GENETIC ANALYSIS OF PROGENIES FROM DIALLEL CROSSES AMONG EIGHT VARIETIES OF DIFFERENT MATURITY GROUPS OF MAIZE (*Zea mays* L.)

BY

IBRAHIM, AMINU KURAWA

MSc/AGRIC/O6399/2008-2009

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AHMADU BELLO UNIVERSITY, ZARIA

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A THESIS SUBMITTED TO THE SCHOOL OF POSTGRADUATE STUDIES, AHMADU BELLO UNIVERSITY, ZARIA, NIGERIA

IN PARTIAL FULFILMENT FOR THE AWARD OF MASTER OF SCIENCE IN PLANT BREEDING

DEPARTMENT OF PLANT SCIENCE

FACULTY OF AGRICULTURE

AHMADU BELLO UNIVERSITY, ZARIA

MARCH, 2012

DECLARATION

I hereby declare that this thesis entitled "Genetic analysis of progenies from diallel crosses among eight varieties of different maturity groups of maize (*Zea mays* L.)" was written by me and is a documentation of my research findings. The information derived from literature has been duly acknowledged in the text and a list of references provided. No part of this thesis has previously been submitted for a degree or any other qualification. References made to published and unpublished literature have been duly acknowledged.

…….. **……..**

IBRAHIM, AMINU KURAWA **Date**

CERTIFICATION

This thesis titled "GENETIC ANALYSIS OF PROGENIES FROM DIALLEL CROSSES AMONG EIGHT VARIETIES OF DIFFERENT MATURITY GROUPS OF MAIZE (*Zea mays* L.)" by Ibrahim, Aminu Kurawa meets the regulations governing the award of the degree of Master of Science of Ahmadu Bello University, Zaria and is approved for its contribution to knowledge and literary presentation.

Prof. S. G. Ado ...…….…….. …….

Chairman, Supervisory Committee (Signature) (Date)

Prof. D. A. Aba ……. …….

Member, Supervisory Committee (Signature) (Date)

Dr. M. D. Katung ……. …….

Member, Supervisory Committee (Signature) (Date)

Dr. I. S. Usman …… ……..

Head, Department of Plant Science (Signature) (Date)

Prof. A. A. Joshua …….. ……...

Dean, School of Postgraduate Studies (Signature) (Date)

DEDICATION

This work is dedicated to Alliance for a Green Revolution in Africa (AGRA) who sponsored the training, to my parents (Malam Ibrahim Muhammad Kurawa and Malama Khadija Ibrahim Kurawa) and to Dr. Sanusi Gaya Muhammad of Bayero University, Kano.

ACKNOWLEDGEMENTS

All thanks be to the Creator of the universe, and peace and blessings of Allah be on to the first of all creations, his household, companions as well as all his followers till the day of judgement. My sincere appreciation goes to my supervisory team Prof. S.G. Ado, Prof. D.A. Aba and Dr. M.D. Katung for their support, guidance, motivation and priceless counsel throughout the preparation, planning and execution of this work. I do not have wards to express my happiness, thanks and appreciation for what Prof S.G. Ado did to me and only *Allah* can reward him. May HE (*Allah)* reward him with *jannatulfirdausi*, ameen. I wish to deeply express my appreciation to AGRA, my sponsor, and particularly to Dr.Ruparo M. Madakadze and Dr. M.F. Ishiyaku for their moral support both academically and financially till the end of the programme. I will not forget to acknowledge the precursor to be part of this programme, Dr. S.G.Muhammad of Bayero University Kano who used to guide and assist me whenever I met him no matter the condition, as well as Jamilu Mudi Guda who informed me about it. May Allah reward them and take good care of them and their families, a*meen*. I would like to acknowledge the Head of Department, Dr. I.S. Usman and the entire lecturers of Plant Science Department especially Prof. C.A. Echekwu, Prof. M.Y.Yeye, Dr. U.S. Abdullahi, and Mr. Alhasan Usman as well as the non academic staff especially Muhammad Ahmad (Bello Library), Mallam Bello Bala (*Maiunguwa*), Hussaini Musa and those who assisted me during the field work particularly Mallam Muhammad Bashir (Maize unit), Mallam Garba (IAR Samaru, irrigation site), Abdullahi Sani (Farm Manager, Kadawa) and Danlami Lawan. My appreciation also goes to my parents (Mallam Ibrahim Muhammad Kurawa and Malama Khadija Ibrahim Kurawa) as well as to my sisters and brothers

especially Dr. Musa Ibrahim Kurawa, Mujtapha Ibrahim Kurawa, Abubakar Ibrahim Kurawa, Nura Ibrahim Kurawa, Eng. Adamu Ibrahim Kurawa, Arch. Salisu Ibrahim Kurawa, Usman Ibrahim Kurawa, Aliyu Aminu Ringim, Halima Ibrahim Kurawa, Zainab Ibrahim Kurawa, Aisha Ibrahim Kurawa, Amina Ibrahim Kurawa, Umar Lawan Abdullahi, Rufa'i Umar Mohd, Kabiru Dawaki Dauda and my wife to be *Insha'Allah* Halima Dawaki Dauda for their support, guidance, encouragement, advice and prayers. May Allah reward them with *Jannatulfirdausi, ameen*. I deeply appreciate the contributions and encouragement of Mallam Abdulmumini of Sa'adatu Rimi College of Education Kano (Deputy Registrar Establishment) and my colleagues (Aminou, Habibou, Mustapha, Abubakar, Richard, Evilla, Debora, Hajara and Balkissa). Mohd Nura Ashiru, Tijjani Saidu and Salisu Abdullahi Ibrahim would also not be forgotten. Once again all thanks are due to Almighty Allah who destined me to be part of this programme and granted me the opportunity to complete it. May He bless the knowledge acquired and continue to be my guide, *ameen*.

ABSTRACT

A full-diallel cross comprising eight varieties belonging to four different maturity groups was developed and studied for fifteen characters to determine general and specific combining ability (GCA,SCA), nature of gene action of parents and hybrids, and heterosis. Eighty one genotypes comprising the crosses, reciprocals, selfs, parents and nine checks were evaluated at Kadawa under irrigation in two different environments (sowing dates). Analysis of variance revealed significant differences for GCA and SCA, indicating presence of additive as well as non-additive gene action. In both environments, the GCA mean squares were highly significant and higher than the SCA mean squares for all traits except cob diameter at environment one, and four traits at environment two. The study revealed significant GCA x environment interaction indicating different parental varieties behaved differently under different environments, hence there is need to select different parental varieties for hybrid production for a specific environment. Significant SCA x environment interaction indicate hybrid performance varies with respect to environments. For that reason, specific hybrids could be produced for specific environments. Sammaz 17 was the best general combiner for both earliness and high yield in environment one while Sammaz 27 was the best general combiner for high yield, earliness and other traits in environment two and across the environments. The crosses which showed significant SCA effect for yield were Sammaz 17 x Sammaz 36 and Sammaz 17 x Sammaz 29. They were from high x low general combiners (Sammaz 17 (high) and Sammaz 36 and Sammaz 29 (low)). These varieties could be exploited for inbred line development to produce commercial hybrids. For earliness and grain yield, Sammaz 19 x Sammaz 27 and Sammaz 36 x Sammaz 29 were the best, they were from low x high and high x high general combiners, respectively. Heterotic patterns observed revealed that at environment one, eighteen hybrids out of twenty eight had positive heterosis for grain yield which ranged from 1.6% to 927.0%. The hybrid Sammaz 36 x Sammaz 35 exhibited highly significant heterobeltiosis for grain yield. Fifteen hybrids out of twenty eight exhibited positive heterosis for grain yield in environment two which ranged from 17.8% to 397.1%. Sammaz 19 x Sammaz 27 exhibited highly significant positive heterobeltiosis for grain yield. High percent heterosis was observed among crosses involving the parents Sammaz 35, Sammaz 36, and Sammaz 27. The results indicate that inter variety hybrid development programme can be an effective breeding approach to exploit the heterotic potential of these varieties.

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CHAPTER ONE

INTRODUCTION

1.1 INTRODUCTION

Zea is a genus belonging to the grass family, Poaceae in the Andropogoneae tribe but is commonly cited in the literature to belong to the tribe Maydeae (Mangelsdorf, 1974). *Zea* was derived from an old Greek name for a food grass. The genus *Zea* consists of four species of which only *Zea mays spp.* is economically important (Mangelsdorf, 1974). The number of chromosomes in *Zea mays* is 2n = 20, 21, 22, 24 (FAO, 2000a). The centre of origin for *Zea mays spp*. *mays* has been established as Mesoamerican region, now Mexico and Central America (Mangelsdorf, 1974). Archaeological records suggest that domestication of maize began at least 6,000 years ago occurring independently in regions of the South-western United States, Mexico, and Central America (Mangelsdorf, 1974). Under natural conditions, maize reproduces only by seed production. Pollination occurs with the transfer of pollen from the tassel to the silks of the ear. About 95% of the ovules are cross-pollinated and the rest are self pollinated (Poehlman, 1959).

Maize is grown from 58^0N latitude without interruption through the temperate, subtropical and tropical regions of the world to 40^0S latitude (Hallauer and Miranda, 1981), with growing cycle ranging from 3 to 13 months (CIMMYT, 2000). It is the third most important crop in the world (FAO 2000b). Developing countries account for 64% of the world's maize area and 43% of global maize (FAO, 2007). In 2008, the world production was about 1142.3 million tonnes, United States of America was the largest producer with 326.5 million tonnes, and

Nigeria's production figure was 26 million tonnes on 3,845,000 ha of land (FAO 2008).The northern states of Nigeria account for more than half of the total production in the country (Anon., 1987).

A rainfall of 75-150cm per annum is usually considered adequate, but it can also be grown in areas of lower rainfall if farmers practice deep cultivation to conserve the ground water and to prevent too much evaporation. It does well in areas where temperature is between 21^0C and 27^0C but it can tolerate temperatures up to 34^0C. It performs better on fertile, well-drained soil which can be sandy–loam to clay–loam with a pH range of 5-8 (Falusi, 1988).

Maize has become a major food item in Nigeria and it is consumed in many forms. It is consumed as green maize when the ear is boiled or roasted. When dry, the grain may be processed into different forms of products such as pap (*ogi*) and starch, it is also an industrial crop in Nigeria (Fakorede *et al.*, 2008). It is an important food crop in Sub-Saharan Africa, providing 50% of the calories in diets in Southern Africa, 30% in Eastern Africa and 15% in West and Central Africa (Vivek *et al*., 2009). Maize represents a staple food for a significant proportion of the world's population and supplements the diets of millions of many. Overall, 21% of the total world maize production is consumed as food, with consumption and utilization varying greatly around the world (Morris, 1998). Availability of early and extra-early varieties is a strategy for adopting maize to the gradually shortening rainy season so that maize could escape the drought stress that occurs during the grain-filling stage in the late season. The early and

extra-early varieties were specifically developed for cultivation in the northern fringes of the Northern Guinea Savanna (NGS) and the Sudan Savanna (SS) (Fajemisin, 1989; Badu-Apraku and Fakorede, 1999; Onyibe *et al*., 1995). The use of extra-early maize results in production of two or more crops in relays especially where irrigation facilities are available. The extra-early maize is also very useful to "catch-up" with the season in situations where rainfall started late or rainfall distribution is so adverse as to require replanting. The use of extra-early varieties is an effective way of escaping havoc caused by drought (Ado *et al.*, 2007). Despite the importance of maize, for maize production to remain sustainable, research is necessary but the immediate task that faces hybrid production programmes in Research Institutes is where to obtain information on combining ability and heterotic patterns of various germplasm materials.

1.2 JUSTIFICATION

Due to an increasing interest in hybrid maize development in the National Agricultural Research Programmes and private seed companies conducting various researches related to hybrid development, information about heterotic patterns and combining abilities among crosses of progenies from different maturity periods of maize will play an important role. This information is not available from the varieties released in the country. Hallauer and Miranda (1981) reported that diallel mating design provides the basis for generating information regarding heterotic patterns among maize populations. Also identification of cultivars with good combining abilities can be derived from diallel crosses (Hohls *et al.*, 1994). This is why the present study involving eight varieties was carried out to obtain information required for maize cultivar development for the benefit of mankind.

1.3 OBJECTIVES

The major objectives of this work were to:

1. Determine the combining ability and heterotic patterns for grain yield and other agronomic traits among extra-early, early, medium and late maturing maize varieties.
2. Determine genotype by environment interaction effects on the traits considered.

The specific objectives were to:

3. Identify appropriate germplasm for hybrid development and
4. Advice on appropriate breeding procedures for development of new cultivars.

CHAPTER TWO

LITERATURE REVIEW

2.1 DIALLEL MATING DESIGN

As the name implies, crosses are made in pairs for n number of parents (Hallauer and Miranda, 1981). Diallel crossing schemes and analyses have been developed for parents that range from inbred lines to broad genetic based varieties. After the crosses are made, evaluated, and analyzed, inferences regarding the types of gene action can be made. If one has a complete diallel, it will include all possible crosses and parents, it is obvious as the number of parents increases, the number of possible crosses increases also. It is therefore apparent that the number of parents one can include to produce the crosses is an important factor in the diallel mating design (Hallauer and Miranda, 1981). Griffing (1956) provided four methods specified according to the nature of entries in the diallel table under two models (fixed and random). In this approach, using a suitable statistical model, the component variances due to general and specific combining ability are estimated which, in turn, may be translated into genetical components such as additive variance and dominance variance (Singh and Chaudhary, 1985). The four methods of the diallel depend on the material involved in the analysis: (i) parents (n), n (n-1)/2, F_1s and reciprocals (ii) parents and F_1s only. (iii) F_1s and reciprocals. (iv) F_1s only. It may be noted that the procedure for the analysis of variance remain the same in both models, but the expectations of mean sums of squares due to various items are different. In each method, two steps are involved in the analysis of the data. The first step consists of analysis of data for testing the null hypothesis that no genotypic differences among the F_1s, parents and reciprocals. Only when the significant differences among these are established, then there will be the need to proceed to the second step of analysis i.e. the combining ability analysis. In

testing of significance in model I, both the General Combining Ability (GCA) and Specific Combining Ability (SCA) mean squares are tested against error mean squares, contrary to model II where the GCA mean squares is tested against the SCA mean squares which in turn, is tested against the error mean squares (Singh and Chaudhary, 1985). In model I (fixed effect) the parents are the population, whereas in model II (random effect) the parents are a random sample from the population. The distinction between the two models is important not only for the analysis of variance but for the information derived from analysis of variance. Because the parents are the population for model I, estimation of components of variance is not appropriate but estimation of the effects of each pair of parents for specific crosses (SCA) and for all crosses that include a common parent (GCA) is appropriate and valid (Hallauer and Miranda, 1981).The model I analysis therefore yield considerable information about the fixed set of parents included - information that can be useful for the selection of parents that have good general combining ability in a series of crosses and good specific combining ability for specific pairs of parents. The diallel cross is feasible only for a relatively small number of genotypes or lines (Hallauer and Miranda, 1981).

2.2 COMBINING ABILITY

Sprague and Tatum (1941) introduced the concept of general combining ability (GCA) and specific combining ability (SCA) to distinguish between the average performance of parents in crosses or margins (GCA) and the deviation of individual crosses from the average in the margin (SCA). The concept of GCA and SCA are extensively used in plant breeding and has particular significance to the diallel mating design. Results from studies on combining ability of tropical early and intermediate maturity germplasm were reported by Beck *et al*. (1990) and for tropical late maturity yellow maize germplasm by Beck *et al.* (1991). Beck *et al.* (1991) reported highly significant positive GCA effect for yield for populations 42, 47, and 34 in Mexico and for pool 41 in the USA. In Nigeria, Ojo *et al.* (2007) reported that GCA and SCA mean squares were not significant for ear length, ear diameter and shelling percentage. Both GCA and SCA variances were, however, highly significant for all the characters reported by Uddin *et al*. (2006). Ivy and Hawlader (2000) found higher GCA variances for plant height, ear height and days to maturity. Das and Islam (1994) reported predominance of non-additive gene action for grain yield in maize. The performance of the parents, observed by Uddin *et al.* (2006) revealed that none of them was a good general combiner for all the characters considered. Ivy and Hawlader (2000) reported that parents that are good general combiners do not always have high SCA effects in their hybrid combinations.

2.3 HETEROSIS AND INBREEDING DEPRESSION

Heterosis is defined as the difference between the hybrid and the mean of the two parents (Falconer and Mackay, 1996) usually called mid-parent heterosis. However, higher parent heterosis is usually taken into cognizance especially when the goal is to identify a better hybrid superior to either of the parents. For grain yield/plant, heterosis over better parent was found in the range of 8.23 to 25.78 percent (Uddin *et al.* 2006). Higher parent heterosis for ear diameter were positive for all the hybrids with 2 x 6, 3 x 5 and 3 x 6 having the highest values of 39.77%, 35.73% and 33.22%, respectively, (Ojo *et al.*, 2007).

Heterosis is opposite and complementary to inbreeding depression (reduction in fitness as a direct result of inbreeding). The heterosis observed on crossing is expected to be equal to the depression upon inbreeding in a large number of crosses between lines derived from a single base population (Acquaah, 2007). Reduction in fitness is usually manifested as a reduction in vigour, fertility, and productivity. The effect of inbreeding is more severe in the early (5-8) generations (Acquaah, 2007). Just like heterosis, inbreeding depression is not uniformly manifested in plants. The study of the effects of self fertilization in maize was reported by Jones (1918; 1939). A gradual reduction in yield and plant height was observed, but environmental effects for estimating rate of inbreeding depression were obvious.

2.4 GENOTYPE BY ENVIRONMENT INTERACTION

The Genotype x Environment interaction implies that the behaviour of the genotypes depend upon the particular environment in which they are grown, thus the performance of any one of the genotypes relative to the remaining genotypes grown in the same environment will be inconsistent (Hill, 1975). Such inconsistencies result in either alteration to the ordering of the genotypes from one environment to another or to changes in the absolute differences between genotypes. Therefore the interactions act to confound comparison among lines/genotypes in most field situations. Genotype A may be superior to genotype B under one environment, equal in another environment but inferior to it in yet another environment. This type of variation arising from the differential performance of genotypes in different environments leading to change of ranks or even relative performance is known as genotype environment (GE) interaction (Chahal and Gosal, 2006). Such a differential expression of genotypes across environments reduces association between phenotypic and genotypic value with the result that difference between a pair of genotypes does not remain same in all the environments. A breeder shall have to decide whether the same variety can be grown under a wide range of environments or separate varieties should be developed for specific environmental situations. The existence of GE interactions influences both the breeding objectives as well as breeding strategies which may be aimed either at avoidance or exploitation of such interactions.

2.4.1 Types of Environments

The sum total of the effects of physical, chemical and biological factors of an individual other than its genotype is known as environment. Comstock and Moll (1963) classified environments into two categories:

i. Micro-environment: It is the environment of a single organism as opposed to that of another organism growing at the same time and in almost the same place. It includes physical and chemical attributes of soil, climatic variables, solar radiation, insect pests and diseases.
ii. Macro-environment: It is the environment which is associated with a given location or area at a particular period of time.

Allard and Bradshaw (1964) classified environments into predictable and unpredictable environments. The predictable environment includes the regular and more or less permanent features of the environment such as climate as determined by its longitude and latitude, soil type, rainfall and day length. It also includes what are called controllable variables (Perkins and Jinks, 1971) which include: level of fertilizer application, sowing date and sowing density, amount of irrigation which can be artificially created. The unpredictable one or uncontrollable environment includes weather fluctuations such as differences between seasons in terms of amount and distribution of rainfall and the prevailing temperature during crop growth.

2.4.2 Classification of GE Interactions

When two genotypes A and B are grown in two different environments X and Y, six types of interactions are possible (Chahal and Gosal, 2006). Some of these interactions could be due to crossovers and others due to non-crossovers (Allard and Bradshaw, 1964). The two varieties may show similar behaviour (parallel lines when grown in two environments) which indicates independence in the performance of genotype and environment. The presence of genotype-environment interactions leads to non-parallel response curves of varieties without intersecting of each other or with intersection. The existence of non-intersecting but non parallel lines suggests the relative ranking of varieties which remains same, though their absolute differences vary with the environment. The G x E interaction is considered as crossover or qualitative if it leads to change in relative ranking of genotypes in different environments. The non-crossover or quantitative G x E interaction, on the other hand results in differential change of mean but not of ranking of different genotypes. The situation for possible types of G x E becomes very complex with the increase in the number of genotypes and environments. For *m* genotypes and *n* environments, the possible types of interaction will be $mn!/m!n!$ (Chahal and Gosal, 2006). Among such a large number of possible interactions, there is only one type in which the same genotype is the best under all the environments. The crossover interactions are of interest in plant breeding because these affect the genotypes to be selected in a given environment. Such interactions also suggest that genotypes are specifically adapted to environments. The non-crossover interactions, on the other hand, influence the nature and magnitude of components of genetic variances and other related parameters like heritability and genetic advance.

CHAPTER THREE

MATERIALS AND METHODS

3.1 ORIGIN AND DESCRIPTION OF THE VARIETIES

The materials consisted of eight varieties of maize belonging to different maturity groups (extra-early, early, medium and late) and nine checks used for the evaluation. Brief description of the varieties is presented in Table 3.1

Table 3.1 Origin and descriptions of the varieties

S/N	Variety	Maturity period	Days to mid-silk	Source, description
1	Sammaz 19 (S.14 DKD DT)	Late (100-120 days)	62 days	IAR, White flint
2	Sammaz 37 (Pop 66 SR/Acr91 Suwan-1-SR)	Late (100-120 days)	62 days	IITA, Yellow flint
3	Sammaz 17 (Acr Sakatifu)	Medium (91-95 days)	58 days	IAR, White dent
4	Sammaz 36 (Cm 2007 pool QPM-Y)	Medium (91-95 days)	56 days	IAR, Yellow flint
5	Sammaz 27 (EV 99 DT-W-STR)	Early (86-90 days)	52 days	IITA,White flint,*Striga* resistant
6	Sammaz 35 (2000 EV DT-Y STRC4)	Early (86-90 days)	52 days	IITA, Yellow flint,*Striga* resistant
7	Sammaz 29(2000 syn EE-W-STR)	Extra-Early (80-85 days)	50 days	IITA, White flint

8	Sammaz 28 (99 TZEE-Y-STR)	Extra-Early (80-85 days)	50 days	IITA, Yellow flint

Source: Usman (2009).

3.2 CROSSING NURSERY

The parent materials used for the diallel mating comprised of eight open pollinated varieties. The varieties were crossed in a complete diallel pattern at Samaru, Zaria in April, 2010. Samaru is located within $11^0$11'N, $07^0$38'E at an altitude of 686m above sea level, in the northern guinea savanna zone of Nigeria, with a mean annual rainfall of 1050mm distributed within five months. The soil type is loamy. The crosses were made in all possible combinations as illustrated in Table 3.2.

Table 3.2 Crossing nursery

♀ \ ♂	1	2	3	4	5	6	7	8
1	1x1	1x2	1x3	1x4	1x5	1x6	1x7	1x8
2	2x1	2x2	2x3	2x4	2x5	2x6	2x7	2x8
3	3x1	3x2	3x3	3x4	3x5	3x6	3x7	3x8
4	4x1	4x2	4x3	4x4	4x5	4x6	4x7	4x8
5	5x1	5x2	5x3	5x4	5x5	5x6	5x7	5x8
6	6x1	6x2	6x3	6x4	6x5	6x6	6x7	6x8
7	7x1	7x2	7x3	7x4	7x5	7x6	7x7	7x8
8	8x1	8x2	8x3	8x4	8x5	8x6	8x7	8x8

3.3 FIELD EVALUATION

Nine checks which included late maturing group (Sammaz 11, Sammaz 14, Sammaz 16), medium maturing (Sammaz 15), early maturing (Sammaz 18, Sammaz 20, Sammaz 34) and extra-early maturing (Sammaz 12, Sammaz 13), the eight parents and the sixty four resultant F_1 (8x8 full diallel cross) totalling eighty one entries were evaluated at Kadawa irrigation site in two different sowing dates (environment one on January 1, 2011 and environment two on March 16, 2011). Each sowing date was considered as an environment. The meteorological data for the two environments are presented below:

Table 3.3 Meteorological data for environments one and two 2011

Days	January		February		March		April		May		June		July	
	Max T(^{o}c)	Min T(^{o}c)	Max T(^{o}c)	Min T(^{o}c)	Max T(^{o}c)	Min T(^{o}c)	Max T(^{o}c)	Min T(^{o}c)	Max T(^{o}c)	Min T(^{o}c)	Max T(^{o}c)	Min T(^{o}c)	Max T(^{o}c)	Min T(^{o}c)
1	35	29	31	35	35	27	30	22	36	29	39	29	36	25
2	32	28	32	27	37	26	29	20	34	28	40	24	40	25
3	32	29	33	28	36	24	32	27	37	26	39	24	38	24
4	33	27	34	29	37	25	32	27	35	25	35	25	39	25
5	33	27	35	30	39	26	32	27	36	26	35	23	40	25
6	34	23	36	29	36	27	32	27	35	27	36	24	36	40
7	34	27	37	28	37	28	32	22	35	25	37	25	42	25
8	35	31	36	29	38	24	32	22	35	25	38	27	38	26
9	35	30	35	28	32	25	32	25	37	27	26	39	37	24
10	30	27	34	27	33	26	32	20	34	28	32	23	36	25
11	31	29	35	28	34	27	32	25	34	25	33	24	36	26
12	30	28	36	29	35	26	35	25	33	25	34	25	40	25
13	31	28	37	29	30	28	38	26	33	26	35	26	40	25
14	30	26	36	29	30	27	38	25	34	27	33	27	40	25
15	30	25	37	32	33	26	38	25	35	28	36	26	35	25
16	32	24	30	27	32	26	37	25	37	27	37	22	35	24
17	33	25	32	26	33	27	32	25	37	28	37	23	38	26
18	33	26	31	26	33	28	32	25	36	27	38	24	35	24
19	35	26	34	27	24	29	32	25	32	28	39	26	35	24
20	35	25	33	22	34	27	32	26	32	29	38	27	35	24
21	34	26	34	23	35	28	37	26	34	25	36	28	35	24
22	34	27	35	24	36	29	32	25	34	26	37	26	36	26
23	32	28	34	25	36	28	35	25	34	27	36	28	37	24
24	33	29	30	25	34	29	38	26	34	27	34	26	36	23
25	34	23	30	26	36	28	38	27	35	28	35	27	35	23
26	33	24	33	27	35	27	38	24	35	28	35	28	34	23
27	33	25	34	27	37	27	38	24	34	28	35	29	35	24
28	34	24	30	26	36	28	38	25	35	28	36	30	38	24
29	35	25			37	27	38	26	34	27	37	26	36	33
30	36	26			37	25	38	27	36	28	36	29	38	33
31	32	27			32	27	34	29						
Total	1023	824	944	768	1069	832	1065	775	1042	808	1074	790	1111	769
Mean	33	27	34	27	35	27	34	25	35	27	36	26	37	25.6

Source: Meteorological data records IRS/IAR/ABU Kadawa, 2011

The 81 entries evaluated in each environment are given in Table 3.4

Table 3.4 Entries evaluated

S/N	Varieties/hybrids	Status
1	Sammaz 19	Parent
2	Sammaz 37	Parent
3	Sammaz 17	Parent
4	Sammaz 36	Parent
5	Sammaz 27	Parent
6	Sammaz 35	Parent
7	Sammaz 29	Parent
8	Sammaz 28	Parent
9	Sammaz 19 X Sammaz 19	Self
10	Sammaz 19 X Sammaz 37	Hybrid
11	Sammaz 19 X Sammaz 17	Hybrid
12	Sammaz 19 X Sammaz 36	Hybrid
13	Sammaz 19 X Sammaz 27	Hybrid
14	Sammaz 19 X Sammaz 35	Hybrid
15	Sammaz 19 X Sammaz 29	Hybrid
16	Sammaz 19 X Sammaz 28	Hybrid
17	Sammaz 37 X Sammaz 19	Reciprocal
18	Sammaz 37 X Sammaz 37	Self
19	Sammaz 37 X Sammaz 17	Hybrid
20	Sammaz 37 X Sammaz 36	Hybrid
21	Sammaz 37 X Sammaz 27	Hybrid
22	Sammaz 37 X Sammaz 35	Hybrid
23	Sammaz 37 X Sammaz 29	Hybrid

24	Sammaz 37 X Sammaz 28	Hybrid
25	Sammaz 17 X Sammaz 19	Reciprocal
26	Sammaz 17 X Sammaz 37	Reciprocal
27	Sammaz 17 X Sammaz 17	Self
28	Sammaz 17 X Sammaz 36	Hybrid
29	Sammaz 17 X Sammaz 27	Hybrid
30	Sammaz 17 X Sammaz 35	Hybrid
31	Sammaz 17 X Sammaz 29	Hybrid
32	Sammaz 17 X Sammaz 28	Hybrid
33	Sammaz 36 X Sammaz 19	Reciprocal
34	Sammaz 36 X Sammaz 37	Reciprocal
35	Sammaz 36 X Sammaz 17	Reciprocal
36	Sammaz 36 X Sammaz 36	Self
37	Sammaz 36 X Sammaz 27	Hybrid
38	Sammaz 36 X Sammaz 35	Hybrid

Table 3.4 contineud

S/N	Varieties/hybrids	Status
39	Sammaz 36 X Sammaz 29	Hybrid
40	Sammaz 36 X Sammaz 28	Hybrid
41	Sammaz 27 X Sammaz 19	Reciprocal
42	Sammaz 27 X Sammaz 37	Reciprocal
43	Sammaz 27 X Sammaz 17	Reciprocal
44	Sammaz 27 X Sammaz 36	Reciprocal
45	Sammaz 27 X Sammaz 27	Self
46	Sammaz 27 X Sammaz 35	Hybrid

47	Sammaz 27 X Sammaz 29	Hybrid
48	Sammaz 27 X Sammaz 28	Hybrid
49	Sammaz 35 X Sammaz 19	Reciprocal
50	Sammaz 35 X Sammaz 37	Reciprocal
51	Sammaz 35 X Sammaz 17	Reciprocal
52	Sammaz 35 X Sammaz 36	Reciprocal
53	Sammaz 35 X Sammaz 27	Reciprocal
54	Sammaz 35 X Sammaz 35	Self
55	Sammaz 35 X Sammaz 29	Hybrid
56	Sammaz 35 X Sammaz 28	Hybrid
57	Sammaz 29 X Sammaz 19	Reciprocal
58	Sammaz 29 X Sammaz 37	Reciprocal
59	Sammaz 29 X Sammaz 17	Reciprocal
60	Sammaz 29 X Sammaz 36	Reciprocal
61	Sammaz 29 X Sammaz 27	Reciprocal
62	Sammaz 29 X Sammaz 35	Reciprocal
63	Sammaz 29 X Sammaz 29	Self
64	Sammaz 29 X Sammaz 28	Hybrid
65	Sammaz 28 X Sammaz 19	Reciprocal
66	Sammaz 28 X Sammaz 37	Reciprocal
67	Sammaz 28 X Sammaz 17	Reciprocal
68	Sammaz 28 X Sammaz 36	Reciprocal
69	Sammaz 28 X Sammaz 27	Reciprocal
70	Sammaz 28 X Sammaz 35	Reciprocal
71	Sammaz 28 X Sammaz 29	Reciprocal
72	Sammaz 28 X Sammaz 28	Self
83	Sammaz 11 (Acr 97 TZL Comp 1)	Check (C1)

74	Sammaz 16 (TZL Com1 syn W-1)	Check (C2)
75	Sammaz 14 (Obatampa)	Check (C3)
76	Sammaz 15 (IWDC2 syn F_2)	Check (C4)

Table 3.4 continued

S/N	Varietes/Hybrids	Status
77	Sammaz 34 (IAR Multicob)	Check (C5)
78	Sammaz 20 (TZE Comp 3)	Check (C6)
79	Sammaz 18 (Tillering maize)	Check (C7)
80	Sammaz 13 (TZEE-Y)	Check (C8)
81	Sammaz 12 (TZEE-W)	Check (C9)

3.3.1 Description of Experimental Site

Kadawa is located within latitude $11^0$56'N, $08^0$45'E and is 496m above sea level. It is situated in sudan savanna zone, and is characterized by mean annual rainfall of 830mm, with monomodal distribution falling between June and October (Singh and Balasubramanium, 1983). The mean daily temperature ranged from 29^0C to 38^0C (Kowal and Knabe, 1972). The soil type is sandy loam. Kadawa is located along the largest irrigation scheme in the country, the Hadejia-Jama'are River Basin.

3.3.2 Experimental Design

The 81 entries (Table 3.4) were arranged in 9 x 9 lattice design with three replications in each environment. One row of 5m long spaced 0.75m apart was used as a plot. Three seeds were planted at intra row spacing of 50cm and later thinned to two plants per hill. Three hoe weedings were carried out, first one at two weeks after planting, second at four weeks after planting and earthing up at six weeks after planting with a split fertilizer application of compound fertilizer (NPK 20:10:10) as basal dressing and urea (46 % N) as top dressing, giving a total plant nutrient of 120 kg N, 60 kg P_2O_5 and 60 kg K_2O per hectare.

3.3.3 Data Collection and Observations

Assessment of plant characters was started two weeks after planting and continued till maturity. Data were collected on the following parameters:

1. Days to 50% pollen shed: Number of days after planting to when 50% of the plants in a plot shed pollen.
2. Days to 50% silking: The number of days after planting to when 50% of the plants in a plot produced silk.
3. Plant height (cm): The height from soil level to the flag leaf.
4. Days to maturity: The number of days from planting to physiological maturity.
5. Ear height (cm): Height from the soil level to the node bearing the top most ear.
6. Ears per plot: Number of ears in each plot at harvest.
7. Number of leaves per plant: The average number of leaves per plant recorded from each plot after flowering.
8. Ear length (cm): The average length of the ear from the end of the peduncle to the end of the cob.
9. Ear diameter (cm): The average diameter of the ear taken from central part of the uppermost ear.
10. Kernel row number: The average number of rows in the central part of the uppermost ear.
11. Kernels per row: The average number of kernels per row.
12. Cob diameter (cm): The average diameter of the cobs per plant.
13. Cob weight (kg): The weight of the cobs with grains per plot.
14. Threshing percentage: (kernel weight/cob weight) x 100.
15. Grain yield per hectare (kg): 10,000 x kernels weight in a plot)/ Area of a plot

Length, weight and diameter were measured using measuring tape, weighing balance and vernia calliper, respectively.

3.4 DATA ANALYSIS

Analyses of variance (ANOVA) for individual environment as well as for combined environments were computed using Statistical Application for the Sciences Software (SAS, 1986). The ANOVA was computed on plot mean values for all characters across the two environments. The form of ANOVA for one environment is presented in Table 3.5 below:

Table 3.5 Form of ANOVA for one environment

Source of variation	df	MS	EMS
Replication	(r-1)	M_3	
Genotype	(g-1)	M_2	$\sigma^2_e + r\sigma^2_g$
Error	(g-1) (r-1)	M_1	σ^2_e
Total	(rg-1)		

Where r and g are the number of replications and genotypes, respectively and σ^2_e and σ^2_g are error and genotype variances, respectively (Obi, 1986).

The following model (Bohren *et al.,* 1963) was used for one environment:

$$x_{ijk} = \mu + r_i + g_j + e_{ijk}$$

Where:

x_{ijk} = Observation of the i^{th} variety and j^{th} variety in the k^{th} replication

μ = The population mean

r_i = Effect of the i^{th} variety due to replication

g_j = Effect of the j^{th} variety due to genotype; e_{ijk} = Experimental error

The form of ANOVA for combined analysis across environments is presented in Table 3.6 below:

Table 3.6 Form of combined ANOVA across environments

Source of variation	df	MS	EMS
Environment	(l-1)		
Replication in environment	l(r-1)	m_l	
Genotype	(g-1)	m_g	$\sigma^2_e + r\sigma^2_{gl} + rl\sigma^2_g$
Genotype x environment	(g-1)(l-1)	m_{gl}	$\sigma^2_e + r\sigma^2_{gl}$
Error	l(r-1)(g-1)	m_e	σ^2_e
Total	lgr-1		

Where: l and g represent environment and genotype, respectively.

σ^2_{gl} = genotype x environment interaction variance

σ^2_g = variance due to genotype

σ^2_e = error variance

The statistical model for the combined ANOVA across environments is presented as:

$$x_{ijk} = \mu + l_i + r_{ij} + g_k + (rl)_{ij} + (gl)_{ik} + e_{ijk}$$

Where:

x_{ijk} = Observation of the i^{th} variety and j^{th} variety in k^{th} replication

$\mu =$ Overall mean

$l_i =$ The effect of the i^{th} environment

$r_{ij} =$ The effect of the j^{th} replication in the i^{th} environment

$g_k =$ The effect of the k^{th} genotype

$(rl)_{ij} =$ Replication x environment interaction

$(jl)_{ik} =$ The interaction effect between k^{th} genotype in the i^{th} environment

$e_{ijk} =$ Experimental error

$i =$ Environment (1, 2)

$j =$ Replications (1, 2, 3)

$k =$ Genotypes (1, 2…..81)

3.5.0 GENETIC ANALYSIS

3.5.1 Combining Ability Estimation

The form of analysis of variance for combining ability for individual environment is presented in Table 3.7 below: (Matzinger *et al.,* 1959; Kempthorne, 1956).

Table 3.7 Form of ANOVA for combining ability for individual environment

Source of variation	df	MS	EMS
Crosses	$n[(n-1)/2]-1$	m_n	
Parents	$(n-1)$	m_p	$\sigma^2_e + rgs\ \sigma^2_p$
Parents Vs Crosses	1		
GCA	$(n-1)$	m_g	$\sigma^2_e + rsp\ \sigma^2_g$
SCA	$n(n-3)/2$	m_s	$\sigma^2_e + rpg\ \sigma^2_s$
Reciprocal	$n(n-1)/2$	m_r	$\sigma^2_e + sgp\ \sigma^2_r$
Error	$(r-1)[(n(n+1)/2]-1$	m_e	σ^2_e

Key: r= reciprocal; p= parent; g= GCA; s= SCA and e=error, n= number of parents.

Parent Vs cross was calculated using the formula (Singh and Chaudhary, 1985)

$$S.S(P.Vs.C) = [\sum^a (c \sum Y)]^2 / n \sum^a c^2$$

Where:

$n =$ Number of replications

$c =$ Coefficient of contrast

$a =$ Number of groups

$\sum Y =$ Sum of entries in a contrasted set

Plot-mean values were used in the diallel analysis of fixed effects method 1 model 1 (Otsuka *et al.*, 1972). The following model was used.

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

Where:

y_{ijk} = The performance of the k^{th} plot of the cross between the i^{th} and j^{th} parents.

μ = Overall mean

g_i = Effect common to all progeny of the i^{th} parent

g_j = Effect common to all progeny of the of the j^{th} parent

s_{ij} = Effect specific to the progeny of mating i^{th} x j^{th} parent

e_{ijk} = Experimental error

The form of analysis of variance for combining ability across environments is presented in Tale 3.8 below:

Table 3.8 Form of ANOVA for combining ability across environments

Source of variation	df	MS	EMS
Environment	$(l-1)$		
Parent Vs cross	1		
GCA	$(n-1)$	m_7	$\sigma^2_e + r\sigma^2_{lgs} + rs\,\sigma^2_g$
SCA	$n(n-1)/2$	m_6	$\sigma^2_e + r\sigma^2_{lgs} + rg\ \sigma^2_s$
Reciprocal	$n(n-1)2$	m_5	$\sigma^2_e + r\sigma^2_{lgs} + sg\ \sigma^2_r$
GCA x environment	$(n-1)(l-1)$	m_4	$\sigma^2_e + r\sigma^2_{lgs} + rs\,\sigma^2_{gl}$
SCA x environment	$(n(n-1)/2)(l-1)$	m_3	$\sigma^2_e + r\sigma^2_{lgs} + rg\ \sigma^2_{sl}$
Error		m_1	σ^2_e

The model below was used for combining ability analysis across the environments:

$$y_{ijkt} = \mu + g_i + g_j + s_{ij} + l_t + (gl)_{it} + (sl)_{ijt} + r_{kt} + e_{ijkt}$$

Where:

y_{ijkt} = The performance of a cross between i^{th} and j^{th} parents in the k^{th} replication in the t^{th} environment.

μ= Overall mean

g_i = Effect common to all progeny of the i^{th} parent

g_j = Effect common to all progeny of the j^{th} parent

s_{ij} = Effect specific to the progeny of mating i^{th} and j^{th} parents

l_t = The average effect of the t^{th} environment

$(gl)_{it}$ = Genotype x environment interaction effect in the i^{th} parent in that environment.

$(gl)_{jt}$ = Genotype x environment interaction effect in the j^{th} parent in that environment

$(sl)_{ijt}$ = Specific effect of mating i^{th} parent and j^{th} parent in that environment

r_{kt} = Effect of the k^{th} replication in l^{th} environment

e_{ijkt} = Experimental error

i = 1-8 parents, j = 1-8 parents, k = 1-3 replications, l = 1-2 environments.

The GCA and SCA effects were estimated using Griffing (1956) method 1, model 1, where the genotype effect was fixed. The relative importance of additive and non-additive effects was estimated by the ratio of the variances of fixed effects (Singh and Chaudhary, 1985).

Component due to GCA was determined from Table 3.7 using the formula below:

$$\sigma^2_g = m_g - m_e / 2n = 1/_{n-1} \sum g^2_i$$

Component due to SCA was determined from Table 3.7 using the formula below:

$$\sigma^2_s = m_s - m_e = 2/n(n-1) \sum \sum s^2_{ij}$$

Component due to reciprocal was estimated from Table 3.7 thus:

$$\sigma^2_r = m_r - m_e / 2 = 2/n(n-1) \sum g^2_i$$

Where:

σ^2_g = Variance due to GCA effect

σ^2_s = Variance due to SCA effects

σ^2_r = Variance due to reciprocal effects

g_i = The GCA effects of the i^{th} parent

s_{ij} = The SCA effects of the cross ixj

r_{ij} = Measure of the reciprocal effect

The ratio of GCA variance to SCA variance was calculated using (Singh and Chaudhary, 1985) formula:

$$(1/n-1)\sum_i g_i^2 /(2/n(n-1)\sum\sum_{i<j} s_{ij}^2 = (m_g - m_e/2n)/(m_s - m_e).$$

General, specific and reciprocal combining ability effects were calculated using Singh and Chaudhary (1985) formula below:

$$g_i = 1/2n(Y_{i.} + Y_{.j}) - 1/n^2 Y_{..}$$
$$s_{ij} = 1/2(Y_{ij} + Y_{ji}) - 1/2n(Y_i + Y_{.i} + Y_j + Y_{IJ}) + 1/n^2 Y_{..}$$

$$r_{ij} = 1/2(Y_{ij} - Y_{ji})$$

Where:

g_i =GCA for parent i

S_{ij} =SCA for parents i and j

n =Number of parents

Y_i = Array means of parent i

Y_j =Array mean of parent j

$Y_{..}$ = Grand total of the crosses

The significance of general and specific combining ability effects was tested using the formula of Cox and Frey (1984).

$$t = GCA \ / \mathrm{SE}_{GCA}$$

$$t = SCA \ / SE_{SCA}$$

$$SE = \sqrt{m}_{e} / r$$

Where:

m_e = Error mean square

r = Number of replications

SE = Standard error

3.6 HETEROSIS ESTIMATION

Heterosis for individual crosses was estimated based on the difference between F_1 and high parent:

High parent heterosis (H_{PH})

$$H_{PH} = \frac{F_1 - H_P}{H_P} \times 100$$

Where:

F_1 = Average performance of hybrid formed between j^{th} and i^{th} parents

H_P = Average performance of the high parent

The significance of heterosis was tested using Paschal and Wilcox (1975) formula:

$$SD = \sqrt{2MSE / r}$$

Where

SD = Standard difference between F_1 and High parent required for significance at 5% and 1% probability levels.

MSE = Mean Square of error

r = number of replications

3.7. INBREEDING DEPRESSION

Inbreeding depression was calculated using Hallauer *et al. (1988)* formula:

$$\text{ID relative to self} = (s_o - p)/s_o X100$$

Where:

ID= Inbreeding depression percentage

$s_o = \text{Mean of the self}$

$p = \text{Parent mean}$

ID relative to $F_1 = ((x_o - x_f)/x_o)X100$

Where:

$x_o = \text{Mean of the parents}$

$x_f = \text{Mean of the hybrid}$

CHAPTER FOUR

RESULTS

4.1 ANALYSIS OF VARIANCE

The analyses of variance for environment one, two and combined across environments are presented in Tables 4.1, 4.2 and 4.3, respectively. The result of analysis of variance for fifteen traits measured at environment one indicated the mean squares due to genotypes (parents, crosses, reciprocals, selfs and checks) were highly significant ($p \leq 0.01$) for eleven traits (Table 4.1), and significant ($p \leq 0.05$) for number of leaves per plant, plant height and kernel row number. Ear height, ear diameter and cob diameter were not significant. The results of environment two indicated highly significant ($p \leq 0.01$) differences for seven traits (Table 4.2), while cob diameter was significant at $p \leq 0.05$. The result of the combined analysis across environments (Table 4.3) indicated highly significant ($p \leq 0.01$) differences for genotype, for eight traits. Days to 50% tasselling, days to 50% silk and number of leaves per plant were significant ($p \leq 0.05$). The differences in the genotypes for days to maturity, ear length, kernel row number, ear diameter and cob diameter were statistically not significant. The mean squares for genotype x environment interaction were highly significant for seven traits. Days to maturity and ear length were significant at $p \leq 0.05$ whereas the genotype x environment interaction for days to 50% silking, number of leaves per plant, plant height, ear height, ear diameter and cob diameter were not significant.

Table 4. 1 Mean squares for fifteen agronomic characters for environment one

Source of variation	df	Daf	Das	NL	PH	EH	DM	Ep	EL
Replication	2								
Genotype	80	31.39**	36.99**	2.69*	615.74*	267.40	44.22**	61.28**	9.29**
Error	159	12.80	17.73	1.75	414.46	197.69	18.00	25.05	3.95
Total	241								

Table 4 .1 continued

Source of variation	df	KRN	KPR	ED	CD	Cw	Tp	Gy
Replication	2							
Genotype	80	3.52*	72.24**	6.02	0.05	1.05**	298.47**	4386929.1**

Error	159	2.48	41.34	8.54	0.07	0.54	135.22	2187249.3
Total	241							

**,* significantly different at 1% and 5% levels of probability, respectively.

KEY: df; Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4. 2 Mean squares for fifteen agronomic characters for environment two

Source of variation	df	Daf	Das	NL	PH	EH	DM	Ep	EL
Replication	2								
Genotype	80	26.28	28.89	5.00	914.64	274.54**	29.74	58.74**	71.57
Error	160	28.67	32.89	4.16	696.97	177.96	42.80	34.53	56.98
Total	242								

Table 4. 2 continued

Source of variation	df	KRN	KPR	ED	CD	Cw	Tp	Gy
Replication	2							
Genotype	80	6.90**	84.42**	8.69	0.06*	0.32**	345.43**	1586512.6**
Error	160	4.35	46.97	7.93	0.04	0.20	135.86	904096.7
Total	242							

**,* significantly different at 1% and 5% levels of probability, respectively.

KEY: df; Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4. 3 Mean squares for fifteen agronomic characters combined across environments

Source of variation	df	Daf	Das	NL	PH	EH	DM	Ep	EL
Env	1								
Rep (Env)	4								
Genotype	80	27.78*	33.59*	4.18*	901.72**	299.80**	31.55	55.65**	39.42
Genotype x Env	80	30.98**	33.31	3.51	631.23	242.16	42.53*	65.24**	41.47*
Error	319	20.76	25.34	2.96	556.16	187.80	30.44	29.80	30.55
Total	484								

Table 4 .3 continued

Source of variation	df	KRN	KPR	ED	CD	Cw	Tp	Gy
Env	1							

Rep (Env)	4							
Genotype	80	3.85	82.67**	6.84	0.05	0.70**	314.81**	3027724.4**
Genotype x Env	80	6.57**	73.96**	7.87	0.06	0.67**	329.21**	2944919.6**
Error	319	3.42	44.16	8.23	0.06	0.37	135.54	1543662
Total	484							

**,* significantly different at 1% and 5% levels of probability, respectively.

KEY: df; Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernels row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

4.2 MEAN PERFORMANCE

The mean performance of the parents, crosses, reciprocals, selfs and checks for fifteen traits at environment one, environment two and across environments are presented in Tables 4.4, 4.5 and 4.6, respectively. At environment one the ranges for days to 50% tasselling, days to 50% silk, number of leaves per plant, plant height, ear height and days to maturity (Table 4.4) were 77-98, 84-105, 11-16, 105-182, 39.67-87, and 113-130 , respectively. The hybrid 8x3 was earliest to tassel (77 days), check C5 was earliest to silk (84days), check C7 produced highest number of leaves (16), hybrid 1x6 was the tallest (182cm), while hybrid 5x6 was the earliest to mature (113days). The records for ear length, kernel row number, kernels per row, ear diameter, cob diameter, cob weight, threshing percentage and yield ranged from 19-11cm, 15-9, 39-18, 7.3-6cm, 2-1cm, 3-0.2kg, 81-34%, and 5316-2131kg/ha, respectively. The hybrid 4 x 1 had the longest ears (19cm), parent 2 had the highest kernel row number (15), hybrid 4 x 6 had the largest kernels per row (39), hybrid 1 x 5 had the largest ear diameter (7.3cm), reciprocal cross 6 x 4 had the largest cob diameter (2cm), hybrid 3 x 7 had the heaviest cobs (3kg), parent 6 had the largest threshing percentage (81%) and hybrid 3 x 7 had the highest yield (5316kg/ ha).

The mean performance in environment two (Table 4.5) indicated that, the ranges for days to 50% tasselling and silk, number of leaves per plant, plant height, ear height and days to maturity were 62-75, 68-81, 14-8, 158-72cm, 90-26cm and 88-103, respectively. The reciprocal cross 5 x 3 (62days) was earliest to tassel and to silk (68 days). Check C2 (14) had the highest number of leaves, hybrid 5 x 7 was the tallest (158cm), hybrid 5 x 7 had the longest ear height

(90cm), hybrid 1 x 5 was the earliest to mature (88days). Mean ranges for ear length, kernel row number, kernels per row, ear diameter, cob diameter, threshing percentage and grain yield were 19.5-7cm, 16-7, 36-8, 8.5-4cm, 2-1cm, 92-53%, and 3049-124kg/ha, respectively. Parent 6 had the highest kernel row number (16), reciprocal 6 x 3 had the highest kernels per row (36), self 4 x 4 had the largest ear diameter (8.5cm), hybrid 5 x 8 had the largest cob diameter (2cm), hybrid 1 x 5 (2kg), hybrid 4 x 7had the highest threshing percentage (92%) and hybrid 1 x 5 had the highest yield (3049kg/ha).

Across environments (Table 4.6) showed that days to 50 % tasselling and silk, number of leaves per plant, plant height, ear height and days to maturity range between 72-81days, 77-88days, 10-14, 100-155cm, 39-74cm and 100-114days, respectively. The hybrid 1 x 5 was earliest to tassel (72days), hybrid 4 x 7 was earliest to silk (77days), reciprocal 7 x 5 had the highest number of leaves (14), reciprocal 7 x 5 was the tallest (155cm) and hybrid 5 x 7 had tallest ear height (74cm) and reciprocal 7 x 1was earliest to mature (100 days). The result revealed that check C4 had the longest ear (18cm), hybrid 1 x 5 had the highest kernel row number (14), reciprocal 6 x 3had the highest kernels per row (36), self 4 x 4 had the highest ear diameter (8cm), hybrid 5 x 8 had the widest cob diameter (2cm), hybrid 4 x 6 had the highest threshing percentage (86.%) and hybrid 5 x 6 had the highest yield (3524kg/ha).

Table 4. 4 Mean performance of parents, crosses, reciprocals, selfs and checks for fifteen agronomic characters in environment one

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 19	1	98.5^{a}	104.5^{a}	14.0^{a-c}	164.5^{a-c}	58.0^{a-h}	117.5^{f-h}	3.0^{k-l}
Sammaz 37	2	82.3^{c-n}	88.0^{d-k}	13.3^{a-d}	140.3^{a-i}	68.0^{a-h}	122.3^{a-f}	13.0^{a-k}
Sammaz 17	3	78.7^{i-n}	85.3^{g-k}	12.7^{b-d}	129.3^{b-i}	57.0^{b-h}	120.7^{c-h}	16.0^{a-g}
Sammaz 36	4	88^{b-d}	96.3^{b-e}	12.7^{b-d}	152.7^{a-h}	53.0^{b-h}	128.7^{a-d}	2.3^{l}
Sammaz 27	5	80.7^{d-n}	87.7^{e-k}	13.3^{a-d}	137.3^{b-i}	58.3^{a-h}	122.0^{a-f}	14.7^{a-h}
Sammaz 35	6	85^{b-l}	90.3^{b-k}	13.3^{a-d}	134.3^{b-i}	56.7^{b-h}	125.3^{a-f}	4.3^{i-l}
Sammaz 29	7	79.0^{h-n}	86.0^{f-k}	12.7^{b-d}	117.0^{f-i}	52.3^{c-h}	122.0^{a-f}	7.0^{g-l}
Sammaz 28	8	81.7^{c-n}	87.3^{f-k}	10.7^{c}	104.7^{i}	41.3^{g-h}	121.0^{c-h}	8.3^{e-l}
Sammaz 19 X Sammaz 19	1x1	85.3^{b-k}	90.7^{b-k}	12.7^{b-d}	131.7^{b-i}	56.3^{b-h}	125.3^{a-f}	14.0^{a-j}
Sammaz 19 X Sammaz 37	1x2	87^{b-f}	92.7^{b-j}	14.7^{a-c}	151.0^{a-h}	64.0^{a-h}	124.3^{a-f}	20.0^{a-c}
Sammaz 19 X Sammaz 17	1x3	86^{b-i}	91.7^{b-k}	13.3^{a-d}	147.7^{a-h}	64.3^{a-h}	130.3^{a}	19.7^{a-c}
Sammaz 19 X Sammaz 36	1x4	85.3^{b-k}	92.7^{b-j}	14.0^{a-c}	156.0^{a-g}	65.3^{a-h}	124.3^{a-f}	15.3^{a-g}
Sammaz 19 X Sammaz 27	1x5	81.3^{c-n}	88.0^{d-k}	14.0^{a-c}	132.0^{b-i}	52.3^{c-h}	122.7^{a-f}	15.0^{a-h}
Sammaz 19 X Sammaz 35	1x6	84^{b-n}	90.0^{c-k}	14.0^{a-c}	182.0^{a}	87.0^{a}	124.0^{a-f}	19.0^{a-d}

Sammaz 19 X Sammaz 29	1x7	85.7^{b-j}	89.3^{d-k}	14.0^{a-c}	148.0^{a-h}	60.3^{a-h}	125.3^{a-f}	15.3^{a-g}
Sammaz 19 X Sammaz 28	1x8	81.7^{c-n}	88.0^{d-k}	12.0^{c-d}	132.0^{b-i}	57.3^{b-h}	120.0^{d-h}	17.7^{a-f}
Sammaz 37 X Sammaz 19	2x1	83^{b-n}	89.3^{d-k}	13.3^{a-d}	161.0^{a-e}	77.3^{a-e}	123.7^{a-f}	19.3^{a-c}
Sammaz 37 X Sammaz 37	2x2	86.7^{b-g}	93.7^{b-h}	13.3^{a-d}	128.3^{b-i}	54.3^{b-h}	122.3^{a-f}	17.3^{a-g}
Sammaz 37 X Sammaz 17	2x3	84.7^{b-m}	93.7^{b-h}	14.7^{a-c}	141.7^{a-i}	62.3^{a-h}	123.3^{a-f}	19.7^{a-c}
Sammaz 37 X Sammaz 36	2x4	83.0^{b-n}	88.3^{d-k}	14.0^{a-c}	132.0^{b-i}	59.0^{a-h}	123.3^{a-f}	19.3^{a-c}
Sammaz 37 X Sammaz 27	2x5	85.3^{b-k}	92.7^{b-j}	13.3^{a-d}	125.7^{c-i}	51.0^{d-h}	127.0^{a-e}	12.7^{b-k}
Sammaz 37 X Sammaz 35	2x6	83.3^{b-n}	89.7^{c-k}	14.7^{a-c}	143.0^{a-i}	67.3^{a-h}	121.7^{a-f}	15.0^{a-h}
Sammaz 37 X Sammaz 29	2x7	84.7^{b-m}	91.7^{b-k}	14.0^{a-c}	134.0^{b-i}	65.7^{a-h}	123.0^{a-f}	18.7^{a-e}

Table 4.4 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 37 X Sammaz 28	2x8	82.0^{c-n}	90.3^{b-k}	12.7^{b-d}	138.7^{b-i}	63.0^{a-h}	121.3^{b-g}	19.7^{a-c}
Sammaz 17 X Sammaz 19	3x1	83.3^{b-n}	90.7^{b-k}	13.3^{a-d}	151.7^{a-h}	72.0^{a-f}	124.7^{a-f}	15.3^{a-g}
Sammaz 17 X Sammaz 37	3x2	86.3^{b-h}	92.0^{b-k}	12.0^{c-d}	131.7^{b-i}	53.0^{b-h}	125.0^{a-f}	13.7^{a-j}
Sammaz 17 X Sammaz 17	3x3	85.3^{b-k}	91.3^{b-k}	14.0^{a-c}	120.7^{d-i}	47.3^{f-h}	128.0^{a-e}	23.3^{a}
Sammaz 17 X Sammaz 36	3x4	82.7^{c-n}	89.7^{c-k}	12.7^{b-d}	128.3^{b-i}	54.7^{b-h}	128.7^{a-d}	14.0^{a-j}
Sammaz 17 X Sammaz 27	3x5	84.3^{b-n}	93.0^{b-i}	12.7^{b-d}	138.0^{b-i}	68.3^{a-h}	124.3^{a-f}	20.3^{a-c}

Sammaz 17 X Sammaz 35	3x6	85.0^{b-l}	92.3^{b-k}	14.7^{a-c}	161.0^{a-e}	78.3^{a-d}	123.7^{a-f}	19.0^{a-d}
Sammaz 17 X Sammaz 29	3x7	81.7^{c-n}	87.7^{e-k}	13.3^{a-d}	137.0^{b-i}	53.7^{b-h}	122.7^{a-f}	19.7^{a-c}
Sammaz 17 X Sammaz 28	3x8	85^{b-l}	90.3^{b-k}	14.0^{a-c}	135.3^{b-i}	57.0^{b-h}	124.0^{a-f}	16.0^{a-g}
Sammaz 36 X Sammaz 19	4x1	85^{b-l}	91.7^{b-k}	14.0^{a-c}	169.7^{a}-^{b}	82.0^{a}-^{b}	122.7^{a-f}	19.7^{a-c}
Sammaz 36 X Sammaz 37	4x2	85.3^{b-k}	91.0^{b-k}	13.3^{a-d}	149.3^{a-h}	73.3^{a-f}	125.7^{a-f}	18.3^{a-e}
Sammaz 36 X Sammaz 17	4x3	83.7^{b-n}	90.0^{c-k}	14.7^{a-c}	148.7^{a-h}	55.3^{b-h}	124.0^{a-f}	12.3^{b-k}
Sammaz 36 X Sammaz 36	4x4	87^{b-f}	94.3^{b-f}	14.7^{a-c}	152.3^{a-h}	63.3^{a-h}	126.0^{a-f}	17.0^{a-g}
Sammaz 36 X Sammaz 27	4x5	85.7^{b-j}	94.3^{b-f}	14.7^{a-c}	142.0^{a-i}	54.7^{b-h}	125.0^{a-f}	12.7^{b-k}
Sammaz 36 X Sammaz 35	4x6	84.3^{b-n}	88.0^{d-k}	14.0^{a-c}	138.7^{b-i}	65.0^{a-h}	124.3^{a-f}	14.3^{a-i}
Sammaz 36 X Sammaz 29	4x7	84^{b-n}	86.3^{f-k}	14.3^{a-c}	154.0^{a-h}	71.7^{a-f}	126.0^{a-f}	17.3^{a-g}
Sammaz 36 X Sammaz 28	4x8	84.3^{b-n}	90.3^{b-k}	14.0^{a-c}	143.3^{a-i}	58.0^{a-h}	123.0^{a-f}	14.3^{a-i}
Sammaz 27 X Sammaz 19	5x1	80.0^{e-n}	86.3^{f-k}	12.7^{b-d}	127.0^{c-i}	60.0^{a-h}	122.0^{a-f}	13.0^{a-k}
Sammaz 27 X Sammaz 37	5x2	81.0^{d-n}	87.3^{f-k}	13.3^{a-d}	142.3^{a-i}	64.3^{a-h}	120.7^{c-h}	18.7^{a-e}
Sammaz 27 X Sammaz 17	5x3	88.7^{bc}	98.3^{a-c}	14.0^{a-c}	151.3^{a-h}	67.7^{a-h}	130.0^{a}-^{b}	18.3^{a-e}
Sammaz 27 X Sammaz 36	5x4	87.3^{b-e}	94.3^{b-f}	13.3^{a-d}	127.3^{b-i}	58.0^{a-h}	129.0^{a-c}	21.3^{a-c}
Sammaz 27 X Sammaz 27	5x5	82.0^{c-n}	87.3^{f-k}	12.7^{b-d}	137.7^{b-i}	72.7^{a-f}	123.3^{a-f}	21.3^{a-c}
Sammaz 27 X Sammaz 35	5x6	80.7^{d-n}	88.0^{d-k}	15.3^{a}-^{b}	161.7^{a-d}	81.7^{a-c}	112.7^{h}	19.0^{a-d}

Sammaz 27 X Sammaz 29	5x7	83.0^{b-n}	90.3^{b-k}	14.0^{a-c}	133.0^{b-i}	57.0^{b-h}	123.7^{a-f}	17.7^{a-f}
Sammaz 27 X Sammaz 28	5x8	80.0^{e-n}	87.7^{e-k}	13.3^{a-d}	142.7^{a-i}	59.7^{a-h}	123.7^{a-f}	15.7^{a-g}

Table 4.4 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 35 X Sammaz 19	6x1	83.3^{b-n}	91.3^{b-k}	15.3^{a-b}	142.3^{a-i}	62.3^{a-h}	126.0^{a-f}	15.0^{a-h}
Sammaz 35 X Sammaz 37	6x2	84.3^{b-n}	91.0^{b-k}	14.7^{a-c}	159.0^{a-f}	67.3^{a-h}	124.0^{a-f}	18.3^{a-e}
Sammaz 35 X Sammaz 17	6x3	79.7^{f-n}	85.7^{f-k}	12.0^{c-d}	127.3^{b-i}	58.0^{a-h}	124.3^{a-f}	17.7^{a-f}
Sammaz 35 X Sammaz 36	6x4	86^{b-i}	92.7^{b-j}	13.3^{a-d}	126.7^{c-i}	58.0^{a-h}	123.0^{a-f}	22.0^{a-b}
Sammaz 35 X Sammaz 27	6x5	82.3^{c-n}	90.7^{b-k}	12.7^{b-d}	115.3^{g-i}	51.3^{d-h}	122.3^{a-f}	13.0^{a-k}
Sammaz 35 X Sammaz 35	6x6	80.0^{e-n}	87.0^{f-k}	12.0^{c-d}	126.7^{c-i}	48.0^{e-h}	122.0^{a-f}	12.7^{b-k}
Sammaz 35 X Sammaz 29	6x7	82.7^{c-n}	89.7^{c-k}	13.3^{a-d}	125.7^{c-i}	59.0^{a-h}	123.0^{a-f}	19.3^{a-c}
Sammaz 35 X Sammaz 28	6x8	82.3^{c-n}	86.0^{f-k}	14.7^{a-c}	153.0^{a-h}	63.3^{a-h}	123.3^{a-f}	17.7^{a-f}
Sammaz 29 X Sammaz 19	7x1	79.7^{f-n}	87.7^{e-k}	13.3^{a-d}	135.0^{b-i}	68.3^{a-h}	102.7^{i}	16.3^{a-g}
Sammaz 29 X Sammaz 37	7x2	82.0^{c-n}	88.7^{d-k}	12.0^{c-d}	125.0^{c-i}	50.0^{d-h}	120.0^{d-h}	7.3^{f-l}
Sammaz 29 X Sammaz 17	7x3	81.0^{d-n}	87.7^{e-k}	14.0^{a-c}	144.3^{a-i}	67.7^{a-h}	120.3^{c-h}	22.0^{a-b}
Sammaz 29 X Sammaz 36	7x4	85.7^{b-j}	94.0^{b-g}	13.3^{a-d}	124.0^{c-i}	39.7^{h}	123.0^{a-f}	14.3^{a-i}
Sammaz 29 X Sammaz 27	7x5	82.7^{c-n}	90.0^{c-k}	15.3^{a-b}	160.3^{a-e}	78.7^{a-d}	122.7^{a-f}	15.7^{a-g}

Sammaz 29 X Sammaz 35	7x6	80.0^{e-n}	85.0^{h-k}	12.7^{b-d}	128.0^{b-i}	57.7^{b-h}	121.0^{c-h}	16.0^{a-g}
Sammaz 29 X Sammaz 29	7x7	83.0^{b-n}	89.0^{d-k}	12.0^{c-d}	120.0^{d-i}	48.0^{e-h}	126.3^{a-f}	15.3^{a-g}
Sammaz 29 X Sammaz 28	7x8	81.0^{d-n}	86.7^{f-k}	13.3^{a-d}	118.3^{e-i}	53.0^{b-h}	121.3^{b-g}	15.3^{a-g}
Sammaz 28 X Sammaz 19	8x1	81.7^{c-n}	89.3^{d-k}	12.0^{c-d}	132.7^{b-i}	58.0^{a-h}	121.7^{a-f}	14.0^{a-j}
Sammaz 28 X Sammaz 37	8x2	79.3^{g-n}	85.7^{f-k}	12.7^{b-d}	134.3^{b-i}	62.3^{a-h}	121.0^{c-h}	16.7^{a-g}
Sammaz 28 X Sammaz 17	8x3	77.0^{n}	84.7^{j-k}	12.7^{b-d}	127.3^{b-i}	60.0^{a-h}	119.3^{e-h}	15.7^{a-g}
Sammaz 28 X Sammaz 36	8x4	80.7^{d-n}	86.0^{f-k}	12.7^{b-d}	141.0^{a-i}	59.0^{a-h}	113.0^{g-h}	13.0^{a-k}
Sammaz 28 X Sammaz 27	8x5	78.3^{j-n}	85.3^{g-k}	14.0^{a-c}	141.7^{a-i}	66.7^{a-h}	119.7^{e-h}	16.3^{a-g}
Sammaz 28 X Sammaz 35	8x6	77.3^{l-n}	84.7^{j-k}	13.3^{a-d}	133.0^{b-i}	56.0^{b-h}	119.7^{e-h}	18.3^{a-e}
Sammaz 28 X Sammaz 29	8x7	80.0^{e-n}	85.7^{f-k}	13.3^{a-d}	129.0^{b-i}	60.0^{a-h}	121.0^{c-h}	17.7^{a-f}
Sammaz 28 X Sammaz 28	8x8	77.7^{l-n}	84.0^{j-k}	12.0^{c-d}	126.0^{c-i}	58.3^{a-h}	120.7^{c-h}	12.7^{b-k}
Sammaz 11	C1	84.3^{b-n}	90.0^{c-k}	13.3^{a-d}	148.0^{a-h}	69.0^{a-h}	125.7^{a-f}	19.7^{a-c}

Table 4.4 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 16	C2	90.3^{b}	99.0^{a-b}	12.7^{b-d}	138.7^{b-i}	56.0^{b-h}	127.0^{a-e}	14.0^{a-j}
Sammaz 14	C3	85^{bl}	90.3^{b-k}	14.0^{a-c}	154.3^{a-h}	70.0^{a-g}	126.3^{a-f}	11.0^{c-l}
Sammaz 15	C4	90.3^{b}	96.7^{b-d}	14.7^{a-c}	151.3^{a-h}	75.3^{a-f}	126.0^{a-f}	20.3^{a-c}

Sammaz 34	C5	78.0^{k-n}	83.7^{k}	13.3^{a-d}	140.7^{a-i}	53.0^{b-h}	120.7^{c-h}	19.3^{a-c}
Sammaz 20	C6	83.7^{b-n}	90.7^{b-k}	13.3^{a-d}	112.3^{h-i}	41.7^{g-h}	127.0^{a-e}	7.3^{f-l}
Sammaz 18	C7	84.7^{b-m}	92.3^{b-k}	16.0^{a}	169.7^{a}-^{b}	76.7^{a-f}	128.0^{a-e}	8.7^{d-l}
Sammaz 13	C8	88^{b-d}	93.3^{b-i}	13.3^{a-d}	129.0^{b-i}	52.3^{c-h}	120.7^{c-h}	4.0^{j-l}
Sammaz 12	C9	79.3^{g-n}	87.7^{e-k}	13.3^{a-d}	121.7^{d-i}	49.7^{d-h}	125.0^{a-f}	5.0^{h-l}
Mean		83.27	89.84	13.47	138.80	60.93	123.13	15.49
CV %		4.30	4.69	9.83	14.67	23.08	3.45	32.32

KEY: Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot.

Table 4.4 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 19	1	19.0^{a-c}	12.0^{b-f}	29.0^{a-l}	6.3^{b}	1.2^{ab}	1.3^{a-m}	52.7^{d-g}	1907^{b-l}
Sammaz 37	2	17.0^{a-i}	15.3^{a}	35.0^{a-f}	6.9^{b}	1.6^{ab}	1.4^{a-m}	69.2^{a-e}	2373^{a-l}
Sammaz 17	3	13.6^{h-m}	13.3^{a-d}	30.3^{a-l}	6.7^{b}	1.4^{ab}	1.5^{a-m}	70.5^{a-e}	2764^{a-l}
Sammaz 36	4	15.3^{a-m}	12.0^{b-f}	23.3^{c-l}	6.1^{b}	1.1^{ab}	0.2^{m}	57.9^{a-f}	213^{l}
Sammaz 27	5	14.5^{e-m}	14.0^{a-c}	29.3^{a-l}	6.9^{b}	1.2^{ab}	1.5^{a-m}	68.9^{a-e}	2587^{a-l}
Sammaz 35	6	13.2^{i-m}	9.3^{f}	22.7^{d-l}	4.8^{b}	1.3^{ab}	0.2^{lm}	80.9^{a}	418^{kl}
Sammaz 29	7	11.7^{l-m}	10.7^{d-f}	19.7^{j-l}	6.4^{b}	1.3^{ab}	0.6^{h-m}	62.0^{a-f}	1129^{g-l}
Sammaz 28	8	13.7^{h-m}	10.0^{e-f}	21.3^{g-l}	5.8^{b}	1.2^{ab}	1.4^{a-m}	77.5^{a-c}	2933^{a-l}

Sammaz 19 X Sammaz 19	1x1	14.1^{f-m}	12.0^{b-f}	21.0^{h-l}	6.8^{b}	1.1^{ab}	0.5^{i-m}	53.3^{c-g}	676^{j-l}
Sammaz 19 X Sammaz 37	1x2	18.4^{a-e}	14.0^{a-c}	27.3^{a-l}	6.2^{b}	1.1^{ab}	1.1^{c-m}	52.9^{d-g}	1573^{d-l}
Sammaz 19 X Sammaz 17	1x3	17.2^{a-i}	13.3^{a-d}	32.3^{a-k}	6.5^{b}	1.2^{ab}	1.0^{d-m}	58.6^{a-f}	1636^{d-l}
Sammaz 19 X Sammaz 36	1x4	16.8^{a-j}	13.3^{a-d}	28.7^{a-l}	7.0^{b}	1.4^{ab}	1.7^{a-m}	65.3^{a-e}	2853^{a-l}
Sammaz 19 X Sammaz 27	1x5	15.4^{a-m}	14.7$^{a\ b}$	27.7^{a-l}	7.3^{a}	1.2^{ab}	1.7^{a-l}	73.0^{a-e}	3342^{a-k}
Sammaz 19 X Sammaz 35	1x6	18.7^{a-d}	12.7^{a-e}	36.3^{a-c}	6.3^{b}	1.2^{ab}	1.8^{a-k}	65.5^{a-e}	3547^{a-j}
Sammaz 19 X Sammaz 29	1x7	16.5^{a-k}	12.7^{a-e}	28.3^{a-l}	6.2^{b}	1.2^{ab}	1.2^{b-m}	61.3^{a-f}	2178^{b-l}
Sammaz 19 X Sammaz 28	1x8	15.1^{c-m}	12.7^{a-e}	25.3^{b-l}	6.1^{b}	1.2^{ab}	0.9^{e-m}	53.3^{c-g}	1200^{f-l}
Sammaz 37 X Sammaz 19	2x1	16.9^{a-i}	14.0^{a-c}	33.3^{a-i}	6.8^{b}	1.3^{ab}	2.3^{a-f}	70.0^{a-e}	4418^{a-e}
Sammaz 37 X Sammaz 37	2x2	15.7^{a-l}	12.7^{a-e}	34.0^{a-i}	6.9^{b}	1.4^{ab}	1.0^{e-m}	59.5^{a-f}	1449^{e-l}
Sammaz 37 X Sammaz 17	2x3	14.3^{f-m}	13.3^{a-d}	33.0^{a-j}	6.3^{b}	1.5^{ab}	1.6^{a-m}	67.9^{a-e}	2809^{a-l}
Sammaz 37 X Sammaz 36	2x4	16.2^{a-k}	11.3^{c-f}	27.3^{a-l}	6.3^{b}	1.2^{ab}	1.0^{d-m}	61.2^{a-f}	1724^{d-l}
Sammaz 37 X Sammaz 27	2x5	14.2^{f-m}	12.0^{b-f}	29.0^{a-l}	6.7^{b}	1.4^{ab}	1.0^{d-m}	67.0^{a-e}	1858^{b-l}
Sammaz 37 X Sammaz 35	2x6	16.5^{a-k}	11.3^{c-f}	30.0^{a-l}	6.2^{b}	1.3^{ab}	1.0^{e-m}	52.9^{d-g}	1324^{e-l}
Sammaz 37 X Sammaz 29	2x7	17.8^{a-g}	12.7^{a-e}	34.3^{a-h}	6.7^{b}	1.4^{ab}	1.7^{a-l}	67.3^{a-e}	3058^{a-l}
Sammaz 37 X Sammaz 28	2x8	16.0^{a-k}	12.7^{a-e}	27.7^{a-l}	6.1^{b}	1.4^{ab}	1.6^{a-m}	49.7^{e-g}	2036^{b-l}
Sammaz 17 X Sammaz 19	3x1	18.2^{a-f}	13.3^{a-d}	28.3^{a-l}	6.9^{b}	1.4^{ab}	1.9^{a-i}	71.2^{a-e}	3760^{a-j}

Table 4.4 continued

Genotype	Entry	EL	NKR	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 17 X Sammaz 37	3x2	17.2^{a-i}	14.0^{a-c}	21.7^{f-l}	6.4^{b}	1.4^{ab}	1.0^{d-m}	53.3^{c-g}	1493^{e-l}
Sammaz 17 X Sammaz 17	3x3	17.7^{a-h}	13.3^{a-d}	33.0^{a-j}	6.9^{b}	1.4^{ab}	1.6^{a-m}	61.0^{a-f}	2631^{a-l}
Sammaz 17 X Sammaz 36	3x4	17.7^{a-h}	11.3^{c-f}	25.3^{b-l}	6.5^{b}	1.2^{ab}	2.0^{c-m}	53.6^{c-g}	1680^{d-l}
Sammaz 17 X Sammaz 27	3x5	16.5^{a-k}	14.0^{a-c}	34.3^{a-h}	7.2^{b}	1.4^{ab}	2.6^{a-c}	70.0^{a-e}	4836^{a-c}
Sammaz 17 X Sammaz 35	3x6	19.3^{a}-^{b}	14.0^{a-c}	33.7^{a-i}	6.9^{b}	1.4^{ab}	2.5^{a-d}	67.4^{a-e}	4658^{a-d}
Sammaz 17 X Sammaz 29	3x7	17.7^{a-h}	14.0^{a-c}	34.0^{a-i}	6.7^{b}	1.5^{ab}	2.8^{a}	72.8^{a-e}	5316^{a}
Sammaz 17 X Sammaz 28	3x8	17.8^{a-g}	14.0^{a-c}	34.7^{a-g}	6.9^{b}	1.2^{ab}	2.1^{a-h}	66.1^{a-e}	3591^{a-j}
Sammaz 36 X Sammaz 19	4x1	19.3^{a}	14.0^{a-c}	35.3^{a-e}	6.7^{b}	1.4^{ab}	2.7^{ab}	71.6^{a-e}	5262^{a}
Sammaz 36 X Sammaz 37	4x2	17.2^{a-i}	13.3^{a-d}	31.0^{a-k}	6.3^{b}	1.5^{ab}	1.5^{a-m}	63.8^{a-f}	2658^{a-l}
Sammaz 36 X Sammaz 17	4x3	15.8^{a-k}	12.7^{a-e}	26.0^{a-l}	6.4^{b}	1.5^{ab}	0.9^{e-m}	67.9^{a-e}	1636^{d-l}
Sammaz 36 X Sammaz 36	4x4	18.1^{a-f}	12.7^{a-e}	30.7^{a-l}	6.1^{b}	1.2^{ab}	0.8^{f-m}	59.2^{a-f}	1227^{f-l}
Sammaz 36 X Sammaz 27	4x5	16.9^{a-i}	13.3^{a-d}	34.7^{a-g}	6.7^{b}	1.3^{ab}	1.5^{a-m}	65.2^{a-e}	2631^{a-l}
Sammaz 36 X Sammaz 35	4x6	18.8^{a-d}	13.3^{a-d}	39.3^{a}	7.0^{b}	1.5^{ab}	1.9^{a-j}	79.6^{ab}	4293^{a-f}
Sammaz 36 X Sammaz 29	4x7	16.8^{a-i}	127^{a-e}	22.0^{e-l}	6.5^{b}	1.3^{ab}	1.1^{c-m}	52.2^{d-g}	1973^{b-l}
Sammaz 36 X Sammaz 28	4x8	14.9^{c-m}	13.3^{a-d}	26.7^{a-l}	7.2^{b}	1.4^{ab}	1.6^{a-m}	66.6^{a-e}	2791^{a-l}

Sammaz 27 X Sammaz 19	5x1	14.8^{d-m}	13.3^{a-d}	19.7^{j-l}	6.7^{b}	1.1^{ab}	1.2^{b-m}	61.6^{a-f}	2409^{a-l}
Sammaz 27 X Sammaz 37	5x2	15.8^{a-k}	13.3^{a-d}	29.7^{a-l}	6.2^{b}	1.3^{ab}	1.5^{a-m}	59.5^{a-f}	2729^{a-l}
Sammaz 27 X Sammaz 17	5x3	14.2^{f-m}	12.0^{b-f}	29.7^{a-l}	6.6^{b}	1.1^{ab}	1.3^{a-m}	67.7^{a-e}	2418^{a-l}
Sammaz 27 X Sammaz 36	5x4	16.6^{a-k}	12.7^{a-e}	35.3^{a-e}	7.1^{b}	1.4^{ab}	1.8^{a-k}	76.3^{a-d}	3476^{a-k}
Sammaz 27 X Sammaz 27	5x5	14.5^{e-m}	14.0^{a-c}	33.0^{a-j}	7.2^{b}	1.1^{ab}	2.0^{a-h}	66.9^{a-e}	3431^{a-k}
Sammaz 27 X Sammaz 35	5x6	17.1^{a-i}	12.7^{a-e}	34.7^{a-g}	7.2^{b}	1.4^{ab}	2.4^{a-e}	76.4^{a-d}	4942^{ab}
Sammaz 27 X Sammaz 29	5x7	15.0^{a-l}	12.7^{a-e}	29.7^{a-l}	6.9^{b}	1.3^{ab}	1.5^{a-m}	65.7^{a-e}	2604^{a-l}
Sammaz 27 X Sammaz 28	5x8	16.5^{a-k}	14.0^{a-c}	34.3^{a-h}	7.1^{b}	1.5^{ab}	2.0^{a-i}	68.3^{a-e}	3609^{a-j}
Sammaz 35 X Sammaz 19	6x1	15.3^{a-m}	12.7^{a-e}	32.0^{a-k}	6.4^{b}	1.1^{ab}	1.0^{d-m}	70.1^{a-e}	1778^{c-l}
Sammaz 35 X Sammaz 37	6x2	16.3^{a-k}	14.0^{a-c}	26.0^{a-l}	6.1^{b}	1.6^{ab}	2.1^{a-h}	63.8^{a-f}	4089^{a-i}

Table 4.4 continued

Genotype	Entry	EL	NKR	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 35 X Sammaz 17	6x3	18.4^{a-e}	12.7^{a-e}	35.7^{a-d}	6.8^{b}	1.2^{ab}	2.0^{a-i}	76.1^{a-d}	4089^{a-i}
Sammaz 35 X Sammaz 36	6x4	17.7^{a-h}	12.7^{a-e}	34.7^{a-g}	6.7^{b}	1.6^{a}	2.0^{a-i}	75.3^{a-d}	3920^{a-i}
Sammaz 35 X Sammaz 27	6x5	14.5^{e-m}	14.7^{a-b}	26.3^{a-l}	6.4^{b}	1.4^{ab}	1.1^{c-m}	63.4^{a-f}	1707^{d-l}
Sammaz 35 X Sammaz 35	6x6	15.7^{a-l}	12.7^{a-e}	30.7^{a-l}	6.7^{b}	1.2^{ab}	1.5^{a-m}	62.2^{a-f}	2240^{a-l}
Sammaz 35 X Sammaz 29	6x7	18.4^{a-e}	14.0^{a-c}	33.0^{a-j}	6.2^{b}	1.4^{ab}	1.8^{a-k}	66.0^{a-e}	3351^{a-k}

Sammaz 35 X Sammaz 28	6x8	16.8^{a-j}	13.3^{a-d}	37.7^{a_b}	6.5^{b}	1.2^{ab}	1.7^{a-k}	69.8^{a-e}	3316^{a-k}
Sammaz 29 X Sammaz 19	7x1	14.4^{e-m}	14.0^{a-c}	33.0^{a-j}	6.8^{b}	1.2^{ab}	2.3^{a-f}	74.7^{a-d}	4596^{a-d}
Sammaz 29 X Sammaz 37	7x2	13.8^{g-m}	14.0^{a-c}	19.0^{k-l}	6.5^{b}	1.3^{ab}	0.3^{k-m}	34.0^{g}	1111^{h-l}
Sammaz 29 X Sammaz 17	7x3	16.3^{a-k}	13.3^{a-d}	34.0^{a-i}	7.2^{b}	1.4^{ab}	2.3^{a-g}	69.5^{a-e}	4222^{a-g}
Sammaz 29 X Sammaz 36	7x4	12.5^{k-m}	12.0^{b-f}	22.7^{d-l}	6.2^{b}	1.3^{ab}	1.2^{c-m}	58.4^{a-f}	1822^{c-l}
Sammaz 29 X Sammaz 27	7x5	17.4^{a-h}	12.7^{a-e}	36.0^{a-d}	6.9^{b}	1.3^{ab}	2.0^{a-h}	72.6^{a-e}	3947^{a-i}
Sammaz 29 X Sammaz 35	7x6	15.4^{a-l}	12.7^{a-e}	26.7^{a-l}	6.3^{b}	1.2^{ab}	1.4^{a-m}	70.8^{a-e}	2791^{a-l}
Sammaz 29 X Sammaz 29	7x7	16.3^{a-k}	12.0^{b-f}	29.7^{a-l}	6.6^{b}	1.1^{ab}	0.9^{e-m}	65.1^{a-e}	1582^{d-l}
Sammaz 29 X Sammaz 28	7x8	13.7^{h-m}	12.7^{a-e}	26.3^{a-l}	6.4^{b}	1.4^{ab}	1.4^{a-m}	71.$^{a-e}$	2711^{a-l}
Sammaz 28 X Sammaz 19	8x1	16.2^{a-k}	13.3^{a-d}	28.0^{a-l}	6.6^{b}	1.4^{ab}	1.5^{a-m}	64.5^{a-e}	2622^{a-l}
Sammaz 28 X Sammaz 37	8x2	15.2^{a-m}	11.3^{c-f}	27.7^{a-l}	6.9^{b}	1.5^{ab}	1.6^{a-m}	64.2^{a-e}	2791^{a-l}
Sammaz 28 X Sammaz 17	8x3	17.4^{a-h}	13.3^{a-d}	29.3^{a-l}	6.6^{b}	1.2^{ab}	1.5^{a-m}	64.6^{a-e}	2756^{a-l}
Sammaz 28 X Sammaz 36	8x4	15.2^{b-m}	14.0^{a-c}	28.3^{a-l}	6.8^{b}	1.2^{ab}	0.7^{h-m}	66.6^{a-e}	1671^{d-l}
Sammaz 28 X Sammaz 27	8x5	15.9^{a-k}	13.3^{a-d}	24.0^{c-l}	6.4^{b}	1.3^{ab}	1.3^{a-m}	64.6^{a-e}	2293^{a-l}
Sammaz 28 X Sammaz 35	8x6	16.4^{a-k}	14.0^{a-c}	28.7^{a-l}	5.9^{b}	1.3^{ab}	1.3^{a-m}	69.0^{a-e}	2409^{a-l}
Sammaz 28 X Sammaz 29	8x7	16.7^{a-j}	13.3^{a-d}	31.0^{a-k}	6.4^{b}	1.4^{ab}	1.8^{a-k}	71.9^{a-e}	3333^{a-k}
Sammaz 28 X Sammaz 28	8x8	17.7^{a-h}	13.3^{a-d}	24.7^{b-l}	6.3^{b}	1.3^{ab}	1.2^{b-m}	62.9^{a-f}	1938^{b-l}

Sammaz 11	C1	17.3^{a-h}	14.7^{a-b}	36.7^{a-c}	7.0^{b}	1.4^{ab}	2.0^{a-i}	67.0^{a-e}	3440^{a-k}
Sammaz 16	C2	14.3^{e-m}	14.7^{a-b}	24.7^{b-l}	6.6^{b}	1.1^{ab}	0.7^{g-m}	57.8^{a-f}	1067^{i-l}
Sammaz 14	C3	17.8^{a-g}	12.7^{a-e}	31.3^{a-k}	6.7^{b}	1.2^{ab}	0.9^{e-m}	63.8^{a-f}	1324^{e-l}

Table 4.4 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 15	C4	16.2^{a-k}	14.0^{a-c}	29.3^{a-l}	6.8^{b}	1.2^{ab}	0.9^{e-m}	56.2^{b-g}	1378^{e-l}
Sammaz 34	C5	17.5^{a-h}	14.7^{a-b}	32.3^{a-k}	6.7^{b}	1.3^{ab}	2.1^{a-h}	72.9^{a-e}	4169^{a-h}
Sammaz 20	C6	12.7^{j-m}	12.0^{b-f}	20.7^{i-l}	6.3^{b}	1.2^{ab}	0.6^{h-m}	40.3^{fg}	444^{kl}
Sammaz 18	C7	18.7^{a-d}	13.3^{a-d}	29.7^{a-l}	6.4^{b}	1.2^{ab}	0.8^{f-m}	65.7^{a-e}	1698^{d-l}
Sammaz 13	C8	11.3^{m}	10.7^{d-f}	17.5^{l}	6.4^{b}	1.0^{b}	0.3^{k-m}	12.4^{h}	764^{j-l}
Sammaz 12	C9	14.3^{e-m}	12.7^{a-e}	26.3^{a-l}	6.1^{b}	1.2^{ab}	0.4^{j-m}	61.9^{a-f}	702^{j-l}
Mean		16.12	13.03	29.34	6.73	1.30	1.42	70.90	2572.22
CV %		12.34	12.09	21.91	43.41	21.01	51.66	94.96	57.50

KEY: EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4.5 Mean performance of parents, crosses, reciprocals, selfs and checks for fifteen agronomic characters in environment two

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 19	1	66.0^{a-c}	72.3^{a-c}	12.0^{a-d}	134.7^{a-g}	51.7^{b-h}	92.3^{a-c}	12.0^{a-k}
Sammaz 37	2	69.7^{a-c}	75.3^{a-c}	10.7^{a-d}	135.0^{a-g}	51.7^{b-h}	95.7^{a-c}	7.7^{e-k}
Sammaz 17	3	67.0^{a-c}	74.3^{a-c}	11.3^{a-d}	96.0^{c-h}	33.0^{gh}	94.3^{a-c}	7.3^{e-k}
Sammaz 36	4	72.0^{a-c}	79.0^{a-c}	11.3^{a-d}	119.7^{a-h}	50.0^{b-h}	99.7^{a-c}	13.3^{a-k}
Sammaz 27	5	72.7^{a-c}	78.7^{a-c}	12.0^{a-d}	140.0^{a-d}	53.7^{b-h}	99.7^{a-c}	12.0^{a-k}
Sammaz 35	6	68.7^{a-c}	75.3^{a-c}	12.7^{a-c}	154.3^{ab}	66.3^{a-d}	94.7^{a-c}	19.3^{a-e}
Sammaz 29	7	64.3^{a-c}	71.3^{a-c}	10.0^{a-d}	102.7^{b-h}	42.7^{c-h}	95.3^{a-c}	13.7^{a-k}
Sammaz 28	8	64.3^{a-c}	71.0^{a-c}	10.0^{a-d}	107.0^{a-h}	44.0^{b-h}	95.7^{a-c}	9.3^{b-k}
Sammaz 19 X Sammaz 19	1x1	65.0^{a-c}	72.0^{a-c}	12.7^{a-c}	126.7^{a-g}	61.0^{b-f}	92.0^{a-c}	16.0^{a-i}
Sammaz 19 X Sammaz 37	1x2	66.7^{a-c}	73.7^{a-c}	11.3^{a-d}	123.0^{a-h}	55.0^{b-g}	96.7^{a-c}	15.0^{a-j}
Sammaz 19 X Sammaz 17	1x3	65.7^{a-c}	76.3^{a-c}	13.3^{ab}	129.0^{a-g}	50.7^{b-h}	92.7^{a-c}	8.3^{d-k}
Sammaz 19 X Sammaz 36	1x4	71.0^{a-c}	76.7^{a-c}	11.3^{a-d}	106.3^{a-h}	43.3^{c-h}	95.0^{a-c}	4.0^{i-k}
Sammaz 19 X Sammaz 27	1x5	61.7^{c}	68.3^{bc}	12.7^{a-c}	117.3^{a-h}	46.0^{b-h}	87.7^{c}	17.0^{a-h}
Sammaz 19 X Sammaz 35	1x6	70.3^{a-c}	77.0^{a-c}	12.0^{a-d}	116.7^{a-h}	47.3^{h}-^{h}	98.3^{a-c}	6.7^{f-k}

Sammaz 19 X Sammaz 29	1x7	66.0^{a-c}	72.3^{a-c}	10.7^{a-d}	135.0^{a-g}	50.0^{b-h}	90.7^{a-c}	14.0^{a-k}
Sammaz 19 X Sammaz 28	1x8	70.7^{a-c}	76.7^{a-c}	10.0^{a-d}	109.7^{a-h}	46.0^{b-h}	98.0^{a-c}	6.0^{g-k}
Sammaz 37 X Sammaz 19	2x1	68.0^{a-c}	76.0^{a-c}	9.3^{b-d}	118.7^{a-h}	51.7^{b-h}	96.3^{a-c}	9.7^{a-k}
Sammaz 37 X Sammaz 37	2x2	69.3^{a-c}	75.7^{a-c}	13.3^{ab}	105.0^{a-h}	53.0^{b-h}	93.3^{a-c}	13.7^{a-k}
Sammaz 37 X Sammaz 17	2x3	65.7^{a-c}	73.3^{a-c}	12.7^{a-c}	125.0^{a-h}	48.3^{b-h}	93.7^{a-c}	9.7^{a-k}
Sammaz 37 X Sammaz 36	2x4	71.7^{a-c}	79.0^{a-c}	12.0^{a-d}	121.7^{a-h}	44.0^{b-h}	98.7^{a-c}	8.3^{d-k}
Sammaz 37 X Sammaz 27	2x5	70.3^{a-c}	77.0^{a-c}	10.7^{a-d}	105.0^{a-h}	51.0^{b-h}	98.0^{a-c}	12.0^{a-k}
Sammaz 37 X Sammaz 35	2x6	70.0^{a-c}	76.7^{a-c}	10.7^{a-d}	118.3^{a-h}	45.0^{b-h}	94.3^{a-c}	8.7^{c-k}
Sammaz 37 X Sammaz 29	2x7	67.0^{a-c}	73.7^{a-c}	10.7^{a-d}	102.3^{b-h}	39.3^{d-h}	93.7^{a-c}	11.3^{a-k}
Sammaz 37 X Sammaz 28	2x8	69.3^{a-c}	77.0^{a-c}	11.3^{a-d}	120.7^{a-h}	49.0^{b-h}	96.0^{a-c}	17.3^{a-h}

Table 4.5 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 17 X Sammaz 19	3x1	66.0^{a-c}	76.0^{a-c}	11.3^{a-d}	98.0^{c-h}	40.0^{d-h}	93.0^{a-c}	9.7^{a-k}
Sammaz 17 X Sammaz 37	3x2	67.3^{a-c}	74.0^{a-c}	12.0^{a-d}	130.7^{a-g}	49.0^{b-h}	92.3^{a-c}	10.0^{a-k}
Sammaz 17 X Sammaz 17	3x3	69.0^{a-c}	76.3^{a-c}	10.7^{a-d}	93.3^{d-h}	47.0^{b-h}	94.7^{a-c}	7.3^{e-k}
Sammaz 17 X Sammaz 36	3x4	67.3^{a-c}	72.7^{a-c}	10.3^{a-d}	98.0^{c-h}	48.3^{b-h}	95.0^{a-c}	7.7^{e-k}
Sammaz 17 X Sammaz 27	3x5	73.0^{ab}	81.3^{a}	12.7^{a-c}	96.0^{c-h}	55.0^{b-g}	100.7^{a-c}	13.3^{a-k}

Sammaz 17 X Sammaz 35	3x6	67.7^{a-c}	75.7^{a-c}	11.3^{a-d}	118.0^{a-h}	52.0^{b-h}	96.7^{a-c}	11.0^{a-k}
Sammaz 17 X Sammaz 29	3x7	72.0^{a-c}	78.0^{a-c}	10.0^{a-d}	109.7^{a-h}	51.7^{b-h}	97.7^{a-c}	2.667^{k}
Sammaz 17 X Sammaz 28	3x8	68.7^{a-c}	75.3^{a-c}	11.3^{a-d}	135.0^{a-g}	44.0^{b-h}	97.0^{a-c}	12.7^{a-k}
Sammaz 36 X Sammaz 19	4x1	69.3^{a-c}	76.3^{a-c}	10.7^{a-d}	129.7^{a-g}	53.3^{b-h}	96.0^{a-c}	9.3^{b-k}
Sammaz 36 X Sammaz 37	4x2	67.7^{a-c}	72.0^{a-c}	12.7^{a-c}	141.0^{a-d}	55.0^{b-g}	94.3^{a-c}	15.0^{a-j}
Sammaz 36 X Sammaz 17	4x3	63.0^{bc}	69.7^{a-c}	12.7^{a-c}	138.3^{a-e}	52.7^{b-h}	89.3^{a-c}	18.0^{a-g}
Sammaz 36 X Sammaz 36	4x4	67.0^{a-c}	73.3^{a-c}	10.0^{a-d}	110.0^{a-h}	41.7^{c-h}	94.0^{a-c}	9.7^{a-k}
Sammaz 36 X Sammaz 27	4x5	69.3^{a-c}	75.3^{a-c}	11.3^{a-d}	110.0^{a-h}	53.7^{b-h}	92.7^{a-c}	9.0^{b-k}
Sammaz 36 X Sammaz 35	4x6	72.7^{a-c}	78.7^{a-c}	9.7^{b-d}	116.3^{a-h}	45.0^{b-h}	103.0^{a}	4.3^{i-k}
Sammaz 36 X Sammaz 29	4x7	61.7^{c}	68.0^{c}	9.3^{b-d}	117.3^{a-h}	38.3^{e-h}	88.3^{bc}	14.0^{a-k}
Sammaz 36 X Sammaz 28	4x8	72.3^{a-c}	78.7^{a-c}	12.0^{a-d}	113.3^{a-h}	48.0^{b-h}	98.0^{a-c}	10.7^{a-k}
Sammaz 27 X Sammaz 19	5x1	72.0^{a-c}	78.7^{a-c}	13.3^{ab}	133.3^{a-g}	62.0^{b-f}	95.3^{a-c}	20.0^{a-d}
Sammaz 27 X Sammaz 37	5x2	65.3^{a-c}	71.3^{a-c}	12.0^{a-d}	131.7^{a-g}	48.0^{b-h}	91.0^{a-c}	8.7^{c-k}
Sammaz 27 X Sammaz 17	5x3	61.7^{c}	68.0^{c}	10.7^{a-d}	114.7^{a-h}	46.7^{b-h}	90.0^{a-c}	6.0^{g-k}
Sammaz 27 X Sammaz 36	5x4	69.7^{a-c}	77.0^{a-c}	12.7^{a-c}	124.0^{a-h}	53.7^{b-h}	94.3^{a-c}	13.0^{a-k}
Sammaz 27 X Sammaz 27	5x5	67.3^{a-c}	73.7^{a-c}	13.3^{ab}	113.7^{a-h}	51.7^{b-h}	91.0^{a-c}	13.0^{a-k}
Sammaz 27 X Sammaz 35	5x6	69.0^{a-c}	76.0^{a-c}	10.7^{a-d}	133.0^{a-g}	62.0^{b-f}	96.3^{a-c}	15.0^{a-j}

Sammaz 27 X Sammaz 29	5x7	71.7^{a-c}	77.7^{a-c}	13.3^{ab}	158.0^{a}	90.0^{a}	96.7^{a-c}	17.0^{a-h}
Sammaz 27 X Sammaz 28	5x8	68.7^{a-c}	75.3^{a-c}	10.7^{a-d}	130.0^{a-g}	59.0^{b-g}	96.7^{a-c}	21.7^{a}
Sammaz 35 X Sammaz 19	6x1	72.0^{a-c}	78.7^{a-c}	13.3^{ab}	129.3^{a-g}	68.3^{a-c}	92.3^{a-c}	7.3^{e-k}

Table 4.5 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 35 X Sammaz 37	6x2	65.7^{a-c}	72.0^{a-c}	11.3^{a-d}	105.0^{a-h}	46.0^{b-h}	94.3^{a-c}	13.3^{a-k}
Sammaz 35 X Sammaz 17	6x3	65.7^{a-c}	72.0^{a-c}	10.7^{a-d}	140.0^{a-d}	71.7^{ab}	93.0^{a-c}	13.3^{a-k}
Sammaz 35 X Sammaz 36	6x4	72.0^{a-c}	78.7^{a-c}	9.3^{b-d}	115.3^{a-h}	39.3^{d-h}	98.7^{a-c}	7.7^{e-k}
Sammaz 35 X Sammaz 27	6x5	71.0^{a-c}	76.7^{a-c}	10.7^{a-d}	139.7^{a-e}	26.3^{h}	99.0^{a-c}	11.3^{a-k}
Sammaz 35 X Sammaz 35	6x6	71.7^{a-c}	79.0^{a-c}	8.0^{d}	90.0^{d-h}	40.3^{d-h}	98.3^{a-c}	3.3^{jk}
Sammaz 35 X Sammaz 29	6x7	72.0^{a-c}	78.7^{a-c}	12.0^{a-d}	116.0^{a-h}	50.3^{b-h}	100.0^{a-c}	10.0^{a-k}
Sammaz 35 X Sammaz 28	6x8	68.3^{a-c}	75.3^{a-c}	11.3^{a-d}	111.3^{a-h}	48.3^{b-h}	92.3^{a-c}	10.0^{a-k}
Sammaz 29 X Sammaz 19	7x1	70.3^{a-c}	77.7^{a-c}	11.7^{a-d}	81.7^{f-h}	43.0^{c-h}	97.3^{a-c}	10.0^{a-k}
Sammaz 29 X Sammaz 37	7x2	74.7^{a}	81.3^{a}	13.3^{ab}	133.3^{a-g}	62.3^{b-f}	98.3^{a-c}	11.7^{a-k}
Sammaz 29 X Sammaz 17	7x3	69.3^{a-c}	79.7^{a-c}	12.0^{a-d}	121.3^{a-h}	41.7^{c-h}	97.0^{a-c}	13.3^{a-k}
Sammaz 29 X Sammaz 36	7x4	71.3^{a-c}	77.7^{a-c}	12.7^{a-c}	124.3^{a-h}	47.7^{b-h}	90.7^{a-c}	9.3^{b-k}
Sammaz 29 X Sammaz 27	7x5	68.3^{a-c}	74.3^{a-c}	13.3^{ab}	149.7^{a-c}	62.0^{b-f}	94.0^{a-c}	18.0^{a-g}

Sammaz 29 X Sammaz 35	7x6	70.0^{a-c}	76.3^{a-c}	9.3^{b-d}	71.7^{h}	36.7^{e-h}	94.7^{a-c}	4.0^{i-k}
Sammaz 29 X Sammaz 29	7x7	65.0^{a-c}	71.7^{a-c}	12.7^{a-c}	133.3^{a-g}	63.3^{b-e}	100.0^{a-c}	10.3^{a-k}
Sammaz 29 X Sammaz 28	7x8	65.7^{a-c}	72.0^{a-c}	12.0^{a-d}	135.0^{a-g}	49.7^{b-h}	90.3^{a-c}	12.7^{a-k}
Sammaz 28 X Sammaz 19	8x1	66.3^{a-c}	73.3^{a-c}	12.7^{a-c}	110.0^{a-h}	48.3^{b-h}	95.0^{a-c}	12.3^{a-k}
Sammaz 28 X Sammaz 37	8x2	65.0^{a-c}	69.3^{a-c}	12.7^{a-c}	126.3^{a-h}	52.3^{b-h}	91.0^{a-c}	12.7^{a-k}
Sammaz 28 X Sammaz 17	8x3	71.3^{a-c}	79.0^{a-c}	10.7^{a-d}	84.7^{e-h}	43.3^{c-h}	96.7^{a-c}	4.7^{i-k}
Sammaz 28 X Sammaz 36	8x4	70.3^{a-c}	77.0^{a-c}	11.3^{a-d}	98.3^{c-h}	34.7^{f-h}	95.0^{a-c}	6.7^{f-k}
Sammaz 28 X Sammaz 27	8x5	73.0^{ab}	79.0^{a-c}	13.3^{ab}	142.7^{a-d}	50.3^{b-h}	96.7^{a-c}	17.7^{a-g}
Sammaz 28 X Sammaz 35	8x6	66.0^{a-c}	72.7^{a-c}	11.3^{a-d}	110.7^{a-h}	44.7^{b-h}	101.7^{ab}	9.3^{b-k}
Sammaz 28 X Sammaz 29	8x7	66.3^{a-c}	73.0^{a-c}	10.7^{a-d}	120.7^{a-h}	53.0^{b-h}	95.3^{a-c}	13.3^{a-k}
Sammaz 28 X Sammaz 28	8x8	68.7^{a-c}	75.0^{a-c}	9.3^{b-d}	102.7^{b-h}	44.7^{b-h}	92.3^{a-c}	5.3^{h-k}
Sammaz 11	C1	71.7^{a-c}	78.3^{a-c}	11.3^{a-d}	136.7^{a-f}	52.0^{b-h}	92.3^{a-c}	11.0^{a-k}
Sammaz 16	C2	64.7^{a-c}	71.3^{a-c}	14.0^{a}	143.3^{a-c}	53.3^{b-h}	90.7^{a-c}	20.7^{a-c}

Table 4.5 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 14	C3	72.3^{a-c}	80.3^{ab}	12.0^{a-d}	140.0^{a-d}	58.3^{b-g}	99.0^{a-c}	18.7^{a-f}
Sammaz 15	C4	72.3^{a-c}	79.7^{a-c}	13.3^{ab}	129.7^{a-g}	68.3^{a-c}	98.3^{a-c}	21.0^{ab}

Sammaz 34	C5	67.7^{a-c}	75.3^{a-c}	8.7^{cd}	80.0^{gh}	35.3^{f-h}	96.7^{a-c}	3.7^{jk}
Sammaz 20	C6	71.0^{a-c}	77.3^{a-c}	12.0^{a-d}	100.0^{b-h}	44.0^{b-h}	97.7^{a-c}	8.0^{d-k}
Sammaz 18	C7	68.0^{a-c}	74.3^{a-c}	10.0^{a-d}	101.7^{b-h}	33.0^{gh}	93.7^{a-c}	7.7^{e-k}
Sammaz 13	C8	71.0^{a-c}	77.3^{a-c}	11.3^{a-d}	113.3^{a-h}	46.0^{b-h}	97.7^{a-c}	13.3^{a-k}
Sammaz 12	C9	70.3^{a-c}	76.3^{a-c}	10.0^{a-d}	105.3^{a-h}	41.3^{c-h}	92.7^{a-c}	8.7^{c-k}
Mean		68.66	75.41	11.45	118.59	49.65	95.17	11.25
CV %		7.80	7.61	17.82	22.26	26.87	6.87	52.23

KEY: Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot.

Table 4.5 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 19	1	13.7^{b}	12.0^{a-e}	21.0^{b-k}	5.7^{b}	1.3^{b-f}	0.3^{d-g}	69.3^{a-n}	613.3^{e-j}
Sammaz 37	2	5.3^{b}	11.3^{b-f}	9.7^{jk}	5.1^{b}	1.1^{e-f}	0.1^{g}	64.3^{c-n}	240.0^{j}
Sammaz 17	3	9.0^{b}	10.0^{d-g}	17.7^{b-k}	5.4^{b}	1.7^{a-d}	0.3^{e-g}	75.0^{a-n}	497.8^{g-j}
Sammaz 36	4	12.8^{b}	12.7^{a-e}	22.0^{b-k}	8.0^{b}	1.7^{a-c}	0.6^{b-g}	66.2^{b-n}	1102.2^{a-j}
Sammaz 27	5	16.0^{b}	11.3^{b-f}	26.3^{a-g}	6.3^{b}	1.6^{a-d}	0.2^{e-g}	68.9^{a-n}	417.8^{g-j}
Sammaz 35	6	19.0^{b}	16.0^{a}	30.0^{a-e}	7.1^{b}	1.6^{a-d}	1.0^{a-g}	86.6^{a-f}	2248.9^{a-i}
Sammaz 29	7	12.2^{b}	12.0^{a-e}	17.7^{b-k}	6.5^{b}	1.5^{a-d}	0.6^{b-g}	82.5^{a-j}	1333.3^{a-j}
Sammaz 28	8	11.2^{b}	12.0^{a-e}	20.3^{b-k}	6.3^{b}	1.6^{a-d}	0.3^{c-g}	73.4^{a-n}	551.1^{e-j}
Sammaz 19 X Sammaz 19	1x1	14.2^{b}	14.0^{a-d}	26.3^{a-g}	6.3^{b}	1.7^{a-c}	0.6^{b-g}	78.6^{a-m}	1235.6^{a-j}
Sammaz 19 X Sammaz 37	1x2	12.2^{b}	12.7^{a-e}	25.0^{a-i}	5.5^{b}	1.2^{d-f}	0.8^{a-g}	83.1^{a-i}	1600.0^{a-j}
Sammaz 19 X Sammaz 17	1x3	13.7^{b}	10.0^{d-g}	29.3^{a-f}	6.4^{b}	1.5^{a-f}	0.5^{c-g}	88.5^{a-c}	1137.8^{a-j}
Sammaz 19 X Sammaz 36	1x4	14.5^{b}	14.0^{a-d}	17.3^{c-k}	6.3^{b}	1.6^{a-d}	0.3^{d-g}	60.6^{h-n}	426.7^{g-j}
Sammaz 19 X Sammaz 27	1x5	14.6^{b}	11.3^{b-f}	26.0^{a-g}	7.9^{b}	1.6^{a-d}	1.5267^{a}	77.9^{a-m}	3048.9^{a}
Sammaz 19 X Sammaz 35	1x6	9.8^{b}	14.0^{a-d}	16.7^{d-k}	6.1^{b}	1.5^{a-f}	0.2^{g}	61.9^{g-n}	231.1^{j}
Sammaz 19 X Sammaz 29	1x7	12.3^{b}	11.3^{b-f}	22.0^{b-k}	6.6^{b}	1.4^{a-f}	0.4^{c-g}	69.4^{a-n}	728.9^{e-j}

Sammaz 19 X Sammaz 28	1x8	14.7^{b}	13.3^{a-e}	30.7^{a-d}	7.4^{b}	1.3^{b-f}	0.2^{fg}	54.6^{mn}	862.2^{e-j}
Sammaz 37 X Sammaz 19	2x1	12.0^{b}	12.7^{a-e}	19.7^{b-k}	5.9^{b}	1.3^{c-f}	0.2^{fg}	71.5^{a-n}	328.9^{h-j}
Sammaz 37 X Sammaz 37	2x2	12.8^{b}	12.7^{a-e}	24.7^{a-i}	6.7^{b}	1.4^{a-f}	0.4^{c-g}	63.7^{d-n}	693.3^{e-j}
Sammaz 37 X Sammaz 17	2x3	14.2^{b}	12.0^{a-e}	28.3^{a-f}	7.2^{b}	1.5^{a-e}	0.9^{a-g}	76.1^{a-m}	1715.6^{a-j}
Sammaz 37 X Sammaz 36	2x4	11.8^{b}	12.0^{a-e}	21.0^{b-k}	5.2^{b}	1.4^{a-f}	0.5^{c-g}	72.2^{a-n}	675.6^{e-j}
Sammaz 37 X Sammaz 27	2x5	13.0^{b}	10.7^{c-g}	29.7^{a-e}	6.0^{b}	1.4^{b-f}	0.8^{a-g}	84.3^{a-h}	1857.8^{a-j}
Sammaz 37 X Sammaz 35	2x6	11.5^{b}	12.0^{a-e}	22.0^{b-k}	6.1^{b}	1.3^{b-f}	0.9^{a-g}	73.7^{a-n}	1680.0^{a-j}

Table 4.5 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 37 X Sammaz 29	2x7	10.7^{b}	11.3^{b-f}	16.3^{e-k}	5.9^{b}	1.4^{a-f}	0.9^{a-g}	74.3^{a-n}	2968.9^{a-c}
Sammaz 37 X Sammaz 28	2x8	13.6^{b}	11.3^{b-f}	19.7^{b-k}	6.4^{b}	1.3^{b-f}	0.9^{a-g}	81.5^{a-j}	1991.1^{a-j}
Sammaz 17 X Sammaz 19	3x1	12.7^{b}	12.7^{a-e}	21.3^{b-k}	6.1^{b}	1.4^{a-f}	0.5^{c-g}	81.2^{a-k}	1128.9^{a-j}
Sammaz 17 X Sammaz 37	3x2	13.4^{b}	11.3^{b-f}	15.3^{f-k}	6.4^{b}	1.7^{a-c}	1.1^{a-e}	67.7^{b-n}	1911.1^{a-j}
Sammaz 17 X Sammaz 17	3x3	13.0^{b}	10.7^{c-g}	21.0^{b-k}	6.3^{b}	1.5^{a-e}	0.2^{e-g}	71.5^{a-n}	453.3^{g-j}
Sammaz 17 X Sammaz 36	3x4	12.2^{b}	10.0^{d-g}	21.0^{b-k}	6.1^{b}	1.3^{b-f}	0.5^{c-g}	84.3^{a-h}	1022.2^{b-j}
Sammaz 17 X Sammaz 27	3x5	12.8^{b}	12.7^{a-e}	30.0^{a-e}	7.4^{b}	1.6^{a-d}	0.5^{c-g}	78.0^{a-m}	951.1^{e-j}
Sammaz 17 X Sammaz 35	3x6	12.8^{b}	12.0^{a-e}	21.7^{b-k}	6.0^{b}	1.4^{a-f}	0.4^{c-g}	81.1^{a-k}	782.2^{e-j}

Sammaz 17 X Sammaz 29	3x7	6.3^{b}	10.7^{c-g}	11.7^{h-k}	3.7^{b}	1.1^{f}	0.2^{e-g}	75.4^{a-n}	462.2^{g-j}
Sammaz 17 X Sammaz 28	3x8	13.5^{b}	9.0^{e-g}	25.3^{a-h}	6.9^{b}	1.6^{a-d}	0.4^{c-g}	72.8^{a-n}	844.4^{e-j}
Sammaz 36 X Sammaz 19	4x1	14.7^{b}	12.0^{a-e}	24.3^{a-i}	6.2^{b}	1.5^{a-f}	0.4^{c-g}	85.3^{a-g}	942.2^{e-j}
Sammaz 36 X Sammaz 37	4x2	13.8^{b}	12.0^{a-e}	29.0^{a-f}	6.9^{b}	1.5^{a-e}	0.3^{c-g}	88.2^{a-c}	791.1^{e-j}
Sammaz 36 X Sammaz 17	4x3	15.2^{b}	12.0^{a-e}	26.3^{a-g}	7.3^{b}	1.7^{a-c}	0.6-^{g}	84.4^{a-h}	1200.0^{a-j}
Sammaz 36 X Sammaz 36	4x4	15.0^{b}	13.3^{a-e}	21.7^{b-k}	20.1^{a}	1.6^{a-c}	0.3^{c-g}	59.6^{i-n}	382.2^{h-j}
Sammaz 36 X Sammaz 27	4x5	13.3^{b}	12.0^{a-e}	23.0^{a-j}	5.8^{b}	1.5^{a-f}	0.5^{c-g}	77.8^{a-m}	995.6^{d-j}
Sammaz 36 X Sammaz 35	4x6	11.0^{b}	12.7^{a-e}	15.3^{f-k}	4.7^{b}	1.5^{a-f}	0.1^{g}	92.5^{a}	328.9^{h-j}
Sammaz 36 X Sammaz 29	4x7	14.1^{b}	10.0^{d-g}	22.0^{b-k}	5.6^{b}	1.5^{a-f}	1.2^{a-d}	92.3^{a}	2977.8^{ab}
Sammaz 36 X Sammaz 28	4x8	11.5^{b}	14.0^{a-d}	21.3^{b-k}	5.7^{b}	1.4^{a-f}	0.6^{a-g}	80.1^{a-l}	1297.8^{a-j}
Sammaz 27 X Sammaz 19	5x1	15.0^{b}	11.3^{b-f}	27.0^{a-g}	6.3^{b}	1.4^{a-f}	0.7^{a-g}	74.8^{a-n}	1315.6^{a-j}
Sammaz 27 X Sammaz 37	5x2	13.8^{b}	11.3^{b-f}	27.7^{a-g}	7.1^{b}	1.6^{a-d}	1.4^{ab}	77.4^{a-m}	2933.3^{a-d}
Sammaz 27 X Sammaz 17	5x3	14.1^{b}	12.7^{a-e}	22.7^{a-j}	6.0^{b}	1.5^{a-d}	0.4^{c-g}	79.4^{a-l}	915.6^{e-j}
Sammaz 27 X Sammaz 36	5x4	14.1^{b}	13.3^{a-e}	27.0^{a-g}	6.5^{b}	1.4^{a-f}	1.2^{a-c}	75.8^{a-n}	2515.6^{a-e}
Sammaz 27 X Sammaz 27	5x5	14.3^{b}	12.0^{a-e}	28.3^{a-f}	6.4^{b}	1.4^{a-f}	0.5^{c-g}	51.8^{n}	711.1^{e-j}
Sammaz 27 X Sammaz 35	5x6	16.8^{b}	14.0^{a-d}	28.7^{a-f}	7.1^{b}	1.5^{a-e}	1.1^{a-f}	73.9^{a-n}	2106.7^{a-j}
Sammaz 27 X Sammaz 29	5x7	15.8^{b}	15.3^{ab}	29.7^{a-e}	7.8^{b}	1.8^{a}	1.1^{a-f}	80.7^{a-k}	2400.0^{a-g}

Table 4.5 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 27 X Sammaz 28	5x8	14.8^{b}	12.7^{a-e}	29.0^{a-f}	6.7^{b}	1.8^{a}	1.1^{a-e}	84.6^{a-h}	2497.8^{a-f}
Sammaz 35 X Sammaz 19	6x1	7.3^{b}	7.3^{fg}	11.0^{i-k}	5.7^{b}	1.5^{a-f}	0.6^{b-g}	80.5^{a-k}	1173.3^{a-j}
Sammaz 35 X Sammaz 37	6x2	12.3^{b}	12.0^{a-e}	24.3^{a-i}	5.6^{b}	1.3^{c-f}	0.3^{d-g}	74.8^{a-n}	533.3^{e-j}
Sammaz 35 X Sammaz 17	6x3	17.3^{b}	12.7^{a-e}	36.3^{a}	6.7^{b}	1.5^{a-f}	0.7^{a-g}	84.6^{a-h}	1653.3^{a-j}
Sammaz 35 X Sammaz 36	6x4	12.7^{b}	13.3^{a-e}	23.0^{a-j}	7.0^{b}	1.6^{a-d}	0.6^{b-g}	80.2^{a-k}	1235.6^{a-j}
Sammaz 35 X Sammaz 27	6x5	15.3^{b}	14.0^{a-d}	28.3^{a-f}	6.8^{b}	1.5^{a-f}	0.5^{c-g}	87.9^{a-d}	1066.7^{b-j}
Sammaz 35 X Sammaz 35	6x6	10.3^{b}	12.7^{a-e}	19.0^{b-k}	5.6^{b}	1.6^{a-c}	0.1^{g}	64.3^{c-n}	124.4^{j}
Sammaz 35 X Sammaz 29	6x7	14.3^{b}	12.7^{a-e}	22.3^{a-k}	6.7^{b}	1.4^{a-f}	0.7^{a-g}	74.1^{a-n}	1448.9^{a-j}
Sammaz 35 X Sammaz 28	6x8	12.7^{b}	12.7^{a-e}	24.7^{a-i}	6.5^{b}	1.5^{a-f}	0.5^{b-g}	77.2^{a-m}	1111.1^{a-j}
Sammaz 29 X Sammaz 19	7x1	15.7^{b}	12.7^{a-e}	26.3^{a-g}	6.9^{b}	1.5^{a-f}	0.3^{d-g}	82.5^{a-j}	622.2^{e-j}
Sammaz 29 X Sammaz 37	7x2	14.7^{b}	11.3^{b-f}	22.7^{a-j}	6.0^{b}	1.7^{a-c}	0.2^{fg}	73.5^{a-n}	328.9^{h-j}
Sammaz 29 X Sammaz 17	7x3	13.7^{b}	12.0^{a-e}	24.3^{a-i}	6.5^{b}	1.7^{ab}	0.5^{c-g}	89.5^{ab}	1120.0^{a-j}
Sammaz 29 X Sammaz 36	7x4	13.8^{b}	12.0^{a-e}	24.0^{a-i}	6.5^{b}	1.3^{b-f}	0.5^{c-g}	73.8^{a-n}	1013.3^{c-j}
Sammaz 29 X Sammaz 27	7x5	15.8^{b}	14.7^{a-c}	31.0^{a-c}	7.2^{b}	1.6^{a-d}	0.7^{a-g}	78.9^{a-l}	1591.1^{a-j}
Sammaz 29 X Sammaz 35	7x6	10.7^{b}	11.3^{b-f}	14.0^{g-k}	5.2^{b}	1.4^{a-f}	0.2^{g}	63.1^{e-n}	248.9^{j}

Sammaz 29 X Sammaz 29	7x7	12.3^{b}	13.3^{a-e}	24.7^{a-i}	6.8^{b}	1.5^{a-f}	0.7^{a-g}	70.9^{a-n}	1111.1^{a-j}
Sammaz 29 X Sammaz 28	7x8	15.8^{b}	12.7^{a-e}	31.7^{ab}	6.0^{b}	1.7^{a-c}	1.1^{a-f}	85.6^{a-g}	2311.1^{a-h}
Sammaz 28 X Sammaz 19	8x1	12.7^{b}	12.7^{a-e}	18.7^{b-k}	6.0^{b}	1.4^{b-f}	0.4^{c-g}	81.1^{a-k}	817.8^{e-j}
Sammaz 28 X Sammaz 37	8x2	16.1^{b}	14.0^{a-d}	30.0^{a-e}	6.5^{b}	1.5^{a-f}	1.1^{a-e}	78.5^{a-m}	2284.4^{a-h}
Sammaz 28 X Sammaz 17	8x3	12.7^{b}	12.7^{a-e}	21.3^{b-k}	6.0^{b}	1.3^{c-f}	0.8^{a-g}	68.8^{a-n}	1413.3^{a-j}
Sammaz 28 X Sammaz 36	8x4	8.5^{b}	7.0^{g}	8.3^{k}	5.0^{b}	1.3^{b-f}	0.3^{e-g}	61.9^{g-n}	389.3^{h-j}
Sammaz 28 X Sammaz 27	8x5	10.5^{b}	11.3^{b-f}	18.3^{b-k}	6.1^{b}	1.3^{c-f}	0.5^{c-g}	55.9-^{n}	871.1^{e-j}
Sammaz 28 X Sammaz 35	8x6	12.3^{b}	12.0^{a-e}	25.3^{a-h}	5.3^{b}	1.3^{c-f}	0.3^{e-g}	87.0^{a-e}	604.4^{e-j}
Sammaz 28 X Sammaz 29	8x7	12.8^{b}	9.3^{e-g}	23.0^{a-j}	5.7^{b}	1.4^{b-f}	0.9^{a-g}	67.9^{b-n}	1733.3^{a-j}
Sammaz 28 X Sammaz 28	8x8	15.7^{b}	11.3^{b-f}	22.0^{b-k}	6.5^{b}	1.6^{a-c}	0.6^{b-g}	57.1^{k-n}	871.1^{e-j}

Table 4.5 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 11	C1	15.8^{b}	11.3^{b-f}	31.7^{ab}	6.8^{b}	1.4^{a-f}	0.6^{b-g}	81.0^{a-k}	1360.0^{a-j}
Sammaz 16	C2	12.8^{b}	13.3^{a-e}	20.0^{b-k}	6.2^{b}	1.6^{a-d}	0.4^{c-g}	69.7^{a-n}	826.7^{e-j}
Sammaz 14	C3	13.7^{b}	12.7^{a-e}	27.7^{a-g}	6.6^{b}	1.3^{c-f}	0.7^{a-g}	62.6^{f-n}	1200.0^{a-j}
Sammaz 15	C4	19.5^{a}	14.0^{a-d}	25.0^{a-i}	7.1^{b}	1.5^{a-d}	0.4^{c-g}	58.7^{j-n}	613.3^{e-j}
Sammaz 34	C5	11.2^{b}	10.0^{d-g}	20.0^{b-k}	5.3^{b}	1.5^{a-e}	0.4^{c-g}	29.5^{o}	204.4^{j}

Sammaz 20	C6	12.5^{b}	14.0^{a-d}	23.7^{a-j}	6.1^{b}	1.5^{a-e}	0.3^{c-g}	75.2^{a-n}	657.8^{e-j}
Sammaz 18	C7	11.8^{b}	12.0^{a-e}	23.7^{a-j}	5.9^{b}	1.4^{a-f}	0.1^{g}	83.4^{a-i}	275.6^{ij}
Sammaz 13	C8	12.5^{b}	12.7^{a-e}	23.3^{a-j}	5.8^{b}	1.5^{a-d}	0.4^{c-g}	92.6^{a}	1120.0^{a-j}
Sammaz 12	C9	13.0^{b}	13.3^{a-e}	24.3^{a-i}	5.7^{b}	1.3^{c-f}	0.2^{e-g}	86.8^{a-f}	515.6^{f-j}
Mean		13.58	12.14	23.26	6.44	1.47	0.55	78.50	1142.04
CV %		55.57	17.18	29.47	43.72	13.99	80.06	57.76	83.26

KEY: EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4. 6 Mean performance of parents, crosses, reciprocals, selfs and checks for fifteen agronomic characters combined across environments

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 19	1	79.0^{a-d}	85.2^{a-e}	12.8^{a-f}	146.6^{a-d}	54.2^{a-i}	102.4^{f-g}	8.4^{h-l}
Sammaz 37	2	76.0^{a-g}	81.7^{a-g}	12.0^{a-g}	137.7^{a-h}	59.8^{a-h}	109.0^{a-f}	10.3^{c-l}
Sammaz 17	3	72.8^{c-g}	79.8^{c-g}	12.0^{a-g}	111.3^{e-i}	45.0^{f-i}	107.5^{a-g}	11.7^{b-l}
Sammaz 36	4	80.0^{ab}	87.7^{ab}	12.0^{a-g}	136.2^{a-h}	51.5^{b-i}	114.2^{a}	7.8^{j-l}
Sammaz 27	5	76.7^{a-g}	83.2^{a-g}	12.7^{a-f}	138.7^{a-h}	56.0^{a-i}	110.8^{a-e}	13.3^{a-l}
Sammaz 35	6	76.8^{a-g}	82.8^{a-g}	13.0^{a-e}	144.3^{a-f}	61.5^{a-h}	110.0^{a-f}	11.8^{b-l}
Sammaz 29	7	71.7^{f-g}	78.7^{d-g}	11.3^{c-g}	109.8^{f-i}	47.5^{d-i}	108.7^{a-f}	10.3^{c-l}

Sammaz 28	8	73.0^{c-g}	79.2^{d-g}	10.3^{fg}	105.8^{hi}	42.7^{hi}	108.3^{a-f}	8.5^{h-l}
Sammaz 19 X Sammaz 19	1x1	75.2^{a-g}	81.3^{a-g}	12.7^{a-f}	129.2^{a-i}	58.7^{a-i}	108.7^{a-f}	15.0^{a-k}
Sammaz 19 X Sammaz 37	1x2	76.8^{a-g}	83.2^{a-g}	13.0^{a-e}	137.0^{a-h}	59.5^{a-h}	110.5^{a-f}	17.5^{a-d}
Sammaz 19 X Sammaz 17	1x3	75.8^{a-g}	84.0^{a-g}	13.3^{a-d}	138.3^{a-h}	57.5^{a-i}	111.5^{a-e}	14.0^{a-l}
Sammaz 19 X Sammaz 36	1x4	78.2^{a-g}	84.7^{a-g}	12.7^{a-f}	131.2^{a-i}	54.3^{a-i}	109.7^{a-f}	9.7^{c-l}
Sammaz 19 X Sammaz 27	1x5	71.5^{g}	78.2^{e-g}	13.3^{a-d}	124.7^{a-i}	49.2^{d-i}	105.2^{c-g}	16.0^{a-i}
Sammaz 19 X Sammaz 35	1x6	77.2^{a-g}	83.5^{a-g}	13.0^{a-e}	149.3^{a-c}	67.2^{a-e}	111.2^{a-e}	12.8^{a-l}
Sammaz 19 X Sammaz 29	1x7	75.8^{a-g}	80.8^{a-g}	12.3^{a-g}	141.5^{a-g}	55.2^{a-i}	108.0^{a-f}	14.7^{a-l}
Sammaz 19 X Sammaz 28	1x8	76.2^{a-g}	82.3^{a-g}	11.0^{d-g}	120.8^{a-i}	51.7^{b-i}	109.0^{a-f}	11.8^{b-l}
Sammaz 37 X Sammaz 19	2x1	75.5^{a-g}	82.7^{a-g}	11.3^{c-g}	139.8^{a-h}	64.5^{a-g}	110.0^{a-f}	14.5^{a-l}
Sammaz 37 X Sammaz 37	2x2	78.0^{a-g}	84.7^{a-g}	13.3^{a-d}	116.7^{b-i}	53.7^{a-i}	107.8^{a-f}	15.5^{a-k}
Sammaz 37 X Sammaz 17	2x3	75.2^{a-g}	83.5^{a-g}	13.7^{a-c}	133.3^{a-i}	55.3^{a-i}	108.5^{a-f}	14.7^{a-l}
Sammaz 37 X Sammaz 36	2x4	77.3^{a-g}	83.7^{a-g}	13.0^{a-e}	126.7^{a-i}	51.5^{b-i}	111.0^{a-e}	13.8^{a-l}
Sammaz 37 X Sammaz 27	2x5	77.8^{a-g}	84.8^{a-f}	12.0^{a-g}	115.3^{b-i}	51.0^{c-i}	112.5^{a-d}	12.3^{b-l}
Sammaz 37 X Sammaz 35	2x6	76.7^{a-g}	83.2^{a-g}	12.7^{a-f}	130.7^{a-i}	56.2^{a-i}	108.0^{a-f}	12.0^{b-l}

Table 4.6 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 37 X Sammaz 29	2x7	75.8^{a-g}	82.7^{a-g}	12.3^{a-g}	118.2^{b-i}	52.5^{b-i}	108.3^{a-f}	15.0^{a-k}
Sammaz 37 X Sammaz 28	2x8	75.7^{a-g}	83.7^{a-g}	12.0^{a-g}	129.7^{a-i}	56.0^{a-i}	108.7^{a-f}	18.5^{ab}
Sammaz 17 X Sammaz 19	3x1	74.7^{a-g}	83.3^{a-g}	12.3^{a-g}	124.8^{a-i}	56.0^{a-i}	108.8^{a-f}	12.5^{b-l}
Sammaz 17 X Sammaz 37	3x2	76.8^{a-g}	83.0^{a-g}	12.0^{a-g}	131.2^{a-i}	51.0^{c-i}	108.7^{a-f}	11.8^{b-l}
Sammaz 17 X Sammaz 17	3x3	77.2^{a-g}	83.8^{a-g}	12.3^{a-g}	108.3^{g-i}	47.2^{e-i}	111.3^{a-e}	15.3^{a-k}
Sammaz 17 X Sammaz 36	3x4	75.0^{a-g}	81.2^{a-g}	11.5^{b-g}	113.2^{d-i}	51.5^{b-i}	111.8^{a-e}	10.8^{b-l}
Sammaz 17 X Sammaz 27	3x5	78.7^{a-e}	87.2^{a-c}	12.7^{a-f}	117.0^{b-i}	61.7^{a-h}	112.5^{a-d}	16.8^{a-f}
Sammaz 17 X Sammaz 35	3x6	76.3^{a-g}	84.0 $^{a-g}$	13.0^{a-e}	139.5^{a-h}	65.2^{a-f}	110.2^{a-f}	15.0^{a-k}
Sammaz 17 X Sammaz 29	3x7	76.8^{a-g}	82.8^{a-g}	11.7^{b-g}	123.3^{a-i}	52.7^{b-i}	110.2^{a-f}	11.2^{b-l}
Sammaz 17 X Sammaz 28	3x8	76.8^{a-g}	82.8^{a-g}	12.7^{a-f}	135.2^{a-h}	50.5^{c-i}	110.5^{a-f}	14.3^{a-l}
Sammaz 36 X Sammaz 19	4x1	77.2^{a-g}	84.0^{a-g}	12.3^{a-g}	149.7^{ab}	67.7^{a-d}	109.3^{a-f}	14.5^{a-l}
Sammaz 36 X Sammaz 37	4x2	76.5^{a-g}	81.5^{a-g}	13.0^{a-e}	145.2^{a-e}	64.2^{a-g}	110.0^{a-f}	16.7^{a-g}
Sammaz 36 X Sammaz 17	4x3	73.3^{b-g}	79.8^{c-g}	13.7^{a-c}	143.5^{a-g}	54.0^{a-i}	106.7^{a-g}	15.$^{a-k}$
Sammaz 36 X Sammaz 36	4x4	77.0^{a-g}	83.8^{a-g}	12.3^{a-g}	131.2^{a-i}	52.5^{b-i}	110.0^{a-f}	13.3^{a-l}
Sammaz 36 X Sammaz 27	4x5	77.5^{a-g}	84.8^{a-f}	13.0^{a-e}	126.0^{a-i}	54.2^{a-i}	108.8^{a-f}	11.0^{b-l}
Sammaz 36 X Sammaz 35	4x6	78.5^{a-e}	83.3^{a-g}	11.8^{a-g}	127.5^{a-i}	55.0^{a-i}	113.7^{ab}	9.3^{e-l}

Sammaz 36 X Sammaz 29	4x7	72.8^{c-g}	77.2^{g}	11.8^{a-g}	135.7^{a-h}	55.0^{a-i}	107.2^{a-g}	15.7^{a-k}
Sammaz 36 X Sammaz 28	4x8	78.3^{a-f}	84.5^{a-g}	13.0^{a-e}	128.3^{a-i}	53.0^{b-i}	110.5^{a-f}	12.5^{b-l}
Sammaz 27 X Sammaz 19	5x1	76.0^{a-g}	82.5^{a-g}	13.0^{a-e}	130.2^{a-i}	61.0^{a-h}	108.7^{a-f}	16.5^{a-h}
Sammaz 27 X Sammaz 37	5x2	73.2^{c-g}	79.3^{d-g}	12.7^{a-f}	137.0^{a-h}	56.2^{a-i}	105.8^{b-g}	13.7^{a-l}
Sammaz 27 X Sammaz 17	5x3	75.2^{a-g}	83.2^{a-g}	12.3^{a-g}	133.0^{a-i}	57.2^{a-i}	110.0^{a-f}	12.2^{b-l}
Sammaz 27 X Sammaz 36	5x4	78.5^{a-e}	85.7^{a-e}	13.0^{a-e}	125.7^{a-i}	55.8^{a-i}	111.7^{a-e}	17.2^{a-e}
Sammaz 27 X Sammaz 27	5x5	74.7^{a-g}	80.5^{b-g}	13.0^{a-e}	125.7^{a-i}	62.2^{a-h}	107.2^{a-g}	17.2^{a-e}
Sammaz 27 X Sammaz 35	5x6	74.8^{a-g}	82.0^{a-g}	13.0^{a-e}	147.3^{a-d}	71.8^{ab}	104.5^{d-g}	17.0^{a-f}

Table 4.6 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 27 X Sammaz 29	5x7	77.3^{a-g}	84.0^{a-g}	13.7^{a-c}	145.5^{a-e}	73.5^{a}	110.2^{a-f}	17.3^{a-e}
Sammaz 27 X Sammaz 28	5x8	74.3^{b-g}	81.5^{a-g}	12.0^{a-g}	136.3^{a-h}	59.3^{a-h}	110.2^{a-f}	18.7^{ab}
Sammaz 35 X Sammaz 19	6x1	77.7^{a-g}	85.0^{a-f}	14.3^{a}	135.8^{a-h}	65.3^{a-f}	109.2^{a-f}	11.2^{b-l}
Sammaz 35 X Sammaz 37	6x2	75.0^{a-g}	81.5^{a-g}	13.0^{a-e}	132.0^{a-i}	56.7^{a-i}	109.2^{a-f}	15.8^{a-j}
Sammaz 35 X Sammaz 17	6x3	72.7^{d-g}	78.8^{d-g}	11.3^{c-g}	133.7^{a-i}	64.8^{a-f}	108.7^{a-f}	15.5^{a-k}
Sammaz 35 X Sammaz 36	6x4	79.0^{a-d}	85.7^{a-e}	11.3^{c-g}	121.0^{a-i}	48.7^{d-i}	110.8^{a-e}	14.8^{a-l}

Sammaz 35 X Sammaz 27	6x5	76.7^{a-g}	83.7^{a-g}	11.7^{b-g}	127.5^{a-i}	38.8^{i}	110.7^{a-e}	12.2^{b-l}
Sammaz 35 X Sammaz 35	6x6	75.8^{a-g}	83.0^{a-g}	10.0^{g}	108.3^{g-i}	44.2^{g-i}	110.2^{a-f}	8.0^{i-l}
Sammaz 35 X Sammaz 29	6x7	77.3^{a-g}	84.2^{a-g}	12.7^{a-f}	120.8^{a-i}	54.7^{a-i}	111.5^{a-e}	14.7^{a-l}
Sammaz 35 X Sammaz 28	6x8	75.3^{a-g}	80.7^{a-g}	13.0^{a-e}	132.2^{a-i}	55.8^{a-i}	107.8^{a-f}	13.8^{a-l}
Sammaz 29 X Sammaz 19	7x1	75.0^{a-g}	82.7^{a-g}	12.5^{a-g}	108.3^{g-i}	55.7^{a-i}	100.0^{g}	13.2^{a-l}
Sammaz 29 X Sammaz 37	7x2	78.3^{a-f}	85.0^{a-f}	12.7^{a-f}	129.2^{a-i}	56.2^{a-i}	109.2^{a-f}	9.5^{d-l}
Sammaz 29 X Sammaz 17	7x3	75.2^{a-g}	83.7^{a-g}	13.0^{a-e}	132.8^{a-i}	54.7^{a-i}	108.7^{a-f}	17.7^{a-c}
Sammaz 29 X Sammaz 36	7x4	78.5^{a-e}	85.8^{a-d}	13.0^{a-e}	124.2^{a-i}	43.7^{hi}	106.8^{a-g}	11.8^{b-l}
Sammaz 29 X Sammaz 27	7x5	75.5^{a-g}	82.2^{a-g}	14.3^{a}	155.0^{a}	70.3^{a-c}	108.3^{a-f}	16.8^{a-f}
Sammaz 29 X Sammaz 35	7x6	75.0^{a-g}	80.7^{a-g}	11.0^{d-g}	99.8^{i}	47.2^{e-i}	107.8^{a-f}	10.0^{c-l}
Sammaz 29 X Sammaz 29	7x7	74.0^{b-g}	80.3^{b-g}	12.3^{a-g}	126.8^{a-i}	55.7^{a-i}	113.2^{a-c}	12.8^{a-l}
Sammaz 29 X Sammaz 28	7x8	73.3^{b-g}	79.3^{d-g}	12.7^{a-f}	126.7^{a-i}	51.3^{c-i}	105.8^{b-g}	14.0^{a-l}
Sammaz 28 X Sammaz 19	8x1	74.0^{b-g}	81.3^{a-g}	12.3^{a-g}	121.3^{a-i}	53.2^{b-i}	108.3^{a-f}	13.2^{a-l}
Sammaz 28 X Sammaz 37	8x2	72.2^{e-g}	77.5^{fg}	12.7^{a-f}	130.3^{a-i}	57.3^{a-i}	106.0^{a-g}	14.7^{a-l}
Sammaz 28 X Sammaz 17	8x3	74.2^{b-g}	81.8^{a-g}	11.7^{b-g}	106.0^{hi}	51.7^{b-i}	108.0^{a-f}	10.2^{c-l}
Sammaz 28 X Sammaz 36	8x4	75.5^{a-g}	81.5^{a-g}	12.0^{a-g}	119.7^{b-i}	46.8^{e-i}	104.0^{e-g}	9.8^{c-l}
Sammaz 28 X Sammaz 27	8x5	75.7^{a-g}	82.2^{a-g}	13.7^{a-c}	142.2^{a-g}	58.5^{a-i}	108.2^{a-f}	17.0^{a-f}

Sammaz 28 X Sammaz 35	8x6	71.7^{f-g}	78.7^{d-g}	12.3^{a-g}	121.8^{a-i}	50.3^{c-i}	110.7^{a-e}	13.8^{a-l}

Table 4.6 continued

Genotype	entry	Daf	Das	NL	PHcm	EHcm	DM	Ep
Sammaz 28 X Sammaz 29	8x7	73.2^{c-g}	79.3^{d-g}	12.0^{a-g}	124.8^{a-i}	56.5^{a-i}	108.2^{a-f}	15.5^{a-k}
Sammaz 28 X Sammaz 28	8x8	73.2^{c-g}	79.5^{d-g}	10.7^{e-g}	114.3^{c-i}	51.5^{b-i}	106.5^{a-g}	9.0^{f-l}
Sammaz 11	C1	78.0^{a-g}	84.2^{a-g}	12.3^{a-g}	142.3^{a-g}	60.5^{a-h}	109.0^{a-f}	15.3^{a-k}
Sammaz 16	C2	77.5^{a-g}	85.2^{a-e}	13.3^{a-d}	141.0^{a-h}	54.7^{a-i}	108.8^{a-f}	17.3^{a-e}
Sammaz 14	C3	78.7^{a-e}	85.3^{a-e}	13.0^{a-e}	147.2^{a-d}	64.2^{a-g}	112.7^{a-d}	14.8^{a-l}
Sammaz 15	C4	81.3^{a}	88.2^{a}	14.0^{ab}	140.5^{a-h}	71.8^{ab}	112.2^{a-e}	20.7^{a}
Sammaz 34	C5	72.8^{c-g}	79.5^{d-g}	11.0^{d-g}	110.3^{e-i}	44.2^{g-i}	108.7^{a-f}	11.5^{b-l}
Sammaz 20	C6	77.3^{a-g}	84.0^{a-g}	12.7^{a-f}	106.2^{hi}	42.8^{hi}	112.3^{a-d}	7.7^{k-l}
Sammaz 18	C7	76.3^{a-g}	83.3^{a-g}	13.0^{a-e}	135.7^{a-h}	54.8^{a-i}	110.8^{a-e}	8.2^{i-l}
Sammaz 13	C8	79.5^{a-c}	85.3^{a-e}	12.3^{a-g}	121.2^{a-i}	49.2^{d-i}	109.2^{a-f}	8.7^{g-l}
Sammaz 12	C9	74.8^{a-g}	82.0^{a-g}	11.7^{b-g}	113.5^{d-i}	45.5^{f-i}	108.8^{a-f}	6.8^{l}
Mean		75.95	82.61	12.46	128.67	55.28	109.12	13.37
CV %		6.00	6.09	13.82	18.33	24.79	5.06	40.85

KEY: Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot.

Table 4.6 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha

Sammaz 19	1	15.8^{b}	12.0^{a-e}	24.2^{c-j}	6.0^{b}	1.3^{b-d}	0.7^{c-m}	62.7^{d-k}	1130.7^{f-n}
Sammaz 37	2	11.2^{b}	13.3^{a-c}	22.3^{d-j}	6.0^{b}	1.3^{a-d}	0.6^{b-m}	66.8^{b-k}	1306.7^{c-n}
Sammaz 17	3	11.3^{b}	11.7^{a-e}	24.0^{c-j}	6.1^{b}	1.5^{a-d}	0.9^{a-m}	72.8^{a-h}	1631.1^{b-n}
Sammaz 36	4	14.1^{b}	12.3^{a-e}	22.7^{d-j}	7.1^{b}	1.4^{a-d}	0.4^{j-m}	62.075^{e-k}	657.8-^{n}
Sammaz 27	5	15.3^{b}	12.7^{a-e}	27.8^{a-j}	6.6^{b}	1.4^{a-d}	0.8^{b-m}	68.9^{a-j}	1502.2^{b-n}
Sammaz 35	6	16.1^{b}	12.7^{a-e}	26.3^{a-j}	6.0^{b}	1.4^{a-d}	0.6^{f-m}	83.8^{ab}	1333.3^{c-n}
Sammaz 29	7	11.9^{b}	11.3^{b-e}	18.7^{j}	6.5^{b}	1.40^{a-d}	0.6^{e-m}	72.2^{a-h}	1231.1^{d-n}
Sammaz 28	8	12.4^{b}	11.0^{c-e}	20.8^{h-j}	6.1^{b}	1.4^{a-d}	0.9^{a-m}	75.5^{a-g}	1742.2^{a-n}
Sammaz 19 X Sammaz 19	1x1	14.1^{b}	12.3^{a-e}	23.7^{c-j}	6.6^{b}	1.4^{a-d}	0.5^{h-m}	65.9^{c-k}	1031.1^{g-n}
Sammaz 19 X Sammaz 37	1x2	15.3^{b}	12.0^{a-e}	25.3^{b-j}	5.9^{b}	1.13^{d}	1.0^{a-m}	68.0^{b-k}	955.6^{i-n}
Sammaz 19 X Sammaz 17	1x3	15.4^{b}	13.7 $^{a-c}$	30.8^{a-g}	6.5^{b}	1.4^{a-d}	0.8^{b-m}	73.5^{a-h}	1586.7^{b-n}
Sammaz 19 X Sammaz 36	1x4	15.6^{b}	12.3^{a-e}	23.0^{d-j}	6.6^{b}	1.5^{a-c}	1.0^{a-m}	63.0^{d-k}	1386.7^{b-n}
Sammaz 19 X Sammaz 27	1x5	15.0^{b}	14.3^{a}	26.8^{a-j}	7.6^{b}	1.4^{a-d}	1.7^{ab}	75.5^{a-g}	1640.0^{b-n}
Sammaz 19 X Sammaz 35	1x6	14.3^{b}	12.0^{a-e}	26.5^{a-j}	6.2^{b}	1.4^{a-d}	1.0^{a-m}	63.7^{c-k}	3195.6^{ab}
Sammaz 19 X Sammaz 29	1x7	14.4^{b}	13.0^{a-d}	25.2^{b-j}	6.4^{b}	1.3^{a-d}	0.8^{b-m}	65.4^{c-k}	1888.9^{a-n}
Sammaz 19 X Sammaz 28	1x8	14.9^{b}	12.7^{a-e}	28.0^{a-j}	6.8^{b}	1.3^{a-d}	0.5^{h-m}	53.9^{i-k}	1453.3^{b-n}
Sammaz 37 X Sammaz 19	2x1	14.5^{b}	13.3^{a-c}	26.5^{a-j}	6.4^{b}	1.3^{a-d}	1.3^{a-k}	70.7^{a-i}	2373.3^{a-n}

Sammaz 37 X Sammaz 37	2x2	14.3^{b}	12.3^{a-e}	29.3^{a-i}	6.8^{b}	1.4^{a-d}	0.7^{c-m}	61.6^{e-k}	1071.1^{f-n}
Sammaz 37 X Sammaz 17	2x3	14.2^{b}	12.7^{a-e}	30.7^{a-h}	6.8^{b}	1.5^{a-d}	1.2^{a-k}	72.0^{a-h}	2262.2^{a-n}
Sammaz 37 X Sammaz 36	2x4	14.0^{b}	11.0^{c-e}	24.2^{c-j}	5.8^{b}	1.3^{a-d}	0.7^{c-m}	66.7^{b-k}	1200.0^{e-n}
Sammaz 37 X Sammaz 27	2x5	13.6^{b}	12.0^{a-e}	29.3^{a-i}	6.3^{b}	1.4^{a-d}	0.9^{a-m}	75.7^{a-g}	1857.8^{a-n}
Sammaz 37 X Sammaz 35	2x6	14.0^{b}	11.3^{b-e}	26.0^{b-j}	6.20^{b}	1.3^{a-d}	0.9^{a-m}	63.3^{c-k}	1502.2^{b-n}

Table 4.6 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 37 X Sammaz 29	2x7	14.3^{b}	12.0^{a-e}	26.0^{b-j}	6.3^{b}	1.4^{a-d}	1.3^{a-i}	70.8^{a-i}	3013.3^{a-e}
Sammaz 37 X Sammaz 28	2x8	14.8^{b}	12.7^{a-e}	23.7^{c-j}	6.3^{b}	1.4^{a-d}	1.3^{a-j}	65.6^{c-k}	2013.3^{a-n}
Sammaz 17 X Sammaz 19	3x1	15.4^{b}	12.3^{a-e}	24.8^{b-j}	6.5^{b}	1.4^{a-d}	1.2^{a-l}	76.2^{a-g}	2444.4^{a-m}
Sammaz 17 X Sammaz 37	3x2	15.3^{b}	12.3^{a-e}	18.5^{j}	6.4^{b}	1.5^{a-c}	1.1^{a-m}	60.5^{f-k}	1702.2^{a-n}
Sammaz 17 X Sammaz 17	3x3	15.3^{b}	11.7^{a-e}	27.0^{a-j}	6.6^{b}	1.5^{a-d}	0.9^{a-m}	66.3^{c-k}	1542.2^{b-n}
Sammaz 17 X Sammaz 36	3x4	15.0^{b}	12.0^{a-e}	23.2^{d-j}	6.3^{b}	1.3^{b-d}	0.8^{b-m}	69.0^{a-j}	1351.1^{b-n}
Sammaz 17 X Sammaz 27	3x5	14.7^{b}	13.0^{a-d}	32.2^{a-d}	7.3^{b}	1.5^{a-c}	1.5^{a-d}	74.0^{a-h}	2893.3^{a-f}
Sammaz 17 X Sammaz 35	3x6	16.0^{b}	12.3^{a-e}	27.7^{a-j}	6.4^{b}	1.4^{a-d}	1.4^{a-g}	74.3^{a-h}	2720.0^{a-i}

Sammaz 17 X Sammaz 29	3x7	12.0^{b}	11.5^{b-e}	22.8^{d-j}	5.2^{b}	1.3^{a-d}	1.5^{a-e}	74.1^{a-h}	2888.9^{a-f}
Sammaz 17 X Sammaz 28	3x8	15.7^{b}	13.0^{a-d}	30.0^{a-i}	6.9^{b}	1.4^{a-d}	1.2^{a-k}	69.5^{a-j}	2217.8^{a-n}
Sammaz 36 X Sammaz 19	4x1	17.0^{b}	13.0^{a-d}	29.8^{a-i}	6.5^{b}	1.5^{a-d}	1.6^{a-c}	78.5^{a-e}	3102.2^{a-c}
Sammaz 36 X Sammaz 37	4x2	15.5^{b}	12.7^{a-e}	30.0^{a-i}	6.7^{b}	1.5^{a-c}	0.9^{a-m}	76.0^{a-g}	1724.4^{a-n}
Sammaz 36 X Sammaz 17	4x3	15.5^{b}	13.0^{a-d}	26.2^{b-j}	6.8^{b}	1.6^{a-c}	0.8^{b-m}	76.2^{a-g}	1417.8^{b-n}
Sammaz 36 X Sammaz 36	4x4	16.6^{b}	12.3^{a-e}	26.2^{b-j}	8.0^{a}	1.4^{a-d}	0.6^{g-m}	59.4^{g-k}	804.4^{j-n}
Sammaz 36 X Sammaz 27	4x5	15.1^{b}	13.0^{a-d}	28.8^{a-i}	6.^{b}	1.4^{a-d}	1.0^{a-m}	71.5^{a-h}	1813.3^{a-n}
Sammaz 36 X Sammaz 35	4x6	14.9^{b}	11.7^{a-e}	27.3^{a-j}	5.9^{b}	1.5^{a-d}	1.0^{a-m}	86.1^{a}	2311.1^{a-n}
Sammaz 36 X Sammaz 29	4x7	15.5^{b}	13.3^{a-c}	22.0^{e-j}	6.1^{b}	1.4^{a-d}	1.2^{a-l}	72.3^{a-h}	2475.6^{a-l}
Sammaz 36 X Sammaz 28	4x8	13.2^{b}	12.3^{a-e}	24.0^{c-j}	6.4^{b}	1.4^{a-d}	1.1^{a-m}	73.4^{a-h}	2044.4^{a-n}
Sammaz 27 X Sammaz 19	5x1	14.9^{b}	12.3^{a-e}	23.3^{d-j}	6.5^{b}	1.3^{b-d}	1.0^{a-m}	68.2^{b-j}	1862.2^{a-n}
Sammaz 27 X Sammaz 37	5x2	14.8^{b}	13.7^{a-c}	28.7^{a-i}	6.7^{b}	1.5^{a-d}	1.5^{a-f}	68.5^{b-j}	2831.1^{a-h}
Sammaz 27 X Sammaz 17	5x3	14.1^{b}	12.3^{a-e}	26.2^{b-j}	6.3^{b}	1.3^{a-d}	0.9^{a-m}	73.5^{a-h}	1666.7^{b-n}
Sammaz 27 X Sammaz 36	5x4	15.3^{b}	13.0^{a-d}	31.2^{a-f}	6.8^{b}	1.4^{a-d}	1.5^{a-f}	76.1^{a-g}	2995.6^{a-e}
Sammaz 27 X Sammaz 27	5x5	14.4^{b}	13.0^{a-d}	30.7^{a-h}	6.8^{b}	1.3^{a-d}	1.3^{a-j}	59.4^{g-k}	2071.1^{a-n}

Table 4.6 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 27 X Sammaz 35	5x6	17.0^{b}	13.3^{a-c}	31.7^{a-e}	7.1^{b}	1.4^{a-d}	1.7^{a}	75.2^{a-g}	3524.4^{a}
Sammaz 27 X Sammaz 29	5x7	15.7^{b}	14.0^{ab}	29.7^{a-i}	7.4^{b}	1.5^{a-c}	1.3^{a-j}	73.2^{a-h}	2502.2^{a-l}
Sammaz 27 X Sammaz 28	5x8	15.7^{b}	13.3^{a-c}	31.7^{a-e}	6.93^{b}	1.63^{a}	1.5^{a-d}	76.5^{a-g}	3053.3^{a-d}
Sammaz 35 X Sammaz 19	6x1	11.3^{b}	10.0^{e}	21.5^{f-j}	6.1^{b}	1.3^{a-d}	0.8^{b-m}	75.3^{a-g}	1475.6^{b-n}
Sammaz 35 X Sammaz 37	6x2	14.3^{b}	13.0^{a-d}	25.2^{b-j}	5.9^{b}	1.4^{a-d}	1.2^{a-l}	69.3^{a-j}	2311.1^{a-n}
Sammaz 35 X Sammaz 17	6x3	17.9^{b}	12.7^{a-e}	36.0^{a}	6.8^{b}	1.3^{a-d}	1.4^{a-i}	80.4^{a-c}	2871.1^{a-g}
Sammaz 35 X Sammaz 36	6x4	15.2^{b}	13.0^{a-d}	28.8^{a-i}	6.9^{b}	1.6^{ab}	1.3^{a-j}	77.7^{a-f}	2577.8^{a-j}
Sammaz 35 X Sammaz 27	6x5	14.9^{b}	14.3^{a}	27.3^{a-j}	6.6^{b}	1.5^{a-d}	0.8^{b-m}	75.7^{a-g}	1386.7^{b-n}
Sammaz 35 X Sammaz 35	6x6	13.0^{b}	12.7^{a-e}	24.8^{b-j}	6.1^{b}	1.4^{a-d}	0.8^{b-m}	63.2^{c-k}	1182.2^{e-n}
Sammaz 35 X Sammaz 29	6x7	16.4^{b}	13.3^{a-c}	27.7^{a-j}	6.5^{b}	1.4^{a-d}	1.3^{a-j}	70.1^{a-i}	2400.0^{a-m}
Sammaz 35 X Sammaz 28	6x8	14.7^{b}	13.0^{a-d}	31.2^{a-f}	6.5^{b}	1.4^{a-d}	1.1^{a-l}	73.5^{a-h}	2213.3^{a-n}
Sammaz 29 X Sammaz 19	7x1	15.1^{b}	13.3^{a-c}	29.7^{a-i}	6.9^{b}	1.4^{a-d}	1.3^{a-i}	78.6^{a-e}	2608.9^{a-j}
Sammaz 29 X Sammaz 37	7x2	14.3^{b}	12.7^{a-e}	20.8^{h-j}	6.2^{b}	1.5^{a-c}	0.2^{m}	53.8^{i-k}	720.0^{k-n}
Sammaz 29 X Sammaz 17	7x3	15.0^{b}	12.7^{a-e}	29.2^{a-i}	6.8^{b}	1.63^{ab}	1.4^{a-i}	79.5^{a-d}	2671.1^{a-i}

Sammaz 29 X Sammaz 36	7x4	13.2^{b}	12.0^{a-e}	23.3^{d-j}	6.3^{b}	1.3^{a-d}	0.8^{b-m}	66.1^{c-k}	1417.8^{b-n}
Sammaz 29 X Sammaz 27	7x5	16.6^{b}	13.7^{a-c}	33.5^{a-c}	7.1^{b}	1.5^{a-d}	1.4^{a-h}	75.8^{a-g}	2768.9^{a-i}
Sammaz 29 X Sammaz 35	7x6	13.1^{b}	12.0^{a-e}	20.3^{ij}	5.8^{b}	1.3^{a-d}	0.8^{b-m}	67.0^{b-k}	1520.0^{b-n}
Sammaz 29 X Sammaz 29	7x7	14.3^{b}	12.7^{a-e}	27.3^{a-j}	6.7^{b}	1.3^{a-d}	0.8^{b-m}	68.0^{b-k}	1346.7^{c-n}
Sammaz 29 X Sammaz 28	7x8	14.8^{b}	12.7^{a-e}	29.0^{a-i}	6.2^{b}	1.5^{a-c}	1.2^{a-k}	78.6^{a-e}	2511.1^{a-k}
Sammaz 28 X Sammaz 19	8x1	14.4^{b}	13.0^{a-d}	23.3^{d-j}	6.3^{b}	1.4^{a-d}	0.9^{a-m}	72.8^{a-h}	1720.0^{a-n}
Sammaz 28 X Sammaz 37	8x2	15.7^{b}	12.7^{a-e}	28.8^{a-i}	6.7^{b}	1.5^{a-d}	1.3^{a-i}	71.3^{a-h}	2537.8^{a-k}
Sammaz 28 X Sammaz 17	8x3	15.1^{b}	13.0^{a-d}	25.3^{b-j}	6.3^{b}	1.3^{b-d}	1.2^{a-l}	66.7^{b-k}	2084.4^{a-n}

Table 4.6 continued

Genotype	Entry	EL	KRN	KPR	EDcm	CDcm	Cwkg	Tp%	Gykg/ha
Sammaz 28 X Sammaz 36	8x4	11.8^{b}	10.5^{d-e}	18.3^{j}	5.9^{b}	1.3^{b-d}	0.5^{i-m}	64.2^{c-k}	1030.2^{g-n}
Sammaz 28 X Sammaz 27	8x5	13.2^{b}	12.3^{a-e}	21.2^{g-j}	6.2^{b}	1.3^{a-d}	0.9^{a-m}	60.3^{g-k}	1582.2^{b-n}
Sammaz 28 X Sammaz 35	8x6	14.4^{b}	13.0^{a-d}	27.0^{a-j}	5.6^{b}	1.3^{a-d}	0.8^{b-m}	78.0^{a-e}	1506.7^{b-n}
Sammaz 28 X Sammaz 29	8x7	14.8^{b}	11.3^{b-e}	27.0^{a-j}	6.1^{b}	1.4^{a-d}	1.4^{a-i}	70.0^{a-i}	2533.3^{a-k}

Sammaz 28 X Sammaz 28	8x8	16.7^{b}	12.3^{a-e}	23.3^{d-j}	6.4^{b}	1.5^{a-d}	0.9^{a-m}	60.0^{g-k}	1404.4^{b-n}
Sammaz 11	C1	16.6^{b}	13.0^{a-d}	34.2^{ab}	6.9^{b}	1.4^{a-d}	1.3^{a-i}	74.0^{a-h}	2400.0^{a-m}
Sammaz 16	C2	13.6^{b}	14.0^{ab}	22.3^{d-j}	6.4^{b}	1.3^{a-d}	0.6^{f-m}	63.7^{c-k}	946.7^{i-n}
Sammaz 14	C3	15.8^{b}	12.7^{a-e}	29.5^{a-i}	6.7^{b}	1.2^{c-d}	0.8^{b-m}	63.2^{c-k}	1262.2^{c-n}
Sammaz 15	C4	18^{a}	14.0^{ab}	27.2^{a-j}	7.0^{b}	1.4^{a-d}	0.6^{d-m}	57.5^{h-k}	995.6^{h-n}
Sammaz 34	C5	14.3^{b}	12.3^{a-e}	26.2^{b-j}	6.0^{b}	1.4^{a-d}	1.3^{a-k}	51.2^{k}	2186.7^{a-n}
Sammaz 20	C6	12.6^{b}	13.0^{a-d}	22.2^{e-j}	6.2^{b}	1.4^{a-d}	0.5^{i-m}	57.7^{h-k}	551.1^{n}
Sammaz 18	C7	15.3^{b}	12.7^{a-e}	26.7^{a-j}	6.2^{b}	1.3^{a-d}	0.5^{i-m}	74.6^{a-h}	986.7^{h-n}
Sammaz 13	C8	11.9^{b}	11.7^{a-e}	20.4^{ij}	12.3^{a}	1.3^{b-d}	0.4^{k-m}	52.5^{jk}	941.8^{i-n}
Sammaz 12	C9	13.7^{b}	13.0^{a-d}	25.3^{b-j}	5.9^{b}	1.3^{b-d}	0.3^{ml}	74.4^{a-h}	608.9^{mn}
Mean		14.85	12.59	26.29	6.59	1.38	0.98	69.54	1855.65
CV %		37.23	14.69	25.28	43.56	17.44	61.42	16.74	66.95

KEY: EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha.

4.3.0 GENETIC ANALYSIS

4.3.1 ANOVA for Combining Ability

The analyses of variance for combining ability for fifteen traits measured at Kadawa environments one, two and combined across environments are presented in Tables 4.7, 4.8 and 4.9, respectively. In Table 4.7, the mean squares due to crosses at environment one were significantly different ($p \leq 0.05$) for days to maturity and grain yield. The parents mean squares were significantly different ($p \leq 0.05$) for days to 50% tasselling. The parents vs. crosses mean squares were highly significant ($p \leq 0.01$) for number of leaves per plant and grain yield and significant ($p \leq 0.05$) for plant height, ear height and cob weight. The mean squares due to general combining ability (GCA) were highly significant ($p \leq 0.01$) for ear diameter and grain yield and significant ($p \leq 0.05$) for plant height, ear height, days to maturity, ear length, kernels per row and cob weight. The mean squares due to specific combining ability (SCA) were not significant for all the traits measured. The mean squares due to reciprocals were significant ($p \leq 0.05$) for number of leaves per plant and ear length only.

The mean squares due to crosses were highly significant ($p \leq 0.01$) at environment two (Table 4.8) for ear length and significant ($p \leq 0.05$) for cob diameter, cob weight, and grain yield. The mean squares due to parents were highly significant ($p \leq 0.01$) for number of leaves per plant and ear diameter. The mean squares due to parents vs. crosses were highly significant ($p \leq 0.01$) for grain yield and significant ($p \leq 0.05$) for cob weight. The mean squares due to general combining ability (GCA) were highly significant ($p \leq 0.01$) for number of ears per plot, number of kernels per row, and grain yield and significant ($p \leq 0.05$) for ear height, ear length, cob diameter

and cob weight. The mean squares due to specific combining ability (SCA) were significant ($p \leq 0.05$) for ear length. The mean squares due to reciprocal were highly significant ($p \leq 0.01$) for number of kernels per row, and threshing percentage and significant ($p \leq 0.05$) for ear length and grain yield.

Results in Table 4.9 are for the combining ability across the environments. The mean squares due to environment were highly significant ($p \leq 0.01$) for all traits measured except days to 50% silk, number of leaves per plant and ear diameter. The mean squares due to general combining ability (GCA) were highly significant ($p \leq 0.01$) for days to 50% tasselling and significant ($p \leq 0.05$) for number of ears per plot, number of kernels per row, and threshing percentage. The mean squares due to specific combining ability (SCA) were highly significant ($p \leq 0.01$) for ear length and threshing percentage and significant ($p \leq 0.05$) for plant height and ear diameter. The mean squares due to reciprocal were highly significant ($p \leq 0.01$) for number of kernels per row and threshing percentage and significant ($p \leq 0.05$) for grain yield. The mean squares due to GCA x environment interaction were highly significant ($p \leq 0.01$) for days to 50% tasselling and ear length and significant ($p \leq 0.05$) for days to maturity, number of ears per plot, number of kernels per row, threshing percentage and grain yield. The mean squares due to SCA x environment interaction were highly significant ($p \leq 0.01$) for ear length, kernel row number and ear diameter and significant ($p \leq 0.05$) for number of kernels per row. The reciprocal x environment interaction mean squares were highly significant ($p \leq 0.01$) for ear length and significant ($p \leq 0.05$) for days to maturity and threshing percentage.

Table 4.7 Mean squares for combining ability for fifteen agronomic characters in environment one

Source of variation	df	Daf	Das	NL	PH	EH	DM	Ep	EL
Crosses	27	9.74	16.11	1.77	532.7	229.04	27.26*	17.24	6.35
Parents	7	33.28*	37.14	3.02	332.55	232.71	19.31	46.14	6.86
Parents Vs Crosses	1	0.91	1.65	16.10**	2499.43*	813.41*	8.60	3.15	4.46
GCA	7	14.84	28.20	2.01	862.57*	395.64*	38*	24.52	11.60*
SCA	20	7.95	11.87	1.68	417.25	170.73	23.50	14.69	4.51
Reciprocal	28	14.83	17.94	2.63*	515.667	279.10	27.33	27.33	6.22*
Error	70	12.34	20.38	1.66	384.50	183.80	15.22	26.62	4.03

Table 4.7 continued

Source of variation	df	KRN	KPR	ED	CD	Cw	Tp	Gy
Crosses	27	2.31	55.12	0.43	0.04	0.7982	211.54	3978784.05*
Parents	7	1.43	61.31	0.35	0.04	0.7658	52.45	2251239.67
Parents Vs Crosses	1	1.06	36.84	0.03	0.13	3.3963*	236.82	19113765.61**
GCA	7	2.84	99.38*	0.96**	0.04	1.4997*	278.04	8197783.57**

SCA	20	2.12	39.63	0.24	0.04	0.5527	188.26	2502134.22
Reciprocal	28	2.07	55.76	0.28	0.04	0.8623	247.88	3822686.21
Error	70	2.06	38.86	0.28	0.07	0.5513	140.36	2212349.5

**,* significantly different at 1% and 5% levels, respectively

KEY: df; Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4.8 Mean squares for combining ability for fifteen agronomic characters in environment two

Source of variation	df	Daf	Das	NL	PH	EH	DM	Ep	EL
Crosses	27	27.51	27.60	3.28	527.32	262.43	38.97	58.94	13.32**
Parents	7	15.42	22.27	12.36**	646.95	218.57	29.90	56.48	8.71
Parents Vs Crosses	1	15.48	30.67	0.13	1564.45	0.02	21.19	29.73	3.74
GCA	7	16.10	17.22	2.33	405.71	438.11*	28.95	120.76**	14.14*
SCA	20	31.51	31.23	3.62	569.88	200.94	42.48	37.30	13.03*

Reciprocal	28	32.10	39.09	3.99	809.92	260.51	33.02	37.18	10.40*
Error	70	23.17	26.76	3.89	743.05	189.28	29.43	39.69	6.30

Table 4.8 continued

Source of variation	df	KRN	KPR	ED	CD	Cw	Tp	Gy
Crosses	27	6.04	83.24	2.45	0.07*	0.41*	5548.73	2099136.32*
Parents	7	3.05	28.76	71.49**	0.03	0.13	225.96	419284.52
Parents Vs Crosses	1	0.60	0.21	61.24	0.14	1.06*	9923.95	10424590.88**
GCA	7	8.43	152.16**	4.07	0.10*	0.71*	4670.91	4041133.72**
SCA	20	5.20	59.11	1.88	0.06	0.30	5855.97	1419437.23
Reciprocal	28	6.01	91.36**	1.78	0.07	0.31	269.11**	1668394.61*
Error	70	5.61	51.58	16.99	0.04	0.24	4423.01	3293888.74

**,* significantly different at 1% and 5% levels, respectively

KEY: df: Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4.9 Mean squares for combining ability across environments for fifteen agronomic characters

Source of variation	df	Daf	Das	NL	PH	EH	DM	Ep	EL
Environment	1	20039.26**	92.04	0.38	41854.38**	13171.88**	74509.90**	3168.25**	973.82**
Parents Vs crosses	1	11.94	15.72	9.56	4009.37	411.12	1.40	26.11	0.02
Replication in environment	4	89.19**	107.96	5.49	6995.93**	5730.41**	85.00	688.044**	89.19**
GCA	7	41.67	309.48**	5.12	624.04	378.16	37.20	71.68*	3.99
SCA	28	15.92	14.58	2.67	875.84*	284.46	28.80	32.07	11.61**
Reciprocal	28	19.68	68.32	3.07	669.47	217.13	33.10	38.58	6.55
GCA x Environment	7	68.30**	26.66	6.06	899.43	226.50	81.92*	83.48*	21.59**

SCA x Environment	28	16.05	29.44	2.85	480.39	185.17	36.75	44.13	9.30**
Error	252	20.55	90.93	4.78	554.374	190.20	30.31	31.31	4.75

Table 4.9 continued

Source of variation	df	KRN	KPR	ED	CD	Cw	Tp	Gy
Environment	1	104.17**	4088.57**	1.49	2.25**	85.59**	11068.32**	234800192.7**
Parents Vs crosses	1	1.62	21.34	32.09	0.00	4.13	6613.41	28886885.00
Replication in environment	4	6.04	197.65**	11.80	0.55**	1.09	3145.68**	4329082*
GCA	7	6.21	110.02*	9.12	0.05	0.86	295.43*	3580089.67
SCA	28	3.13	60.12	8.37*	0.06	0.49	266.99**	2213226.94
Reciprocal	28	3.92	88.84**	1.21	0.06	0.66	247.88**	3069879.09*
GCA x Environment	7	4.21	108.32*	7.26	0.07	0.98	248.57*	4670088.91*
SCA x Environment	28	6.32**	73.62*	10.01**	0.05	0.63	162.64	2665003.83
Error	252	3.17	41.86	5.08	0.06	0.41	119.49	1763172

**,* significantly different at 1% and 5% levels, respectively

KEY: df: Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

4.3.2 Estimates of General and Specific Combining Ability Variances

The components for GCA variance, SCA variance, reciprocal variance and GCA/SCA variance ratios for fifteen traits measured at environments one, two and combined across environments are presented in Tables 4.10, 4.11 and 4.12, respectively. Table 4.10 indicated positive GCA/SCA ratios for all the characters except days to 50% tasselling, days to 50% silk, ear height and ear diameter. GCA variances were higher than SCA variances for all traits except plant height, number of days to maturity, ear length, kernel row number and threshing percentage. High reciprocal variances were observed for plant height, ear height, days to maturity, number of kernels per row, threshing percentage and grain yield. Positive GCA/SCA ratios were observed at environment two (Table 4.11) for number of leaves per plant, plant height, ear height, ear length, number of kernels per row, ear diameter, cob diameter, cob weight and threshing percentage. GCA variances were higher than SCA variances for all characters except days to maturity, ear length, number of kernels per row, cob diameter, cob weight and threshing percentage. High reciprocal variances were observed for days to 50% silk, plant height, ear height and number of kernels per row.

The combined data (Table 4.12) revealed positive GCA/SCA ratios for plant height, ear height, number of ears per plot, number of kernels per row, ear diameter, cob weight, threshing percentage and grain yield. GCA variances were higher than SCA variances for all the traits except plant height, ear height, ear length, number of kernels per row, ear diameter, cob diameter, cob weight, threshing percentage, and grain yield. High reciprocal variances were observed for plant height, ear height, number of kernels per row, threshing percentage and grain yield.

Table 4.10 Estimates of combining ability variance components for fifteen agronomic characters for environment one

Characters	Daf	Das	NL	PH	EH	DM	Ep	EL
GCA	0.16	0.49	0.02	29.88	13.24	1.42	-0.13	0.47
SCA	-4.39	-8.51	0.02	32.75	-13.08	8.27	-11.93	0.48
Reciprocal	1.25	-1.22	0.48	65.58	47.65	6.06	0.36	1.10
GCA/SCA Ratio	-0.04	-0.06	1.25	0.91	-1.01	0.17	0.01	0.99

Table 4.10 continued

Characters	KRN	KPR	ED	CD	Cw	Tp	Gy
GCA	0.05	3.78	0.04	-0.0021	0.06	8.61	374090
SCA	0.06	0.77	-0.04	-0.03	0.0014	47.91	289785
Reciprocal	0.01	8.45	0.001	-0.02	0.16	53.76	805168
GCA/SCA Ratio	0.89	4.91	-1.07	0.07	41.49	0.18	1.29

KEY: df: Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4.11 Estimates of combining ability variance components for fifteen agronomic characters for environment two

Characters	Daf	Das	NL	PH	EH	DM	Stnd	Ep	EL
GCA	-0.44	-0.60	-0.10	-21.08	15.55	-0.03	5.16	5.0667	0.49
SCA	8.34	4.47	-0.27	-173.17	11.66	13.05	29.06	-2.399	6.73
Reciprocal	4.47	6.17	0.05	33.44	35.61	1.80	16.77	-1.258	2.05

GCA/SCA Ratio	-0.05	-0.13	0.36	0.12	1.33	-0.002	0.18	-2.112	0.07

Table 4.11 continued

Characters	KRN	KPR	ED	CD	Cw	Tp	Gy
GCA	0.18	6.29	-0.81	0.004	0.03	15.50	46702.81
SCA	-0.41	7.54	-15.12	0.02	0.06	1433	-1874452
Reciprocal	0.20	19.89	-7.61	0.01	0.03	-2077	-812747
GCA/SCA Ratio	-0.43	0.83	0.05	0.19	0.53	0.01	-0.03

KEY: df: Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4.12 Estimates of combining ability variance components across environments for fifteen agronomic characters

Characters	Daf	Das	NL	PH	EH	DM	Ep	EL
GCA	1.32	13.66	0.02	4.35	11.75	0.43	2.52	-0.05
SCA	-4.63	-76.35	-2.12	321.47	94.26	-1.51	0.76	6.86
Reciprocal	-0.44	-11.30	-0.86	57.55	13.47	1.40	3.63	0.90
GCA/SCA Ratio	-0.29	-0.18	-0.01	0.01	0.13	-0.29	3.34	-0.01

Table 4.12 continued

Characters	KRN	KPR	ED	CD	Cw	Tp	Gy
GCA	0.19	4.26	0.25	-0.001	0.03	11	113557
SCA	-0.04	18.27	3.29	0.001	0.07	147.51	450055
Reciprocal	0.38	23.49	-1.94	0.002	0.12	64.19	653354
GCA/SCA Ratio	-4.86	0.23	0.08	-1.13	0.39	0.08	0.25

KEY: df: Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

4.3.3 Estimates of Combining Ability Effects

The estimates of GCA, reciprocal and SCA effects for fifteen traits in environments one, two and combined across environments are presented in Tables 4.13, 4.14 and 4.15, respectively. In environment one (Table 4.13), highly significant GCA effects for Sammaz 35 were recorded for two traits while four significant GCA effects were observed for the variety. Similarly, Sammaz 37 GCA effects were highly significant for one trait and significant for three other traits. Sammaz 29 x Sammaz 37 cross showed significant and highly significant reciprocal effects for three and two traits, respectively. Sammaz 29 x Sammaz 19 exhibited positive significant and highly significant reciprocal effects for days to 50% tasselling, and days to maturity, respectively. Sammaz 17 x Sammaz 36 showed negative significant SCA effects for kernel row number and grain yield.

In environment two, Sammaz 27 showed significant to highly significant GCA effects (Table 4.14) for seven traits. Sammaz 19 x Sammaz 27 showed negative significant SCA effects for days to 50% tasselling, days to 50% silk, and days to maturity. The hybrid also indicated positive significant SCA effects for cob weight and grain yield.

The combined data (Table 4.15) indicated that Sammaz 27 had significant GCA effects for four traits and highly significant positive GCA effects for two traits. Sammaz 36 had highly significant negative GCA effects for days to 50% silk. Sammaz 29 x Sammaz 37 showed significant positive reciprocal effects for two traits including grain yield. Sammaz 17 x Sammaz

35 had positive significant SCA effects for ear height, number of ears per plot and number of kernels per row.

Table 4.13 GCA, Reciprocal and SCA effects for fifteen characters in environment one

Genotype	status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy
Sammaz 19	G	0.97	0.43	-0.15	9.13	2.03	1.00	0.36	0.19	0.31	-1.82	-0.16	-0.12	-0.32	-3.97	-671.85*
Sammaz 37	G	0.81	1.54	0.18	-4.65	-1.03	-0.167	0.86*	-0.58	-0.69*	-1.38	-0.33	-0.01	-0.37*	-5.82	-996.30**
Sammaz 17	G	0.69	1.43	-0.26	-0.82	0.03	2.00*	1.41	0.59	0.42	1.74	0.08	0.02	0.39*	0.45	694.07*
Sammaz 36	G	0.69	-0.01	0.13	0.07	-1.69	1.61	-2.08	0.19	-0.47	-2.15	0.12	0.01	-0.24	-0.40	-402.22
Sammaz 27	G	-0.81	0.71	0.07	-3.15	-2.31	-1.00	-1.14*	-0.78	0.31	1.24	0.45	0.02	0.22	5.34	577.04
Sammaz 35	G	-0.47	-1.01	0.63*	11.85*	10.53	-2.06*	0.58	1.45**	-0.03	4.63**	-0.03	0.02	0.30	5.24	845.19*
Sammaz 29	G	-0.42	-1.35	-0.10	-7.32	-3.03	0.00	0.58	-0.05	-0.03	-1.54	-0.14	0.04	0.03	0.54	138.52
Sammaz 28	G	-1.47	-1.74	-0.49	-5.10	-4.53	-1.39	-0.58	-1.03	0.19	-0.71	-0.01	0.01	-0.01	-1.39	-184.45
Sammaz 37 X Sammaz 19	R	2.00	-5.67	-0.67	-5.00	-6.67	0.33	0.33	0.75	0.00	-3.00	-0.32	-0.12	-0.60	-1.37	-1422.22*
Sammaz 17 X Sammaz 19	R	1.33	-0.83	0.00	-2.00	-3.83	2.83	2.17	-0.52	0.00	2.00	-0.20	-0.07	-0.45	-1.34	-1062.22
Sammaz 17 X Sammaz 37	R	-0.83	2.33	-0.33	5.00	4.67	-0.83	3.00	-1.45	-0.33	5.67*	-0.05	0.05	0.26	5.74	657.78
Sammaz 36 X Sammaz 19	R	0.17	-4.17	-0.67	-6.83	-8.33	0.83	-2.17	-1.28	-0.33	-3.33	0.12	0.00	-0.52	-7.74	-1204.44
Sammaz 36 X Sammaz 37	R	-1.17	1.67	-0.33	-8.67	-7.17	-1.17	0.50	-0.50	-1.00	-1.83	-0.03	-0.18	-0.23	-4.67	-466.67
Sammaz 36 X Sammaz 17	R	-0.50	1.83	-0.33	-10.67	-0.33	2.33	0.83	0.92	-0.67	-0.33	0.07	-0.15	0.08	-3.60	22.22
Sammaz 27 X Sammaz 19	R	0.67	-1.50	-0.33	2.50	-3.83	0.33	1.00	0.30	0.67*	4.00	0.32	0.03	0.23	3.64	466.67
Sammaz 27 X Sammaz 37	R	2.167	5.33	0.33	-8.33	-6.67	3.17	-3.00	-0.83	-0.67	-0.33	0.22	0.02	-0.25	3.60	-435.56

Sammaz 27 X Sammaz 17	R	-2.17	-0.83	0.00	-6.67	0.33	-2.83	1.00	1.17	1.00	2.33	0.30	0.15	0.65*	0.22	1208.89
Sammaz 27 X Sammaz 36	R	-0.83	3.50	1.00	7.33	-1.67	-2.00	-4.33*	0.17	0.33	-0.33	-0.18	-0.05	-0.12	-2.29	-422.22
Sammaz 35 X Sammaz 19	R	0.33	-5.67	0.67	19.83*	12.33	-1.00	2.00	1.67*	0.00	2.17	-0.05	0.07	0.39	-5.79	884.44
Sammaz 35 X Sammaz 37	R	-0.50	0.50	0.00	-8.00	0.00	-1.17	-1.67	0.10	-1.33*	2.00	0.05	-0.15	-0.56	-3.00	-1382.22*
Sammaz 35 X Sammaz 17	R	2.67	-2.83	0.33	16.83	10.17	-0.33	0.67	0.42	0.67	-1.00	0.02	0.08	0.26	-3.06	284.44
Sammaz 35 X Sammaz 36	R	-0.83	0.67	0.33	6.00	3.50	0.67	-3.83	0.55	0.33	2.33	0.15	-0.07	0.00	4.17	106.67
Sammaz 35 X Sammaz 27	R	-0.83	-3.17	-1.00	23.17*	15.17*	-4.83**	3.00	1.31	-1.00	4.17	0.38	-0.03	0.64*	-0.24	1617.78*

Table 4.13 continued

Genotype	status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy
Sammaz 29 X Sammaz 19	R	3.00*	-1.00	0.67	6.50	-4.00	11.33**	-0.50	1.05	-0.67	-2.33	-0.33	-0.02	-0.56	-6.61	-1208.89
Sammaz 29 X Sammaz 37	R	1.33	1.67	1.17	4.50	7.83	1.50	5.67**	2.00*	-0.67	7.67**	0.12	0.03	0.58	8.51*	1315.56*
Sammaz 29 X Sammaz 17	R	0.33	1.50	0.67	-3.67	-7.00	1.17	-1.17	0.67	0.33	0.00	-0.23	0.05	0.26	-2.69	546.67
Sammaz 29 X Sammaz 36	R	-0.83	1.33	1.67	15.00	16.00*	1.50	1.50	2.17**	0.33	-0.33	0.17	0.00	-0.01	3.09	75.56
Sammaz 29 X Sammaz 27	R	0.17	3.67	-0.67	-13.67	-10.83	0.50	1.00	-0.90	0.00	-3.17	0.00	-0.03	-0.29	-1.25	-671.11
Sammaz 29 X Sammaz 35	R	1.33	4.00	1.33	-1.17	0.67	1.00	1.67	1.50	0.67	3.17	-0.05	0.07	0.21	1.56	280.00
Sammaz 28 X Sammaz 19	R	0.00	2.50	1.00	-0.33	-0.33	-0.83	1.83	-0.55	-0.33	-1.33	-0.25	-0.08	-0.32	-9.41*	-711.11
Sammaz 28 X Sammaz 37	R	1.33	0.00	-0.67	2.17	0.33	0.17	1.50	0.38	0.67	0.00	-0.38	-0.05	0.04	-2.86	-377.78
Sammaz 28 X Sammaz 17	R	4.00**	-6.17	-1.00	4.00	-1.50	2.33	0.17	0.20	0.33	2.67	0.15	-0.03	0.28	1.37	417.78
Sammaz 28 X Sammaz 36	R	1.83	-3.67	0.00	1.17	-0.50	5.00**	0.67	-0.15	-0.33	-0.83	0.17	0.12	0.39	4.58	693.33
Sammaz 28 X Sammaz 27	R	0.83	-4.67	-0.33	0.50	-3.50	2.00	-0.33	0.32	0.33	5.17*	0.38	0.08	0.35	8.10*	657.78

Sammaz 28 X Sammaz 35	R	2.50	-2.17	-0.67	10.00	3.67	1.83	-0.33	0.17	-0.33	4.50	0.30	-0.05	0.20	-2.29	453.33
Sammaz 28 X Sammaz 29	R	0.50	-4.00	-1.33	-5.33	-3.50	0.17	-1.17	-1.50	-0.33	-2.33	0.00	-0.03	-0.18	4.36	-311.11
Sammaz 19 X Sammaz 37	S	1.63	0.73	0.79	4.54	0.36	-0.07	1.66	2.12	1.32	-0.46	0.04	-0.13	0.21	-2.16	332.91
Sammaz 19 X Sammaz 17	S	0.74	-0.16	-0.10	-2.63	-0.37	3.76	0.77	-0.30	-0.46	1.43	-0.08	0.00	-0.64	-2.74	-1295.24
Sammaz 19 X Sammaz 36	S	0.07	2.29	0.18	4.82	2.36	-1.85	-0.06	-0.31	0.43	1.65	0.37	0.22	0.60	4.89	1018.84
Sammaz 19 X Sammaz 27	S	-2.43	-3.10	0.24	-15.96	-10.03	-0.91	-1.34	-0.74	0.99	-2.74	0.37	-0.06	0.18	6.86	528.47
Sammaz 19 X Sammaz 35	S	-0.10	0.62	-0.32	19.04	11.80	1.48	0.94	0.33	-0.68	2.54	-0.19	0.01	0.21	-0.55	464.76
Sammaz 19 X Sammaz 29	S	1.52	0.29	0.41	4.21	-1.31	0.76	-2.73	-0.30	-0.68	0.71	-0.18	-0.05	-0.13	-0.09	-197.46
Sammaz 19 X Sammaz 28	S	-1.43	-0.66	-1.21	-14.02	-2.81	-3.18	0.77	-0.79	-0.91	-3.13	-0.34	0.012	-0.43	-6.21	-852.28
Sammaz 37 X Sammaz 17	S	-0.43	0.73	0.91	5.15	0.69	-2.07	0.27	-2.44*	0.54	1.65	-0.08	0.14	-0.08	8.44	202.54
Sammaz 37 X Sammaz 36	S	-3.00	-3.16	-0.15	-5.41	-0.92	-1.68	3.44	-0.14	-0.57	-0.13	-0.17	-0.15	0.04	2.58	214.39
Sammaz 37 X Sammaz 27	S	1.74	0.45	-0.76	-8.52	-8.31	4.60*	-4.18	-1.18	-0.68	-1.85	-0.10	0.04	-0.45	2.66	-631.53
Sammaz 37 X Sammaz 35	S	-0.60	-0.83	0.02	-6.18	-4.81	0.32	-3.56	-1.04	-1.02	-4.24	-0.05	-0.05	-0.57	-11.34	-1433.02
Sammaz 37 X Sammaz 29	S	0.68	1.51	0.07	3.98	7.08	-0.41	0.10	1.76	0.32	6.26	0.52	0.05	0.45	7.75	1006.98

Table 4.13 continued

Genotype	status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy
Sammaz 37 X Sammaz 28	S	-0.93	0.56	-0.87	6.43	5.91	-0.68	2.27	0.91	0.096	-1.24	-0.17	0.09	0.42	-7.91	307.73
Sammaz 17 X Sammaz 36	S	-2.32	-1.71	-1.04	-12.91	-6.31	0.15	-2.45	0.20	-1.68*	-5.24	-0.32	-0.18	-0.67	-11.24	-1520.42*
Sammaz 17 X Sammaz 27	S	0.85	0.90	-0.98	-0.02	7.97	1.48	2.94	-0.00	0.21	0.37	0.01	0.04	0.37	-0.61	655.87
Sammaz 17 X Sammaz 35	S	1.189	1.96	0.46	7.98	5.14	-0.24	-0.12	0.54	0.54	-3.68	0.16	0.02	0.20	-3.10	209.95

Sammaz 17 X Sammaz 29	S	-2.21	-2.39	-0.15	3.15	-5.98	-2.91	0.55	0.44	0.54	2.82	0.10	0.15	0.74*	7.00	1574.39*
Sammaz 17 X Sammaz 28	S	2.19	0.68	0.91	-0.74	-1.14	-0.18	-1.95	1.58	0.32	2.65	0.21	-0.18	0.08	2.24	172.91
Sammaz 36 X Sammaz 27	S	2.19	3.68	0.63	3.10	-3.98	0.82	-1.23	0.82	0.43	4.60	-0.47	-0.05	-0.10	-4.54	-452.28
Sammaz 36 X Sammaz 35	S	0.52	-0.94	-0.60	-15.24	-6.48	1.21	-1.29	0.43	0.76	5.87	0.30	0.13	0.22	17.46*	941.80
Sammaz 36 X Sammaz 29	S	0.13	-2.27	0.46	19.26	13.75	0.82	1.71	-0.00	0.10	-5.29	-0.12	-0.04	-0.29	-12.73	-671.53
Sammaz 36 X Sammaz 28	S	1.52	2.12	0.52	6.37	1.58	-0.79	-0.12	-0.993	0.54	-1.46	0.42	0.07	0.20	3.59	469.21
Sammaz 27 X Sammaz 35	S	-1.66	-1.66	0.79	10.98	10.80	-7.85**	2.44	-0.24	-0.68	-2.18	0.14	0.02	0.25	1.04	611.43
Sammaz 27 X Sammaz 29	S	0.63	1.01	0.18	1.48	-0.31	1.10	1.10	-0.27	-0.68	-1.02	-0.02	-0.11	-0.39	-4.95	-1019.68
Sammaz 27 X Sammaz 28	S	-1.32	-1.27	-0.10	8.93	3.86	2.48	0.27	1.61	0.43	2.82	0.06	0.12	0.13	-0.45	307.72
Sammaz 35 X Sammaz 29	S	-0.04	2.06	-1.04	-20.85	-11.14	1.48	1.05	0.34	0.98	-1.07	-0.24	-0.01	-0.15	-4.61	-541.16
Sammaz 35 X Sammaz 28	S	0.69	-1.21	0.68	4.26	-5.31	3.21	0.55	-0.35	0.10	2.76	-0.13	-0.11	-0.16	1.10	-253.76
Sammaz 29 X Sammaz 28	S	-0.71	-0.21	0.071	-11.24	-2.09	-0.85	-1.79	-1.95	-0.57	-2.41	-0.06	-0.00	-0.23	7.63	-151.54

**,* significant at 1% and 5% levels, respectively. G, R and S are General Combining Ability, Reciprocal and Specific Combining Ability effects, respectively.

KEY: df: Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length,

KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4.14 GCA, Reciprocal and SCA effects for fifteen characters in environment two

Genotype	status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy
Sammaz 19	G	-1.58	-1.35	0.33	0.88	-2.38	-1.61	-1.11	0.11	0.24	0.24	0.38	-0.03	-0.14	21.54	-346.67
Sammaz 37	G	-0.14	0.21	0.00	-2.63	-3.49	0.39	0.83	-0.70	-0.88	-0.60	-0.27	-0.10*	0.16	-6.14	395.56
Sammaz 17	G	-0.25	0.60	0.39	-3.51	-0.43	0.78	-2.06	-0.95	-0.49	0.35	-0.03	-0.05	-0.22	-9.67	-533.33*
Sammaz 36	G	0.75	-0.01	-0.56	-8.13	-5.32	0.33	-3.22*	-0.44	-0.43	-4.04*	-0.74	-0.01	-0.19	-9.07	-398.52
Sammaz 27	G	0.36	0.32	0.44	2.93	10.68*	0.00	4.61**	1.69**	1.24*	5.13**	0.81	0.15**	0.32	-9.50	623.70*
Sammaz 35	G	1.42	1.49	-0.28	-0.35	-0.43	2.06	-1.94	-0.36	-0.43	-2.32	-0.14	-0.03	-0.12**	-11.87	-404.44
Sammaz 29	G	-0.92	-1.46	-0.22	6.93	2.79	-1.89	0.67	-0.28	0.51	-1.60	-0.26	0.01	0.16	-5.01	530.37*
Sammaz 28	G	0.36	0.21	-0.11	3.88	-1.43	-0.06	2.22	0.92	0.24	2.85	0.26	0.06	0.04	29.71*	133.33
Sammaz 37 X Sammaz 19	R	-0.67	-3.67	-1.33	2.17	1.67	0.17	2.67	0.08	-1.33	2.50	-0.20	-0.03	0.31	5.82	635.56
Sammaz 17 X Sammaz 19	R	-0.17	3.17	1.33	15.50	5.33	-0.17	-0.67	0.50	1.33	4.00	0.13	0.02	0.02	3.65	4.44
Sammaz 17 X Sammaz 37	R	-0.83	0.17	1.00	-2.83	-0.33	0.67	-0.17	0.37	0.67	6.50*	0.38	-0.08	-0.11	4.21	-97.78
Sammaz 36 X Sammaz 19	R	0.83	-2.50	0.00	-11.67	-5.00	-0.50	-2.67	-0.12	-0.33	-3.50	0.03	0.07	-0.07	-12.35*	-257.78
Sammaz 36 X Sammaz 37	R	2.00	-3.83	1.00	-9.67	-5.50	2.17	-3.33	-1.00	-0.67	-4.00	-0.83	-0.03	0.01	-8.04	-57.78
Sammaz 36 X Sammaz 17	R	2.17	-0.50	0.00	-20.17	-2.17	2.83	-5.17*	-1.50	-0.33	-2.67	-0.58	-0.17	-0.07	-0.07	-88.89
Sammaz 27 X Sammaz 19	R	-5.17*	2.83	-0.33	-8.00	-8.00	-3.83	-1.50	-0.22	1.33	-0.50	0.83	0.08	0.43*	1.55	866.67*
Sammaz 27 X Sammaz 37	R	2.50	3.83	0.33	-13.33	1.50	3.50	1.67	-0.42	-1.00	1.00	-0.53	-0.12	-0.30	3.45	-537.78
Sammaz 27 X Sammaz 17	R	5.67*	1.17	0.67	-9.33	4.17	5.33*	3.67	-0.63	-0.33	3.67	0.70	0.03	0.03	-0.69	17.78
Sammaz 27 X Sammaz 36	R	-0.17	1.67	-0.50	-7.00	0.00	-0.83	-1.83	-0.37	-0.33	-2.00	-0.35	0.03	-0.36	0.97	-760.00

Sammaz 35 X Sammaz 19	R	-0.83	-1.67	-0.33	-6.33	-10.50	3.00	-0.33	1.25	2.00*	2.83	0.18	0.00	-0.21	-9.29	-471.11
Sammaz 35 X Sammaz 37	R	2.17	0.83	-2.00*	6.67	-0.50	0.00	-2.17	-0.42	-0.33	-1.17	0.23	0.03	0.32	-0.54	573.33
Sammaz 35 X Sammaz 17	R	1.00	-3.50	0.00	-11.00	-9.83	1.83	-1.17	-2.28*	-1.00	-7.33**	-0.37	-0.03	-0.19	-1.75	-435.56
Sammaz 35 X Sammaz 36	R	0.33	-3.50	-0.67	0.50	2.83	2.17	-1.67	-0.83	-1.67	-3.83	-1.12	-0.05	-0.23	6.16	-453.33
Sammaz 35 X Sammaz 27	R	-1.00	-0.50	-0.33	-3.33	17.83*	-1.33	1.83	0.75	0.00	0.17	0.12	0.02	0.32	-7.00	520.00
Sammaz 29 X Sammaz 19	R	-2.17	-2.00	-1.33	26.67*	3.50	-3.33	2.00	-1.67	0.33	-2.17	-0.13	-0.02	0.06	-6.52	53.33
Sammaz 29 X Sammaz 37	R	-3.83	2.00	-0.67	-15.50	-11.50*	-2.33	-0.17	-2.00	0.00	-3.17	-0.05	-0.12	0.49*	0.40	991.11*

Table 4.14 continued

Genotype	status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy
Sammaz 29 X Sammaz 17	R	1.33	1.00	-0.33	-5.83	5.00	0.33	-5.33*	-3.70*	-1.50	-6.33*	-1.37	-0.33**	-0.11	-7.02	-328.89
Sammaz 29 X Sammaz 36	R	-4.83*	1.00	0.67	-3.50	-4.67	-1.17	2.33	0.15	1.00	-1.00	-0.43	0.07	0.33	9.26	982.22*
Sammaz 29 X Sammaz 27	R	1.67	-2.00	-0.67	4.17	14.00*	1.33	-0.50	0.00	0.33	-0.67	0.32	0.10	0.18	0.92	404.44
Sammaz 29 X Sammaz 35	R	1.00	1.33	0.00	22.17*	6.83	2.67	3.00	1.83	0.67	4.17	0.75	0.02	0.29	5.51	600.00
Sammaz 28 X Sammaz 19	R	2.17	-4.83	-1.00	-0.17	-1.17	1.50	-3.17	1.00	0.00	6.00*	0.70	-0.02	-0.00	-13.22*	-240.00
Sammaz 28 X Sammaz 37	R	2.17	-3.67	0.33	-2.83	-1.67	2.50	2.33	-1.27	-0.67	-5.17	-0.03	-0.07	-0.09	1.51	-146.67
Sammaz 28 X Sammaz 17	R	-1.33	1.50	0.33	25.17*	0.33	0.17	4.00	0.42	-0.33	2.00	0.43	0.13	-0.19	1.99	-284.44
Sammaz 28 X Sammaz 36	R	1.00	4.17	-0.67	7.50	6.67	1.50	2.00	1.50	2.17*	6.50*	0.32	0.03	0.19	9.12	454.22
Sammaz 28 X Sammaz 27	R	-2.17	-2.83	0.33	-6.33	4.33	0.00	2.00	2.18	0.67	5.33	0.32	0.25*	0.30	14.36**	813.33*
Sammaz 28 X Sammaz 35	R	1.17	0.67	-1.00	0.33	1.83	-4.67	0.33	0.17	0.33	-0.33	0.60	0.08	0.14	-4.91	240.00
Sammaz 28 X Sammaz 29	R	-0.33	-5.67	1.00	7.17	-1.67	-2.50	-0.33	1.50	1.67	4.33	0.17	0.15	0.07	8.86	288.89

Sammaz 19 X Sammaz 37	S	-0.40	-0.78	-0.33	5.93	10.49	2.37	4.18	-0.26	-1.54	1.42	-0.89	-0.13	0.11	-20.05	106.03
Sammaz 19 X Sammaz 17	S	-1.29	1.50	1.28	12.82	3.10	-2.02	0.41	1.50	2.07	5.14	-0.23	0.08	0.20	-11.12	572.70
Sammaz 19 X Sammaz 36	S	3.05	2.44	0.22	-5.24	0.66	0.75	-2.76	1.81	-0.65	-2.47	0.39	0.18	-0.06	-39.60	-273.23
Sammaz 19 X Sammaz 27	S	-5.90*	-6.22*	0.56	-5.29	-12.68	-6.25*	2.41	-0.25	0.35	-2.97	0.47	-0.01	0.69**	-21.92	1326.77*
Sammaz 19 X Sammaz 35	S	1.71	1.28	0.61	-2.68	-0.23	2.37	3.35	-2.93*	-0.65	-4.86	-0.42	0.06	-0.25	-35.52	-462.86
Sammaz 19 X Sammaz 29	S	-0.29	-0.44	-0.78	8.37	-0.79	-1.36	-1.37	-0.51	0.41	-0.25	0.24	-0.01	-0.28	-34.85	-899.89
Sammaz 19 X Sammaz 28	S	3.10	2.22	-1.56	-13.91	-0.56	4.14	-6.21*	0.63	0.02	3.98	0.45	-0.16	-0.40	163.06*	-369.52
Sammaz 37 X Sammaz 17	S	-2.73	-3.06	0.94	12.32	1.88	-3.02	-0.21	2.80*	1.18	4.98	1.23	0.19	0.29	4.14	408.26
Sammaz 37 X Sammaz 36	S	2.27	3.22	1.22	13.60	2.44	2.42	-0.37	-0.05	-0.21	2.03	-0.03	0.09	-0.29	-0.36	-766.56
Sammaz 37 X Sammaz 27	S	1.33	0.89	-1.11	-14.13	-6.56	2.09	-4.54	-1.01	-0.54	1.53	-0.81	-0.14	-0.32	12.20	-606.56
Sammaz 37 X Sammaz 35	S	-0.06	-0.61	-0.39	2.48	-1.45	-3.64	-0.98	-0.46	0.46	1.31	0.20	0.00	0.21	3.99	243.81
Sammaz 37 X Sammaz 29	S	-0.73	-0.67	-0.44	-20.79	-10.34	-0.36	-1.26	-1.37	-0.48	-5.08	0.16	0.06	-0.08	29.87	597.89
Sammaz 37 X Sammaz 28	S	0.33	1.00	0.11	0.60	3.55	0.14	3.18	0.34	1.13	-6.19	0.14	-0.08	0.07	-29.80	17.14
Sammaz 17 X Sammaz 36	S	-1.95	-3.50	-0.83	-9.18	3.71	-1.64	1.85	0.54	1.41	1.09	0.60	-0.07	0.20	15.30	508.99

Table 4.14 continued

Genotype	status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy
Sammaz 17 X Sammaz 27	S	4.10	4.83	0.50	-22.24	-5.62	4.37	-0.32	-0.92	-0.93	0.92	0.39	0.04	-0.30	9.43	-584.34
Sammaz 17 X Sammaz 35	S	-2.29	-2.00	-0.11	3.04	2.49	-1.69	3.91	1.06	-0.60	0.03	-0.10	0.01	0.05	14.89	274.92
Sammaz 17 X Sammaz 29	S	4.38	3.28	-1.50	-12.57	-1.06	3.25	-7.04	-5.51**	-3.21**	-10.69*	-2.25	-0.36*	-0.36	2.34	-979.90
Sammaz 17 X Sammaz 28	S	-0.23	-1.06	-0.28	15.82	-4.51	0.75	1.41	0.53	0.07	-1.47	0.36	0.10	-0.07	-34.98	-200.63

Sammaz 36 X Sammaz 27	S	-0.56	-0.56	0.11	-3.63	-2.06	-3.19	-3.15	-0.94	-0.32	-1.69	-0.54	-0.13	-0.31	8.58	-674.71
Sammaz 36 X Sammaz 35	S	1.71	1.61	-0.83	5.98	0.38	5.09	-1.60	-1.22	-1.32	-1.91	-0.66	0.04	-0.22	25.70	-313.23
Sammaz 36 X Sammaz 29	S	-6.95*	-6.11*	-1.22	-0.29	-9.51	-5.64	5.46	1.84	1.74	4.03	0.36	0.00	0.55	18.67	1400.85*
Sammaz 36 X Sammaz 28	S	2.44	2.89	1.33	-1.24	4.38	2.20	0.57	-1.99	-0.65	-1.08	-0.13	-0.11	0.13	-28.29	117.88
Sammaz 27 X Sammaz 35	S	-1.56	-1.39	-0.83	11.60	1.38	-1.25	1.24	1.41	1.02	2.25	0.12	-0.08	0.22	7.54	442.33
Sammaz 27 X Sammaz 29	S	3.44	3.22	1.78	29.32*	26.16**	3.03	0.63	2.49	1.41	2.53	0.98	0.18	-0.07	7.49	-199.16
Sammaz 27 X Sammaz 28	S	-0.84	-0.78	-1.00	4.37	-0.62	1.20	3.74	-0.79	-0.98	-2.58	-0.61	0.14	0.09	-23.33	295.66
Sammaz 35 X Sammaz 29	S	2.71	3.06	1.17	-9.41	-2.40	4.31	0.18	1.96	0.41	2.64	0.79	-0.01	0.03	3.28	-122.12
Sammaz 35 X Sammaz 28	S	-2.23	-1.94	0.39	-11.02	-0.18	-5.19	-1.37	-0.90	0.68	0.53	0.07	-0.03	-0.04	-19.88	-62.86
Sammaz 29 X Sammaz 28	S	-2.56	-2.33	1.00	5.37	-2.06	-3.25	-1.32	2.19	-0.26	6.81	-0.28	0.14	0.22	-26.60	202.33

**,* significant at 1% and 5% levels, respectively. G, R and S are General Combining Ability, Reciprocal and Specific Combining Ability effects, respectively.

KEY: df: Degrees of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length, KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

Table 4. 15 GCA, Reciprocal and SCA effects of fifteen characters combined across environments

Genotype	Status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy
Sammaz 19	G	-0.04	1.47	0.11	3.24	2.64	-0.44	-0.01	-0.06	0.03	-0.90	-0.06	-0.05*	-0.09	-0.60	-157.07
Sammaz 37	G	0.40	-1.02	-0.13	0.61	0.15	-0.10	0.59	-0.23	-0.18	-0.30	-0.19	0.00	-0.05	-3.08*	-150.96
Sammaz 17	G	-0.09	1.51	-0.22	-2.36	-0.93	0.86	0.02	0.32	-0.10	0.65	-0.02	0.02	0.06	1.70	91.82
Sammaz 36	G	1.10	-2.59**	0.29	1.28	-2.03	0.52	-0.79	0.20	-0.25	-0.92	0.66*	0.02	-0.12	0.67	-217.68
Sammaz 27	G	-0.03	1.92*	0.22	3.42	3.12	-0.13	1.68*	0.17	0.57**	2.23**	0.23	0.01	0.18*	0.85	367.65*
Sammaz 35	G	0.19	-1.24	-0.16	-1.48	-0.43	0.66	-1.13	-0.15	-0.07*	0.42	-0.28	-0.01	0.00	1.96	23.76

Sammaz 29	G	-0.28	1.58	0.20	-1.26	-0.16	-0.45	0.03	-0.20	0.08	-0.44	-0.15	0.01	0.02	0.40	124.04
Sammaz 28	G	-1.24	-1.63	-0.31	-3.46	-2.37	-0.92	-0.39	-0.03	-0.08	-0.75	-0.19	-0.00	-0.01	-1.90	-81.57
Sammaz 37 X Sammaz 19	R	0.67	-4.67	-1.00	-1.42	-2.50	0.25	1.50	0.42	-0.67	-0.25	-0.26	-0.08	-0.15	-1.37	-393.33
Sammaz 17 X Sammaz 19	R	0.58	1.17	0.67	6.75	0.75	1.33	0.75	-0.01	0.67	3.00	-0.03	-0.03	-0.22	-1.34	-528.89
Sammaz 17 X Sammaz 37	R	-0.83	1.25	0.33	1.08	2.17	-0.08	1.42	-0.54	0.17	6.08**	0.17	-0.02	0.07	5.74	280.00
Sammaz 36 X Sammaz 19	R	0.50	-3.33	-0.33	-9.25	-6.67	0.17	-2.42	-0.70	-0.33	-3.42	0.08	0.03	-0.29	-7.74	-731.11
Sammaz 36 X Sammaz 37	R	0.42	-1.08	0.33	-9.17	-6.33	0.50	-1.42	-0.75	-0.83	-2.92	-0.43	-0.11	-0.11	-4.67	-262.22
Sammaz 36 X Sammaz 17	R	0.83	0.67	-0.17	-15.17	-1.25	2.58	-2.17	-0.29	-0.50	-1.50	-0.26	-0.16	0.01*	-3.60	-33.33
Sammaz 27 X Sammaz 19	R	-2.25	0.67	-0.33	-2.75	-5.92	-1.75	-0.25	0.04	1.00	1.75	0.58	0.06	0.33	3.64	666.67
Sammaz 27 X Sammaz 37	R	2.33	4.58	0.33	-10.83	-2.58	3.33	-0.67	-0.63	-0.83	0.33	-0.16	-0.05	-0.28	3.60	-486.67
Sammaz 27 X Sammaz 17	R	1.75	0.17	0.33	-8.00	2.25	1.25	2.33	0.27	0.33	3.00	0.50	0.09	0.34	0.24	613.33
Sammaz 27 X Sammaz 36	R	-0.50	2.58	0.25	0.17	-0.83	-1.42	-3.08	-0.10	0.00	-1.17	-0.27	-0.01	-0.24	-2.29	-591.11
Sammaz 35 X Sammaz 19	R	-0.25	-3.67	0.17	6.75	0.92	1.00	0.83	1.46	1.00	2.50	0.07	0.03	0.09	-5.79	206.67
Sammaz 35 X Sammaz 37	R	0.83	0.67	-1.00	-0.67	-0.25	-0.58	-1.92	-0.16	-0.83	0.42	0.14	-0.06	-0.12	-3.00	-404.45
Sammaz 35 X Sammaz 17	R	1.83	-3.17	0.17	2.92	0.17	0.75	-0.25	-0.93	-0.17	-4.17	-0.18	0.03	0.04	-3.06	-75.56
Sammaz 35 X Sammaz 36	R	-0.25	-1.42	-0.17	3.25	3.17	1.42	-2.75	-0.14	-0.67	-0.75	-0.48	-0.06	-0.13	4.17	-133.33
Sammaz 35 X Sammaz 27	R	-0.92	-1.83	-0.67	9.92	16.50	-3.08**	2.42	1.03	-0.50	2.17	0.25	-0.01	0.48	-0.24	1068.89*
Sammaz 29 X Sammaz 19	R	0.42	-1.50	-0.33	16.58*	-0.25	4.00	0.75	-0.31	-0.17	-2.25	-0.23	-0.02	-0.25	-6.61	-577.78

Table 4.15 continued

Genotype	Status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy

Sammaz 29 X Sammaz 37	R	-1.25	1.83	0.25	-5.50	-1.83	-0.42	2.75	0.00	-0.33	2.25	0.03	-0.04	0.54*	8.51*	1146.67*
Sammaz 29 X Sammaz 17	R	0.83	1.25	0.17	-4.75	-1.00	0.75	-3.25	-1.52	-0.58	-3.17	-0.80	-0.14	0.07	-2.69	108.89
Sammaz 29 X Sammaz 36	R	-2.83	1.17	1.17	5.75	5.67	0.17	1.92	1.16	0.67	-0.67	-0.13	0.03	0.16	3.10	528.89
Sammaz 29 X Sammaz 27	R	0.92	0.83	-0.67	-4.75	1.58	0.92	0.25	-0.45	0.17	-1.92	0.16	0.03	-0.06	-1.26	-133.33
Sammaz 29 X Sammaz 35	R	1.17	2.67	0.67	10.50	3.75	1.83	2.33	1.67	0.67	3.67	0.35	0.04	0.25	1.56	440.00
Sammaz 28 X Sammaz 19	R	1.08	-1.17	0.00	-0.25	-0.75	0.33	-0.67	0.23	-0.17	2.33	0.23	-0.05	-0.21	-9.41*	-344.44
Sammaz 28 X Sammaz 37	R	1.75	-1.83	-0.17	-0.33	-0.67	1.33	1.92	-0.44	0.00	-2.58	-0.21	-0.06	-0.03	-2.86	-262.22
Sammaz 28 X Sammaz 17	R	1.33	-2.33	-0.33	14.58	-0.58	1.25	2.08	0.31	0.00	2.33	0.29	0.05	0.05	1.37	66.67
Sammaz 28 X Sammaz 36	R	1.42	0.25	-0.33	4.33	3.08	3.25	1.33	0.68	0.92	2.83	0.24	0.08	0.32	4.58	507.11
Sammaz 28 X Sammaz 27	R	-0.67	-3.75	0.00	-2.92	0.42	1.00	0.83	1.25	0.50	5.25*	0.35	0.17*	0.32	8.10*	735.56
Sammaz 28 X Sammaz 35	R	1.83	-0.75	-0.83	5.17	2.75	-1.42	0.00	0.17	0.00	2.08	0.45	0.02	0.17	-2.29	353.33
Sammaz 28 X Sammaz 29	R	0.08	-4.83	-0.17	0.92	-2.58	-1.17	-0.75	0.00	0.67	1.00	0.08	0.06	-0.05	4.36	-11.11
Sammaz 19 X Sammaz 37	S	0.03	-1.40	-0.47	5.86	3.40	1.81	1.54	0.38	0.22	0.71	-0.20	-0.14*	0.18	2.75	275.96
Sammaz 19 X Sammaz 17	S	-0.40	0.41	0.29	2.00	-0.77	0.77	-0.65	0.37	0.48	1.35	-0.00	0.01	-0.06	3.48	-31.26
Sammaz 19 X Sammaz 36	S	0.82	0.01	0.11	7.19	4.59	0.44	-1.00	1.40	0.29	1.49	-0.60	0.12	0.41	0.36	733.79
Sammaz 19 X Sammaz 27	S	-1.96	0.50	-0.16	-7.95	-6.49	-1.49	0.70	0.02	0.14	-2.99	0.31	-0.05	0.12	1.28	306.24
Sammaz 19 X Sammaz 35	S	1.49	-0.84	0.06	12.11	8.23	0.97	-0.74	-1.79*	-1.55*	-2.26	-0.11	-0.02	-0.10	-2.13	-196.54
Sammaz 19 X Sammaz 29	S	-0.04	1.00	0.19	-5.77	-2.87	-4.10	0.01	0.21	0.46	2.01	0.28	-0.02	0.05	1.89	52.07
Sammaz 19 X Sammaz 28	S	1.12	0.43	-0.58	-1.39	-1.24	0.49	-2.12	0.48	0.62	1.47	0.11	-0.11	0.12	-1.26	344.50
Sammaz 37 X Sammaz 17	S	-0.08	-1.02	-0.81	5.30	-1.86	-1.15	-1.24	-0.12	0.19	-2.45	0.25	0.09	0.07	-2.67	29.29
Sammaz 37 X Sammaz 36	S	-0.37	-0.08	-0.32	5.40	3.91	1.10	1.57	-0.01	-0.33	1.61	-0.84	-0.01	-0.09	3.47	-181.21

Sammaz 37 X Sammaz 27	S	-0.65	-0.43	0.08	-6.57	-5.50	0.42	-3.15	-0.52	-0.16	0.38	-0.11	0.01	0.00	3.99	115.68
Sammaz 37 X Sammaz 35	S	-0.53	1.48	0.46	3.50	0.89	-0.95	0.58	-0.24	-0.18	-1.23	-0.08	-0.03	0.05	-2.85	21.79
Sammaz 37 X Sammaz 29	S	1.19	-1.01	0.85	-4.39	-1.47	0.32	-2.25	-0.11	-0.17	-2.87	0.05	0.06	-0.26	-5.31	-118.49
Sammaz 37 X Sammaz 28	S	-2.45	-1.40	0.68	17.40	5.52	0.32	2.06	0.78	0.24	-2.64	-0.32	0.05	0.58	5.71	1135.06

Table 4.15 continued

Genotype	Status	Daf	Das	NL	PH	EH	DM	Ep	EL	KRN	KPR	ED	CD	Cw	Tp	Gy
Sammaz 17 X Sammaz 36	S	-2.63	-1.20	-0.39	0.71	-0.09	-1.11	-0.12	-0.10	0.26	-1.76	-0.62	-0.02	-0.24	-0.09	-501.76
Sammaz 17 X Sammaz 27	S	1.26	0.79	0.17	-4.76	1.42	1.55	-1.09	-0.88	-0.40	-0.40	0.04	-0.01	-0.12	0.93	-191.54
Sammaz 17 X Sammaz 35	S	-1.38	0.78	-0.28	11.72	10.56*	-1.08	2.48*	1.99	0.08	4.08*	0.35	-0.04	0.27	3.37	667.90
Sammaz 17 X Sammaz 29	S	0.59	-0.29	0.36	3.00	-1.05	0.03	0.48	-1.43	-0.49	-0.90	-0.37	0.02	0.28	4.40	552.07
Sammaz 17 X Sammaz 28	S	-0.52	-0.87	0.08	13.34	5.35	-0.30	-2.67	0.38	1.31	2.06	0.17	-0.13	0.36	5.43	782.28
Sammaz 36 X Sammaz 27	S	1.15	0.15	0.75	-7.58	-1.89	0.88	-0.69	0.08	0.08	1.99	-0.92	-0.03	0.11	1.97	242.40
Sammaz 36 X Sammaz 35	S	1.68	-0.70	0.55	-4.26	-1.51	2.09	0.12	0.18	0.06	1.89	-0.57	0.12	0.20	8.99*	626.29
Sammaz 36 X Sammaz 29	S	-0.94	3.06	-1.15*	1.19	-4.28	-2.06	0.62	-0.46	0.24	-2.67	-0.86	-0.06	0.03	-2.18	28.24
Sammaz 36 X Sammaz 28	S	2.26	0.62	-0.07	-2.43	-2.25	-1.30	-2.56	-3.81**	-1.08	-5.17	-6.11**	-0.07	0.12	11.99	596.78
Sammaz 27 X Sammaz 35	S	-0.19	-0.29	-0.22	6.77	-3.16	-1.92	0.15	1.14	0.74	0.16	0.37	0.05	0.01	2.32	52.07
Sammaz 27 X Sammaz 29	S	0.95	-2.12	-0.59	19.38**	13.15**	0.85	1.49	1.41	0.58	3.10	0.57	0.09	0.07	2.95	131.79
Sammaz 27 X Sammaz 28	S	1.54	-2.71	0.53	20.46	2.24	2.79	2.74	0.22	0.49	-1.27	0.24	0.20	0.13	11.72	695.89
Sammaz 35 X Sammaz 29	S	0.48	-1.13	0.13	-15.64*	-4.30	0.48	-0.45	0.28	0.06	-2.67	-0.03	-0.04	-0.08	-4.14	-199.87
Sammaz 35 X Sammaz 28	S	-0.91	0.97	0.31	20.65	10.85	0.67	5.09	1.43	0.34	5.42	-0.20	-0.07	0.19	16.38	783.11

Sammaz 29 X Sammaz 28	S	0.21	0.38	-0.66	1.28	0.46	-5.69	2.34	0.28	-0.50	0.98	-0.51	0.17	0.56	8.57	1381.17

**,* significant at 1% and 5% levels, respectively. G, R and S are General Combining Ability, Reciprocal and Specific Combining Ability effects, respectively.

KEY: df: Degrese of freedom, Daf: Days to flower, Das: Days to silk, NL: Number of leaves, PH: Plant height, EH: Ear height, DM: Days to maturity, Ep: Ears per plot, EL: Ear length,

KRN: Kernel row number, KPR: Kernels per row, ED: Ear diameter, CD: Cob diameter, CW: Cob weight, Tp: Threshing percentage, Gy: Grain yield/ha

4.3.4 Estimates of Heterosis and inbreeding depression

The percent heterosis for environments one and two are presented in Tables 4.16 and 4.17, respectively. Table 4.16 indicated high parent heterosis for six traits at environment one. Ten out of twenty eight hybrids exhibited negative heterosis for grain yield. The magnitude of percent heterosis for the trait ranged from -59.09 to 927.03. Sammaz 36 x Sammaz 35 exhibited highly significant positive heterosis for cob weight and grain yield. The values for number of leaves, plant height, ear height, and cob weight ranged from -14.3 to 13.2, -19.8 to 19.9, -13.2 to 40 and -39.4 to 862.5, respectively. Percentage for high parent heterosis for environment two (Table 4.17) indicated that thirteen out of twenty eight hybrids exhibited negative heterosis. The magnitude of percent heterosis ranged from -87 to 480 for cob weight and -89.7 to 397.1 for grain yield. Sammaz 19 x Sammaz 27 exhibited highly significant positive heterosis for cob weight and grain yield. At environment one (Table 4.18) the estimate of inbreeding depression indicated that four selfs out of eight had a positive value for grain yield and days to tasselling. Sammaz 19 x Sammaz 19 recorded high negative estimate for grain yield (-182.10%). Five out of eight had negative values for days to silk and plant height whereas for days to maturity only three selfs out of eight had negative values. Sammaz 35 x Sammaz 35 recorded high negative value (-273). Negative heterosis for grain yields in hybrids ranged from -9.36% (Sammaz 37 x Sammaz 17) to -1260.70% (Sammaz 36 x Sammaz 35). The results for days to tasselling, days to silk, plant height, and days to maturity ranged from -6.03 to 9.34, -8.08 to 8.41, -28 to 12.53 and -9.45 to 8.41, respectively. In environment two (Table 4.19), four selfs out of the eight had negative estimates of inbreeding depression. Sammaz 35 x Sammaz 35 (-1707.80%) recorded high negative value for grain yield. Four, five and three out of eight selfs had positive estimates for days to tasselling, days to silk and days to maturity, respectively. The results indicated that seven out of the eight selfs had negative values for plant height. Sammaz 35 x Sammaz 35

recorded high negative value (-71.48). The estimates for yields of hybrids ranged from -491.39% (Sammaz 19 x Sammaz 27) to 83.85% (Sammaz 19 x Sammaz 35). The values for days to tasselling, days to silk, plant height and days to maturity ranged from -9.64 to 11, -7.09 to 9.53, -33 to 23.64 and -6 to 8.68, respectively. For the combined data across environments (Table 4.20), five out of the eight selfs recorded high negative estimates for grain yield. Four out of the eight selfs recorded high negative estimates for days to tasselling and days to maturity. Three and six selfs recorded high negative values for days to silk and plant height, respectively. The reduction in yields for the hybrids ranged from 21.59% (Sammaz 19 x Sammaz 37) to -162.16% (Sammaz 36 x Sammaz 29). The results for days to tasselling, days to silk, plant height, and days to maturity ranged from -6.34 to 8.14, -6.95 to 7.21, -24.49 to 16.53 and -6.24 to 5.36, respectively.

Table 4.16 Percent Heterosis of five characters in environment one

Genotype	NL	PH	EH	Cw	Gy
Sammaz 19 x Sammaz 37	4.8	-8.2	-5.9	-16.1	-33.7
Sammaz 19 x Sammaz 17	-4.8	-10.2	10.9	-29.9	-40.8
Sammaz 19 x Sammaz 36	0	-5.2	12.6	28.0	49.6
Sammaz 19 x Sammaz 27	0	-19.8	-10.3	16.8	29.2
Sammaz 19 x Sammaz 35	0	10.6	50	38.5	86.0
Sammaz 19 x Sammaz 29	0	-10.0	4.0	-7.7	14.2
Sammaz 19 x Sammaz 28	-14.3	-19.8	-1.2	-39.4	-59.1
Sammaz 37 x Sammaz 17	10.0	1.0	-8.3	4.1	1.6
Sammaz 37 x Sammaz 36	5.0	-13.5	-13.2	-23.0	-27.4
Sammaz 37 x Sammaz 27	0	-10.5	-25	-30.3	-28.2
Sammaz 37 x Sammaz 35	10.0	1.9	-1.0	-28.4	-44.2
Sammaz 37 x Sammaz 29	5.0	-4.5	-3.4	27.2	28.9
Sammaz 37 x Sammaz 28	-5.0	-1.2	-7.4	15.5	-30.6
Sammaz 17 x Sammaz 36	0	-15.9	-4.1	-26.3	-39.2
Sammaz 17 x Sammaz 27	-5.0	0.5	17.1	74.8	75
Sammaz 17 x Sammaz 35	10.0	19.9	37.4	68.5	68.5
Sammaz 17 x Sammaz 29	5.3	5.9	-5.8	86.8	92.3
Sammaz 17 x Sammaz 28	10.5	4.6	0	39.8	22.4
Sammaz 36 x Sammaz 27	10.0	-7.0	-6.3	3.9	1.7

Sammaz 36 x Sammaz 35	5.0	-9.2	14.7	862.5**	927.0**
Sammaz 36 x Sammaz 29	13.2	0.9	35.2	91.5	74.8
Sammaz 36 x Sammaz 28	10.5	-6.1	9.4	968	-4.8
Sammaz 27 x Sammaz 35	15	17.7	40.0	64.2	91.0
Sammaz 27 x Sammaz 29	5.0	-3.2	-2.3	1.8	0.7
Sammaz 27 x Sammaz 28	0	3.9	2.3	34.4	23.1
Sammaz 35 x Sammaz 29	-0.0	-6.5	4.1	205.1	196.8
Sammaz 35 x Sammaz 28	10.0	13.9	11.8	22.5	13.1
Sammaz 29 x Sammaz 28	5.3	1.2	1.3	-0.9	-7.6
SE±	1.34	20.26	13.35	0.84	1710.20

Table 4.17 Percent Heterosis for two characters in environment two

Genotype	Cw	Gy
Sammaz 19 x Sammaz 37	198.8	160.9
Sammaz 19 x Sammaz 17	86.1	85.5
Sammaz 19 x Sammaz 36	-55.9	-61.3
Sammaz 19 x Sammaz 27	480**	397.1**
Sammaz 19 x Sammaz 35	-85.5	-89.7
Sammaz 19 x Sammaz 29	-35.7	-45.3
Sammaz 19 x Sammaz 28	-46.6	40.6
Sammaz 37 x Sammaz 17	254.7	244.6
Sammaz 37 x Sammaz 36	-44.7	-38.7
Sammaz 37 x Sammaz 27	298.3	344.7
Sammaz 37 x Sammaz 35	-8.1	-25.3
Sammaz 37 x Sammaz 29	45.4	122.7
Sammaz 37 x Sammaz 28	216.0	261.3
Sammaz 17 x Sammaz 36	-29.3	-7.3
Sammaz 17 x Sammaz 27	82.7	91.1
Sammaz 17 x Sammaz 35	-63	-65.2
Sammaz 17 x Sammaz 29	-62.2	-65.3
Sammaz 17 x Sammaz 28	36.4	53.2
Sammaz 36 x Sammaz 27	-23.4	-9.7
Sammaz 36 x Sammaz 35	-86.5	-85.4
Sammaz 36 x Sammaz 29	88.3	123.3
Sammaz 36 x Sammaz 28	1.1	17.8
Sammaz 27 x Sammaz 35	9.1	-6.3

Sammaz 27 x Sammaz 29	74.0	80.0
Sammaz 27 x Sammaz 28	276.2	353.2
Sammaz 35 x Sammaz 29	-26.9	-35.6
Sammaz 35 x Sammaz 28	-46.1	-50.6
Sammaz 29 x Sammaz 28	75.1	73.3
SE±	0.47	1028

Table 4.18 percent inbreeding depression in environment one

Genotype	Status	Daf	Das	PH	DM	GY
Sammaz 19 x Sammaz 19	Self	-15.43	-15.26	-24.93	6.25	-182.10
Sammaz 37 x Sammaz 37	Self	4.99	6.05	-9.35	0.00	-63.77
Sammaz 17 x Sammaz 17	Self	7.81	6.57	-7.18	5.73	-5.06
Sammaz 36 x Sammaz 36	Self	-1.15	-2.12	-0.22	-2.12	82.64
Sammaz 27 x Sammaz 27	Self	1.63	-0.38	0.25	1.08	24.60
Sammaz 35 x Sammaz 35	Self	-6.25	-3.83	-6.05	-2.73	81.34
Sammaz 29 x Sammaz 29	Self	4.82	3.37	2.50	3.43	28.63
Sammaz 28 x Sammaz 28	Self	-5.15	-3.97	16.93	-0.28	-51.34
Sammaz 19 x Sammaz 37	Hybrid	3.78	3.72	0.93	-3.68	26.50
Sammaz 19 x Sammaz 17	Hybrid	2.92	3.42	-0.51	-9.45	29.95

Sammaz 19 x Sammaz 36	Hybrid	8.49	7.72	1.63	-1.02	-169.15
Sammaz 19 x Sammaz 27	Hybrid	9.21	8.41	12.53	-2.44	-48.73
Sammaz 19 x Sammaz 35	Hybrid	8.45	7.61	-21.81	-2.13	-205.12
Sammaz 19 x Sammaz 29	Hybrid	3.47	6.21	-5.15	-4.66	-43.48
Sammaz 19 x Sammaz 28	Hybrid	9.34	8.25	1.92	-0.63	50.41
Sammaz 37 x Sammaz 17	Hybrid	-5.18	-8.08	-5.07	-1.51	-9.36
Sammaz 37 x Sammaz 36	Hybrid	2.54	4.16	9.90	1.73	-33.33
Sammaz 37 x Sammaz 27	Hybrid	-4.70	-5.50	9.48	-3.96	25.08
Sammaz 37 x Sammaz 35	Hybrid	0.40	-0.56	-4.13	1.75	5.12
Sammaz 37 x Sammaz 29	Hybrid	-4.96	-5.36	-4.15	-0.68	-74.64
Sammaz 37 x Sammaz 28	Hybrid	0.00	-3.04	-13.20	0.27	23.26
Sammaz 17 x Sammaz 36	Hybrid	0.80	1.28	8.99	-3.21	-12.87
Sammaz 17 x Sammaz 27	Hybrid	-5.86	-7.51	-3.50	-2.47	-80.75
Sammaz 17 x Sammaz 35	Hybrid	-3.87	-5.12	-22.13	-0.54	-192.77
Sammaz 17 x Sammaz 29	Hybrid	-3.59	-2.34	-11.23	-1.10	-173.11
Sammaz 17 x Sammaz 28	Hybrid	-6.03	-4.63	-15.67	-2.62	-26.07
Sammaz 36 x Sammaz 27	Hybrid	-1.58	-2.54	2.07	0.27	-87.93
Sammaz 36 x Sammaz 35	Hybrid	2.51	5.71	3.37	2.10	-1260.70
Sammaz 36 x Sammaz 29	Hybrid	-0.60	5.30	-14.21	-0.53	-194.04
Sammaz 36 x Sammaz 28	Hybrid	0.59	1.63	-11.39	1.47	-77.43
Sammaz 27 x Sammaz 35	Hybrid	2.62	1.12	-19.02	8.89	-228.92
Sammaz 27 x Sammaz 29	Hybrid	-3.97	-4.03	-4.59	-1.37	-40.15
Sammaz 27 x Sammaz 28	Hybrid	1.44	-0.19	-17.91	-1.78	-30.76
Sammaz 35 x Sammaz 29	Hybrid	-0.81	-1.70	0.00	0.54	-333.23
Sammaz 35 x Sammaz 28	Hybrid	1.20	3.19	-28.03	-0.14	-97.91
Sammaz 29 x Sammaz 28	Hybrid	-0.83	0.00	-6.76	0.14	-33.48

Table 4.19 percent inbreeding depression in environment two

Genotype	Status	Daf	Das	PH	DM	GY
Sammaz 19 x Sammaz 19	Self	-1.54	-0.46	-6.32	-0.36	50.36
Sammaz 37 x Sammaz 37	Self	-0.48	0.44	-28.57	-2.50	65.38
Sammaz 17 x Sammaz 17	Self	2.90	2.62	-2.86	0.35	-9.82
Sammaz 36 x Sammaz 36	Self	-7.46	-7.73	-8.79	-6.03	-188.38
Sammaz 27 x Sammaz 27	Self	-7.92	-6.79	-23.16	-9.52	41.25
Sammaz 35 x Sammaz 35	Self	4.19	4.64	-71.48	3.73	-1707.80
Sammaz 29 x Sammaz 29	Self	1.03	0.47	23.00	4.67	-20.00
Sammaz 28 x Sammaz 28	Self	6.31	5.33	-4.22	-3.61	36.74
Sammaz 19 x Sammaz 37	Hybrid	1.72	0.22	8.78	-2.84	-275.01
Sammaz 19 x Sammaz 17	Hybrid	1.25	-4.09	-11.85	0.71	-104.81
Sammaz 19 x Sammaz 36	Hybrid	-2.90	-1.32	16.39	1.04	50.25
Sammaz 19 x Sammaz 27	Hybrid	11.06	9.49	14.57	8.68	-491.39
Sammaz 19 x Sammaz 35	Hybrid	-4.45	-4.29	19.26	-5.17	83.85
Sammaz 19 x Sammaz 29	Hybrid	-1.28	-0.70	-13.76	3.37	25.11
Sammaz 19 x Sammaz 28	Hybrid	-8.44	-6.98	9.24	-4.26	-48.09
Sammaz 37 x Sammaz 17	Hybrid	3.90	2.00	-8.23	1.40	-365.06
Sammaz 37 x Sammaz 36	Hybrid	-1.18	-2.38	4.45	-1.02	-0.67
Sammaz 37 x Sammaz 27	Hybrid	1.17	0.00	23.64	-0.34	-464.85
Sammaz 37 x Sammaz 35	Hybrid	-1.20	-1.77	18.20	0.88	-35.00
Sammaz 37 x Sammaz 29	Hybrid	0.00	-0.46	13.89	1.92	-277.41
Sammaz 37 x Sammaz 28	Hybrid	-3.48	-5.24	0.27	-0.35	-403.38
Sammaz 17 x Sammaz 36	Hybrid	3.12	5.22	9.12	2.06	-27.78
Sammaz 17 x Sammaz 27	Hybrid	-4.53	-6.32	18.64	-3.78	-107.75
Sammaz 17 x Sammaz 35	Hybrid	0.25	-1.11	5.72	-2.29	43.04

Sammaz 17 x Sammaz 29	Hybrid	-9.64	-7.09	-10.40	-2.99	49.52
Sammaz 17 x Sammaz 28	Hybrid	-4.57	-3.67	-33.00	-2.11	-61.01
Sammaz 36 x Sammaz 27	Hybrid	4.15	4.44	15.28	7.02	-31.00
Sammaz 36 x Sammaz 35	Hybrid	-3.32	-1.94	15.09	-6.00	80.37
Sammaz 36 x Sammaz 29	Hybrid	9.53	9.53	-5.54	9.40	-144.53
Sammaz 36 x Sammaz 28	Hybrid	-6.11	-4.89	0.00	-0.34	-57.00
Sammaz 27 x Sammaz 35	Hybrid	2.36	1.30	9.63	0.86	-58.00
Sammaz 27 x Sammaz 29	Hybrid	-4.62	-3.56	-30.22	0.85	-174.11
Sammaz 27 x Sammaz 28	Hybrid	-0.24	-0.67	-5.26	1.02	-415.60
Sammaz 35 x Sammaz 29	Hybrid	-8.27	-7.27	9.73	-5.26	19.11
Sammaz 35 x Sammaz 28	Hybrid	-2.76	-2.96	14.80	2.98	20.64
Sammaz 29 x Sammaz 28	Hybrid	-2.07	-1.17	-28.77	5.41	-145.29

Table 4.20 percent inbreeding depression combined across environments

Genotype	Status	Daf	Das	PH	DM	GY
Sammaz 19 x Sammaz 19	Self	-5.10	-4.75	-13.49	5.77	-9.66
Sammaz 37 x Sammaz 37	Self	2.56	3.54	-18.00	-1.08	-22.00
Sammaz 17 x Sammaz 17	Self	5.62	4.77	-2.77	3.44	-5.76
Sammaz 36 x Sammaz 36	Self	-3.90	-4.57	-3.81	-3.78	18.18
Sammaz 27 x Sammaz 27	Self	-2.68	-3.31	-10.34	-3.42	27.47
Sammaz 35 x Sammaz 35	Self	-1.32	0.20	-33.23	0.15	-12.78
Sammaz 29 x Sammaz 29	Self	3.15	2.07	13.40	3.98	8.58
Sammaz 28 x Sammaz 28	Self	0.23	0.42	7.43	-1.72	-24.05

Sammaz 19 x Sammaz 37	Hybrid	0.86	0.32	3.61	-4.54	21.59
Sammaz 19 x Sammaz 17	Hybrid	0.11	-1.80	-7.26	-6.24	-14.90
Sammaz 19 x Sammaz 36	Hybrid	1.68	2.04	7.22	-1.28	-55.10
Sammaz 19 x Sammaz 27	Hybrid	8.14	7.15	12.60	1.36	-24.58
Sammaz 19 x Sammaz 35	Hybrid	0.96	0.61	-2.66	-4.68	-159.38
Sammaz 19 x Sammaz 29	Hybrid	-0.66	1.34	-10.36	-2.34	-59.95
Sammaz 19 x Sammaz 28	Hybrid	-0.22	-0.18	4.27	-3.45	-1.17
Sammaz 37 x Sammaz 17	Hybrid	-1.01	-3.41	-7.09	-0.23	-54.01
Sammaz 37 x Sammaz 36	Hybrid	0.86	1.18	7.49	0.52	-22.17
Sammaz 37 x Sammaz 27	Hybrid	-1.96	-2.93	16.53	-2.35	-32.28
Sammaz 37 x Sammaz 35	Hybrid	-0.33	-1.11	7.33	1.37	-13.80
Sammaz 37 x Sammaz 29	Hybrid	-2.71	-3.12	4.51	0.46	-137.47
Sammaz 37 x Sammaz 28	Hybrid	-1.57	-4.04	-6.51	0.00	-32.07
Sammaz 17 x Sammaz 36	Hybrid	1.85	3.08	8.55	-0.90	-18.92
Sammaz 17 x Sammaz 27	Hybrid	-5.24	-6.95	6.40	-3.05	-84.68
Sammaz 17 x Sammaz 35	Hybrid	-2.00	-3.28	-9.13	-1.30	-83.51
Sammaz 17 x Sammaz 29	Hybrid	-6.34	-4.52	-11.53	-1.93	-101.87
Sammaz 17 x Sammaz 28	Hybrid	-5.37	-4.19	-24.49	-2.39	-31.49
Sammaz 36 x Sammaz 27	Hybrid	1.06	0.68	8.31	3.26	-67.87
Sammaz 36 x Sammaz 35	Hybrid	-0.11	2.25	9.09	-1.42	-132.13
Sammaz 36 x Sammaz 29	Hybrid	3.96	7.21	-10.30	3.81	-162.16
Sammaz 36 x Sammaz 28	Hybrid	-2.40	-1.30	-6.06	0.67	-70.33
Sammaz 27 x Sammaz 35	Hybrid	2.50	1.20	-4.12	5.36	-148.59
Sammaz 27 x Sammaz 29	Hybrid	-4.27	-3.81	-17.10	-0.38	-83.09
Sammaz 27 x Sammaz 28	Hybrid	0.67	-0.41	-11.52	-0.53	-88.22
Sammaz 35 x Sammaz 29	Hybrid	-4.15	-4.23	4.92	-1.98	-87.18

Sammaz 35 x Sammaz 28	Hybrid	-0.56	0.41	-5.67	1.22	-43.93
Sammaz 29 x Sammaz 28	Hybrid	-1.38	-0.53	-17.47	2.46	-68.91

CHAPTER FIVE

DISCUSSION

In this study there were significant differences among the genotypes in environment one for all traits measured except ear height, ear diameter and cob diameter, indicating presence of genetic variability in the genotypes. The non-significant differences of the genotypes for ear height, ear diameter and cob diameter in environment one indicate that they may be conditioned by the same genes and are genetically related for these characters. The resemblance of the genotypes for these characters is not unexpected considering the source of the parents which mainly came from IITA, Ibadan. It might be possible that the genotypes are related through some remote ancestors. The significant genotype x environment interaction for nine traits indicated that the traits were influenced by differences in environments. For that reason, suitable hybrids could be developed for specific environments. In other words, specific hybrids can be developed for early planting in the dry season at Kadawa while some other hybrids will be suitable for planting late in the season represented as environment two in this study. Sammaz 27 x Sammaz 35, Sammaz 27 x Sammaz 17, Sammaz 36 x Sammaz 29, Sammaz 19 x Sammaz 27 and Sammaz 29 x Sammaz 19 are better and more suitable for early planting in environment one while Sammaz 19 x Sammaz 17 and Sammaz 36 x Sammaz 35 are better for late planting in environment two. Similar results were observed by Leta (2011) in studies for combining ability across environments for grain yield, ear height, plant height and days to maturity in maize.

The mean performance of the hybrids at environment one showed that parents from diverse genetic background can combine effectively to produce good hybrids. Parents with different maturity groups showed similar mean performance, especially Sammaz 28 and Sammaz 29 for days to 50% tasselling. Among the varieties, Sammaz 19 had longest days to 50% tasselling (99 days) while Sammaz 17 had the shortest (79 days). Among the hybrids Sammaz 28 x Sammaz 17 had the shortest days to 50% tasselling (77 days). The days to tasselling, silking and maturity were longer in both environments than in the usual wet season because the dry season is characterised by the cool harmattan which reduces maize growth rate (Table 3.3). Sammaz 19 had the highest performance for plant height (165cm), while Sammaz 19 x Sammaz 35 was the tallest (182cm) suggesting overdominance gene action for the character in the cross. The same hybrid (Sammaz 19 x Sammaz 35) was also the tallest for ear height (87cm), indicating that plant height was associated with ear height. Sammaz 19 x Sammaz 17 had the longest number of days to maturity (130 days) revealing the importance of the parents in genetic improvement in days to maturity. Sammaz 27 x Sammaz 35 had the shortest days to maturity (113 days) but the parents were of intermediate maturity group. In general, the maturity periods of the genotypes grown under irrigation were longer than when grown under rain fed condition due to difference in temperature in the two distinct seasons. Simultaneous emergence of weeds and maize seedlings under irrigation was observed. As such weed competition under irrigation if not checked can affect the yield significantly. Sammaz 36 x Sammaz 19 and Sammaz 36 x Sammaz 35 had the highest mean performance for ear length (19cm) and number of kernels per row (39), respectively. Interestingly, Sammaz 17 x Sammaz 29 had the highest mean performance for cob weight (2.7kg) and grain yield (5316 kg/ha) suggesting the effect of diversity in origin of the parental lines towards grain yield. The results also revealed that the traits were positively associated (the heavier the cob, the higher the grain yield).

At environment two, Sammaz 27 x Sammaz 17 had the shortest number of days to 50% tasselling (62 days) and silking (68 days), expressing that the hybrid could be used for early planting under irrigation. The parents were from early and medium maturing groups. Sammaz 19 x Sammaz 27 had the shortest days to maturity (88days) and also had the highest mean performance for cob weight (2kg) and grain yield (3049 kg/ha), showing that, inbred lines extracted from these parents (Sammaz 19 and Sammaz 27) may likely produce single cross hybrids with early maturity and high grain yields when planted under irrigation in the month of March in Kadawa. Sammaz 27 x Sammaz 29 was the tallest (158cm) and had longest ear height (90cm) indicating the taller the plant, the taller the height of the ear.The result suggests that plant height and ear height are genetically associated.

The mean performance for the combined data across environments revealed that Sammaz 36 x Sammaz 29 had the shortest days to 50% silk (78 days). The results also indicated that, the crosses involving Sammaz 19 had the highest mean performance for number leaves (14), plant height (155cm), ear height (74cm) and days to maturity (100), indicating that Sammaz 19 could be selected for extraction of inbred lines for commercial hybrid development for such traits. Sammaz 27 x Sammaz 28, Sammaz 27 x Sammaz 35 and Sammaz 27 x Sammaz 35 were the best for cob diameter (2cm), cob weight (2kg) and grain yield (3524kg/ha), respectively, suggesting Sammaz 27 to be the best combiner for these traits and could be selected for improvement.

The mean squares for combining ability at environment one (Table 4.7) revealed significant differences for crosses with respect to days to maturity and grain yield. This implies that suitable inbred lines can be extracted from the parents to develop suitable hybrids for different maturity groups with high grain yields. Parents vs. crosses were significantly different for number of leaves per plant, plant height, ear height, cob weight, kernel weight and grain yield expressing that the hybrids formed were better than at least one of the parents for such traits. The parents vs. crosses comparison are a test for heterosis which is due to nonadditive genetic effects (Hallauer and Miranda, 1981). The GCA mean squares were significant for eight traits including ear length, ear diameter and ear height. This was contrary to the finding of Ojo *et al.* (2007) who reported non-significant differences for ear length and ear diameter. The differences of the result with that of Ojo *et al*. (2007) can be explained on the basis of differences in the genotypes used and the testing environments. Different genetic materials are expected to perform differently under different experimental conditions. The GCA mean squares were, however, higher than the SCA mean squares for all traits except cob diameter, indicating preponderance of additive type of gene action for the traits except cob diameter. Additive gene action can be utilized in population improvement for the affected characters including grain yield. Thus, recurrent selection procedure can be utilized to improve the populations and composite varieties can be developed from the genotypes. Similarly, early maturing as well as late maturing populations can be developed through selection for maturity period. The height of the population can similarly be improved through cyclical selection and accumulation of genes for desired plant and ear heights. Significant reciprocal effects exist for number of leaves per plant and ear length indicating the influence of maternal parent for these characters. Improvement of these traits should take due cognisance of the maternal parents during recombination of selected parents. The GCA mean squares were highly significant for

grain yield. Ojo *et al.* (2007) and Zambezi *et al.* (1986) reported similar results in maize. Similar findings were also reported by Ivy and Hawlader (2000) for plant height, ear height and days to maturity in maize. The ratio of GCA compared to SCA observed in this study is in agreement with the findings of Ojo *et al.* (2007), Kim and Ajala (1996), Ogunbodede *et al*. (2000) and Windstorm *et al.* (1932) for grain yield parameter.

The results for environment two (Table 4.8) revealed that the mean squares due to hybrids were higher than those of the parents for days to 50% tasselling and silking, ear height, days to maturity, ears per plot, ear length, kernel row number, cob diameter, cob weight, threshing percentage and grain yield suggesting the importance of heterosis for the characters including grain yield. The GCA mean squares were higher than those of SCA for ten traits indicating the importance of additive type of gene action controlling the inheritance of these traits. Number of days to 50% tasselling and silking, number of leaves per plant and plant height had higher SCA indicating non-additive type of gene action. Where non-additive gene action is implied in the genotypes, suitable inbreds can be identified for hybrid development. Where both GCA and SCA mean squares are significant like in the case of ear length, the importance of additive as well as non–additive type of gene action is implied. Similar results were reported by Uddin *et al.* (2006) for plant height, ear height, cob diameter, ear length and grain yield parameters.

The combining ability analysis across environments (Table 4.9) revealed significant GCA x environment interaction for seven traits including days to 50% tasselling, days to maturity,

ears per plot and grain yield suggesting that different parental varieties behaved differently with respect to those traits under different environments. This shows the need to select different parental varieties for hybrid production for specific environments for the affected traits. The significant SCA x environment interaction for ear length, kernel row number, kernels per row and ear diameter indicated that hybrid performance for the traits varies with respect to environment, revealing that specific hybrids should be produced for specific environments under consideration. In other words, specific hybrids will do better for each of the planting dates used in this study. Similar results were reported by Paroda and Hayes (1971) and Pixley and Bjarnason (1993) who reported that both GCA and SCA can interact with the environment.

A relatively large GCA/SCA variance ratio suggests the importance of additive gene effects while low ratio implies the presence of dominant and/or epistatic gene effects (Griffing, 1956). Additivity shows that the performance of heterozygote is intermediate to that of the homozygote, therefore, an intermediate heterozygote reflect no-dominance of one allele over the other. The departure of the heterozygote (Aa) from the mean of two homozygotes (AA or aa) at a locus reflects the extent of dominance. The results for environments one, two and combined across environments, revealed that the magnitudes of GCA components were much higher than that of SCA for days to 50% tasselling, days to 50% silk, number of leaves per plant and number of kernels per row indicating the predominance of additive gene action controlling the traits. Where SCA is small relative to GCA, performance of single cross progeny can be predicted on the basis of the GCA of the parents. Those traits having higher SCA components to that of GCA were controlled by non-additive type of gene action. The variance components due to reciprocals were high for plant height, ear height and grain yield for both environments and

combined across environments indicating the importance of maternal effects for these characters.

The general, reciprocal and SCA effects for environment one (Table 4.13) indicated that Sammaz 35 showed positive significant GCA effects for number of leaves per plant, plant height, ear length, number of kernels per row and grain yield and significant negative value for days to maturity. The result of Table 4.13 also revealed that Sammaz 37 had negative significant GCA effects for kernel row number, cob weight and grain yield and significant positive GCA effects for ears per plot and cob weight. Negative significant GCA effect observed for days to maturity for Sammaz 35 suggests that it is a good combiner for earliness to maturity, hence, can be crossed to obtain early hybrid combinations or selfed to obtain promising genotypes for inbred development. Roy *et al*. (1998) and Hussain *et al.* (2003) reported similar results for GCA effects for for maize. Sammaz 17 also had significant GCA effects for days to maturity, cob weight and grain yield indicating the parent may be a good combiner for late maturity and high yields. The significant reciprocal effect of the cross Sammaz 35 x Sammaz 27 for days to maturity and grain yield and Sammaz 29 x Sammaz 37 for cob weight, threshing percentage and grain yield, revealed that the maternal parents had great influence in improving the performance of those traits. The result also revealed that Sammaz 29 x Sammaz 19 and Sammaz 28 x Sammaz 17 had positive significant reciprocal effects for days to 50% tasselling indicating the crosses can produce hybrids that would shed pollen late. Sammaz 29 x Sammaz 19 also showed positive significant reciprocal effect for days to 50% tasselling indicating its usefulness in developing late flowering varieties. Specific combining ability effects showed that Sammaz 17 x Sammaz 36 had the highest significant negative SCA effects for kernel row number and grain yield. Sammaz 17

x Sammaz 29 had the highest significant positive SCA effects for cob weight and grain yield. These two hybrids (Sammaz 17 x Sammaz 36 and Sammaz 17 x Sammaz 29) are from high x low general combiners. Sammaz 17 had high GCA whereas Sammaz 29 had low GCA. The results also revealed that the parent with higher GCA (Sammaz 17) produced hybrid (Sammaz 17 x Sammaz 29) with high estimate of SCA for grain yield (1574.4). Similar results were also observed by Poul and Duara (1991) who reported that the parents with high GCA always produced hybrids with high estimates of SCA.

The effects for GCA, reciprocal and SCA for environment two (Table 4.14) indicated that Sammaz 17 showed significant negative GCA effect for grain yield. Sammaz 27 showed significant positive GCA effects for ear height, ears per plot, ear length, kernel row number, kernels per row, cob diameter and grain yield. Hence Sammaz 27 is a good combiner for both high yield and other traits and can be crossed with another good combiner to accumulate desirable alleles through recurrent selection method. Similar results were observed by Uddin *et al*. (2006) who reported significant positive GCA effects for grain yield. Significant reciprocal effects were recorded for Sammaz 27 x Sammaz 19 for three traits (days to 50% tasselling, cob weight and grain yield). Sammaz 29 x Sammaz 17 had significant reciprocal effects for days to 50% tasselling and grain yield. Sammaz 27 x Sammaz 17 showed high positive significant reciprocal effects for days to 50% tasselling and days to maturity indicating importance of maternal effects. Sammaz 19 x Sammaz 27 involved low x high general combiners (Sammaz 19 low and Sammaz 27 high) and had significant negative SCA effects for days to 50% tasselling, days to 50% silk and days to maturity and significant positive SCA for cob weight and grain yield, indicating good specific combination for earliness and grain yield. Similar results were reported

by Uddin *et al*. (2006) who observed significant SCA effect for grain yields in maize. Sammaz 36 x Sammaz 29 involve high x high general combiners (parents with high GCA) had significant SCA effects for days to 50% tasselling, days to 50% silk and grain yield indicating the parents are good specific combiners for earliness and grain yield. Significant SCA effects for grain yield were also reported by Uddin *et al*. (2006).

The GCA, reciprocal and SCA effects from combined data across environments (Table 4.15) revealed that Sammaz 27 had the highest positive significant GCA effects for days to 50% tasselling, ears per plot, kernel row number, kernels per row, cob weight, and grain yield. Thus, Sammaz 27 was a good combiner for both high yield, early tasselling and other traits. Sammaz 36 had significant negative GCA effects for days to 50% tasselling and significant positive GCA for ear diameter, suggesting earliness in pollen shedding and big ears. Hence the two varieties (Sammaz 27 and Sammaz 36) can be crossed to accumulate desirable alleles through recurrent selection. The reciprocal cross Sammaz 29 x Sammaz 37 had the highest significant positive reciprocal effects for cob weight, threshing percentage and grain yield, pointing maternal effect.

The performance of a hybrid is a function of the genes it received from its parents but can be judged by its phenotypic performance in terms of the amount of heterosis it expressed. Many breeders (and geneticists) believe that the magnitude of heterosis is directly related to the degree of genetic diversity between the parents. In other words, it is assumed that the more the parents are genetically different, the greater the heterosis will be. It is common in most hybrid breeding programmes to maintain two or more distinct germplasm

(heterotic groups). Breeding and development is carried out within each source and the different genetic sources are only combined in the actual production of new hybrid cultivars (Brown and Caligari, 2008). It has proved difficult to clearly and convincingly define the underlying causes of heterosis in crop plants. There are very few instances where heterozygous advantage *per se* has been shown to result from over dominance. The counterpart to heterosis, inbreeding depression, is generally attributed to the fixation of unfavourable recessive alleles and so it is argued that heterosis should simply reflect the converse effect (Brown and Caligari, 2008). Therefore unfavourable recessive alleles in one line would be masked in the cross between them by dominant alleles from the other. If this is all that there is to it, then heterosis should be fixable in true breeding lines (Brown and Caligari, 2008).

It is a common belief in plant breeding that heterosis manifested by a cross of two populations increases with genetic diversity (Munguma and Pollak, 1988). Based on high-parent heterosis in environment one (Table 4.16), eighteen hybrids out of twenty eight had positive heterosis for grain yield which ranged from 1.63% to 927.03%. Sammaz 36 x Sammaz 35 exhibited highly significant positive heterobeltiosis for cob weight and grain yield. Fifteen hybrids out of twenty eight exhibited positive heterosis for grain yield in environment two (Table 4.17) which ranged from 17.75% to 397.1%. Sammaz 19 x Sammaz 27 exhibited highly significant positive heterobeltiosis for cob weight and grain yield. The high per cent heterosis manifested in this study by crosses Sammaz 36 x Sammaz 35 and Sammaz 19 x Sammaz 27 corroborated the fact that wide genetic distances on the basis of origin, adaptation and maturity contribute to genetic diversity and to higher heterosis. Hence these parents are the best for a concomitant improvement of grain yield through reciprocal recurrent selection. Inter variety

hybrid development programme can be an effective breeding approach to exploit the heterotic potential of these varieties.

High reduction in yield with self fertilization was observed in Sammaz 19, Sammaz 35 and Sammaz 28 for environments one, two and combined across environments, respectively. Jones (1918) reported similar results on the first 11 generations of self fertilization for four inbred lines. In environment one,the hybrid Sammaz 36 x Sammaz 35 recorded high negative inbreeding depression estimate for grain yield (-1260.70%), thus indicating additive gene action controlling the character. Similarly in environment two, Sammaz 19 x Sammaz 27 had a high negative inbreeding depression value (-491.39%), indicating additive type of gene action. For the combined data across environments, Sammaz 36 x Sammaz 29 had highest negative estimate of inbreeding depression (-162.16%) indicating that the parents may have similar recessive genes in common resulting in the reduction in yield in the hybrid combination similar to self fertilzation.

CHAPTER SIX

SUMMARY, CONCLUSION AND RECOMMENDATIONS

6.1 SUMMARY

The study was conducted to determine the combining ability and heterotic patterns for grain yield and other agronomic traits among extra early, early, medium and late maturing maize varieties. The parental materials comprised of eight genotypes, which were crossed in a complete diallel pattern. The matings were made in all possible combinations which generated crosses, reciprocals and selfs. Eighty one genotypes comprising the crosses, reciprocals, selfs, parents and nine checks were evaluated at Kadawa in two sowing dates at three months interval. The sowing dates were considered as separate environments.

The results of the study indicated significant differences among the genotypes in environment one for all traits measured except ear height, ear diameter and cob diameter, indicating genetic variability in the parents used, whereas in environment two seven traits were not significant (days to 50% tasselling and silking, number of leaves, plant height, days to maturity, ear length and ear diameter). A significant genotype x environment interaction was observed, indicating that suitable hybrids could be produced for specific environments. Sammaz 27 x Sammaz 35, Sammaz 27 x Sammaz 17, Sammaz 36 x Sammaz 29, Sammaz 19 x Sammaz 27 and Sammaz 29 x Sammaz 19 are better and more suitable for early planting in environment one while Sammaz 19 x Sammaz 17, and Sammaz 36 x Sammaz 35 are better for late planting in environment two.

The mean squares for combining ability at environments one and two revealed significant parents vs. crosses for cob weight and grain yield, showing that, the hybrids formed were better than at least one of the parents. The Parents vs. crosses signifies test for heterosis which was due to non-additive genetic effects. The GCA mean squares were highly significant and higher than SCA means squares for ear height, ear length, kernels per row, cob weight and grain yield, indicating preponderance of additive type of gene action for the traits. The significant GCA x environment interaction indicated that different parental varieties behaved differently under different environments hence there was need to select different parental varieties for hybrid production for specific environments. The significant SCA x environment interaction revealed that hybrid performance varies with respect to environments; hence specific hybrids could be produced for specific environments. Sammaz 27 x Sammaz 35, Sammaz 27 x Sammaz 17, Sammaz 36 x Sammaz 29, Sammaz 19 x Sammaz 27 and Sammaz 29 x Sammaz 19 are better and more suitable for environment one while hybrids Sammaz 19 x Sammaz 17 and Sammaz 36 x Sammaz 35 are better in environment two.

Significant GCA effects were observed for Sammaz 35 for number of leaves per plant, plant height, ear length, number of kernels per row, grain yield and days to maturity. Similarly significant GCA effects were observed for Sammaz 37 for kernel row number, cob weight, grain yield, ears per plot and cob weightwhile Sammaz 17 showed significant GCA effects for days to maturity, cob weight and grain yield pointing that, the parents could be useful in hybrid breeding programme with a view to increase yield. Significant negative GCA observed for days to maturity for Sammaz 36 indicated it is a good combiner for earliness to maturity, hence can be crossed to identify optimal hybrid combinations for selecting promising lines within

segregating generations. Sammaz 29 x Sammaz 19 and Sammaz 28 x Sammaz 17 showed significant positive reciprocal effect for days to 50% tasselling indicating the crosses can produce hybrids that would shed pollen early. Specific combining ability effects showed Sammaz 17 x Sammaz 36 had the highest significant SCA effect for kernel row number and grain yield whereas Sammaz 17 x Sammaz 29 had the highest significant SCA effect for cob weight and grain yield. These hybrids (Sammaz 17 x Sammaz 36 and Sammaz 17 x Sammaz 29) are from high x low general combiners, Sammaz 17 (high GCA), Sammaz 36 and Sammaz 29 (low GCA), thus the parent with higher GCA estimate (Sammaz 17) produced hybrids with high estimate of SCA (Sammaz 17 x Sammaz 29) for grain yield.

Sammaz 27 showed significant positive GCA effect for seven traits including grain yield suggesting that it is a good combiner for both high yield and other traits. Intra-population improvement could be used to accumulate desirable alleles through recurrent selection method. The GCA effect for combining ability across environments revealed that Sammaz 27 and Sammaz 36 had the highest significant GCA effects. They are good combiners for earliness, high yield and other traits. Hence the two varieties could be crossed to accumulate desirable alleles through reciprocal recurrent selection approach.

Sammaz 36 x Sammaz 35 showed highly significant positive heterobeltiosis for cob weight and grain yield in environment one. Sammaz 19 x Sammaz 27 also showed highly significant positive heterobeltiosis for cob weight and grain yield in environment two. The result corroborates the fact that wide genetic distances on the basis of origin, adaptation and maturity

contribute to genetic diversity and high heterosis. Hence the parents in these hybrids are the best for a concomitant improvement of grain yield through reciprocal recurrent selection. Inter variety hybrid development programme can be used as an effective breeding approach to exploit heterotic potential of the varieties.

6.2 CONCLUSION

The study revealed significant GCA x environment interaction indicating different parental varieties behaved differently in different environments and this shows the need to select different parental varieties for hybrid production for specific environments for affected traits. The significant SCA x environment interaction was observed, indicate that specific hybrids must be produced for specific environments under consideration. In other words, specific hybrids will do better for each of the planting dates used in this study. Sammaz 27 and Sammaz 36 had significant GCA effects combined across environments, they are good combiners for early maturity and grain yield hence can be crossed to accumulate desirable alleles through recurrent selection approach.

6.3 RECOMMENDATIONS

Based on the results of this study, the following recommendations are hereby made:

1. There is need to select different parental varieties for hybrid production for specific environments. Specific hybrids should be produced for specific planting dates under irrigation.

2. Inter variety hybrid development programme is recommended as an effective breeding approach to exploit heterotic potential of the varieties.
3. Sammaz 35, Sammaz 37, Sammaz 17, Sammaz 36 and Sammaz 27 are the best combiners for early days to maturity and high yield. They are recommended for extraction of inbred lines for hybrid and composite variety development.

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LIST OF TABLES

ABBREVIATIONS

ABU: Ahmadu Bello University

ANOVA: Analysis of variance

C1- C9: Checks 1-9

CD: Cob diameter (cm)

CV: Coefficient of variability

Cw : Cob weight (kg)

Daf: Days to 50% tasselling

Das: Days to 50% silk

df : Degrees of freedom

DM: Days to maturity

ED: Ear diameter (cm)

EH: Ear height (cm)

EL: Ear length (cm)

EMS: Expectation of mean squares

Ep : Ears per plot

F_1 : Hybrid (First filial generation)

GCA: General combining ability

GE: Genotype by environment interaction

Gy : Grain yield (kg/ha)

IAR: Institute for Agricultural Research, Samaru

ID: Inbreeding depression

IITA: International Institute of Tropical Agriculture, Ibadan

KPR: Kernels per row

KRN: Kernel row Number

Kw : Kernel weight (kg)

Max: Maximum

Min: Minimum

MS: Mean Squares

NGS: Northern Guinea Savanna

NL: Number of leaves per plant

^{o}C: Degree Celsius

PH: Plant height (cm)

R: Reciprocal

S/N: Serial number

SCA: Specific combining ability

SS: Sudan Savanna

T: Temperature

Tp : Threshing percentage (%)

Vs: Versus