GENETICS OF SOME AGRONOMIC AND YIELD TRAITS IN RICE (*Oryza sativa* L.)

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ZARIA

MARCH, 2012

DECLARATION

I hereby declare that this thesis titled **"Genetics of some Agronomic and Yield Traits in Rice (*Oryza sativa* L.)"** was written by me and is a record of my own research work. It has not been presented before in any previous application for a Higher Degree. References made to published and unpublished literature have been duly acknowledged.

ISMAILA ABUBAKAR …….. ……..

(Student) Signature Date

The above declaration is confirmed:

Prof. C. A. ECHEKWU …… ……..… …….

(Chairman, Supervisory Committee) Signature Date

CERTIFICATION

This thesis titled **"Genetics of some Agronomic and Yield Traits in Rice (*Oryza sativa* L.)"** by **ISMAILA ABUBAKAR** 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 scientific knowledge and literary presentation.

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DEDICATION

This work is dedicated to God Almighty in whose wisdom I live and to my beloved Parents (Mall Ismaila Adamu & Mallama Fatima) and those who stood by me for the success of this work.

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ABSTRACT

Six rice genotypes (FARO20 and FARO52 as female parents and FARO31, FARO39, FARO45 and FARO46 males) were crossed in a line x tester mating fashion to develop eight (8) F_1 hybrids. The parents along with the F_1 population were evaluated during the off season in 2010 at the screen house of the Institute for Agricultural Research (I.A.R), Samaru in a completely randomized design with three replicates to obtain information on estimates of genetic variations, combining ability, heterosis and heritability. Data were taken on seedling vigour, plant height, number of tillers, days to 50% flowering, panicle length, panicle weight, yield per plant and 1000grain-weight. Results from analysis of variance showed highly significant differences among the genotypes for all the traits. This is an indication of the presence of considerable amount of genetic variability in the materials, which could be used to initiate selection for population improvement. Phenotypic Coefficient of variation (PCV) values were slightly greater than Genotypic Coefficient of variation (GCV). However maximum GCV were obtained for yield per plant (28.94%), panicle weight (21.22%), 1000-grain weight (19.43%) and number of tillers (17.74%). Estimates of variance due to GCA and SCA and their ratios revealed preponderance of non-additive gene action for all characters except for days to 50% flowering. Positive GCA and SCA effects were observed among the lines and testers for yield per plant and other agronomic characters studied. Significant heterosis were revealed for most of the characters studied. Among the hybrids, FARO20 x FARO45 recorded the highest significant Positive heterosis for mid (115.27%) and high parent (80.06%) heterosis for yield per plant while FARO20 x FARO39 revealed negative heterosis for plant height and days to 50% flowering which is highly desirable as it confers resistance to lodging and early maturity. Broad sense heritability estimates were high for all the traits coupled with high genetic advance for yield per plant, 1000grain-weight, panicle weight, number of tillers and plant height, while the lowest genetic advance was observed in panicle length. Correlation studies revealed that genotypic correlations were generally higher than the phenotypic correlations for most of the traits. However, yield per plant correlate positively and significantly with seedling vigour, plant height and panicle weight at genotypic level.

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ABBREVIATIONS

B.P: Before present

cd: Critical difference

cm: centimeter

df: Degree of freedom

DTF: Days to 50% flowering

EMS: Expected mean square

$F_{1:}$ Hybrids

g: grams

GA: Genetic Advance

GCA: General Combining Ability

GCV: Genotypic coefficient of variation

GM: Grand Mean

HP: High Parent

I.A.R: Institute for Agricultural Research

MP: Mid Parent

N.C.R.I: National Cereals Research Institute

NT: Numbers of Tillers

PANL: Panicle Length

PANW: Panicle Weight

PCV: Phenotypic coefficient of variation

PLH: Plant height

$r_{g:}$ Genotypic Correlation

$r_{ph:}$ Phenotypic Correlation

SCA: Specific Combining Ability

SE: Standard Error

SV: Seedling Vigour

Y/P: Yield per Plant

σ^2: Variance

CHAPTER ONE

INTRODUCTION

Rice (*Oryza sativa* Linn) is one of the most important food crops (Gregory *et al.,* 2000). It is the second most important cereal in the world after Wheat (*Tritium astivum* L.) in terms of production and utilization (Jones, 1995). Rice is indigenous to south East Asia and has been cultivated for more than seven thousand years (Grist, 1986). The total world production of paddy rice in 2008 was estimated at 685 million metric tons out of which 23 million metric tons were produced in Africa (FAO, 2009).

1.1 ORIGIN AND DISTRIBUTION OF RICE

Evidence of the presence of rice in food of the early man has been found around 5000 BC in China and India from archeological excavations (Sharma *et al*., 2000). The archaeological evidence and more consensus among experts in support of an early domestication of *O. sativa* from its wild relative *O. rufipogon*, in the middle Yangtze valley in China about 7,000 years before present, or BP (Crawford and Shen, 1998; Higman and Lu, 1998; Vaughan and Morishima, 2003). Chang (1976) presented evidence for early rice cultivation in the Indian Himalayas 2450-3950 BP and in China 5230 BP, proposing multiple, independent, concurrent domestication events across the region stretching from the foothills of the Indian Himalayas to southwestern and southern China. Separate domestication of the two varieties, *indica* and *japonica*, has been proposed (Second, 1982) and alternatively, domestication of *indicas* from wild rice, then derivation of *japonicas* from *indicas* (Oka, 1988), but the evidence is equivocal (Cheng *et al*., 2003; Lu *et al*., 2002;

Yamanaka *et al*., 2003). Domesticated rice spread throughout Asia, the Mediterranean (2,300 BP), Madagascar (1,500 BP), Southern Europe (500 - 600 BP) and more recently as a result of European colonization, to Africa, North and South America respectively (300-500 BP) (Oka, 1988).

Introduction of *O. sativa* to Africa also brought it in contact with the more recently domesticated (3,500 BP), closely related West African domesticated species *O. glaberrima* (Chang, 1976). Rice (*Oryza glaberrima* Steud) is indigenous to Nigeria and has been cultivated for the past 3,500 years (Hardcastle, 1959). The earliest cultivation of improved rice varieties (*O. sativa* L.) started in about 1890 with the introduction of upland varieties to the high forest zone in Western Nigeria (Hardcastle, 1959; Atanda *et al.,* 1978). Consequently, by 1960 *O. sativa* had taken over from *O. glaberrima*, which is now limited to some deep-flooded plains of the Sokoto-Rima river basin and other isolated pockets of deep swamps all over the country (Atanda *et al.,* 1978, Imolehin, 1991).

1.2 TAXONOMY AND BOTANY

Rice is a member of the grass family (Poaceae) and belongs to the genus *Oryza* under the tribe Oryzeae. The genus *Oryza* includes twenty wild species and two cultivated species. The wild species are widely distributed in the humid tropics and subtropics of Africa, Asia, Central and South America, and Australia (Chang, 1976). Vaughan (1994) described 23 distinct species in the genus *Oryza* and classified them into four species complexes; *O. sativa* complex, *O. officinalis* complex, *O. meyeriana* complex and *O. ridleyi*

complex. *O. schlechteri* was thought to be extinguished, but recently recollected from Papua New Guniea by Vaughan (1994). *O. sativa* complex comprises two cultigen; *Oryza sativa* (indica and japonica rice) and *O. glaberrima* (African cultivated rice) and six wild species (Singh and Khush, 2000). *O. sativa* is grown worldwide. It is annual species but has tendency to grow as perennial. *O. glaberrima* is domesticated to tropical West Africa. All species included in *Oryza sativa* complex have 2n=24 chromosomes and AA genome. *Oryza officinalis* is the largest complex in the genus and include 10 species out of which five species are diploid (2n=24), four tetraploid (2n=48) and one (*O. punctata*) which has both diploid and autotetraploid ecotypes. The species of this complex are found in Asia, Africa and Latin America.

Rice is the seed of a monocot plant and morphologically, is an annual grass and one of the most important cereal crops. Although it can grow in diverse environments, it grows faster and more vigorously in wet and warm conditions. This plant develops a main stem and many tillers which may range from 0.6 to 6.0 meters (floating rice) in height (Anon, 2004). The inflorescence of rice is known as panicle which bears single flowered spikelets. Typically rice flower is different than those of other cereals in having six stamens. Blooming of flowers takes place between 8-11 a. m (Adair, 1934). After the appearance of panicle from boot leaf, most of the flower bloom between two to four days. Blooming of the spikelets starts at the apex of panicle and then proceeds downwards (Adair, 1934). Rice flower is normally self pollinated and the crossing range varies from 0-3 % (Bredero, 1965).

1.3 ECONOMIC IMPORTANCE OF RICE

Africa, accounts for 32 percent of the global imports and is a big international player in the rice marketing arena with a record level of 9 million tons in 2006 (A.R.C., 1998). Africa's emergence as a big rice importer is explained by the fact that in the last decade, rice became the most rapidly growing food source in sub-Saharan Africa (Sohl, 2005). The crop has grown in importance as a component of Nigerian diets. An average Nigerian consumes about 24.8 kg of rice per year, representing 9 per cent of total caloric intake and 23 percent of the total cereal consumption (FAO, 2003). Rice is also used for making wine, bear, and confectioneries. Starch made from rice is used in foods, cosmetics, and textile manufacture. Rice straw is used in feeding livestock and also used for the manufacture of straw board and ceiling board, braiding baskets, mats, mushroom culture, thatching roof, and mulching pineapples. Rice serves as an important source of vitamin B complex especially when the kernel is not polished (Araragi and Nara, 1991). Improving rice productivity would contribute to hunger eradication, poverty alleviation, national food security and economic development (Khurram *et al*., 2007).

1.4 RICE PRODUCTION

DARE and ICAR (2002) reported that of all staple food crops, rice accounts for the dietary energy requirements of almost half of the world population and with over 90 percent of it being produced and consumed in Asia. It is the second most important crop in the world (after wheat, which has an annual cultivation area of 213 million hectares) and is grown annually on 151.54 million hectares, with an annual production of 593 million tons and an

average productivity of 3.91 tons per hectare (FAOSTAT, 2002). In sub-Saharan Africa, rice is produced in five main ecosystems, namely rainfed uplands, rainfed lowlands, inland swamps, irrigated ecosystem and mangrove swamps (Norman and Otoo, 2003). West Africa remains the hub of rice production in sub-Saharan Africa but the shortfall in rice production has increased significantly as consumption rises at a rate well above that of production growth. In 2006, paddy rice production in sub-Saharan Africa was estimated at 14.2million tones. Rice production in sub-Saharan Africa grew at 3.23% per annum from 1961 to 2005. This growth rate was higher than the yearly population growth rate of 2.90% during the same period (A.R.C., 2007).

Rice production started in Nigeria in 1500 BC with the low-yielding indigenous red grain species *O. glaberrima* Steud, then widely grown in the Niger delta area (Hardcastle, 1959). The high-yielding white grain *O. sativa* L. was introduced in about 1890, and by 1960 it accounted for more than 60 percent of the rice grown in the country. Imolehin and Wada (2000) reported that, the country has potential land area for rice production of between 4.6 million and 4.9 million hectares. However, only 1.7 million ha, or 35 percent of Nigeria's total land mass is put into rice production. Paddy rice production in Nigeria first experienced a boom in 1967 when output stood at 385 thousand tons. During this period, area cultivated to rice stood at 262 thousand hectares while average national yield was 1.47 tons per hectare. Another significant improvement in rice production in Nigeria occurred in 1980 when output increased to 1 million tons while area cultivated and yield rose to 550 thousand hectares and 1.98 tons per hectare respectively. Throughout the 1980s, rice output

and yield increased. However, in the 1990s, while rice output increased, the yield of rice declined, suggesting extensive rice cultivation (Godwin *et al.,* 2001).

1.5 JUSTIFICATION

Breeding programmes depend on the knowledge of key traits, genetic systems controlling their inheritance, as well as the genetic and environmental factors that influence their expression. The characters of importance in rice breeding may include reduced plant height, strong culms; moderate tillering, short and erect leaves, large and compact panicles, and earliness of maturation others are drought tolerance, pest and diseases resistance and grain yield .(Miller *et al.,* 1993; Nemoto *et al*., 1995; Mackill and Lei, 1997; Wayne and Dilday, 2003; Paterson *et al*., 2005). Yield of paddy rice is a complex quantitative character controlled by many genes each interacting with the environment and is the product of many factors called yield components. Thus, selection of parents based on yield alone is often misleading. Therefore, there is the need to study the relationship between yield and its contributing characters in other to get better understanding of inheritance and select or identify superior genotypes. In view of this, present study was designed to achieve the following objectives;

- To estimate general and specific combining ability of parents and their hybrids, respectively for yield and yield contributing traits;
- To determine heritability, and expected gains from selection; and
- To determine the nature and direction of correlations among the traits.

CHAPTER TWO

LITERETURE REVIEW

2.1 GENETICS AND COMBINING ABILITY OF RICE

To establish a sound basis for any breeding programme aimed at achieving higher yield, breeders must have genetic information on the nature of combining ability of the parents, their behaviour and performance in the hybrid combination (Chawla and Gupta, 1984). The knowledge of combining ability is essential for selection of suitable parents for hybridization and identification of promising hybrids for future exploitation in a breeding programme (Alabi *et al*., 1987). The concepts of general and specific combining ability were introduced by Sprague and Tatum (1942). General combining ability (GCA) is the average performance of a line in hybrid combination and specific combining ability (SCA) is the deviation of crosses on the basis of average performance of the lines involved. General combining ability is associated with additive genetic effects while specific combining ability is associated with non-additive genetic effects (Falconer and Mackay, 1996).

Several studies on combining ability indicated that GCA is more important than SCA, although specific effects are of sufficient importance to merit attention in breeding programmes (Rosenow, 1970). Combining ability for eight quantitative characters in rice was studied which include days to heading, plant height, panicle length, number of panicles per plant and number of productive tillers, others are number of spikelets per panicle, 1000-grain weight and grain yield through line × tester analysis by Rogbell and Subbaraman (1997). The values of variance of GCA, SCA, and their ratio (GCA: SCA) indicated the

preponderance of non-additive type of gene actions for all the traits. Sreedhar and Kulkarni (1997) investigated the nature of gene action for rice grain and yield components through line × tester analysis. Non-additive gene action was of higher magnitude for plant height, tillers per hill, filled grains per panicle, 100-grain weight and grain yield but additive gene action for days to 50% flowering and panicle length. Ramalingam *et al*. (1993) carried out combining ability analysis through line × tester analysis for major yield attributes (days to heading, panicle length, number of panicles per plant, spikelet sterility, number of spikelets per panicle, harvest index and 1000-grain weight and grain yield) in rice. A preponderance of non-additive gene action was observed for all the traits except for 100-grain weight.

Surek and Korkut (1998) crossed eight rice cultivars in all possible combinations to assess the nature of gene action for nine agronomic characters. The additive genetic variance was greater than non-additive genetic variance for days to heading, plant height, panicle length, number of panicles per plant, spikelet sterility, number of spikelets per panicle, harvest index and 1000-grain weight except for grain yield in F_1 and F_2 generations. Dwivedi *et al*. (1999) conducted combining ability studies involving 10 rice lines and their 45 hybrids without reciprocals in diallel fashion for yield and yield components. The estimates of SCA effects were higher than GCA effects for all traits except for 1000-grain weight. Petchiammal and Kumar (2007) studied the nature of combining ability in 42 hybrids derived from seven diverse rice genotypes with full diallel mating design. Significant role of additive gene action was observed for days to 50% flowering, plant height, panicle length, grains per panicle, yield per plant, spikelet fertility, 1000-grain weight and harvest index.

Sadhukhan and Chattopadhyay (2006) determined the combining ability of yield and yield components in five rice cultivars. The general and specific combining ability variances were highly significant for yield per plant, harvest index, days to 50% flowering, plant height and number of productive tillers, indicating significance of both additive and non-additive gene action in the expression of these traits.

Ramalingam *et al*. (2000) conducted line × tester analysis and generation mean analysis for the genetic analysis of economic traits in rice. The SCA variance was greater than GCA showing presence of non-additive gene action for productive tillers. The GCA: SCA variance showed equal importance of both additive and non-additive gene actions for the control of ear length and 100-grain weight. Similarly SCA variance was higher than GCA variance signifying the non-additive gene action for grain yield. Vanaja *et al.* (2003) reported the importance of additive and non-additive gene effects in yield and most of the yield components from diallel crosses without reciprocals among eight parents in rice. Additive gene action was important for 1000-grain weight and plant height. Sharma and Mani (2005) hypothesized that the crosses involving at least one parent with good GCA effects could be attributed to additive × additive and / or additive × dominant gene interaction in sizable amount while the crosses involving average × average, poor × average and poor × poor GCA effects could be attributed to complementary type of gene interaction that might be explored in succeeding generations. In such crosses where non-additive gene effects played a dominant role in association with additive components, the recurrent and reciprocal recurrent selection could be used to exploit both components at the same time.

2.2 HETEROSIS

Heterosis is defined as the increased vigour of the F_1 generation over the mean of the parents or over the mean of the better parent (Hayes *et al*., 1955). Shull (1914) first coined the term heterosis and Whaley (1952) extended the term for increased vigour of F_1 over the better parent which is now termed as 'heterobeltiosis'. Janardhanam *et al*. (2002) assessed estimates of heterosis from 4 line × 4 tester experiment with 16 F_1 hybrids of rice. Ten hybrids exhibited significant mid-parent heterosis for plant height and number of grains per panicle while 13 hybrids exhibited significant mid-parent heterosis for yield. Eleven hybrids showed significant high-parent heterosis for plant height, 18 for panicle length and nine hybrids for number of grains per panicle. Out of 10 hybrids with significantly high-parent heterotic effects, seven (7) showed 80% increase over the high-parent for yield per plant. Li *et al*. (2002) reported heterosis from an incomplete diallel experiment in which six male sterile lines were crossed with three types to form 18 cross combinations. All F_1 hybrids showed highly significant positive heterosis for plant height, 1000-grain weight and yield. Significant negative heterosis was found for number of days to heading. Four crosses showed significant positive heterosis for grain yield per plant.

In another investigation involving rice genotypes, Mishra and Pandey (1998) derived information on heterosis from data on 10 yield related traits in 36 F_1 hybrids, 17-20% of all the hybrids manifested significant and positive heterosis for seed yield in the range of 44.7 to 230.9% due to significant and positive heterosis for panicle length and 1000-grain weight. Patil *et al*. (2003) determined the extent of heterosis in seven male sterile lines and 12 non-

male sterile lines through their 84 crosses. Six crosses showed high heterosis for early flowering. Two hybrids exhibited heterosis for high tillering, panicle length, number of grains per panicle and yield per plant. Mid and better parent heterosis for grain yield per plant were significant. Iftekharuddaula *et al*. (2004) assessed the nature and extent of heterosis in an eight half diallel cross in rice. The highest amount of heterosis was recorded in grain yield per plant followed by number of panicles per plant and number of filled grains per panicle. Punitha *et al*. (2004) worked out heterosis from 3 line × 4 tester experiment including their 12 F_1 hybrids. They reported mid-parent heterosis ranging from 70.79 to 93.81% and -54.74 to -14.70% for better parent in case of grain yield per plant.

2.3 HERITABILITY

Heritability estimates the amount of genetic variation existing in a set of genetic materials and can be used to predict the magnitude of genetic improvement that can be achieved when selection is practiced (Abubakar, 2002). Heritability estimates for agro-morphological traits in rice are sparse and contradictory, depending on the genetic materials used (Falconer, 1989). Ali *et al*. (2000) reported significant genetic variability and broad sense heritability for some selected yield and yield components except for number of tillers per plant and panicle length. Heritability estimates were maximum for plant height, 100-seed weight, number of tillers per plant and panicle length, but maximum genetic gain was recorded for number of tillers per plant and plant height. Rao *et al*. (1997) evaluated 20 high quality rice genotypes for yield components. Analysis of variance indicated significant genetic differences between and within the lines. Broad sense heritability for 1000-grain

weight, panicle length and straw yield was from 0.70 to 0.93. Yadav (2000) worked out genetic variability for yield and yield components in 15 rice genotypes. Appreciable amount of genetic variability, heritability and genetic advance was observed for total grains per panicle and grain yield per plant.

Agrawal (2003) studied genetic parameters in seven parental lines and their 21 F_2 populations in rice. Grain weight per panicle, yield per plant and number of grains per panicle showed high heritability and genetic advance. However, days to flowering, days to maturity, tillers per plant and panicle length indicated high heritability but low genetic advance. In another investigation, Vaithiyalingan and Nadarajan (2006) estimated variability parameters for quantitative characters of F_2 populations of different inter sub-specific crosses of rice. Grain yield showed high heritability with high genetic advance as percent of mean followed by fertility, productive tillers per plant and number of grains per panicle. Elayaraja *et al*. (2005) studied the nature and amount of induced genetic variability in rice. High heritability coupled with moderate to high genetic advance as percent of means were observed for number of productive tillers per plant, panicle length, number of grains per panicle, 100-grain weight and grain yield per plant. Swati and Ramesh (2004) evaluated 50 rice genotypes and reported that grain yield, number of secondary branches per panicle exhibited high heritability while flag leaf area, number of tillers per plant, 1000-grain weight and plant height showed moderate heritability. However panicle length and number of primary branches per panicle recorded low heritability. Shanthi and Singh (2002) conducted an experiment on 16 F_6 generations of induced mutants along with the non-mutant Mahsuri rice. The analysis of variance indicated that genotypes considerably varied for plant height,

number of tillers per plant, panicle length, number of grains per panicle, 1000-grain weight and yield per plant. Heritability in broad sense was high (more than 80%) for all the characters with the exception of grain yield per plant (78.99%) and number of tillers per plant (63.04%). The maximum genetic advance was recorded for number of grains per panicle (107.13%). High heritability coupled with high genetic advance was observed in plant height, number of grains per panicle and 1000-grain weight.

2.4 CORRELATION

Correlation studies measures the degree of association among traits. The knowledge of correlation is useful in plant breeding for taking decision in indirect selection of traits that show low heritability or are difficult to measure (Cuatero and Cubero, 1982). Hallauer (1981) reported that direct selection based on the phenotypic performance of a quantitatively controlled complex character such as yield may be subjective, but that based on indirect selecting superior genotypes from the population. If genetic association exists, selection for one trait will cause changes in the other traits; such changes are known as correlated response (Falconer, 1960; Fakorede and Obilana, 1979).

The relationship between rice yield and yield components has been studied extensively at phenotypic level; Sharma and Choubey (1985) and Dhanraj and Jagadish (1987) reported that yield per plant was positively correlated with the number of productive tillers per plant, the number of panicles per plant and spikelets per plant and 1000 grain weight. Prasad *et al*. (1988) observed positive correlations between rice grain yield per plant

and the number of spikelets per panicle, the number of fertile grains per panicle and 1000 grain weight. Bai *et al*. (1992) reported that grain yield is positively correlated with the number of productive tillers per plant, and the number of grains per panicle. Sürek and Korkut (1998) reported that grain yield per plant was significantly correlated with the number of panicles per plant and 1000 grain weight. Sadeghi (2011) reported positive significant association in rice for grain yield with grains per panicle, days to maturity, number of productive tillers and days to flowering.

CHAPTER THREE

MATERIALS AND METHODS

3.1 EXPERIMENTAL SITE

The experiment was conducted in the screen house of Institute for Agricultural Research (I.A.R.) Ahmadu Bello University Samaru, Zaria ($11^0$11'N, $7^0$38'E), 600m above sea level in the Northern guinea savanna within the period of June 2010 to July 2011.

3.2 GENETIC BACKGROUND AND DESCRIPTION OF MATERIALS

The plant materials for this study comprised two lines of rice used as female parents viz: FARO 52, FARO 20, and four testers used as male parents FARO 31, FARO 39, FARO 45 and FARO 46. The six genotypes were obtained from National Cereals Research Institute (N.C.R.I) Badeggi. The origin, pedigree and description of the genotypes are presented in Table 1.

3.3 POPULATION DEVELOPMENT

Rice (*Oryza Sativa L*) is a self pollinated; thus hand emasculation was carried out and female plants were pollinated with selected male varieties to produce F_1 hybrids. Line x tester mating fashion was used to produce eight F_1 crosses. The parents and F_1 hybrids were evaluated in the Screen house.

Table 1. Origin, Pedigree and Description of the Genotypes used in the study

Variety Name	Common Names	Origin/Pedigree	Brief Description
FARO 20	BP1 - 79 (BICol)	Philippines/unknown	Irrigated lowland, medium varieties (125-130days) with a height ranging from 90-100cm and has the potential yield of 2.5-4.0t/ha.
FARO 31	FAROX228-3-1-1	Nigeria(NCRI)/FARO15/IR28	Irrigated lowland, medium varieties (110-115days) with a height ranging from 120-125cm and has the potential yield of 3.0-4.0t/ha.
FARO 39	IRAT144	Nigeria(IAR&T)/IRAT13/IRAT 10	Early maturing (100-105days) upland rice. Plant height ranging from 95-105cm and has the potential yield of 1.5-3.5t/ha.
FARO 45	ITA257	Nigeria(IITA)/IRAT13/(Dourado precoce689//Tox490-1)	Early maturing (95-105days) upland rice varieties with Plant height ranging from 90-100cm and has the potential yield of 2.0-3.0t/ha.
FARO 46	ITA150	Nigeria(IITA)/63-83/(Dourado precoce/ROK1/SF363G)	Short variety (80-90cm) upland rice and medium maturing (115-120days) with potential yield of 2.0-3.5t/h.
FARO 52	WITA4	Nigeria (IITA)/Unknown	Irrigated lowland, medium varieties (125-130days) with a height ranging between 90-105cm with yield of 3.5-4.5t/h.

Source, NCRI

3.4 EXPERIMENTAL DESIGN

The six parents and their eight F_1 hybrids making a total of fourteen entries were evaluated in the screen house at Samaru. Plots were laid in a completely randomized design with three replications. Each genotype was assigned into six plastic pots of 25cm in diameter filled with soils, each pot containing three seedlings per pot. The pots were well labeled accordingly and arranged randomly in rows on platform and watered once daily. All other cultural practices were carried out according to the recommendation of National Cereals Research Institute.

3.5 DATA COLLECTION

Data were collected on the following agronomic characters.

1. Seedling vigour: vigour of the plants 20 days after sowing was scored based on a 1-5 scale.

   1 = least vigorous plant 2 = less vigorous plant 3 = vigorous plant

   4 = more vigorous plant 5 = most vigorous plant

2. Plant height (cm): The distance from ground level to the base of flag leaf at maturity.
3. Number of tillers per plant: The numbers of tillers per plant were counted for each genotype.
4. Days to 50% flowering: The number of days from sowing to when 50% of the plants in each plot are at anthesis.

5. 1000 grain weight (g):100 seeds were counted and weighed. 1000-grain weights were obtained as follows.

   1000-grain weight = X/100 *1000

6. Panicle length (cm): The distance from the base to the tip of the top most grain of the panicle.
7. Panicle weight (g): The weight of the dry panicle, ear or head.
8. Yield per plant (g): The weight of threshed grains per plant measured in grams.

3.6 STATISTICAL ANALYSIS

The linear Model (Comstock and Robinson, 1948; Kang, 1994) used for analysis of variance is expressed as

$$y_{ijk} = \mu + m_i + f_j + (m \times f)_{ij} + e_{ijk}$$

Where;

y_{ijk} = is the response of the k^{th} observation in the *ith* environment of the plant;

μ =general mean;

m_i = the effect of ith male;

f_j = the effect of the jth female;

mf_{ij} = the interaction effect;

e_{ijk} = the error associated with each observation

Table 2. Form of Analysis of Variance for Line x Tester analysis

Source:	d.f	M.S	Expected mean square
Replication	$r-1$		
Treatment	$T-1$		
Parents	$p-1$		
Crosses	$c-1$		
Parents vs. crosses	1		
Lines	$l-1$	M_l	$\sigma^2{}_e + r\sigma_{lt}{}^2 + rt\sigma_l{}^2$
Testers	$t-1$	M_t	$\sigma^2{}_e + r\sigma_{lt}{}^2 + rl\sigma_t{}^2$
L x T	$(l-1)(t-1)$	M_{lxt}	$\sigma^2{}_e + r\sigma_{lt}{}^2$
Error	$(t-1)(r-1)$	M_e	$\sigma^2{}_e$
Total	$rlt-1$		

M = observed mean square of the subscripted effect.

3.6.1 Estimation of GCA and SCA Effects

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

GCA effects of lines = $gi = \frac{x_{i}..}{tr} - \frac{x...}{ltr}$

Where;

$x_{i}.$ = total of i^{th} lines over testers

$x....$ = grand total

l = number of lines

t = number of testers

r = number of replications

GCA effects of testers = $g_{t} = \frac{x._{j}}{lr} - \frac{x..}{ltr}$

Where,

$x._{j}$ = total of the j^{th} tester over lines

$x...$ = grand total

l = number of lines

t = number of testers

$r =$ number of replications

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

Where;

x_{ij} = value of the j^{th} lines with *ith* testers,

x_{i} = total of i^{th} over all tester,

$x._{j}$ = total of j^{th} tester over all lines,

$x..$ = grand total crosses,

l = number of lines,

t = number of testers; and

r = number of replication.

The standard errors of the estimates were computed as the square roots of their variances as shown below.

i. S.E. (*gca* for line) = $\left(\frac{Me}{rt}\right)^{1/2}$

ii. S.E. (*gca* for testers) = $\left(\frac{Me}{rl}\right)^{1/2}$

iii. S.E. (*sca* effect) = $\left(\frac{Me}{r}\right)^{1/2}$

Where,

Me: MSS due to error

r: Number of replications

l: Number of female parents

t: Number of male parents

Genetic components of variance were estimated according to Singh and Chaudhary (1985);

$$\text{Cov H.S (line)} = \frac{m_l - m_{l\times t}}{r \times t}$$

$$\text{Cov H.S. (testers)} = \frac{m_t - m_{l\times t}}{r \times l}$$

$$\text{Cov H.S. average} = \frac{1}{r(2lt - l - t)}\left(\frac{(l-1)(m_l) + (t-1)(m_t) - m_{l\times t}}{l + t - 2}\right)$$

Where;

m_l = mean square lines

m_t = Mean square testers

$m_{l\times t}$ = Line x tester interaction mean square

r = number of replication

t = number of testers

l = number of lines

3.6.2 Proportional Contribution of Lines, Testers and Line × Tester Interaction

Contribution of lines, testers and their interaction to the total variance were calculated in accordance with Singh and Chaudhary (1985).

Contribution of lines = $\frac{SS(lines)}{SS(crosses)} \times 100$

Contribution of testers = $\frac{SS(testers)}{SS(crosses)} \times 100$

Contribution of *(l × t)* = $\frac{SS(l \times t)}{SS(crosses)} \times 100$

Where *SS*(*lines*), *SS*(*testers*), *SS*(*crosses*) and *SS*(*line × tester*) were the sum of square of lines, testers, crosses and line × tester, respectively.

3.6.3 Phenotypic and Genotypic Co-efficient of Variation

The formula suggested by Singh and Chaudhary (1985) was followed for computation of these parameters.

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma_g^2}}{\overline{X}} \times 100$

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma_{ph}^2}}{\overline{X}} \times 100$

Where,

σ_g^2 = Genotypic variance

σ_{ph}^2 = Phenotypic variance

$\overline{X}$ = Mean trait in question

3.6.4 Estimation of Heterosis

The estimates of heterosis for individual crosses expressed as percentage increase or decrease of hybrid mean over both the mid (%MP) and high (%HP) parents were computed as per Fehr (1987) mentioned here under.

High parent heterosis = $\frac{\overline{F_1} - Hp}{Hp} \times 100$

Mid parent heterosis = $\frac{\overline{F_1} - Mp}{Mp} \times 100$

Where;

F_1 = performance of hybrid

Mp = average performance of parents per se $\left(\frac{parent1 + parent2}{2} \right)$

Hp = performance of best parent

Test of Significance

The heterosis was tested by least significant difference at 5% and 1% level of significance as follows.

For testing heterosis over mid parent

$$\text{S.E (diff) } Mp = \left(\frac{3Me}{2r}\right)^{1/2}$$

For testing heterosis over better parent (HP)

$$\text{S.E (diff) } Hp = \left(\frac{2Me}{2r}\right)^{1/2}$$

Where,

Me = Error mean sum of square

r = number of replication

Critical difference:

C.D = SE (diff) x t (at 5 and 1% level for error df)

Heterosis was considered significant when F_1 – MP or F_1 – HP was higher than critical difference.

3.6.5 Estimation of Heritability

Heritability in broad sense (h^2_b) was calculated as the ratio of genotypic variance to the phenotypic variance (Falconer, 1989).

$$h_b^2 = \sigma_g^2 \Big/ \sigma_{p_h}^2$$

Where;

h_b^2 = broad sense heritability estimate

σ^2_g = genotypic variance

σ^2_{ph} = phenotypic variance

Narrow-sense heritability (h^2_n) estimates were calculated as the ratio of additive genetic variance to total phenotypic variance (Acquaah, 2007).

$$h^2_n = \sigma_a^2 / \sigma_{ph}^2$$

Where,

σ_a^2 = Additive variance

σ_{ph}^2 = Phenotypic variance

3.6.6 Genetic Advance

Genetic advance in next generation in response to selection was determined as suggested by Falconer and Mackey (1996) as under:

$$GA = K \times \sigma p_h \times h^2$$

Where;

K = Selection intensity at 0.05 = 2.06

σp_h = Standard deviation of the phenotypic variance under selection

h^2 = Heritability in broad sense

GA = Genetic Advance

Genetic advance in term of percentage of mean = *GA/GM*100*

Where;

GM = Grand Mean (parents and hybrids)

The range of genetic advance in percentage of mean was classified as suggested by Johnson *et al.* (1995).

Low = less than 10%, moderate = 10-20% and high = more than 20%

3.6.7 Estimation of Genotypic and Phenotypic Correlations

Estimates of genotypic and phenotypic correlations were obtained using the formula suggested by Singh and Chaudhary (1979).

Genotypic correlation $r_{gxgy} = \frac{\sigma^2_{gxgy}}{\sqrt{\sigma^2_{gx} * \sigma^2_{gy}}}$

Where;

r_{gxy} = correlation coefficient of character X and Y,

σ^2_{gxgy} = Genotype covariance of character X and Y

σ^2_{gx} = genotype variance of character X

σ^2_{gy} = genotypic variance of character Y

Phenotypic correlation coefficient;

$$r_{ph} = \frac{m_{gxgy}}{\sqrt{m_{gx} * m_{gy}}}$$

Where;

r_{ph} = phenotypic correlation of character X and Y

m_{gx} = entry mean square of the character X,

m_{gy} = entry mean square of the character Y,

m_{gxgy} = entry mean product of the character X and Y

CHAPTER FOUR

RESULTS

4.1 ANALYSIS OF VARIANCE

The Mean squares from the analysis of variance for all traits measured are presented in Table 3. The results depicted highly significant differences among the rice genotypes for all the characters studied. Genotypic mean squares were further partitioned into parents, crosses and parents' vs. crosses. The parents showed significant differences for all traits. However, the crosses revealed the existence of highly significant differences for all the traits except for seedling vigour for which the differences was not significant. Parent's vs. crosses showed highly significant differences for all the traits. However, non significant differences existed among lines and testers for these traits. Estimates of variance due to general combining ability ($\sigma^2 gca$) effects were lower than those of variance due to specific combining ability ($\sigma^2 sca$) effects for all the traits except for days to 50% flowering for which the variance was due to general combining ability ($\sigma^2 gca$) effects. The ratio of variance due to general to specific combining ability ($\sigma^2 gca/\sigma^2 sca$), were less than unity for all the traits and degree of dominance being greater than unity.

Table 3. Mean squares from Analysis of variance for different agronomic characters in rice

Sources	df	SV	PLH	NT	DTF	PANL	PANW	1000GW	Y/P
Rep	2	0.0264	38.5	1.2695	34.381	1.3067	4.1295	5.8095	5.7874
Treatment	13	0.7295**	434.42**	14.3968**	316.0092**	4.9484**	39.5639**	97.1795**	45.2778**
Parents	5	0.5209**	656.49**	26.4009**	329.6000**	2.1582*	36.0179**	936556**	31.3049**
Crosses	7	0.0971	287.55**	7.3000**	250.4226**	6.8095**	35.0095**	106.2321**	39.7893**
P vs. C	1	6.2000**	352.17**	4.8420*	707.1607**	5.8717**	89.1746**	51.4306**	153.5620**
Lines	1	0.2204	916.37	18.0267	782.0417	0.6017	14.7267	222.0417	9.1267
Testers	3	0.0126	183.82	6.2828	201.8194	1.5133	15.5033	110.1528	19.6872
L x T	3	0.1404	181.67**	4.4789**	121.8194*	14.1750**	61.2767**	63.7083**	70.1122**
Error	26	0.0798	41.09	0.9849	40.2784	0.839	6.0267	5.3223	4.3307
$\sigma^2 gca$		0.0026	40.9461	0.8529	41.1235	1.4575	5.1291	11.3765	6.1895
$\sigma^2 sca$		0.0202	46.86	1.1647	27.1803	4.4453	18.4167	19.462	21.9272
$\sigma^2 gca/\sigma^2 sca$		0.1287	0.8739	0.7323	1.513	0.3279	0.2785	0.5845	0.2823

*Significant at 0.05 probability level, ** Significant at 0.01 probability level.

Key: SV = seedling vigour, PLH = plant height, NT= numbers of tillers, DTF= days to 50% flowering, PANL = panicle length, PANW= panicle weight, 1000GW= thousand grain weight Y/P=yield per plant.

4.2 MEAN PERFORMANCE OF GENOTYPES

The mean performances of the parents and crosses for seedling vigour, plant height, number of tillers per plant, days to 50% flowering, panicle length, panicle weight, 1000-grain weight and yield per plant are presented in Table 4. There were significant differences between the parents for all the traits measured, FARO 46 has the highest grain yield with superior performance for panicle weight and early flowering, while FARO 31 and FARO 39 ranked second and third respectively with regards to grain yield per plant. The lowest yielder and poor performing parents in terms of panicle weight were FARO 52 and FARO 20. FARO 39 exhibited the highest panicle length, 1000-grain weight and seedling vigour, while FARO 52 revealed the lowest for panicle length and seedling vigour.

The F_1 hybrids revealed high means performance with FARO20 x FARO39 has the highest grain yield with good performance for panicle weight and panicle length. Hybrids FARO52 x FARO31 ranked second for yield per plant and panicle weight. The lowest yielder and poor performing F_1 hybrid in terms of panicle weight was observed in FARO20 x FARO 31. FARO20 x FARO46 was observed to have the highest 1000-grain weight and early flowering, while other parents exhibited good performance for these traits. All hybrids exhibited good performance for seedling vigour.

The general means with standard errors, ranges, genotypic and phenotypic coefficient of variations are presented in Table 5. Wide range were obtained for plant height, days to 50% flowering, panicle weight and yield per plant. GCV was found to be

highest for yield per plant followed by panicle weight and 1000-grain weight. Similar trend was observed for PCV.

Table 4. Mean performance of rice lines and hybrids for different agronomic characters

Parents	SV	PLH (cm)	NT	DTF	PANL	PANW	1000GW	Y/P
Faro 20	3.73^{ed}	70.60^{c}	10.93^{edf}	99.67^{cbd}	23.40^{dc}	9.77^{c}	29.67^{c}	7.20^{d}
Faro 31	3.73^{ed}	60.97^{d}	13.87^{bac}	112.67^{a}	22.47^{def}	14.93^{b}	25.67^{d}	11.97^{cb}
Faro 39	4.27^{bc}	93.30^{a}	6.70^{g}	101.67^{cb}	24.07^{bc}	15.87^{b}	39.33^{a}	11.67^{cb}
Faro 45	3.50^{e}	54.97^{e}	14.47^{ba}	102.67^{cb}	23.33^{dc}	14.27^{b}	23.00^{ed}	10.70^{c}
Faro 46	4.13^{dc}	92.37^{a}	12.77^{bdc}	75.33^{g}	22.63^{de}	22.33^{a}	31.33^{c}	19.73^{a}
Faro 52	3.00^{f}	56.50^{e}	10.03^{ef}	111.67^{a}	21.63^{ef}	9.97^{c}	31.00^{c}	5.63^{d}
Faro20xFaro31	4.43^{bac}	69.30^{c}	12.30^{dc}	95.00^{fe}	23.50^{dc}	13.87^{b}	20.67^{e}	10.37^{c}
Faro20 xFaro39	4.43^{bac}	93.70^{a}	9.63^{f}	92.33^{f}	25.13^{ba}	22.53^{a}	19.67^{e}	20.13^{a}
Faro20 xFaro45	4.23^{bc}	73.03^{c}	12.30^{dc}	97.00^{ed}	25.43^{a}	14.33^{b}	20.67^{e}	12.37^{cb}
Faro20xFaro46	4.733^{a}	81.63^{b}	12.10^{dc}	75.67^{g}	21.67^{ef}	17.73^{b}	36.33^{ba}	14.47^{b}
Faro52xFaro31	4.20^{bc}	60.56^{d}	15.30^{a}	103.00^{b}	22.40^{def}	21.53^{a}	31.33^{c}	19.27^{a}
Faro52 xFaro39	4.60^{bac}	78.00^{b}	11.60^{ed}	98.00^{ced}	25.23^{ba}	14.83^{b}	33.00^{bc}	12.37^{cb}
Faro52 xFaro45	4.57^{bac}	72.10^{c}	12.67^{dc}	102.67^{cb}	24.10^{bc}	14.53^{b}	24.67^{d}	11.67^{cb}
Faro52 xFaro46	4.67^{ba}	70.40^{c}	12.20^{dc}	77.67^{g}	21.23^{f}	14.06^{b}	32.33^{c}	11.13^{cb}
CV (%)	5.89	2.8	8.19	2.68	3.11	13.9	4.61	15.53
SE±	0.14	1.18	0.56	1.49	0.42	1.26	0.77	1.34

In each column, any two means having a common letter are not significantly different at p = 0.05 based on Duncan's Multiple Range Test.
Key: SV=seedling vigour, PLH= plant height, NT=numbers of tillers, DTF= days to 50% flowering, PANL=panicle length, PANW= panicle weight, 1000GW= thousand grain weight Y/P=yield per plant.

Table 5. General mean, Standard error (SE±), Range, Genotypic (GCV) and Phenotypic (PCV) Coefficient of variation for different agronomic traits

Traits	Means	Range	GCV(%)	PCV (%)
SV	4.1584 ± 0.41	3.50 - 4.73	11.19	13.09
PHT	73.3876 ± 1.19	54.97 - 93.30	15.60	17.88
NT	11.9193 ± 0.56	6.70 - 15.30	17.74	19.60
DTF	96.0729 ± 1.45	75.67 - 111.67	9.98	11.97
PANL	23.3014 ± 0.42	21.23 - 25.43	5.02	6.38
PANW	15.7536 ± 1.26	9.77 - 22.53	21.22	26.33
1000GW	28.4764 ± 0.76	19.67 - 39.33	19.43	21.05
Y/P	12.7629 ± 1.14	5.63 - 19.73	28.94	33.23

Key: SV = seedling vigour, PLH = plant height, NT = numbers of tillers, DTF = days to 50% flowering, PANL = panicle length, PANW = panicle weight, 1000GW = thousand grain weight Y/P = yield per plant.

4.3 ESTIMATION OF HETEROSIS

The estimates of mid and high parent heterosis are presented in Table 6 and revealed significant mid-parent heterosis for seedling vigour ranging from 5.83% to 41.54% percent and that of high-parent heterosis from 10.94% to 31.43% percent. FARO20 x FARO39 exhibited highly significant negative mid and high Parent heterosis. FARO52 x FARO39 was the most promising combination for heterotic response since it showed highly significant positive heterosis for number of tillers and also exhibited highly significant negative heterosis for days to 50% flowering. Most of the hybrids recorded significant positive heterotic values for grain yield per plant. FARO52 x FARO31 and FARO20 x FARO45 recorded the highest mid and high-Parent heterosis for yield per plant and panicle weight. FARO52 x FARO31 showed highly significant positive heterosis for panicle length. The mean mid and high parent heterosis ranged from -8.45% to 54.18% and -15.17% to 18.52% respectively with yield per plant recording the highest mean.

4.4 PROPORTIONAL CONTRIBUTION OF LINES, TESTERS AND THEIR INTERACTIONS

The proportional contribution of lines, testers and their interaction for the traits studied is presented in Table 7. It is evident from the table that lines played important role towards plant height and days to 50% flowering indicating predominant maternal influence for these traits. Testers were more important for number of tillers, and 1000-

grain weight. It revealed preponderance influence for these traits. The contribution of line x tester were high for seedling vigour, panicle length, panicle weight and yield per plant.

Table 6. Percentage Mid and High parent heterosis for different characters in rice

Crosses	SV		PLH		NT		DTF		PANL		PANW		Y/P		1000GW	
	MP	HP	MP	HP	MP	HP	MP	HP	MP	HP	MP	HP	MP	HP	MP	HP
FARO20xFARO31	18.75**	18.75**	5.35**	-1.84	-0.81	-11.3**	-10.52**	-15.68**	2.47*	0.43	12.28*	-7.14	8.17	-13.37**	-25.3**	-30.34**
FARO20xFARO39	5.83*	-0.78	-10.88**	-21.72**	39.51**	12.5**	-3.64	-4.59**	7.16**	5.68**	11.83*	-9.66*	34.28**	8.57	-40.10**	-47.46**
FARO20xFARO45	16.13**	12.50**	-3.53	-14.21**	20.47**	5.76**	1.81	0.32	-4.14**	-4.27**	79.20**	50.93**	115.27**	80.06**	18.99**	5.62**
FARO20xFARO46	20.7**	19.13**	-3.05	-7.72**	3.54	-6.40**	12.00**	3.01	4.40**	2.99**	2.35	-22.00**	8.53	-18.41**	-15.91**	-16.85**
FARO52xFARO31	31.68**	18.75**	59.53**	53.69**	-19.39**	-30.53**	-17.68**	-18.05**	13.98**	11.87**	80.99**	50.89**	128.79**	68.25**	-18.82**	-25.81**
FARO52xFARO39	30.28**	10.94**	8.99**	-12.5**	44.62**	20.60**	-29.06**	-32.24**	-5.18**	-9.97**	37.29**	11.76**	67.24**	24.00**	3.32**	-7.63**
FARO52xFARO45	41.54**	31.43**	39.95**	38.05**	-5.31*	-19.82**	-8.55**	-12.24**	12.23**	8.14**	22.42**	3.97	51.43**	15.58**	22.22**	6.45**
FARO52xFARO46	29.76**	15.65**	5.62*	-9.00**	4.38	-9.11**	-11.95**	-22.99**	-0.3	-2.78*	7.93	-17.17**	19.73**	-16.55**	-2.22*	-5.38**
AVERAGE	24.33	15.8	12.75	3.09	10.88	-4.79	-8.45	-12.81	3.83	1.51	31.79	7.7	54.18	18.52	-7.23	-15.17

*Significant at 0.05 probability level, ** Significant at 0.01 probability level.

Key: SV = seedling vigour, PLH = plant height, NT= numbers of tillers, DTF = days to 50% flowering, PANL= panicle length, PANW= panicle weight, 1000GW = thousand grain weight Y/P = yield per plant.

Table 7. Proportional contribution of lines, testers and their interactions to total variance in rice

Source	SV	PLH	NT	DTF	PANL	PANW	Y/P	1000GW
Due to lines	32.43	45.53	35.83	44.61	1.26	6.01	3.28	29.86
Due to testers	5.58	27.40	37.46	34.54	9.52	18.98	21.21	44.44
Due to line x testers	61.99	27.08	26.71	20.85	89.21	75.01	75.52	25.70

Key: SV = seedling vigour, PLH= plant height, NT=numbers of tillers, DTF = days to 50% flowering, PANL = panicle length, PANW = panicle weight, 1000GW= thousand grain weight

Y/P = yield per plant.

4.5 COMBINING ABILITY EFFECTS

The estimates of General combining Ability (GCA) effects of males and females are presented in Table 8. Among the female (lines) parents, FARO20 was a good combiner for most of the traits studied because it has high positive GCA effects for number of tillers and panicle length and as well as high negative GCA effects for plant height. The other female parent, FARO52 was found to be a good combiner for, days to 50% flowering, panicle weight, 1000grain weight and yield per plant.

Among the testers FARO45 was observed to be a good general combiner as it exhibited high negative GCA for plant height and exhibited high positive GCA for number of tillers, 1000-grain weight and yield per plant. Another tester, FARO31 exhibited positive GCA effects for panicle length, panicle weight and yield per plant. FARO39 had high negative GCA for days to 50% to flowering.

Specific combining ability (SCA) effects are presented in Table 9. The cross combination FARO52 x FARO31 was the best specific cross combination with the highest positive SCA effects for grain yield along with desirable SCA effects for all other traits except for panicle length, and seedling vigour. This was followed by the cross FARO20 x FARO39 which had desirable SCA effects for yield per plant and other traits which include panicle weight and panicle length. The cross FARO52 x FARO45 exhibited desirable SCA effect for most of the characters except for days to 50%

flowering, plant height, and number of tillers. The cross FARO20 x FARO46 had desirable SCA effects for all characters except for panicle length.

Table 8. Estimates of GCA effects for different agronomic traits

	SV	PLH	NT	DTF	PANL	PANW	1000GW	Y/P
Lines								
Faro 20	-0.0958	-6.1792	0.8667	5.7083	0.1583	-0.7833	-3.0417	-0.6167
Faro 52	0.0958	6.1792	-0.8667	-5.7083	-0.1583	0.7833	3.0417	0.6167
S.E. (gca lines)	0.0815	1.8505	0.2865	1.8321	0.2644	0.7087	0.666	0.6007
Testers								
Faro 31	-0.0208	6.5708	-1.3083	-0.0417	0.6167	1.3500	-5.5417	1.1417
Faro 39	0.0292	2.4042	-0.0750	-7.375	-0.1500	-0.8167	1.1250	-0.5417
Faro 45	-0.0542	-5.6458	1.1750	6.7917	0.1167	1.3333	4.7917	1.7083
Faro 46	0.0458	-3.3292	0.2083	0.6250	-0.5833	-1.8667	-0.3750	-2.3083
S.E. (gca testers)	0.1153	2.6169	0.4052	2.5910	0.3739	1.0022	0.9418	0.8496

Key: SV = seedling vigour, PLH = plant height, NT= numbers of tillers, DTF = days to 50% flowering, PANL= panicle length, PANW = panicle weight, 1000GW = thousand grain weight, Y/P = yield per plant.

Table 9. Estimates of SCA effects for different agronomic traits

Crosses	SV	PLH	NT	DTF	PANL	PANW	1000GW	Y/P
FARO20x FARO31	0.0958	-6.0208	0.4667	-4.375	-0.975	-3.55	1.875	-4.2667
FARO20x FARO39	-0.0958	6.0208	-0.4667	4.375	0.975	3.55	-1.875	4.2667
FARO20x FARO45	-0.1542	1.8792	-0.7667	4.9583	1.725	-0.9167	-4.7917	-0.2833
FARO20x FARO46	0.1542	-1.8792	0.7667	-4.9583	-1.725	0.9167	4.7917	0.2833
FARO52x FARO31	-0.1042	-2.5375	0.9833	-3.2083	-1.575	4.1333	2.2083	4.0667
FARO52 x FARO39	0.1042	2.5375	-0.9833	3.2083	1.575	-4.1333	-2.2083	-4.0667
FARO52 x FARO45	0.1625	6.6792	-0.6833	2.625	0.825	0.3333	0.7083	0.4833
FARO52 x FARO46	-0.1625	-6.6792	0.6833	-2.625	-0.825	-0.3333	-0.7083	-0.4833
S.E. (sca effect)	0.1631	3.7009	0.573	3.6642	0.5288	1.4147	1.332	1.2015

Key: SV = seedling vigour, PLH = plant height, NT= numbers of tillers, DTF = days to 50% flowering, PANL = panicle length, PANW= panicle weight, 1000GW = thousand grain weight, Y/P = yield per plant.

4.6 HERITABILITY AND GENETIC ADVANCE

Heritability and genetic advance estimates for the eight characters studied are presented in Table 10. High broad sense heritability were recorded for all the traits studied, Yield per plant recorded the highest broad sense heritability estimates which was followed by numbers of tillers. Panicle length recorded the least broad sense heritability estimates of 0.6202.

Narrow sense heritability estimates were high for panicle length, panicle weight and yield per plant; yield per plant recorded the highest narrow sense heritability estimates. Other traits recorded moderate narrow sense heritability estimates with the values ranged from 0.1158 for number of tillers to 0.2923 for1000-grain weight.

Genetic advance estimates express as percentage of mean ranged from 8.1482 (panicle length) to 51.9551 (yield per plant). Yield per plant recorded the highest genetic advance estimates which were followed by 1000-grain weight, seedling vigour and days to 50% flowering expressed moderate genetic advance estimates. Panicle length recorded the least genetic advance estimates of 8.1482.

Table 10. Estimation of heritability and genetic advance for different agronomic traits

	SV	PLH	NT	DTF	PANL	PANW	Y/P	1000GW
H^2_b	0.7307	0.7614	0.8195	0.6953	0.6202	0.6497	0.8432	0.7591
h^2_n	0.2341	0.1435	0.1158	0.2270	0.3271	0.3562	0.3935	0.2923
G A	19.7059	28.0454	33.0801	17.1409	8.1482	35.2416	51.9551	36.9468

Key: H^2_b = broad sense heritability, h^2_n = narrow sense heritability, GA = genetic advance, SV = seedling vigour, PLH = plant height, NT= numbers of tillers, DTF = days to 50% flowering, PANL = panicle length, PANW= panicle weight, 1000GW = thousand grain weight, Y/P = yield per plant.

4.7 CORRELATION

The estimates of genotypic and phenotypic correlation coefficients among all the traits studied are presented in Table 11. The genotypic correlation coefficients were higher than the phenotypic correlation coefficients for most of the traits. In this study, yield per plant showed significant positive correlation with plant height, panicle weight and seedling vigour at both genotypic and phenotypic level except for seedling vigour which the phenotypic correlation was not significant. Plant height revealed significant positive genotypic correlation with panicle length, seedling vigour, panicle weight and 1000grain-weight, and significant negative correlation with number of tillers per plant and days to 50% flowering. Phenotypic correlations for plant height followed similar trend with the genotypic correlations except for seedling vigour that was not significant. Days to 50% flowering correlates negatively with most of the characters studied at both genotypic and phenotypic levels.

Table 11. Phenotypic (P_h) and Genotypic (G) correlation coefficients between yield, and yield components obtained from fourteen genotypes in I.A.R. screen house Samaru

		1000GW	DTF	Y/P	PLH	PANL	NT	SV	PANW
DTF	P_h	-0.2462							
	G	-0.2673							
Y/P	P_h	-0.0043	-0.3572*						
	G	-0.0019	-0.4313**						
PLH (cm)	P_h	0.3168*	-0.5658**	0.4396**					
	G	0.3318*	-0.5674**	0.5157**					
PANL	P_h	-0.3977**	0.0023	0.1545	0.3796**				
	G	-0.4187**	0.2272	0.2063	0.3840**				
NT	P_h	-0.1749	-0.3352*	0.1732	-0.4491**	-0.2816			
	G	-0.4071**	-0.0128	0.2262	-0.6234**	-0.2975			
SV	P_h	0.0583	-0.2285	0.0725	0.2066	-0.1145	-0.0041		
	G	0.1544	-0.6713**	0.5597**	0.6131**	0.2541	-0.0698		
PANW	P_h	0.0733	-0.4597**	0.8408**	0.5578**	0.1154	0.122	0.1716	
	G	0.0795	-0.4621**	0.9928**	0.5595**	0.1153	0.1805	0.5174**	

*Significant at 0.05 probability level, ** Significant at 0.01 probability level.
Key: SV = seedling vigour, PLH = plant height, NT= numbers of tillers, DTF = days to 50% flowering, PANL = panicle length, PANW= panicle weight, 1000GW = thousand grain weight, Y/P = yield per plant.

CHAPTER FIVE

DISCUSSION

The presence of significant differences was observed among the parents for all the traits measured. This result indicates that appreciable amount of genetic variability exist in the parent inbred lines used for the crosses. Falconer (1981), pointed out that the amount of improvement that can be achieved by selection among a number of crosses is dependent on the amount of variation between the crosses and the intensity of selection, since selection is ultimately applied to the crosses. Therefore, this result implies that the inbred parents that produced these crosses which showed significant differences for these traits could be selected for genetic improvement in grain yield and other agronomic traits. The relative estimates of variance due to specific combining ability ($\sigma^2 sca$) effects were predominant for all the characters studied. Thus, indicating the predominance of non additive component, except for days to 50% flowering which is preponderance of additive components of genetic variation indicating both additive and non additive gene variation are important. The ratio of variances ($\sigma^2 gca/\sigma^2 sca$) due to general and specific combining ability effects ranged from -0.2785 to 0.8739. Similar results indicating the predominance of non additive gene action for the above traits mentioned were reported earlier by (Annaduri and Nadarajan, 2001; Radhidevi *et al*., 2002; Sarker *et al.,* 2002 and Ganash *et al.,* 2004).

Existence of genetic variation among the parental breeding materials is one of the most important pre-requisite for any crop improvement programme. The choice of genotypes and breeding system to use to initiating an improvement programme will depend

upon the mean performance and on the magnitude and quality of genetic variation present (Eckebili *et al*., 1977).

For most of the characters considered, the mean performance indicated presence of significant genetic variability among the genotypes. However neither of the lines nor the testers manifested significant mean performance for all the traits. Generally none of the hybrid showed superior mean performance for all the traits studied. However, for yield per plant FARO20 x FARO39 recorded the highest mean value with divergence in parents. Similar results had been reported that crosses of unrelated lines yielded better than crosses of related lines (Kim *et al*., 1987; Pollak *et al*., 1991 and Melchinger and Gumber, 1998). This indicates that genetic variability for the improvement of these traits is important in hybrid production. For most of the characters considered, the range values were wide and the mean differences observed were significant. This wide range suggests the possibility of selection as may be pertinent for each character. But for an improved population, a wide range in the expression of a character may not be desirable. Coefficient of variation truly provides a relative measure of variability among the different traits. Genotypic Coefficient of variation (GCV) gives good implication for genetic potential in crop improvement through selection (Johnson *et al*., 1955). Genotypic Coefficient of variation (GCV) was high for yield per plant, panicle length and 1000-grain weight. Similar trend was observed for phenotypic Coefficient of variation (PCV). Close relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing very little influence of environment for their expression. This implies that there is a good scope for yield improvement through phenotypic selection for grain yield.

The phenomenon of superiority of F_1 over its parents is heterosis (Syn. Hybrid vigor). This phenomenon has been a powerful force in the evolution of plants and has been exploited extensively in crop production. The degree of heterosis varied from cross to cross and from character to character. Alam *et al*. (2004) in upland rice observed the varying degree of heterosis for yield and its related traits. For plant height and days to 50% flowering negative heterosis were desirable but for rest of the characters positive heterosis were desirable. This implies that, negative heterosis for plant height and days to 50% flowering are desirable as it confers resistance to lodging and earliness respectively.

Highly significant mid parent heterosis were observed for seedling vigour, panicle length, panicle weight, 1000-grain weight and yield per plant. These results confirmed the earlier findings of Watanesk (1993) and Rao *et al*. (1996), Li *et al*. (1997), Perera *et al*. (2001) and Nuruzzaman *et al*. (2002) found high heterosis for grain yield and its components in rice. FARO 20 x FARO 39 was the most promising combination since it showed highly significant negative heterosis for plant height and for days to 50% flowering. Yield per plant, being the ultimate objective, is very important to rice breeders FARO20 x FARO45 recorded the highest significant Positive heterosis for mid and high parent heterosis. This result corroborates with the findings of Banumathy *et al*. (2003) who reported high magnitude of mid-parent heterosis and heterobeltiosis for grain yield from rice hybrid IR69616A/ IR10198-66-2R.

The maximum contribution to the total variance of plant height and 50% days to flowering were made by female parents indicating predominant maternal influence for these

traits. Testers were more important for number of tillers, and 1000-grain weight. It revealed preponderance influence for these traits. Line × tester interactions contributed more than lines and testers for seedling vigour, panicle length, panicle weight and yield per plant. This finding is in agreement with that of Thirumeni *et al.* (2000) who reported significant contribution of line × tester for yield per plant.

Combining ability refers to the ability of a parent to transmit desirable performance to its hybrid progeny or crosses. Combining ability analysis helps in the evaluation of inbred in terms of their genetic value and in the selection of suitable parents for hybridization. The selection of parents based on *per se* performance may not always result in producing superior segregants. Dhillon (1975) pointed out that combining ability of parents gives useful information on the choice of parent's in terms of expected performance of their progenies. Negative GCA effect is required for plant height and days to 50% flowering, to protect the crop from lodging and for earliness. In the present investigation, among the lines, FARO20 was found to be a good general combiner in the right directions for plant height, number of tillers per plant and panicle length. These findings are in accordance with those of Gnanasekaran *et al.* (2006) and Sharma (2006) who reported several parents with desirable GCA effects for plant height in rice. The line FARO52 also showed positive GCA effect for panicle weight, 1000-grain weight and yield per plant.

Among testers FARO 45 and FARO 46 exhibited both positive and negative GCA effects for plant height and number of tillers per plants respectively, which are potential

parents for use in subsequent breeding programmes aim at generating new varieties with more number of tillers per plant. These results are in line with those of Gnanasekaran *et al.* (2006) and Akram *et al.* (2007) who registered promising lines and testers with high GCA effects for number of tillers per plant. Testers FARO31 and FARO45 with positive GCA effects can play a vital role in increased yield per plant. The parents with high GCA effects can be utilized for hybridization programme for selection of superior recombinants in segregating progenies as suggested by Rojas and Sprague (1952).

Specific combining ability effect is the index to determine the usefulness of a particular cross combination in the exploitation of heterosis. Short statured plant height is desirable trait of rice crop. Four hybrids FARO20 x FARO39, FARO20 x FARO45, FARO52 x FARO39 and FARO52 x FARO45 expressed positive SCA effects reflecting an increase in plant stature, therefore these were undesirable. The remaining four hybrids, FARO20 x FARO31, FARO20 x FARO46, FARO52 x FARO31 and FARO52 x FARO46 showed negative SCA lying in the category of average effects. The cross FARO52 x FARO46 exhibited the best showing negative SCA effect for plant height indicating that improvement in plant height in term of intermediate or short statured can be brought by exploitation of hybrid vigour in this cross combination. Number tillers per plant and increased panicle length are also desirable traits for rice increased yield per plant. The cross combinations FARO52 x FARO31 and FARO20 x FARO46 possess positive SCA effects for number tillers per plant. These results are in conformity with the reports of Mehla *et al*. (2000), Sharma *et al.* (2005) and Sharma (2006) had similar SCA estimates relating to number of tillers per plant and recommended potential high tillering hybrids for the

development of hybrid variety(s) or cultivar(s). FARO52 x FARO31 and FARO20 x FARO39, recorded positive SCA effect for panicle weight, while FARO20 x FARO46 exhibited positive SCA effects for 1000-grain weight. These results are in line with the findings of Roy and Mandal (2001) and Singh and Kumar (2004). Yield per plant is the ultimate objective of rice breeding programmes. The cross combinations, FARO20 x FARO39 and FARO52 x FARO31 had positive SCA effect for yield per plant indicating relative importance of non additive gene effects for this traits. Dhaliwal and Sharma (1990) reported that non-additive gene effects were predominant for yield and its components. In the present study, it was observed that cross combinations, which expressed high SCA effects for grain yield, invariably exhibited positive SCA effects for one or more yield related traits also. Singh *et al*. (1996) and Rogbell *et al*. (1998) found good specific cross combinations in rice. None of the cross combinations were found to be good specific cross combinations for all the characters studied. Generally, in most of the good specific cross combinations at least one low general combiner parents were involved for all the characters along with grain yield. It also indicated both additive and non-additive types of gene action. While selecting the best specific combination for yield, it would be important to give due considerations to yield related traits.

Heritability estimates provide the information about index of transmissibility of the quantitative characters of economic importance and are essential for an effective crop breeding strategy. The magnitude of heritability also helps in predicting the behaviour of succeeding generations by devising the appropriate selection criteria and assessing the level of genetic improvement. Similarly, genetic advance gives clear picture and precise view of

segregating generations for possible selection. Higher estimates of heritability coupled with better genetic advance confirm the scope of selection in developing new genotypes with desirable characteristics. High broad sense heritability was exhibited for all the eight characters studied. Dabholkar (1992) classified heritability estimates as low (5-10%), medium (10-30%) and high (>30%). Accordingly, all of the agronomic characters considered showed high broad sense heritability constituting high breeding value which has more additive genetic effects which is important for crop improvement. Similar results have been reported by Bhandarkar *et al*. (2002), Kuldeep *et al*. (2004), Patra *et al*. (2006), Sabesan *et al*. (2009) and Jayasudha and Sharma (2010). Although, the presence of high heritability values indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication to the amount of genetic progress for selecting the best individuals which is possible by using the estimates of genetic advance. High heritability coupled with high genetic advance were observed for yield per plant followed by 1000grain-weight, panicle weight, number of tillers per plant, and plant height. Hence, heritability with high genetic advance indicates the preponderance of additive gene action and such characters could be improved through selection. Similar results were also reported by Singh and Singh (2003), Sarkar *et al*. (2007), Anbanandan *et al*. (2009), Sabesan *et al*. (2009) and Jayasudha and Sharma (2010). Days to 50% flowering revealed high heritability and moderate genetic advance. However, Mishra *et al.* (2003) and Agrawal (2003) reported high estimates of broad sense heritability along with low genetic advance for days to 50% flowering proposing that selection for these characters must be taken in advance generations.

Narrow sense heritability measures the relative importance of the additive portion of the genetic variance that can be transmitted to the next generation of offspring (Fehr, 1987). A high value for narrow sense heritability therefore, indicates that the additive gene action is important for controlling the character, while a low value signifies non additive gene influence. Moderate narrow sense heritability value would mean that both additive and non additive gene action are important in influencing the expression of the character, and that an appreciable amount of variation exist for improvement. The estimate of narrow sense heritability were high for panicle length, panicle weight and yield per plant indicating the presence of additive gene action controlling these characters, On the other hand, seedling vigour, plant height, number of tillers, days to 50% flowering, 1000grain-weight, were due exhibited moderate narrow sense heritability values which indicates that both additive and non additive gene action are important in influencing the expression of the character.

The degree of correlation among the characters is an important factor especially in economic and complex character as yield. Steel and Torrie (1984) stated that correlations are measures of the intensity of association between traits. The selection for one trait results in progress for all characters that are positively correlated and retrogress for traits that are negatively correlated. In general, the genotypic correlations were higher than the phenotypic correlation for most of the traits studied. Genotypic correlation result indicated that yield per plant correlated positively and significantly with plant height, panicle weight, seedling vigour. This result corroborates with the findings of Rasheed *et al*. (2002) and Girish *et al*. (2006) also reported the positive association of yield per with plant height at genotypic level. This implies that increase in plant height may increase grain yield (Hallauer and Miranda,

1988). Malcomson (1976) in a similar study reported that plant vigour is positively correlated to yield suggesting that during selection emphasis should be placed on plant with vigour as this would be translated with good yield.

CHAPTER SIX

SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

Result obtained from Analysis of variance depicted highly significant differences among rice genotypes for all the characters studied. The relative estimates of variance due to specific combining ability ($\sigma^2 sca$) effects were predominant for all the characters studied indicating the predominance of non additive component, except for 50% Days to flowering for which the variance due to general combining ability ($\sigma^2 gca$) effects were more suggesting preponderance of additive components of genetic variation. The additive effect for these traits would enhance population generations in rice while the non-additive genetic effects could assist breeders in devising strategies to exploit these genetic effects to enhance gain in selection for these traits.

Performance information from this indicated relatively wide ranges for most traits indicating existence of genetic variability. Close relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing very little influence of environment for their expression.

Heterosis studies revealed that the performance of most hybrids was based on the relatedness of the parental inbred lines. Most of the crosses that performed well were from parents with different genetic background. FARO20 x FARO45 recorded the highest significant Positive heterosis for yield per plant.

Parents that exhibit high combining abilities in hybridization programs could be more useful to plant breeders than those with low combining ability effect. However, positive GCA and SCA effects were observed among the genotypes for yield per plant and other agronomic characters studied.

Broad sense heritability estimates were high for the entire traits coupled with high genetic advance for most traits and low narrow sense heritability was observed. In the correlation studies, it was observed that most of the traits were positively correlated with yield per plant except days to 50% flowering which had negative association with yield per plant. However, the genotypic correlations were always higher than the phenotypic correlation in most cases.

The significance of GCA and SCA mean squares suggests the importance of both additive and non-additive variances for all the characters studied. The tester FARO31 demonstrates the ability to distinguish the merit of the female lines. However, the higher GCA effects of female line FARO 52 and male tester FARO 31 for majority of the traits indicate that both these parents may be preferred for hybridization and selection programmes. The SCA effects reveal that, for hybrid crop development, cross FARO 52 x FARO 31could be the better choice for most of the traits including yield.

Based on the findings from this study, it is recommended that the information obtained will be used for the formulation of breeding strategies to improve desired traits

based on understanding of gene action. The result from this study warrants further investigations to validate these findings under natural environment.

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