ICSA 11 X NR71168	0.6811ns	-0.8031**	-2.1209**	0.6102ns	0.3444*	0.6551**
ICSA 11 X SPV 422	-0.3822ns	0.3591**	0.4613**	-0.5187ns	-0.3411*	-0.5927**
ICSA 11 X SAMSORG 8	-0.1911ns	0.1791**	-0.5787**	0.1224ns	-0.1211ns	0.354*
ICSA 38 X CHOKWE	-0.6824ns	-0.356**	1.2889**	0.0773ns	-0.2253*	0.1369ns
ICSA 38 X CF35.5	-0.148ns	-0.6738**	-0.4467**	-0.2993ns	0.0091ns	0.1147ns
ICSA 38 X NR71168	-0.2269ns	-1.5338**	0.1044*	-0.2571ns	-0.2109ns	-0.7909**
ICSA 38 X SPV 422	0.8431*	2.1218**	-0.48**	0.6207ns	0.4102*	0.5713**
ICSA 38 X SAMSORG 8	0.2142ns	0.4418**	-0.4667**	-0.1416ns	0.0169ns	-0.032ns
SE ±	0.3741	0.0127	0.0678	0.424	0.1014	0.1243

***, **:** Significant at 0.05 and 0.01probabilitylevel respectively.ns= non significant

4.3.4 Combined Analysis of Variance for Combining Ability Analysis for Malting/proximate Quality Traits

Estimate of variance components showed that the ratio of GCA variance to SCA variance in relation to the total genotypic variances indicated that non-additive genes were in control of these characters. The contribution of testers to the total variance was higher for all traits except β –amylase, while the contribution of the interaction component of lines x tester was more than that of the testers and lines for all traits. The SCA variances were higher than the GCA variances for all traits. The ratio of the variances of GCA to SCA was less than unity for all traits.

The estimate of general combining ability effects of lines and testers are presented in Table 4.21. The estimates of general combining ability effects indicate that amongst the three females, ICSA 731 exhibited positive significant GCA effect for malting loss and α-amylase but showed negative significant SCA effect for germination capacity and β-amylase. ICSA11 showed positive significant SCA effect for germination capacity and β-amylase but indicated negative SCA effects for malting loss. This is a good general combiner in developing hybrid with good malting quality for breweries. ICSA38 showed negative significance SCA effect for β-amylase .Among the testers, it was observed that Chokwe, showed highly positive significant GCA estimate for malting loss. The tester CF35.5 was a good general combiner for germination capacity, malting loss and β-amylase as it exhibited positive significant GCA effects for these traits. NR71168 exhibited negative significant GCA effect for germination capacity while SPV22 showed negative significant GCA effect for malting loss.

Specific combining ability effect across location are shown in Table 4.22.Eight hybrids showed positive SCA effect for germination capacity with ICSA11 X NR71168 recording the highest significant positive value while seven hybrids indicated negative SCA effect

with ICSA731 X NR71168 recording the lowest significant negative value for germination capacity. Eleven hybrids showed significant SCA effects for malting loss, five of these exhibited positive significant effects while six hybrids showed negative significant effects. Six hybrids exhibited significant SCA effects for α-amylase, three of these indicated positive effects while the other three showed negative effects. Seven hybrids express positive SCA effect for β- amylase with ICSA731 X CHOKWE indicating the highest positive values while ICSA 731 X NR71168 recorded the lowest negative SCA effect. Six hybrids express positive SCA effect for starch with ICSA11 X NR71168 indicating the highest positive values while ICSA 731 X NR71168 recorded the lowest negative SCA effect. Only two hybrids showed significant SCA effect for protein, ICSA731 X CHOKWE indicated positive significant SCA values while ICSA38 X NR71168 expresses negative significant SCA effects.

Table 4.21: Combined General Combining Ability (GCA) Effect, variance component estimate and proportional contribution to total variance For Malting Quality Traits.

GENOTYPE	%Germination Capacity	%5malting Loss	α-Amylase(µg/100)	β-Amylase(µg/100)	%Starch	%Protein
LINES						
ICSA731	-0.3984*	0.3182**	0.2804*	-0.3594*	-0.0307ns	-0.214ns
ICSA11	0.4806*	-0.3558**	-0.1909ns	0.5822**	-0.01ns	0.1407ns
ICSA38	-0.0821ns	0.0376ns	-0.0896ns	-0.2228*	0.0407ns	0.0733ns
TESTERS						
Chokwe	0.0819ns	0.9322**	-0.3344ns	-0.1057ns	-0.0131ns	-0.0079ns
CF.35.5	0.478*	0.3322*	-0.2622ns	0.4227*	0.0552ns	0.091ns
NR71168	-0.7692*	-0.0967ns	0.2678ns	0.086ns	-0.0237ns	0.1104ns
SPV422	0.1191ns	-0.8544**	0.37ns	-0.1118ns	-0.0009ns	0.0177ns
SAMSORG 8	0.0902ns	-0.3133*	-0.0411ns	-0.2912ns	-0.0176ns	-0.2112ns
S.E (GCA for line)	0.1450	0.0880	0.1198	0.1062	0.0860	0.0826
S.E (GCA for Tester)	0.2367	0.1438	0.1956	0.1734	0.1405	0.1348
Variance Component Estimate						
σ^2GCA	0.218308	-0.39077	-0.58222	0.31996	-0.03112	-0.02519
σ^2SCA	2.0245	10.4667	8.7826	0.4961	0.3753	0.9583
σ^2GCA/σ^2SCA	0.1078	-0.03733	-0.06629	0.62547	-0.08291	-0.02628
Proportional contribution to total variance						
LINES	26.26%	5.57%	4.56%	56.66%	2.39%	19.07%
TESTERS	33.75%	26.47%	8.68%	19.34%	2.18%	10.56%
LINES X TESTERS	39.99%	67.96%	86.76%	24.00%	95.43%	70.37%

*, **: Significant at 0.05 and 0.01 probability level respectively.ns= non significant .σ^2GCA=Variance of General Combining Ability.

σ^2SCA = Variance of Specific Combining Ability

Table 4.22: Combined Specific Combing Ability (SCA) effect for malting quality traits across the two locations

GENOTYPES	%Germination Capacity	Malting Loss. (Log Ug/100g)	α-Amylase (Ug/100g)	β-Amylase (Ug/100g)	%Starch	%Protein
ICSA 731 X CHOKWE	0.3484ns	1.6851**	-1.1749**	0.53ns	0.0884ns	0.4729*
ICSA731 X CF35.5	0.3873ns	-0.9716*	-1.2438**	0.0833ns	-0.1299ns	-0.3693ns
ICSA 731 X NR71168	-1.0938*	1.4273**	1.4529**	-0.3217ns	-0.291ns	0.1479ns
ICSA 731 X SPV 422	0.0696ns	-1.4916**	0.4707ns	-0.1939ns	0.0046ns	-0.126ns
ICSA731 X SAMSORG 8	0.2884ns	-0.6493*	0.4951ns	-0.0978ns	0.3279ns	-0.1254ns
ICSA 11 X CHOKWE	-0.0739ns	-0.9842**	-0.2002ns	-0.32ns	-0.0256ns	-0.4484ns
ICSA 11 X CF35.5	-0.2133ns	1.0158**	1.3542**	0.205ns	-0.0322ns	0.2193ns
ICSA 11 X NR71168	0.9739*	-0.5153*	-1.3258**	0.2067ns	0.3533ns	0.3216ns
ICSA 11 X SPV 422	-0.3911ns	0.1924ns	0.072ns	-0.2722ns	-0.2161ns	-0.289ns
ICSA 11 X SAMSORG 8	-0.2956ns	0.2913**	0.0998ns	0.1806ns	-0.0794ns	0.1966ns
ICSA 38 X CHOKWE	-0.2746ns	-0.7009*	1.3751**	-0.21ns	-0.0629ns	-0.0244ns
ICSA 38 X CF35.5	-0.174ns	-0.0442ns	-0.1104ns	-0.2883ns	0.1621ns	0.15ns
ICSA 38 X NR71168	0.1199ns	-0.912ns	-0.1271ns	0.115ns	-0.0623ns	-0.4694*
ICSA 38 X SPV 422	0.3216ns	1.2991**	-0.5427ns	0.4661ns	0.2116ns	0.415ns
ICSA 38 X SAMSORG 8	0.0071ns	0.358ns	-0.5949ns	-0.0828ns	-0.2484ns	-0.0711ns
SE ±	0.41	0.249	0.3387	0.3003	0.2434	0.2335

*, **: Significant at 0.05 and 0.01 probability level respectively. ns:non significant

4.4 HETEROSIS

Heterosis is the performance of the hybrids over the mid-parents or high parent.

The estimate of heterosis for individual location is presented in tables 4.23.

Location 1 (Samaru)

Heading date is one of the traits utilized for selecting early cross combination in hybrid development. The heterosis over best- parent ranged from -43.38 to 25.52 percent. Eight hybrids showed significant negative heterosis. The highest negative heterosis was shown by the hybrid ICSA 11 X NR 71168, which is considered to be the earliest hybrid.

With respect to plant height, a high degree of high parent heterosis was exhibited ranging from -15.78 to 46.64 percent .Twelve hybrids showed significant positive heterosis, indicating that most of the hybrid combinations were tall. The hybrid ICSA 38 X NR 71168 recorded the highest heterosis (46.64%) while ICSA11 X SPV422 recorded the lowest heterosis(-15.78%).

For panicle length, fifteen hybrids showed significant negative heterosis. Heterosis for panicle length ranged from -41.36 to -8.05 percent, none indicating positive heterosis.

For 1000grain weight, the heterosis range from -33.44 to 26.51 percent. Only three hybrids showed highly significant positive heterosis. All the other hybrids indicated highly significant but negative heterosis.

Heterosis for grain yield ranged from -4 to 32.0 percent. Fourteen out of the fifteen hybrids showed positive highly significant heterosis. The hybrids ICSA731 X NR71168 gave the highest high parent heterosis value of 32.08 percent followed by ICSA 38 X CF 35.5 (29.17%) and ICSA11 X SPV 422 (29.09%) while ICSA11 X SAMSORG 8 indicated 0% heterosis.

4.4.1 Heterosis for Malting/Proximates Quality - Samaru

The estimates of heterosis for Samaru location for different malting/proximate quality traits are presented in Table 4.24.

Alpha -amylase is one of the traits utilized for selecting good cross combination in commercial hybrid development for industrial use. The high parent heterosis ranged from-9.14 to 8.0%. Fourteen hybrids showed highly significant high-parent heterosis out of which only four are positive. The highest positive high-parent heterosis was exhibited by the hybrid ICSA731×SPV422 (8.0%).

The high-parent heterosis for β-amylase ranged from-7.19 to 9.81%. Five out of the fifteen hybrids showed positive highly significant high parent heterosis. The hybrids ICSA11 ×CF35.5 gave the highest high parent heterosis value of 9.81% followed by ICSA11 ×Samsorg8 (KSV14) (6.74%) and ICSA11×NR71168 (6.39%). With respect to germination capacity, the high parent heterosis ranged from -8.24 to 12.44%. Five hybrids showed highly significant positive heterosis, ICSA731×Chokwe showing the highest positive estimate (12.44%).

Estimated values for Malting loss ranged from-5.35 to 4.08%. Three hybrids exhibited highly significant positive heterosis, while nine hybrids showed highly significant negative heterosis. Five hybrids expressed highly significant positive heterosis for starch, also five hybrids showed highly significant negative heterosis. The magnitude of the heterosis ranged from-20.57 to 19.70%. ICSA38×Chokwe showed the highest heterosis of 19.70% for starch, followed by ICSA11×NR71168 (18.48%) For protein, the magnitude of the heterosis ranged from-4.43 to 3.57%. Seven hybrids showed positive significant heterosis for protein.

Table 4.23: Estimates of high- parent (HP) heterosis for agronomic traits at Samaru in 2010.

GENOTYPES	Heading Date	Plant height(cm)	Panicle length(cm)	1000 Grain weight(gm)	Grain yield per hectare(kg)
ICSA731 X CHOKWE	-17.69**	8.23**	-13.98**	-13.73**	7.55**
ICSA731 X CF35.5	-10.82**	21.25**	-20.9**	-12.22**	-1.89**
ICSA731 X NR71168	-15.15**	-5.04**	-14.83**	-23.7**	32.08**
ICSA731 X SPVA22	-35.77**	-0.58**	-14.41**	-25.30**	18.18**
ICSA731 X SAMSORG 8	4.33**	23.74**	-8.05**	-10.05**	15.09**
ICSA11 X CHOKWE	15.38**	17.71**	-25.91**	-25.86*8	1.92*
ICSA11 X CF35.5	8.81**	40.45**	-41.36**	-33.44**	6.25**
ICSA11 X NR71168	-43.38**	34.53**	-30.23**	-23.88**	14**
ICSA11 X SPV422	-7.72**	-15.78**	-20.68**	-27**	29.09**
ICSA11 X SAMSORG 8	25.52**	31.21**	-25.68**	-15.99**	0
ICSA38 X CHOKWE	-15**	8.48**	-34.39**	20.08**	25**
ICSA38 X CF35.5	8.29**	45.43**	-10.18**	-8.04**	29.17**
ICSA38 X NR71168	3.65**	46.64**	-30.41**	26.51**	-4*
ICSA38 X SPV422	-2.03*	7.83**	-24.91**	-24.72**	21.82**
ICSA38 X SAMSORG 8	3.9**	17.77**	-21.17**	6.83**	3.77**

*, ** Significant at 0.05 and 0.01 probability levels, respectively. ns:non-significant.

Table 4.24: Estimates of high- parent (HP) heterosis for malting quality traits at Samaru in 2010.

Genotypes	α-Amylase ug /100	β – Amylase ug/100	%Germination capacity	%Malting loss	%Starch	%Proteins
ICSA11XNR71168	-1.27**	6.39**	-2.38**	2.80**	18.48**	-2.83**
ICSA11XCHOKWE	-7.00**	1.48ns	2.65**	0.00	-2.88**	2.22**
ICSA11XSPV422	1.08**	5.57**	-0.24ns	-1.01**	-1.75**	-2.71**
ICSA11XCF35-5	-7.82**	9.81**	-1.05**	1.38**	6.35**	-2.00**
ICSA11XSAMSORG8	1.36**	6.74**	2.65**	-1.01**	-2.41**	2.06**
ICSA38 X NR71168	-2.62**	1.94ns	2.11**	-5.35**	1.54**	-3.89**
ICSA38XCHOKWE	-0.36**	-7.19*	-8.24**	-1.02**	19.70ns	-0.55*
ICSA38XSPV422	-2.52**	-0.50ns	-6.37ns	-1.01**	-7.20ns	0.00
ICSA38XCF35-5	-9.09**	-0.26ns	0.00	0.00**	-12.09ns	1.79**
ICSA38XSAMSORG8	-6.39**	-2.29*	-6.12**	-1.01**	14.94ns	0.82**
ICSA731XNR71168	6.56**	0.32ns	1.24**	4.08**	8.61**	0.00
ICSA731XCHOKWE	-9.14**	0.09ns	12.44**	-1.02**	-20.57**	3.05**
ICSA731XSPV422	8.00**	-1.20ns	-4.53**	-1.01**	-9.36	-4.43**
ICSA731XCF35-5	-9.06**	4.84**	-1.53*	0.00	-4.84**	0.41*
ICSA731XSAMSORG8	0.03ns	0.42ns	-4.15**	-1.01**	3.37**	3.57**

*, **Significant at 0.05 and 0.01 probability levels, respectively. ns:non significant.

α:Alpha,β:Beta.

Location 2(Kadawa)

The heterosis estimates over the best parents for the different agronomic traits in Kadawa are presented in Table 4.25.

For heading date, twelve hybrids indicated significant negative heterosis over the best parent. The best parent heterosis varied from -41.04 to 22.87 percent. The hybrid ICSA731 x SPV422 recorded the highest significant negative high parent heterosis of (-41.04%). It is considered to be the earliest. Twelve hybrids showed significant negative heterosis.

With respect to plant height, high heterosis values were exhibited. The best parent heterosis ranged from -12.09 to 46.72 percent. Fourteen hybrids recorded significant positive heterosis. The hybrid ICSA38XChokwe recorded the highest significant positive best parents heterosis of (46.72%) followed by ICSA 731X Chokwe.(46.45%) .

Heterosis observed for panicle length ranged from -39.91 to 18.03 percent. The hybrid ICSA731 X SAMSORG8 gave the highest heterosis of (18.03%). All the other hybrids showed highly significant negative heterosis.

With respect to 1000 grain weight, nine hybrids showed significant negative best-parent heterosis ranging from -21.87 to -1.11 percent. Only five hybrids showed significant positive heterosis. The highest estimated heterosis over the best parent was recorded by the hybrid ICSA 731 x CF35.5.

For grain yield, the best parents' heterosis varied from-12.12 to 31.25 percent. Nine hybrids exhibited highly significant positive heterosis over the best parent while four hybrids showed highly significant negative value. The highest estimate was obtained

from hybrid ICSA731 x chokwe (31.25%) while the lowest was from ICSA11 X NR71168 (-12.12%).

4.4.2 Malting /Proximate Quality Traits - Kadawa

The heterosis estimates over the best parents for the different malting/proximate quality traits in Kadawa are presented in Table 4.26.

For α-amylase, seven hybrids recorded highly significant positive heterosis. The values ranged from1.91 to 10.47%. ICSA38×NR71168 had the highest positive heterosis of 10.47% followed closely by ICSA38×Chokwe (9.89%) while eight hybrids indicated significant negative heterosis with ICSA731 X CF35.5 showing the lowest value of -16.53%.

With respect to β-amylase, the high heterosis ranged from-2.15 to 7.07%. Three hybrids exhibited significant positive heterosis. ICSA38×CF35.5 had the highest value. This hybrid can be used for the development of malting beverages.

The magnitude of heterosis for germination capacity ranged from-1.96 to 1.87%.Seven hybrids showed significant high parent heterosis out of which only two are positive. ICSA38×NR71168 showed the highest positive heterosis of 1.87%.

Estimated values for malting loss ranged from-10.53 to 17.75%.Three hybrids exhibited highly significant positive heterosis, while four hybrids exhibited highly significant negative heterosis. ICSA731× CHOKWE indicated the highest positive heterosis of 17.75% and ICSA38×NR71168 shows the lowest negative value of -10.53%.

Heterosis observed for starch ranged from -1.43 to 0.23%.ICSA11 X CF35.5 indicated the highest heterosis of 0.23% while the lowest negative was exhibited byICSA38 X CHOKWE(-1.43).

With respect to protein eleven hybrids exhibited significant high parent heterosis ranging from-18.94 to 11.72%.Only three hybrids exhibited highly significant positive heterosis while eight hybrids shows significant negative heterosis. ICSA731×Chokwe recorded the highest positive heterosis of 11.72% and ICSA11 X CHOKWE shows the lowest estimated heterosis of -18.94%.

Table 4.25: Estimates of high-parent (HP) heterosis for agronomic traits at Kadawa in 2010.

Entry	Heading Date	Plant height(cm)	Panicle length(cm)	1000Grain weight(g)	Grain yield per hectare(kg)
ICSA731 X CHOKWE	-24.7**	46.45**	-21.53**	15.19**	31.25**
ICSA731 X CF35.5	-28.29**	41.71**	-8.56**	27.2ns	-3.64**
ICSA731 X NR71168	-37.85**	-12.09**	-16.99**	-14.33**	-10.61**
ICSA731 X SPVA22	-41.04**	-2.71**	-10.51**	-21.87**	16.07**
ICSA731XSAMSORG 8	-31.08**	22.74**	18.03 ns	-8.52**	17.91**
ICSA11 X CHOKWE	1.96**	1.2**	-31.33**	-5.1**	22.92**
ICSA11 X CF35.5	11.76**	37.1**	-39.91**	-6.69**	5.45**
ICSA11 X NR71168	-15.69**	37.79**	-21.14**	12.08**	-12.12**
ICSA11 X SPV422	-28.87**	15.34**	-11.48**	-0.87**	30.36**
ICSA11 X SAMSORG 8	22.88**	35.05**	-20.6**	-8.7**	-7.46**
ICSA38 X CHOKWE	-6.34**	46.72**	-30.11**	7.71**	25.49**
ICSA38 X CF35.5	-12.2**	32.78**	-10.8**	1.86**	21.82**
ICSA38 X NR71168	-23.41**	22.09**	-16.99**	5.32**	0.00
ICSA38 X SPV422	-23.41**	14.3**	-10.51**	-11.18**	30.36**
ICSA38 XSAMSORG 8	-34.63**	35.52**	-5.11**	-1.1**	-10.45 ns

*,** Significant at 0.05 and 0.01 probability levels, respectively.. ns= non significant

Table 4.26: Estimates of high-parent (HP) heterosis for malting quality traits at KADAWA in 2010

Genotypes	α-Amylase µg /100	β –Amylase µg /100	% Germination capacity	% Malting loss	% Starch	% Proteins
ICSA11xNR71168	-8.7**	3.11ns	0.38ns	-2.35ns	0.18ns	-0.52ns
ICSA11xCHOKWE	-6.16**	0.3ns	0.09**	2.42ns	-0.16**	-18.94**
ICSA11xSPV422	2.72**	-2.15ns	-0.48ns	0ns	-0.72ns	-14.77**
ICSA11xCF35-5	9.51**	3.18ns	0.62ns	4.09ns	0.23ns	0.62ns
ICSA11xSAMSORG8	-8.88**	-0.06ns	-0.34ns	10.44**	-0.69**	-10.64**
ICSA38 x NR71168	10.47**	4.45ns	1.87*	-10.53**	-1.39**	-17.6**
ICSA38xCHOKWE	9.89**	2.74ns	-1.96*	-2.34ns	-1.43*	-9.32**
ICSA38xSPV422	6.23**	5.37**	-0.67ns	0.62ns	-0.37ns	-4.97**
ICSA38xCF35-5	-0.24**	7.07**	-0.95ns	-8.11**	-0.53**	-6.51**
ICSA38 x SAMSORG8	1.91**	5.74**	-1.37*	-4.09**	-1.25**	-16.78**
ICSA731xNR71168	2.07**	0ns	-1.83**	15.09**	-1.42**	11.68**
ICSA731xCHOKWE	-16.58**	0.86ns	-0.22ns	17.75**	-1.07**	11.72**
ICSA731xSPV422	-6.45**	5.37ns	-1.73ns	-9.12**	-1.22**	-6.73ns
ICSA731xCF35-5	-16.53**	2.79ns	-0.35*	1-35ns	-0.71**	7.37**
ICSA731xSAMSORG8	-8.48**	-0.61ns	-1.34**	2.98ns	-1.26**	0.70ns

*, **Significant at 0.05 and 0.01 probability levels, respectively.ns= non significant.α :Alpha, β:Beta.

4.4.3 Combined High Parents Heterosis for Agronomic Traits

The combined analysis revealed that the magnitudes of heterotic responses were high for all traits' studied (Table 4.27).

Thirteen hybrids indicated highly significant negative best parent heterosis for heading dates with the values ranging from -28.63 to -1.22 percent. The hybrid ICSA11x CF35.5 indicated the highest best parent heterosis value of 13.92%. ICSA11 X CHOKWE was the earliest among them with a highly significant negative value of-1.22%.

Plant height estimates of high parent heterosis were moderately high by the entire crosses and positive for most of the hybrids. The estimates varied from 4.93 to 51.58 percent. All the estimates were highly significant and positive. The hybrids ICSA38x CF35.5 indicated heterosis value of 51.58%.

For panicle length, all the fifteen hybrids exhibited highly significant negative heterosis, the values ranging from -32.68 to -8.60percent. The highest best parent (-8.60%) heterosis values were recorded by the hybrid ICSA731x CF35.5.

In the case of 1000grain weight, the range of best parent heterosis varied from -22.62 percent for the hybrid ICSA 731X SAMSORG8(KSV14) to 16.13 percent for the hybrid ICSA38 x Chokwe, Five hybrids showed highly significant positive heterosis over the best parent, the rest were negative.

For grain yield, the range of best parent heterosis was -9.18 to 43.99%.Nine out of fifteen hybrids showed highly significant positive best parents heterosis while four hybrids exhibited significant negative heterotic effect over the best parent. The hybrids ICSA38x CHOKWE recorded the highest heterosis value (43.99%).

Table 4.27: High parent Heterosis for five agronomic traits combined over two locations. 2010

GENOTYPES	Heading Date	Plant height(cm)	Panicle length(cm)	**1000** Grain weight **(g)**	Grain yield per hectare(kg)
ICSA731xChokwe	-16.38**	26.67**	-17.93**	4.86**	20.00**
ICSA 731 X CF35.5	-14.31**	39.37**	-8.60**	-1.84ns	16.50**
ICSA731 X NR71168	-14.31**	28.58**	-20.49**	6.76**	-5.41**
ICSA731 X SPV422	-19.91**	4.93**	-11.56**	-4.70**	-1.8ns
ICSA731 X SAMSORG8	-28.63**	16.83**	-27.22**	-22.62**	-9.18**
ICSA11XChokwe	-1.22ns	19.95**	-14.3**	-11.67**	29.00**
ICSA11 X CF35.5	13.92**	8.44**	-31.42**	-11.67**	25.24**
ICSA11 X NR71168	-27.91**	36.37**	-25.56**	1.57ns	-8.65**
ICSA 11 X SPV422	-12.72**	11.22**	-32.68**	2.46**	2.71ns
ICSA11X SAMSORG8	-4.96**	12.89**	-28.48**	-18.67**	8.33**
ICSA38 X Chokwe	-10.98**	18.53**	-12.24**	16.13**	43.99**
ICSA38 X CF35.5	-2.93**	51.58**	-16.91**	-22.14**	35.94**
ICSA38 X NR71168	0.98ns	28.13**	-10.03**	9.67**	20.69**
ICSA38 X SPV422	-2.49**	16.04**	-19.67**	-6.67**	3.59*
ICSA38 XSAMSORG8	-15.37**	27.30**	-13.03**	2.19ns	-4.16**

*, **Significant at0.05 and 0.01 probability levels, respectively..ns= non significant.

4.4.4 Conbined Malting /Proximates Quality Traits

The combined analysis revealed that the magnitudes of heterotic responses were high for all traits studied. Table 4.28. For α-amylase, the range of high parent heterosis varied from-10.24 to 4.89%. Eight hybrids exhibited highly significant positive heterosis with the hybrid ICSA38×NR71168 showing the highest heterosis value of 4.85 followed by ICSA38×Chokwe (4.57%).

In the case of β-amylase, eleven hybrids showed significant high parent heterosis ranging from -2.06 to 6.38%. Out of these, nine hybrids showed significant positive high parent heterosis while only two indicated significant negative heterosis. The highest heterosis estimates was by the hybrid ICSA11×CF35.5 (6.38%) and lowest negative byICSA38 X CHOKWE, (-2.06%)

Germination capacity estimates of high parent heterosis values ranged from -2.96 to 1.69%. Only two hybrids exhibited highly significant positive heterosis with ICSA11×CF35.5 indicating the highest value of 1.69%.while six hybrids indicated highly significant negative values with ICSA731×NR71168 having the lowest value of-2.96%. For malting loss, thirteen hybrids recorded significant heterosis ranging from -6.77 to 15.15%. Seven hybrids indicated highly significant negative high parent heterosis while six hybrids showed highly significant positive high parent heterosis. The lowest negative heterosis values was by ICSA731X SPV422 (-6.77%)

In the case of starch, heterosis estimates ranged from -3.66 to 0.79%.Thirteen hybrids exhibited significant heterosis, out of which nine indicated highly significant positive heterosis.ICSA731 X CHOKWE exhibited the highest value of 0.79%.

For protein, eight hybrids indicated positive highly significant heterosis, the over-all heterosis estimates ranged from-5.49 to 6.97%.ICSA731×Chokwe recorded the highest value for high parent heterosis of 6.97% followed by ICSA11×NR71168, (6.24%)

Table 4.28: Combined High parent (HP) Heterosis for six malting/proximate traits over two locations 2010.

Genotypes	α-Amylase µg /100	β – Amylase µg /100	% Germination capacity	% Malting loss	% Starch	% Proteins
ICSA11XNR71168	-5.13ns	4.95**	1.63**	-2.36**	0.29**	6.24**
ICSA11XCHOKWE	-3.28 ns	0.87 ns	0.05 ns	2.69**	0.65**	-3.46 ns
ICSA11XSPV422	1.93**	2.06*	-0.74 ns	4.7**	-0.41**	-3.44 ns
ICSA11XCF35-5	1.5**	6.38**	1.69**	4.31**	0.29**	4.91**
ICSA11X SAMSORG8	0.13**	3.23**	0.16 ns	7.75**	-0.16**	1.36ns
ICSA38 X NR71168	4.89**	3.15**	-1.45**	-0.25ns	-3.66ns	-3.66 ns
ICSA38XCHOKWE	4.57**	-2.06**	-0.98 ns	-4.33**	0.67**	-0.11ns
ICSA38XSPV422	3.09**	2.49**	-0.59 ns	-3.46**	0.3**	3.37**
ICSA38XCF35-5	-4.7 ns	4.82**	-0.48**	-4.1**	0.66**	2.86**
ICSA38X SAMSORG8	-2.05 ns	2.56**	-0.69**	-5.1**	-0.33*	-2.82ns
ICSA731XNR71168	4.14**	0.56 ns	-2.96**	9.16**	-0.69ns	4.94**
ICSA731XCHOKWE	-10.24 ns	0.49 ns	-0.62 ns	15.15**	0.79**	6.97**
ICSA731XSPV422	0.22**	-0.93**	-1.17 ns	-6.77**	-0.11**	-5.49ns
ICSA731XCF35-5	-10.22ns	3.78**	-0.17**	-1.37**	0.12**	3.46**
ICSA731XSAMSORG8	-1.5 ns	-0.11 ns	-0.67**	-0.66 ns	0.42**	2.36**

*, **Significantat 0.05 and 0.01 probability levels, respectively.ns = non significant.α :Alpha, β:Beta.

4.5 FERTILITY RESTORATION

The availability of restorers is a prerequisite for exploitation of the cytoplasmic male sterility (CMS) or the successful production of hybrid seeds. At maturity, seeds set under the selfing bags were counted; there was a high percentage (more than 80%) of seeds produced on each inflorescence. Pollen fertility restoration ability of all the pollinators proved to be effective restorers of the A1 system of cytoplasmic male sterility used in the study.

4.6 ANALYSIS OF GENOTYPIC AND PHENOTYPIC CORRELATION FOR MALTING QUALITY AND AGRONOMIC TRAITS.

The result of genotypic correlation amongst some agronomic, malting and proximate traits in some Sorghum genotypes and hybrids evaluated at Samaru and Kadawa is presented in Table 4.29. Highly negative significant genotypic correlation was shown between yields per hectare with Alpha Amylase (r = -0.79, $P< 0.01$) and positively correlated with plant height (r = 0.56, $P< 0.01$). There was also highly significant correlation between plant height with heading date (r = 0.93, $P< 0.01$), heading date was also positively correlated with malting quality trait Beta Amylase (r = 0.78, $P < 0.01$) .Significant correlations were recorded between yields per hectare with heading date, protein,1000grain weight, Malting Loss, Beta Amylase and starch at ($P <0.05$). Heading date was significantly and positively correlated with Germination Capacity and Beta Amylase at ($P< 0.05$).

The result of phenotypic correlation amongst some agronomic, malting and proximate traits evaluated across the two locations is presented in Table 4.29. Highly positive significant phenotypic correlation was shown between Beta Amylase and starch at (r = 0.569, $P< 0.01$) and Alpha Amylase was negatively correlated with starch at (r = -0.436, $P< 0.05$), respectively.

Table 4.29: Genotypic and Phenotypic correlation amongst agronomic, malting traits in some Sorghum crosses across two location. (Samaru and Kadawa in 2010)

		YLD/H	HD	PHT	PROT	GWT	GC	ML	APHA	BETA	STCH
YLD/H	G										
	P										
	G	0.46*									
HD	P	-0.0013									
PHT	G	0.56**	0.93**								
	P	0.073	0.0029								
PROT	G	0.47*	0.091	0.26							
	P	-0.85	0.0008	0.051							
GWT	G	0.46*	0.001	0.01	0.024						
	P	0.03	0.079	0.016	0.140						
GC	G	0.46*	0.40*	0.01	0.0008	-0.07					
	P	-0.24	-0.017	0.075	0.0034	0.0169					
ML	G	0.47*	0.40*	0.08	0.0008	0.006	-0.0012				
	P	-0.0086	0.071	0.034	0.159	0.423	-0.0048				
	G	-0.79**	0.0002	0.21	0.014	0.073	-0.0047	0.0025			
APHA	P	-0.0023	0.117	0.001	-0.103	-0.103	-0.009	0.0058			
BETA	G	0.48*	0.78**	0.02	0.005	0.002	-0.0034	0.038	0.0029		
	P	0.0011	0.0012	0.193	0.103	0.569**	-0.095	0.282	0.263		
	G	0.48*	0.0002	0.077	0.039	0.0057	0.0077	0.0008	0.26	0.059	
STCH	P	-0.0011	0.0024	0.014	0.0104	0.119	0.012	0.0512	-0.436*	0.0159	

*, ** Significant at 0.05 and 0.01 probability levels. YLD/H= Yield per hectare,HD=Heading date, PHT=Plant height,PROT= Protein, GWT= Grainweight, GC = Germination Capacity, ML= Malting Loss, α= Alpha Amylase, β=Beta Amylase, STCH= Starch.

CHAPTER 5

5.0 DISCUSSION

Combining ability studies aim at identifying parents which are good combiners and cross combination showing high specific combining ability effects. The information derived from such studies in turn helps in selecting the parents to be included in hybridization or cultivar improvement programs.

In this study, the significant differences observed for all the malting and agronomic characters among the entries indicated that the parent studied could be selected for genetic improvement. Significant mean squares were observed among the hybrids for the different malting and agronomic character that could be used in selection for genetic improvement of grain yield and malting quality traits.

The mean squares of location x entry source of variation were significant for all the malting and agronomic characters. This showed that, the entries performed differently in different location indicating that suitable hybrids can be developed for specific locations.

The combined analyses of variances over the two locations further confirmed the diversity of the genotypes and their differences in location responses.

The mean performances of the hybrids for agronomic and malting quality traits in Samaru, Kadawa and across locations shows similar trend. Generally, grain yield varied appreciably among crosses in each environment. However, some high yielding hybrids like ICSA38 X CHOKWE, ICSA38 XCF35.5 and ICSA38 X NR 71168 were consistent in their performance despite the varying locations.ICSA11 X CF35.5, ICSA11 X NR71168, ICSA11 X SAMSORG 8 and ICSA11 X SPV422 were consistent for β-amylase across location. The parents and the checks gave a considerable yield and β-

amylase in Samaru and Kadawa. Although the differences were not significant, generally across the location, parents which gave high yields were not always high performing in their crosses. This result is in agreement with Niehaus and Pickett (1966) who reported from a study of heterosis and combining ability in sorghum that parent performance was not always a good indicator of hybrid performance.

A non-significant GCA value indicates that a particular inbred is average in its combining ability, while a significant GCA value indicates that an inbred is relatively better than the remaining line with which it is compared. Significant GCA value also provides an indication of the importance of genes involved in cross combination. A non-significant SCA indicates that the hybrids involved in a particular combination have performed fairly well on the basis of their general combining ability, while a significant SCA indicates that some combinations perform relatively better than others. SCA is largely dependent on dominant gene effect and epistasis while GCA provides an indication of the importance of genes which are largely additive in their effects. In this study, the estimates of general combining ability (GCA) effects of parents revealed considerable differences among the parents.

The variance components estimates of SCA were greater than that of GCA for all agronomic and malting quality traits except β-amylase. It implies that non-additive gene action was of major importance in the inheritance of most of the traits measured.

The proportional contribution to total variance for line × Tester was greater than that of the lines and the testers for all agronomic and malting quality traits except heading date, panicle length and β-amylase where line and tester was greater; indicating the presence of wide variability among the crosses for these traits. The ratio of the variance component showed that the ratio of GCA to SCA was less than unity for the entire trait except β-

amylase which was 3 for Samaru and 2.8 for Kadawa but less than unity across location revealing the preponderance of non-additive gene action over bothlocations.

This result tends to suggest that specific combining ability was the predominant factor in explaining variation among crosses in this study.

These results are in agreement with Mahdy *et al* (2011), and Mohammed (2009). The magnitude of GCA/SCA variance ratio for β-amylase was specifically sizable, indicating the predominance of additive gene action. Several workers have indicated that additive and non additive components of genetic variance were important for agronomic and malting quality traits studied. (Can *et al.,* 1997; Amir, 1999;Birader; *et al.*,2000; Mostafa and El-meshawi2001,Kenga *et al.,*2004;Hovny *et al*.,2005; Mohamed, 2007; Mohmoud, 2007; Abd-El-Mottalab, 2009).

Several lines have been identified as good general combiners in this study. Among the Lines, ICSA731 showed good general combining ability for grain yield, negative effect for plant height which is desirable, good combiner for α-amylase and protein. On the basis of its desirable GCA effects, this may be used to produce dwarf statured high yielding hybrid with high α-amylase content. The line ICSA11 was a good combiner for early flowering, positive GCA value for germination capacity, β-amylase however, it showed negative GCA effect for grain yield per hectare and malting loss. It may be used for producing early maturing hybrids with good malting quality traits. The ICSA38 on the other hand was a good combiner for 1000grain weight, panicle length, and starch. ICSA38 is a good general combiner for long panicle.

A parent line showing high GCA effect for grain yield and its components with low GCA effects for plant height and heading date will offer greater scope in developing short to medium height and early maturing hybrids. On the other hand a parent line showing high

GCA effect for grain yield and its components with positive GCA for germination capacity proteins α and β-amylase will offer greater scope in developing hybrids with good malting quality which is on high demand in the brewery industries.

Among the Testers, NR71168 and CF35.5 were the best general combiners for earliness and β-amylase, while SPV422 was a good general combiner for grain yield and short statured hybrid. In terms of malting quality, SPV422 showed positive germination capacity and negative value for malting loss. It will offer a greater scope in developing hybrids with good malting quality. SAMSORG 8(KSV14) on the other hand was a good general combiner for long panicle length, 1000 grain weight, germination capacity, malting loss, α-amylase, starch and protein. Apparently, from the point of view of developing early maturing, medium hybrid with a high potential for grain yield and malting quality traits, these parent lines would be the most desirable.

The parent ICSA731, ICSA11, ICSA38, SPV422, SAMSORG 8 (KSV14), and CF35.5 though produced high grain yield and high α and β-amylase, they also exhibited negative GCA effects. A comparison of GCA effects for individual line for grain yield, α and β-amylase showed that much of the positive GCA obtained was contributed by the lines:- ICSA731 ICSA38, SPV422, CF35.5, NR71168, SAMSORG8(KSV14)and Chokwe suggesting that these lines might be quite useful in a hybrid programme.

The crosses which recorded high SCA effects, coupled with high per se performance for agronomic and malting quality traits involved either one or both of the parents with a good GCA for the trait being considered. The significant and desirable SCA effects of the crosses:-ICSA731x Chokwe, ICS731× NR71168, ICSA731× KSV14, ICSA11 × Chokwe, ICSA11 × CF35.5, ICSA11 × NR71168, ICSA38 × CF35.5, ICSA38 ×

Chokwe, ICSA38 × NR71168, ICSA38 × SPV422; reflected on the good combining ability of the parent involved in these crosses.

ICSA11×NR71168 turned out to be the best specific combiner for earliness, long panicle, 1000 grain weight, high germination capacity, high starch content and beta-amylase. ICSA731 × Chokwe and ICSA38×NR71168 are good specific combiners for beta-amylase. ICSA731×CF35.5 is a good specific combiner for less malting loss. ICSA38 X Chokwe is a good specific combiner for α-amylase and grain yield. ICSA11×Chokwe is a good specific combiner for long panicle length and grain yield. ICSA38×SPV422 is a good specific combiner for protein. ICSA11×CF35.5 turned out to be the best specific combiner for short stature and grain yield. ICSA11×SPV422 is a good specific combiner for grain weight. These hybrids are very promising and are worthy to be use in further sorghum breeding improvements for high yield and high malting/proximate quality.

Thus, for hybridization programme, the parents showing GCA effects in desired direction could be used as parent materials.

These results are in agreement with those obtained by Ali(2000), Birader *et al*(2000) Kenga*et al.(*2004), Hovny *et al*, (2005), Mahmoud(2007), Hovny and El-Dsouky(2007), Abd-El-Mottaleb(2009) and Essa (2000). Rojas and Sprague (1952) reported that the variance for specific combining effects became relatively more important than the variance for general combining ability effects when the lines under test had been subjected to previous testing and selection. The male lines used in the present study, represent a wide range of different sorghum genotype available in the sub-region. Therefore, it would be expected that the estimates of variance of specific combining ability will be high in the crosses evaluated. In addition, the female lines are often being

utilized in various hybrid development programs. Therefore, a high level of male × female interaction was expected.

Significant GCA effects were observed for grain yield, plant height, panicle length, heading date, α and β-amylase and malting loss in most of the parental lines, suggesting that additive gene effects also contributed to the variation expressed for these traits.

Therefore, in hybrid breeding procedures testing of parent lines for GCA should be supplemented by the evaluation of individual F_1 hybrids for specific combining ability and heterotic responses. As such, in certain population, biparental mating as well as mating of selected plants in early segregating generations could help in developing potential populations. Further exploitation of such population would lead to the development of high yielding line which may be use in hybrid breeding programs.

Heterosis designates the increased growth or other augmented action resulting from crossing; (Wengui, 2003). The essence of the superiority of the hybrid over the better parent and the local check can be profitably exploited for commercial production.

Heterosis has been defined as the increased vigor of a hybrid over the mean of its parents or over the high parent. From a practical stand point of view, increase over the high parent is more important, because it implies the improvement of desirable traits over its existing maximal.

Both positive and negative heterotic values were recorded for all malting and agronomic characters studied. However, the negative heterosis observed for heading date, plant height and malting loss are desirable in breeding for earliness, short statured hybrid that could resist lodging and high malting quality hybrid. The negative heterosis recorded for characters like panicle length, grain weight, grain yield, α-amylase, β-amylase,

germination capacity, starch and protein could be due to linkage, inadequate statistical and genetic models, inadequate experimental procedure and the influence of location on the genotypes. Similarly it could be attributable to similar genetic base of the materials used in the development of the parents. ICSA11XNR71168 exhibited the highest negative heterosis for earliness whereas; ICSA38X CHOKWE exhibited the highest positive heterosis for grain yield while ICSA11XCF35.5 expresses the highest positive heterosis for β-amylase. The significant mean squares of line x tester and significant heterosis observed showed that testing parental lines for GCA should be supplemented by the evaluation of individual hybrids for specific combining ability and heterosis response. These results are in harmony with those obtained by Ali (2000), Thawari *et al*, (2000), Prabhakar (2001), Kenga *et al.* (2004). Hovny *et al*. (2005), Abo-Zaid (2007), Hovny and El-Dsouky (2007), Abd-El-Mottaleb (2009), Essa (2009) and Mahdy *et al.* (2010).

The pollen fertility restoration ability of the pollinators was highly uniform in the study. All the pollinators were effective restorers of the A1 cytoplasmic – nuclear male – sterility. This was not unexpected since the previous search for restorer in most Sorghum breeding programmes had been primarily restricted to A1 cytoplasmic – nuclear male sterility. It is currently the only system used commercially to produce sorghum hybrids seeds worldwide. Similar observation was reported by Kenga, (2001).

Knowledge of correlation between traits of economic importance are not only of interest from theoretical consideration of quantitative inheritance of characters, but of practical value since selection is usually concerned with changing two or more traits simultaneously. The magnitudes of genetic correlation coefficients were higher than those of phenotypic correlation coefficients.

Genetic correlation coefficients provide a measure of genetic association between characters and this helps to identify the more important characters to be considered in breeding programmes. Johnson *et al* (1955) explained that where the genetic correlation coefficients are high, there is a strong heritability between characters. This means that selection for these characters can be carried out irrespective of the locations. Correlation coefficients ranged from low to high values. The low values of correlation coefficient obtained may slow down the progress for selection. The high negative values of correlation coefficients were obtained for some characters. This showed that selection for some of these characters would affect each other in the opposite direction. Yeye (2000) reported higher genotypic correlation of characters than phenotypic correlation among millet populations. Similarly, Diz and Shark (1995) obtained genotypic and phenotypic correlation coefficient, which in some case differ in magnitude and sign and in another case, did not differ and had the same sign.

Heading date was positively and significantly correlated with many of the agronomic and malting characters. Theoretically, it means that heading date could be used as a selection index to improve the agronomic and malting quality traits. Most of the yield components were positively and significantly correlated among themselves. Grain yield shows positive and significant correlation with heading date, plant height and1000grain weight and grain weight per plant at genotypic level. This implies that selecting individuals with bold seeds and heavy panicles can affect improvement of grain yield. **The magnitude of the direct effect of correlation, which was similar to the magnitude of correlation between grain weight per plant and grain yield per hectare indicates that correlations explains the true relationships and selection for high grain weight per plant will mean indirectly selecting for high grain yield.** A high positive correlation at genotypic levels between heading date and germination capacity implies that as the plants

gets matured, germination energy increases. This result confirmed the findings of Yeye and Usman (2008) in the study of genetic variability for agronomic and malting quality of sorghum.It was observed from this study that plant height, heading date, protein,and 1000grain weight, malting loss, β-amylase and starch all exhibited positive genetic correlations with grain yield. This showed that selection for any of these characters would lead to selection for grain yield and could also be use to improve the malting characteristics of sorghum grains.

On the basis of the hybrid performance in agronomic and malting quality traits, the following hybrids stand out for food due to their high grain yield: ICSA38 × Chokwe (3199.8kg/ha),ICSA38× CF35.5(3111.3kg/ha), ICSA38×NR71168(3111.2kg/ha). They were significantly superior to the best check (ICSA38×NR71176 (3022kg/ha).

For the industries, the hybrids that had higher α-amylase than the best checks are: ICSA731×NR71168(23.4µg/100),ICSA731×SPV422(22.52µg/100),ICSA731×KSV14(22.14µg/100),ICSA11×CF35.5(22.3µg/100),ICSA38×Chokwe(22.35µg/100),ICSA38×SPV422(21.13µg/100),ICSA11×SPV422(21.65µg/100)and.ICSA38×NR71168(21.45µg/100).

In the case of β-amylase, the following hybrids were superior the best existing malting sorghum (ICSV400 and SK5912). The hybrids are: ICSA11×KSV14(24.19 µg/100), ICSA11×NR71168(24.6 µg/100),ICSA11 X CF35-5(24.93 µg/100),ICSA11 X SPV422(23.92 µg/100), ICSA38×SPV422(23.85 µg/100), ICSA38×KSV14(23.13 µg/100), ICSA38×CF35.5(23.65 µg/100), ICSA38×Chokwe(23.19 µg/100), ICSA11×Chokwe(23.88 µg/100), ICSA731×NR71168(23.13 µg/100), ICSA731×CF35.5(23.87 µg/100) and ICSA731×Chokwe(23.79 µg/100).

For starch,ICSA11X NR71168(67.85%) and protein ICSA11 X CF35.5(3.43%)

CHAPTER 6

6.0 SUMMARY,CONCLUSION AND RECOMMENDATIONS

6.1 SUMMARY

This study was carried out to examine the application of heterosis and combining ability for agronomicand malting quality traits in sorghum (*Sorghum bicolor* (L) Meonch), to evaluate a comparative expression to heterosis among the F1 hybrids generated and to determine the food (proximate) and malting quality trait of the hybrids.

Line X tester procedure described by Singh and Chaudhary (1985) was used to intermate three A – lines and five restorer lines to generate fifteen hybrids. Twenty – seven entries consisting of fifteen hybrids, eight parental lines and four checks were arranged as a factorial arrangement in a Randomized Complete Block Design (RCBD) with three replications and were evaluated in two locations in 2010: Samaru and Kadawa. The male parents used in the production of the hybrids represented different groups of sorghum cultivated in the West and central Africa. The females involved are Kafir – milo derivative and have the same cytosterile mechanism. Data were taken on both agronomic and malting quality traits and subjected to analysis of variance.

Significant mean squares were observed among entries and hybrids for all the agronomic and malting/proximate characters. This was an indication of the presence of considerable amount of genetic diversity in the materials, which could be used to enhance selection for further population improvement.

Mean performance differed significantly in the two locations of evaluation for some traits, while for some other mean performances were not significantly different from each other. Each trait exhibited a considerable range for its expression.

For each cross, analysis of variances were made for combining ability for agronomic traits: heading date, plant height, panicle length, 1000 grain weight, and grain yield also for malting quality trait:- germination capacity, malting loss, alpha – amylase, B – amylase, starch and protein. Estimate of general and specific combining ability were obtained for each male inbred, female parents and for all hybrids at individual and across the two locations.

From the combining analysis across location, general combining ability estimate were high for both agronomic and malting quality traits. The testers CF35.5, SPV 422, NR71168, Samsorg8 (KSV14) contributed high GCA estimate for grain yield, protein, alpha and beta- amylase .The GCA estimates for the female parents was greater than those of the male parents. It was observed that the parents that showed high GCA effects for grain yield, also showed high to average GCA for each yield components, suggesting that GCA effects for grain yield are possibly related to combining ability affects of yield and malting contributing traits.

The effects of specific combining ability were more important in most of the traits. The majority of the cross combinations involved either good x good(ICSA38 X NR71168) or good x poor combiners(ICSA11 X SAMSORG 8). It was not always the case that the parents who were the best general combiners produced the best hybrid combinations for agronomic of malting traits. This difficulty in predicting the malting and productivity level of the hybrid should necessitate testing of specific male x female combinations.

The variance components estimates of the testers (male parents) were higher than those of the lines (female parents). The SCA variances were greater than those of the GCA. The proportional contribution to total variance for line x tester was greater than that of the line and the tester. The proportion of GCA to SCA was less than unity for most of the traits

studied, emphasizing the importance of non – addictive gene effects. However, significant GCA effects were also obtained for β – amylase; suggesting that addictive gene effects also contributed to the variances expressed for these traits. That is to say that both addictive and non – addictive gene actions were operatives in the expression of these traits.

In the present study, high yields and malting quality obtained from ICSA38 X CHOKWE,ICSA38XNR71168,ICSA38XCF35.5,ICSA731X NR71168,ICSA731XSPV422,ICSA11 X SPV422 andICSA11 X CF35.5 indicated that there is ample potential to improve the current yield and malting quality of grain sorghum in Nigeria. Striking level of heterosis was observed for all the agronomic and malting quality traits.

The parent vs hybrid mean squares were significant for most of the traits, indicating the presence of high level of heterosis and that non additive gene effects were also important for these traits.. That is high × high crosses sometimes gave the lowest yield and low × low or high × low gave the highest yield. The relative magnitude of heterosis values varied from one location to another. The fact that the pattern was inconsistent may be interpreted as supporting evidence that the levels of heterosis observed were influenced by location effect.

Generally, hybrids were taller with high grain yield, alpha-amylase, β-amylase, high germination capacity and high starch content; however, most of these hybrids contain low protein. The genotypic mean squares for combine analysis were highly significant for both agronomic and malting quality traits. The significant mean squares due to line × tester, and significant heterosis estimates suggested that testing of parental lines for GCA should be supplemented by the evaluation of individual hybrid for specific combining

ability and heterosis response. Across the two locations, ICSA11was a good general combiner for germination capacity, malting loss, β-amylase and protein, Lines ICSA731 is a good general combiner for α-amylase while ICSA38 is a good general combiner for starch.

Among the Testers, CF35.5 is a good general combiner for germination capacity, and β-amylase and may be used for producing good malting hybrid. NR71168 is a good general combiner for α-amylase and protein while SPV422 is a best general combiner for α-amylase and low malting loss. This may be use in producing hybrid with good malting quality traits.

The highest grain yielding entries across locations were: ICSA38 × Chokwe (3199.8kg/ha),ICSA38× CF35.5(3111.3kg/ha), ICSA38×NR71168(3111.2kg/ha). They were significantly superior to the best check ICSA38×NR71176 (3022kg/ha). For malting quality traits, the hybrids that had higher α-amylase than the best checks are: ICSA731×NR71168(23.4µg/100),ICSA731×SPV422(22.52µg/100),ICSA731×KSV14(22.14µg/100),ICSA11×CF35.5(22.3µg/100),ICSA38×Chokwe(22.35µg/100),ICSA38×SPV422(21.13µg/100),ICSA11×SPV422(21.65µg/100) and ICSA38×NR71168(21.45µg/100).

In the case of β-amylase, the following hybrids were superior the best existing malting sorghum (ICSV400 and SK5912). The hybrids are: ICSA11×KSV14(24.19 µg/100), ICSA11×NR71168(24.6 µg/100),ICSA11 X CF35-5(24.93 µg/100),ICSA11 X SPV422(23.92 µg/100), ICSA38×SPV422(23.85 µg/100), ICSA38×KSV14(23.13 µg/100), ICSA38×CF35.5(23.65 µg/100), ICSA38×Chokwe(23.19 µg/100), ICSA11×Chokwe(23.88 µg/100), ICSA731×NR71168(23.13 µg/100), ICSA731×CF35.5(23.87 µg/100) and ICSA731×Chokwe(23.79 µg/100).

For starch,ICSA11X NR71168(67.85%) and protein ICSA11 X CF35.5(3.43%)

6.2 CONCLUSION

It is interesting to note that the majority of hybrids shown by this study as being the best to display heterosis and SCA effects for some traits, were also among the best performing for the same trait; hence, utilizing heterosis in improving such traits might be rewarding. Furthermore, although malting quality traits and yield are usually reported to be adversely associated (Sanderson *et al.* 1993; Moyer *et al*. 2003), some hybrids in this study depicted a good compromise between yield and some malting quality traits pointing to the possibility of developing hybrids with better yield and malting quality.

Evaluation of fertility restoration indicated that the pollen fertility restoration ability of all the pollinators was highly uniform. All pollinators proved to be effective restorers of A1 system cytoplasmic male sterility. This presents the possibility of producing hybrids with most of the inbred lines selected in the region.

There is potential of increased sorghum yields through the use of hybrids. Hybrids high in α and β-amylase percentages appeared to be attainable without sacrificing high yield level.

Male sterility of female parent is an important biological mechanism for the commercial production of hybrid seed. This should be exploited to produce hybrid sorghum seed for commercial production in Nigeria.

From this study, it was observed across locations that most of the malting attributing factors (malting loss, Beta-amylase, germination capacity and starch) were positively correlated with grain yield. Consequently, selection for any of these characters could lead to indirect selection for grain yield. Simultaneous selection for these characters can be made for the improvement of grain yield and malting quality.

In conclusion, the exploitation of heterosis provides an excellent opportunity to increase and stabilize the performance of sorghum in terms of high yield and quality.

6.3 RECOMMENDATIONS

ICSA731 showed good general combining ability for grain yield, negative effect for plant height, good combiner for α-amylase and protein may be used to produce high yielding, dwarf statured hybrid with high α-amylase content. The line ICSA11 was a good combiner for earliness, positive GCA value for germination capacity, β-amylase and low malting loss may be used for producing early maturing hybrids with good malting quality traits. The ICSA38 on the other hand was a good combiner for 1000grain weight, panicle length, and starch is recommended for use in developing hybrid for the food industry.

The following hybrids due to their high yielding potentials are recommended for use by farmers producing Sorghum for food: ICSA38 X CHOKWE, ICSA38 X CF35.5 and ICSA38 X NR71168.

For the industries (brewery), the following hybrids are recommended base on their high malting quality traits:ICSA11×KSV14, ICSA11×NR71168, ICSA11 X CF35-5,ICSA11 X SPV422, ICSA11×Chokwe ICSA38×SPV422, ICSA38×KSV14, ICSA38×CF35.5, 1CSA38×Chokwe, ICSA38 X NR71168 , ICSA731×NR71168, ICSA731×CF35.5, ICSA731×Chokwe,ICSA731 X SAMSORG 8, and ICSA731 X SPV422.

For both food and industries, the following hybrids are recommended:ICSA38X CHOKWE, ICSA38 X NR71168, ICSA731 X CHOKWE, ICSA731 XCF35.5, ICSA731 XSAMSORG 8, ICSA38 X SAMSORG8, ICSA11 X SAMSORG8, ICSA11XCF35.5andICSA11XNR71168, due to their high grain yield, high α-amylase, β-amylase, germination capacity and low malting loss.

More emphasis is needed on maintaining the malting potential of current hybrids. This can be achieved through the incorporation of resistance to biotic factors and quick growth to meet the multiple demands of sorghum.

The identification and development of male-sterile lines and restorers suitable for malting sorghum hybrid productions are also important.

Malting sorghum improvement programmes are beset with lack of information on variability and useful genetic stocks for various traits. Therefore, concerted and planned efforts are needed to collect, evaluate, catalogue, and maintain germplasm exclusively for malting sorghum. This is possible through the use of biotechnology techniques.

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