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“GENETIC ANALYSIS OF QUANTITATIVE TRAITS IN AEROBIC RICE (*Oryza sativa* L.)”

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ABSTRACT

GENETIC ANALYSIS OF QUANTITATIVE TRAITS IN AEROBIC RICE [*Oryza sativa* L.]

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ABSTRACT

The present investigation entitled "Genetic analysis of quantitative traits in aerobic rice [*Oryza sativa* L.] " was carried out at Regional Rice Research Station, Navsari Agricultural University, Vyara during *kharif*-2013.

The material comprising of five genetically diverse genotypes of rice (Gurjari, Jaya, GR 4, GR 5 and IET 18654) selected on the basis of their geographic origin and wide variation in morphological characters. Four crosses (Gurjari x GR-5, GR-4 x IET-18654, Jaya x IET-18654 and Jaya x GR-5) obtained by crossing five diverse lines during *kharif*-2012 at Regional Rice Research Station, Navsari Agricultural University, Vyara. These F_1's along with their parents were grown during summer 2012-13, where fresh F_1's and back crosses were developed. Parent and F_1's plant were selfed during the same season to obtain seeds of parents and F_2 generations of each cross.

The experimental material consisting of four families, each having six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were evaluated in Compact Family Block Design with three replications during *kharif*-2013. The individual replication was represented by four family blocks, one row each of P_1, P_2 and F_1, four rows of F_2 and two rows each of BC_1 and BC_2. Total 10 plants were accommodated in each row. The inter and intra row spacing was 30 and 10 cm, respectively.

The observations recorded for 10 different characters *viz.*, Days to flowering, plant height, productive tillers per plant, panicle length, grains per panicle, 100 grain weight, grain yield per plant, kernel length, length/breadth ratio and straw yield per plant were subjected to generation mean analysis to assess the gene effects controlling these traits to estimate the heterosis, inbreeding depression, heritability and genetic advance.

The analysis of variance for grain yield per plant and its component traits revealed significant differences among generations in all the characters studied in all four crosses.

The scaling tests (A, B, C and D) indicated appreciable amount of epistasis present in different characters of four crosses under the study, indicated the failure of a simple genetic model to explain the genetic system controlling the studied traits in the three crosses studied.

Generation mean analysis revealed that different gene effects were responsible for the inheritance of the same trait in different crosses and for different traits in the same cross, specific handling of individual cross in segregating generations would be advantageous for improvement of these traits. In the present investigation, non-allelic interaction played pertinent role in determination of various characters in aerobic rice. Thus, breeding methods involving high volume crossing like biparental, recurrent and diallel selective mating design that take care of both additive and non-additive gene action seemed more promising for the improvement of various characters studied.

Highly significant and positive heterosis over mid parent and better parent was recorded for grain yield per plant and its related traits in three crosses *viz.*, Gurjari x GR-5, Jaya x IET-18654 and Jaya x GR-5. Crosses which depicted significant and positive heterosis for grains yield per plant also exhibited significant and

positive heterosis for its components traits like grains per panicle, panicle length and straw yield per plant, which indicated that heterotic effect for grain yield per plant was mainly due to manifestation of heterosis in yield components. The crosses which exhibited heterosis for grain yield per plant and its contributing traits also depicted significant inbreeding depression which revealed association between heterotic effects and inbreeding depression.

The estimates of broad sense heritability genetic advance for grain yield per plant its attributes were in general high to moderate. The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotype is good reflection of genotype and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these matric traits, but in case of lower heritability, pedigree, sib or progeny test can be employed to improve it. The moderate to high heritability coupled with moderate to high genetic advance was recorded for most of the traits and therefore in such condition selection would be a beneficial approach to improve such trait.

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CERTIFICATE

This is to certify that the thesis entitled “ **GENETIC ANALYSIS OF QUANTITATIVE TRAITS IN AEROBIC RICE (*Oryza sativa* L.)**” submitted by **PATEL ASHISHKUMAR RAMESHBHAI** in partial fulfilment of the requirement for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **GENETICS AND PLANT BREEDING** of the Navsari Agricultural University is a record of bonafide research work carried out by him under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma or published for other similar title. All the assistance and help received during the course of the investigation have been duly acknowledged by him.

Place: **Navsari**
Date: 4th October, 2014

(Dr. V. P. Patel)

Major Advisor

DECLARATION

This is to declare that the whole of the research work submitted in this thesis for the partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING** is the result of investigation done by the undersigned under the direct guidance and supervision of **Dr. Vipul. P Patel**, Assistant Research Scientist, Regional Rice Research Station, Navsari Agricultural University, Vyara and that no part of the work has been submitted for any other degree so far as a unique research.

Place: Navsari

Date: 4th October, 2014 **(PATEL A. R)**

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Place*: Navsari*
Date*: / /2014* ***(Ashish R. Patel)***

INTRODUCTION

I. INTRODUCTION

Rice (*Oryza sativa* L., 2n=24) belongs to family *Poaceae* and subfamily *Oryzoidae*. It is believed to be originated in South East Asia. Rice is hydrophilic, self pollinated, short day C_3 plant. It is highly adaptable to different climatic conditions and therefore successful varieties needs to be develop in aerobic rice. Rice is the most important grain with regard to human nutrition and caloric intake, providing more than one fifth of the calories consumed worldwide by human species. Rice grain provides 35-80% of total caloric intake to more than 2.7 billion people (Gorantla *et al*. 2005).

Globally rice is cultivated in 144 countries. Global production of rice is 685 million tonnes from 158 million hectares area and its productivity is 4.3 t/ha. Asia is considered as 'Rice bowl' of the world, occupying 90% world's rice cultivation area (193 m/ha) contributing 90 % of the global production (584 mt) and productivity is 4.19 t/ha. India is the largest rice growing country, while China is the largest producer of rice. In India rice is grown in an area of 43 million hectares with a production of 99 million tonnes with productivity of 2300 kg/ha (Anon., 2012a). Area under rice cultivation in Gujarat is 8.08 lakh hectares with production of 14.97 lakh tonnes with productivity of 1852 kg/ha (Anon., 2012b).

Rice consumes more than 50 per cent of water used for irrigation in Asia (Barker *et al*. 1999). Global water crisis threatens the sustainability of irrigated rice. Aerobic rice is new concept of growing rice in non–puddled and non-flooded soil. Aerobic rice is grown like any other crops e.g. maize or sorghum on dry soils with surface irrigation provided when necessary with intensive agronomic practices. Aerobic rice has been projected as sustainable rice production methodology for immediate future to address water scarcity and environmental safety in the scenario of global warming.

Aerobic rice yield on par with irrigated puddled rice with an average of 5.5-6.0 kg/ha. Important advantage with aerobic rice cultivation is that it causes 80-85 percent lesser release of methane gas into the atmosphere thus keeping the environment safe. Economic savings in aerobic rice cultivation are obtained from reduced cost of land preparation, transplanting and reduced labour cost. In the year 2007 first drought tolerant aerobic rice variety MAS 946–1 was released followed by MAS 26 in (2008) by of at University of Agricultural Science, Bangalore, India.

Any successful breeding programme depends upon selection of parents, breeding methodology and critical observation for evaluation of superior genotypes. In general, parents are selected on the basis of per se performance, but many times high yielding genotype may not necessarily transmit its superiority to the next generation. Therefore information on mode of inheritance and type of gene action *i.e.*, genetic architecture of yield and its components is most important for adopting a sound breeding methodology. Partitioning of total genetic variation into all its components *i.e.* additive, dominance and all types of epistatics with regard to individual crosses will be of immense value in formulating effective breeding programme.

One of the common approaches followed to understand the nature of gene action is by growing different generation and carrying out the generation mean analysis, using first degree statistics. Aspects are available in literature on aerobic rice genotype. In spite of the great potential of the aerobic rice crop, very little efforts have been made for genetic improvements of yield and its components. Very little information is available on these aspects. Therefore, the present investigation was planned.

Heterosis refers to the phenomenon in which F_1 obtained by crossing two genetically distinct individuals manifest in a increase or decrease in vigour over mid parent value. Heterosis breeding for genetic improvement of yield can be fully exploited in the form of hybrids and partially in the form of synthetic and composite varieties.

Inbreeding depression refers to reduced fitness and vigour due to inbreeding. The inbreeding depression results due to fixation of unfavorable recessive genes in F_2 while in case of heterosis the unfavorable recessive genes of one line (Parent) are covered by favourable dominant genes of other parent.

The knowledge of nature and magnitude of gene action governing the expression of various traits can be helpful for making an effective and sound breeding programme. The exploitation of hybrid vigour depends upon the direction and magnitude of heterosis. Hence, the study of heterosis and inbreeding depression will also have direct bearing on the breeding methodology to be employed for varietal improvement or hybrid development programs. Further, the estimates of heritability and genetic advance are also useful in predicting the resultant effect of selection of the desired plants.

The present investigation entitled "**Genetic analysis of quantitative traits in aerobic rice (*Oryza sativa* L.)**" was carried out during the year 2012-13 at Regional Rice Research Station, Navsari agriculture University, Vyara with following objective :

1. To study the nature of gene action involved in inheritance of grain yield and its components.
2. To estimate the magnitude of heterosis and inbreeding depression for various traits.
3. To estimate heritability and genetic advance for yield and its components.

REVIEW

OF

LITERATURE

II. REVIEW OF LITERATURE

The available literature pertaining to gene effect, heterosis, inbreeding depression, heritability and genetic advance with reference to yield and yield components reviewed is presented under following sub heads.

2.1 Gene effect

2.2 Heterosis and inbreeding depression

2.3 Heritability and genetic advance

2.1 GENE EFFECT

The nature and magnitude of gene action governing the inheritance of quantitative characters could be of vital importance to the plant breeders in formulating appropriate breeding procedures.

Fisher (1918) was the first to divide the genetic variance into additive, dominance and epistatic components and defined these three as additive genetic variance arising from the additive effect of genes summed at all segregating loci, which gives an average heritable effect of genes. Dominance genetic variance arising due to the deviation from the additive scheme of gene action resulting from intra-allelic interaction of genes at segregating loci, which is unfixable variation and epistatic genetic variance arising due to the deviation of a consequence of inter-allelic interaction of genes at two or more segregating loci. Later on Kempthorne (1956), Hayman (1958) and Cockerham (1961) partitioned total epistasis variance into, (i) additive x additive (ii) additive x dominance (iii) dominance x dominance components for digenic inheritance. The literature pertaining to gene action involved in inheritance of different character of rice have been presented below.

Sharma *et al*. (1986) studied genetic architecture of seven crosses in rice and reported that the epiststic effect (i, j and l) varied in different characters and crosses and were much less than the mean effect (m). For yield, the preponderance of dominance type of gene effect and additive x additive type of epistasis was observed. For number of panicles per plant and grains per panicle, additive x additive epistatic effects were found in higher magnitude.

Chauhan and Chauhan (1994) studied six generations *viz*., P_1, P_2, (Begunbuchi and IRAT 102), F_1, F_2, BC_1, BC_2 of rice and reported the importance of additive and additive x additive gene interactions in inheritance of grains per panicle and 100-grain weight. However, grain yield was predominantly governed by dominance effect and additive x dominance and dominance x dominance interaction effects. Complementary type of epistasis was observed for grains per panicle and 100-grain weight, while duplicate type of epistasis was prominent for grain yield.

The fifteen F_1 hybrids derived from six parents from a diallel crosses were evaluated by Honarnejad (1995) for six quantitative traits. He reported the preponderance of additive gene action for plant height and grain length/breadth ratio while, non-additive gene action was observed in characters *viz*., Panicle length, tillers per plant and 100-grain weight.

Roy and Panwar (1997) studied gene effects in parental, F_1, F_2, B_1 and B_2 generations of two crosses for yield per plant, days to flowering, plant height, panicles per plant, panicle length, grains per panicle, grain length and straw yield per plant. Additive gene action was found significant for all traits under study in both crosses *viz*., HKR 120 X HKR 1 and PR 106 X TN-1. Duplicate epistasis played an important role in the inheritance of days to flowering and plant height in cross, KHR 120 X HKR 1.

Chauhan (1998) estimated gene effects for grain weight, length, breadth and length/breadth in P_1, P_2, F_1, F_2 and F_3 of a cross. Estimates of scaling tests indicated that epistasis played a major role in the inheritance of these traits. Dominant gene effects and dominance x dominance interactions were important for grain weight and length/breadth. However, grain length and breadth were governed predominantly by additive gene effects and their interaction.

Chang *et al.* (2002) studied progenies (F_1, F_2, B_1 and B_2) of a cross, Oochikara x Hwayeongbyeo and were tested to understand gene action for 100-grain weight and grain length in rice. Scaling test and joint scaling test revealed that inheritance of grain traits were fitted to additive-dominance model without epistasis. Additive effects for the traits were much greater than the dominance effects.

Mishra (2004) evaluated six generations P_1, P_2, F_1, F_2, BC_1 and BC_2 of four crosses *i.e.* IR 36 x Annada, Tuljapur 1 x JR 75, JR 75 x IR 36 and Annada x IR 64. The dominance gene effect and dominance x dominance interaction were found prominent for inheritance of grain yield, plant height, number of tillers per plant, panicle length, grains per panicle and test weight.

Sivakumar and Bapu (2005) carried out an experiment to evaluate 13 genotypes as lines and 3 wide compatible cultivars as testers. Preponderance of non-additive gene action was observed for all the seven traits studied *viz.*, Plant height, days to flowering, number of tillers per plant, panicle length, grains per panicle, 100-grain weight and grain yield per plant.

Kumar *et al.* (2006) reported that the predominant role of non-additive gene action for the characters *viz.*, Numbers of tillers per plant, panicle length and grain yield per plant, whereas additive gene action was predominant for days to flowering, plant height and 1000-grain weight.

Saravanan *et al.* (2006) carried out line x tester analysis for yield and quality characters in rice. They revealed that majority of characters like number of grains per panicle, grain yield per plant, 1000-grain weight and panicle length exhibited non-additive variance. They further reported that dominance and epistatic gene interactions were important for controlling all the characters.

Verma *et al.* (2006) studied half diallel involving 21 F_1, F_2 along with seven parents for five characters *viz.*, Days to flowering, panicle length, number of productive tillers per plant, 100 grain weight and grain yield per plant and reported the importance of both additive and non-additive gene actions with preponderance for grain yield per plant.

Nayak *et al.* (2007) evaluated parental F_1, F_2, BC_1 and BC_2 generations of four crosses involving scented and non-scented rice varieties for characters *viz.*, Days to 50 per cent flowering, plant height, panicle number per plant, panicle length, number of grains per panicle, 1000 grain weight and grain yield per plant. The dominance effects were more important than the additive effects in most of the crosses. The duplicate type of epistasis was found for all the characters except panicle length in cross Muskbudhi x Ratna in which the complementary epistasis was observed.

Rabiei *et al.* (2011) determined the gene action in F_1, F_2, BC_1 and BC_2 generations for agronomic traits *viz.*, Plant height, panicle length, panicle number per plant, grain number per panicle, 100 grain weight, days to flowering and grain yield. They reported that the character days to flowering was governed by additive gene action whereas, preponderance of dominance gene action was found for all the characters except grain yield per plant. Grain yield was controlled by both additive and dominance gene actions.

Roy and Senapati (2011) observed that the additive gene effect was significant for all the characters except florets per panicle in IET 6441 x Dudheshwar. Dominant effect was significant for all the characters except days to fifty percent flowering, panicle length and floret per panicle in IET 6441 x Dudheshwar and except for productive tillers per plant, panicle length, 1000 seed weight and grain yield per plant in cross IET 8002 x Basmati 385. Duplicate epistasis was observed for most of the characters under study in all three crosses.

Srivastava *et al*. (2012) studied parents F_1, F_2, BC_1 and BC_2 generations of five crosses to understand the genetics of seven yield and yield components. It was observed that dominance, additive x additive and dominance x dominance were found significant for all the traits studied except dominance for 100-grain weight and additive x additive and dominance x dominance for plant height. Also dominance gene action was significant for all the yield components except plant height and yield per plant. Further, additive x dominance was significant for plant height and panicle length.

Kiani *et al*. (2013) reported that the additive × dominance model was significant for traits in both crosses, except number of panicle length trait in Sang-e-Tarrom x Gerdeh cross. The joint scaling test indicated that the inheritance of traits related to yield was described by additive × dominance components, non-allelic interactions mainly additive × additive and additive × dominance and duplicate epistasis. More than one major gene group appeared to be involved for the expression of 100 grain weight and plant height while the remaining traits showed the presence of at least one major group of genes controlling their inheritance.

2.2 HETEROSIS AND INBREEDING DEPRESSION

Heterosis defined as the superiority of F_1 hybrid over its mid-parental value, though lately some terms like "Heterobeltiosis" and "Economic heterosis" are also used for designating superiority of F_1 hybrid over better parent and best check, respectively (Shull, 1908; East and Shull, 1905 and Fonseca and Patterson, 1968). For the first time heterosis was reported in plants by Koelreuter (1763). He noted that vigour in crosses increase in dissimilarity of parents. Shull (1914) coined the term "Heterosis" and is also known as “Hybrid vigour”. Heterosis being a complex phenomenon no clear-cut or conclusive explanation is available for its manifestation. However, several theories have been postulated to explain heterosis *viz.* dominance of gene (Davenport, 1908; Keeble and Pellow, 1910; Bruce, 1910), over dominance of gene (Shull, 1908; Stadler, 1939; Hull, 1945 and Gustafsson, 1946) and physiological complementation of mitochondrial activities.

Inbreeding means the mating together of individuals which are related to each other by ancestry. Inbreeding depression was noticed as early as 1876 by Darwin (Rai, 1979). It is measured as coefficient of inbreeding, which is the “Probability that two genes at any locus in an individual are identical by descent”.

Deosarkar and Nerkar (1994) reported highly significant positive heterosis over mid-parent in seven crosses for plant height, 100-grain weight and grain yield per plant, while eight crosses for panicle length and ten crosses for number of grains per panicle exhibited highly significant positive heterosis over mid-parent.

Significant and positive heterosis for grain yield over mid parent and better parent was expressed by four hybrids and was invariably followed by inbreeding depression in F_2. High heterosis and high inbreeding depression were observed for effective tillers per plant, filled grains per panicle and yield per plant in all four crosses (Reddy and Nerkar, 1995).

Mishra *et al.* (1998) studied heterosis and inbreeding depression for yield its yield components in six parents, 4 F_1's and 4 F_2's and recorded high magnitude of heterosis for grain yield per plant and panicle weight. High magnitude of inbreeding depression was observed for grain yield per plant.

Singh and Maurya (1999) estimated heterosis and inbreeding depression and reported significant and negative standard heterosis in five hybrids for earliness and four hybrids for dwarfness. In addition, eleven hybrids for effective tillers, panicle length and spikelets per panicle exhibited significant positive standard heterosis. All the hybrids showed negative heterosis for test weight. There was negligible inbreeding depression for days to flowering, plant height, panicle length and test weight and considerable inbreeding depression for grain yield per plant.

Heterosis and inbreeding depression in F_1 progenies were evaluated for grains per panicle, 100-grain weight and grain yield per plant by Agrawal (2003). The higher magnitude of heterosis was observed for grains per panicle, grain weight per panicle and grain yield per plant. The higher inbreeding depression was recorded for 100- grain weight and grain yield per plant.

The magnitude of heterosis and inbreeding depression for eleven traits was analyzed by Alam *et al.* (2004). Significant heterosis was observed for most of the traits under study. Among the ten hybrids, five hybrids *viz.*, 17A x 45R, 25A x 37R, 27A x 39R, 31A x 47R and 35A x 47R expressed highest heterosis for grain yield per ten hills. Both positive and negative inbreeding depressions were found in many crosses for all the characters under investigation, but none was found significant.

Verma *et al.* (2004) studied four generations *viz.*, P_1, P_2, F_1 and F_2 of crosses Jhona 349 x IET 12944 and Narendra 80 x Lalmati. The significant heterosis in desirable direction was observed for all the traits except panicle length in Jhona 349 x IET 12944 and grain yield per plant in Narendra 80 x Lalmati. Similarly, significant and positive inbreeding depression was obtained for all the traits studied except test weight in cross, Jhona 349 x IET 12944.

Raju *et al.* (2005) reported high degree of heterosis for the traits *i.e.*, Days to flowering, productive tillers per plant and grain yield per plant. In case of filled grains per panicle and 100-grain weight, it was found low. The low degree of inbreeding depression was observed in days to flowering and 100 grain weight.

Veni *et al.* (2005) evaluated twenty three crosses and their respective F_2'S to study magnitude of heterosis and inbreeding depression for grain yield and yield attributing traits. Out of twenty three crosses, highly significant and positive average heterosis and heterobeltiosis for grain yield per plant were expressed in four crosses and in each case it was invariably accompanied with inbreeding depression.

An experiment was conducted by Kumar *et al.* (2008) to study heterosis and inbreeding depression for number of filled grains per panicle, 100-grain weight and grain yield per plant using five generations of six rice crosses. High significant positive heterosis was observed for grain yield per plant and was accompanied by higher inbreeding depression.

Krishnan *et al.* (2009) studied heterosis and inbreeding depression in ten F_1 hybrids of rice for plant height, panicles per plant, panicle length, grains per panicle, 100-grain weight, kernel length/breadth ratio and grain yield per plant. All the ten hybrids showed higher values of heterobeltiosis for grain yield and high inbreeding depression for panicle length, grains per panicle, 100-grain weight and grain yield per plant.

Panwar and Ali (2010) conducted an experiment to study the nature and magnitude of heterosis and inbreeding depression in rice for yield and its components. High magnitude of heterosis was observed for plant height, productive tillers per plant, panicle length, filled grains per panicle, test weight and grain yield per plant. Four cross combinations exhibited higher magnitude of heterobeltiosis in F_1 coupled with high inbreeding depression in F_2 for grain yield per plant.

Adilakshmi and Reddy (2011) studied the nature and magnitude of heterosis and inbreeding depression in two crosses and reported significant and positive heterosis for estimation of heterobeltiosis for length/breath ratio and grain yield in the cross Samba Mahsuri x Polasaprabha and grain yield per plant in Samba Mahsuri x Nellore Mahsuri whereas, the significant positive heterosis for length/breadth was found in cross, Samba Mahsuri x Polasaprabha.

Kumar *et al.* (2012) evaluated 3 female, 4 male lines and their 12 F_1 hybrids by using Line x Tester analysis. They reported significant and negative heterosis for 50 per cent flowering and plant height, while positive and significant heterosis was reported for panicles per plant, test weight and grain yield per plant.

Anilkumar and mali (2013) studied heterosis in basmati rice for seven characters *viz.*, Days to 50 per cent flowering, plant height, number of effective tillers per plant, panicle length, number of grains per panicle, 1000-grain weight and grain yield per plant in seven crosses among eight basmati/basmati type parental lines. The magnitude of heterosis varied from cross to cross for all the characters studied and all the crosses exhibited significant inbreeding depression in F_2 generation. High heterotic effects were observed for days to 50 per cent flowering, number of effective tillers per plant, panicle length, number of grains per panicle, 1000-grain weight and grain yield per plant except plant height.

2.3 HERITABILITY AND GENETIC ADVANCE

The improvement in crop can be achieved by breeding high yielding varieties with improved quality, which is dependent upon the extent, nature and magnitude of genetic variability present in the material and the extent to which it is heritable. In crop improvement, only the genetic component of variance is important since, only this component is transmitted to the next generation.

Heritability in broad sense, as the ratio of additive variance to the total variance was proposed by Lush (1949). Later, Hanson *et al.* (1956) proposed heritability in broad sense as the ratio of genotypic variance to total variance in a non-segregating population. Heritability influences the selection programme to a larger extent. According to Allard (1960), heritability of yield alone is less and that of yield components is more. However, the gain from selection for a particular character is the function of its heritability, selection pressure and the variance existing in the base populations. Thus, genetic gain was expressed by Burton and De vane (1953) as the product of heritability, phenotypic standard deviation and selection differential. Though heritability value indicates the relative effectiveness of selection based on phenotypic expression of a trait, the genetic advance is more useful in predicting the actual value of selection as shown by Johnson *et al.* (1955).

Narrow sense heritability is the ratio of additive variance to the total variance which plays important role in the selection of the elite genotypes from the segregating populations. Improvement in mean genotypic values of selected plants over the parental population is the genetic advance which is essential to know the effectiveness of selection.

Lokprakash *et al.* (1992) calculated heritability and genetic advance of F_2 and F_3 populations of three different crosses. High heritability observed in cross HP 19 x IET 7575 for 100-grain weight (92.1 per cent). Genetic advance was moderate to high for 100 grain weight.

Sharma and Sharma (1993) evaluated forty-nine promising Indian genotypes for ten agronomic traits. They reported high heritability estimates coupled with high genetic advance for days to flowering, 100-grain weight, kernel length. High genetic advance was recorded for grain yield per plant and plant height.

Chauhan and Chauhan (1994) studied P_1, P_2, F_1 and F_2 generations of five intervarietal crosses derived from seven promising upland varieties and observed high broad sense heritability, together with high to moderate genetic advance for grain weight, length, breadth and shape, indicated the potential improvement of these traits through selection in the segregating generation.

Kumar *et al.* (1994) tested nine genotypes for heritability and genetic advance in ten quantitative traits and reported that the characters *viz.*, Grains per panicle, grain yield per plant, plant height and days to flowering exhibited high heritability and high to moderate genetic advance and selection would be beneficial for improvement of these traits.

Sawant *et al.* (1994) reported high heritability and high genetic advance for plant height, grains per panicle and 100-grain weight. Grain yield had low heritability with moderate genetic advance.

The heritability and genetic advance of three crosses and its F_2 generations were analyzed by Ganesan (1994). He observed high heritability and high genetic advance for plant height and grain yield per plant.

Heritability and genetic advance were investigated in the F_1 population of 20 crosses. The traits *viz.*, Days to flowering, height, 100-grain weight, number of grains per primary ear and grain yield had high values for heritability and genetic advance (Manonmani *et al.*, 1996).

Moon *et al.* (1996) investigated thirty genotypes for heritability and genetic advance of upland paddy. They observed that the characters *viz.*, Plant height and number of grains per panicle exhibited high heritability and high genetic advance, indicated high scope for selection.

Sharma *et al.* (1996) studied some thirty nine upland rice genotypes and reported that broad sense heritability estimates ranged from 42.2 per cent for grain yield to 99.9 per cent for grain length. High heritability was found for effective tillers, panicle weight and spikelets per panicle. Genetic advance as a percentage of mean was highest for effective tillers (77.3 per cent), followed by panicle weight (53.9 per cent).

Fourty five F_1 progeny its F_2 progeny were studied by Singh and Choudhary (1996) and observed that plant height and number of grains per panicle depicted high heritability and high genetic advance.

A study was conducted with F_2 and F_3 generations of three inter-varietal crosses (Ganesan *et al.*, 1997). High heritability combined with high genetic advance was observed for yield per plant in the F_2 and F_3 of all crosses. Days to panicle emergence had high heritability but low genetic advance.

Information on heritability is derived from data on ten yield components in three male sterile lines and their F_1 hybrids. High heritability estimates were observed for plant height (99.15 per cent) followed by days to 50 per cent flowering (98.2 per cent) and productive tillers/plant (98.19 per cent) (Saravanan and Senthil, 1997).

Verma and Mani (1998) observed that the estimates of heritability and genetic advance as a percentage of mean were generally low for all the characters studied. Genetic advance was highest for grain yield per plant.

Early segregating progenies of crosses were studied by Banumathy and Patil (1999) to quantify the extent of heritability and genetic advance. The highest heritability and genetic advance as percentage of mean were observed for grain yield and number of filled grains.

Thakur *et al*. (1999) studied F_2 populations for yield and its attributing traits and observed high heritability coupled with high genetic advance for biological yield, panicle-weight and grains per panicle.

Heritability observed in F_2 population for all the traits evaluated except for number of tillers per plant and panicle length. Highest heritability was reported for plant height, 100-seed weight, number of tillers per plant and panicle length, but maximum genetic advance was exhibited by number of tillers per plant and plant height (Ali *et al*., 2000).

Kumari *et al*. (2003) assessed fifty-five rice cultivars and their fourty two crosses and found that number of tillers and number of grains per panicle had high heritability and high genetic advance. Plant height, panicle length and 100-grain weight showed high heritability coupled with moderate genetic advance.

Thirty four genotypes were studied to estimate heritability and genetic advance and (Singh *et al*., 2007) observed that high heritability coupled with high genetic advance was recorded for spikelets per panicle. High heritability was observed 50 per cent flowering, test weight and panicle length. Moderate heritability and low genetic advance was recorded for total number of tiller per plant and effective tiller per plant. Days to 50 per cent flowering, plant height, seed setting percentage, grain yield and harvest index showed moderate genetic advance.

Padmaja *et al*. (2008) examined 145 genotypes and reported that heritability and genetic advance were high for all the characters except days to 50 per cent flowering and panicle length, which had moderate genetic advance along with high heritability. The genetic advance expressed as a percentage of mean ranged from 17.34 per cent to 49.54 per cent and the important characters like productive tillers per plant (49.54 per cent), single plant yield (46.87 per cent) and grains per panicle (45.74 per cent) recorded higher estimates.

The heritability and genetic advance study was conducted on twenty seven F_1 hybrids along with their twelve Basmati rice parents to know the pattern of inheritance of some morpho-physiological traits for selecting superior genotypes (Saleem *et al.*, 2008). Estimates of broad sense heritability and expected genetic advance in response to selection in next generation were high for all the traits.

Sedeek *et al.* (2009) studied heritability and genetic advance of twenty four rice varieties and found that heritability in broad sense was high for all studied traits and ranged from 86 per cent to 99.4 per cent. High heritability was observed for number of days to heading, number of filled grains per panicle and grain yield per plant. The expected genetic advance from selection appeared effective and ranged from 3.56 per cent to 44.88 per cent.

Rao *et al.* (2011) reported high heritability coupled with high genetic advance as per cent of mean for productive tillers per plant, grain yield and number grains per panicle.

Babu *et al.* (2012) carried out an investigation to study the genetic parameters for yield, yield attributing, quality and nutritional characters in twenty one rice hybrids. They observed that the characters *viz.*, Number of filled grains per panicle and water uptake exhibited high heritability coupled with high genetic advance indicating that simple selection could be effective for improving these characters.

Satya and Jabera (2013) computed heritability and genetic advance for yield and yield contributing traits. They observed that the traits *viz.*, Productive tillers per plant, panicles per plant and filled grains per panicle had high heritability accompanied with high genetic advance indicated lesser environmental influence importance of selection for improvement of these characters.

MATERIALS

&

METHODS

III. MATERIALS AND MATHOD

3.1 CLIMATIC CONDITIONS

The present investigation entitled "**Genetic analysis of quantitative traits in aerobic rice [*Oryza sativa* L.]**" was carried out at Regional Rice Research Station, Navsari Agricultural University, Vyara, during *kharif*-2013.

Geographically Vyara is situated at 21^0 04 N latitude and 73^0 03 E longitude with an altitude of 69 m above the mean sea level. Vyara is situated in South Gujarat heavy rainfall Agro-climatic region of Gujarat state. The rainy season commences in the second fortnight of June and ends by September. The weather during the growing season was normal and favourable for crop growth. The meteorological data for the cropping season presented in Appendix-I.

3.2 EXPERIMENTAL MATERIAL

The experimental material comprised of four families each representing six generations (P_1, P_2, F_1, F_2, B_1 and B_2). Four families were developed from parents lines viz., Gurjari, GR–4, Jaya, GR–5, IET-18654 (CRR 56-29), which were selected on the basis of their geographic origin and wide variation in morphological characters (Table 3.1).

The seeds of F_1 of each family were obtained by crossing during *kharif*-2012 at Regional Rice Research Station, Navsari Agricultural University, Vyara. These F_1's along with their parents were grown during summer 2012-13, where fresh F_1's and back crosses were developed. Parent and F_1's plant were selfed during the same season to obtain seeds of parents and F_2 generations. Details of four families presented in Table 3.2.

Table 3.1 Detail of parentage/pedigree and morphological characteristics of parental lines used in study.

Particulars	GURJARI	GR-4	JAYA	GR-5	IET-18654 (CRR 56-29)
Parentage Pedigree	Asha/Kranti	Zinnia-31/ IR-8-246	T.N-1/ T-141	Navsari-18	Annanda / RR 151-3
Plant height (cm)	110-115	105-110	80-85	110-115	120-125
Days to 50% flowering	90-95	85-90	95-100	61-67	63-67
Panicle length (cm)	22-23	19-20	23-25	24-25	22-25
1000 grain weight (g)	27.0 - 28.0	13.0-14.0	27.0-28.0	26.5-26.8	19.70
Kernel length (mm)	6.40	5.3	6.11	5.50	5.57
Kernel breath (mm)	2.20	1.40	2.35	2.10	2.30
L/B ratio	2.90	3.78	2.60	2.61	2.42
Grain yield (kg/ha)	5000-8000	4500-4700	4500-5500	1700-2500	2500-3000

Table 3.2 The detail of the experimental material

Cross	Family		Material Studied
1.	Gurjari × GR–5	P_1	Gurjari
		P_2	GR–5
		F_1	Gurjari × GR-5
		F_2	Gurjari × GR–5
		BC_1	(Gurjari × GR-5)× Gurjari
		BC_2	(Gurjari × GR-5)× GR–5
2.	GR-4 × IET-18654 (CRR 56-29)	P_1	GR–4
		P_2	IET-18654 (CRR 56-29)
		F_1	GR- 4 × IET-18654
		F_2	GR- 4 × IET-18654
		BC_1	(GR-4 × IET-18654) x GR-4
		BC_2	(GR-4 × IET-18654) x IET-18654
3.	Jaya × IET-18654 (CRR 56-29)	P_1	Jaya
		P_2	IET-18654 (CRR 56-29)
		F_1	Jaya× IET-18654
		F_2	Jaya× IET-18654
		BC_1	(Jaya× IET-18654) ×Jaya
		BC_2	(Jaya× IET-18654) × IET-18654
4.	Jaya × GR–5	P_1	Jaya
		P_2	GR-5
		F_1	Jaya × GR-5
		F_2	Jaya × GR-5
		BC_1	(Jaya × GR-5) ×Jaya
		BC_2	(Jaya × GR-5) × GR-5

3.3 CROSSING AND SELFING TECHNIQUES

The crossing work was started, when the crop commenced flowering, emasculation was done during evening hours followed by pollination on next day morning. About thirty spikelets, likely to open on the following day or a day after, were left for emasculation; whereas, opened flowers, fully developed floret and under developed floret were removed. The emasculation was done by cutting top one third portions of selected spikelets and the anthers were removed with the help of vaccum emasculator. After removal of anther, a butter paper bag was used to cover the emasculated panicle. On the next day morning, around 7 a.m., fresh flowers (Panicles) of appropriate male parent were collected and placed under the artificial light. Anther comes out after some time and pollination was made by dusting pollen from the dehisced anthers on the stigma of emasculated female flower. After pollination, the florets were again bagged with white butter paper bag and tagged showing crosses (Female × Male) at the bottom.

The seeds of individual parental lines, F_2 seeds from selfed F_1 plants and F_1 seeds including back crosses were harvested separately and were labeled accordingly.

3.4 EXPERIMENTAL DESIGN

The experimental material consisting of four families, each having six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were evaluated in Compact Family Block Design with three replications. The four crosses formed the family blocks; whereas, different generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 of each family represented individual experimental unit within family. The individual replication was represented by four family blocks, one row each of P_1, P_2 and F_1, four rows of F_2 and two rows each of BC_1 and BC_2. Total 10 plants were accommodated in each row. The inter and intra row spacing was 30 cm and 10 cm, respectively. All the recommended agronomical practices and plant protection measures were followed as and when required for raising good crop.

3.5 CHARACTERS STUDIED

Observations for different characters under study were recorded in each experimental unit *i.e.* generation as five plants in each P_1, P_2 and F_1, twenty plants in F_2 and ten plants each of BC_1 and BC_2. The plants for recording observations were selected randomly from the competitive plants excluding border plants. The selected plants were tagged and numbered for recording different observations. An individual observation of each generation of each family was considered for statistical analysis. Procedures followed for recording various observations are as under :

3.5.1 Days to flowering

Days to flowering was recorded as days taken from sowing to occurrence of flowering on each plant.

3.5.2 Plant height (cm)

It was measured in centimeter from ground level to the tip of the main panicle.

3.5.3 Productive tillers per plant

The numbers of productive tillers producing panicles with seed set were counted as productive tillers from each selected plant at the time of harvest.

3.5.4 Panicle length (cm)

The length of panicle was measured from base to the tip of panicle in centimeters at the time of harvest.

3.5.5 Grains per panicle

The total numbers of matured grains of main panicles of randomly selected plants were counted at time of harvest.

3.5.6 100 grain weight (g)

The seeds of all panicles per plant were mixed up thoroughly and 100 grains were taken randomly and weighted in grams.

3.5.7 Kernel length (mm)

Kernel length was measured in millimeters as the distance from base to the tip of kernel with the help of digital image analyzer. Ten kernels were used per sample and average computed.

3.5.8 Kernel L/B ratio

The kernel length : kernel breath ratio was calculated as :

$$\text{L/B ratio} = \frac{\text{Kernel length (mm)}}{\text{Kernel breath(mm)}}$$

3.5.9 Grain yield per plant (g)

Weight of grains from each observational plant was recorded in grams.

3.5.10 Straw yield per plant (g)

Weight of sun dried straw of each selected plant was recorded in gram.

3.6 STATISTICAL METHODS

The data obtained for respective character from the observations recorded on each representative (tagged) plant of each generation (P_1, P_2 and F_1 = 5 plants, F2 = 20, BC_1 and BC_2 = 10 plants) of every family in each replication were used for statistical analysis.

The statistical analysis was done on following aspects:

1) Analysis of variance

a) Between families

b) Within families

2) Estimation of gene effects

3) Estimation of heterosis

4) Estimation of inbreeding depression

5) Estimation of heritability and genetic advance

3.6.1 Analysis of variance

The recorded observations for each character were subjected to standard statistical analysis to test the significance of differences among various families and generations of each family. The family differences were tested through Compact Family Block Design as reviewed by Panse and Sukhatme (1969); whereas, differences among generations were tested through Randomized Complete Block Design as suggested by Snedecor (1938) and reviewed by Panse and Sukhatme (1969). The statistical model for Compact Family Block Design is as under:

$$Y_{ijk} = m + r_i + f_j + p_k + e_{ijk}$$

Where,

Y_{ijk}= Phenotypic value of the k^{th} progeny of j^{th} family in the i^{th} replication.

m = General mean

r_i = Effect of the i^{th} replication,

f_j = Effect of the j^{th} family

$p_{k(f)}$ = Effect of k^{th} generation of j^{th} family

e_{ijk} = Uncontrolled variation due to k^{th} generation of j^{th} family in the i^{th}replication.

The ANOVA for comparing families and generations within family are given in Table 3.3 and Table 3.4, respectively:

Table 3.3 Analysis of variance for family comparisons

Source	d.f.	M.S.	E.M.S.
Replication	(r-1)	Mr	$\sigma^2e + f\ \sigma^2r$
Families	(f-1)	Mf	$\sigma^2e + r\ \sigma^2f$
Error	(r-1)(f-1)	Me	σ^2e
Total	(rf-1)	-	-

Where,

f = Number of families

r = Number of replications

Table 3.4 Analysis of variance for generations within family

Source	d.f.	M.S.	E.M.S.
Replications	(r-1)	Mr	$\sigma^2 e + g\ \sigma^2 r$
Generations	(g-1)	Mg	$\sigma^2 e + r\ \sigma^2 g$
Error	(r-1)(g-1)	Me	$\sigma^2 e$
Total	(rg-1)	-	-

Where,

g= Number of generations

r = Number of replications

3.6.2 Scaling tests and estimation of gene effects

The crosses which showed significant differences among various generations for each of the character under study were subjected to generation mean analysis. For estimation of components of gene effect, simple Scaling Tests (Hayman and Mather, 1955) were applied. The non significance test of all the Simple Scaling Tests suggest adequacy of additive dominance model; hence, principle gene effects additive and dominance were estimated as per Jinks and Jones (1958). For the families and characters, wherein any of the Simple Scaling Test was significant, six parameters (m, d, h, i, j and l) model as suggested by Hayman (1958) was applied to partition gene effect into epistatic components including principle gene effects.

3.6.2.1 Simple Scaling Tests

The Simple Scaling Tests (A, B, C and D) as described by Hayman and Mather (1955) were used to test the adequacy of additive-dominance model for different characters in each family. The adequacy of scales must satisfy two conditions *viz*;

1) Additivity of genes

2) Independence of heritable component from non- heritable ones.

The test of first condition, additivity of genes provides information regarding absence or presence of intra allelic and interallelic interactions. The A, B, C and D scaling tests were applied using following equations for their values and variances.

$A = 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1$

$B = 2\bar{B}_2 - \bar{P}_2 - \bar{F}_1$

$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$

$D = 2\bar{F}_2 - \bar{B}_1 - \bar{B}_2$

The variances for scaling tests were computed using following formulae:

$V_A = 4V(\bar{B}_1) + V(\bar{P}_1) + V(\bar{F}_1)$

$V_B = 4V(\bar{B}_2) + V(\bar{P}_2) + V(\bar{F}_1)$

$V_C = 16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)$

$V_D = 4V(\bar{F}_2) + V(\bar{B}_1) + V(\bar{B}_2)$

The standard error of each test was calculated as square root of the respective variance as under:

S.E. (A) = $(V_A)½$ S.E.(B) = $(V_B)½$

S.E. (C) = $(V_c)½$ S.E.(D) = $(V_D)½$

The significance of each scaling test was tested by calculating ‘t’ value as follow:

t (A) = A/S.E.(A) t(B) = B/S.E.(B)

t (C) = C/S.E.(C) t(D) = D/S.E.(D)

The calculated values of ‘t’ were compared with tabulated values of ‘t’ at 0.05 and 0.01 probability levels i.e. 1.960 and 2.576 table values, respectively.

The significance of any one of these scales would suggest presence of nonallelic interactions

(i) The significance of A and/or B scaling tests provide evidence of presence of 'i' and/or 'j' and/or ‘l’ type of non-allelic interactions.

(ii) The significance of only ‘C’ scaling test suggests evidence of ‘l’ (dominance x dominance) type of digenic interaction.

(iii) The significance of only ‘D’ scaling test provides a test for presence of ‘i’ (additive x additive) type of interallelic interaction.

3.6.2.3 Estimation of gene effects

For the characters and families additive-dominance model was adequate, the estimates and magnitude of principal gene effects were computed as per Jinks and Jones (1958).

3.6.2.4 Three parameter model:

In the absence of interaction as indicated by non-significance of scaling tests following three parameters model was used for estimation of genetic components of variation. According to Jinks and Jones (1958):

$$\hat{d} = \frac{1}{2}\bar{P}1 - \frac{1}{2}\bar{P}2$$

$$\hat{h} = 6\bar{B}1 + 6\bar{B}2 - 8\bar{F}2 - \bar{F}1 - (3/2)\,\bar{P}1 - (3/2)\bar{P}2$$

$$\hat{m} = \frac{1}{2}\bar{P}_1 + \frac{1}{2}\bar{P}_2 + 4\bar{F}_2 - 2\bar{B}_1 - 2\bar{B}$$

The variances of these estimates were obtained using the formulae:

$$\hat{V}m = \frac{1}{4}V(\bar{P}_1) + \frac{1}{4}V(\bar{P}_2) + 16\bar{V}(F_2) + 4V(\bar{B}_1) + 4\bar{V}(B_2)$$

$$\hat{V}d = \frac{1}{4}V(\bar{P}_1) + \frac{1}{4}V(\bar{P}_2)$$

$$\hat{V}h = 36V(\bar{B}_1) + 36V(\bar{B}_2) + 64V(\bar{F}_2) + \bar{V}(F_1) + 9/4\bar{V}(P_1) + 9/4V(P_2)$$

Where,

$V(P_1)$, $V(\bar{P}_2)$, $V(\bar{F}_1)$, $V(\bar{F}_2)$, $V(\bar{B}_1)$, $V(\bar{B}_2)$ are the variances of means of P_1, P_2, F_1, F_2, B_1 and B_2 generation, respectively.

The standard error for each of the gene effect was computed as follow:

$$S.E.\ (m) = V\ (m)^{1/2}$$

S.E. (d) = V (d) ^{½}

S.E. ($\hat{h}$) = V (h) ^{½}

Then, the ‘t’ values were obtained as follow:

t (m) = m/S.E.(m)

t (d) = d/S.E. (d)

t (h) = h/S.E. (h)

When additive-dominance model was inadequate various gene effects were estimated using six-parameter model as suggested by Hayman (1958) and those have been explained as under:

Gene effect	**Symbol**	**Equation for estimation**
Mean	$\hat{M}$	$\overline{F}_2$
Additive	$\hat{D}$	$\overline{B}_1 - \overline{B}_2$
Dominance	$\hat{H}$	$\overline{F}_1 - 4\overline{F}_2 - ½\overline{P}_1 - ½\overline{P}_2 + 2\overline{B}_1 + 2\overline{B}_2$
Additive × Additive	$\hat{i}$	$2\overline{B}_1 + 2\overline{B}_2 - 4\overline{F}_2$
Additive × Dominance	$\hat{j}$	$2\overline{B}_1 - \overline{P}_1 - 2\overline{B}_2 + \overline{P}_2$
Dominance × Dominance	$\hat{l}$	$\overline{P}_1 + \overline{P}_2 + 2\overline{F}_1 + 4\overline{F}_2 - 4\overline{B}_1 - 4\overline{B}_2$

Where,

$\overline{P}_1$, $\overline{P}_2$, $\overline{F}_1$, $\overline{F}_2$, $\overline{B}_1$ and $\overline{B}_2$ are the mean values of P_1, P_2, F_1, F_2, B_1 and B_2 generation, respectively.

3.6.2.5 Test of significance for various gene effects

The test of significance of various gene effects was performed using 't' test for which variance and standard error of each estimate was calculated using following equations:

The variances of these estimates were obtained using following formulae:

$$V(\hat{m}) = V(\overline{F_2})$$

$$V(\hat{d}) = V(\overline{B_1}) + V(\overline{B_2})$$

$$V(\hat{h}) = V(\overline{F_1}) + 16V(\overline{F_2}) + \tfrac{1}{4} V(\overline{P_1}) + \tfrac{1}{4} V(\overline{P_2}) + 4V(\overline{B_1}) + 4V(\overline{B_2})$$

$$V(\hat{i}) = 4V(\overline{B_1}) + 4V(\overline{B_2}) + 16V(\overline{F_2})$$

$$V(\hat{j}) = 4V(\overline{B_1}) + V(\overline{P_1}) + 4V(\overline{B_2}) + V(\overline{P_2})$$

$$V(\hat{l}) = V(\overline{P_1}) + V(\overline{P_2}) + 4V(\overline{F_1}) + 16V(\overline{F_2}) + 16V(\overline{B_1}) + 16(\overline{B_2})$$

Where,

$V(\overline{P_1})$, $V(\overline{P_2})$, $V(\overline{F_1})$, $V(\overline{F_2})$, $V(\overline{B_1})$ and $V(\overline{B_2})$ are the mean values of P_1, P_2, F_1, F_2, B_1 and B_2 generation, respectively.

The standard error for each of the gene effect was computed as follow:

S.E. $(\hat{m}) = V(m)^{½}$ S.E. $(\hat{i}) = V(\hat{i})^{½}$

S.E. $(\hat{d}) = V(d)^{½}$ S.E. $(\hat{j}) = V(\hat{j})^{½}$

S.E. $(\hat{h}) = V(h)^{½}$ S.E. $(\hat{l}) = V(\hat{l})^{½}$

Then, the ‘t’ values were obtained as follow:

$t(\hat{m}) = m/S.E.(\hat{m})$ $\quad$ $t(\hat{i}) = m/S.E.(\hat{i})$

$t(\hat{d}) = d/S.E.(\hat{d})$ $\quad$ $t(\hat{j}) = m/S.E.(\hat{j})$

$t(\hat{h}) = h/S.E.(\hat{h})$ $\quad$ $t(\hat{l}) = m/S.E.(\hat{l})$

The calculated values of ‘t’ were compared with 1.960 and 2.576, which are the tabulated values of ‘t’ at 5 per cent and 1 per cent levels of significance, respectively.

3.6.3 Estimation of heterosis

Heterosis expressed as per cent increase or decrease of F_1 hybrid over its mid parent value (MP) and better parent value (BP) was computed using following formulae.

3.6.3.1 Heterosis over mid parent (Relative heterosis): H_1 (Turner 1953)

Where,

$$MP = \frac{\overline{P_1} + \overline{P_2}}{2} \qquad H_1(\%) = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

P_1 = Mean performance of first parent *i.e.* (female)

P_2 = Mean performance of second parent *i.e.* (male)

$\overline{F_1}$ = Mean value of F_1 hybrid *i.e.* F_1

3.6.3.1 Heterosis over better parent (Heterobeltosis): H_2 (Fonseca and Patterson, 1968)

$$H_2(\%) = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where, BP = Mean performance of better parent

3.6.3.2 Test of significance

The tests of significance for heterosis and heterobeltiosis were carried out following 't' tests as under

$$t = \frac{\overline{F_1} - \overline{MP}}{S.E.\ (\overline{F_1} - \overline{MP})} \quad \text{(for heterosis)}$$

$$t = \frac{\overline{F_1} - \overline{BP}}{S.E.\ (\overline{F_1} - \overline{BP})} \quad \text{(for heterobeltiosis)}$$

Standard errors (S.E.) and critical differences were estimated using the following relation

$$\text{S.E. For } H_1 = \frac{\sqrt{3Me}}{2r} \qquad = \text{S.E.}(H_1) \times t$$

$$\text{S.E. For } H_2 = \frac{\sqrt{2Me}}{r}$$

Where,

Me = Error mean sum of square

r = Number of replication

The test of significance of relative heterosis and heterobeltiosis were carried out by comparing calculated values of 't' with tabulated values of 't' at 5% (1.96) and 1% (2.576) level of significance.

3.6.4 Estimation of inbreeding depression

Inbreeding depression was computed by using the following formulae:

Inbreeding depression (%)

$$= \frac{\overline{F_1} - \overline{F_2}}{\overline{F_1}} \times 100$$

The standard error and 't' value for test of significance for inbreeding depression were calculated as under:

Standard error for inbreeding depression

$$\text{S. E. } (\overline{F_1} - \overline{F_2}) = \sqrt{\frac{Me_1 + Me_2}{r}}$$

't' test for inbreeding depression

$$t\ (\overline{F_1} - \overline{F_2}) = \frac{\overline{F_1} - \overline{F_2}}{\text{S. E. } (\overline{F_1} - \overline{F_2})}$$

Where,

$\overline{F_1}$ = Mean value of F_1 hybrid

$\overline{F_2}$ = Mean value of F_2 generation of respective F_1

Me_1 = Error mean square of F_1 generation

Me_2 = Error mean square of F_2 generation

r = Number of replications

The test of significant of inbreeding depression was performed by comparing, calculated 'f' value with table 't' value at 5 per cent (1.960) and 1 per cent (2.576) level of significance.

3.6.5 Estimation of heritability

3.6.5.1 Heritability in broad sense

The broad sense heritability in per cent was calculated by using formula suggested by Roy Darbeshwar (2000) as follows:

$$h^2b\ (\%) = \frac{VF_2 - 1/3\ (VP_1 + VP_2 + VF_1)}{VF_2} \times 100$$

Where,

h^2b =Heritability in broad sense

VF_2 =Variance of F_2 generation

VP_1=Variance of P_1 generation

VP_2=Variance of P_2 generation

VF_1=Variance of F_1 generation

3.6.5.2 Heritability in Narrow Sense

The Narrow sense heritability in percent was calculated by using formula.

$$h^2n\ (\%) = \frac{2VF_2 - (VB_1 + VB_2)}{VF_2} \times 100$$

3.6.6 Estimation of expected genetic advance under selection:

The expected genetic advance at 5% selection intensity was estimated by using formula suggested by Allard (1960)

$$G.A. = h^2\ (n) \times K \times \sigma p$$

Where,

$h^2\ (n)$ = Heritability in narrow sense

K = Selection differential (K=2.06) at 5% selection intensity

σp = Phenotypic standard deviation

Expected genetic advance as per cent of population mean was obtained by using following formula.

$$\text{Genetic advance as per cent of mean} = \frac{G.A.}{\overline{X}} \times 100$$

Where,

G.A = Genetic Advance

$\overline{X}$ = Mean of the character under study

EXPERIMENTAL RESULTS

IV. EXPERIMENTAL RESULTS

Results of the present investigation on "**Genetic analysis of quantitative traits in aerobic rice (*Oryza sativa* L.)**" are presented in this chapter. Each of the four crosses has been discussed separately under following headings except analysis of variance for generation means which is as follows.

4.1 Analysis of variance and per se performance of six generations
4.2 Scaling tests and estimation of gene effects
4.3 Heterosis, inbreeding depression, heritability and genetic advance.

4.1 Analyses of variance and *per se* performance

Analysis of variance for generation means comprising six generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 was computed for ten characters for each cross and mean sum of squares with their degrees of freedom are presented in Table 4.1. The mean sum of squares data revealed the significant differences among the generations of all the four crosses for all the traits. This indicated sufficient diversity among the materials under study. Mean performance of different generations of each family for various characters are presented in Table 4.1.1 to Table 4.1.4 and results are presented as under.

4.1.1 Cross Gurjari x GR-5

4.1.1.1 Days to flowering

The data in table 4.1.1 revealed that the significant differences were observed amongst the parental, F_1 and back crosses mean for this trait. The F_1 (77.33) mean value being intermediate to the

Table : 4. 1 Analysis of variance for generation means of four crosses for different characters

Mean sum of square											
Source of variance	**df**	**Days to flowering**	**Plant height**	**Productive tillers per plant**	**Panicle length**	**Grains per panicle**	**Grain yield per plant**	**100 grain weight**	**Kernel length (mm)**	**Length/Breath ratio**	**Straw yield per plant**
GURJARI X GR-5											
Replication	2	0.56	5.5	0.2	0.62*	33.11*	0.05	0.009	0.008	0.018	6.12
Generation	5	125.03**	429.91**	6.59**	5.08**	1001.62**	281.63	0.042**	0.168**	0.082**	125.53**
Error	10	2.38	7.4	0.22	0.11	6.07	40.48	0.005	0.025	0.005	2.46
GR-4 x IET-18654											
Replication	2	1.59	5.23	0.77*	1.05	60.96	1.55	0.028	0.002	0.032	6.99*
Generation	5	129.18**	163.34**	1.72**	4.34**	1934.10**	25.40**	0.100**	0.055**	0.173**	82.66**
Error	10	6.48	5.92	0.11	0.29	41.38	1.39	0.008	0.002	0.017	1.47
JAYA x IET-18654											
Replication	2	0.70	6.12	0.50	0.03	42.84	3.14	0.042	0.019	0.002	10.03
Generation	5	120.46**	679.89**	2.50*	4.85**	1888.93**	51.36**	0.080	0.368**	0.012**	156.74
Error	10	2.75	29.29	0.68	0.48	13.51	4.48	0.059	0.017	0.006	55.48
JAYA x GR-5											
Replication	2	0.02	4.63	0.13	0.009	1.01	0.54	0.004	0.001	0.008	9.02*
Generation	5	143.23**	587.68**	13.91*	5.333**	494.73**	25.73**	0.071*	0.055*	0.040*	28.02**
Error	10	3.19	6.96	5.34	0.214	7.72	0.84	0.016	0.009	0.010	1.48

*, ** Significant at 5 and 1 % levels, respectively.

parental means but differed significantly from either of the parents *i.e.* P_1 (92.93) and P_2 (75.20) and back crosses, BC_1 (84.36) and BC_2 (81.80). However, non-significant difference was observed in mean values of F_1 (77.33) generation from the mean of F_2 (77.98).

4.1.1.2 Plant height (cm)

For this trait, all the mean values of respective generation differed significantly from each other (Table 4.1.1). The mean of F_1 (132.53 cm) significantly exceeded the mean of both parents *i.e.* P_1 (100.93 cm) and P_2 (124.46 cm), F_2 (128.73 cm) and both back crosses *i.e.* BC_1 and BC_2 (109.96 and 120.73 cm).

4.1.1.3 Productive tillers per plant

The data pertaining to table 4.1.1 showed that the F_1 (10.26) mean value differed significantly from either of the parents *i.e.*, P_1 and P_2 (10.93 and 8.60), both back crosses BC_1 (8.10) and BC_2 (7.06) and F_2 (7.93) means. The second parent, P_2 was found at par with BC_1, while the mean values of BC_1 and F_2 had non-significant difference. The F_1 mean was found significantly higher than mean of F_2 population.

4.1.1.4 Panicle length (cm)

From the data given in (table 4.1.1), it was observed that the F_1 mean (25.03 cm) differed significantly from either of the parents *i.e.* P_1 (21.42 cm) and P_2 (24.16 cm) and both the back crosses *i.e.* BC_1 (22.83 cm) and BC_2 (23.88 cm) for this trait, but it was differed non-significantly from F_2 (24.72 cm) mean. The mean value of second parent (P_2) was at par with the mean value of BC_2 (23.88 cm).

4.1.1.5 Grains per panicle

The mean value of first parent, P_1 (135.53) was higher than P_2 (87.27) and both are differed significantly from each other. The F_1 (135.80) exhibited higher values than both the parents and non-significantly differed from first parent P_1, while F_2 (116.30) had non-significant difference with BC_1. The mean values of both BC_1 (113.87) and BC_2 (107.90) generations found significantly higher than parent P_2 (Table 4.1.1).

4.1.1.6 Grain yield per plant (g)

The significant differences were observed among the both the parents (17.40 and 8.44 g). F_1 (20.11 g) differed significantly from both the parents and backcrosses *i.e.* BC_1 (13.57 g) and BC_2 (10.32 g). The F_2 (13.39 g) generation had significantly lower mean than mean of F_1 (Table 4.1.1).

4.1.1.7 100 Grain weight (g)

The parent P_1 (3.02 g) had significantly higher 100 grain weight than the parent P_2 (2.70 g), F_1 (2.78 g), F_2 (2.81 g), BC_1 (2.85 g) and BC_2 (2.70 g) (Table 4.1.1). The F_1 mean found intermediate to both the parents and non-significantly differed from P_2, F_2, BC_1 and BC_2. The mean values of BC_1 and BC_2 generations were closer to its respective recurrent parent and BC_1 had significant and higher values than BC_2.

4.1.1.8 Kernel length (mm)

Both the parents differed significantly for their mean performance (Table 4.1.1). Mean value of F_1 (6.44 mm) generation was significantly higher than the parent P_2 (6.05 mm) and closer to parent P_1 (6.55 mm). Mean value of F_1 was at par with means of P_1, F_2 (6.48 mm) and BC_1 (6.37 mm). BC_2 (5.99 mm) differed significantly from all the generations except parent P_2.

4.1.1.9 Length/Breath ratio

Significant difference was reported between the parental mean *i.e.* P_1 and P_2 (2.95 and 2.50) for this trait. F_1 (2.54) mean value was found in between to the parental means but differed significantly

Table 4.1.1 Mean performance of six generations for different characters in cross Gurjari x GR-5

GURJARI × GR-5										
Generation	**Days to flowering**	**Plant height**	**Productive tillers per plant**	**Panicle length**	**Grains per panicle**	**Grain yield per plant**	**100 grain weight**	**Kernel length (mm)**	**Length /Breath ratio**	**Straw yield per plant**
P_1	92.93	100.93	10.93	21.42	135.53	17.40	3.02	6.55	2.95	22.96
P_2	75.20	124.46	8.60	24.16	87.27	8.43	2.70	6.05	2.50	14.50
F_1	77.33	132.53	10.26	25.03	135.80	20.11	2.78	6.44	2.54	22.83
F_2	77.98	128.73	7.93	24.72	116.30	13.38	2.81	6.48	2.79	19.01
BC_1	84.36	109.96	8.10	22.83	113.87	13.57	2.85	6.37	2.68	9.76
BC_2	81.80	120.73	7.06	23.88	107.90	10.32	2.70	5.99	2.62	7.99
S.Em. ±	0.63	1.11	0.19	0.13	1.00	0.82	0.031	0.06	0.029	0.641
C.D. at 5 %	1.98	3.50	0.61	0.43	3.17	2.58	0.098	0.20	0.093	2.02

from all the generations except P_2 and BC_2. The F_2 mean value (2.79) found higher than F_1 and differed significantly from all the generations while, BC_1 (2.68) and BC_2 (2.62) were at par to each other (Table 4.1.1).

4.1.1.10 Straw yield per plant (g)

The high mean value of F_1 (22.83 g) differed significantly from all the generations except Parent P_1 (22.96 g). Both the backcrosses, BC_1 and BC_2 (9.76 g and 7.99 g) were found at par to each other. The means of P_2 (14.50 g) and F_2 population (19.01 g) were found lower than F_1 mean and differed significantly from each other and the rest of the generations. The mean values of both BC_1 and BC_2 generations were slightly lower to its recurrent parents (Table 4.1.1).

4.1.2. Cross GR-4 X IET-18654

4.1.2.1 Days to flowering

Both the parental means *i.e.* P_1 (93.47) and P_2 (74.47) differed significantly from each other and the mean value of their resultant F_1 (84.00) generation. The mean of F_1 was significantly higher than the parent P_2 mean (74.47). Mean value of F_1 was at par with means of BC_1 (85.10) and BC_2 (83.43), while F_2 (90.42) and P_1 were at par to each other. The mean of F_2 was found higher than the mean of F_1, BC_1 and BC_2 generations (Table 4.1.2).

4.1.2.2 Plant height (cm)

For this traits parent P_1 (109.20 cm) and was significantly differed from P_2 (123.84 cm) and F_1 (125.67 cm). F_1 mean didn’t significantly differ from the mean of P_2 and BC_2 (128.10 cm). The mean of F_2 population (118.65 cm) and BC_1 (113.56 cm) were significantly differed and lower than the F_1 mean value. The mean of BC_1 was significantly lower than BC_2 (Table 4.1.2).

4.1.2.3 Productive tillers per plant

The significant differences were observed among both the parental means (9.53 and 7.40) and their resultant F_1's mean (8.53). Mean values of F_2 (8.96) generation was statistically at par with mean values of F_1 and BC_2 (8.83). The F_1 generation had lower mean than F_2 generation. BC_1 (9.33) found better than BC_2 (8.83) generation in respect to productive tillers per plant (Table 4.1.2).

4.1.2.4 Panicle length (cm)

The mean value of P_1 (21.67cm) and P_2 (24.26cm) differed significantly from each other (Table 4.1.2). F_1 (24.25cm) was found very close to the mean of P_2, at par to each other and significantly differed from P_1 and F_2 (22.32cm). The mean of F_1 recorded significantly higher than mean of F_2. Both the backcrosses, BC_1 and BC_2 (23.63cm and 24.65cm) were significantly differed from each other.

4.1.2.5 Grains per panicle

The mean values of both the parents *i.e.* P_1 (191.00) and P_2 (124.53) were significantly differed from each other. F_1 (150.80) and F_2 (142.92) mean were intermediate to both the parents. F_2 mean value was significantly lower than F_1. The mean values of both BC_1 (127.97) and BC_2 (125.80) generations were found closer to each other (Table 4.1.2).

4.1.2.6 Grain yield per plant (g)

The parent P_1 (18.67 g) had significantly higher grain yield per plant than the parent P_2 (9.99 g), F_1 (13.14 g), F_2 (14.89 g), BC_1 (12.32 g) and BC_2 (13.21 g). The F_1 mean found intermediate to both the parents and significantly differed from P_1 and P_2. F_2 recorded significantly higher mean than F_1 (Table 4.1.2).

4.1.2.7 100 Grain weight (g)

From the data given in table 4.1.2, it was observed that the F_1 mean (1.81 g) was intermediate to both the parents and differed significantly from either of the parents *i.e.* P_1 (1.48 g) and P_2 (1.98 g) and BC_1 (1.54 g) for this trait, but it was differed non-significantly from F_2 (1.71 g) and BC_2 (1.78 g) means. The mean of BC_1 was lower than mean of BC_2, while difference between mean values of F_1 and F_2 were found non-significant.

4.1.2.8 Kernel length (mm)

Kernel length was more in P_2 (5.57 mm) compared to P_1 (5.38 mm) and both parents differed significantly from each other and it's F_1 (5.79 mm). The F_1 mean value was found significantly highest than all other five generations. Mean performance of BC_1 (5.51 mm) was lower than the recurrent parent. Mean value of BC_2 (5.63 mm) was significantly higher than BC_1 (Table 4.1.2).

4.1.2.9 Length/Breath ratio

Length/Breath ratio was significantly more in parent P_1 (3.13) compared to P_2 (2.39). The F_1 mean value (2.75) was found intermediate to both parent and differed significantly from both the parents. The F_2 (2.90) had higher mean value P_2, F_1, BC_1 and BC_2. Mean performances of BC_1 (2.79) and BC_2 (2.76) were found at par to each other (Table 4.1.2).

4.1.2.10 Straw yield per plant (g)

Parent P_1 (24.85 g) recorded higher straw yield than parent P_2 (17.20 g) (Table 4.1.2). The mean of F_1 population (17.47 g) differed significantly from all the generations except P_2. The mean value of F_2 (19.58 g) was found significantly higher than F1. The mean value of BC_1 was (8.78 g) significantly lower than BC_2 (19.59 g).

Table 4.1.2 Mean performance of six generations for different characters in cross GR-4 × IET-18654

GR-4 × IET-18654										
Generation	**Days to flowering**	**Plant height**	**Productive tillers per plant**	**Panicle length**	**Grains per panicle**	**Grain yield per plant**	**100 grain weight**	**Kernel length (mm)**	**Length /Breath ratio**	**Straw yield per plant**
$\mathbf{P_1}$	93.47	109.20	9.53	21.67	191.00	18.67	1.48	5.38	3.13	24.85
$\mathbf{P_2}$	74.47	123.84	7.40	24.26	124.53	9.99	1.98	5.57	2.39	17.20
$\mathbf{F_1}$	84.00	125.67	8.53	24.25	150.80	13.14	1.81	5.79	2.75	17.47
$\mathbf{F_2}$	90.42	118.65	8.96	22.32	142.92	14.89	1.71	5.54	2.90	19.58
$\mathbf{BC_1}$	85.10	113.56	9.33	23.63	127.97	12.32	1.54	5.51	2.79	8.78
$\mathbf{BC_2}$	83.43	128.10	8.83	24.65	125.80	13.21	1.78	5.63	2.76	19.59
S.Em. ±	1.04	0.99	0.14	0.22	2.63	0.48	0.037	0.017	0.05	0.50
C.D. at 5 %	3.27	3.13	0.43	0.7	6.27	1.52	0.12	0.06	0.17	1.56

4.1.3. Cross Jaya x IET-18654

4.1.3.1 Days to flowering

From the data given in table 4.1.3, it was observed that the F_1 mean (85.27) found intermediate to both the parents and differed significantly from either of the parents *i.e.* P_1 (93.27) and P_2 (74.27), F_2 (87.73) and BC_1 (88.40) for this trait, but it was differed non-significantly from BC_2 (87.00) mean. Non-significant differences recorded between mean values of BC_1 and BC_2, while mean of F_2 was found significantly higher than F_1.

4.1.3.2 Plant height (cm)

The F_1 (109.60 cm) mean found intermediate to both the parents and significantly differed from the mean all the generation *viz.*, P_1 (87.04 cm), P_2 (127.00 cm), BC_2 (127.24 cm) and F_2 (118.62 cm) except BC_1 (108.82 cm) (Table 4.1.3). The mean of F_2 population was significantly higher than F_1. BC_1 exhibited significantly lower value than BC_2.

4.1.3.3 Productive tillers per plant

The mean of the F_1 (7.13) was slightly closer to P_1 (7.27) and it was significantly differed from P_2 (8.27), BC_1 (9.57) and BC_2 (8.73). The F_2 (8.07) mean was higher than F_1 and both were found at par to each other. The mean values of BC_1 and BC_2 generations were non-significantly differed and higher than its respective recurrent parents (Table 4.1.3).

4.1.3.4 Panicle length (cm)

The F_1 mean value for panicle length (26.69 cm) was found significantly higher than both the parents. Non-significant difference recorded between mean of F_1 and F_2 (27.07 cm). Both parents *viz.*, P_1 (24.11 cm) and P_2 (24.23 cm) were found at par to each other (Table 4.1.3). Mean performance of BC_1 (25.20 cm) was lower than BC_2 (26.30 cm). Both the backcrosses had higher values than their respective recurrent parent.

4.1.3.5 Grains per panicle

The F_1 mean value (160.27) was found significantly higher than four generations *i.e.* P_1 (95.27), P_2 (122.07), F_2 (131.13) and BC_1 (114.63) but found at par to BC_2 (156.93). The mean values of BC_1 (114.63) had significantly lower values than BC_2 (156.93). Both the backcrosses had higher values than their recurrent parent (Table 4.1.3).

4.1.3.6 Grain yield per plant (g)

The highest mean value of F_1 (21.88 g) differed significantly from all the generations (Table 4.1.3). The parent P_1 (19.08) exhibited significantly higher value than P_2 (10.18 g) BC_2 (14.73 g) and F_2 (14.88 g). The mean values of BC_1 (18.61) found significantly higher than BC_2 (14.73 g) generation but lower than recurrent parent.

4.1.3.7 100 Grain weight (g)

The data given in table 4.1.3 showed that F_1 (2.63g) found intermediate to both the parents *i.e.* P_1 (2.82 g) and P_2 (2.36 g) but non-significantly differed from each of the five generations. BC_1 (2.71 g) had slightly higher mean than BC_2 (2.63 g) and lower than its recurrent parent.

4.1.3.8 Kernel length (mm)

The mean value of first parent, P_1 (6.12 mm) was significantly higher than P_2 (5.46 mm). The F_1 (6.26 mm) exhibited higher values than both the parents and non-significantly differed from first parent P_1, F_2 (6.35 mm) and BC_1 (6.27 mm). The mean values of both BC_1 (6.27 mm) and BC_2 (5.77 mm) generations found significantly differed from each other (Table 4.1.3).

Table 4.1.3 Mean performance of six generations for different characters in cross JAYA × IET-18654

JAYA × IET-18654										
Generation	**Days to flowering**	**Plant height**	**Productive tillers per plant**	**Panicle length**	**Grains per panicle**	**Grain yield per plant**	**100 grain weight**	**Kernel length (mm)**	**Length /Breath ratio**	**Straw yield per plant**
P_1	93.27	87.04	7.27	24.11	95.27	19.08	2.82	6.12	2.64	23.22
P_2	74.27	127.00	8.27	24.23	122.07	10.18	2.36	5.46	2.50	17.05
F_1	85.27	109.60	7.13	26.69	160.27	21.88	2.63	6.26	2.52	26.09
F_2	87.73	118.62	8.07	27.07	131.13	14.88	2.76	6.35	2.52	20.80
BC_1	88.40	108.82	9.57	25.20	114.63	18.61	2.71	6.27	2.61	24.33
BC_2	87.00	127.24	8.73	26.30	156.93	14.73	2.63	5.77	2.48	20.37
S.Em. ±	0.68	2.21	0.36	0.28	1.50	0.86	0.1	0.054	0.032	0.92
C.D. at 5 %	2.19	6.96	1.06	0.89	4.73	2.72	0.32	0.17	0.10	2.33

4.1.3.9 Length/Breath ratio

The significant differences were observed among both the parental means (2.64 and 2.50) however, their resultant F_1 (2.52) and F_2 (2.52) expressed non-significant differences among all the generations except parent P_1. BC_1 (2.61) found better than BC_2 (2.48) generation in respect to length/breath ratio (Table 4.1.3).

4.1.3.10 Straw yield per plant (g)

The mean of the F_1 (26.09 g) significantly differed from P_1 (23.22 g), P_2 (17.05 g), and BC_2 (20.37 g) and F_2 (20.80 g). The F_2 (20.80 g) depicted significantly lower mean performance than F_1. Significant difference recorded between back cross generations (Table 4.1.3).

4.1.4 Cross Jaya x GR-5

4.1.4.1 Days to flowering

The data pertaining to (Table 4.1.4) revealed that the significant differences were observed among both the parental means (93.25 and 77.13). BC_1 (88.77) depicted significantly higher values than BC_2 (79.63) generation and lower than its recurrent parent, in respect to days to flowering. The F_2 generation (87.30) expressed significantly higher values than F_1 generation.

4.1.4.2 Plant height (cm)

The F_1 (110.20 cm) mean found intermediate to both the parents and significantly differed from the mean all the generations *viz.*, P_1 (85.64 cm), P_2 (123.35 cm), BC_2 (119.94 cm) and F_2 (120.80 cm) except BC_1 (108.20 cm). Non-significant difference observed between F_1 and F_2. BC_1 exhibited significantly lower value than BC_2 and higher than its recurrent parent (Table 4.1.4).

4.1.4.3 Productive tillers per plant

The mean of the F_1 non-significantly differed from P_1 and BC_1. The mean of F_1 (6.87) had lower mean values than both the parental means (7.73 and 9.13) and F_2 (9.25). The F_2 depicted significantly higher mean performance than F_1. The mean value BC_2 (8.33) found higher than BC_1 (7.37). Both the backcrosses had lower values that their respective recurrent parent (Table 4.1.4).

4.1.4.4 Panicle length (cm)

The F_1 mean value (24.73 cm) was lying between mid-parent values and differed significantly from all the generation means *viz.*, P_1 (22.46 cm), F_2 (23.86 cm), BC_1 (23.87 cm) and BC_2 (26.37 cm) except P_2 (25.16 cm). The mean of F_1 found significantly higher than F_2 mean value. The means of BC_1 (23.87 cm) and BC_2 (26.37 cm) was found higher than their respective recurrent parent (Table 4.1.4).

4.1.4.5 Grains per panicle

For this trait, all the mean values of respective generation differed significantly from each other (Table 4.1.4). The mean of F_1 (121.67) significantly exceeded the mean of both parents *i.e.* P_1 (102.60) and P_2 (84.87), F_2 (112.67) and both back crosses *i.e.* BC_1 and BC_2 (107.73 and 96.77). The BC_1 exhibited significantly higher values than BC_2 while both the backcrosses had significantly higher values than their respective recurrent parent.

4.1.4.6 Grain yield per plant (g)

The data showed that the mean of F_1 population (17.78 g) was higher than five generations *viz.*, P_1 (15.41 g), P_2 (9.48 g), F_2 (15.87 g), BC_1 (14.67 g) and BC_2 (12.36 g) suggesting involvement of over dominance gene effects in the expression of this trait. The mean value of BC_1 significantly exceeded from mean value of BC_2 (Table 4.1.4).

4.1.4.7 100 Grain weight (g)

The F_1 mean value (2.82 g) was lying between mid-parent values and differed significantly from both the parents *viz.*, P_1(3.02 g) and P_2 (2.60 g). The mean value of F_2 (2.87 g) was at par to mean of F_1 generation. The mean values of BC_1 (2.80 g) and BC_2 (2.64 g) found at par to each other however, BC_1 expressed lower values than its recurrent parent (Table 4.1.4).

4.1.4.8 Kernel length (mm)

Non-significant differences were found among the parents *viz.*, P_1 (6.09 mm), P_2 (6.10 mm) and F_1 (6.14 mm). The F_1 value depicted higher performance than its parents but significantly lower than F_2 mean value (6.44 mm). Mean performance of both BC_1 (6.27 mm) and BC_2 (6.28 mm) was at par to each other and significantly higher than its respective recurrent patent (Table 4.1.4).

4.1.4.9 Length/Breath ratio

Length/Breath ratio was significantly more in parent P_1 (2.91) compared to all the generations under study. The F_1 mean value (2.70) was lying between both parental means and higher than F_2 (2.59). Mean performance of BC_2 (2.67) was higher than the recurrent parent but slightly lower than BC_1 (2.77) (Table 4.1.4).

4.1.4.10 Straw yield per plant (g)

The significant differences were recorded among both the parents *i.e.* P_1, P_2 and their resulted F_1. The F_1 (24.01 g) depicted significantly higher mean value than five generations *viz.*, P_1 (20.20 g), P_2 (14.89 g), F_2 (21.06 g), BC_1 (19.49 g) and BC_2 (17.99 g) suggesting involvement of over dominance gene effects in the expression of this trait. The mean value of BC_1 found superior to mean value of and BC_2 and was slightly lower to its recurrent parent (Table 4.1.4).

Table 4.1.4 Mean performance of six generations for different characters in cross JAYA × GR-5

JAYA × GR-5										
Generation	**Days to flowering**	**Plant height**	**Productive tillers per plant**	**Panicle length**	**Grains per panicle**	**Grain yield per plant**	**100 grain weight**	**Kernel length (mm)**	**Length/ Breath ratio**	**Straw yield per plant**
P_1	93.53	85.64	7.73	22.46	102.60	15.41	3.02	6.09	2.91	20.20
P_2	77.13	123.35	9.13	25.16	84.87	9.48	2.60	6.10	2.62	14.89
F_1	77.07	110.20	6.87	24.73	121.67	17.78	2.82	6.14	2.70	24.01
F_2	87.30	120.80	9.25	23.86	112.67	15.87	2.87	6.44	2.59	21.06
BC_1	88.77	108.20	7.37	23.87	107.73	14.67	2.80	6.27	2.77	19.49
BC_2	79.63	119.94	8.33	26.37	96.77	12.36	2.64	6.28	2.67	17.99
S.Em. ±	0.73	1.077	0.30	0.19	1.13	0.37	0.05	0.04	0.04	0.50
C.D. at 5 %	2.30	3.39	0.94	0.60	3.57	1.10	0.16	0.13	0.13	1.57

4.2 SCALING TESTS AND ESTIMATION OF GENE EFFECTS

The mean values of all the six generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 for ten different characters of all the four crosses were first subjected to genetic analysis. The test of adequacy of scale is important because in most of the cases the estimation of additive and dominance components of variances is made assuming the absence of gene interaction. When the scale is adequate, the values of A, B, C and D should be zero within the limits of their respective standard errors. The significance of any one of these scales (A, B, C and D) indicated the presence of non-allelic interaction. Individual simple scaling tests (A, B, C and D) of Hayman and Mather, 1955 were employed to detect the presence of epistasis. For the families and characters, wherein any of the Simple Scaling Test was significant, six parameters (m, d, h, i, j and l) model as suggested by Hayman (1958) and Jinks and Jones (1958) was applied to partition gene effect into epistatic components including principle gene effects. The character and cross-wise results are presented in Table 4.2.1 to 4.2.4. Significance of ‘m’ parameter for all the characters studied in all the crosses with most of the approaches suggested that different generations of a respective cross significantly differed and sufficient variability was existing among the generations incorporated for the study, hence this component has not been explained individually.

4.2.1 Cross Gurjari x GR-5

4.2.1.1 Days to flowering

Presence of non-allelic interaction was indicated by the significance of A, B, C and D scales (Table 4.2.1). The genetic parameters *viz.*, additive (8.86), dominance (43.60) found highly significant. The interaction additive x additive (20.40), additive x dominance (-6.30) and dominance x dominance (-29.93) were found highly significant. Duplicate type of gene action was found responsible for inheritance of this trait.

4.2.1.2 Plant height (cm)

The data pertaining to plant height (Table 4.2.1) revealed that all four scales A, B, C and D were highly significant which indicated the non allelic interaction. Estimation of genetic parameters revealed that additive (-11.76) and dominance (-117.30) were highly significant. The two interaction *viz.*, additive x additive (-53.86) and dominance x dominance (83.26) were also found highly significant. Duplicate type of gene action was occurred for inheritance of this trait.

4.2.1.3 Productive tillers per plant

Scaling tests A, B, C, and D were highly significant (Table 4.2.1), which suggested the inadequate of additive and dominance model. Estimated genetic factors such as additive (1.16) and dominance (-12.03) was highly significant. Similarly additive x additive (-1.40) and dominance x dominance (11.13) were highly significant. Duplicate type of gene action was recorded for inheritance of this trait.

4.2.1.4 Panicle length (cm)

All four scaling test *viz.*, A, B, C, and D were highly significant (Table 4.2.1), that indicated inadequacy of additive and dominance model. Estimation of genetic parameters revealed that additive (-1.31) was non-significant while, dominance (-11.02) was highly significant. As far as interaction concerned additive x dominance (0.26) was significant, while, highly significant values were recorded for additive x additive (-5.44) and dominance x dominance (7.76) interaction. Interaction of this character was governed by duplicate type of gene action.

4.2.1.5 Grains per panicle

Non allelic interaction was reported as the four scaling test A, B, C, and D had highly significant values (Table 4.2.1). Additive (24.13), dominance (-69.80) were highly significant. While epistatic effect *viz.*, additive x additive (-21.66), additive x dominance (-18.16) and dominance x dominance (72.53) were found highly significant. This character was governed by duplicate gene action.

4.2.1.6 Grain yield per plant (g)

Additive-dominance model inadequate as all four scaling tests A, B, C, and D were highly significant (Table 4.2.1). Estimated genetic parameters revealed that additive (4.48), dominance (-22.56) were highly significant. The interaction *viz.*, additive x additive (-5.74), additive x dominance (-1.23) and dominance x dominance (24.01) were also highly significant. The gene action recorded for this trait was duplicate type.

4.2.1.7 100 Grain weight (g)

Non-allelic gene actions were present as the A, B, and D scaling tests revealed highly significant (Table 4.2.1). Genetic analysis revealed that additive (0.16), dominance (-0.56), additive x additive (-0.15) and dominance x dominance (0.33) interaction effects were highly significant. The dominance and dominance x dominance estimates had opposite signs indicating the presence of duplicate type of gene interaction.

4.2.1.8 Kernel length (mm)

For kernel length, highly significant values of A, B, C and D tests indicated digenic interaction for the inheritance of this trait (Table 4.2.1). The results obtained on six parameter model indicated

Table 4.2.1 The results of scaling tests and estimation of gene effects for ten character studied in cross Gurjari x GR-5

Parameter	Days to flowering	Plant height (cm)	Productive tillers per plant	Panicle length (cm)	Grains per panicle	Grain yield per plant (g)	100 grain weight	Kernel length (mm)	Length/ Breath ratio	Straw yield per plant (g)
A	-1.53* ± 0.64	-13.53** ± 1.16	-5.00** ± 0.24	-0.89 ** ± 0.17	-43.60** ± 1.10	-10.37** ± 0.76	-0.11** ± 0.04	-0.25** ± 0.06	-0.11** ± 0.04	-26.26** ± 0.61
B	11.06 ** ± 0.61	-15.86** ± 1.44	-4.73** ± 0.22	-1.42** ± 0.14	-7.26** ± 1.35	-7.9** ± 0.50	-0.07 ** ± 0.01	-0.52** ± 0.06	0.19** ± 0.03	-21.34** ± 0.39
C	-10.20** ± 1.25	24.46** ± 1.27	-8.33** ± 0.22	3.12** ± 0.31	-29.20** ± 2.81	12.52** ± 1.41	-0.03 ± 0.05	0.44** ± 0.11	0.62** ± 0.06	-7.07** ± 1.52
D	-10.20 ** ± 0.44	26.93** ± 0.87	0.70** ±0.13	2.72 ** ±0.15	10.83** ± 1.25	2.87** ±0.55	0.07** ± 0.02	0.61** ± 0.05	0.27** ±0.02	20.26** ± 0.65
m	63.66** ± 0.91	166.56** ± 1.76	11.16** ± 0.27	28.28** ± 0.02	133.06** ± 2.53	18.66** ± 1.15	3.01** ± 0.05	7.52** ± 0.11	3.27** ± 0.05	59.26** ± 1.34
d	8.86** ± 0.19	-11.76** ± 0.28	1.16** ± 0.06	-1.31 ± 0.07	24.13** ± 0.29	4.48** ± 0.35	0.16** ± 0.01	0.25** ± 0.01	0.22** ± 0.01	4.23** ± 0.29
h	43.60** ± 2.10	-117.30** ± 5.12	-12.03** ± 0.84	-11.02** ± 0.75	-69.80** ± 5.80	-22.56** ± 2.60	-0.56** ± 0.11	-3.08** ± 0.27	-1.20** ± 0.13	-124.57** ± 2.82
aa	20.40** ± 0.89	-53.86** ± 1.74	-1.40** ± 0.27	-5.44** ± 0.31	-21.66** ± 2.51	-5.74** ± 1.10	-0.15** ± 0.04	-1.22** ± 0.10	-0.54** ± 0.05	-40.53** ± 1.31
ad	-6.30** ± 0.27	1.16 ± 0.86	-0.13 ± 0.15	0.26* ± 0.11	-18.16** ± 0.65	-1.23** ± 0.40	-0.01 ± 0.02	0.13** ± 0.03	-0.15** ± 0.02	-2.45** ± 0.39
dd	-29.93** ± 1.46	83.26** ± 3.49	11.13** ± 0.58	7.76** ± 0.44	72.53** ± 3.67	24.01** ± 2.53	0.33** ± 0.07	2.00** ± 0.18	0.47** ± 0.09	88.14** ± 1.58
Gene action	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate

highly significant values of additive (0.25), dominance (-3.08), additive x additive (-1.22), additive x dominance (0.13) and dominance x dominance (2.00) gene effects. The dominance and dominance x dominance (l) estimates had opposite signs indicated the presence of duplicate type of gene interaction.

4.2.1.9 Length/Breath ratio

Significance of A, B, C and D scaling tests revealed presence of non-allelic gene effects (Table 4.2.1). The additive (0.22), dominance (-1.20) effects were highly significant. The results obtained on six parameter model indicated highly significant values of additive x additive (-0.54), additive x dominance (-0.15) and dominance x dominance (0.47) gene effects. The opposite sign of dominance and dominance x dominance (l) indicated the presence of duplicate type of gene interaction.

4.2.1.10 Straw yield per plant (g)

Non allelic gene affects were found predominant as the scaling tests A, B, C and D were highly significant (Table 4.2.1). The additive (4.23), dominance (-124.57) effects were highly significant. Highly significant values recorded for additive x additive (-40.53), additive x dominance (-2.45) and dominance x dominance (88.14) gene interaction. Duplicate type of gene interaction was obtained for this trait.

4.2.2 Cross GR-4 XIET-18654

4.2.2.1 Days to flowering

Scaling tests A, B, C, and D were highly significant (Table 4.2.2) that indicated the non-allelic gene action. Estimation of genetic parameters revealed that additive (9.50) and dominance (-48.03) were highly significant. All the three interaction *viz.*, additive x additive, additive x dominance and dominance x dominance were found highly significant. Duplicate type of gene action was found responsible for inheritance of this trait.

4.2.2.2 Plant height (cm)

Inadequate of additive–dominance model was reported for this trait as the scaling tests A, B, C, and D had highly significant values (Table 4.2.2). The estimated six genetic parameters revealed that additive (-7.32) and dominance (25.56), While additive x additive (8.73), additive x dominance (-7.22) and dominance x dominance (-7.68) were highly significant. Duplicate type of gene action was observed the study.

4.2.2.3 Productive tillers per plant

The significant scaling tests A, B and C indicated the presence of non allelic gene action (Table 4.2.2). All five genetic parameters *viz.*, additive (1.06), dominance (3.46), additive x additive (0.53), additive x dominance (-0.56) and dominance x dominance (-2.86) were found highly significant. Duplicate type of gene action was found responsible for inheritance of this trait.

4.2.2.4 Panicle length (cm)

The additive-dominance model was found inadequate as scaling tests A, B, C, and D had significant value (Table 4.2.2). Estimation of genetic parameters revealed that additive (-1.29) and dominance (18.01) were highly significant, In case of interaction additive x additive (7.29), dominance x dominance (-9.43) were highly significant, additive x dominance (0.27) was found significant. The inheritance of character was governed by duplicate type of gene action.

4.2.2.5 Grains per panicle

Scaling tests A, B, C, and D were highly significant (Table 4.2.2) indicating the non allelic gene action. Estimation of genetic parameters revealed that additive (33.23), dominance (-244.83) were highly significant. While interaction such as additive x additive

(-64.13), additive x dominance (-31.06) and dominance x dominance (173.73) were highly significant. Duplicate type of gene action was found prominent for inheritance of this trait.

4.2.2.6 Grain yield per plant (g)

Significance of scaling tests A, B, C and D indicated the inadequate of additive–dominance model (Table 4.2.2). Estimation of genetic parameters revealed that additive (4.34), dominance (-22.02), additive x additive (-8.48), additive x dominance (-5.22) and dominance x dominance (12.35) were highly significant. Duplicate type of gene action was found responsible for inheritance of grain yield per plant.

4.2.2.7 100 Grain weight

Non-allelic gene actions were present as the A, B, C and D scaling tests revealed significant results (Table 4.2.2). Genetic analysis revealed that additive (-0.24), dominance (-0.73) and additive x additive (-0.18) were significant and dominance x dominance (0.63) gene interaction was found highly significant. The dominance and dominance x dominance estimates had opposite signs indicating the presence of duplicate type of gene interaction.

4.2.2.8 Kernel length (mm)

For kernel length, highly significant values of A, B, C and D tests indicated digenic interaction for the inheritance of this trait (Table 4.2.2). The results obtained on six parameter model indicated highly significant values of additive (-0.09) dominance (0.34), additive x additive (0.13), additive x dominance (-0.03) were highly significant, While, dominance x dominance (0.10) gene effect had significant value. Similar signs of dominance and dominance x dominance gene effects indicated that the complementary type of epistasis in expression of this trait.

Table 4.2.2 The results of scaling tests and estimation of gene effect for ten character studied in cross GR -4 x IET-18654

Parameter	Days to flowering	Plant height (cm)	Productive tillers per plant	Panicle length (cm)	Grains per panicle	Grain yield per plant (g)	100 Grain weight	Kernel length (mm)	Length/Breath ratio	Straw yield per plant (g)
A	-7.26** ± 0.94	-7.74** ± 0.71	0.60** ± 0.15	1.34 ** ± 0.26	-85.86** ± 3.11	-7.16** ± 0.45	-0.21** ± 0.02	-0.15** ± 0.02	-0.29** ± 0.07	-24.75** ± 0.40
B	8.40 ** ± 0.80	6.69** ± 1.42	1.73** ± 0.24	0.80* ± 0.33	-23.73** ± 2.92	3.29** ± 0.63	-0.23 ** ± 0.05	-0.08** ± 0.01	0.38** ± 0.06	4.51** ± 0.86
C	25.73** ± 1.76	-9.78** ± 1.26	1.80** ± 0.30	-5.15** ± 0.54	-45.46** ± 4.74	4.60** ± 0.58	-0.25** ± 0.07	-0.37** ± 0.03	0.59** ± 0.09	1.32 ± 1.09
D	12.30 ** ± 1.03	-4.36** ± 0.92	-0.26 ±0.15	-3.64 ** ± 0.01	32.06** ± 1.03	4.24** ±0.39	0.09 * ± 0.04	-0.067** ± 0.009	0.25** ±0.04	10.78** ± 0.48
m	108.56** ± 2.07	107.78** ± 1.85	7.93** ± 0.31	15.67** ± 0.28	221.90** ± 2.44	22.80** ± 0.80	1.91** ± 0.09	5.34** ± 0.01	3.26** ± 0.09	42.59** ± 0.99
d	9.50** ± 0.17	-7.32** ± 0.16	1.06** ± 0.06	-1.29** ± 0.09	33.23** ± 1.31	4.34** ± 0.16	-0.24** ± 0.005	-0.090** ± 0.008	0.368** ± 0.005	3.82** ± 0.21
h	-48.03** ± 4.92	25.56** ± 5.02	3.46** ± 0.83	18.01** ± 0.76	-244.83** ± 7.42	-22.02** ± 2.24	-0.73* ± 0.22	0.34** ± 0.05	-0.93** ± 0.26	-66.94** ± 2.58
aa	-24.60** ± 2.06	8.73** ± 1.84	0.53 ± 0.31	7.29** ± 0.26	-64.13** ± 2.06	-8.48** ± 0.78	-0.18* ± 0.09	0.13** ± 0.01	-0.50** ± 0.09	-21.57** ± 0.97
ad	-7.83** ± 0.61	-7.22** ± 0.76	-0.56** ± 0.13	0.27* ± 0.13	-31.06** ± 1.63	-5.22** ± 0.37	0.008 ± 0.030	-0.03** ± 0.01	-0.34** ± 0.04	-14.63** ± 0.40
dd	23.46** ± 2.93	-7.68* ± 3.26	-2.86** ± 0.55	-9.43** ± 0.65	173.73** ± 37.54	12.35** ± 1.48	0.63** ± 0.13	0.10* ± 0.04	0.41* ± 0.18	41.82** ± 1.75
Gene action	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Complementary	Duplicate	Duplicate

*, ** Significant at 5 and 1 % levels, respectively.

4.2.2.9 Length/Breath ratio

Significance of A, B, C and D scaling tests revealed presence of non-allelic gene effects were highly significant (Table 4.2.2). The additive (0.36), dominance (-0.93) effects were highly significant. The results reported highly significant values for additive x additive (-0.50), additive x dominance (-0.34) gene action. While, dominance x dominance (0.41) had significant value. The opposite sign dominance and dominance x dominance indicated the presence of duplicate type of gene interaction.

4.2.2.10 Straw yield per plant (g)

For this trait results showed the presence of non allelic gene action as scaling test A, B, C and D were found highly significant (Table 4.2.2). The additive (3.82) and dominance (-66.94) effects were highly significant. Among the interaction effects additive x additive (-21.57), additive x dominance (-14.63) and dominance x dominance (41.82) effects were highly significant, indicated that the trait was governed by non-additive gene action. Duplicate type of gene interaction was recorded for inheritance of this trait.

4.2.3 Cross Jaya x IET-18654

4.2.3.1 Days to flowering

Scaling test A was significant B and C were highly significant indicating the non-allelic gene action (Table 4.2.3). Estimation of genetic parameters revealed that additive (9.50), dominance (13.96), additive x dominance (-8.10) and dominance x dominance (-12.60) were highly significant, While additive x additive

(-0.13) was non-significant. Duplicate type of gene action was found for inheritance of this trait.

4.2.3.2 Plant height (cm)

Significance of A, B and C scaling tests suggested presence of non-allelic gene action in the inheritance of this trait (Table 4.2.3). The additive (-19.97), dominance (36.71) gene effects were found highly significant. Among non-allelic gene effect dominance x dominance (-36.50) was highly significant. Duplicate interaction was observed for this trait.

4.2.3.3 Productive tillers per plant

Scaling tests A, B, C and D were significant indicating of non-allelic interaction (Table 4.2.3). The additive (-0.50), dominance (14.83) gene effects were highly significant. Among non-allelic gene effects, additive x additive (4.33), additive x dominance (1.33) and dominance x dominance (-11.13) gene effects were highly significant. Duplicate type of gene action was found responsible for inheritance of this trait.

4.2.3.4 Panicle length (cm)

For panicle length, highly significant values of B, C and D revealed the inadequate of additive, dominance model (Table 4.2.3). The results obtained on six parameter model indicated highly significant values for dominance (-6.77), additive x additive (-5.28), additive x dominance (-1.03) and dominance x dominance (4.02) gene effects. The dominance and dominance x dominance (l) estimates had opposite signs reported the presence of duplicate type of gene interaction.

4.2.3.5 Grains per panicle

Highly significant values of individual scaling tests *viz.*, A, B, C and D analysis indicated the presence of non-allelic interaction

(Table 4.2.3). Further analysis revealed that the additive (-13.40), dominance (94.06), additive x additive (18.60), additive x dominance (-28.90) and dominance x dominance (-23.86) were highly significant. Duplicate type of epistasis was responsible for inheritance of this trait.

4.2.3.6 Grain yield per plant (g)

Highly significant values of A, C, D and significant values of B scaling test indicated the presence of non-allelic interaction (Table 4.2.3). The data further revealed that additive (4.44), dominance (15.23), additive x additive (7.16) were highly significant. Duplicate type of epistasis was reported for this trait.

4.2.3.7 100 Grain weight (g)

Non-allelic gene actions were present as scaling test the B was significant, similarly C and D scaling test were found highly significant. Genetic analysis revealed that additive (0.23) was highly significant and dominance (-0.35) was non- significant. Whereas additive x additive (0.33) gene effect was highly significant and additive x dominance (-0.15) had significant value (Table 4.2.3).

4.2.3.8 Kernel length (mm)

For Kernel length, highly significant values of B, C and D tests indicated digenic interaction for the inheritance of this trait (Table 4.2.3). The results showed highly significant values of additive (-0.33), dominance (-2.18), additive x additive (-1.31 and), additive x dominance (0.16) and dominance x dominance (1.34) gene effects. The dominance and dominance x dominance (l) estimates had opposite signs indicated that presence of duplicate type of gene interaction.

4.2.3.9 Length/Breath ratio

The scaling test C found significant, while D had highly significant (Table 4.2.3) express the presence of non-allelic gene effects. The additive (0.07) effect was highly significant and positive.

Table 4.2.3 The results of scaling tests and estimation of gene effects for ten character studied in cross Jaya x IET- 18654

Parameter	Days to flowering	Plant height (cm)	Productive tillers per plant	Panicle length (cm)	Grains per panicle	Grain yield per plant (g)	100 Grain weight	Kernel length (mm)	Length/Breath ratio	Straw yield Per plant (g)
A	-1.73 * ± 0.84	20.99** ± 2.84	4.73** ± 0.35	-0.40 ± 0.29	-26.26** ± 1.46	-3.74** ± 0.89	-0.01 ± 0.04	0.15 ± 0.09	0.06 ± 0.03	-0.64 ± 0.99
B	14.46 ** ± 0.53	17.88** ± 2.07	2.06** ± 0.36	1.66 ** ± 0.29	31.53** ± 1.14	-2.59* ± 1.09	0.29 * ± 0.12	-0.17** ± 0.03	-0.06 ± 0.04	-2.4** ± 1.13
C	12.86** ± 1.10	41.23** ± 1.86	2.46** ± 0.63	6.54** ± 0.43	-13.33** ± 3.89	-13.49** ± 1.23	0.60** ± 0.12	1.28** ± 0.04	-0.12* ± 0.05	-9.27** ± 1.63
D	0.06 ± 0.51	1.18 ± 1.63	-2.16** ±0.20	2.64 ** ± 0.18	-9.30** ± 1.76	-3.58** ±0.55	0.16 ** ± 0.03	0.65** ± 0.04	-0.06** ±0.02	-3.11** ± 0.50
m	83.90** ± 1.04	109.38** ± 3.32	3.43** ± 0.42	29.45** ± 0.38	90.06** ± 3.55	7.47** ± 1.14	2.91** ± 0.08	7.10** ± 0.09	2.44** ± 0.04	13.91** ± 1.06
d	9.50** ± 0.16	-19.97** ± 0.60	-0.50** ± 0.12	-0.06 ± 0.08	-13.40** ± 0.50	4.44** ± 0.29	0.23** ± 0.06	-0.333** ± 0.005	0.070** ± 0.008	3.08** ± 0.34
h	13.96** ± 2.74	36.71** ± 9.87	14.83** ± 1.13	-6.77** ± 0.75	94.06** ± 7.60	15.23** ± 3.39	-0.35 ± 0.25	-2.18** ± 0.27	-0.20 ± 0.11	15.36** ± 3.10
aa	-0.13 ± 1.06	-2.36 ± 3.27	4.33** ± 0.40	-5.28** ± 0.144	18.60** ± 3.52	7.16** ± 1.10	0.33** ± 0.06	-1.31** ± 0.09	0.12** ± 0.03	6.22** ± 1.00
ad	-8.10** ± 0.17	1.55 ± 1.70	1.33** ± 0.18	-1.03** ± 0.03	-28.90** ± 0.72	-0.57 ± 0.60	-0.15* ± 0.06	0.16** ± 0.04	0.06** ± 0.01	0.87** ± 0.56
dd	-12.60** ± 1.88	-36.50** ± 6.65	-11.13** ± 0.83	4.02** ± 0.75	-23.86** ± 4.40	-0.82 ± 2.45	0.06 ± 0.17	1.34** ± 0.18	-0.12 ± 0.08	-3.18** ± 19.17
Gene action	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	-	Duplicate	-	Duplicate

Among the interaction effects, additive x additive (0.12), additive x dominance (0.06) gene effects were highly significant.

4.2.3.10 Straw yield per plant (g)

The scaling tests C and D were highly significant reported presence of non-allelic gene effects. Similarly significant B scale reported for this trait. The additive (3.08), dominance (15.36) gene effects were highly significant and positive. Among the interaction effects, additive x additive (6.22) were highly significant. The dominance and dominance x dominance (l) estimates had opposite signs indicated the presence of Duplicate type of gene interaction (Table 4.2.3).

4.2.4 Cross Jaya x GR-5

4.2.4.1 Days to flowering

Presence of non-allelic interaction was indicated by the significance of A, B, C and D scales (Table 4.2.4). Estimation of genetic parameters revealed that additive (8.20), dominance (-21.06) and additive x additive (-12.40) gene effects were highly significant. Duplicate type of gene action was found responsible for inheritance of this trait.

4.2.4.2 Plant height

Significance of A, B, C, and D scaling tests suggested presence of non-allelic gene action in the inheritance of this trait (Table 4.2.4). The gene effects calculated on the basis of six parameter model revealed that additive (-18.85), dominance (-21.23) gene effects were found highly significant. Among non-allelic gene effects additive x additive (-26.91), additive x dominance (7.11) gene effects were highly significant. The character governed duplicate type of gene action.

4.2.4.3 Productive tillers per plant

Scaling tests B was significant C and D were highly significant indicated the preponderance of non allelic gene interaction (Table 4.2.4). The genetic parameter *viz.*, additive (-0.70) as well as dominance (-11.96) gene effects were highly significant. Among non-allelic gene effects, additive x additive (-5.60) and dominance x dominance (4.80) gene effects were highly significant, similarly additive x dominance (-0.26) was significant. The opposite sign of dominance (h) and dominance x dominance revealed the duplicate type of gene action for inheritance of this trait.

4.2.4.4 Panicle length (cm)

For panicle length, highly significant values of B, C and D tests indicated digenic interaction for the inheritance of this trait (Table 4.2.4). The results obtained on six parameter model indicated highly significant values of additive (-1.35), dominance (14.39), additive x additive (5.04), additive x dominance (-1.14) and dominance x dominance (-8.43) gene effects. The dominance and dominance x dominance (l) estimates had opposite signs indicating the presence of duplicate type of gene interaction.

4.2.4.5 Grains per panicle

Highly significant values of A, B, C and D scaling tests indicated the presence of non-allelic interaction (Table 4.2.4). It was observed that genetic parameter *viz.*, additive (8.86), dominance (-79.06), additive x additive (-42.60), additive x dominance (2.10) and dominance x dominance (64.40) were highly significant. Duplicate type of epistasis was reported for inheritance of this trait.

4.2.4.6 Grain yield per plant (g)

Highly significant values of individual scaling tests were A, B, C and D indicated the presence of non-allelic interaction (Table 4.2.4). Further analysis revealed that additive (2.96), dominance (-19.88), additive x additive (-9.41), additive x dominance (-0.65) and dominance x dominance (15.79) were highly significant. Duplicate type of epistasis was found responsible for inheritance of this trait.

4.2.4.7 100 Grain weight (g)

Non-allelic gene actions were present as the A, C and D scaling tests were found highly significant and B was significant (Table 4.2.4). Genetic analysis revealed that additive (0.20), dominance (-1.61), additive x additive (-0.62) and dominance x dominance (1.00) gene effects were highly significant. The dominance and dominance x dominance estimates had opposite signs indicating the presence of duplicate type of gene interaction.

4.2.4.8 Kernel length (mm)

For Kernel length, highly significant values of A, B, C and D tests indicated digenic interaction for the inheritance of this trait (Table 4.2.4). The results obtained on six parameter model indicated highly significant values for dominance (-0.66) and additive x additive (-0.66). The dominance and dominance x dominance (l) estimates had similar signs indicating the presence of complementary type of gene interaction.

4.2.4.9 Length/Breath ratio

Among the four scaling test A was significant C and D scaling tests were highly significant that revealed presence of non-allelic gene effects (Table 4.2.4). The additive (0.14) and dominance (0.89) effects were highly significant. Among the interaction effects,

Table 4.2.4 The results of scaling tests and estimation of gene effects for ten character studied in cross Jaya x GR-5

Parameter	**Days to Flowering**	**Plant height (cm)**	**Productive tillers per plant**	**Panicle length (cm)**	**Grains per panicle**	**Grain yield per plant (g)**	**100 Grain weight**	**Kernel length (mm)**	**Length/Breath ratio**	**Straw yield per plant (g)**
A	6.93 ** ± 0.95	20.56** ± 1.01	0.13 ± 0.21	0.55 ± 0.28	-8.80** ± 1.15	-3.84** ± 0.32	-0.23 ** ± 0.02	0.30** ± 0.04	-0.07* ± 0.03	-5.22** ± 0.82
B	5.06 ** ± 0.64	6.33** ± 0.50	0.66* ± 0.30	2.84 ** ± 0.12	-13.00** ± 1.08	-2.54** ± 0.17	-0.14 * ± 0.06	0.32** ± 0.03	0.03 ± 0.04	-2.92** ± 0.69
C	24.40** ± 0.77	53.80** ± 2.35	6.40** ± 0.61	-1.64** ± 0.11	20.80** ± 2.06	3.03** ± 0.76	0.23** ± 0.07	1.28** ± 0.06	-0.55** ± 0.05	1.14 ± 1.37
D	6.20 ** ± 0.53	13.45** ± 1.14	2.80** ±0.23	-2.52** ± 0.14	21.30** ± 0.62	4.70** ±0.33	0.31 ** ± 0.02	0.33** ± 0.03	-0.25** ±0.03	4.64** ± 0.48
m	97.73** ± 1.08	131.41** ± 2.29	14.03** ± 0.48	18.77** ± 0.29	136.33** ± 1.31	21.86** ± 0.68	3.42** ± 0.05	6.76** ± 0.06	2.26** ± 0.06	26.83** ± 0.98
d	8.20** ± 0.16	-18.85** ± 0.13	-0.70** ± 0.08	-1.35** ± 0.04	8.86** ± 0.41	2.96** ± 0.15	0.20** ± 0.02	-0.003 ± 0.005	0.14** ± 0.01	2.65** ± 0.17
h	-21.06** ± 3.17	-21.23** ± 5.00	-11.96** ± 1.07	14.39** ± 0.87	-79.06** ± 3.34	-19.88** ± 1.42	-1.61** ± 0.13	-0.66** ± 0.17	0.89** ± 0.17	-20.25** ± 2.53
aa	-12.40** ± 1.07	-26.91** ± 2.28	-5.60** ± 0.47	5.04** ± 0.29	-42.60** ± 1.25	-9.41** ± 0.66	-0.62** ± 0.04	-0.66** ± 0.06	0.50** ± 0.06	-9.28** ± 0.97
ad	0.93 ± 0.53	7.11** ± 0.45	-0.26* ± 0.11	-1.14** ± 0.15	2.10** ± 0.55	-0.65** ± 0.16	-0.04 ± 0.03	-0.01 ± 0.02	-0.05* ± 0.02	-1.15** ± 0.36
dd	0.40 ± 2.17	0.02 ± 2.91	4.80** ± 0.70	-8.43** ± 0.59	64.40** ± 2.54	15.79** ± 0.78	1.00** ± 0.09	-0.04 ± 0.12	-0.46** ± 0.11	17.43** ± 1.88
Gene action	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Complementary	Duplicate	Duplicate

*, ** Significant at 5 and 1 % levels, respectively.

additive x additive (0.50), dominance x dominance (-0.46) gene effects were highly significant while, additive x dominance (-0.05) was significant indicated that the trait was governed by non-additive gene action. Duplicate type epistatis was found for this trait.

4.2.4.10 Straw yield per plant (g)

Significance of A, B and D scaling tests revealed presence of non-allelic gene effects (Table 4.2.4). The additive (2.65) and dominance (-20.25) gene effects were highly significant. Among the interaction effects, additive x additive (-9.28), additive x dominance (-1.15) and dominance x dominance (17.43) gene effects were highly significant. Duplicate type of epistasis was found responsible for inheritance of this trait.

4.3 HETEROSIS, INBREEDING DEPRESSION, HERITABILITY AND GENETIC ADVANCE

For a successful heterosis breeding programme in any crop, there are two important pre-requisites (1) there must be an ample evidence of the presence of significant heterotic effect in the hybrids that can really be of practical utility, and (2) the production of hybrid seed at commercial scale must be economically feasible. Rice is a self-pollinated crop and hybrid seed production at commercial scale is possible with use of male sterility. Heterosis, particularly heterobeltiosis is useful in deciding the direction of future breeding programme and to identify the promising cross combinations. Heterosis leads to increase in yield, reproductive ability, adaptability, disease and insect resistance, general vigour, quality etc.

Inbreeding depression refers to decrease in fitness and vigour due to inbreeding and decreased heterozygosity. It results due to fixation of unfavorable recessive genes in F_2, while in case of heterosis undesirable recessive genes of one parent are suppressed by favorable dominant genes of other parent.

Estimate of heritability serves as a useful guide to the breeder. The breeder is able to appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, *i.e.* the heritable portion of variation in the first case, and the portion of genetic variation that is fixable in pure lines in the later case. If heritability of a character is very high, selection for the character should be fairly easy because there would be a close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype. But for a character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects. Thus, estimates of heritability are useful in predicting the transmission of characters from the parents to their offspring. Heritability in narrow sense may be more helpful in the selection of elite types from the mixed parental populations or segregating populations.

Heterosis was measured as per cent increase or decrease in F_1 over better parent (heterobeltiosis) for all the traits in four crosses. Inbreeding depression was calculated on the data of F_1 and F_2 generations of all the four crosses. Heritability is a measure of the efficiency of a selection system in separating genotypes. High or low heritability is not rigidly defined, but the following values are generally accepted (Stansfield, 1969).

(i) Low heritability : < 20 %
(ii) Moderate heritability : 20 to 50 %
(iii) High heritability : > 50 %

Similarly, the range of genetic advance as percent of mean is classified as suggested by Johnson *et al.* (1955).

(i) Low genetic advance : < 10 %
(ii) Moderate genetic advance : 10 to 20 %
(iii) High genetic advance : > 20 %

The results obtained on these aspects for different characters in all the four crosses in Table 4.3.1 to 4.3.2. In some of the cases heritability estimates were not reported due to abnormal values (negative on more than 100 %) obtained which might be due to high environmental influence or sampling error or both.

4.3.1 Gurjari x GR-5

4.3.1.1 Days to flowering

For this character, parent having less number of days to first flowering was considered as the better parent (Table 4.3.1). The cross Gurjari x GR-5 exhibited highly significant average heterosis (-8.01 %) and positive but non-significant heterobeltiosis (2.84 %). The non–significant results were obtained for inbreeding depression (-0.84 %). Moderate broad sense heritability (29.00 %) and low narrow sense heritability (0.68 %) reported for this trait with and low genetic advance (4.23 %).

4.3.1.2 Plant height (cm)

The average heterosis and heterobeltiosis (-17.60 and 31.30 %) were found highly significant for the above studied trait. Whereas, the magnitude inbreeding depression (2.86 %) exploited as non-significant. Narrow sense heritability (22.92 %) was found moderate whereas genetic advance (57.04 %) were found positive and high (Table 4.3.1).

4.3.1.3 Productive tillers per plant

Higher number of productive tillers is an important character in rice, in this cross, *i.e.* Gurjari x GR-5 both average heterosis (5.11 %) and heterobeltiosis (-6.09 %) were found non significant while, higher and positive significant inbreeding depression (22.72 %) was recorded for trait under study (Table 4.3.1).

4.3.1.4 Panicle Length (cm)

The magnitudes of average heterosis (9.54 %) and heterobeltiosis were found positive and significant (3.59 %). The inbreeding depression (1.24 %) was recorded as non- significant. High broad sense heritability (57.4 %) whereas low narrow sense heritability (1.07 %) along with low genetic advance (2.60 %) was observed for this trait (Table 4.3.1).

4.3.1.5 Grains per panicle

The estimates of average heterosis (21.90 %) and inbreeding depression (14.36 %) were positive and highly significant while, heterobeltiosis had (0.20 %) non-significant value (Table 4.3.1). High broad sense heritability (72.8 %) recorded for grains per panicle. Whereas low narrow sense heritability (0.93 %) and high genetic advance (30.69 %) were observed for the trait under study.

4.3.1.6 Grain yield per plant (g)

Positive and significant estimates were observed for average heterosis (55.72 %), heterobeltiosis (15.61 %) and inbreeding depression (33.46 %) for grain yield per plant (Table 4.3.1). Moderate broad sense heritability (24.7 %) whereas low narrow sense heritability (0.40 %) reported for this trait.

4.3.1.7 100 Grain weight (g)

The estimated average heterosis (-2.62 %) and inbreeding depression (-1.08 %) had negative and non-significant values whereas, highly significant negative heterobeltiosis (-7.84 %) was recorded for this trait (Table 4.3.1). Low broad sense heritability (8.5 %) reported for this trait.

4.3.1.8 Kernel length (mm)

Magnitude of average heterosis (2.22 %), heterobeltiosis (-1.68 %) and inbreeding depression (-0.62 %) were recorded as non-significant. High broad sense heritability (61.1 %) reported for this trait. Low heritability (1.91 %) along with low genetic advance (1.62 %) was observed for the above studied character (Table 4.3.1).

4.3.1.9 Length/Breath ratio

The estimated average heterosis (-6.91 %), heterobeltiosis (-13.91 %) and inbreeding depression (-9.86 %) were highly significant but in negative direction (Table 4.3.1).

4.3.1.10 Straw yield per plant (g)

For this trait, the average heterosis (21.87 %) and inbreeding depression (16.72 %) were positive and highly significant while, heterobeltiosis was negative and non-significant (Table 4.3.1). The estimated narrow sense heritability (0.095 %) and genetic advance (7.63 %) recorded as low and non-significant. High broad sense heritability (67.1 %) recorded for this trait.

4.3.2 GR-4 X IET-18654

4.3.2.1 Days to flowering

The heterobeltiosis (12.80 %) was highly significant and positive whereas inbreeding depression (-7.64 %) recorded highly significant results but was in negative direction. However, average heterosis (0.04 %) was found positive but non-significant. Broad sense heritability results revealed very high value (93.5 %) for this trait. Low narrow sense heritability (1.57 %) and high genetic advance (41.48 %) were observed for the trait (Table 4.3.1).

4.3.2.2 Plant height (cm)

Magnitude of average heterosis (7.85 %) and heterobeltiosis (15.07 %) as well as inbreeding depression (5.58 %) were found positive and highly significant. The heritability in narrow sense recorded (6.52 %) low positive while, genetic advance was (48.56 %) high positive (Table 4.3.1). High broad sense heritability (78.4 %) reported for this trait.

4.3.2.3 Productive tillers per plant

For this trait, the heterobeltiosis (-10.49 %) and inbreeding depression (-4.88 %) both found highly significant but in negative direction, studied traits had low narrow sense heritability (4.12 %) and moderate genetic advance (15.26 %) (Table 4.3.1). Results revealed moderate value for broad sense heritability (23.50 %).

4.3.2.4 Panicle length (cm)

The average heterosis (5.58 %) and inbreeding depression (7.96 %) were found positive and highly significant. However, non significant heterobeltiosis (-0.05 %) and low genetic advance (3.50 %) was recorded for this trait (Table 4.3.1).

4.3.2.5 Grains per panicle

Magnitude of average heterosis (-4.41 %) and inbreeding depression (5.22 %) were found non-significant. Whereas, negative highly significant heterobeltiosis recorded for this traits (Table 4.3.1). Moderate heritability (25.66 %) along with high genetic advance (67.38 %) was recorded for grains per panicle.

4.3.2.6 Grain yield per plant

Magnitude of average heterosis (-8.27 %) and inbreeding depression (-13.26 %) were negative and non-significant (Table 4.3.1).

While, heterobeltiosis (-29.60 %) had highly significant value but in negative direction. The character is governed by low heritability (10.01 %) and very high genetic advance (87.18 %).

4.3.2.7 100 grain weight (g)

For this trait only heterobeltiosis (-8.58 %) was found significant but in negative direction (Table 4.3.1). Both average heterosis and inbreeding depression were positive but non-significant. The character was governed by low heritability (2.79 %) and low genetic advance (5.94 %). Results revealed very high value of broad sense heritability (93.8 %) for this trait.

4.3.2.8 Kernel length (mm)

The estimation of average heterosis (5.72 %), heterobeltiosis (3.95 %) and inbreeding depression (4.32 %) were positive and highly significant (Table 4.3.1).

4.3.2.9 Length/Breath ratio

For this trait heterobeltiosis (-12.24 %) was found significant but in negative direction. While, average heterosis (-0.54 %) and inbreeding depression (-5.70 %) were negative and non-siginificant. Both heritability (14.49 %) and genetic advance (7.36 %) were low in magnitude (Table 4.3.1).

4.3.2.10 Straw yield per plant (g)

Magnitude of average heterosis (-16.88 %), heterobeltiosis (-29.68 %) and inbreeding depression (-12.05 %) were negative and highly significant (Table 4.3.1). The character was governed by low heritability narrow sense heritability (3.26 %), broad sense heritability (11.9 %) and high genetic advance (67.27 %).

Table 4.3.1 **Magnitude of average heterosis (%), heterobeltiosis (%), inbreeding depression (%), heritability in narrow sense (%) and genetic advance (%) for different traits in four crosses of rice**

GURJARI × GR-5										
Estimates (%)	**Days to flowering**	**Plant height**	**Productive tillers per plant**	**Panicle length**	**Grains per panicle**	**Grain yield per plant**	**100 grain weight**	**Kernel length (mm)**	**Length/Breath ratio**	**Straw yield per plant**
Average Heterosis (%)	-8.01**	17.59**	5.11	9.54**	21.90**	55.72**	-2.62	2.22	-6.91**	21.87**
Heterobeltiosis (%)	2.83	31.30**	-6.09	3.59*	0.20	15.61**	-7.83**	-1.67	-13.91**	-0.58
Inbreeding Depression (%)	-0.84	2.86	22.72**	1.23	14. 36**	33.46**	-1.07	-0.62	-9. 86**	16.72**
Heritability (bs) (%)	29.0	--	--	57.4	72.8	24.7	8.5	61.1	--	67.1
Heritability (ns) (%)	0.68	22.99	--	1.07	0.93	0.40	--	1.91	--	0.09
Genetic advance (%)	4.23	57.04	--	2.60	30.69	24.52	--	1.62	--	7.63

GR-4 × IET-18654										
Estimates (%)	**Days to flowering**	**Plant height**	**Productive tillers per plant**	**Panicle length**	**Grains per panicle**	**Grain yield per plant**	**100 grain weight**	**Kernel length (mm)**	**Length/ Breath ratio**	**Straw yield per plant**
Average Heterosis (%)	0.04	7.85**	0.78	5.58**	-4.41	-8.27	4.52	5.72**	-0.54	-16.88**
Heterobeltiosis (%)	12.80**	15.07**	-10.49**	-0.05	-21.04**	-29.60**	-8.58*	3.95**	-12.24**	-29.68**
Inbreeding Depression (%)	-7.64**	5.58**	-4.88**	7.96**	5.22	-13.26	5.70	4.32**	-5.70	-12.05*
Heritability (bs) (%)	93.5	78.4	23.5	--	--	--	93.8	-	--	11.9
Heritability (ns) (%)	1.57	6.52	4.12	2.74	25.66	10.01	2.79	--	14.49	3.26
Genetic Advance (%)	41.48	48.56	15.26	3.50	67.38	87.18	5.94	--	7.36	67.27

*, ** Significant at 5 and 1 % levels, respectively.

4.3.3 Jaya x IET-18654

4.3.3.1 Days to flowering

The magnitude of heterobeltiosis (14.81 %) was found high significant and in positive direction. The non significant results were obtained for average heterosis (1.79 %) and inbreeding depression (-2.89 %). Moderate genetic advance (17.48 %) along with low narrow sense heritability was recorded for the studied trait (Table 4.3.2). Moderate value of broad sense heritability (26.9 %) recorded for this trait.

4.3.3.2 Plant height (cm)

High heritability (67.63 %), high genetic advance (232.02 %) were observed for the inheritance of the traits. High significant positive heterobeltiosis (25.91 %) was recorded for this trait. The estimated inbreeding depression (-8.23 %) was negative significant (Table 4.3.2).

4.3.3.3 Productive tillers per plant

The negative and non-significant magnitude of heterobeltiosis (-13.71 %), relative heterosis (-8.15 %) and inbreeding depression (-13.08 %) were observed for productive tillers per plant. Estimate of heritability in narrow sense was low (2.79 %), whereas genetic advance was (23.98 %) high (Table 4.3.2).

4.3.3.4 Panicle length (cm)

The positive and highly significant heterobeltiosis (10.15 %) and relative heterosis (10.44 %) observed for panicle length. hereas negative non-significant inbreeding depression (-1.399 %) were observed for this trait (Table 4.3.2). The magnitude of both narrow sense heritability (6.03 %) and genetic advance (9.25 %) were found low.

4.3.3.5 Grains per panicle

Magnitude of heterobeltiosis (31.29 %) and inbreeding depression (18.17 %) were positive and highly significant, while average heterosis (47.48 %) was found positive and significant (Table 4.3.2). The character was governed by low heritability (0.30 %). It had high genetic advance (20.75 %). High value of broad sense heritability (79.8 %) reported for this trait.

4.3.3.6 Grain yield per plant

The positive and highly significant magnitude of heterobeltiosis (14.67 %) average heterosis (49.53 %) and inbreeding depression (31.98 %) were observed for the trait (Table 4.3.2). The character had moderate narrow sense heritability (35.35 %) and high genetic advance (174.19 %).

4.3.3.7 100 grain weight (g)

For this trait heterosis (1.67 %) and heterobeltiosis (-6.76 %) were found non-significant (Table 4.3.2). The character governed by moderate narrow sense heritability (45.45 %) but had low genetic advance (3.85 %).

4.3.3.8 Kernel length (mm)

The average heterosis (8.11 %) was found positive and highly significant while, heterobeltiosis (2.32 %) had non-significant value. Inbreeding depression (-1.38 %) was found negative and non significant. Moderate value of broad sense heritability (36.9 %) recorded for this trait. The low heritability (15.62 %) and low genetic advance (3.41 %) were observed for the inheritance of the trait (Table 4.3.2).

4.3.3.9 Length/Breath ratio

Both heterosis (-1.94 %) and heterobeltiosis (-4.54 %) were observed non-significant and negative. While inbreeding depression was in positive direction (0.26 %) (Table 4.3.2).

4.3.3.10 Straw yield per plant (g)

Positive and significant estimates were observed for average heterosis (29.58 %), heterobeltiosis (12.37 %) and inbreeding depression (20.30 %) for straw yield per plant (Table 4.3.2).

4.3.4 Jaya x GR-5

4.3.4.1 Days to flowering

Heterosis over mid parent (-9.68 %) was highly significant and negative. Highly significant inbreeding depression (13.27 %), recorded for this trait. Moderate narrow sense heritability (29.73 %) and high genetic advance (31.67 %) observed for this trait (Table 4.3.2).

4.3.4.2 Plant height (cm)

Heterosis over mid parent (5.46 %) and better parent (28.67 %) were highly significant and positive (Table 4.3.2).Whereas negative and highly significant inbreeding depression was recorded for this trait. Very high value for broad sense heritability (90.8 %) recorded for this trait. The character was governed by low heritability (0.54 %) and moderate genetic advance (16.99 %).

4.3.4.3 Productive tillers per plant

The estimated average heterosis (-18.57 %), heterobeltiosis (-24.81 %) and inbreeding depression (-34.70 %) were found highly significant but in negative direction. High broad sense (54.9 %) whereas low narrow sense heritability (0.47 %) and low genetic advance (8.87 %) were recorded for trait (Table 4.3.2).

4.3.4.4 Panicle length (cm)

The character exhibited positively significant average heterosis (3.88 %) and inbreeding depression (3.53 %) and non significant heterobeltiosis (-1.70 %) (Table 4.3.2).

4.3.4.5 Grains per panicle

Average heterosis (29.80 %), heterobeltiosis (18.58 %) and inbreeding depression (7.20 %) were highly significant and in positive direction (Table 4.3.2). However, the character governed low heritability (1.77 %) and genetic advance (13.41 %).

4.3.4.6 Grain yield per plant (g)

Both of the heterosis *viz.*, average heterosis (42.80 %) and heterobeltiosis (15.33 %) and inbreeding depression (10.72 %) were found highly significant in desirable direction (Table 4.3.2). High broad sense heritability (66.5 %) whereas very low narrow sense heritability (0.06 %) and low genetic advance (1.44 %) reported for this trait.

4.3.4.7 100 Grain weight (g)

The estimated average heterosis (0.41 %), heterobeltiosis (-6.51 %) and inbreeding depression (-1.89 %) were non-significant. (Table 4.3.2).

4.3.4.8 Kernel length (mm)

Heterosis over mid parent (0.82 %), and better parent (0.76 %) was non-significant. While, inbreeding depression (-4.82 %) was negative and highly significant (Table 4.3.2). Moderate value of broad sense heritability (46.1 %) reported for this trait.

4.3.4.9 Length/Breath ratio

For this character heterobeltiosis (-7.43 %) recorded highly significant results but in negative direction (Table 4.3.2). While, both average heterosis (-2.53 %) and inbreeding depression (3.83 %) were non-significant. The character had moderate broad sense heritability (21.5 %), low narrow sense heritability (8.62 %) and low genetic advance (3.76 %).

4.3.4.10 Straw yield per plant (g)

The character depicted highly significant average heterosis (36.84 %) and inbreeding depression (12.27 %) (Table 4.3.2). While, it had non-significant heterobeltiosis (18.86 %) value. Low narrow sense heritability (2.61 %) and high genetic advance (54.64 %) were recorded for the inheritance of this trait.

Table 4.3.2 Magnitude of average heterosis (%), heterobeltiosis (%), inbreeding depression (%), heritability in narrow sense (%)and genetic advance (%) for different traits in four crosses of rice

JAYA × IET-18654

Estimates (%)	Days to flowering	Plant height	Productive tillers per plant	Panicle length	Grains per panicle	Grain yield per plant	100 grain weight	Kernel length (mm)	Length/B reath ratio	Straw yield per plant
Average Heterosis (%)	1.79	2.40	-8.15	10.44**	47.48*	49.53**	1.67	8.11**	-1.94	29.58**
Heterobeltiosis (%)	14.81**	25.91**	-13.71	10.15**	31. 29**	14.67**	-6.74	2.23	-4.54	12.37**
Inbreeding Depression (%)	-2.89	-8.23*	-13.08	-1. 39	18.17**	31.98**	-4.94	-1.38	0.26	20.30
Heritability (bs) (%)	26.9	--	--	--	79.8	--	--	36.9	--	--
Heritability (ns) (%)	4.05	67.63	2.79	6.03	0. 30	35.35	45.45	15.62	--	12.94
Genetic Advance (%)	17.48	232.02	23.98	9.25	20.75	174.19	3.85	3.41	--	94.81

JAYA × GR-5

Estimates (%)	Days to flowering	Plant height	Productive tillers per plant	Panicle length	Grains per panicle	Grain yield per plant	100 grain weight	Kernel length (mm)	Length/ Breath ratio	Straw yield per plant
Average Heterosis (%)	-9.68**	5.45*	-18.57**	3.88*	29.80**	42.80**	0.41	0.82	-2.53	36.84**
Heterobeltiosis (%)	-0.08	28.67**	-24.81**	-1.70	18.58**	15.33*	-6.51	0.76	-7.43*	18.86
Inbreeding Depression (%)	-13.27**	-9.61**	-34.70**	3.53*	7.20**	10.72**	-1.89	-4.82**	3.83	12.27**
Heritability (bs) (%)	--	90.8	54.9	--	--	66.5	--	46.1		
Heritability (ns) (%)	29.73	0.54	0.47	552.63	1.77	0.06	--	--	8.62	2.61
Genetic Advance (%)	31.67	16.99	8.87	8.86	13.41	1.43	--	--	3.76	54.64

*, ** Significant at 5 and 1 % levels, respectively.

DISUSSION

V. DISCUSSION

Plant breeding can be divided into three stages; assembly or creation of a gene pool of variable germplasm, selection of superior individuals from the gene pool and utilization of the selected individuals directly for commercial cultivation or in hybridization to create a superior variety. The improvement in yield, which is considered as a final product in almost all the crop plants, is usually obtained by screening, evaluating and selecting the suitable genes from a huge collection of germplasm and synthesizing and accumulating them in a productive genotype for commercial cultivation. Hence, the chief aim in any plant breeding programme is to developed high yielding varieties. To fulfill this, the breeding programme can efficiently be planned with prior knowledge of the genetic makeup of complex quantitative characters like yield and its attributes. It is, therefore, necessary to examine the nature of the crops and the genetic architecture of various quantitative characters in relation to breeding behavior of the crops.

In recent year, considerable emphasis has been put on the development of high yielding hybrids and varieties having dwarf and eractophile habits in several crop species like bajra, sorghum, maize, castor, cotton etc. Incorporation of male sterility and its use on commercial scale are the notable examples representing another milestone in our efforts to raise the productivity of several cultivated crops.

For designing an efficient breeding programme in any crop, the breeders should conformed with the problem of choosing parents, because many time the high yielding parents may not be combine well to give good and appropriate hybrids. Parents which produce good hybrids or progenies on crossing are of immense use to the breeders. This necessitates the testing of parents for their ability to exploit heterosis or to accumulate fixable genes through selection.

The genetic yield potential of present varieties of rice can be enhanced by restructuring of plant type. This can be achieved by using diverse gene pool in hybridization programme. Rice is a self-pollinated crop and the scope of exploitation of hybrid vigour will depend on the direction and magnitude of heterosis and the type of gene action involved. Although the advantages of hybrid vigour cannot be exploited easily commercially in self-pollinated crops, the high heterotic F_1's can be used to isolate a higher frequency of productive derivatives in their later generations. The genetic information, specially on the type of gene action involved in the inheritance of economically important quantitative traits is of immense use to the breeder for framing suitable breeding programme. Cockerham (1961) suggested that the production of hybrids, as oppose to inbreds or open pollinated varieties, depend largely on the level of dominance or epistasis or both. The level of dominance and forms of epistasis again will influence the selection of parents to develop open pollinated varieties. Thus estimation of additive, dominance and epistasis components of genetic variation will help in planning crop improvement programme.

Number of genetic models assuming certain basic requirements; have been proposed for the estimation of gene effects. Most of these models were developed to estimate relative importance of additive and dominance gene effects assuming epistatic gene effects to be negligible. However, in quantitative traits in self-pollinated species, epistatic effects have been found to play important role. Partitioning total heritable variance further in to additive and dominance components only will ignore the presence of inter allelic gene actions and would not give a correct picture of the gene actions involved. The nature of gene action governing grain yield per plant and other quantitative characters helps to identify useful source of germplasm. These studies are basic to yield improvement and it is necessary to high light the important contribution of characters often referred to as components of yield. Littlemore work has been done in the past to study the epistatic gene actions in the inheritance of yield and its related traits of rice *viz.*, days to flowering, plant height, number of tillers per plant, grain yield per plant, 100 seed weight by Roy and Panwar (1997), Thakur (1999), Raju (2005), Chang (2002), Mishra (2004), Sivakumar and Bapu (2005), Verma (2006), Rabiei and Ghorbanipour (2011) and Srivastava *et al.* (2012).

The present study was therefore, undertaken using six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) in each of the four crosses of rice to obtain information about digenic epistasis in addition to additive and dominance effects for grain yield per plant and its components. The results obtained in the present investigation are discussed below:

5.1 Analysis of variance and per se performance of six generations

5.2 Scaling test and estimation of gene effects

5.3 Magnitude of heterosis, inbreeding depression,

5.4 Heritability and genetic advance

5.1 Analysis of variance and *per se* performance of six generations

The analysis of variance for individual character was carried out for each of the four crosses for ten traits *viz.*, days to flowering, plant height, productive tillers per plant, panicle length, grains per panicle, 100 grain weight, grain yield per plant, kernel length, length/breadth ration and straw yield per plant (Table 4.1.). The mean sum of squares revealed significant differences among the generations for most of the characters studied in all the crosses indicating considerable variability in the experimental material. The results of *per se* performance for different characters are discussed below.

5.1.1 Days to flowering

In cross Gurjari x GR 5, significant differences were found for mean values of P_1, P_2, F_1, BC_1 and BC_2. F_1 mean deviating from mid parent value towards early parent P_2 indicating partial dominance gene effect. Non-significant difference observed between mean values F_1 and F_2 indicated absence of inbreeding depression for this trait.

In cross GR 4 x IET 18654, mean of F_2 was found higher than the mean of F_1, BC_1 and BC_2 generations indeed the mean values of F_1, BC_1 and BC_2 were at par with each other, revealing possibility of transgressive segregants.

F_1 mean of cross Jaya x GR 5 found intermediate to both the parents and differed significantly from either of the parents. Mean of F_2 was found significantly higher than F_1 suggesting transgressive segregants.

For cross Jaya x GR 5, significant difference observed between mean of both the parents, however non-significant difference between F_1 and early parent P_2 indicated complete dominance gene effect and genes for earliness dominated on the genes of lateness.

5.1.2 Plant height (cm)

For cross Gurjari x GR 5, all the mean values of respective generation differed significantly from each other. The mean of F_1 significantly exceeded the mean of both parents indicating existence of over dominance. Significant difference between F_1 and F_2 indicated presence of inbreeding depression.

In cross GR 4 x IET 18654, parental mean differed significantly from each other. F_1 mean at par with the mean of tall parent P_2 indicating complete dominance gene effect for this trait and genes for tallness dominated the genes for dwarfness.

The F_1 mean of cross Jaya x IET 18654 was found intermediate to both the parents and significantly differed from the mean all the generations. The mean of F_2 population was significantly higher than F_1 suggested transgressive segregation. BC_1 exhibited significantly lower value than BC_2.

For cross Jaya x GR 5, F_1 mean found intermediate to both the parents and significantly differed from the mean all the generations except BC_1. Non-significant difference observed between F_1 and F_2 indicated absence of inbreeding depression. BC_1 exhibited significantly lower value than BC_2 and higher than its recurrent parent.

5.1.3 Productive tillers

In cross Gurjari x GR 5, F_1 mean value differed significantly from parents, back crosses and F_2 means. The F_1 mean was found significantly higher than mean of F_2 population suggested presence of inbreeding depression for this trait.

For productive tillers per plant, significant differences were observed among both the parental means and their F_1's mean in cross GR 4 x IET 18654. Mean values of F_2 generation was statistically at par with mean values of F_1 suggested absence inbreeding depression. The F_1 generation had lower mean than F_2 generation.

The mean of the F_1 was at par with P_1 and it was significantly differed from P_2 revealed complete dominance gene effect for this trait in cross Jaya x IET 18654. The F_2 and F_1 mean were found at par to each other revealed absence of inbreeding depression.

The mean of the F_1 (Jaya x GR 5) non-significantly differed from P_1 and BC_1 suggested complete dominance and genes for low tiller dominated the genes for high tiller. The F_2 depicted significantly higher mean performance than F_1.

5.1.4 Panicle length (cm)

F_1 mean differed significantly from either of the parents and back crosses in cross Gurjari x GR 5. Non-significant difference in F_1 and F_2 mean revealed absence of inbreeding depression.

In cross GR 4 x IET 18654, mean of P_1 and P_2 differed significantly from each other. F_1 mean was at par to parent P_2 showed complete dominance gene effect for this trait. Both the backcrosses were significantly differed from each other.

For cross Jaya x IET 18654, the F_1 mean value for panicle length was found significantly higher than both the parents indicated over dominance gene effect. Absence of inbreeding depression evident from non-significant difference between F_1 and F_2 mean. Mean of F_1 (Jaya x GR 5) and parent P_2 showed non-significant difference, suggested complete dominance gene effect governing this trait.

5.1.5 Grains per panicle

The mean of the F_1 was at par with P_1 and it was significantly differed from P_2 revealed complete dominance gene effect for this trait in cross Gurjari x GR 5.

For cross GR 4 x IET 18654, mean values of both the parents were significantly differed from each other. Presence of inbreeding depression as evident from significantly lower F_2 mean compared to F_1 mean. The mean values of both BC_1 and BC_2 generations were found closer to each other.

The F1 (Jaya x IET 18654) mean value was found significantly higher than parents suggested over dominance gene effect in the inheritance of this trait. Absence inbreeding depression as evident from non-significant mean of F_1 and F_2. The mean values of BC_1 had significantly lower values than BC_2. Both the backcrosses had higher values than their recurrent parent.

For this trait, all the mean values of respective generation differed significantly from each other. The mean of F_1 significantly exceeded the mean of both parents, F_2 and both back crosses revealed over dominance gene effect for this trait (cross Jaya x GR 5). The BC_1 exhibited significantly higher values than BC_2 while both the backcrosses had significantly higher values than their respective recurrent parent.

5.1.6 Grain yield per plant (g)

In cross Gurjari x GR 5, F_1 recorded significantly higher mean than both parents revealed over dominance gene effect for this trait. The F_2 had significantly lower mean than of F_1 showed high inbreeding depression.

In cross GR 4 x IET 18654, the F_1 mean found intermediate to both the parents and significantly differed from P_1 and P_2. F_2 recorded significantly higher mean than F_1 revealed transgressive segregation for this trait.

The highest mean value of F_1 (Jaya x IET 18654) differed significantly from all the generations revealed over dominance gene effect in inheritance of this trait. The mean values of BC_1 found significantly higher than BC_2 generation but lower than recurrent parent.

The data showed that the mean of F_1 (Jaya x GR 5) was higher than five generations suggesting involvement of over dominance gene effects in the expression of this trait. The mean value of BC_1 significantly exceeded from mean value of BC_2.

5.1.7 100 grain weight (g)

For cross Gurjari x GR 5, parent P_1 had significantly higher 100 grain weight compared to all generations. The F_1 mean found intermediate to both the parents and non-significantly differed from P_2, F_2, BC_1 and BC_2 suggests presence of complete dominance and absence of inbreeding depression. The mean values of BC_1 and BC_2 generations were closer to its respective recurrent parent and BC_1 had significant and higher values than BC_2.

In cross GR 4 x IET 18654, F_1 mean was intermediate to both the parents and differed significantly from either of the parents and BC_1 this trait, but it was differed non-significantly from F_2 revealed absence of inbreeding depression.

F_1 (Jaya x IET 18654) found intermediate to both the parents and non-significantly differed from all five generations revealed complete dominance gene effect in the inheritance of this trait. BC_1 had slightly higher mean than BC_2 and lower than its recurrent parent.

The F_1 (Jaya x GR 5) mean value was place between mid-parent values and differed significantly from both the parents. Absence of inbreeding depression as evident from at par mean value of F_1 and F_2 generation.

5.1.8 Kernel length (mm)

In cross Gurjari x GR 5, both the parents differed significantly for their mean performance. Mean value of F_1 was at par with means of P_1, F_2 and BC_1 revealed complete dominance gene effect in inheritance of this trait and absence of inbreeding depression.

For kernel length both parents differed significantly from each other and it's F_1 (GR 4 x IET 18654). The F_1 mean value was found significantly highest than all other five generations showed over-dominance gene effect in the expression of this trait.

Parental line differed significantly from each other for this trait. The F_1 (Jaya x IET 18654) exhibited higher values than both the parents and non-significantly differed from first parent P_1, F_2 and BC_1, BC_2 revealed complete dominance gene effect in inheritance of this trait and absence of inbreeding depression. The mean values of both BC_1 and BC_2 generations found significantly differed from each other.

The F_1 (Jaya x GR 5) mean value depicted higher performance than its parents but significantly lower than F_2 mean value revealed transgressive segregation. Mean performance of both BC_1 and BC_2 was at par to each other and significantly higher than its respective recurrent patent.

5.1.9 length/Breadth ration

Cross Gurjari x GR 5, F_1 mean value was in between to parental means but differed significantly from all the generations except P_2 and BC_2 suggest complete dominance gene effect in the inheritance of this trait.

In cross GR 4 x IET 18654, the F_1 mean value was rest between mid-parent values and differed significantly from both the parents. The F_2 had higher mean value than P_2, F_1, BC_1 and BC_2. Mean performances of BC_1 and BC_2 were found at par to each other.

Cross Jaya x IET 18654, significant differences were observed among parental means. F_1 and F_2 expressed significant differences. Indicating absence of inbreeding depression.

For cross Jaya x GR 5, length/breath ratio was significantly high in parent P_1 compared to all the generations under study. Complete dominance gene effect as evident from non-significant difference between F_1 and P_1 mean. The F_1 mean value was rest between parental means and higher than F_2.

5.1.10 Straw yield per plant (g)

In cross Gurjari x GR 5, mean value of F_1 differed significantly from all the generations except parent P_1 suggest complete dominance gene effect in the inheritance of this trait.

Cross GR 4 x IET 18654, parent P_1 recorded higher straw yield parent P_2. The mean of F_1 and P_2 was non-significant showed complete dominance gene effect in the inheritance of this trait. The mean value of F_2 was found significantly higher than F_1 revealed trangressive segregation.

The mean of the F_1 (Jaya x IET 18654) significantly differed from both the parents revealed over dominance gene effect. The F_2 depicted significantly lower mean performance than F_1 showed high inbreeding depression for this trait.

For cross Jaya x GR 5, significant differences recorded among both the parents and their resulted F_1. The F_1 depicted significantly higher mean value than five generations suggesting involvement of over dominance gene effects in the expression of this trait.

5.2 SCALING TEST AND ESTIMATION OF GENE EFFECTS

Before any model is fitted to estimate gene actions involved on yield and its components, scaling tests were performed as given by Hayman and Mather, 1955. The scaling tests A, B, C and D indicated presence of appreciable amount of epistasis for different characters in all the four crosses. Presence of epistatic gene action for grain yield per plant and its related traits have been reported earlier by Roy and Panwar (1997), Chang *et al.* (2002), Mishra (2004), Sivakumar and Bapu (2005), Kumar *et al.* (2006), Verma *et al.*(2006), Rabiei and Ghorbanipour (2011), Srivastava *et al.* (2012) and Kiani *et al.* (2013) which supported the present results.

Based upon the present findings the gene effect involved in the inheritance of various characters affecting grain yield per plant and its components are discussed below.

5.2.1 Days to flowering

For days flowering non-additive gene effects played a major role in most of the crosses. The additive and dominance gene effects were highly significant in all the crosses. Among the epistasis the magnitude of dominance x dominance effect was high, significant and positive in cross, GR-4 x IET-18654. However, additive x additive effect found significant and positive in cross, Gurjari x GR-5. Duplicate epistasis was present in all the crosses. Similar results were obtained by Sivakumar and Bapu (2005), Sivakumar and Bapu (2005), Kumar *et al.* (2006), Verma *et al.* (2006) and Rabiei *et al.* (2011).

5.2.2 Plant height (cm)

Additive and non-additive type gene actions appeared to play role in the inheritance of this trait. The dominance gene effects were highly significant in all the crosses. However, additive gene effects also found significant and negative in four crosses viz., Gurjari x GR-5, GR-4 x IET-18654, Jaya x IET-18654 and Jaya x GR-5. Thus further change in early maturity could be possible through selection in this population. Among epistasis additive x additive and dominance x dominance had greater contribution in the variation. Additive x additive gene effects were highly significant and positive in one cross, GR-4 x IET-18654. While, it was negative in two crosses, Gurjari x GR-5 and Jaya x GR-5. Dominance x dominance gene effects was found significant for Gurjari x GR-5, Jaya x IET-18654 and GR-4 x IET-18654. The F_2 means were smaller than F_1 means in two crosses *viz.*, Gurjari x GR-5 and GR-4 x IET-18654 indicating the presence of interaction of dominance and/ or epistatic nature. Inheritance of this trait in all the crosses was under the control of duplicate type of epistasis. These results are similar to the findings of Mishra (2004), Sivakumar and Bapu (2005), Sivakumar and Bapu (2005), Kumar *et al.* (2006), Rabiei *et al.* (2011), Srivastava *et al.*(2012) and Kiani *et al.* (2013).

5.2.3 Productive tillers per plant

For this trait both additive and dominance effects were highly significant in all of crosses, but magnitude of dominance effect was higher compared to additive in majority the crosses which suggested its greater role in the expression of this trait. Duplicate type of gene action was observed in all the crosses indicated that phenotypic selection would be effective for isolating superior genotypes for this trait this findings are associated to the findings of Mishra (2004), Sivakumar and Bapu (2005), Kumar *et al.* (2006), Verma *et al.* (2006), Rabiei and Ghorbanipour (2011) and Kiani *et al.* (2013).

5.2.4 Panicle length (cm)

For this character both additive and dominance effects were highly significant in cross GR-4 x IET-18654 and Jaya x GR-5. However, the magnitude of dominance effect was highly significant in Gurjari x GR-5 and Jaya x IET-18654. Additive x additive, additive x dominance and dominance x dominance components contributed effectively in all four crosses. Duplicate type of epistasis was present in all four crosses. Similar kind of results were reported by Honarnejad (1995), Mishra (2004), Sivakumar and Bapu (2005), Kumar *et al.* (2006), Saravanan *et al.* (2006), Rabiei and Ghorbanipour (2011) and Srivastava *et al.*(2012).

5.2.5 Grains per panicle

The gene effects *viz.*, additive and dominance were highly significant in all four crosses. For this trait additive x additive and dominance x dominance effects were positive in majority of crosses. However, in all four crosses duplicate type gene interaction played a prominent role for the inheritance of this trait and Chauhan (1994), Mishra (2004), Sivakumar and Bapu (2005), Chauhan Kumar *et al.* (2006), Saravanan *et al.* (2006), Verma *et al.*(2006) and Rabiei and (2011) reported the similar findings as quoted above.

5.2.6 Grain yield per plant (g)

Digenic epistatic model, based on six generations, showed that on an average dominance gene effect contributed towards seed yield. Additive as well as dominance gene effects were contributed for grain yield per plant in four crosses. However in cross, Jaya x IET-18654 additive effect contributed more to grain yield per plant than dominance.

The F_2 means were smaller than F_1 means in most of the crosses suggested the presence of interaction of dominance or epistatic nature. Among digenic epistasis, major role in the inheritance of grain yield per plant was showed by additive x additive and dominance x dominance gene interactions. The additive x additive gene effects were positive and highly significant in cross, Jaya x IET-18654 while dominance x dominance gene effects had positive and significant effect in Gurjari x GR-5, GR-4 x IET-1865 and Jaya x GR-5. Among gene actions, sign attached to dominance and dominance x dominance effect are more important. In general, interactions divide in two groups; complementary and duplicate. If, dominance and dominance x dominance interactions have similar signs (positive or negative) then interactions will be complmentry and if both have opposite signs then interaction will be duplicate. Duplicate type of epistasis played significant role in the inheritance of grain yield per plant in crosses Gurjari x GR-5, GR-4 x IET-18654, Jaya x IET-18654 and Jaya x GR-5. The similar findings were reported by Sivakumar and Bapu (2005), Sivakumar and Bapu (2005), Kumar *et al.* (2006), Saravanan *et al.* (2006), Verma *et al.*(2006), Rabiei and Ghorbanipour (2011) and Srivastava *et al.*(2012).

5.2.7 100 grain weight (g)

For this character both additive and dominance effects were significant in crosses *viz.*, Gurjari x GR-5, GR-4 x IET-18654 and Jaya x GR-5. However, the magnitude of dominance effect was much higher compared to additive in all the crosses which suggested its predominant role in the expression of this trait. Additive x additive and dominance x dominance components contributed maximum in two crosses. While, in cross GR-4 x IET-18654 additive x additive gene effect was significant, dominance x dominance gene effect was highly significant. In cross Jaya x IET-18654 additive x additive gene effect was highly significant. Duplicate type of epistasis was present in all four crosses. The same results also reported by Chauhan and Chauhan (1994), Chang *et al.* (2002), Mishra (2004), Sivakumar and Bapu (2005), Kumar *et al.* (2006), Saravanan *et al.* (2006), Verma *et al.*(2006), Rabiei *et al.* (2011), Srivastava *et al.*(2012) and Kiani *et al.* (2013).

5.2.8 Kernel length (mm)

Highly significant and negative additive effects in two crosses except GR-4 x IET-18654 and Jaya x IET-18654 suggested the gain expected in advance generation through selection in these two crosses. In cross, Gurjari x GR-5 additive gene actions were highly significant and positive suggested the potential for obtaining further improvement in this trait through selection. However, dominance effect in all four crosses and dominance x dominance in crosses Gurjari x GR-5, GR-4 x IET-18654 and Jaya x IET-18654 were more importance in the expression of this trait. Duplicate epistasis was present in two crosses *viz.*, Gurjari x GR-5 and Jaya x IET 18654, while in crosses, GR-4 X IET-18654 and Jaya x GR-5 the gene interactions were complementary which reduced the expression of the heterosis. The expression of complementary and duplicate gene interactions for kernel length was also reported by the scientists *viz.*, Mishra (2004) and Rabiei and Ghorbanipour (2011).

5.2.9 Length/Breath ratio

Additive and dominance gene effect was highly significant in three crosses except Jaya x IET-18654. Among epistasis, additive x additive components contributed maximum in four crosses, whereas dominance x dominance in crosses Gurjari x GR-5, Jaya x GR-5 were highly significant and GR-4 x IET-18654 was found significant.

Duplicate epistasis was present in three crosses. Complementary gene effect reported in cross Jaya x IET-18654. Honarnejad (1995) reported the same results for this character.

5.2.10 Straw yield per plant (g)

For straw yield, magnitude of additive gene effect was found highly significant and positive for all crosses. While, dominance gene effect was found highly significant in three crosses but it was found positively significant in a single cross *i.e.* Jaya x IET 18654. Among the epistasis, dominance x dominance components contributed more in all four crosses. In all four crosses of additive x additive and additive x dominance component were highly significant. Duplicate type of epistasis was recorded in all the crosses. Roy and Panwar (1997) quoted the same findings in their studies.

5.3 MAGNITUDE OF HETEROSIS AND INBREEDING DEPRESSION

Exploitation of hybrid vigour in commercial crop is more significant when judged in relation to better parent or other hybrids rather than with mid-parental mean (Average heterosis). Fonseca and Patterson (1968) emphasized the utilization of hybrid vigour in express of the better parent for the production of commercial hybrids and coined the term "Heterobeltiosis".

The estimates of heterotic effects in the present study revealed that the magnitude of heterosis was in general medium for all the characters. The relative ranking of most heterotic crosses for different characters was quite different with change, indicating appreciable influence of environment in the expression of various traits. The top significant most heterotic crosses for different characters are presented

Table: 5.1 The top heterotic crosses for different characters in rice over better parent

Sr. No.	**Characters**	**Crosses**
1.	Days to flowering	GURJARI × GR-5
2.	Plant height (cm)	GURJARI × GR-5, GR-4 x IET-18654, JAYA X IET-18654, JAYA X GR-5
3.	Productive tillers per plant	GURJARI x GR-5
4.	Panicle length (cm)	JAYA × IET-18654, GURJARI × GR-5
5.	Grains per panicle	JAYA × IET-18654, JAYA × GR-5
6.	Grain yield per plant (g)	GURJARI x GR-5, JAYA × IET-18654, JAYA × GR-5
7.	100 Grain weight (g)	GR-4 x IET 18654
8.	Kernel length (mm)	GR-4 × IET-18654
9.	Length/breath ratio	GURJARI × GR-5, GR-4 X IET-18654, JAYA X GR-5
10.	Straw yield per plant (g)	JAYA X IET-18654

that number of single hybrid out of four had expressed the heterotic effect for all the traits under study in Table 5.1.

In case of grain yield per plant per plant out of four crosses three *viz*., Gurjari x GR-5, Jaya x IET-18654, Jaya x GR-5 displayed highly significant average heterosis and heterobeltiosis in desired direction. The three crosses *viz*., Gurjari x GR-5 (15.61 %), Jaya x GR-5 and Jaya x IET-18654 registered significant increase in grain yield per plant as compared to its better parent. Significant and positive average heterosis similarly cross *viz*., Gurjari x GR-5 Jaya x IET-18654 and Jaya x GR-5. It was further observed that the three cross combination for grain yield per plant also occupied significant heterobeltiosis panicle length, grains per panicle, straw yield per plant. The heterotic effects for grain yield per plant and its related traits was also reported by Deosarkar and Nerkar (1994), Reddy and Nerkar, (1995), Mishra *et al*. (1998), Singh and Maurya (1999), Verma *et al*. (2004), Agrawal, (2003), Alam *et al*. (2004), Raju *et al*. (2005), Veni *et al*. (2005), Kumar *et al*. (2008), Krishnan *et al*. (2009), Adilakshmi and Reddy (2011), Kumar *et al*. (2012) and Anilkumar *et al*. (2013).

The magnitude of mean performance of F_2 populations for grain yield per plant and its related traits showed significant inbreeding depression for various characters in majority of crosses studied. The crosses showing significant inbreeding depression for various traits are presented in table 5.2. Out of four crosses depicted inbreeding depression for different characters invariably. It was also found that number of single cross was able to express the significant inbreeding depression for all character study (Table 5.2). The crosses, Gurjari x GR-5, Jaya x IET-18654 and Jaya x GR-5 manifested significant and positive high relative heterosis and heterobeltiosis for grain yield per plant. Showed significant with inbreeding depression. This indicated

Table: 5.2 The crosses showing significant inbreeding depression for various characters in rice.

Sr. No.	Characters	Crosses
1.	Days to flowering	JAYA × GR-5, GR-4 × IET-18654
2.	Plant height (cm)	JAYA × GR-5, JAYA × IET-18654, GR-4 × IET-18654
3.	Productive tillers per plant	GURJARI x GR-5
4.	Panicle length (cm)	JAYA × GR-5, GR-4 × IET-18654
5.	Grains per panicle	JAYA × IET-18654, GURJARI × GR-5, JAYA × GR-5
6.	Grain yield per plant (g)	JAYA × GR-5, JAYA × IET-18654
7.	100 Grain weight (g)	GR-4 xIET-18654
8.	Kernel length (mm)	GR-4 × IET-18654
9.	Length/breath ratio	GURJARI × GR-5
10.	Straw yield per plant (g)	JAYA × GR-5, GURJARI × GR-5

that degree of inbreeding depression expressed by the F_2 populations was somewhat related to the amount of heterosis in F_1 for grain yield per plant. The results further revealed that the crosses which depicted significant inbreeding depression for grain yield per plant also exhibited positive inbreeding depression for its related traits also. Crosses Gurjari x GR-5, Jaya x IET-18654 and Jaya x GR-5 exhibited positive inbreeding depression for yield components like grains per panicle, panicle length, Straw yield per plant. Thus, it revealed that the expression of heterosis and inbreeding depression for grain yield per plant was dependent on its attributing traits. The results are matching with the results of Singh and Maurya (1999) and Raju *et al*. (2005).

Significant positive heterosis for grain yield per plant per plant and its related traits followed by significant inbreeding depression indicated that non-additive gene actions played major role in the inheritance of grain yield per plant and its attributes. These findings are similar to those of Veni *et al*. (2005), Kumar *et al*. (2008), Krishnan *et al*. (2009), Adilakshmi and Reddy (2011).

5.4 HERITABILITY AND GENETIC ADVANCE

In crop improvement, only genetic component of variation is important since only that component is transmitted to the next generation. Heritability indicates the effectiveness with the selection of genotypes could be based on phenotypic performance. This could be achieved through determining heritability and genetic gain under selection.

High broad sense heritability recorded for traits *viz*., panicle length, grains per panicle, kernel length and straw yield per plant in cross Gurjari x GR-5. Similarly high broad sense heritability reported for traits *viz*., days to flowering, plant height and 100 grain weight in cross GR-4 x IET-18654. In cross Jaya x GR-5 plant height, productive tillers per plant, grains yield per plant recorded high broad sense heritability.

Low narrow sense heritability was observed for days to flowering, panicle length, grains per panicle, grain yield per plant, kernel length and straw yield per plant in Gurjari x GR-5; productive tillers per plant, panicle length, grain yield per plant, days to flowering, plant height, 100 grain weight, length/breath ratio and straw yield in GR-4 x IET-18654; days to flowering, productive tillers per plant, panicle length, grains per panicle and kernel length in Jaya x IET-18654 and plant height, productive tillers per plant, grains per panicle, grain yield per plant, length/breath ratio and straw yield in cross Jaya x GR-5.

Moderate heritability was recorded for plant height in Gurjari x GR-5; grains per panicle in GR-4 x IET-18654; grain yield per plant, 100 grain weight in cross Jaya x IET18654 and days to flowering in Jaya x GR-5 .

The high heritability was identified for plant height in cross Jaya x IET-18654; panicle length in cross Jaya x GR-5.

The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotype is good reflection of genotype and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these matric traits but in case of lower heritability, pedigree, sib or progeny test can be employed to improve it. These results are similar to the findings of different scientists *viz*., Lokprakash *et al*. (1992), Sharma and Sharma (1993), Kumar *et al*. (1994), Manonmani *et al*. (1996), Moon *et al*. (1996), Sarma *et al*. (1996), Singh and Choudhary (1996), Saravanan and Senthil, (1997), Banumathy and Patil, (1999), Thakur *et al*. (1999), Kumari *et al*.

(2003), Saleem *et al.* (2008), Rao *et al.* (2011), Babu *et al.* (2012) and Satya and Jabera (2013).

In the present investigation, low genetic advance was recorded for almost all the traits except plant height and grains per panicle. However, most of the crosses revealed moderate to high genetic advance for three or more traits. Low genetic advance was reported for days to flowering, panicle length, kernel length and straw yield per plant in cross Gurjari x GR-5; panicle length, 100 grain weight and length/breath ratio in cross GR-4 x IET-18654; panicle length, 100 grain weight and kernel length in cross Jaya x IET-18654 and productive tillers per plant, panicle length, grains per panicle and length/breath ratio in cross Jaya x GR-5.

Moderate genetic advance was recorded for grain yield per plant in cross Gurjari x GR-5; productive tillers per plant in cross GR-4 x IET-18654; days to flowering in cross Jaya x IET-18654; plant height and grains per panicle in cross Jaya x IET-18654.

High genetic advance was recorded for plant height, grains per panicle in cross Gurjari x GR-5; days to flowering, plant height, grains per panicle, grain yield per plant and straw yield per plant in cross GR-4 x IET 18654; plant height, productive tillers per plant, grains per panicle and grain yield per plant in cross Jaya x IET-18654; days to flowering and straw yield per plant in cross Jaya x GR-5.

Shift in the gene frequency towards selection pressure is termed as genetic advance. Johnson *et al.* (1955) found it more useful to estimate heritability values together with genetic advance in predicting the ultimate choice of best individuals by selection. High genetic gain along with high heritability showed most effective condition for selection.

Breeding methodology:

Overall, it appeared that different gene effects were responsible for inheritance of the same trait in different crosses and for different traits in the same cross, specific handling of individual cross in segregating generations would be advantageous for improvement of these traits. In the present investigation, non-allelic interaction played pertinent role in determination of various characters in aerobic rice. Thus, breeding methods involving high volume crossing like biparental, recurrent and diallel selective mating design that take care of both additive and non-additive gene action seemed more promising for the improvement of various characters studied. Moderate level of heterosis for different characters reported, yet it varied a lot among the crosses and was cross specific.

SUMMARY

&

CONCLUSION

VI SUMMARY AND CONCLUSIONS

The present investigation entitled "**Genetic analysis of quantitative traits in aerobic rice [*Oryza sativa* L.]** " was carried out at Regional Rice Research Station, Navsari Agricultural University, N.A.U., Vyara, during k*harif*-2013.

The material comprising of five genetically diverse genotypes of rice (Gurjari, Jaya, GR 4, GR 5 and IET 18654) selected on the basis of their geographic origin and wide variation in morphological characters. Four crosses (Gurjari x GR 5, GR 4 x IET 18654, Jaya x IET 18654 and Jaya x GR 5) obtained by crossing five diverse lines during *kharif*-2012 at Regional Rice Research Station, Navsari Agricultural University, Vyara. These F_1's along with their parents were grown during summer 2012-13, where fresh F_1's and back crosses were developed. Parent and F_1's plant were selfed during the same season to obtain seeds of parents and F_2 generations. The experimental material consisting of four families, each having six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were evaluated in Compact Family Block Design with three replications during *kharif*-2013. The individual replication was represented by four family blocks, one row each of P_1, P_2 and F_1, four rows of F_2 and two rows each of BC_1 and BC_2. Total 10 plants were accommodated in each row. The inter and intra row spacing was 30 cm and 10 cm, respectively.

The observations recorded for 10 different characters *viz*., days to flowering, plant height, productive tillers per plant, panicle length, grains per panicle, 100 grain weight, grain yield per plant, kernel length, length/breadth ration and straw yield per plant were subjected to generation mean analysis to assess the gene effects controlling these traits to estimate the heterosis, inbreeding depression, heritability and genetic advance. Salient findings of the present study are summarized as below.

1. The analysis of variance for grain yield per plant and its component traits revealed significant differences among generations in all the characters studied in all four crosses.
2. The mean value of F_1 was significantly higher than parental mean value in three out of crosses *viz.*, Jaya x GR-5, Gurjari x GR-5 and Jaya x IET-18654 for grain yield per plant suggesting the importance of over dominance gene effect in the inheritance of this trait. The mean of F_2 generation was significantly lower than F_1 revealed high inbreeding depression.
3. Using A, B, C and D scaling tests as given by Mather (1949), non- allelic gene action was detected in most of the crosses for different characters studied. The scaling test A, B, C and D were found significant (either positive or negative) in all crosses *viz.*,Gurjari x GR-5, GR-4 x IET-18654, Jaya x IET-18654 and Jaya x GR-5 for grain yield per plant.
4. For days to flowering, dominance gene effects were significant and negative in two crosses *viz.*, GR-4 x IET-18654 and Jaya x GR-5. Among epistatic interactions, additive x additive and dominance x dominance effects shared major contribution in the inheritance. Duplicate type of epistasis was observed in majority of crosses.
5. For plant height, dominance as well as additive gene effects were significant in majority of crosses. While additive gene effects found to be significant and negative in majority of crosses. Among epistatic interactions, additive x additive and dominance x

dominance effects shared major contribution in the inheritance. Duplicate type of epistasis was observed in majority of crosses.

6. For productive tillers per plant, dominance as well as additive gene effects contributed for inheritance in four crosses. Additive x additive and dominance x dominance types of non-allelic gene action was useful for the inheritance of plant height. Additive x additive interaction effects showed diminishing effect in the expression of this trait in two crosses. Duplicate type of epistasis was observed for inheritance of this trait.
7. Dominance gene effects played major role in the inheritance of panicle length in most of the crosses. Among the epistasis, both additive x additive and dominance x dominance effects were important in majority of crosses. Duplicate type of epistasis was noticed in all four crosses.
8. For grains per panicle additive and dominance gene effects were appreciable in most of the crosses. However, additive effects were greater than dominance. Among non- allelic interactions additive x additive and dominance x dominance contributed major role in all four crosses. Duplicate type of epistasis was important for inheritance of this trait in all the crosses.
9. For grain yield per plant additive and dominance gene effects were highly significant in all four crosses. However, highly significant and positive additive effects in four crosses revealed its predominant role in the expression of this trait. Among epistasis, dominance x dominance had enhancing effects while additive x additive epistasis exhibited retardant effect in three of four crosses. Duplicate type of epistasis was observed in the expression of this trait in most of the crosses.

10. For 100 grain weight additive and dominance gene effects were appreciable in most the crosses. However, additive effects were greater than dominance. Additive x additive and dominance x dominance components contributed maximum in most of the crosses. Duplicate type of epistasis was noticed in all four crosses.
11. Additive and dominance gene action played important role in the expression of kernel length in most of the crosses. Dominance x dominance shared significantly higher and positive contribution in three crosses. Duplicate type of non-allelic interaction was important for inheritance of this trait.
12. For length/breath ratio magnitude of additive gene effects were positive and significant in four crosses which suggested its greater contribution in the expression of this trait. Among epistasis, additive x additive components contributed maximum in four crosses while dominance x dominance gene effects were important in three crosses. Duplicate type of epistasis played important role in inheritance of length/breath ratio in three crosses *viz.*,Gurjari x GR-5, GR-4 x IET-18654 and Jaya x GR-5.
13. For straw yield per plant, additive gene had positive highly significant effect for the inheritance of this trait. Among the epistasis, additive x additive and dominance x dominance gene interaction were more important for inheritance of this trait. Duplicate type of epistasis played important role in expression of this trait.
14. Highly significant and positive heterosis over mid parent and better parent was recorded for grain yield per plant and its related traits in three out of four crosses *viz.*, Gurjari x GR-5, Jaya x IET-18654 and Jaya x GR-5. Crosses which depicted significant and positive heterosis for grains yield per plant also exhibited

significant and positive heterosis for its components traits like, grains per panicle, panicle length, and straw yield per plant, which indicated that heterotic effect for grain yield per plant was mainly due to manifestation of heterosis in yield components.

15. The crosses which exhibited heterosis for grain yield per plant and its contributing traits also depicted significant inbreeding depression which revealed non-additive gene actions played major role in the inheritance of grain yield per plant and its attributes.
16. The estimates of broad sense heritability for grain yield per plant its attributes were in general high to moderate. The high broad sense heritability was observed from Jaya x GR-5 and moderate narrow sense heritability for Jaya x IET-18654 for grain yield per plant. The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotype is good reflection of genotype and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these matric traits but in case of lower heritability, pedigree, sib or progeny test can be employed to improve it. The high genetic advance was reported in crosses, Gurjari x GR-5, GR-4 x IET-18654 and Jaya x IET-18654 for grain yield per plant. Magnitude of genetic advance for majority of traits was high to moderate.
17. The breeding method that can be employed for improvement of character depends upon the type of gene action involved in its expression. The magnitude and type of gene effects differed for the same trait in different cross combinations and for different traits in the same cross combination. Therefore, for improvement of trait, segregating generations of individual crosses should be

handled in specific manner as per the gene action involved in its inheritance.

18. Different gene effects were responsible for inheritance of the same trait in different crosses and for different traits in the same cross, specific handling of individual cross in segregating generations would be advantageous for improvement of these traits. In the present investigation, non-allelic interaction played pertinent role in determination of various characters in aerobic rice. Thus, breeding methods involving high volume crossing like biparental, recurrent and diallel selective mating design that take care of both additive and non-additive gene action seemed more promising for the improvement of various characters studied. Moderate level of heterosis for different characters reported, yet it varied a lot among the crosses and was cross specific.

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APPENDICES

APPENDIX –I

Meteorological data recorded at Vyara (June – November 2013)

Month & Year	Temp. (^{0}C)		Relative humidity (%)		Rainfall (mm)	Rainy days
	Max.	Min.	Max.	Min.		
June 2013	29.5	20.5	-	-	203	12
July 2013	28.8	20.0	-	-	801	27
August 2013	29.9	21.0	-	-	320	14
September 2013	30.4	22.0	-	-	447.3	15
October 2013	34.8	22.0	-	-	83.9	6
November 2013	33.8	17.4	-	-	-	-

Source: Regional Rice Research Station N.A.U, Vyara.

CERTIFICATE

This is to certify that I have no objection for supplying to any scientist only one copy any part of this at a time through reprographic process, if necessary for rendering reference service in a libray or documentation center.

Place: Navsari

Date: 4th /10/2014 **(Ashish R. Patel)**