Genetic studies for yield and its contributing components in rice (*Oryza sativa* L.) under salt affected soil

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"I would like to dedicate my dissertation to my beloved Grandparents, Mom & Dad and my sister Dr. Archana, who always picked me upon time and encouraged me to go on every adventure especially this one."

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CERTIFICATE-I

This is to certify that the thesis entitled **"Genetic studies for yield and its contributing components in rice (*Oryza sativa* L.) under salt affected soil''** submitted for the degree of **'Doctor of philosophy'** in the subject of **Genetics and Plant Breeding** to the Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) is a bonafide research work carried out by **Miss. Preeti Kumari**, **Id. No. A-5226/10/14/16,** under my supervision and that no part of this thesis has been submitted for any other degree.

The assistance and help received during the course of investigation has been duly acknowledged.

Narendra Nagar
June, 2019

(M. P. Chauhan)
Major Advisor and Chairman,
Advisory Committee

CERTIFICATE-II

This is to certify that the thesis entitled "**Genetic studies for yield and its contributing components in rice (*Oryza sativa* L.) under salt affected soil**'' submitted by **Miss. Preeti Kumari**, **Id. No. A-5226/10/14/16** to the Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya U.P.) in partial fulfillment of the requirements for the degree of **'Doctor of philosophy'** in the subject of **Genetics and Plant Breeding** has been approved by the Student's Advisory Committee after an oral examination on the same in collaboration with an external examiner.

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CHAPTER-I

INTRODUCTION

Rice (*Oryza sativa* L.) is a *Kharif* season crop, belongs to **Kingdom:** Plantae, **Division:** Magnoliophyta, **Class:** Liliopsida, **Order:** Cyperales, **Family:** Gramineae (Poaceae), **Genus:** *Oryza,* **Species:** *sativa,* **Subspecies:** *Indica* with chromosome number 2n= 24, n=12, x=5. Rice is tetraploid plant with two genome A and B. The genus *Oryza* of the Gramineae family has 24 species. Two of the 24 species, *O. sativa* L. and *O. glaberrima* Steud., are cultivated cereals and 22 are wild species distributed in different geographic locations worldwide (Khush 1997, Vaughan 1989). *O. sativa* is cultivated as a major cereal crop in most parts of Asia and consumed as a staple food. The African cultivated rice, *O. glaberrima* is grown in small areas in West Africa. Asian cultivated rice has evolved into three eco-geographic races - *indica*, *japonica* and *javanica*.

Rice (*Oryza sativa* L.) is the most economically important food crop in the world and provides two third of calorie intake of more than three billion people in Asia and one-third of calorie intake of nearly 1.5 billion people in Africa and Latin America (Khush 2005).

World total rice acreage is 162.08 million hectare, with total production of 495.88 million tonnes of milled rice (USDA 2017-18). India has world's largest rice harvesting area. In India, area under rice is 42.90 million hectare with total output of 112.76 million tonnes with an average productivity of 39.40 q/ha (USDA 2017-18). It is grown in almost all the states of India *viz*. West Bengal, Uttar Pradesh, Andhra Pradesh, Punjab, Tamilnadu, Bihar, Chhattisgharh, Orissa, Assam, Karnataka, Kerala, Madhya Pradesh and Maharashtra and contribute to total 92% of area and production. In Uttar Pradesh it covers an area of 5.6 m ha with a production of 11.620 m tonnes and average productivity of 20.42 q/ ha (DRDPAT, 2015-2016).

Rice is a crop of tropical climate. However, it is also grown successfully in humid to sub-humid regions under subtropical and temperate climate. Rice is cultivated in almost all types of soils with varying productivity. Under high temperature, high humidity with sufficient rainfall and irrigation facilities, rice can be grown in any type of soil. The major soil groups where rice is grown are riverine alluvium, red-yellow, red loamy, hill and sub-mountain, Tarai, laterite, costal alluvium, red sandy, mixed red, black, medium and shallow black soils.

Rice is grown under many different conditions and production systems, but submerged in water is the most common method used worldwide. Rice is the only cereal crop that can grow for long periods of time in standing water (International year of rice 2004). More than half (57%) of rice is grown on irrigated land, 25% on rainfed lowland, 10% on the uplands, 6% in deepwater, and 2% in tidal wetlands (Chopra and Prakash 2002). Rice can be a short, medium or long grain size. It can also be waxy (sticky) or non-waxy. Some rice varieties are aromatic (Alford and Duguid, 1998, Chaudhary *et al.,* 2007). Rice also comes in many different colors including brown, red, purple and black (International Year of Rice, 2004).

Rice cultivation in the world extends from 39°S latitude (Australia) to 45°N latitude (Japan) and 50°N latitude (China). Most extensive rice growing areas are within 45°N of the equator. In India rice is grown under widely varying conditions of altitude and climate. Rice cultivation in India extends from 8 to 35°N latitude and from sea level to as high as 3000 meters elevation. Rice being a tropical and sub-tropical plant, requires a fairly high temperature, ranging from 20° to 40°C.The optimum temperature of 30°C during day time and 20°C during night time seems to be more favorable for the development and growth of rice crop. Sunlight is very essential for the development and growth of the plants. The yield of rice is influenced by the solar radiation particularly during the last 35 to 45 days of its ripening period. Bright sunshine with low temperature during ripening period of the crop helps in the development of grains. Rainfall has direct impact on deciding the ecosystem. Rice requires abundant rainfall, ranging from 150 cm to 200 cm. Rice requires a rainfall of 125 cm during vegetative stage. Heavy downpour at anthesis and flowering leads to sterility. No standing water is required at ripening stage. Relative humidity (RH) directly influences the water relations of plant and indirectly affects leaf growth, photosynthesis, pollination, occurrence of diseases and finally economic yield. The incidence of insect pests and diseases is high under high humidity conditions. Majority of pest and diseases are commonly seen during rainy season while aphids, thrips, scales, mealy bugs and mites are relatively more severe during summer. Moderate rainfall, relative humidity of around 80% and a wide range of atmospheric temperature of 20-33°c appear to be highly conducive to the brown plant hopper.

Improving the productivity of rice systems would contribute to hunger eradication, poverty alleviation, national food security and economic development. According to FAO estimates, there are about 840 million undernourished people, including more than 200 million children in developing countries.

However, rice production is facing serious constraints including a declining rate of growth in yields, depletion of natural resources, labour shortages, gender-based conflicts, institutional limitations and environmental pollution. Overcoming hunger, poverty and malnutrition - while protecting the environment - requires collective action by all stakeholders. The diversity of the regions, peoples, and resources connected within the world's rice-based systems, requires a diverse approach for global rice-based development that includes participation from the local to the international level.

Rice-based production systems provide the main income and employment for more than 50 million households. Rice (genus *Oryza*) is tolerant to desert, hot, humid, flooded, dry and cool conditions, and grows in saline, alkaline and acidic soils.

Rice is therefore, on the frontline in the fight against world’s hunger and poverty. Rice is also a symbol of both cultural identity and unity. For all these reasons, “Rice is life” and therefore, the United Nations General Assembly (UNGA) during its 57th session on 16th December 2002 declared 2004 as the International Year of Rice. This dedication of an International Year of Rice, for rice as a single crop, is unique precedence in the UNGA’s history. It reflects the fact that rice is not only a fundamental commodity and primary food source for more than half of the world’s population, but also a focus within a complex rice-based ecosystem that influences issues of global concern such as food security, poverty alleviation, presentation of cultural heritage and sustainable development. Rice, being the staple food for more than 70 per cent of our national population and source of livelihood for 120 to 150 million rural households, is backbone of the Indian Agriculture.

The area for rice cultivation has decreased in the context of economic development and urbanization. It is evident that rice yield cannot be increased by simply expanding the cultivation area. In light of this, it is important to pay attention to increasing rice yield per unit area. There are two major approaches for achieving this goal: improving cultivation conditions and technology, and breeding rice varieties with higher yield potential. In order to improve the cultivation technique, selecting superior cultivars is essential. Practices in rice science and production have shown that high-yield breeding of rice is essential for yield increase, and a breakthrough is usually made through discovery and effective utilization of specific germplasm (gene)

Out of total area in India about 5.5 million ha area is affected due to sodicity, out of which Uttar Pradesh shares about 1.37 m ha under sodicity (CSSRI, 2018). Rice area with salt problem in state is estimated to be ≤ 2%. Inland salinity areas are mainly concentrated in Raibareilly, Azamgarh, Sultanpur, Faizabad, Lucknow, Unnao and Pratapgarh districts.

Salt affected areas have increased day by day because of excessive use of irrigation water with improper drainage coupled with the poor quality irrigation water. Development of varieties for underutilized soil is the only option to increase the production. Thus, adoption of high yielding rice varieties to various stress environment and underutilized land such as saline-alkalinity affected soil would be an important strategy to meet this challenge. The salt tolerant rice varieties are sparse and the success of any breeding programme mainly depends on presence of genetic variability in the germplasm.

Yield enhancement is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic and molecular variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of the genetic variability parameters, *viz.* genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability (h^2) and genetic advance (GA) for different traits of economic importance is a major pre-requisite for any plant breeder to work with crop improvement programs. Further, information on correlation coefficients between grain yield and its component characters is essential for yield improvement, since grain yield in rice is a complex entity and highly influenced by several component characters. Studies on path co-efficient also provide useful information regarding the direct and indirect effects of different yield component characters on grain yield and thus aid in the identification of effective selection criteria for effective yield improvement.

Varietal adaptability to environmental fluctuations is important for the stabilization of crop production over both the regions and years. An information on genotype x environment interaction leads to successful evaluation of stable genotype, which could be used for general cultivation. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations; hence, the selection for superior genotypes based on yield per se at a single location in a year may not be very effective. Thus, evaluation of genotypes for stability of performance under varying environmental conditions for yield has become an essential part of any breeding programme. An understanding of the causes of genotype x environment interaction can help in identifying traits and environments for better cultivar evaluation. For developing stable varieties, some stability parameters for which Finlay and Wilkinson (1963), Eberhart and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971) have given some models and have been used in the search for an understanding of the causes of G x E interaction. Development of rice hybrids with high yield and desirable grain quality for different environments is one of the exciting research leads to successful evaluation of stable genotype, which could be used for general cultivation. Therefore, the present investigation was carried out, identifying stable genotypes with high yield using Eberhart and Russell model.

In order to meet the domestic demand of the increasing population, the present day production of 116 million tonnes (Annonymous, 2015- 2016) of milled rice has to be increased to 125 million tonnes by the year 2030. Since the yield of high yielding varieties (HYVs) of rice is plateauing, it is rather difficult to achieve this target with the present day inbred varieties. Therefore, to sustain the self sufficiency in rice, additional production of 1.17 million tonnes is needed every year. Among many genetic approaches being explored to break the yield barrier in rice and increased productivity, hybrid rice technology appears to be the most feasible and readily adaptable one. In a hybrid breeding program, choice of suitable parents is of primary importance since *per se* performance of parents is not always a true indicator of its combining ability in hybrid combination (Swamy *et al.*, 2003). Therefore, performance of a F_1 hybrid depends on choice of parents.

Several methods like *per se* performance, genetic diversity, combining ability *etc.*, have been attempted to select the parents. Among them combining ability analysis offers a powerful tool for estimating the value of a parent to produce superior hybrid. The combining ability studies of the parents provide information which helps in the selection of better parents for effective breeding. Its role is important to decide parents, crosses and appropriate breeding procedure to be followed to select desirable segregates (Salgotra *et al.,* 2009)

The success of a plant breeding programme greatly depends on correct choice of parents for hybridization and the gene action of different economic traits. Combining ability analysis provides such information so as to frame the breeding programme effectively. The line x tester analysis gives reliable information about the nature and magnitude of gene action and combining ability effects present in the genetic materials. Dhillon (1975) pointed out that combining ability gives useful information on the choice of parents in terms of expected performance of the hybrids and their progenies.

The scope for exploitation of hybrid vigour depends on the direction and magnitude of heterosis and ease with which hybrids seeds can be produced (Kumar 2017). Further, the extent of heterosis will have direct effect on breeding methodology in varietal improvement programme. Therefore, in the present investigation, a study was conducted to estimate the extent of heterosis for grain yield and its component traits over better parent (BP) and standard parent (SP) in hybrid rice (*Oryza sativa* L.) through line× tester analysis.

There are several biotic and abiotic factors behind the less productivity as compared to other major rice growing countries. Therefore, keeping in view the importance and seriousness of the salinity stress, planning and execution of a successful breeding programme aimed at development of superior rice varieties for stress environments like salinity conditions is vital. Line × tester analysis technique has been extensively used in almost all the major field crops to estimate *gca* and *sca* variances and their effects, and to understand the nature of gene action involved in the expression of various quantitative traits.

The present investigation was undertaken in this context to elucidate information on variability, heritability, genetic advance, genetic divergence, character associations, path analysis, stability index, gene action, combining ability and heterosis of promising rice genotypes. A good knowledge of genetic resources might also help in identifying desirable genotypes for future hybridization program. Therefore, present investigation was undertaken with following objectives:

1. To examine the genetic variability and evaluate the rice genotype for various traits.
2. To compute association at genotypic and phenotypic levels among different characters.
3. To assess the stability of rice genotypes.
4. To study the combining ability variances and their effects.
5. To find out gene action involved in the inheritance of various characters.
6. To estimate heterosis over better-parent and standard varieties, and
7. To identify promising parents and superior hybrids for exploitation in breeding programme.

CHAPTER-II

REVIEW OF LITERATURE

The development of improved cultivars has made a major contribution to the increased productivity and quality of plants. The prime objective of breeder is to bread varieties better than the best existing ones by improving those characteristics of a plant species that contribute to its economic value (yield). This requires availability of sufficient genetic variability in the breeding populations on which direct and indirect selection can be applied effectively. Modern high-yielding rice varieties developed since 1960's are occupying about 60% of the world's rice area. Since 1965, increase in productivity coupled with expansion of the area planted under rice cultivation has doubled world'srice production. Today, there is no more available land to bring under rice cultivation and growth rate of rice production has decreased (Khush, 1997). By 2020, we would require 60% more rice to keep up with the world's increasing rice consuming population. Further, there is need to improve yield potential of modern rice varieties from 8-10 tonnes per hectare to 10-13 tonnes per hectare. India has achieved self sufficiency in food production during the past decade and to keep pace with growing population, the country must now increase food production by at least 5.00 million tonnes and rice by 2.00million tonnes every year to sustain the current level of self-sufficiency. Hybrid rice technology is the most important new scientific approach for meeting this challenge to increase rice production.

In this regard, past studies form the basis for formulating new strategy. Hence, a brief review of literature available in rice in respect of various aspects of present investigation was collected and is presented in this chapter under following sub heads:

1. To examine the genetic variability and evaluate the rice genotype for various traits.
2. To compute association studies at genotypic and phenotypic levels among different characters

3. To assess the stability of rice genotype.

4. To study the combining ability variances and their effects,

5. To find out gene action involved in the inheritance of various characters,

6. To estimate heterosis over better-parent and standard varieties, and

7. To identify promising parents and superior hybrids for exploitation in breeding programme.

2.1 Genetic variability

The genetic variability existing in the germplasm collections serves as raw material to the plant breeder on which selection is exercised to evolve superior genotypes. Thus, availability of sufficient genetic variability is the basic requirement for its efficient utilization in any crop improvement programme. The variation exploited in most breeding programmes is derived from naturally occurring variants and the wild relatives of main crop species as well as artificially developed strains and genetic stocks by human efforts. The reservoir of variability for different characters of a plant species resulting from available naturally or artificially synthesized variants or strains constitute its germplasm. Thus, germplasm may include improved strains, primitive cultivars, wild relatives, obsolete cultivars, special genetic stocks, seeds, pollen and vegetative parts etc. Germplasm forms the most valuable natural resource in modern agriculture as it provides donors for important agronomic and economic traits for engineering superior genotypes in a crop improvement programme (Hawkes, 1981). Sometimes introduction of superior genotypes from the germplasm collections of other area may in certain cases accomplish the same purpose as development of superior varieties in breeding programmes.

Vavilov (1926) was the first to realize the essential need for a broad genetic base of germplasm for plant improvement. Vavilov (1951) advocated for genetic resource management and its enhancement through extensive explorations and systematic studies of the collection of land races from various parts of the world. He suggested the geographical centers of genetic diversity of the cultivated plant species and their wild relatives.

Harlan (1956) also speculated the problem of germplasm conservation while discussing natural variability of plants and pointed out that centers of diversity are in constant process of genetic erosion as “partial or complete destruction of genetic resources in short span of time” which is greatly accelerated in areas of intensive agricultural production. Thus, in centers of plant origin, the primitive forms of cultivated plants and related wild species are fast disappearing (Hawkes 1971; Harlan 1972, 1975).

Development of high yielding and disease resistant cultivars is ultimately causing elimination of old traditional cultivars and land races from the cultivation. Thus, infinite number of valuable natural variants is vanishing gradually for ever while they might have potential genes for different useful characters under changed environment and time (Frankel, 1970). Therefore, apart from increasing productivity, it is equally important to conserve the existing germplasm and make it available for future breeding work by marking them as potential donor for important traits.

Fisher (1918) was the first person to partition the total variability into genetic and environmental components. He further divided the genetic variance into additive, dominance and epistatic components. Phenotypic differences among the plants are correlated in lesser or larger extent with the corresponding genotypic differences among them, while selecting an individual on basis of phenotype, we actually select indirectly the genotype responsible for it. The coefficients of variation at genotypic, phenotypic and environmental levels provide clear understanding of existing variability in a crop and relative importance of genetic and environmental components.

A brief review of literature in respect of studies on genetic variability in rice is presented below:

Devi *et al.* (2016ii) noticed that general mean for grain yield per plant (21.48 ± 0.95 g) was greater than the mean of parents (20.83 g) and crosses (21.45 g) under salinity condition. In general, the magnitude of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. High estimates of phenotypic and genotypic coefficient of variation (>20%) were recorded for grains per panicle. Panicle bearing tillers per plant exhibited high estimate for PCV and moderate for GCV. High heritability coupled with very high and high genetic advance in per cent of mean were observed for the characters like flag leaf area, spikelets per panicle, grains per panicle, 1000-grain weight, biological yield per plant, harvest-index and grain yield per plant under saline condition.

Kumari *et al.* (2018) grouped forty one indigenous and exotic rice in to seven clusters based on the relative magnitudes of D^2 values following Tocher's method of cluster formation. Cluster II is the largest cluster consisting of 12 genotypes while Cluster I was the smallest with only a single genotype. The maximum intra cluster distance (D = 133.58) was found in cluster III consisting of 5 varieties. In the present study, maximum inter cluster distance was estimated between cluster III and VII ($\sqrt{D}2$ = 913.36) which was followed by clusters II and VI ($\sqrt{D}2$ = 755.83). Based on the rank totals, the characters which contributed maximum towards genetic divergence in the present studies were spikelets per panicle (30.24%) followed by days to 50% flowering (16.59%), flag leaf area (16.34%), plant height (14.39%), biological yield per plant (9.15%), spikelet fertility (5.12%), length/breadth ratio (3.41%), 1000 grain weight (3.17%), harvest index (1.46%) and panicle length (0.12%). Hence, these traits could be focused for selection while improving quantitative traits. On the basis of their greater inter cluster distance, high value of cluster mean and performance of the individual germplasm for the character, the germplasm could be used in hybridization programme for improvement of different plant characters of the rice.

Divya *et al.* (2018) conducted experiment with thirty three genetically diverse genotypes. They found that analysis of variance was found to be significant for all the traits, indicated that there is existence of genetic variability for all the traits varying from lower to higher coefficients of variance. The results found that the moderate genotypic and phenotypic coefficients of variance were recorded for number of productive tillers per plant, number of grains per panicle and seed yield per plant. High heritability with high genetic advance was observed for number of productive tillers per plant, 1000 grain weight, number of grains per panicle and seed yield per plant.

The traits were found to have higher values of variance and selection for such traits will be practiced based on phenotypic observation.

Sandeep *et al.* (2018) observed highly significant differences among the genotypes for all the characters indicating sufficient variability existed in the present material selected for the study. Environmental influence was very meager on the expression of all the characters as there is a narrow difference between genotypic and phenotypic coefficients of variation. Genotypic and phenotypic coefficients of variability were high for single plant yield, number of grains per panicle, number of tillers per hill, pollen viability and spikelet fertility. The characters *viz.,* spikelet fertility, plant height, single plant yield, number of grains per panicle, number of tillers per hill, pollen viability, number of productive tillers per hill, panicle length and 1000 grain weight exhibited high heritability estimates coupled with high genetic advance as per cent of mean which suggested that these traits were amenable for further improvement by following simple selection methods.

Saha *et al.* (2019) observed higher value of phenotypic co-efficient of variation (PCV) compared to the corresponding genotypic coefficient of variation (GCV) for all the studied traits indicated that there was an influence of the environment. Number of unfilled grains per panicle exhibited high estimates of PCV and GCV followed by number of filled grains per panicle, number of grains per panicle, flag leaf area. High heritability coupled with high genetic advance was observed in flag leaf area, pollen fertility, number of grains per panicle and number of filled grains per panicle which reflected that the direct selection of these characters based on phenotypic expression by simple selection method for yield improvement would be more reliable. Grain yield per plant showed significant and positive association with days to 50% flowering, days to maturity, flag leaf area, number of total tillers per hill, number of effective tillers per hill, pollen fertility, number of grains per panicle, number of filled grains per panicle indicating selection of these characters for yield improvement may be rewarding. Both at phenotypic and genotypic level, days to 50% flowering, flag leaf area, number of effective tillers per hill, pollen fertility, panicle length, number of grains per panicle and100 seed weight had direct positive effect on yield per plant indicating their importance during selection in yield improvement program.

2.2 Correlation and path coefficient analysis

The grain yield in rice, like in other crops, has a very complex existence because its expression depends on several other plant characters. The genetic architecture of grain yield in rice can be better resolved through components rather than yield *per se*, as yield is the end product of multiplicative interactions between various yield components (Grafius, 1959). The correlation coefficient provides information about inter-relationship among yield and its components. The information on character associations may be used in the prediction of correlated response to directional selection, construction of selection indices and identification of some characters which may have no value by themselves, but are useful as indicators of the more important ones under consideration (Johnson *et al.,* 1955).

Wright (1921) developed the concept of path coefficient as an attempt to analyze statistically the causes and effects in correlated variables and critically examine the real contribution of individual variables to the ultimate complex end product like yield. Li (1956) gave a detailed account of both basic and applied aspects of path coefficient analysis. Dewey and Lu (1959) applied this technique for the first time in plant breeding in crested wheat grass (*Agropyron cristatum*).

Dwivedi *et al.* (2012) studied direct and indirect influences on grain yield in 58 rice introgression lines including check varieties. The path coefficient analysis indicated that biological yield and harvest index had maximum direct effect on grain yield at phenotypic and genotypic level under drought condition. Biological yield and harvest index had maximum direct effect on grain yield at phenotypic level and grains per panicle and panicles per plant had maximum direct effect on grain yield at genotypic level under control condition. Seedling height, leaves per seedling and plant height exerted very high positive indirect effect on grain yield at phenotypic and genotypic level under control conditions *via* harvest index.

Rai *et al.* (2014) conducted experiment with 40 genotypes of rice during *Kharif*2013 in randomized block design. The data were recorded for 13 quantitative characters to study path coefficient. Correlation and path-coefficient analysis, concluded that, biological yield per plant and harvest index exhibited maximum positive direct effect on grain yield seems to be primary yield contributing characters and could be relied upon for selection of genotypes to improve genetic yield potential of rice. Hence, utmost importance should be given to these characters during selection for single plant yield improvement.

Kumar (2015) carried out an investigation to assess the nature and magnitude of character association in rice using 57 genotypes. The effective tillers (0.474), spikelet fertility (0.323),biological yield (0.723) and harvest index (0.744) in land races, plant height (0.542), panicle length (0.356),effective tillers (0.436), spikelet fertility (0.317), biological yield (0.766) and harvest index (0.744) in new plant types and panicle length (0.386), spikelets and grains per panicle (0.459, 0.498), biological yield (0.627) and harvest index (0.627)in japonicas were positively associated with grain yield indicating that these are the important characters and can be strategically used to improve the yield of rice.

Dwivedi *et al.* (2015) reported that grain yield per plant showed positive and significant correlation with L:B ratio, biological yield per plant and harvest index in saline conditions emerge as most important associates of grain yield in rice. Path analysis identified harvest-index, biological yield and grains per panicle as most important direct yield contributing traits. Grains per panicle, 1000 grain weight, kernel length, kernel breadth, L:B ratio exhibited high and positive indirect effect on grain yield *via* biological yield per plant and harvest index.

Devi *et al.* (2016 i) carried out experiment with fifteen characters with 18 lines and 3 testers. The correlation studies revealed strong positive association of yield with biological yield per plant followed by 1000-grain weight and harvest index. The result of path analysis indicated that the number of grains per panicle had maximum direct effect on biological yield per plant followed by harvest-index and grains per panicle under saline condition.

Kumari *et al.* (2017) carried out an experiment consisted of 41 rice genotypes including check Narendra Usar Dhan 3. The experiment was conducted under saline-alkali soil (pH = 8.9; EC = 2.21dSm^{-1}; ESP = 45%) in randomized complete block design with three replications. In each block 41 entries were accommodated. The spacing between rows to row and plant to plant were 20 cm and 15 cm, respectively. Length of row was 5m and 3 rows of each entry were planted in a plot. The nursery was planted after the period of 30 days. The yield and yield contributing traits were utilized for estimation of correlation coefficients. The genotypic correlations coefficients were generally similar in nature and higher in magnitude with the corresponding phenotypic correlation coefficients. Days to 50% flowering, biological yield per plant, harvest-index, spikelet fertility, spikelets per panicle, plant height and panicle bearing tillers per plant showed very strong significant and positive correlation with grain yield per plant in rice at both phenotypic and genotypic levels.

Sumithra *et al.* (2019) conducted experiment to evaluate the nature and magnitude of variability and character association among 36 rice genotypes. The divergent studies showed the significant variation among the genotypes for all the characters studied. Correlation studies revealed that number of tillers/plant, 100 grain weight and grain length registered, positive correlation with grain yield per plant. Path analysis revealed that the traits grain breadth and grain L/B ratio had very high positive direct effect on grain yield. The traits days to 50% flowering, number of tillers per plant, number of grains per panicle, grain breadth and grain L/B ratio had high positive direct effect on grain yield per plant.

Sreedhar and Reddy (2019) reported that number productive tillers per m^2 and 1000-grain weight exhibited significant positive correlation with yield at both genotypic and phenotypic levels. Significant negative correlation was observed between number of unfilled grains per panicle and yield. Path coefficient analysis revealed positive direct effect of number of productive tillers per m^2 and days to 50% flowering on grain yield at both genotypic and phenotypic levels.

2.3 Combining ability

Sprague and Tatum (1942) gave the concept of general combining ability (gca) and specific combining ability (sca) based on gene interactions. They suggested that the general combining ability (gca) means the average performance of a line in hybrid combinations, while specific combining ability (sca) refers to those cases in which certain combinations do relatively better or worse than would be expected on the basis of average performance of the lines involved. Good general combining parent results in higher frequency of heterotic hybrids than poor general combining parent. From the genetic point of view, general combining ability represents additive gene effects and specific combining ability results non-additive gene effects, depending on genes with dominance (intra-allelic interactions) and epistasis (inter-allelic interactions). In a hybrid breeding programme, plant breeder generally identifies parental lines with good general combining ability and crosses with high specific combining ability effects.

Griffing (1956) gave generalized concepts and methodologies for combining ability analysis. He pointed out that gca involved both additive effects and additive × additive interaction effects which are fixable in nature. He outlined the procedure for determining the gca and sca effects and variances from diallel sets of varied composition.

Kempthorne (1957) suggested a procedure known as line × tester mating design, which is used to estimate genetic parameters and general and specific combining ability variances and their effects from a set of homozygous lines.

Dwivedi *et al.* (1999) studied combining ability for grain yield and its contributing characters in a 10 parents F_1diallel in rice over three environment, E_1: normal sowing time and high fertility, E_2: normal sowing time and optimum fertility and E_3: late sowing time and high fertility. The parental lines were four tropical japonicas *viz.*, BSI 10, BSI 16, B4116 and B 4122 having wide compatibility gene(s) and six indicas*viz.*, Govind, Manhar, Pant Dhan 4, Sarjoo 52, Pant Dhan 12 and

Narendra 359. Both general combining ability (gca) and specific combining ability (sca) were influenced by environments. Studies on combining ability over range of environments are suggested for obtaining unbiased estimates. Both additive and non-additive genetic variances were important in the expression of all the characters. The magnitude of sca variances was relatively higher than the gca variances and thus predominance of non-additive gene action was indicated for all the characters, except 100-seed weight in E_1 environment, where the additive gene action played major role in its inheritance. *Per se* performance of the parents gave a good indication of their gca effects. General combining ability effects pooled over environments indicated that parents Pant Dhan 4, Sarjoo 52, Narendra 359, B 4122 and BSI 10 to be good general combiners for grain yield and most of its components. Based on sca effects, the crosses BSI 10/Narendra 359, B 4122/Pant Dhan 4 and B 4122/Narendra 359 were suggested for the isolation of high yielding lines through conventional methods, while crosses BSI 10/Govind, BSI 10/Pant Dhan 12 and B 4122/Pant Dhan 12 that involved diverse indica and tropical japonicas can be exploited for heterosis at the inter-subspecific levels.

Devi *et al.* (2017 i) conducted experiment to evaluate line × tester performance of 54 F1 hybrids along with 18 parents in rice. Analysis of variance revealed highly significant differences among treatments, parents, crosses and lines × testers for number of panicle bearing tillers per plant, panicle length, spikelets per panicle, and grains per panicle, spikelets fertility, biological yield per plant, harvest index and grain yield per plant under both normal and saline conditions. Parents vs. crosses were significant for panicle bearing tillers per plant, spikelets per panicle, grains per panicle, spikelets fertility, biological yield per plant and grain yield per plant in normal condition while in saline condition for spikelets per panicle, grains per panicle, spikelets fertility, biological yield per plant and harvest index. Lines were significant for panicle length, biological yield per plant and harvest index in normal condition but in case of saline condition panicle length and grain yield per plant were found significant. Testers were non-significant for all the traits in both conditions. The estimates of variance of specific combining ability effects, ratio of variance of general combining ability to specific combining ability and degree of dominance indicated preponderance of non-additive gene effects for each trait. On over all bases, role of lines in the expression of most of the yield components was more than testers and line × tester interaction under both conditions.

Devi ***et al.*** **(2017 iii)** conducted experiment to evaluate line × tester performance of 54 F1 hybrids along with 18 parents in rice. Analysis of variance revealed highly significant differences in treatment for 1000 grain weight, kernel length, kernel breadth, L:B ratio and grain yield per plant under both normal and saline conditions except kernel breadth which found significant for normal condition. Analysis of variance revealed highly significant differences among crosses and lines × testers for 1000 grain weight, kernel length, kernel breadth, L:B ratio and grain yield per plant under both normal and saline conditions. Parents *vs*. crosses were for kernel length and grain yield per plant for normal condition while in case of saline condition kernel breadth was found highly significant. Lines were highly significant and significant for 1000 grain weight and grain yield per plant in normal and saline condition, respectably. Testers were non-significant for all the traits in both conditions except kernel length in normal condition which was found significant. The estimates of variance of specific combining ability effects, ratio of variance of general combining ability to specific combining ability and degree of dominance indicated preponderance of non-additive gene effects for each trait. On over all bases, role of lines in the expression of most of the quality traits were more than testers and line × tester interaction under both conditions.

Devi ***et al.*** **(2017 iv)** observed that analysis of variance revealed highly significant difference in treatments, parents, crosses and line × tester for days to 50% flowering, plant height, flag leaf area and grain yield per plant under both normal and saline conditions. Parent *vs.* crosses were highly significant for plant height and grain yield per plant while significant for days to 50% flowering and flag leaf area in normal condition but in case of saline condition highly significant differences were found for plant height and flag leaf area and non-significant for days to 50% flowering and grain yield per plant. Analysis of variance revealed highly significant differences among lines for grain yield per plant under both normal and saline conditions while plant height for saline condition. Tester was non-significant for all the characters under both normal and saline conditions. The estimates of variance of specific combining ability effects, ratio of variance of general combining ability to specific combining ability and degree of dominance indicated preponderance of non-additive gene effects for each trait. On over all bases, role of lines in the expression of most of the morphological traits were more than testers and line × tester interaction under both conditions.

Parimala *et al.* (2018) studied that analysis of variance revealed the prevalence of non-additive gene action for the traits studied except for days to 50% flowering. The CMS lines IR-79156A and IR-58025A and testers WGL-3962, RNR-15038 and RNR-2781 were best combiners for most important yield contributing traits, like number of productive tillers per plant, number of filled grains per panicle and grain yield per plant by exhibiting positive *gca* effects. The hybrids, IR-58025A x RNR-15038, IR-79156A x NWGR-3132, IR-58025A x RNR-2781, IR-79156A x RNR-2781 and APMS-6A x RNR-15038 were considered as potential cross combinations for grain yield and its attributes based on *per se* performance, *sca* effects, *gca* effects of parents and standard heterosis. These hybrids could be further evaluated in multi locational trials for commercial use.

2.4 Heterosis

The term heterosis was first used by Shull in 1914. Heterosis may be defined as the superiority of an F_1 over either of its parents in terms of yield or some other character(s). Generally, heterosis is manifested as an increase in vigour, size, growth rate, yield or some other characteristics, but in some cases, the hybrid may be inferior to the weaker parent.

The exploitation of heterosis is considered as an outstanding application of the principles of the science of genetics in agriculture. Heterosis breeding had led to a breakthrough in yield increase in several crop plants. For the exploitation of heterosis, it is imperative to study the magnitude of heterosis. The expression of heterosis is greatly influenced by the magnitude of genetic differences among parents involved in the crosses. The parents with optimal to intermediate genetic diversity have been found to show maximum heterosis (Moll and Stuber 1974). Varying levels of heterosis in grain yield and yield components have been reported by several workers in rice.

A brief review of literature pertaining to studies on heterosis for different characters in rice is presented in the following paragraphs:

Dwivedi *et al.* (1998) reported moderate to high heterosis for yield and ten related characters in 45 crosses involving six indica (I) and four tropical japonica (J) varieties of rice under three (E_1- optimum sowing and high fertility, E_2-both optimum sowing and fertility and E_3 late sowing and high fertility) environments. Trends of magnitude of heterosis for grain yield and plant height were I/J>I/I>J/J and for days to 50%flowering was I/J>J/J>I/I hybrids. Estimates of standard heterosis (%) for grain yield were -65.5 to 146.1 in E_1, -70.4 to 82.2 in E_2 and -67.2 to 63.8 in E_3. Environment E_1 seemed to be more favorable for higher heterosis expression than others. Higher heterosis in yield also accompanied heterosis in panicle number, dry matter and spikelets and grain number per panicle. Most estimates for days to 50% flowering were negative. Heterotic I/J hybrids also recorded maximum heterosis for earliness. Moderate to low standard heterosis for plant height across environments (2.0 to 13.7%) was recorded. Hybrids were identified in specific environments for direct exploitation in hybrid breeding. Hybrids B4116/Sarjoo 52, B4122/Pant Dhan 4 and B4122/Narendra 359 were more stable than others over three envornments.

Dwivedi and Pandey (2012) evaluated 45 hybrid rice along with six semi-dwarf, early to mid-early duration and high yielding indicas (Govind, Manhar, Pant Dhan 4, Sarjoo 52, Pant Dhan 12 and Narendra 359) along with four tropical japonicas cultivars (BSI10, BSI16, B4116 and B4122) having wide compatibility gene(s), in relation to analyze gene action and heterosis for grain yield and associated traits. The experiment was conducted in randomized complete design and data collected on various traits were analyzed for heterosis and combining ability. Both additive and non-additive gene action were found to control the expression of all characters. The ratio of general combining ability (GCA) to specific combining ability (SCA) variances exhibited greater relevance of non-additive gene action governing yield and its associated traits. Parent B4122 and Sarjoo 52 were found to be the best general combiner for maximum characters, including grain yield per plant. The crosses B4116 × Sarjoo 52, BSI10×Pant Dhan 12, BSI10×Narendra 359, B4122×Manhar and B4122×Govind recorded the highest SCA effects for grain yield per plant. Heterosis over mid-parent, better parent and standard variety ranged between -54.17 to 169.70, -58.31 to 150.32 and -64.55 to 146.15%, respectively. The trends of magnitude of heterosis for grain yield and plant height were I/J>I/I>J/J and for days to 50% flowering I/J>J/J> I/I hybrids. The crosses B4116×Sarjoo 52, BSI10×Pant Dhan 12 and BSI10×Narendra 359 were identified as the best hybrids on the basis of per se performance, high heterosis and combining ability effects. Most of the heterotic cross combinations identified in this study involved indica and tropical japonica lines having wide compatibility gene as their parents. Interspecific hybrids exhibited high heterobeltiosis and economic heterosis.

Devi *et al.* (2017 ii) observed that potential of hybrid rice to increase productivity, the present experiment was done with a fixed model i.e. line x tester mating design involving 3 tester (male) and 18 line (female) toidentify the best heterotic combinations. The results indicated that the heterobiltiosis for grain yield wassignificantly superior for 2 hybrids ranging from -59.40 to 27.12%. Standard heterosis ranged from -52.52 to 48.64% and 16 hybrids showed significantly and positive standard heterosis over Narendra User Dhan 2009. Cross, NDRK 50001 × Narendra Usar Dhan 2009 exhibited heterobiltiosis for grain yield perplant, also showed significant heterobiltiosis for plant height, biological yield per plant and 1000 grainweight. This hybrid also recorded high standard heterosis for grain yield per plant along with significant standard heterosis for panicle bearing tillers per plant, spikeltes per panicle, grains per panicle, kernel length, biological yield per plant, 1000 grain weight and L: B Ratio. Cross NDRK 5035 × Narendra Usar Dhan 3 also exhibited significant heterobiltiosis and standard heterosis for grain yield per plant along with other quantitative traits.

Gokulakrishnan (2018) studied that majority of the crosses showed positive heterosis for the characters *viz.,* productive tillers, filled grains per panicle, spikelet fertility, 1000 grain weight, grain yield per plant, grain length, grain breadth, grain L/B ratio, kernel L/B ratio, milling recovery, head rice recovery, and amylose content. Negative heterosis was recorded for the characters namely days to first flowering, plant height, panicle length, kernel length, kernel breadth and alkali digestion value. Hybrids IR58025A×ASD19, IR62829A× ASD16 and PUSA3A× IR42 were found to record high per se performance, higher percentage of standard heterosis for majority of the traits.

Budhlakoti *et al.* (2019) estimated standard heterosis by using Pant Dhan4 as a check parent. Cross combinations namely PR113×HKR47 (-4.273) and UPR-3905-22-2-2-1×HKR 47 (-5.512) showed significant negative standard heterosis for days to 50% flowering and days to maturity, respectively. Highly significant and maximum standard heterosis was showed by cross combinations UPR3037-2-2-1-3×PD 24 (5.138), UPR3037-2-2-1-3×PD 24 (13.515), UPR3037-2-2-1-3×HKR47 (7.811) and UPRI 2015-2×PD 24 (18.728) for grain length, grain width, 1000 grain weight and grain yield per plant.

Stability index

Genotype-environment interaction differs from population to population, being smaller for heterozygous and cross-fertilized population than the homozygous and self-fertilized population (Allard, 1961).

The occurrence of G×E interaction has long posed a major challenge to a fuller understanding of the nature of genetic variation. Thus, G×E interaction have assumed greater importance in plant breeding in the sense they violently interfere with the precise estimates of genetic parameters and with stability of genotypic values under diverse environments.

The presence of G×E interaction in plant breeding experiments aimed at gathering information on genetic variance causes biased estimates. The additive and non-additive components the biased estimates of variance components, a faulty breeding method may be commissioned.

Eberhart and Russell (1966) considered that an ideal variety in one which has high mean, unit regression coefficients (bi=1) and least deviation from regression (S^2 di=0).

Several works have reported the analysis of G×E interaction and genotype adaptation in rice.

Nassir and Ariyo (2011) studied twelve rice varieties which were cultivated in inland hydromorphic lowland over a four year-season period in tropical rainforest ecology to the genotype x environment (G x E) interaction and yield stability and to determine the agronomic and environmental factors responsible for the interaction. Data on yield and agronomic characters and environmental variables were analyzed using the Additive Main Effect and Multiplicative Interaction (AMMI), Genotype and Genotype x Environment Interaction (GGE) and the yield stability using the modified rank-sum statistic (YSi). AMMI analysis revealed environmental differences as accounting for 47.6% of the total variation. The genotype and G×E interaction accounted for 28.5 and 24%, respectively. The first and second interaction axes captured 57 and 30% of the total variation due to G×E interaction. The analysis identified 'TOX 3107' as having a combination of stable and average yield. The GGE captured 85.8%of the total G×E. 'TOX 3226-53-2-2-2' and 'ITA 230' were high yielding but adjudged unstable by AMMI. These two varieties along with 'WITA 1' and 'TOX 3180-32-2-1-3-5' were identified with good inland swamp environment, which is essentially moisture based. The two varieties ('TOX 3226-53-2-2-2' and 'ITA 230'), which were equally considered unstable for yield by the stability variance, sigma $^2{}_i$, were selected by YSi in addition to 'TOX 3107', 'WITA 1', 'IR 8' and 'M 55'. The statistic may positively complement AMMI and GGE in selecting varieties suited to specific locations with peculiar fluctuations in environmental indices. Correlation of

PC scores with environmental and agronomic variables identified total rainfall up to the reproductive stage, variation in tillering ability and plant height as the most important factors underlying the G×E interaction.

Additional information from the models can be positively utilized in varietal development for different ecologies.

Krishnamurthy *et al.* (2016) reported that breeding for salt tolerant varieties is the cost-effective way of addressing this problem. The development and dissemination of these high yielding and salinity tolerant varieties to different agro-ecological zones of the country involves conducting multi-location trials. In the current study, one such trial was conducted using 44 genotypes which were tested across seven salt stress environments during **Kharif,** 2014. The data recorded for days to 50% flowering and grain yield were analyzed through both Genotype and Genotype × Environment interaction (GGE) and Additive Main Effects and Multiplicative Interactions (AMMI) analyses. GGE biplots accounted for 92.5% and 87.5% of the interaction variance, whereas, AMMI biplots could explain 95.7% and 88.5% for days to 50% flowering and grain yield, respectively. The location Aligarh (ENV6) was found the most discriminating for both the characters. Furthermore, it was found the most favorable environment. For days to 50% flowering, two mega environments were identified while for grain yield one mega-environment through GGE biplot and three through AMMI biplot could be demarcated. Both AMMI and GGE have led to similar conclusions with minor differences. However, the GGE biplot was found comparatively more advantageous over AMMI. The genotypes RP 5898-18-5-2-1-1, Bulk 18, NDRK 50043, CSR 11-121, CSR 23, RP 5898-38-7-2-1-1 and CSR 55 were found stable with above average yields across saline and sodic soils. These rice lines could be used for commercial cultivation for improving the productivity in salt affected soils.

Krishnamurthy *et al.* (2017) tested a total of 53 promising salt-tolerant genotypes across 18 salt-affected diverse locations for three years. An attempt was made to identify ideal test locations and mega environments using GGE biplot analysis. The CSSRI sodic environment was the most discriminating location in individual years as well as over the years and could be used to screen out unstable and salt sensitive genotypes. Genotypes CSR36, CSR-2K-219, and CSR-2K-262 were found ideal across years. Overall, Genotypes CSR-2K-219, CSR-2K-262, and CSR-2K-242 were found superior and stable among all genotypes with higher mean yields. Different sets of genotypes emerged as winners in saline soils but not in sodic soils; however, genotype CSR-2K-262 was the only genotype that was best under both saline and alkaline environments over the years. The lack of repeatable associations among locations and repeatable mega-environment groupings indicated the complexity of soil salinity. Hence, a multilocation and multi-year evaluation is indispensable for evaluating the test sites as well as identifying genotypes with consistently specific and wider adaptation to particular agro-climatic zones. The genotypes identified in the present study could be used for commercial cultivation across edaphically challenged areas for sustainable production.

Dewi *et al.* (2019) studied stability parameters of grain yield of rice mutant lines across sixteen different environments and to select lines having wide and/or specific adaptation to environment. Yield stability of genotypes was estimated by using regression lines proposed by Finlay and Wilkinson. The result of yield stability analysis indicated that five mutant lines were OBS 1901/Psj, OBS 1904/Psj, OBS 1906/Psj, OBS 1907/Psj, and OBS 1908/Psj having wide adaptability to the environment. All rice mutant lines had highest yield compare than parent and check varieties with mean yield ranged from 7.54 to 7.89 t. ha^{-1}. Finally, regarding both mean yield and most of stability characteristics, genotypes OBS 1901/Psj and OBS 1908/Psj were found to be the most stable genotypes.

CHAPTER III

MATERIALS AND METHODS

The present investigation entitled **"**Genetic studies for yield and its contributing components in rice (*Oryza sativa* L.) under salt affected soil**"** was conducted at Genetics & Plant Breeding (GPB) Research Farm and Student Instructional Farm of N. D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya.

Geographically this place is located in between 26.47^0N latitude, 82.12^0E longitude and at an altitude of 113 meters above from mean sea level. This area falls in sub-tropical climatic zone. The climate of district Ayodhya is semi-arid with hot summer and cold winter.

The detail of weather conditions recorded during evaluation period of *Kharif,* 2016 and 2017 (21 May to 2nd December) is presented in Table 3.1.

Table 3.1: Weather condition during the crop season *Kharif* 2016 and 2017

Standard week 2016	**Temperature ^{0}c**		**Average relative humidity (%)**	**Total Rainfall (mm)**	**Sunshine (hrs)**
	Min.	Max.			
21-27 May	24.6	37.6	53.3	02.4	07.9
28-3 June	29.5	38.6	57.0	12.8	07.5
4-10 June	25.5	38.0	60.9	87.7	08.4
11-17 June	27.0	36.6	43.5	04.4	07.1
18-24 June	27.0	34.6	75.2	01.2	05.1
25-1 July	27.3	36.8	69.6	00.0	05.1
2-8 July	25.7	32.2	84.9	168.5	02.8
9-15 July	27.2	31.5	79.7	0.50	03.9
16-22 July	24.9	31.3	86.1	114.8	00.0
23-29 July	26.0	31.5	84.2	27.6	02.8

30-05 Aug.	25.8	32.2	79.5	62.6	02.8
06-12 Aug	25.9	32.7	82.6	21.8	02.5
13-19 Aug.	25.9	32.2	85.4	71.8	02.5
20-26 Aug.	26.3	32.8	78.9	03.2	04.8
27-2 Sept.	26.9	34.9	78.2	15.0	05.9
03-9 Sept.	26.5	34.4	75.6	02.2	03.5
10-16 Sept.	26.0	32.8	84.7	09.2	01.1
17-23 Sept.	25.7	32.8	80.6	00.0	01.5
24-30 Sept.	24.2	30.5	85.4	76.2	01.0
1-7 Oct.	25.7	34.0	76.6	09.8	03.1
08-14 Oct.	21.8	32.7	74.5	25.3	05.1
15-21 Oct.	17.9	32.8	68.1	00.0	05.9
22-28 Oct.	16.3	32.4	64.9	00.0	03.0
29-04 Nov	14.1	31.0	65.4	00.0	04.5
05-11 Nov	12.7	29.7	67.2	00.0	01.5
12-18 Nov.	11.8	29.0	67.4	00.0	01.5
19-25 Nov.	11.1	27.3	67.4	00.0	02.4
26-02 Dec.	12.2	25.8	79.9	00.0	02.0
2017					
30-6May	23.1	39.6	40.2	00.0	08.8
7-13 May	22.7	38.5	62.3	10.6	08.3
14-20 May	25.6	39.3	51.5	00.0	08.9
21-27 May	25.7	40.5	46.1	00.0	08.9
28-03 June	25.8	37.9	56.1	00.0	08.4
04-10 June	27.2	37.8	64.1	07.3	05.8
11-17 June	24.7	37.4	62.9	57.4	07.5
18-24 June	26.8	36.0	67.7	07.2	06.6
25-01 July	28.7	37.2	67.5	00.0	07.3
2-8 July	25.8	30.6	90.8	120.6	00.8
09-15 Aug.	26.1	30.7	85.1	52.6	02.5
16-22 July	26.9	33.7	79.0	151.8	06.2
23-29 July	26.2	32.1	82.6	51.4	03.6
30-05 Aug.	26.9	32.6	85.7	20.6	02.3

06-12 Aug.	26.6	33.2	90.7	87.6	03.3
13-19 Aug.	26.8	31.9	84.4	01.0	03.7
20-26 Aug..	26.3	32.9	84.7	38.6	04.7
27-2 Sept.	25.6	33.0	81.3	100.6	06.2
03-09 Sept.	26.0	34.0	80.1	49.4	03.8
10-16 Sept..	26.7	34.7	78.7	00.0	07.3
17-23 Sept.	25.8	32.7	84.8	88.2	05.2
24-30 Sept.	25.2	33.1	82.4	20.6	05.3
01-07 Oct.	24.8	33.8	79.9	00.0	06.8
08-14 Oct.	23.9	33.0	78.1	00.0	07.0
15-21 Oct.	21.4	33.7	71.7	00.0	07.6
22-28 Oct	16.7	32.7	67.5	00.0	06.5
29-04 Nov.	17.0	29.9	75.2	00.0	05.8
05-11 Nov.	15.3	29.2	73.6	00.0	04.3
12-18 Nov.	13.9	29.9	66.7	00.0	04.5
19-25 Nov.	11.9	26.8	66.0	00.0	05.6
26-02 Dec.	08.1	25.9	63.0	00.0	05.1

EXPERIMENTAL MATERIALS

The technical programme of the present investigation was based on two sets of experiments as follows:

Experiment I:

Forty nine diverse genotypes of rice including two checks IRSSTN 143 (IR 28) and CSR 43 were evaluated in Randomized Complete Block Design with three replications in saline soil at GPB farm and in normal soils at Students Instructional Farm during *Kharif* 2016. Three rows plots of 3m length were used following intra and inter-row spacing of 15 cm and 20 cm, respectively. Recommended cultural practices were followed to raise a good crop. Details of genotypes are given in Table 3.2.

Table: 3.2 Detail of rice genotypes

Sl. No.	Genotypes		Sl. No.	Genotypes	
	Code	Name		Code	Name
1	IRSSTN-101	IR 13T106	**25**	IRSSTN-125	IR11T184
2	IRSSTN-102	IR 89331-19-2-1-2-2-1	**26**	IRSSTN-126	IR11T189
3	IRSSTN-103	IR 89331-36-2-3-3-2-1	**27**	IRSSTN-127	IR 86385-194-2-1-B
4	IRSSTN-104	IR 90362-B-22-1-1-2-B	**28**	IRSSTN-128	IR11T205
5	IRSSTN-105	IR 90384-B-25-2-3-3-3	**29**	IRSSTN-129	IR 11T208
6	IRSSTN-106	IR 90477-36-3-2-B-B	**30**	IRSSTN-130	IR 11T213
7	IRSSTN-107	IR 91669-25-2-2-AJY 3	**31**	IRSSTN-131	IR 86385-84-1-1-B
8	IRSSTN-108	IR 91669-25-2-3-AJY 3	**32**	IRSSTN-132	IR11T230
9	IRSSTN-109	IR 9168-48-1-1-AJY 2	**33**	IRSSTN-133	IR11T232
10	IRSSTN-110	IR 91682-6-2-1-1	**34**	IRSSTN-134	IR12T266
11	IRSSTN-111	IR 91683-27-3-2-AJY 2	**35**	IRSSTN-135	IR12T210
12	IRSSTN-112	IR 91684-20-3-3-3	**36**	IRSSTN-136	IR13T144
13	IRSSTN-113	IR 91716-60-BAY 1-1	**37**	IRSSTN-137	IR13T145
14	IRSSTN-114	IR 91716-60-BAY 1-3	**38**	IRSSTN-138	IR13T147
15	IRSSTN-115	IR 92831-22-BAY 2-1	**39**	IRSSTN-139	IR13T148
16	IRSSTN-116	IR 92860-26-CUM 1-2-CMU 3-AJY B	**40**	IRSSTN-140	A 69-1
17	IRSSTN-117	IR 92860-39-CUM-2-1-CMU 2-AJY B	**41**	IRSSTN-141	CSR 28
18	IRSSTN-118	IR12T193	**42**	IRSSTN-142	CSR-90-IR-2
19	IRSSTN-119	IR13T141	**43**	IRSSTN-143 Check 1	IR 28
20	IRSSTN-120	IR12T127	**44**	IRSSTN-144	IR 45427-2B-2-2B-1-1
21	IRSSTN-121	IR12T195	**45**	IRSSTN-145	IR 55179-3B-11-3
22	IRSSTN-122	IR11T171	**46**	IRSSTN-146	IR 58443-6B-10-3
23	IRSSTN-123	IR12T147	**47**	IRSSTN-147	IRRI 147
24	IRSSTN-124	IR11T183	**48**	IRSSTN-148	IR 66946-3R-178-1-1
			49	Check 2	CSR 43

Experiment II:

A line × tester set of 48 hybrids (F_1s) were derived by crossing 16 lines (female) with three high yielding testers (male) *viz.,* Improved Pusa Basmati 1, CSR 10 and NDR 359 during *Kharif* 2016. The sixteen lines were IRSSTN 101, IRSSTN 105, IRSSTN 107, IRSSTN 116, IRSSTN 117, IRSSTN 120, IRSSTN 124, IRSSTN 129, IRSSTN 135, IRSSTN 136, IRSSTN 139, IRSSTN 142, IRSSTN 143, IRSSTN 144, IRSSTN 152 and IRSSTN 155.

The 48 F_1s along with their parents (16 lines +3 testers) and two check varieties (IR-28 and CSR 43) were evaluated in Randomized Complete Block design with three replications at Genetics and Plant Breeding Farm under saline soil during *Kharif*, 2017. Single row plots of 3m length were used for transplanting single seedling per hill for each genotype (treatment) in each replication following intra and inter-row spacing of 15 cm and 20 cm, respectively. Recommended cultural practices were followed to raise a good crop.

The fertilizers were applied @ 120 kg nitrogen, 60 kg phosphorus and 60 kg potash per hectare through urea, DAP and murate of potash, respectively. The full dose of phosphorus and potash and half dose of nitrogen were applied as basal and rest of nitrogen was applied in two split doses as top dressing at tillering and panicle initiation stage of crop growth.

The pH, EC and ESP of were 8.9, 0.28 dSm^{-1} and 68%, respectively for saline soil.

3.3 Observations recorded

The observations were recorded on five randomly selected competitive plants of a genotype in a plot in each replication for thirteen characters. The mean values of observations recorded on five plants of each plot were used for analysis. The observations for different characters were recorded as follows:

3.3.1 Days to 50 % flowering

The number of days taken from date of sowing to panicle emergence in 50% plants in a row plot was counted as days to 50% flowering.

3.3.2 Plant height (cm)

Plant height of a plant was recorded in centimeters from ground level to the tip of the main panicle excluding awns at maturity.

3.3.3 Flag leaf area (cm^2)

The flag leaf area was calculated by measuring and multiplying the length and highest breadth of flag leaf and further multiplying the value by factor 0.75.

3.3.4 Panicle bearing tillers per plant

The number of panicle bearing tillers was counted in a plant at the time of maturity.

3.3.5 Panicle length (cm)

The length of main panicle was measured in centimeters from the base to the tip of the panicle excluding awns.

3.3.6 Spikelets per panicle

The total numbers of spikelets from the main panicle of five plants were counted and averages were taken.

3.3.7 Grains per panicle

Filled grains were counted from the main panicle of five plants and averages were taken.

3.3.8 Spikelet fertility (%)

Spikelet fertility in per cent was recorded for each randomly selected plant as:

$$\text{Spikelet fertility (\%)} = \frac{\text{Number of filled spikelets}}{\text{Total number of spikelets}} \text{ x } 100$$

3.3.9 1000-grain weight (g)

The weight of 1000-filled grains sampled from five randomly selected plants was weighed in grams.

3.3.10 L:B ratio

This was recorded as the ratio of length of kernel to breadth of kernel computed from ten measured grains.

3.3.11 Biological yield per plant (g)

The total biomass excluding roots of a plant was sun-dried and dry matter was weighed in grams.

3.3.12 Harvest-index (%)

The ratio of grain yield (g) to biological yield (g) of a plant was considered as harvest-index and expressed in percentage. The value was calculated as:

$$\text{Harvest index (\%)} = \frac{\text{Grain yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

3.3.13 Grain yield per plant (g)

The grains of each selected plant were hand threshed and sun-dried. The weight of the grains obtained from a plant was taken on an electronic balance in grams.

3.4 Statistical analyses

The experimental data collected on all the thirteen characters in respect of experiment of the present study were compiled by taking the mean values over five randomly selected plants in each plot in each replication. It was then subjected to various statistical and genetically analysis.

3.4.1 Analysis of variance for randomized complete block design

Analysis of variance for randomized complete block design was carried out following Panse and Sukhatme (1967) as follows:

Source of variation	**d.f.**	**S.S**	**M.S.**	**F ratio**
Replications	(r-1)	SSR	MSR	MSR/MSE
Treatments	(t-1)	SST	MST	MST/MSE
Error	(r-1) (t-1)	SSE	MSE	-
Total	(rt-1)	TSS	-	-

Where,

r = Number of replications

t = Number of treatments

MSR = Mean squares due to replications

MST = Mean squares due to treatments

MSE = Mean squares due to error

d.f. = Degrees of freedom

The standard error and critical difference were calculated as follows:

SE of mean = $\sqrt{2MSE/r}$

Critical difference (CD) = $\sqrt{2MSE/r}$ x 't' value at 5% or 1% level of significance at error degree of freedom.

The analysis of variance was further extended to partition the variance due to treatments (genotypes) in to various components such as parents, crosses, parents *vs.* crosses, females, males and females *vs.* males as outlined below:

Source of variation	**d.f.**	**S.S.**	**M.S.**	**F-ratio**
Replications	(r-1)	SSR	MSR	MSR/MSE
Treatments	(t-1)	SST	MST	MST/MSE
Parents	(p-1)	SSP	MSP	MSP/MSE
Females	(f-1)	FSS	MSF	MSF/MSE
Males	(m-1)	MSS	MSM	MSM/MSE
Females vs Males	1	FSS vs. MSS	MSF vs. MSM	MSF vs. MSM/MSE
Crosses	(F_1-1)	F_1SS	MSF$_1$	MSF$_1$/MSE
Parents vs Crosses	1	SSP vs. F_1SS	MSP vs. MSF$_1$	MSP vs. MSF$_1$/MSE
Error	(r-1) (t-1)	SSE	MSE	-

Where,

r = number of replications
t = number of treatments
p = number of parents
f= number of females
m = number of males
F_1 = number of hybrids
S.S. = Sum of squares
M.S. = Mean sum of squares
d.f. = Degree of freedom

3.4.2 Coefficients of variation

Phenotypic (PCV), genotypic (GCV) and environmental (ECV) coefficients of variation for different characters were estimated by following formulae suggested by Burton and de Vane (1953):

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\text{Phenotypicvariance}}}{\bar{X}} \times 100$

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\text{Genotypic variance}}}{\bar{X}} \times 100$

Environmental coefficient of variation (ECV) = $\frac{\sqrt{\text{Environmental variance}}}{\bar{X}} \times 100$

Where, $\bar{X}$ = Mean of the characters.

3.4.3 Heritability in broad sense

Heritability in broad sense (h^2b) was calculated as suggested by Hanson *et.al.* (1956).

$$h^2b\,(\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

σ^2g = genotypic variance
σ^2p = phenotypic variance

3.4.4 Genetic advance in per cent of mean

The expected genetic advance (Ga) was estimated using formula suggested by Johnson *et al.* (1955).

$$Ga = h^2b \times \sigma p \times K$$

Where,

h^2b = Heritability

σp = Phenotypic standard deviation

K = Standardized selection differential (2.06) a constant at 5% selection intensity.

Genetic advance as per cent of mean (Ga) was worked out as:

$$(\overline{Ga})\ (\%) = \frac{GA}{\overline{X}} \times 100$$

Where,

Ga = Genetic advance $\overline{X}$ = Mean of the character

3.4.5 Estimation of correlations coefficients

The simple correlation coefficient between different characters was estimated according to Searle (1961) as follows:

Correlation coefficient (r) between characters x and y $r_{xy} = \frac{Cov.xy}{\sqrt{(Var.x\ X\ var.y)}}$

Where,

r_{xy}= Correlation coefficient between characters x and y.

Cov.xy = Covariance between characters x and y.

Var.x = Variance for x character.

Var.y = Variance for y character.

The significance of correlation coefficient was tested by comparing at an appropriate level of significance the significant values of (r) at (n-2) degrees of freedom, where ‘n’ is number of genotypes.

3.4.6 Path coefficient analysis

Path coefficient analysis was carried out according to Dewey and Lu (1959). Grain yield per plant was assumed to be dependent variable (effect) which was influenced by the other characters, the independent variables (causes), directly as well as indirectly through other characters. The variation in grain yield per plant unexplained by the traits (causes) was presumed to be contributed by a residual factor (x) which is uncorrelated with other factors. Path-coefficients were estimated by solving the following simultaneous equations indicating the basic relationship between correlation and path coefficient. The equations used are as follows:

$$r_{iy} = P_{iy} + \sum_{j=1}^{13} r_{ij} P_{jy} \text{ for } i = 1,2,\ldots\ldots\ldots 13.$$

$$r_{iy} = \sum_{j=1}^{13} r_{ij} P_{jy} \text{ for}_{ii} = 1$$

The above equations can be written in the form of matrix:

$$[A]_{13\times1} = [B]_{13\times1} \ [C]_{13\times1}$$

Where,

A is column vector of correlations r_{iy},

B is the correlation matrix of r_{ij},and

C is the column vector of direct effects, P_{iy}

Residual factor was calculated as follows:

$$P_{xy} = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_j P_{iy}\, r_{iy}$$

The r_{ij}'s i.e. $r_{1.2}$ to $r_{12.13}$ denote correlations between all possible combinations of independent characters and P_{1y} to P_{13y} denote direct effects of various characters on character y.

r_{iy} = Correlation coefficient between i^th^and y character.

3.4.7 Genetic divergence (D^2) analysis

The genetic divergence among 49 genotypes of rice was worked out using Mahalanobis' D^2 statistic (Rao, 1952). The calculation of D^2-values involves the following steps:

(i) A set of uncorrelated linear combinations (Y's) was obtained by the pivotal condensation of the common dispersion matrix (Rao, 1952) of a set of correlated variables (X's). The common dispersion matrix was arranged with the help of error mean sum of squares and sum of products.

(ii) Using the relationship between Y's and X's, the mean values of different genotypes for different characters (X_1 to X_{11}) were transformed in to the mean values of a set of uncorrelated linear combinations (y_1 to y_{11}).

(iii) The D^2 between i^th^ and j^th^ genotypes for K characters was calculated as:

$$D^2_{ij} = \sum (Y_{it}-Y_{jt})^2$$

Where,

t=1

The K components were calculated separately and added to get D^2_{ij}

(iv) The K components of D^2_{ij} for each combination were ranked in descending order of magnitude.

(v) These ranks were added up for each component over all the combinations of i and j and the rank totals were obtained.

(vi) Testing D^2_{ij} as the generalized statistical distance between it hand j^th^populations, the populations were grouped into number of clusters on the basis of D^2 values.

Any two genotypes belonging to the same cluster had the smallest possible intra-cluster distance. On an average intra-cluster distance was less than the inter-cluster distance (Tocher's method).

(vii) Per cent contribution of each character towards genetic divergence was calculated as below:

$$\text{Percentage contribution of character x} = \frac{\text{N x 100}}{\text{C}}$$

Where,

N= Number of genotype combinations which was ranked first for character x.

C= All possible combinations of genotype.

Group constellation

The D^2 values were arranged in an increasing order of magnitude. The grouping of the strains into different cluster was done by using Tocher's method (Rao, 1952). The two most closely associated groups were chosen and third group was found which had the smaller average D^2 value form the first two. Similarly, the fourth was chosen to have the smallest average D^2 from the first three and so on. The D^2 value did not fit in with the former group and was therefore, taken as another cluster.

Intra and Inter – cluster distance

The intra – cluster D^2 was calculated as the sum of n (n-1)/2 genotypes with in a cluster divided by total number of combinations.

All possible D^2 values between the groups of two cluster were added and then divided by $n_1 \times n_2$ for computing inter-cluster distance.

Where,

$n_1$and n_2 = number of genotype in two clusters.

Cluster mean

The cluster mean for a particular character is the summation of mean values of the strains included in a cluster divided by number of strains in the cluster.

Testing of the significance of D^2 values

The D^2 values obtained for a pair of population were taken as the calculated values of X^2 and are tested against the tabulated value of X^2 for ‘p’ degree of freedom.

Where,

p = number of character considered.

3.4.8. Phenotypic stability analysis

The statistical technique proposed by Eberhart and Russel (1966) was utilized to estimate stability parameters and genotype × environment interactions for different genotypes with respect to different characters.

Stability index: Stability index was calculated by using formula.

$$\textbf{Stability Index} = \boxed{\frac{\text{Normal Condition} - \text{Stress Condition}}{\text{Stress Condition}}}$$

3.4.9. Combining ability analysis

The combining ability analysis was carried out following line×tester mating design outlined by Kempthorne (1957) and further elaborated by Arunachalam (1974). Line× tester analysis was used to estimate general combining ability (gca) and specific combining ability (sca) variances and their effects using the observations taken on F_1 generation of the line×tester sets of crosses. In this mating system, a random sample of ‘l’ lines is taken and each line is mated to each of the ‘t’ testers (Singh and Chaudhary, 1977).

The model underlying this analysis is as follows:

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

Where,

μ = General mean

g_i = gca effect of the i^{th} male (tester), i = 1,2,…m.

g_j = gca effect of j^{th} female (line), j = 1,2,…f.

s_{ij} = sca effect of the i^{th} tester and j^{th} line cross combination

e_{ijk} = Error associated with ijk^{th} observation, k = 1,2,…r.

The individual effects were estimated as follows:

(i) $\mu = \frac{X...}{mfr}$

Where,

X... = total of all hybrid combinations

(ii) $g_i = \frac{X_i..}{fr} - \frac{X...}{mfr}$

Where,

$X_i..$ = total of i^{th} male over all the females and replications.

(iii) $g_j = \frac{X._j.}{mr} - \frac{X...}{mfr}$

Where,

$X._j.$ = total of j^{th} female over all males and replications.

(iv) $s_{ij} = \frac{X_{ij}.}{r} - \frac{X_i..}{fr} - \frac{X._j.}{mr} + \frac{X...}{mfr}$

Where,

$X_{ij.}$ = total of ij^{th} combination over all replications.

Standard errors for combining ability estimates were calculated as given below:

SE (gca for line) = $(Me/rm)^{1/2}$

SE (gca for tester) = $(Me/rf)^{1/2}$

SE (sca effect) = $(Me/r)^{1/2}$

SE (g_i-g_j) line = $(2Me/rm)^{1/2}$

SE (g_i-g_j) tester = $(2Me/rf)^{1/2}$

SE (S_{ij}-S_{kl}) = $(2Me/r)^{1/2}$

Where,

Me = Error MS

Critical differences (CD) were calculated as:

CD = SEd × t at 5% and 1% probability levels at error d.f.

The analysis of variance for combining ability is as follows:

Source of variation	**d.f.**	**S.S.**	**M.S.**	**Expected MS**
Replications	(r-1)	-	-	-
Lines (females)	(l-1)	SS (l)	MS (l)	$\sigma^2 e + r$ (Cov. F.S.-2 Cov. H.S.) + rtCov. H.S.
Testers (males)	(t-1)	SS (t)	MS (t)	$\sigma^2 e + r$ (Cov. F.S.-2 Cov. H.S.) + rlCov. H.S.
Lines × Testers	(l-1) (t-1)	SS (l × t)	MS (l × t)	$\sigma^2 e + r$ (Cov. F.S.-2 Cov. H.S.)
Error	(rlt-1)	SS (e)	MS (e)	$\sigma^2 e$

Where,

r = number of replications

l = number of lines

t = number of testers

$\sigma^2 e$ = variance due to error

Genetic components

$$\text{Cov. Half sib (line)} = \frac{M_f - M_{fm}}{rm}$$

$$\text{Cov. Half sib (tester)} = \frac{M_m - M_{fm}}{rf}$$

$$\text{Cov. Half sib (average)} = \frac{1}{r(2fm - f - m)}\left[\frac{(f-1)M_f + (m-1)M_m}{f + m - 2} - M_{fm}\right]$$

$$\text{Cov. F.S. (average)} = \frac{(M_f - M_e) + (M_m - M_e) + (M_{fm} - M_e)}{3r} +$$

$$\frac{6r\ \text{Cov. H.S. (average)} - r\,(f + m)\ \text{Cov. H.S. (average)}}{3r}$$

Where,

M_f = Mean squares due to lines (females)

M_m = Mean squares due to testers (males)

M_{fm} = Mean squares due to line × tester interactions

M_e = Mean squares due to error

r = number of replications

f = number of lines

m = number of testers

gca variance (σ^2gca) = Cov. H.S. (average) = $\left[\frac{1 + F}{4}\right] \sigma^2 A$

Therefore,

Additive genetic variance (σ^2A) = 2 Cov. H.S. (average), if F = 1 and

(σ^2A) = 4 Cov. H.S. (average), If F = 0

sca variance (σ^2sca) $= \frac{(M_{fm} - M_e)}{r}$

$\sigma^2\text{sca} = \left[\frac{1+F}{2}\right]^2 \sigma^2 D$

Therefore,

Dominance variance (σ^2D) = σ^2sca with F = 1, and

σ^2D = 4σ^2sca, if F = 0

Where,

F = Inbreeding coefficient

Average degree of dominance

It was calculated using formula given by Kempthorne and Curnow (1961).

$$\text{Average degree of dominance} = \sqrt{(\sigma^2 \text{sca})/(2\sigma^2 \text{gca})} \text{ or } \sqrt{(\sigma^2 \text{D})/(\sigma^2 \text{A})}$$

Where, σ^2sca = Estimated variance due to sca.

σ^2gca = Estimated variance due to gca

Predictability ratio

It was suggested by Baker (1978) and was calculated as follows:

$$\text{Predictability ratio} = \frac{2\sigma^2 g}{2\sigma^2 g + \sigma^2 s}$$

Heritability in narrow sense

Heritability in narrow sense (h^2n) was calculated as suggested by Kempthorne (1957).

$$h^2 n\,(\%) = \frac{2\sigma^2 g}{2\sigma^2 g + \sigma^2 s + \sigma^2 e} \text{ x } 100$$

Where,

σ^2g = variance due to gca

σ^2s = variance due to sca

σ^2e = variance due to error

Proportional contribution of lines, testers and their interactions

$$\text{Contribution of lines (\%)} = \frac{\text{S.S. (lines)}}{\text{S.S. (crosses)}} \text{ x } 100$$

$$\text{Contribution of testers (\%)} = \frac{\text{S.S. (testers)}}{\text{S.S. (crosses)}} \text{ x } 100$$

$$\text{Contribution of lines} \times \text{testers} = \frac{\text{S.S. (lines x testers)}}{\text{S.S. (crosses)}} \text{ x } 100$$

3.4.10. Estimation of heterosis

The term heterosis was given by Shull (1914). The heterosis was computed as per cent increase or decrease of the mean values of crosses (F_1) over better parent (Heterobeltiosis) and standard variety (Standard Heterosis).

1. $\text{Heterosis over better parent (Heterobeltiosis)} = \dfrac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$
2. $\text{Heterosis over standard variety (Standard heterosis)} = \dfrac{\overline{F}_1 - \overline{SV}}{\overline{SV}} \times 100$

Where,

$F_1 = \text{Mean of } F_1$

$\overline{BP} = \text{Mean of better - parent}$

$\overline{SV} = \text{Mean of standard variety or check variety}$

The test of significance was applied to determine the significance of heterosis by using the following formula:

$$'t'\ (\text{Heterobeltiosis}) = \frac{\overline{F}_1 - BP}{S.E.}$$

$$'t'\ (\text{Standard heterosis}) = \frac{\overline{F}_1 - \overline{SV}}{S.E.}$$

$$\text{S.E. of heterosis over better parent and standard variety} = \sqrt{2Me/r}$$

Where,

Me = Mean error variance

r = Number of replications.

Thus, C.D. = SE ×‘t’ value at error d.f. at 5 or 1% probability level. Critical difference was used to test the significance of difference mean value of F_1 over better parent and standard variety which signified significance of the respective heterosis.

CHAPTER-IV

EXPERIMENTAL FINDINGS

The results obtained in respect of various aspects of the experiment conducted on the present investigation have been described in this chapter under the following sections.

1. To examine the genetic variability and evaluate the rice genotype for various traits.
2. To compute association at genotypic and phenotypic levels among different characters.
3. To assess the stability of rice genotypes.
4. To study the combining ability variances and their effects.
5. To find out gene action involved in the inheritance of various characters.
6. To estimate heterosis over better-parent and standard varieties, and
7. To identify promising parents and superior hybrids for exploitation in breeding programme.

4.1 Analysis of variance

The results of analysis of variance for randomized complete block design for thirteen characters of 49 rice genotypes under two conditions *i.e.* saline and normal condition have been presented in tables 4.1(a) and 4.1(b), respectively. The mean sum of squares due to treatments was highly significant for all the characters in both conditions under the study.

4.2 Mean performance of genotypes

The mean, general mean and range of 49 rice genotypes including checks IRSSTN 143 (IR 28) and CSR 43 for thirteen characters is presented in Appendix 1(a) and 1(b) for salinity and normal conditions, respectably and results are describe here character wise.

Table 4.1(a): Analysis of variance for randomized block design for 13 characters in rice genotypes under salinity condition

Characters	Sources of variation		
	Replications	Treatments	Error
d.f.	2	48	96
Days to 50% flowering	2.37	73.34**	2.47
Plant height (cm)	17.87	250.21**	7.33
Flag leaf area (cm^2)	2.93	55.92**	1.92
Panicle bearing tillers per plant	0.52	5.93**	2.71
Panicle length (cm)	1.08	12.06**	2.35
Spikelets per panicle	11.74	556.05**	25.28
Grains per panicle	35.91	481.36**	14.65
Spikelet fertility (%)	4.41	63.16**	4.39
1000- grains weight (g)	0.03	9.15**	0.41
L:B ratio	0.002	0.473**	0.002
Biological yield per plant (g)	0.28	181.86**	5.73
Harvest-index (%)	0.65	79.46**	11.54
Grains yield per plant(g)	4.43	28.56**	1.77

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

Table 4.1 (b): Analysis of variance for randomized block design for 13 characters in rice genotypes under normal condition

Characters	Sources of variation		
	Replications	Treatments	Error
d. f.	2	48	96
Days to 50% flowering	10.78	115.59**	4.49
Plant height (cm)	9.99	223.29**	15.89
Flag leaf area (cm^2)	2.02	55.40**	1.63
Panicle bearing tillers per plant	0.25	7.35**	7.78
Panicle length (cm)	1.04	8.48**	1.93
Spikelets per panicle	107.66	1843.22**	71.98
Grains per panicle	107.17	1276.85**	44.86
Spikelet fertility (%)	3.81	56.25**	6.74
1000- grains weight (g)	0.003	8.34**	0.08
L:B ratio	0.002	0.507**	0.005
Biological yield per plant (g)	5.07	185.36**	6.51
Harvest-index (%)	4.70	16.71**	7.12
Grains yield per plant(g)	0.14	37.18**	1.55

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

4.2.1 Days to 50% flowering

The days to 50% flowering among genotypes ranged from 77.67 (IRSSTN-106) to 104.00 days (IRSSTN-115). The general mean was 97.48 ± 2.07 days among all the genotypes. Only one genotype was highly significant over CRS 43 and five genotypes were significant and 20 genotypes were highly significant over IR 28. The best five early flowering lines were IRSSTN-106 (77.67), CSR 43 (83.00), IRSSTN-107 (86.66), IRSSTN-130 (89.66) and IRSSTN-113 (93.00) under salinity condition. The days to 50% flowering among genotypes ranged from 77.00 (IRSSTN-107) to 113.00 days (IRSSTN-131). The general mean was 87.71± 2.26 days among all the genotypes. Only one genotype was significant and four genotypes were highly significant over CSR 43 and fourty seven genotypes were highly significant over IR 28. Top five genotypes having flowering significantly earlier than the both checks were lower were IRSSTN-107 (77.00), IRSSTN-106 (77.67), IRSSTN-130 (77.67), IRSSTN-113 (78.67) and IRSSTN-105 (80.33) in normal condition.

4.2.2 Plant height (cm)

Plant height varied from 70.20 (IRSSTN-116) to 111.53 cm (IRSSTN-138). The grand mean was 88.06± 1.47 cm. One genotype was significant and and 30 genotypes were highly significant over check variety CSR 43, where as, 26 genotypes were highly significant over IR 28. The top five genotypes recorded short plant hieght over both checks were IRSSTN-116 (70.20), IRSSTN-109 (74.25), IRSSTN-102 (75.10), IRSSTN-107 (76.10) and IRSSTN-106 (76.30) under salinity condition.

Under normal condition plant height of genotypes varied from 76.08 (IRSSTN-122) to 114.13cm (IRSSTN-126). The grand mean was 95.86 ±1.57 cm among all the genotypes. Four genotypes were significant and 17 genotypes were highly significant over check variety CSR 43, whereas, three genotypes were significant and six genotypes were highly significant over check variety IR 28. Top five short statured genotypes over both checks were IRSSTN-122 (76.08), IRSSTN-106 (76.30), IRSSTN-124 (76.76), IRSSTN-123 (80.27) and IRSSTN-121 (83.00).

4.2.3 Flag leaf area (cm^2)

Among genotypes, minimum and maximum flag leaf area were recorded as 16.75 cm^2 (IRSSTN-108) and 36.52cm^2 (IRSSTN-104), respectively. The general mean was 24.13 cm^2 among all the genotypes. Ten genotypes recorded highly significance flag leaf area over CSR 43, while, one genotype was significant and eight were highly significant over check variety IR 28. The best five genotypes for flag leaf area were IRSSTN-104 (36.52), IRSSTN-131 (30.77), IRSSTN-125 (29.84), IRSSTN-111 (29.58) and IRSSTN-103 (29.50) over both the checks under salinity condition.

In case of normal soil condition minimum and maximum flag leaf area were recorded in IRSSTN-108 (17.79 cm^2) and IRSSTN-135 (37.77cm^2), respectively. The general mean was 25.16 ±1.28 cm^2. Two genotypes recorded significant and ten highly significant flag leaf area over CSR 43, while, one genotype was significant and seven genotypes were highly significant over check variety IR 28. The top highly significant genotypes having better flag leaf area over both checks were IRSSTN- 135 (37.77), IRSSTN-131 (31.30), IRSSTN-104 (30.75), IRSSTN-111 (30.50) and IRSSTN-125 (30.49).

4.2.4 Panicle bearing tillers per plant

Panicle bearing tillers per plant ranged from 6.49 (IRSSTN-143) to 12.5 (IRSSTN-115) among all genotypes. The general mean was recorded 9.38 ± 1.14. Six genotypes were significant and one genotype was highly significant over CSR43, while 15 entreis were significant and 14 entries were highly significant over check variety IR 28. The best five genotypes were IRSSTN-115 (12.5), IRSSTN-135 (11.87), IRSSTN-119 (11.75), IRSSTN-126 (11.21) and IRSSTN-111(11.20) over both checks in salinity condition

In normal condition it ranged from 6.59 (IRSSTN-142) to 12.81 (IRSSTN-135). The general mean was 10.32±0.63 among all the genotypes. Three genotypes were significant and four genotypes were highly significant over CSR43, while five entreis were significant and six entries were highly significant over check variety IR 28. The top five genotypes showed high number of panicle per plant over both the checks were IRSSTN-135 (12.81), IRSSTN-124 (12.62), IRSSTN-121 (12.37), IRSSTN-111 (12.36) and IRSSTN-132 (12.30).

4.2.5 Panicle length (cm)

The panicle length varied from 17.62 (IRSSTN-137) to 25.68 cm (IRSSTN-107) with general mean of 22.22 ± 1.22 cm among all the genotypes. Seven genotypes were significant and eight genotypes were highly significant over CSR43, while six entreis were significant and nine entries were highly significant over check variety IR 28. Top five genotypes recorded long panicle length were IRSSTN-107 (25.68), IRSSTN-109 (25.64), IRSSTN-103 (25.58), IRSSTN-112 (25.53) and IRSSTN-104 (25.41) under salinity condition.

In normal soil condition panicle length varied from 19.05 (IRSSTN-119) to 26cm (IRSSTN-126). The general mean for panicle length was 23.34 ±0.97 cm among all the genotypes. Eight genotypes were significant and 12 genotypes were highly significant over CSR43, while 8 genotypes were significant and four were highly significant over check variety IR 28. The genotypes IRSSTN-126 (26.00), IRSSTN-146 (25.83), IRSSTN-107 (25.55), IRSSTN-135 (25.46) and IRSSTN-141(25.45) were recommended top five genotypes over both checks.

4.2.6 Spikelets per panicle

In salinity condition, minimum and maximum spikelets per panicle were recorded as 102.09 (IRSSTN-102) and 171.82 (IRSSTN-115), respectively. The general mean was 119.46 ± 2.20 among all the genotypes. One genotype was significant and five genotypes were highly significant over CSR43, while two genotypes were significant and 19 genotypes were highly significant over check variety IR 28. The genotypes IRSSTN-115 (171.82), IRSSTN-119 (147.42), IRSSTN-134 (142.15), IRSSTN-139 (141.08) and IRSSTN-130 (138.08) were significantly superior over both checks.

In case of normal condition minimum and maximum spikelets per panicle were recorded in IRSSTN-103 (89.84) and IRSSTN-126 (194.37), respectively with general mean of 129.97±2.18 spikelets. One genotype was significant and six genotypes were highly significant over CSR43, while four genotypes were significant and 23 genotypes were highly significant over check variety IR 28. Among entries, genotypes IRSSTN-126 (194.37), IRSSTN-108 (190.08), IRSSTN-135 (188.88), IRSSTN-115 (183.66) and IRSSTN-104 (166.24) were at top performing over both checks.

4.2.7 Grains per panicle

Among genotypes, minimum and maximum number of grains per panicle were recorded as 64.81 (IRSSTN-143) and 141.84 (IRSSTN-115), respectively having general mean 94.59 ± 2.35 among all the genotypes. Two genotypes were significant and 12 genotypes were highly significant over CSR43, while 46 genotypes were highly significant over check variety IR 28. Top five genotypes for grains per panicle were IRSSTN-115 (141.84), IRSSTN-119 (119.99), IRSSTN-139 (115.61), IRSSTN-134 (113.60) and IRSSTN-145 (111.34) over both checks in salinity condition.

In case of normal condition, minimum and maximum grains per panicle were recorded in 74.46 (IRSSTN-103) and 159.11 (IRSSTN-108), respectively with general mean of 106.12± 2.31 among all the genotypes. Six genotypes were significant and 30 genotypes were highly significant over CSR43, while six genotypes were significant and 25 genotypes were highly significant over check variety IR 28. The top five best performing genotypes were IRSSTN-108(159.11), IRSSTN-126 (158.36), IRSSTN-115 (156.06), IRSSTN-135 (144.01) and IRSSTN-104 (131.92) over both the checks..

4.2.8 Spikelet fertility (%)

Spikelet fertility varied from 59.27 (IRSSTN-143) to 85.78% (IRSSTN-113). The grand mean was 79.14±1.88%. Four genotypes were significant and 34 genotypes were highly significant over CSR43, while 48 genotypes were highly significant over check variety IR 28. Top five genotypes for spikelet fertility were IRSSTN-113 (85.78), IRSSTN-148 (83.80), IRSSTN-114 (83.56), IRSSTN-112 (83.40) and IRSSTN-142 (83.34) over both checks under salinity condition.

In normal condition it varied from 60.81 (IRSSTN-130) to 87.53% (IRSSTN-117) and grand mean was 81.75±1.82% among all the genotypes. Six genotypes were significant and 30 genotypes were highly significant over CSR43, while 6 genotypes were significant and 25 were highly significant over check variety IR 28. The top six genotypes were IRSSTN-117 (87.53), IRSSTN-113 (87.37), IRSSTN-146 (86.57), IRSSTN-116 (85.58), IRSSTN-137 (85.54) and IRSSTN-123 (85.54) over both checks. .

4.2.9 1000 grain weight (g)

In salinity condition among 49 genotypes, 1000-grain weight ranged from 18.61 (IRSSTN-131) and 24.75 g (IRSSTN-115), with general mean of 21.97 ± 0.95 g. Five and 42 genotypes were highly significant over CSR43 and IR 28, respectively. Top five genotypes for bolder seed size were IRSSTN-115 (24.75), IRSSTN-138 (24.70), IRSSTN-102 (24.50), IRSSTN-141(24.45) and IRSSTN-104 (24.41) over both the checks.

In normal condition, it varied from 18.77 (IRSSTN-123) to 25.64 g (IRSSTN-146) with general mean 22.78±0.98 g. One genotype was highly significant over CSR43, while one genotype was significant and 45 genotypes were highly significant over check variety IR 28. IRSSTN-146 (25.64) was top performing genotype over both checks, while other top performing genotypes were IRSSTN-101(24.77), IRSSTN-141 (24.70), IRSSTN-148 (24.64) and IRSSTN-113 (24.61). Over check variety IR 28.

4.2.10 L: B ratio

The lowest L: B ratio was recorded in genotypes 2.17(IRSSTN-120) while highest in parent 3.47 (IRSSTN-132). For this character, the general mean was 2.71 ± 0.22 among all the genotypes. Four and 24 genotypes were highly significant over CSR43 and IR 28, respectively. Top five genotypes were IRSSTN-132 (3.47),

IRSSTN-116 (3.28), IRSSTN-114 (3.24), IRSSTN-108 (3.22) and IRSSTN-112 (3.19) over both checks in salinity condition.

The lowest L: B ratio was recorded in genotypes IRSSTN-124 (2.05) while highest in IRSSTN-143 (3.68). For this character, the general mean was 2.81 ± 0.21 in normal condition. Only single genotype IRSSTN-143 (3.68) exhibited highly significant L: B ratio over both checks. The other having higher L: B ratio was CSR 43 (3.43), IRSSTN-111 (3.34), IRSSTN-114 (3.33) and IRSSTN-115 (3.32).

4.2.11 Biological yield per plant

The biological yield per plant ranged from 27.2 (IRSSTN-107) to 59.33g (IRSSTN-135). The grand mean was 38.77 ± 1.55g among all the genotypes. Twelve genotypes were highly significant over CSR43, while one was significant and 26 genotypes were highly significant over check variety IR 28. The top five genotypes were IRSSTN-135 (59.33), IRSSTN-137(52.33), IRSSTN-139 (51.33), IRSSTN-129 (51.33), IRSSTN-131(50.67) and IRSSTN-132 (50.67) over both checks in salinity condition.

In normal condition ranged from 23.73 (IRSSTN-119) to 58.74g (IRSSTN-101) having general mean of 37.15 ± 1.87 g. Three genotypes were highly significant over CSR43, while one genotype was significant and 4 were highly significant over check variety IR 28. IRSSTN-101(58.74), IRSSTN-132 (52.77) and, IRSSTN-136 (50.05) were top five recommended genotypes over both checks..

4.2.12 Harvest-index (%)

Minimum and maximum harvest index was recorded in 22.47% (IRSSTN-101) and 41.78% (IRSSTN-130), respectively with general mean 33.38 ± 1.90% among all the genotypes. Seven genotypes were significant and 25 genotypes were highly significant over IR 28. Genotypes IRSSTN-130 (41.78), IRSSTN-110 (41.54), CSR 43 (41.27), IRSSTN-108 (41.25) and IRSSTN-105 (40.55) were best performing genotypes for harvest index in salinity condition.

Among the fourty nine genotypes, minimum and maximum harvest index was recorded in IRSSTN-145 (31.13%) and CSR 43 (42.53%), respectively. The general mean was 37.68±1.81% among all the genotypes. One genotype was significant and one was highly significant over check IR 28. Top five recommended genotypes were CSR 43(42.53), IRSSTN-136 (42.03), IRSSTN-141 (41.08), IRSSTN-132 (40.44) and IRSSTN-115 (40.40) in normal condition.

4.2.13 Grain yield per plant

The grain yield per plant varied from 7.92 (IRSSTN-143) to 20.48 g (IRSSTN-135) with general mean of 12.88 ± 0.99g among all the genotypes. One genotype was significant and two genotypes were highly significant over CSR 43, while, four genotypes were significant and 35 genotypes were highly significant over IR 28. The top five high yielding genotypes were IRSSTN-135 (20.48), IRSSTN-115 (18.56), IRSSTN-131 (17.80), IRSSTN-128 (17.29) and IRSSTN-125 (17.18) in salinity condition.

In case of normal condition grain yield ranged from 8.55 (IRSSTN-119) to 23.46 g (IRSSTN-101). The general mean for grain yield per plant was 14.07 ± 0.95 g among all the genotypes. Two genotypes were significant and one genotype was highly significant over CSR43, while 2 genotypes were significant and 26 were highly significant over check variety IR 28. The IRSSTN-101 (23.46), IRSSTN-132 (21.32), IRSSTN-136 (21.03), CSR 43 (18.93) and IRSSTN-137 (18.25) were top five genotypes over checks. Four genotypes were significant and 34 genotypes were highly significant over CSR43, while 48 genotypes were highly significant over check variety IR 28.

4.3 Coefficients of variation

The phenotypic (PCV) and genotypic (GCV) coefficients of variation for the thirteen characters under study have been presented in table 4.2 (a) and 4.2 (b) under salinity and normal conditions, respectably. In general, the magnitude of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits.

Under salinity condition, the high estimates of phenotypic and genotypic coefficient of variation (> 20%) were estimated for grains yield per plant (g) but high PCV and moderate GCV for biological yield per plant (g) and panicle bearing tillers per plant. The moderate estimates (10-20%) of PCV and GCV were recorded for plant height, spikelets per panicle, grains per panicle, L:B ratio, harvest-index and flag leaf area, while moderate PCV and low GCV was recorded for panicle length. Days to 50% flowering, spikelet fertility (%) and 1000- grains weight (g) showed low estimates (<10%) for both parameters in salinity condition.

Under normal condition, high estimates of phenotypic and genotypic coefficient of variation (>20%) were recorded for biological yield per plant (g) and grain yield per plant. High estimates of PCV and moderate estimate of GCV was recorded for grains per panicle. Moderate PCV and GCV (10 - 20%) were noted for flag leaf area, panicle bearing tillers per plant and L:B ratio. Low estimate (<10%) of PCV and GCV were recorded by days to 50% floweing, plant height, panicle length, spikelet fertility and harvest index.

4.4 Heritability and genetic advance

The estimates of heritability in broad sense (h^2_{bs}) and genetic advance in per cent of mean for thirteen characters have been presented in table 4.2 (a) and 4.2 (b) under salinity and normal conditions, respectably. High estimates of broad sense heritability (>75%) were recorded for all traits under study except panicle bearing tillers per plant and harvest index. Harvest index (66.25%) showed moderate heritability whereas, panicle beraing tillers per plant (28.43%) having low heritability under salinity condition.

High estimates of broad sense heritability (>75%) under normal condition were recorded for the characters like days to 50% flowering (89.18), plant height (81.30), flag leaf area (91.65), spikelets per panicle (89.13), grains per panicle (90.15), 1000 grain weight (96.94), L:B ratio (96.67), biological yield per plant (90.16) and grain yiled per plant (88.42). Moderate heritability (50-75%) was recorded for spikelet fertility (70.98), panicle length (53.15) and panicle bearing tillers per plant (50.91). Low estimate of heritability (<50%) was found for the character harvest index (30.99) under normal soil condition.

None of the characters was found having very high (>50%) estimates of genetic advance in per cent of mean in salinity condition. Plant height (20.16), flag leaf area (34.43), spikelets per panicle (21.45), grains per panicle (25.97), L:B ratio (29.99), biological yield per plant (38.86), harvest-index (23.90) and grain yield per plant (43.64) showed high estimates of genetic advance in per cent of mean (>20%). The characters viz., panicle bearing tillers per plant (12.15), panicle length (12.69), spikelet fertility (10.41) and 1000 grain weight (16.23) revealed moderate estimates of genetic advance in per cent of mean (>10 to <20%). Days to 50% flowering showed low estimate (9.77) of genetic advance in per cent of mean (>20%).

None of the characters was found to have very high (>50%) genetic advance in per cent of mean under normal condition. Flag leaf area, spikelets per panicle, grains per panicle, biological yield per plant and grains yield per plant exhibited high genetic advance in per cent of mean (>20 - 50%). Moderate (>10-20%) genetic advance in per cent of mean were observed for days to 50% flowering, plant height, panicle bearing tillers per plant and 1000-grains weight, while, panicle length, spikelet fertility and harvest-index (%) recorded low genetic advance (<10%) under normal condition.

Under salinity condition high estimates of broad sense heritability coupled with high genetic advance in per cent of mean were recorded for plant height, flag leaf area, spikelets per panicle, grains per panicle, L:B ratio, biological yield per plant and grain yield per plant, while, in normal condition high heritability coupled with high genetic advance in per cent of mean were observed for flag leaf area, spikelets per panicle, grains per panicle, L:B ratio, biological yield per plant and grain yield per plant.

4.5 Correlation coefficient

The estimates of simple correlation coefficients (phenotypic) computed between thirteen characters are presented in table 4.3(a) and 4.4 (a) for salinity and normal conditions, respectively.

In salinity condition the grain yield per plant exhibited highly significant and positive correlation with biological yield per plant (0.70) followed by harvest-index (%) (0.58) and panicle bearing tillers per plant (0.42). Harvest index showed significant and positive correlation with panicle bearing tillers per plant (0.27). Biological yield per plant possessed positive and highly significant correlation with grains per panicle (0.41) and positive and significant correlation with spikelets per panicle (0.34) followed by plant height (cm) (0.32). Spikelet fertility (%) showed positive and high significant correlation with grains per panicle (0.48) and positive and significant association with panicle bearing tillers per plant (0.28), while, in case of grains per panicle showed positive and highly significant association with spikelets per panicle (0.90). The estimates of correlation coefficients between remaining six character pairs were found to be non-significant in this analysis.

Under normal soil grain yield per plant exhibited highly significant and positive correlation with biological yield per plant (0.94) followed by 1000-grains weight (g) (0.61), harvest-index (%) (0.52) and plant height (cm) (0.44), while, panicle bearing tillers per plant (0.31), grains per panicle (0.30) and spikelets per panicle (0.28) showed significant and positive association with grain yield per plant. Harvest index showed positive and significant association with biological yield per plant (0.29). Biological yield per plant possessed positive and highly significant correlation with 1000 grain weight (0.65) followed by plant height (cm) (0.46) and significant with grains per panicle (0.30) followed by panicle bearing tillers per plant (0.29) and spikelets per panicle (0.27). The L:B ratio showed positive and significant correlation with plant height (cm) (0.30). Grains per panicle showed positive and highly significant association with spikelets per panicle (0.95), while, positively significant with plant height (0.33) followed by panicle length (cm)

(0.27). Spikelets per panicle exhibited significant and positive association with plant height (0.32) followed by flag leaf area (cm^2) (0.27). Panicle length exhibited positive and significant correlation with plant height (cm) (0.34). The estimates of correlation coefficients between remaining six character pairs were found to be non-significant in this analysis.

4.6 Path coefficient analysis

The direct and indirect effects of 13 characters on grain yield per plant estimated by path coefficient analysis using simple correlations (phenotypic) are given in table 4.5 (a) for salinity condition and in table 4.6 (a) for normal condition.

Under salinity condition the highest positive direct effect on grain yield per plant was exerted by biological yield per plant (0.807) followed by harvest-index (0.694), spikelets per panicle (0.495), spikelet fertility (%) (0.201) and flag leaf area (cm^2) (0.039). While highest negative direct effect on grain yield per plant was exerted by grains per panicle (-0.52) followed by panicle bearing tillers per plant (-0.04), plant height (cm) (-0.04). The direct effects of remaining characters were too low to be considered important.

Spikelets per panicle showed maximum positive indirect effects on grain yield per plant *via* grains per panicle (0.445) followed by *via* biological yield per (g) (0.170) and days to 50% flowering (0.108). Biological yield per (g) showed highest positive indirect effects on grain yield per plant *via* grains per panicle (0.333) followed by spikelets per panicle (0.277), panicle bearing tillers per plant (0.269), plant height (cm) (0.261) and spikelet fertility (%) (0.203). Harvest index (%) exhibited highest positive indirect effects on grain yield per plant *via* panicle bearing tillers per plant (0.186) followed by 1000-grains weight (g) (0.158) and L:B ratio (0.131).

Highest negative indirect effect on grain yield per plant was exerted by grains per panicle *via* spikelets per panicle (-0.464) followed by spikelet fertility (%) (-0.248), biological yield per plant (g) (-0.213), days to 50% flowering (-0.161), panicle bearing tillers per plant (-0.138). Biological yield per plant (g) showed

Table 4.2 (a): Estimates of general mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2b) and genetic advance in per cent of mean for 13 characters in ricegenotypes under salinity condition

Characters		Grand mean	Range		PCV	GCV	h^2	Genetic Advance in % of mean
			Min.	Max.				
1.	**Days to 50% flowering**	**97.48**	77.67	104.00	5.24	4.99	90.52	9.77
2.	**Plant height (cm)**	**88.06**	70.20	111.53	10.67	10.22	91.70	20.16
3.	**Flag leaf area (cm^2)**	**24.13**	16.75	36.52	18.50	17.58	90.35	34.43
4.	**Panicle bearing tillers per plant**	**9.38**	6.49	12.50	20.75	11.06	28.43	12.15
5.	**Panicle length (cm)**	**22.22**	17.62	25.68	10.64	8.10	57.94	12.69
6.	**Spikelets per panicle**	**119.46**	102.09	171.82	11.90	11.13	87.5	21.45
7.	**Grains per panicle**	**94.59**	64.81	141.84	13.79	13.19	91.39	25.97
8.	**Spikelet fertility (%)**	**79.14**	59.27	85.78	6.19	5.59	81.68	10.41
9.	**1000- grains weight (g)**	**21.97**	18.61	24.75	7.99	7.93	98.66	16.23
10.	**L:B ratio**	**2.71**	2.17	3.47	14.71	14.64	98.95	29.99
11.	**Biological yield per plant (g)**	**38.77**	27.20	59.33	20.71	19.76	91.11	38.86
12.	**Harvest-index (%)**	**33.38**	22.47	41.78	17.52	14.26	66.23	23.90
13.	**Grains yield per plant(g)**	**12.88**	7.92	20.48	25.40	23.20	83.39	43.64

Table 4.2 (b): Estimates of general mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2b) and genetic advance in per cent of mean for 13 characters in rice genotypes under normal condition

Characters		Grand mean	Range		PCV	GCV	h^2	Genetic Advance in % of mean
			Min.	Max.				
1.	**Days to 50% flowering**	87.71	77.00	113.00	7.35	6.94	89.18	13.50
2.	**Plant height (cm)**	95.86	76.08	114.13	9.62	8.67	81.30	16.11
3.	**Flag leaf area (cm^2)**	25.16	17.79	37.77	17.58	16.83	91.65	33.19
4.	**Panicle bearing tillers per plant**	10.32	6.59	12.81	18.49	13.20	50.91	19.40
5.	**Panicle length (cm)**	23.34	19.05	26.00	8.69	6.34	53.15	9.52
6.	**Spikelets per panicle**	129.97	89.84	194.37	19.80	18.70	89.13	36.36
7.	**Grains per panicle**	106.12	74.46	159.11	20.11	19.10	90.15	37.35
8.	**Spikelet fertility (%)**	81.75	60.81	87.53	5.90	4.97	70.98	8.62
9.	**1000- grains weight (g)**	22.78	18.77	25.64	7.40	7.28	96.94	14.77
10.	**L:B ratio**	2.81	2.05	3.68	14.78	14.54	96.67	29.44
11.	**Biological yield per plant (g)**	37.15	23.73	58.74	21.89	20.78	90.16	40.65
12.	**Harvest-index (%)**	37.68	31.13	42.53	8.53	4.75	30.99	5.44
13.	**Grains yield per plant(g)**	14.07	8.55	23.46	26.04	24.49	88.42	47.43

highest negative indirect effect on grain yield per plant *via* panicle length (-0.165) followed by 1000-grains weight (g) (-0.115) and harvest index (%) (-0.081). Harvest index (%) exhibited maximum negative indirect effect on grain yield per plant *via* biological yield per plant (g) (-0.081), plant height (cm) (-0.071) and panicle length (-0.022).

The rest of the estimates of indirect effects obtained in path analysis were negligible. The estimate of phenotypic residual factors obtained in path analysis was 0.2106.

Under normal condition highest positive direct effect on grain yield per plant was exerted by biological yield per plant (g) (0.876) followed by harvest index (%) (0.263), spikelets per panicle (0.241). While highest negative direct effect on grain yield per plant was exerted by grains per panicle (-0.229). The direct effects of remaining characters were too low to be considered important.

Under normal condition the spikelets per panicle showed maximum positive indirect effects on grain yield per plant *via* grain yield per plant (0.230). Biological yield per plant (g) *via* 1000-grains weight (g) (0.566) followed by plant height (cm) (0.406), grains per panicle (0.262), panicle bearing tillers per plant (0.258), harvest index (%) (0.252), spikelets per panicle (0.239) and panicle length (0.224).

Highest negative indirect effect on grain yield per plant was exerted by grains per panicle *via* spikelets per panicle (-0.218) followed by plant height (cm) (-0.075), biological yield per plant (g) (-0.068), panicle length (-0.062) and flag leaf area (-0.051).

The indirect effects of remaining characters were too low to be considered important.The estimate of residual factors (0.0570) obtained in path analysis was low.

4.7 Genetic divergence analysis

The study of genetic divergence among 49 genotypes of rice under salt affected and normal soil was performed by employing Mahalanobis' D^2 statistics as described by Rao (1952). Intra cluster distance showed divergence among the genotypes within a cluster while inter cluster distances expressed relative divergence between the clusters. The 49 genotypes were grouped into 8 different non-overlapping clusters as presented in table 4.7(a) and 4.7(b) under salinity and normal conditions, respectively.

The estimates of intra and inter-cluster distances represented by D^2 values have been depicted in table 4.8(a) and 4.8(b), the intra cluster groups means for 13 characters are given in table 4.9 (a) and 4.9 (b) and *per cent* contribution of different characters on total genetic diversity are presented in table 4.10 (a) and (b) under salinity and normal conditions, respectively.

Cluster 6 contained highest numbers of 9 genotypes followed by cluster 2, 3, 4 and 5 with 7 genotypes each, cluster 8 with 5 genotypes, clusters 7 with 4 genotypes and cluster 1 with 3 genotypes under salinity condition. Under normal condition cluster 6 contained highest numbers of 14 genotypes followed by cluster 8 with 10 genotypes, cluster 2 with 8 genotypes, clusters 7 with 5 genotypes and cluster 1 with 4 genotypes

Under salinity condition the intra-cluster distances ranged from 115.23 (cluster 3) to 407.84 (cluster 8). The maximum inter-cluster distance was observed between cluster 3 and 8 (1188.00) followed by cluster 3 and 7 (1077.27), cluster 2 and 7 (947.08), cluster 2 and 8 (935.58), cluster 1 and 8 (855.55) and cluster 3 and 6 (822.32). The minimum estimate for inter-cluster distance was recorded between cluster 2 and 3 (307.65) followed by cluster 3 and 4 (308.86) and cluster 2 and 5 (310.20).

Under normal condition the intra-cluster distances ranged from 85.32 (cluster 2) to 152.60 (cluster 7). The maximum inter-cluster distance was observed between cluster 2 and 8 (672.83) followed by cluster 2 and 6 (622.82), cluster 2 and 7 (523.82), cluster 2 and 5 (498.49) and cluster 2 and 3 (491.83). The minimum estimate for inter-cluster distance was recorded between cluster 1 and 5 (152.78) followed by cluster 6 and 7 (186.86), cluster 5 and 7 (204.04), cluster 1 and 4 (204.69) and cluster 5 and 8 (206.29).

The intra cluster groups means for 13 characters presented in table 4.9 (a) and 4.9 (b) for salinity and normal condition, revealed marked differences between the clusters in respect of cluster means for different characters.

1. Days to 50% flowering

Cluster mean for days to 50% flowering ranged from 85.17 (cluster 6) to 102.17 days (cluster 8). Maximum mean for days to 50% flowering was recorded for cluster 8 (102.00 days) followed by cluster 7 (99.73 days) and cluster 5 (99.09 days), while, minimum mean was recorded for cluster 6 (85.17 days) followed by cluster 2 (95.33 days) and cluster 3 (97.87 days) in salinity condition.

Cluster mean in case of normal condition ranged from 84.11 (cluster 1) to 102.67 days (cluster 2). Maximum mean for days to 50% flowering was recorded for cluster 2 (102.67 days) followed by cluster 7 (96.25 days) and cluster 6 (88.56 days) while, minimum mean was recorded for cluster 1 (84.11 days) followed by cluster 3 and 5 (85.67 days).

2. Plant height

The cluster mean for plant height ranged from 81.63 (cluster 6) to 97.97 cm (cluster 4). Maximum mean for plant height was recorded for cluster 4 (97.97 cm) followed by cluster 8 (96.47 cm) and cluster 3 (90.17) while, minimum mean was recorded for cluster 6 (81.63 cm) followed by cluster 7 (83.03) and cluster 2 (85.55 cm), under salinity condition.

Plant height ranged from 91.86 (cluster 4) to 113.07 cm (cluster 3) in normal condition. Maximum mean for plant height was recorded for cluster 3 (113.07 cm) followed by cluster 6 (102.01 cm) and cluster 7 (98.78 cm) while, minimum mean was recorded for cluster 4 (91.86 cm) followed by cluster 8 (92.03 cm) and cluster 5 (94.54 cm).

Table.4.3 (a): Estimate of phenotypic correlation coefficients between 13 characters of rice genotype under salinity condition

Character	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant (g)
Days to 50% flowering	1.00	0.14	-0.11	0.12	0.00	0.22	0.31	0.26	-0.03	-0.25	0.19	-0.05	0.12
Plant height (cm)		1.00	0.06	0.02	-0.11	0.17	0.15	0.00	-0.24	0.12	0.32*	-0.10	0.16
Flag leaf area (cm^2)			1.00	-0.04	0.11	0.10	0.08	0.00	-0.07	-0.08	-0.08	0.03	0.00
Panicle bearing tillers per plant				1.00	0.00	0.17	0.27	0.28*	0.08	-0.08	0.33*	0.27*	0.42**
Panicle length (cm)					1.00	-0.19	-0.15	0.03	0.23	0.12	-0.20	-0.03	-0.17
Spikelets per panicle						1.00	0.90**	0.07	-0.12	-0.19	0.34*	-0.01	0.31*
Grains per panicle							1.00	0.48**	-0.10	-0.19	0.41**	0.04	0.37**
Spikelet fertility (%)								1.00	0.01	-0.05	0.25	0.08	0.24
1000- grains weight (g)									1.00	-0.12	-0.14	0.23	0.04
L:B ratio										1.00	-0.03	0.19	0.09
Biological yield per plant (g)											1.00	-0.12	0.70**
Harvest-index (%)												1.00	0.58**
Grains yield per plant (g)													1.00

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

Table 4.3 (b): Estimate of genotypic correlation coefficients between 13 characters of rice genotype under salinity condition

Character	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant (g)
Days to 50% flowering	**1.00**	0.16	-0.13	0.32	-0.03	0.23	0.32	0.29	-0.02	-0.26	0.22	-0.06	**0.15**
Plant height (cm)		**1.00**	0.06	-0.13	-0.17	0.22	0.18	0.01	-0.25	0.12	0.35	-0.19	**0.17**
Flag leaf area (cm^2)			**1.00**	-0.18	0.10	0.08	0.07	0.00	-0.07	-0.08	-0.07	0.01	**-0.01**
Panicle bearing tillers per plant				**1.00**	-0.04	0.36	0.57	0.64	0.09	-0.15	0.73	0.25	**0.79**
Panicle length (cm)					**1.00**	-0.32	-0.25	0.04	0.31	0.18	-0.24	-0.08	**-0.28**
Spikelets per panicle						**1.00**	0.92	0.13	-0.12	-0.20	0.40	0.01	**0.35**
Grains per panicle							**1.00**	0.52	-0.09	-0.20	0.46	0.04	**0.41**
Spikelet fertility (%)								**1.00**	0.01	-0.05	0.29	0.10	**0.29**
1000- grains weight (g)									**1.00**	-0.12	-0.16	0.27	**0.03**
L:B ratio										**1.00**	-0.03	0.23	**0.10**
Biological yield per plant (g)											**1.00**	-0.13	**0.76**
Harvest-index (%)												**1.00**	**0.56**
Grains yield per plant(g)													1.00

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

Table.4.4 (a): Estimate of phenotypic correlation coefficients between 13 characters of rice genotype under normal condition

Character	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000- grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant (g)
Days to 50% flowering	1.00	0.03	0.04	0.04	0.00	-0.08	-0.03	0.13	0.02	0.12	0.01	0.03	0.02
Plant height (cm)		1.00	-0.02	-0.16	0.34*	0.32*	0.33*	0.04	0.26	0.30*	0.46**	0.23	0.44**
Flag leaf area (cm^2)			1.00	0.03	0.05	0.27*	0.22	-0.11	0.19	0.12	0.20	0.01	0.16
Panicle bearing tillers per plant				1.00	-0.02	0.02	0.06	0.13	0.17	-0.11	0.29*	0.15	0.31*
Panicle length (cm)					1.00	0.24	0.27*	0.13	0.21	0.20	0.26	0.10	0.25
Spikelets per panicle						1.00	0.95**	-0.11	0.10	0.19	0.27*	0.15	0.28*
Grains per panicle							1.00	0.20	0.11	0.15	0.30*	0.14	0.30*
Spikelet fertility (%)								1.00	0.04	-0.14	0.10	-0.02	0.09
1000- grains weight (g)									1.00	0.13	0.65**	0.19	0.61**
L:B ratio										1.00	0.15	0.19	0.19
Biological yield per plant (g)											1.00	0.29*	0.94**
Harvest-index (%)												1.00	0.52**
Grains yield per plant(g)													1.00

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

Table 4.4(b): Estimate of genotypic correlation coefficients between 13 characters of rice genotype under normal condition

Character	**Days to 50% flowering**	**Plant height (cm)**	**Flag leaf area (cm^2)**	**Panicle bearing tillers per plant (cm)**	**Panicle length (cm)**	**Spikelets per panicle**	**Grains per panicle**	**Spikelet fertility (%)**	**1000-grains weight (g)**	**L:B ratio**	**Biological yield per plant (g)**	**Harvest index (%)**	**Grains yield per plant (g)**
Days to 50% flowering	**1.00**	0.04	0.04	0.07	0.05	-0.09	-0.04	0.17	0.01	0.12	0.01	0.07	**0.03**
Plant height (cm)		**1.00**	-0.03	-0.17	0.52	0.42	0.41	0.00	0.30	0.34	0.52	0.42	**0.53**
Flag leaf area (cm^2)			**1.00**	0.04	0.09	0.28	0.24	-0.09	0.20	0.13	0.21	0.03	**0.18**
Panicle bearing tillers per plant				**1.00**	0.04	0.01	0.07	0.21	0.25	-0.15	0.41	0.39	**0.42**
Panicle length (cm)					**1.00**	0.32	0.36	0.19	0.29	0.27	0.38	0.19	**0.36**
Spikelets per panicle						**1.00**	0.96	-0.07	0.10	0.20	0.30	0.28	**0.31**
Grains per panicle							**1.00**	0.21	0.12	0.16	0.32	0.26	**0.33**
Spikelet fertility (%)								**1.00**	0.07	-0.17	0.12	-0.07	**0.10**
1000- grains weight (g)									**1.00**	0.14	0.70	0.32	**0.65**
L:B ratio										**1.00**	0.16	0.33	**0.20**
Biological yield per plant (g)											**1.00**	0.68	**0.99**
Harvest-index (%)												**1.00**	**0.83**
Grains yield per plant(g)													**1.00**

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

Table 4.5 (a): Estimate of phenotypic direct and indirect (path coefficient) effect of 13 characters on grains yield per plant in rice genotypes under salinity condition

Character	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant (g)
Days to 50% flowering	**0.016**	-0.006	-0.004	-0.005	0.000	0.108	-0.161	0.053	0.000	0.002	0.150	-0.034	**0.119**
Plant height (cm)	0.002	**-0.043**	0.002	-0.001	-0.002	0.086	-0.076	0.000	0.002	-0.001	0.261	-0.071	**0.160**
Flag leaf area (cm^2)	-0.002	-0.003	**0.039**	0.002	0.002	0.049	-0.043	-0.001	0.001	0.001	-0.061	0.021	**0.005**
Panicle bearing tillers per plant	0.002	-0.001	-0.002	**-0.041**	0.000	0.086	-0.138	0.057	-0.001	0.001	0.269	0.186	**0.418**
Panicle length (cm)	0.000	0.005	0.004	0.000	**0.018**	-0.093	0.078	0.006	-0.002	-0.001	-0.165	-0.022	**-0.170**
Spikelets per panicle	0.003	-0.007	0.004	-0.007	-0.003	**0.495**	-0.464	0.014	0.001	0.001	0.277	-0.005	**0.309**
Grains per panicle	0.005	-0.006	0.003	-0.011	-0.003	0.445	**-0.516**	0.097	0.001	0.001	0.333	0.024	**0.374**
Spikelet fertility (%)	0.004	0.000	0.000	-0.011	0.001	0.035	-0.248	**0.201**	0.000	0.000	0.203	0.056	**0.241**
1000- grains weight (g)	0.000	0.010	-0.003	-0.003	0.004	-0.057	0.049	0.001	**-0.008**	0.001	-0.115	0.158	**0.037**
L:B ratio	-0.004	-0.005	-0.003	0.003	0.002	-0.096	0.098	-0.009	0.001	**-0.007**	-0.021	0.131	**0.090**
Biological yield per plant (g)	0.003	-0.014	-0.003	-0.014	-0.004	0.170	-0.213	0.051	0.001	0.000	**0.807**	-0.081	**0.704**
Harvest-index (%)	-0.001	0.004	0.001	-0.011	-0.001	-0.004	-0.018	0.016	-0.002	-0.001	-0.095	**0.694**	**0.584**

Residual effect = 0.2106., Bold figures indicate the direct effects.

Table 4.5 (b): Estimate of genotypic direct and indirect (path coefficient) effect of 13 characters on grains yield per plant in rice genotypes under salinity condition

Character	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000- grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant (g)
Days to 50% flowering	**-0.040**	0.058	-0.029	0.390	0.008	-0.069	0.063	-0.158	-0.001	-0.045	-0.010	-0.017	**0.151**
Plant height (cm)	-0.006	**0.365**	0.013	-0.152	0.041	-0.066	0.035	-0.005	-0.009	0.021	-0.016	-0.056	**0.166**
Flag leaf area (cm^2)	0.005	0.022	**0.223**	-0.214	-0.026	-0.023	0.014	-0.002	-0.002	-0.014	0.003	0.002	**-0.013**
Panicle bearing tillers per plant	-0.013	-0.046	-0.040	**1.203**	0.010	-0.106	0.112	-0.349	0.003	-0.026	-0.033	0.075	**0.792**
Panicle length (cm)	0.001	-0.060	0.023	-0.050	**-0.251**	0.095	-0.049	-0.021	0.010	0.030	0.011	-0.023	**-0.283**
Spikelets per panicle	-0.009	0.080	0.017	0.427	0.079	**-0.299**	0.181	-0.072	-0.004	-0.035	-0.018	0.003	**0.349**
Grains per panicle	-0.013	0.065	0.015	0.689	0.063	-0.276	**0.196**	-0.281	-0.003	-0.034	-0.020	0.013	**0.415**
Spikelet fertility (%)	-0.012	0.004	0.001	0.774	-0.010	-0.040	0.102	**-0.542**	0.000	-0.009	-0.013	0.030	**0.286**
1000- grains weight (g)	0.001	-0.093	-0.016	0.111	-0.078	0.035	-0.018	-0.008	**0.034**	-0.021	0.007	0.080	**0.033**
L:B ratio	0.011	0.045	-0.018	-0.180	-0.044	0.061	-0.039	0.028	-0.004	**0.171**	0.001	0.070	**0.103**
Biological yield per plant (g)	-0.009	0.128	-0.017	0.875	0.060	-0.120	0.090	-0.155	-0.005	-0.004	**-0.045**	-0.038	**0.759**
Harvest-index (%)	0.002	-0.069	0.001	0.302	0.019	-0.003	0.008	-0.055	0.009	0.040	0.006	**0.300**	**0.562**

Residual effect = 0.226., Bold figures indicate the direct effects.

Table 4.6 (a): Estimate of phenotypic direct and indirect (path coefficient) effect of 13 characters on grains yield per plant in rice genotypes under normal condition

Character	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000- grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant (g)
Days to 50% flowering	**0.005**	-0.001	-0.001	0.001	0.000	-0.018	0.007	0.009	0.000	0.003	0.011	0.009	**0.024**
Plant height (cm)	0.000	**-0.036**	0.001	-0.002	0.003	0.078	-0.075	0.003	-0.001	0.007	0.406	0.061	**0.445**
Flag leaf area (cm^2)	0.000	0.001	**-0.032**	0.000	0.000	0.064	-0.051	-0.008	-0.001	0.003	0.174	0.003	**0.156**
Panicle bearing tillers per plant	0.000	0.006	-0.001	**0.015**	0.000	0.005	-0.014	0.009	0.000	-0.003	0.258	0.040	**0.314**
Panicle length (cm)	0.000	-0.012	-0.002	0.000	**0.008**	0.058	-0.062	0.010	-0.001	0.005	0.224	0.026	**0.253**
Spikelets per panicle	0.000	-0.012	-0.008	0.000	0.002	**0.241**	-0.218	-0.008	0.000	0.005	0.239	0.040	**0.280**
Grains per panicle	0.000	-0.012	-0.007	0.001	0.002	0.230	**-0.229**	0.015	0.000	0.004	0.262	0.037	**0.302**
Spikelet fertility (%)	0.001	-0.001	0.003	0.002	0.001	-0.026	-0.045	**0.074**	0.000	-0.004	0.086	-0.005	**0.085**
1000- grains weight (g)	0.000	-0.009	-0.006	0.003	0.002	0.024	-0.025	0.003	**-0.003**	0.003	0.566	0.051	**0.608**
L:B ratio	0.001	-0.011	-0.004	-0.002	0.002	0.046	-0.033	-0.010	0.000	**0.025**	0.127	0.051	**0.191**
Biological yield per plant (g)	0.000	-0.017	-0.006	0.004	0.002	0.066	-0.068	0.007	-0.002	0.004	**0.876**	0.076	**0.942**
Harvest-index (%)	0.000	-0.009	0.000	0.002	0.001	0.036	-0.033	-0.001	-0.001	0.005	0.252	**0.263**	**0.516**

Residual effect = 0.0570, Bold figures indicate the direct effects.

Table 4.6 (b): Estimate of genotypic direct and indirect (path coefficient) effect of 13 characters on grains yield per plant in rice in normal condition

Character	Days to 50% Flowering	Plant Height (cm)	Flag leaf area (cm^2)	Panicle Bearing Tillers/ Plant	Panicle Length (cm)	Spikelets per panicle	Grains per panicle	Spiklet Fertility (%)	1000 Grain Weight (g)	Length/ Breadth Ratio	Biological Yield per Plant (g)	harvest Index %	Grain Yield/ Plant (g)
Days to 50% flowering	**0.007**	0.000	0.000	-0.003	0.000	-0.258	0.111	0.138	0.000	-0.002	0.009	0.024	**0.026**
Plant height (cm)	0.000	**-0.012**	0.000	0.008	-0.002	1.162	-1.166	0.001	0.009	-0.006	0.382	0.155	**0.532**
Flag leaf area (cm^2)	0.000	0.000	**-0.001**	-0.002	0.000	0.774	-0.688	-0.070	0.006	-0.002	0.155	0.012	**0.183**
Panicle bearing tillers per plant	0.001	0.002	0.000	**-0.049**	0.000	0.034	-0.191	0.167	0.008	0.003	0.304	0.143	**0.420**
Panicle length (cm)	0.000	-0.006	0.000	-0.002	**-0.003**	0.885	-1.017	0.151	0.009	-0.005	0.282	0.069	**0.363**
Spikelets per panicle	-0.001	-0.005	0.000	-0.001	-0.001	**2.769**	-2.723	-0.055	0.003	-0.004	0.222	0.104	**0.309**
Grains per panicle	0.000	-0.005	0.000	-0.003	-0.001	2.662	**-2.833**	0.171	0.004	-0.003	0.240	0.097	**0.328**
Spikelet fertility (%)	0.001	0.000	0.000	-0.010	-0.001	-0.188	-0.593	**0.816**	0.002	0.003	0.089	-0.025	**0.096**
1000- grains weight (g)	0.000	-0.003	0.000	-0.012	-0.001	0.277	-0.329	0.056	**0.030**	-0.003	0.514	0.117	**0.646**
L:B ratio	0.001	-0.004	0.000	0.007	-0.001	0.567	-0.452	-0.136	0.004	**-0.019**	0.116	0.121	**0.204**
Biological yield per plant (g)	0.000	-0.006	0.000	-0.020	-0.001	0.832	-0.920	0.098	0.021	-0.003	**0.740**	0.252	**0.994**
Harvest-index (%)	0.000	-0.005	0.000	-0.019	-0.001	0.778	-0.747	-0.055	0.010	-0.006	0.505	**0.369**	**0.830**

Residual effect = 0.0570, Bold figures indicate the direct effects.

3. Flag leaf area

For flag leaf area cluster cluster mean ranged from 23.11 (cluster 5) to 27.42 cm^2 (cluster 6). The maximum mean for flag leaf area were recorded for cluster 6 (27.42 cm^2) followed by cluster 1 (24.90 cm^2) and cluster 8 (24.22 cm^2), while, minimum mean was recorded for cluster 5 (23.11 cm^2) followed by cluster 7 (23.28 cm^2) and cluster 4 (23.55 cm^2) under salinity condition.

In normal condition, it ranged from 18.18 (cluster 3) to 32.36 cm^2 (cluster 7). The maximum mean for flag leaf area were recorded for cluster 7 (32.36 cm^2) followed by cluster 5 (25.84 cm^2) and cluster 8 (25.39 cm^2), while, minimum mean was recorded for cluster 3 (18.18 cm^2) followed by cluster 4 (23.26 cm^2) and cluster 6 (24.24 cm^2).

4. Panicle bearing tillers per plant

Under salinity condition the cluster mean for panicle bearing tillers per plant ranged from 8.61 (cluster 6) to 11.08 (cluster 8). Maximum mean for panicle bearing tillers per plant was recorded for cluster 8 (11.08) followed by cluster 3 (9.79) and cluster 2 (9.73), while, minimum mean was recorded for cluster 6 (8.61) followed by cluster 5 (8.86) and cluster4 (9.09).

Under normal condition, it varied from 9.23 (cluster 2) to 11.60 (cluster 7). Maximum mean for panicle bearing tillers per plant was recorded for cluster 7 (11.60) followed by cluster 8 (11.16) and cluster 3 (10.88), while minimum mean was recorded for cluster 2 (9.23) followed by cluster 1 (9.25) and cluster 4 (9.48).

5. Panicle length

The cluster mean for panicle length ranged from 20.56 (cluster 3) to 23.33 cm (cluster 2). Maximum mean for panicle length was recorded for cluster 3 (23.33 cm) followed by cluster 8 (23.25 cm) and cluster 5 (23.13 cm), while, minimum mean was recorded for cluster 3 (20.56 cm) followed by cluster 1 (21.22 cm) and cluster 7 (22.31 cm) under salinity condition.

In normal condition, it ranged from 22.44 (cluster 2) to 25.65 cm (cluster 3). Maximum mean for panicle length was recorded for cluster 3 (25.65 cm) followed by cluster 7 (25.01 cm) and cluster 6 (23.92 cm), while, minimum mean was recorded for cluster 2 (22.44 cm) followed by cluster 8 (22.48 cm) and cluster 4 (22.71 cm).

6. Spikelets per panicle

Cluster mean for spikelets per panicle ranged from 109.82 (cluster 2) to 141.95 (cluster 8). Maximum mean for spikelets per panicle was recorded for cluster 8 (141.95) followed by cluster 3 (126.68) and cluster 4 (124.26), while, minimum mean was recorded for cluster 2 (109.82) followed by cluster 6 (112.63) and cluster 5 (113.15) under salinity condition.

In case of normal condition, it ranged from 111.18 (cluster 2) to 192.22 (cluster 3). Maximum mean for spikelets per panicle was recorded for cluster 3 (192.22) followed by cluster 7 (169.13) and cluster 1 (132.25), while, minimum mean was recorded for cluster 2 (111.18) followed by cluster 5 (118.26) and cluster 4 (120.87).

7. Grains per panicle

Under salinity condition, cluster mean for grains per panicle ranged from 84.28 (cluster 6) to 114.86 (cluster 8). Maximum mean for grains per panicle was recorded for cluster 8 (114.86) followed by cluster 3 (102.17) and cluster 1 (100.03), while, minimum mean was recorded for cluster 6 (84.28) followed by cluster 2 (87.02) and cluster 5 (91.31) .

In normal condition, it ranged from 85.40 (cluster 2) to 158.73 (cluster 3). Maximum mean for panicle length was recorded for cluster 3 (158.73) followed by cluster 7 (138.99) and cluster 6 (107.44), while, minimum mean was recorded for cluster 2 (85.40) followed by cluster 5 (95.54) and cluster 4 (99.63).

Table 4.7(a). Clustering pattern of 48 rice genotype on the basis on D^2 analysis for 13 characters unders salinity condition

Cluster no.	No of genotype	Genotype
1	3	IRSSTN-102, IRSSTN-106, IRSSTN-107
2	7	IRSSTN-103, IRSSTN-108, IRSSTN-112, IRSSTN-113, IRSSTN-116, IRSSTN-117, IRSSTN-143
3	7	IRSSTN-104, IRSSTN-109, IRSSTN-118, IRSSTN-110, IRSSTN-127, IRSSTN-141, IRSSTN-140
4	7	IRSSTN-105, IRSSTN-111, IRSSTN-114, IRSSTN-122, IRSSTN-144, IRSSTN-146, CSR 43
5	7	IRSSTN-123, IRSSTN-128, IRSSTN-130, IRSSTN-131, IRSSTN-132, IRSSTN-137, IRSSTN-139
6	9	IRSSTN-101, IRSSTN-115, IRSSTN-120, IRSSTN-121, IRSSTN-133, IRSSTN-134, IRSSTN-136, IRSSTN-138, IRSSTN-145
7	4	IRSSTN-119, IRSSTN-129, IRSSTN-135, IRSSTN-142
8	5	IRSSTN-124, IRSSTN-125, IRSSTN-126, IRSSTN-147, IRSSTN-148

Table 4.7(b). Clustering pattern of 41 rice genotype on the basis on D^2 analysis for 13 characters under normal condition

Cluster no	No of genotype	Genotype
1	4	IRSSTN-106, IRSSTN-110, IRSSTN-128, IRSSTN-134
2	8	IRSSTN-101, IRSSTN-103, IRSSTN-112, IRSSTN-125, IRSSTN-129, IRSSTN-130,IRSSTN-138, IRSSTN-139
3	2	IRSSTN-119, IRSSTN-123
4	3	IRSSTN-116, IRSSTN-122, IRSSTN-124
5	3	IRSSTN-108, IRSSTN-115, IRSSTN-126
6	14	IRSSTN-104, IRSSTN-107, IRSSTN-111, IRSSTN-114, IRSSTN-131, IRSSTN-132, IRSSTN-135, IRSSTN-136, IRSSTN-137, IRSSTN-140, IRSSTN-141, IRSSTN-146, IRSSTN-148, CSR 43
7	5	IRSSTN-118, IRSSTN-127, IRSSTN-133, IRSSTN-142, IRSSTN-143
8	10	IRSSTN-102, IRSSTN-105, IRSSTN-109, IRSSTN-113, IRSSTN-117, IRSSTN-120, IRSSTN-121, IRSSTN-144, IRSSTN-145, IRSSTN-147

Table 4.8 (a): Estimates of average intra and inter-cluster distances for 8 clusters in rice under salinity condition.

Cluster No.	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	**201.27**	819.53	592.03	365.58	777.78	682.50	413.03	855.55
Cluster 2		**164.29**	307.65	378.46	310.20	509.19	947.08	935.58
Cluster 3			**115.23**	308.86	637.43	822.32	1077.27	1188.00
Cluster 4				**236.13**	447.04	526.90	585.96	751.67
Cluster 5					**168.10**	356.44	543.30	449.89
Cluster 6						**291.53**	478.91	642.59
Cluster 7							**128.05**	405.86
Cluster 8								**407.84**

Bold figures represent intra-cluster distance.

Table 4.8 (b): Estimates of average intra and inter-cluster distances for 8 clusters in rice under normal condition

Cluster No.	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	**99.93**	280.50	213.89	204.69	152.78	231.33	253.92	262.72
Cluster 2		**85.32**	491.83	344.29	498.49	622.82	523.82	672.83
Cluster 3			**59.52**	357.25	302.86	266.52	308.57	388.16
Cluster 4				**112.86**	325.00	449.78	461.55	243.00
Cluster 5					**108.54**	180.41	204.04	206.29
Cluster 6						**80.96**	186.86	249.92
Cluster 7							**152.60**	330.60
Cluster 8								**121.52**

Bold figures represent intra-cluster distance.

8. Spikelet fertility (%)

Cluster mean for spikelet fertility (%) ranged from 74.22 (cluster 4) to 80.91% (cluster 1). Maximum mean for spikelet fertility was recorded for cluster 1 (80.91%) followed by cluster 3 (80.73%) and cluster 5 (80.69%), while, minimum mean was recorded for cluster 4 (74.22%) followed by cluster 6 (74.94%) and cluster 7 (78.82%) under salinity condition.

Cluster mean for spikelet fertility (%) ranged from 76.82 (cluster 2) to 83.18 % (cluster 6). Maximum mean for spikelet fertility was recorded for cluster 6 (83.18%) followed by cluster 3 (82.73%) and cluster 4 (82.60%), while, minimum mean was recorded for cluster 2 (76.82%) followed by cluster 1 (78.92%) and cluster 5 (81.04%) under normal condition.

9. 1000-Grain weight (g)

Cluster mean under salinity condition for 1000-grain weight ranged from 19.39 (cluster 3) to 24.73g (cluster 8). Maximum mean for 1000-grain weight was recorded for cluster 8 (24.73g) followed by cluster 7 (23.85 g) and cluster 6 (23.26 g), while, minimum mean was recorded for cluster 3 (19.39 g) followed by cluster 4 (20.78 g) and cluster 1 (20.93 g).

In normal condition cluster mean for 1000-grain weight ranged from 19.42 (cluster 2) to 24.01 g (cluster 7). Maximum mean for 1000-grain weight was recorded for cluster 7 (24.01 g) followed by cluster 5 (23.82 g) and cluster 8 (23.24 g), while, minimum mean was recorded for cluster 2 (19.42 g) followed by cluster 4 (20.43 g) and cluster 1 (21.89 g).

10. Length/breadth ratio

Cluster mean for length/breadth ratio ranged from 2.27 (cluster 7) to 3.23 (cluster 2). The maximum mean for length/breadth ratio was recorded for cluster 2 (3.23) followed by cluster 5 (306) and cluster 3 (3.02), while, minimum mean was recorded for cluster 7 (2.27) followed by cluster 1 (2.29) and cluster 8 (2.71) under salinity condition.

While in normal condition varied from 2.30 (cluster 8) to 3.68 (cluster 2). The maximum mean for length/breadth ratio was recorded for cluster 2 (3.68) followed by cluster 7 (3.16) and cluster 1 (3.12) while, minimum mean was recorded for cluster 8 (2.30) followed by cluster 4 (2.53) and cluster 3 (301).

11. Biological yield per plant (g)

Cluster mean for biological yield per plant ranged from 30.97 (cluster 6) to 47.89g (cluster 3). The maximum mean for biological yield per plant was recorded for cluster 3 (47.89 g) followed by cluster 8 (45.50 g) and cluster 1 (40.81 g), while, minimum mean was recorded for cluster 6 (30.97 g) followed by cluster 5 (35.26 g) and cluster 2 (36.67 g) under salinity condition.

Cluster mean ranged from 27.45 (cluster 2) to 48.89 g (cluster 6). The maximum mean for biological yield per plant was recorded for cluster 6 (48.89 g) followed by cluster 2 (42.90 g) and cluster 7 (41.65 g), while, minimum mean was recorded for cluster 2 (27.45 g) followed by cluster 4 (28.21 g) and cluster 1 (28.21 g) under normal condition.

12. Harvest index (%)

Under salinity condition, cluster mean for harvest index ranged from 30.83 (cluster 4) to 36.38% (cluster 5). The maximum mean for harvest index was recorded for cluster 5 (36.38%) followed by cluster 8 (36.31%) and cluster 3 (35.33%), while, minimum mean was recorded for cluster 4 (30.83%) followed by cluster 1 (31.63%) and cluster 2 (32.24%).

In case of normal condition, cluster mean ranged from 36.13 (cluster 1) to 40.64% (cluster 6). The maximum mean for harvest index was recorded for cluster 6 (40.64%) followed by cluster 3 (38.82%) and cluster 7 (38.50%), while, minimum mean was recorded for cluster 1 (36.13%) followed by cluster 2 (36.63%) and cluster 4 (36.78%).

13. Grain yield per plant (g)

Cluster mean for grain yield per plant ranged from 10.77 (cluster 6) to 16.80g (cluster 3). The maximum mean for grain yield per plant was recorded for cluster 3 (16.80) followed by cluster 8 (16.59) and cluster 1 (12.88), while, minimum mean was recorded for cluster 6 (10.77) followed by cluster 2 (11.61) and cluster 4 (11.63) under salinity condition.

Cluster mean ranged from 10.07 (cluster 2) to 19.83g (cluster 6). The maximum mean for grain yield per plant was recorded for cluster 6 (19.83) followed by cluster 3 (16.64) and cluster 7 (16.07), while, minimum mean was recorded for cluster 2 (10.07) followed by cluster 4 (10.37) and cluster 2 (10.07).

4.8 Per cent contribution of defined character on total genetic variability

Per cent contribution of different characters towards total genetic diversity ranged from 1.00 (grains per panicle,) to 24% (1000 grain weight). Maximum *per cent* contribution was recorded by 1000 grain weight (1000 grain weight) followed by length/breadth ratio (22%), grains yield per plant(g) (12%), panicle bearing tillers per plant (10%), harvest-index (%) (8%), panicle length (cm) (5%), biological yield per plant (4%), days to 50% flowering, plant height (cm), flag leaf area (cm^2) spikelets per panicle, (3%), spikelet fertileity (%) (2%) and grains per panicle (1%) under salinity condition.

In normal condition contribution of different character towards total genetic diversity ranged from 2.00 plant height (cm) and grains per panicle (g) to 15% Grains yield per plant (g). Maximum per cent contribution was recorded by Grains yield per plant(g) (15%) followed by panicle bearing tillers per plant (12%), 1000-

grains weight (g) (11%), L:B ratio (10%), flag leaf area (cm^2) (10%), harvest-index (%) (9%), spikelets per panicle (8%), biological yield per plant (g) days to 50% flowering (6%), spikelet fertility (%) (5%), panicle length (cm) (4%), plant height (cm) and grains per panicle (2%).

4.9 Stability index analysis

The stability index analysis for grain yield per plant is presented in table 4.11. Among germplasm the genotypes IRSSTN-139 (-0.43), IRSSTN-123 (-0.40), IRSSTN-119 (-0.40), IRSSTN-130 (-0.29), IRSSTN-122I (-0.27), IRSSTN-118 (-0.18), RSSTN-114 (-0.16), IRSSTN-121 (-0.11), IRSSTN-116 (-0.11), IRSSTN-128 (-0.10), IRSSTN-131 (-0.09), IRSSTN-124 (-0.07), IRSSTN-117 (-0.07), IRSSTN-145 (-0.06), IRSSTN-133 (-0.06), IRSSTN-115 (-0.06)and IRSSTN-129 (-0.03) showed good performance for grain yield per plant under salinity condition. Genotypes IRSSTN-112 (0.00) showed good performance in both conditions and other genotypes IRSSTN-104 (0.95), IRSSTN-107 (0.88), IRSSTN-132 (0.79), IRSSTN-111 (0.70), IRSSTN-140 (0.62), IRSSTN-147 (0.59), IRSSTN-134 (0.56), IRSSTN-126 (0.43), IRSSTN-136 (0.38), IRSSTN-148 (0.33), IRSSTN-120 (0.30), IRSSTN-146 (0.30), IRSSTN-106 (0.28), IRSSTN-143 (0.27), IRSSTN-144 (0.25), IRSSTN-113 (0.23), CSR 43 (0.23), IRSSTN-101 (0.20), IRSSTN-105 (0.19), IRSSTN-108 (0.19), IRSSTN-109 (0.19), IRSSTN-141 (0.19), IRSSTN-142 (0.16), IRSSTN-135 (0.15), IRSSTN-102 (0.11), IRSSTN-137 (0.10), IRSSTN-127 (0.08), IRSSTN-103 (0.04), IRSSTN-125 (0.03) and IRSSTN-138 (0.01) showed good performance only in normal condition.

Table 4.9 (a): Cluster means for 13 characters of rice (*Oryza sativa* L.) under salinity condition

Clusters	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Yield/ Plant (g)
Cluster 1	98.85	89.60	24.90	9.46	21.22	123.75	100.03	80.91	20.93	2.29	40.81	31.63	12.88
Cluster 2	95.33	85.55	23.59	9.73	23.33	109.82	87.02	79.34	21.15	3.23	36.67	32.24	11.61
Cluster 3	97.87	90.14	23.96	9.79	20.56	126.68	102.17	80.73	19.39	3.02	47.89	35.33	16.80
Cluster 4	98.43	97.97	23.55	9.09	22.35	124.26	92.72	74.22	20.78	2.79	38.11	30.83	11.63
Cluster 5	99.09	86.48	23.11	8.86	23.13	113.15	91.31	80.69	23.15	3.06	35.26	36.38	12.71
Cluster 6	85.17	81.63	27.42	8.61	22.78	112.63	84.28	74.94	23.26	2.78	30.97	34.34	10.77
Cluster 7	99.73	83.03	23.28	9.39	22.31	117.40	92.56	78.82	23.85	2.27	37.98	32.81	12.47
Cluster 8	102.17	96.47	24.22	11.08	23.25	141.95	114.86	80.61	24.73	2.71	45.50	36.31	16.59

Table 4.9 (b): Cluster means for 13 characters of rice (*Oryza sativa* L.) under normal condition

Clusters	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grain Yield/ Plant (g)
Cluster 1	84.11	95.92	24.81	9.25	23.69	132.25	103.91	78.92	21.89	3.12	31.98	36.13	11.59
Cluster 2	102.67	96.37	27.17	9.23	22.44	111.18	85.40	76.82	19.42	3.68	27.45	36.63	10.07
Cluster 3	85.67	113.07	18.18	10.88	25.65	192.22	158.73	82.73	22.10	3.01	42.90	38.82	16.64
Cluster 4	87.66	91.86	23.26	9.48	22.71	120.87	99.63	82.60	20.43	2.53	28.21	36.78	10.37
Cluster 5	85.67	94.54	25.84	9.97	23.16	118.26	95.54	81.04	23.82	3.02	36.59	37.28	13.61
Cluster 6	88.56	102.01	24.24	10.73	23.92	129.31	107.44	83.18	24.47	3.07	48.89	40.64	19.83
Cluster 7	96.25	98.78	32.36	11.60	25.01	169.13	138.99	82.43	24.01	3.16	41.65	38.50	16.07
Cluster 8	86.76	92.03	25.39	11.16	22.48	122.30	100.82	82.31	23.24	2.30	38.48	37.27	14.35

Table 4.10 (a): Per cent contribution of defined character on total genetic variability in rice under salinity condition

Sl. No.	Source	Contribution %
1.	Days to 50% flowering	3
2.	Plant height (cm)	3
3.	Flag leaf area (cm^2)	3
4	Panicle bearing tillers per plant	10
5.	Panicle length (cm)	5
6.	Spikelets per panicle	3
7.	Grains per panicle	1
8.	Spikelet fertility (%)	2
9.	1000- grains weight (g)	24
10.	L:B ratio	22
11.	Biological yield per plant (g)	4
12.	Harvest-index (%)	8
13.	Grains yield per plant(g)	12

Table 4.10 (b): Per cent contribution of defined character on total genetic variability in rice under normal condition

Sl. No.	Source	Contribution %
1.	Days to 50% flowering	6
2.	Plant height (cm)	2
3.	Flag leaf area (cm^2)	10
4	Panicle bearing tillers per plant	12
5.	Panicle length (cm)	4
6.	Spikelets per panicle	8
7.	Grains per panicle	2
8.	Spikelet fertility (%)	5
9.	1000- grains weight (g)	11
10.	L:B ratio	10
11.	Biological yield per plant (g)	6
12.	Harvest-index (%)	9
13.	Grains yield per plant(g)	15

Table 4.11: Stability index of germplasm for grain yield per plant

S. No.	**Genotype**	**Salinity**	**Normal**	**Stability**
1	IRSSTN-101	9.43	11.37	0.20
2	IRSSTN-102	10.82	12.00	0.11
3	IRSSTN-103	10.97	11.45	0.04
4	IRSSTN-104	9.28	18.10	0.95
5	IRSSTN-105	13.15	15.66	0.19
6	IRSSTN-106	9.33	11.95	0.28
7	IRSSTN-107	8.25	15.54	0.88
8	IRSSTN-108	13.47	15.98	0.19
9	IRSSTN-109	9.99	11.88	0.19
10	IRSSTN-110	13.77	10.30	-0.25
11	IRSSTN-111	10.08	17.14	0.70
12	IRSSTN-112	10.13	10.12	0.00
13	IRSSTN-113	10.89	13.39	0.23
14	IRSSTN-114	15.02	12.60	-0.16
15	IRSSTN-115	18.56	17.46	-0.06
16	IRSSTN-116	10.40	9.26	-0.11
17	IRSSTN-117	15.35	14.29	-0.07
18	IRSSTN-118	13.75	11.33	-0.18
19	IRSSTN-119	14.25	8.55	-0.40
20	IRSSTN-120	11.04	14.39	0.30
21	IRSSTN-121	17.15	15.20	-0.11
22	IRSSTN-122	12.73	9.33	-0.27
23	IRSSTN-123	15.30	9.17	-0.40
24	IRSSTN-124	12.46	11.55	-0.07
25	IRSSTN-125	17.18	17.76	0.03
26	IRSSTN-126	12.12	17.31	0.43
27	IRSSTN-127	11.39	12.33	0.08
28	IRSSTN-128	17.29	15.56	-0.10
29	IRSSTN-129	12.02	11.60	-0.03

30	IRSSTN-130	17.11	12.08	-0.29
31	IRSSTN-131	17.80	16.13	-0.09
32	IRSSTN-132	11.92	21.32	0.79
33	IRSSTN-133	11.00	10.33	-0.06
34	IRSSTN-134	8.83	13.76	0.56
35	IRSSTN-135	20.48	23.46	0.15
36	IRSSTN-136	15.23	21.03	0.38
37	IRSSTN-137	16.61	18.25	0.10
38	IRSSTN-138	14.63	14.77	0.01
39	IRSSTN-139	16.98	9.75	-0.43
40	IRSSTN-140	9.30	15.12	0.62
41	IRSSTN-141	15.12	18.00	0.19
42	IRSSTN-142	9.89	11.47	0.16
43	IRSSTN-143	7.92	10.07	0.27
44	IRSSTN-144	10.67	13.31	0.25
45	IRSSTN-145	11.83	11.12	-0.06
46	IRSSTN-146	13.70	17.83	0.30
47	IRSSTN-147	8.99	14.31	0.59
48	IRSSTN-148	12.09	16.04	0.33
49	CSR 43	15.43	18.93	0.23

Line × Tester analysis

4.10: Analysis of variance for design of experiment

Analysis of variance was carried out with respect to thirteen characters to test the significance of differences between various treatments (genotypes) *viz.,* sixteen lines, three testers and forty eight F_1s as depicted under salinity condition in table 4.12. The mean sum of squares due to treatments was highly significant for all the thirteen characters which showed presence of sufficient variability in the study materials.

4.11 Mean performance of genotypes

Mean performance of parents and crosses in respect of thirteen characters has been presented in Appendix 2.

4.11.1 Days to 50% flowering

The days to 50% flowering among parents ranged from 77.67 (IRSSTN 107) to 95.33 days (IRSSTN 116). Among crosses, it varied from 84.67 (IRSSTN-107xCSR 10) to 100.33 days (IRSSTN 155×CSR 10). The general mean was 92.89±0.79 days in between the means of the parents (88.12 days) and crosses (94.60 days) uner salinity condition.

4.11.2 Plant height

Plant height of parents varied from 77.75 (IRSSTN-124) to 110.42 cm (IRSSTN-129). Among the crosses, plant height ranged from 76.00 (IRSSTN 155×CSR 10) to 106.49 cm (IRSSTN-135×NDR 359). The grand mean (95.32±1.82 cm) was in between the mean of the parents (94.32 cm) and crosses (95.54 cm) under salinity condition.

4.11.3 Flag leaf area (cm^2)

Among parents, minimum and maximum flag leaf area were recorded in IRSSTN-116 (19.40cm^2) and IRSSTN-117 (29.62cm^2), respectively. It varied from 24.85 (IRSSTN-120 × NDR 359) to 37.01 cm^2 (IRSSTN-142 × Improved Pusa Basmati 1) among the crosses. The general mean (28.27±0.97cm^2) was in between the mean of parents (25.52 cm^2) and crosses (29.40 cm^2) under salinity condition.

4.11.4 Panicle bearing tillers per plant

Panicle bearing tillers per plant ranged from 5.86 (IRSSTN 152) to 13.16 (IRSSTN 135) among parents and from 6.00 (IRSSTN-101×Improved Pusa Basmati 1) to 15.67 (IRSSTN-120×Improved Pusa Basmati 1) among crosses. The general mean (11.21±0.79) was found within the mean of crosses (11.84) and parents (9.92).

Table 4.12: Analysis of variance for randomized block design for 13 characters in L ×T crosses in rice under salinity condition

Characters	Sources of variation		
	Replications	**Treatments**	**Error**
d.f.	**2**	**68**	**136**
Days to 50% flowering	3.42	72.02**	1.87
Plant height (cm)	8.12	153.85**	9.92
Flag leaf area (cm^2)	3.81	37.47**	2.89
Panicle bearing tillers per plant	4.40	18.78**	1.85
Panicle length (cm)	1.50	8.29**	1.49
Spikelets per panicle	55.98	1898.16**	59.12
Grains per panicle	89.37	1269.26**	43.39
Spikelet fertility (%)	2.89	63.53**	6.29
1000- grains weight (g)	0.016	7.19**	0.105
L:B ratio	0.008	0.41**	0.003
Biological yield per plant (g)	23.40	500.37**	9.88
Harvest-index (%)	0.66	23.62**	6.16
Grains yield per plant(g)	6.64	57.24**	1.96

**** Significant at 1% probability levels,**

4.11.5 Panicle length

The panicle length varied from 19.59 (IRSSTN-129) to 23.41 cm (IRSSTN-120) in parents. Among crosses, it ranged from 19.71 (IRSSTN-120×Improved Pusa Basmati 1) to 26.47 cm (IRSSTN-136×CSR 10). The general mean for panicle length (22.27±0.71 cm) was in between the mean of parents (20.75 cm) and crosses (22.65 cm).

4.11.6 Spikelets per panicle

Among parents, minimum and maximum spikelets per panicle were recorded in IRSSTN-116 (93.61) and IRSSTN-139 (148.27), respectively. It varied from 107.54 (IRSSTN-129×Improved Pusa Basmati 1) to 194.33 (IRSSTN-101×NDR 359) among the crosses. The general mean (145.45±4.44) was in between mean of crosses (153.67) and parents (121.83) under salinity condition.

4.11.7 Grains per panicle

Among parents, minimum and maximum grains per panicle were recorded in IRSSTN-124 (71.17) and IRSSTN-139 (117.01), respectively. It varied from 67.75 (IRSSTN-117×Improved Pusa Basmati 1) to 162.48 (IRSSTN-101×NDR 359) among the crosses. The general mean (111.02±3.80) was in between mean of crosses (116.69) and parents (92.53) under salinity condition.

4.11.8 Spikelet fertility (%)

Spikelet fertility of parents varied from 68.78 (IRSSTN-124) to 82.48% (IRSSTN-101), while in crosses it ranged from 60.1 (IRSSTN-117×Improved Pusa Basmati 1) to 84.24% (IRSSTN-101×CSR 10). The grand mean (76.30±1.45%) was in higher than the mean of parents (75.99%) and crosses (75.86 %).

4.11.9 1000 grain weight

Among parents, minimum and maximum 1000-grain weight was recorded in IRSSTN-116 (19.95g) and IRSSTN-144 (24.26 g), respectively. In crosses, it varied from 18.85 (IRSSTN-143×Improved Pusa Basmati 1) to 24.30 g (IRSSTN-105 x NDR 359). The general mean (22.08± 0.19 g) was slightly higher than the mean of parents (21.87 g) and crosses (22.01 g) under salinity condition.

4.11.10 L: B ratio

The lowest L: B ratio was recorded in parent IRSSTN-101 (2.22) while highest in parent IRSSTN-139 (3.32). Among crosses, it ranged from 2.10 (IRSSTN-117×Improved Pusa Basmati 1) to 3.42 (IRSSTN-136×Improved Pusa Basmati 1). For this character, the general mean (2.61±0.03) was greater than the mean of parents (2.96) and crosses (2.50) under salinity condition.

4.11.11 Biological yield per plant

Biological yield per plant ranged from 25.93 (IRSSTN-116) to 58.74 g (IRSSTN-135) in parents and from 26.15 (IRSSTN-135×CSR 10) to 72.00 g

(IRSSTN-116×Improved Pusa Basmati 1) in crosses. The grand mean (43.88±1.82g) was in between the mean of parents (36.14 g) and crosses (46.63 g).

4.11.12 Harvest-index (%)

Among parents, minimum and maximum harvest index was recorded in IRSSTN-116 (31.33 %) and IRSSTN-136 (42.77%), respectively. In crosses, it varied from 31.88 (IRSSTN-135×Improved Pusa Basmati 1) to 42.01 % (IRSSTN 152×CSR 10). The general mean (36.79 ± 1.43%) was in between the mean of parents (37.27%) and crosses (36.59%).

4.11.13 Grain yield per plant

The grain yield per plant varied from 8.12 (IRSSTN-116) to 22.26 g (IRSSTN-135) in parents and from 9.43 (IRSSTN-135×CSR 10) to 24.53 g (IRSSTN-139×NDR 359) in crosses. The general mean for grain yield per plant (15.97±0.81 g) was in between the mean of parents (13.54 g) and crosses (16.89 g) under salinity condition.

4.12 Coefficients of variation

The phenotypic (PCV) and genotypic (GCV) coefficients of variation for the thirteen characters under study have been presented in Table 4.13. In general, the magnitude of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. The high estimates of phenotypic and genotypic coefficient of variation (>20%) were estimated for biological yield per plant but high PCV for panicle bearing tillers per plant and GCV for grain yield per plant, panicle bearing tillers per plant. The moderate estimates (10-20%) of PCV and GCV were recorded for grains per panicle, spikelets per panicle, L:B ratio, flag leaf area, while moderate PCV was recorded for grians yield per plant. Plant height, 1000 grain weight, panicle length, harvest index, spikelet fertility and days to 50% flowering showed low estimates (<10%) for both parameters under salinity condition.

4.13 Heritability and genetic advance

The estimates of heritability in broad sense (h^2_{bs}) and genetic advance in per cent of mean for thirteen characters have been presented in table 4.13. High estimates of broad sense heritability (>75%) was recorded for the characters 1000 grain weight (95.76), biological yield per plant (94.30), days to 50% flowering (92.57), spikelets per panicle (75.19), grain per panicle (90.40), grains yield per plant (90.37), plant height (82.85), flag leaf area (79.91), panicle bearing tillers per plant (75.21) and spikelet fertility (75.19). Panicle length (60.19) which exhibited moderate estimate of heritability (50-75%) while harvest index (48.57) showed low estimates of heritability (<50%) under salinity condition.

The genetic advance in per cent of mean was found to be very high (>50%) for biological yield per plant (58.30) and grain yield per plant (52.72). Panicle bearing tillers per plant (38.09), grains per panicle (35.84), spikelets per panicle (33.64), L:B ratio (28.90) and flat leaf area (22.16) showed high estimates for this parameter (>20-50%). Moderate genetic advance in per cent of mean (10-20%) were noted for 1000 grain weight (14.04), plant height (13.62), panicle length (10.83), days to 50% flowering (10.34) and spikelet fertility (10.23) while low (<10%) for harvest index (9.43).

High heritability coupled with very high and high genetic advance in per cent of mean were observed for biological yield per plant, grain yield per plant, panicle bearing tillers per plant, grains per panicle, spikelets per panicle, L:B ratio and flag leaf area.

4.14 Correlation coefficient

The estimates of simple correlation coefficients (phenotypic) computed between thirteen characters under study are presented in table 4.15. The grain yield per plant exhibited highly significant and positive correlation with biological yield per plant (0.952) and panicle bearing tillers per plant (0.359). Biological yield per plant possessed positive and highly significant correlation with panicle bearing tillerss per plant (0.372). L:B ratio showed nigative and highly significant correlation with grains per panicle (-0.317) followed by 1000- grains weight (-0.303) and spikelets per panicle (-0.287) possessed nigative and significant correlation. Spikelet fertility showed positive and highly significant correlation with grains per panicle (0.350) while in case of grains per panicle showed positive and highly significant association with spikelets per panicle (0.940). Spikelet per panicle showed positive and significant association with flag leaf area (0.289). Panicle length and flag leaf area possessed positive and highly significant association with days to 50% flowering (0.371) and (0.370), respectively. The estimates of correlation coefficients between remaining character pairs were found to be non-significant in this analysis.

4.15 Path coefficient analysis

The direct and indirect effects of 12 characters on grain yield per plant estimated by path coefficient analysis using simple correlations (phenotypic) are given in table 4.17.

The highest positive direct effect on grain yield per plant was exerted by biological yield per plant (1.0113) followed by harvest-index (0.2708), spikelet per panicle (0.1061), spikelet fertility (0.0290), panicle bearing tillers per plant (0.0247), flag leaf area (0.0064) and L:B ratio (0.0055) and highest negative direct effect on grain yield per plant was exerted by grains per panicle (-0.1199) followed by 1000 grain weight (-0.0207), panicle length (-0.0116), plant height (-0.0053) and days to 50% flowering (-0.0032). Maximum positive indirect effects on grain yield per plant exhibited for panicle bearing tillers per plant (0.3766) followed by plant height (cm) (0.1563) days to 50% flowering (0.0942) and panicle length (cm) (0.0898) *via* biological yield per plant. Grains per panicle *via* spikelet per panicle (0.0998). The maximum negative indirect effect on grain yield per plant possessed by harvest-index (%) via biological yield per plant (-0.2509). The rest of the estimates of indirect effects obtained in path analysis were negligible. The estimate of residual factors (0.090) obtained in path analysis was low.

Table 4.13: Estimates of general mean, phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability in broad sense (h^2b) and genetic advance in per cent of mean for 13 characters in L×T crosses of rice under salinity condition

Characters	General mean ±SE	Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
		PCV	GCV		
Days to 50% flowering	92.70±0.79	5.22	5.42	92.57	10.34
Plant height (cm)	95.34±1.81	7.27	7.98	82.85	13.62
Flag leaf area (cm^2)	28.21±0.98	12.04	13.46	79.91	22.16
Panicle bearing tillerss per plant	11.14±0.78	21.32	24.59	75.21	38.09
Panicle length (cm)	22.21±0.70	6.78	8.74	60.19	10.83
Spikelets per panicle	144.79±4.41	17.10	17.91	91.20	33.64
Grains per panicle	110.47±3.78	18.30	19.25	90.40	35.84
Spikelet fertility (%)	76.27±1.44	5.73	6.61	75.19	10.23
1000- grains weight (g)	22.08±0.19	6.96	7.12	95.76	14.04
L:B ratio	2.63±0.03	14.17	14.31	97.99	28.90
Biological yield per plant (g)	43.87±1.80	29.15	30.01	94.30	58.30
Harvest-index (%)	36.74±1.42	6.57	9.42	48.57	9.43
Grains yield per plant(g)	15.95±0.80	15.95	28.32	90.37	52.72

Table 4.14: Estimate of genotypic correlation coefficients between 13 characters in L×T crosses of rice under salinity condition

Characters	**Days to 50% flowering**	**Plant height (cm)**	**Flag leaf area (cm^2)**	**Plant bearing tillers per plant**	**Panicle length (cm)**	**Spikelet per panicle**	**Grains per panicle**	**Spikelet fertility (%)**	**1000-grains weight (g)**	**L:B ratio**	**Biological yield per plant (g)**	**Harvest index (%)**	**Grains yield per plant(g)**
Days to 50% flowering	**1.000**	-0.054	0.415**	0.214	0.466**	0.188	0.154	-0.078	-0.164	-0.299*	0.100	-0.031	**0.097**
Plant height (cm)		**1.000**	0.076	0.025	0.178	-0.057	-0.037	0.054	-0.096	-0.048	0.179	0.064	**0.197**
Flag leaf area (cm^2)			**1.000**	0.129	0.197	0.367**	0.244*	-0.310**	-0.144	-0.075	0.065	0.121	**0.109**
Panicle bearing tillerss per plant				**1.000**	-0.062	0.072	0.014	-0.202	-0.033	-0.229	0.426**	-0.169	**0.429****
Panicle length (cm)					**1.000**	0.196	0.262*	0.252*	0.067	-0.251*	0.127	0.123	**0.126**
Spikelets per panicle						**1.000**	0.952**	0.067	0.095	-0.301**	-0.085	0.090	**-0.081**
Grains per panicle							**1.000**	0.373**	0.132	-0.333**	-0.094	0.114	**-0.092**
Spikelet fertility (%)								**1.000**	0.124	-0.153	-0.053	0.106	**-0.062**
1000- grains weight (g)									**1.000**	-0.313**	-0.051	0.158	**-0.047**
L:B ratio										**1.000**	-0.191	-0.177	**-0.219**
Biological yield per plant (g)											**1.000**	-0.328**	**0.977****
Harvest-index (%)												**1.000**	**-0.123**
Grains yield per plant(g)													**1.000**

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

Table 4.15: Estimate of phenotypic correlation coefficients between 13 characters in L×T crosses of rice under salinity condition

Characters	**Days to 50% flowering**	**Plant height (cm)**	**Flag leaf area (cm^2)**	**Plant bearing tillers per plant**	**Panicle length (cm)**	**Spikelet per panicle**	**Grains per panicle**	**Spikelet fertility (%)**	**1000- grains weight (g)**	**L:B ratio**	**Biological yield per plant (g)**	**Harvest index (%)**	**Grains yield per plant(g)**
Days to 50% flowering	**1.000**	-0.044	0.370**	0.175	0.371**	0.180	0.152	-0.059	-0.155	-0.287*	0.093	-0.007	0.091
Plant height (cm)		**1.000**	0.055	0.006	0.132	-0.040	-0.024	0.036	-0.087	-0.048	0.155	0.063	0.168
Flag leaf area (cm^2)			**1.000**	0.096	0.197	0.289*	0.185	-0.242	-0.122	-0.069	0.062	0.095	0.096
Panicle bearing tillerss per plant				**1.000**	-0.023	0.047	-0.005	-0.145	-0.028	-0.195	0.372**	-0.163	0.359**
Panicle length (cm)					**1.000**	0.153	0.185	0.137	0.055	-0.217	0.089	0.094	0.093
Spikelets per panicle						**1.000**	0.940**	0.034	0.090	-0.287*	-0.066	0.089	-0.052
Grains per panicle							**1.000**	0.350**	0.122	-0.317**	-0.077	0.111	-0.065
Spikelet fertility (%)								**1.000**	0.103	-0.135	-0.051	0.055	-0.056
1000- grains weight (g)									**1.000**	-0.303**	-0.051	0.131	-0.042
L:B ratio										**1.000**	-0.184	-0.121	-0.204
Biological yield per plant (g)											**1.000**	-0.248	0.952**
Harvest-index (%)												**1.000**	0.009
Grains yield per plant(g)													**1.000**

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

4.16 Combining ability analysis

4.16.1 Analysis of variance for line × tester set

The analysis of variance for sixty seven treatments of line × tester set comprising of forty eight crosses and ninteen parents is presented in table 4.18. The analysis of variance revealed that mean sum of squares due to treatments, parents, parents vs crosses, crosses and line × tester were highly significant for all the characters except plant height and harvest index which showed non-significant for parents *vs.* crosses. The variances due to line were non-significant for all the characters except flage leaf area, panicle length, spikelet fertility and biological yield per plant which show singingicatand harvest index showed highly singnificant. In case of tester, most of the characters showed non-significant mean squares except plant height, flag leaf area and L:B ratio which show highly significant.

4. 16.2 Estimates of components of variance

The estimates of general combining ability (gca) and specific combining ability (sca) variances, average degree of dominance, predictability ratio, additive and dominance variances, heritability in narrow sense and genetic advance in per cent of mean have been presented in table 4.19.

Estimates of sca variance were higher than the corresponding estimates of gca variance for all the traits except flag leaf area. The values of average degree of dominance were more than unity (>1) revealing over dominance for most of the characters, namely, panicle bearing tillers per plant (2.66), spikelets per panicle (2.52), days to 50% flowering (2.24), grains per panicle (2.11), 1000 grain weight (1.98), grain yield (1.89), panicle length (1.88), biological yield per plant (1.85) and spikelet fertility (1.25) while for plant length (0.84), L:B ratio (0.81) and flag leaf area (0.51) showed incomplete dominance. The predictability ratio was lesser than one for all the characters studies except 1000 grain weight.

The estimates of heritability in narrow sense (h^2n) have been classified by Robinson (1966) into three categories *viz.,* high (> 30%), medium (10-30%) and low (<10%). High estimates of heritability in narrow sense were recorded for flag leaf area (73.73), L:B ratio (60.08), plant height (55.57) and spikelet fertility (35.34), while, medium estimates were recorded for biological yield per plant (22.26), harvest index (21.59), grain yield per plant (21.11), 1000-grains weight (19.86), grains per panicle (17.63), days to 50% flowering (15.83), panicle length (15.59), spikelets per panicle (13.16) and panicle bearing tillers per plant (11.21).

The high estimates of genetic advance in per cent of mean (>20%) using broad sense heritability were recorded for panicle bearing tillers per plant (53.12%), grains per panicle (42.33%), spikelets per panicle (41.62%), panicle length (33.96%), biological yield per plant (32.30%), grain yield per plant (26.95%) and plant height (23.52%). Moderate genetic advance (10-20%) were estimated for 1000 grain weight (19.34) followed by flag leaf area (17.11%), L:B ratio (16.59%), kernel length (12.41%) and harvest index (10.27%). Low genetic advance (<10%) using narrow sense heritability were recorded for all the character.

4.16.3 Estimates of general combining ability effects

The estimates of general combining ability (gca) effects in respect of 19 parents (16 lines and 3 testers) for the thirteen characters have been set out in table 4.20

4. 16.3.1 Days to 50% flowering

The parents having negative and significant values of general combining ability effects were considered as good general combiners for this character as early flowering is desirable. The desirable negative and highly-significant gca effects were exhibited by the lines, IRSSTN 136 (-3.38), IRSSTN 101 (-3.27), IRSSTN 117 (-2.38), IRSSTN 139 (-1.27), IRSSTN 107 (-2.21) and IRSSTN 116 (-1.93) while IRSSTN 120 (-1.20) showed desirable negative and significant gca effect for days to 50% flowering but IRSSTN 105 (-0.38) exhibited desirable negative and non-significant. The tester, CSR 10 (-0.50) have desirable negative and significant effect but Improved Pusa Basmati 1 (-0.02) showed desirable negative and non-significant gca effect but NDR 359 (0.51) have undesirable positive and significant gca effect.

Table 4.16: Estimate of genotypic direct and indirect effect of 12 characters on grains yield per plant in rice under salinity condition

Characters	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Plant bearing tillers per plant	Panicle length (cm)	Spikelet per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant(g)
Days to 50% flowering	**0.0081**	0.0001	0.0047	0.0048	-0.0143	0.0935	-0.0836	-0.0124	0.0026	-0.0034	0.1045	-0.0071	**0.0974**
Plant height (cm)	-0.0004	**-0.0016**	0.0009	0.0006	-0.0054	-0.0282	0.0198	0.0086	0.0015	-0.0006	0.1875	0.0147	**0.1973**
Flag leaf area (cm^2)	0.0034	-0.0001	**0.0112**	0.0029	-0.0060	0.1823	-0.1323	-0.0490	0.0023	-0.0009	0.0678	0.0280	**0.1094**
Panicle bearing tillerss per plant	0.0017	0.0000	0.0014	**0.0223**	0.0019	0.0357	-0.0076	-0.0319	0.0005	-0.0026	0.4463	-0.0391	**0.4285**
Panicle length (cm)	0.0038	-0.0003	0.0022	-0.0014	**-0.0306**	0.0972	-0.1421	0.0399	-0.0011	-0.0029	0.1323	0.0284	**0.1255**
Spikelets per panicle	0.0015	0.0001	0.0041	0.0016	-0.0060	**0.4970**	-0.5171	0.0107	-0.0015	-0.0034	-0.0886	0.0209	**-0.0808**
Grains per panicle	0.0013	0.0001	0.0027	0.0003	-0.0080	0.4731	**-0.5432**	0.0592	-0.0021	-0.0038	-0.0981	0.0264	**-0.0922**
Spikelet fertility (%)	-0.0006	-0.0001	-0.0035	-0.0045	-0.0077	0.0334	-0.2028	**0.1585**	-0.0020	-0.0018	-0.0552	0.0245	**-0.0618**
1000- grains weight (g)	-0.0013	0.0002	-0.0016	-0.0007	-0.0020	0.0472	-0.0717	0.0196	**-0.0160**	-0.0036	-0.0537	0.0365	**-0.0473**
L:B ratio	-0.0024	0.0001	-0.0008	-0.0051	0.0077	-0.1497	0.1807	-0.0243	0.0050	**0.0114**	-0.2001	-0.0409	**-0.2185**
Biological yield per plant (g)	0.0008	-0.0003	0.0007	0.0095	-0.0039	-0.0421	0.0509	-0.0084	0.0008	-0.0022	**1.0465**	-0.0758	**0.9766**
Harvest-index (%)	-0.0003	-0.0001	0.0014	-0.0038	-0.0038	0.0449	-0.0620	0.0168	-0.0025	-0.0020	-0.3433	**0.2312**	**-0.1234**

Table 4.17: Estimate of phenotypic direct and indirect effect of 12 characters on grain yield per plant in rice under salinity condition

Characters	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Plant bearing tillers per plant	Panicle length (cm)	Spikelet per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant(g)
Days to 50% flowering	**-0.0032**	0.0002	0.0024	0.0043	-0.0062	0.0191	-0.0182	-0.0017	0.0032	-0.0016	0.0942	-0.0018	**0.0907**
Plant height (cm)	0.0001	**-0.0053**	0.0003	0.0001	-0.0022	-0.0042	0.0028	0.0010	0.0018	-0.0003	0.1563	0.0172	**0.1678**
Flag leaf area (cm^2)	-0.0012	-0.0003	**0.0064**	0.0024	-0.0033	0.0306	-0.0222	-0.0070	0.0025	-0.0004	0.0626	0.0257	**0.0958**
Panicle bearing tillerss per plant	-0.0006	0.0000	0.0006	**0.0247**	0.0004	0.0050	0.0006	-0.0042	0.0006	-0.0011	0.3766	-0.0441	**0.3585**
Panicle length (cm)	-0.0012	-0.0007	0.0013	-0.0006	**-0.0166**	0.0162	-0.0221	0.0040	-0.0011	-0.0012	0.0898	0.0254	**0.0931**
Spikelets per panicle	-0.0006	0.0002	0.0018	0.0012	-0.0025	**0.1061**	-0.1127	0.0010	-0.0019	-0.0016	-0.0669	0.0240	**-0.0519**
Grains per panicle	-0.0005	0.0001	0.0012	-0.0001	-0.0031	0.0998	**-0.1199**	0.0102	-0.0025	-0.0017	-0.0779	0.0300	**-0.0645**
Spikelet fertility (%)	0.0002	-0.0002	-0.0015	-0.0036	-0.0023	0.0036	-0.0420	**0.0290**	-0.0021	-0.0007	-0.0510	0.0148	**-0.0559**
1000- grains weight (g)	0.0005	0.0005	-0.0008	-0.0007	-0.0009	0.0095	-0.0146	0.0030	**-0.0207**	-0.0017	-0.0516	0.0355	**-0.0419**
L:B ratio	0.0009	0.0003	-0.0004	-0.0048	0.0036	-0.0304	0.0380	-0.0039	0.0063	**0.0055**	-0.1861	-0.0327	**-0.2038**
Biological yield per plant (g)	-0.0003	-0.0008	0.0004	0.0092	-0.0015	-0.0070	0.0092	-0.0015	0.0011	-0.0010	**1.0113**	-0.0672	**0.9519**
Harvest-index (%)	0.0000	-0.0003	0.0006	-0.0040	-0.0016	0.0094	-0.0133	0.0016	-0.0027	-0.0007	-0.2509	**0.2708**	**0.0090**

4. 16.3.2 Plant height

The negative and highly significant gca effects for plant height were exhibited by IRSSTN-107 (-5.67), IRSSTN 155 (-5.55), IRSSTN-124 (-5.48), IRSSTN-120 (-3.68) and IRSSTN-139 (-2.88) but IRSSTN-101 (-2.31) have negative and significant gca effect. These female lines were good general combiners for dwarf stature. Line IRSSTN 116 (-1.34) showed negative and non-significantgca effect. Among male testers, CSR 10 (-4.85) showed highly significant and negative gca effects, whereas,Improved Pusa Basmati 1 (1.02) had positive gca effects while NDR 359 (3.84) had highly significant and positive effect on plant height which are poor combiner for plant height.

4. 16.3.3 Flag leaf area

The female lines IRSSTN 144 (2.82), IRSSTN 142 (2.70), IRSSTN 117 (2.01), IRSSTN 107 (1.98) and IRSSTN 143 (1.89) exhibited highly significant and positive gca effects and lines IRSSTN 155 (0.73) andIRSSTN 124 (0.57) having non-significant and positive gca effect for flag leaf area. Tester NarendraUsar Dhan-2 (1.54) showed highly significant and positive gca effect for this character. Improved Pusa basmati 1 (2.62) showed highly significant and positive gca effects among the testers, while CSR 10 (-2.04) exhibited highly-significant and negative gca effects but NDR 359 (-0.58) had non-significant and negative effect for flag leaf area.

4. 16.3.4 Panicle bearing tillers per plant

Among the female lines, highly significant and positive gca effects were exhibited by IRSSTN 139 (2.19)and IRSSTN 120 (1.71) while IRSSTN 116 (0.97) showed significant and positive gca effects. These genotypes emerged as good general combiners for panicle bearing tillers per plant while IRSSTN 129 (0.70), IRSSTN (0.49), IRSSTN 143 (0.42) and IRSSTN 144 (0.39) have non-significant and positive effect which emersed as average general combiner for this character. The tester CSR 10 (0.59) exhibited highly-significant and positive gca effects, while the male tester Improved Pusa basmati 1 (-0.47) had significant

Table 4.18: Analysis of variance for 13 characters of line × tester set of crosses and their parents in rice under salinity condition

Characters	**Sources of variation**								
	Replications	**Treatments**	**Parents**	**Parents *vs* Crosses**	**Crosses**	**Lines**	**Testers**	**Lines × testers**	**Error**
d.f.	**2**	**66**	**18**	**1**	**47**	**15**	**2**	**30**	**132**
Days to 50% flowering	2.87	69.40 **	80.78 **	1489.41**	34.83**	46.20	12.26	30.65**	1.85
Plant height (cm)	7.67	158.39**	195.60**	24.58	146.99**	153.43	943.71**	90.66**	9.99
Flag leaf area (cm^2)	4.77	38.18**	29.47**	658.20**	28.33**	30.07*	272.94**	11.14**	2.92
Panicle bearing tillerss per plant	4.36	18.84**	16.26**	205.73**	15.85**	11.64	13.84	18.09**	1.89
Panicle length (cm)	1.11	8.19**	9.85**	76.48**	6.10**	10.26*	0.49	4.39**	1.52
Spikelets per panicle	50.82	1908.38**	816.07**	34292.63**	1637.68**	2217.68	0.16	1456.85**	60.19
Grains per panicle	84.96	1276.32**	750.87**	16336.36**	1157.13**	1702.85	300.37	941.39**	44.58
Spikelet fertility (%)	2.37	65.16**	62.54**	95.76**	65.51**	99.81*	138.77	43.48**	6.39
1000- grains weight (g)	0.03	7.08**	12.90**	1.94**	4.96**	7.58	1.75	3.87**	0.11
L:B ratio	0.01	0.41**	0.39**	7.17**	0.28**	0.27	2.06**	0.16**	0.00
Biological yield per plant (g)	17.08	515.51**	216.38**	3838.22**	559.38**	911.72*	212.97	406.31**	9.64
Harvest-index (%)	0.84	22.88**	32.95**	19.24	19.10**	34.57**	9.33	12.01**	6.23
Grains yield per plant(g)	5.58	58.73**	36.99**	435.41**	59.04**	83.38	42.54	47.97**	1.97

Table 4.19: Components of genetic variance, average degree of dominance, predictability ratio, heritability in narrow sense and genetic advance in per cent of mean for 13 characters in rice under salinity condition

Characters	**gca variance ($\sigma^2 g$)**	**sca variance ($\sigma^2 s$)**	**Average degree of dominance** $\sqrt{c^1 s/2\sigma^1 g}$	**Predictability ratio** $2\sigma^2 g/2\sigma^3 g+\sigma^2 s)$	**$\sigma^2 A$**	**$\sigma^2 D$**	**Heritability ($h^2 n$ %)**	**Genetic Advance (%)**
Days to 50% flowering	0.96	9.60	2.24	0.17	1.92	9.60	15.83	1.14
Plant height (cm)	18.90	26.89	0.84	0.58	37.79	26.89	55.57	9.44
Flag leaf area (cm^2)	5.21	2.74	0.51	0.79	10.43	2.74	73.73	5.71
Panicle bearing tillers per plant	0.38	5.40	2.66	0.12	0.76	5.40	11.21	0.60
Panicle length (cm)	0.14	0.95	1.88	0.22	0.27	0.95	15.59	0.42
Spikelets per panicle	36.80	465.55	2.52	0.14	73.60	465.55	13.16	6.41
Grains per panicle	33.58	298.94	2.11	0.18	67.16	298.94	17.63	7.09
Spikelet fertility (%)	3.96	12.36	1.25	0.39	7.92	12.36	35.34	3.45
1000- grains weight (g)	0.16	1.25	1.98	2.80	0.32	1.25	19.86	0.52
L:B ratio	0.04	0.05	0.81	0.61	0.08	0.05	60.08	0.46
Biological yield per plant (g)	19.39	132.22	1.85	0.23	38.79	132.22	22.26	6.05
Harvest-index (%)	0.55	1.92	1.32	0.36	1.10	1.92	21.59	1.00
Grains yield per plant(g)	2.14	15.33	1.89	0.21	4.28	15.33	21.11	1.98

and negative gca effect but NDR 359 (-0.12) exhibited non-significant and negative gca effect for panicle bearing tillers per plant. NarendraUsar Dhan-2 (0.14) had non significant and positive gca effect for panicle bearing tillers per plant.

4. 16.3.5 Panicle length

Highly significant and positive gca effects were exhibited by IRSSTN 136 (2.08) and IRSSTN 155 (1.48). Genotypes IRSSTN 143 (1.03) and IRSSTN 135 (0.82) having significant and positive gca effect, while, IRSSTN 152 (0.43), IRSSTN 124 (0.30) and IRSSTN 142 (0.27) recorded non significant and positive gca effect for panicle length. The non-significant and positive gca effect were exhibited by CSR 10 (0.03) and Improved Pusabansmati 1 (0.08) among the male testers. NDR 359 (-0.11) showed non-significant and negative gca effect for panicle length.

4. 16.3.6 Spikelets per panicle

The female lines, IRSSTN-120 (30.67), IRSSTN-101 (18.86), IRSSTN-105 (11.18), IRSSTN-135 (10.35), IRSSTN-107 (9.35), IRSSTN-136 (9.22) and IRSSTN-116 (8.56) exhibited highly significant and positive gca effects for spikelets per panicle, while, IRSSTN 152 (0.22) and IRSSTN 124 (0.13) showed non-significant and positive effect. Tester CSR 10 (0.07) showed non-significant and positive gca effects for spikelets per panicle, while, tester Improved pusa basmati 1 (-0.03) and NDR 359 (-0.04) showed non-significant and negative gca effects for spikelets per panicle.

4. 16.3.7 Grains per panicle

The female lines, IRSSTN-101 (25.62), IRSSTN-120 (24.54), IRSSTN-105 (12.02), IRSSTN-136 (6.35) and IRSSTN-135 (6.32) exhibited highly significant and positive gca effects for grains per panicle emersed as good general combiner. IRSSTN-107 (3.52), IRSSTN 152 (2.70) and IRSSTN-124 (1.89) were average general combiner for grains per panicle, while, tester NDR 359 (2.21) was good general combiner as showed significant and positive gca effects for grains per panicle but CSR 10 (0.51) was average general combiner having non-significant and positive gca effect.

4. 16.3.8 Spikelet fertility

The female lines, IRSSTN-101 (6.50), IRSSTN-139 (4.53) and IRSSTN-105 (2.23) were found to be good general combiners for spikelet fertility having highly significant and positive gcaeffect, while, lines IRSSTN-124 (1.37), IRSSTN-120 (0.67) and IRSSTN-136 (0.01) having non-siginificant and positive gcaeffect.Tester NDR 359 (1.41) showed positive and highly-significant gca effects for spikelet fertility, while, CSR 10 (0.47) exhibited non-significant and positive gca effect but Imporved Pusa Basmati 1 (-1.89) had non-significant and negative effect on this character.

4. 16.3.9 1000-grain weight

Among lines, IRSSTN-135 (1.55), IRSSTN-107 (1.31), IRSSTN-117 (1.13), IRSSTN-105(0.79), IRSSTN-101 (0.58) and IRSSTN-129(0.40) were recorded as good general combiner for 1000-grain weight while significant and positive effect for IRSSNT-139 but IRSSTN-142 (0.02) had non-significant and positive effect. Tester NDR 359 (0.15) showed positive and highly-significant gca effects for 1000 grain weight while, CSR 10 (0.06) exhibited non-significant and positive gca effect but Imporved Pusa Basmati 1(-0.21) had non-significant and negative effect on this character.

4. 16.3.10 L:B ratio

Amongthe female lines, IRSSTN-136 (0.23), IRSSTN-142 (0.22), IRSSTN-144 (0.20), IRSSTN-129 (0.15), IRSSTN-143 (0.12), IRSSTN-120 (0.11) and IRSSTN-101 (0.05) emerged with highly significant and positive gca effects, whereas, IRSSTN-124 (0.04) showed significant and positive gca effects. Tester Improved Pusa Basmati 1 (0.24) recorded highly significant and positive gca effects for L: B ratio. CSR 10 (-0.12) and NDR-359 (-0.12) showed highly-significant and negative gca effect for this trait.

4. 16.3.11 Biological yield per plant

The female lines IRSSTN-116 (22.56), IRSSTN-139 (17.86), IRSSTN-136 (6.44), IRSSTN-124 (4.59), IRSSTN-129 (4.28) and IRSSTN-120 (3.70) exhibited highly significant and positive gca effects for biological yield per plant while line IRSSTN-105 (0.52) and IRSSTN-142 (0.37) and testers NDR 359 (2.36) showed significant and positive gca effect. CSR 10(-1.69) recorded highly significant and negative gca effects for biological yield per plant while Improved Pusa Basmati 1 (-0.66) had non-significant and negative gca effect on this character.

4. 16.3.12 Harvest-index

Among female lines, IRSSTN-152 (4.72) and IRSSTN-143 (3.40) exhibited highly-significant and positive effect for harvest index, while, IRSSTN-144 (1.23), IRSSTN-117 (1.04), IRSSTN-155 (0.65) and IRSSTN-120 (0.13) exhibited non-significant and positive gca effects for harvest-index. Testers NDR 359 (0.50) had non-significant and positive gca effect for harvest-index. Rest two testers CSR 10 (-0.17) and Improved Pusa Basmati 1 (-0.33) showed significant and positive gca effect for harvest-index under salinity condition.

4. 16.3.13 Grain yield per plant

Lines IRSSTN-116 (6.54), IRSSTN-139 (5.41), IRSSTN-136 (2.21), IRSSTN-124 (1.91) and IRSSTN-120 (1.55) possessed highly significant and positive gca effects for grain yield per plant. IRSSTN-129 (042) showed non-significant and positive gca effects. Among the testers NDR 359 (1.07) showed highly-significant and positive gca effects, whereas, CSR 10 (-0.71) exhibited highly-significant and negative gca effect but Improved Pusa Basmati 1 (0.35) exhibited non-significant and positive gca effect of grain yield per plant.

Table 4.20: Estimates of general combining ability (GCA) effects of parents (lines and testers) for 13 characters in rice under salinity condition

S. N.	Line	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Plant bearing tillers per plant	Panicle length (cm)	Spikelet per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant(g)
1	IRSSTN-101	-3.27**	-2.31*	-1.99**	-0.39	-0.35	18.86**	25.62**	6.50**	0.58**	0.05**	-13.70**	-0.38	-4.99**
2	IRSSTN-105	-0.38	0.53	-1.56**	-2.08**	-0.07	11.18**	12.02**	2.23**	0.79**	-0.21**	0.52	-0.56	-0.16
3	IRSSTN-107	-2.21**	-5.67**	1.98**	-0.37	-1.31**	9.35**	3.52	-2.21*	1.31**	-0.05**	-0.33	-0.61	-0.23
4	IRSSTN-116	-1.93**	-1.34	-0.73	0.97*	-1.71**	8.56**	-0.53	-4.27**	-1.08**	0.00	22.56**	-2.67**	6.54**
5	IRSSTN-117	-2.38**	1.70	2.01**	-0.38	-0.95*	-10.58**	-17.49**	-7.39**	1.13**	-0.27**	-3.85**	1.04	-0.93*
6	IRSSTN-120	-1.16*	-3.68**	-0.83	1.71**	-1.66**	30.67**	24.54**	0.67	-0.92**	0.11**	3.70**	0.13	1.55**
7	IRSSTN-124	1.73**	-5.48**	0.57	-0.04	0.30	0.13	1.89	1.37	-0.56**	0.04*	4.59**	-0.15	1.91**
8	IRSSTN-129	0.73	6.17**	-2.13**	0.70	-0.14	-26.00**	-23.05**	-2.94**	0.40**	0.15**	4.28**	-2.34**	0.42
9	IRSSTN-135	1.40**	2.79**	-0.56	0.49	0.82*	10.35**	6.32**	-0.73	1.55**	0.00	-7.00**	-1.70*	-3.05**
10	IRSSTN-136	-3.38**	8.10**	-1.21*	-0.59	2.08**	9.22**	6.35**	0.01	-0.29**	0.23**	6.44**	-0.18	2.21**

11	IRSSTN-139	-1.27**	-2.88**	-2.80**	2.19**	-0.03	-28.00**	-15.74**	4.53**	0.24*	-0.23**	17.86**	-2.01*	5.41**
12	IRSSTN-142	2.73**	2.92**	2.70**	-0.08	0.27	-4.23	-0.46	1.93*	0.02	0.22**	0.37	-0.58	-0.06
13	IRSSTN-143	1.40**	0.20	1.89**	0.42	1.03*	-7.03**	-5.32*	-0.22	-1.68**	0.12**	-7.81**	3.40**	-1.32**
14	IRSSTN-144	2.07**	2.71*	2.82**	0.39	-0.19	-7.80**	-7.89**	-0.74	-0.69**	0.20**	-8.30**	1.23	-2.41**
15	IRSSTN 152	2.29**	1.79	-0.90	-1.85**	0.43	0.22	2.70	2.07*	-0.30**	-0.28**	-13.44**	4.72**	-3.19**
16	IRSSTN 155	3.62**	-5.55**	0.73	-1.09*	1.48**	-14.90**	-12.47**	-0.81	-0.50**	-0.07**	-5.89**	0.65	-1.70**
	SE (gi) line	0.45	1.05	0.57	0.46	0.41	2.59	2.23	0.84	0.11	0.02	1.03	0.83	0.47
	SE(gi – gj)	0.64	1.49	0.81	0.65	0.58	1.12	3.15	1.19	0.15	0.03	1.46	1.18	0.66
	Tester													
	CSR 10	-0.50*	-4.85**	-2.04**	0.59**	0.03	0.07	0.51	0.47	0.06	-0.12**	-1.69**	-0.17	-0.71**
	Improved Pusa Basmati 1	-0.02	1.02*	2.62**	-0.47*	0.08	-0.03	-2.72**	-1.89**	-0.21**	0.24**	-0.66	-0.33	-0.35
	NDR 359	0.51*	3.84**	-0.58*	-0.12	-0.11	-0.04	2.21*	1.41**	0.15**	-0.12**	2.36**	0.50	1.07**
	SE(gi) tester	0.20	0.46	0.25	0.20	0.18	3.66	0.96	0.36	0.05	0.01	0.45	0.36	0.20
	SE(gi – gj)	0.28	0.65	0.35	0.28	0.25	1.58	1.36	0.52	0.07	0.03	0.63	0.51	0.29

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

4. 16.4 Estimates of specific combining ability effects

The estimates of specific combining ability effects for forty eight crosses of line×tester set for thirteen characters are presented in table 4.21. The characters-wise results are given here under:

4. 16.4.1 Days to 50% flowering

As early flowering being desirable, the negative and significant estimates of sca effects were considered as desirable for crosses. The negative and significant sca effects for days to 50% flowering were exhibited by two crosses, while, highly significant by six crosses. The best five crosses having high negative sca effects for days to 50% flowering in order of merit were IRSSTN-105×Improved Pusa Basmati 1 (-6.54), IRSSTN-107×CSR 10 (-6.23), IRSSTN-136×NDR 359 (-5.74), IRSSTN-101×NDR 359 (-3.85) and IRSSTN-117×CSR 10 (-3.73). The undesirable positive and high-significant sca effects for days to 50% flowering were shown by eight crosses under this condition.

4. 16.4.2 Plant height

Nine crosses possessed highly-significant and three crosses significant and negative sca effects for plant height. Short stature in case of rice was considered as desirable. The most promising five cross combinations for short stature were IRSSTN 155×CSR 10 (-9.13), IRSSTN-107×Improved Pusa Basmati 1 (-7.51), IRSSTN-139×CSR 10 (-7.12), IRSSTN-117×NDR 359 (-6.87) and IRSSTN-142×NDR 359 (-6.29). The positive and highly-significant sca effects for plant height were observed in case of seven while positive and significant sca effects for six crosses.

4. 16.4.3 Flag leaf area

One cross recorded desirable positive and highly-significant sca effects for flag leaf area while positive and significant for six crosses and best five among them were IRSSTN-120×Improved Pusa Basmati 1 (2.67), IRSSTN 155×Improved Pusa Basmati 1 (2.34), IRSSTN-142×Improved Pusa Basmati 1 (2.28), IRSSTN-139×Improved Pusa Basmati 1 (2.20) and IRSSTN-136×Improved Pusa Basmati 1 (2.04). Three crosses exhibited negative and highly significant sca effects for flag leaf area while two crosses have negative and significant sca effects under this condition.

4. 16.4.4 Panicle bearing tillers per plant

For number of panicle bearing tillers per plant, nine crosses recorded positive and highly-significant sca effects, while, only two crosses were found positive and significant and the best five crosses wereIRSSTN-143×Improved Pusa Basmati 1 (3.76), IRSSTN-105×NDR 359 (3.72), IRSSTN-129×NDR 359 (2.93), IRSSTN-117×Improved Pusa Basmati 1 (2.78) andIRSSTN-101×NDR 359 (2.67), while, seven crosses exhibited undesirable negative and highly-significant sca effects and one crosses showed undesirable negative and significant sca effects under salinity condition.

4. 16.4.5 Panicle length

Among the forty eight crosses only five crosses recorded positive and significant sca effects for panicle length and these crosses were IRSSTN-124×NDR 359 (1.83), IRSSTN-143×NDR 359 (1.71), IRSSTN-136×CSR 10 (1.70), IRSSTN-139×Improved Pusa Basmati 1 (1.64) and IRSSTN-142×NDR 359 (1.51). Two F_1s possessed negative and significant sca effects, while, 20 crosses showed negative and non-significant sca effect for panicle length.

4. 16.4.6 Spikelets per panicle

The positive and significant sca effects for spikelets per panicle were shown by seventeen crosses, the best five crosses in order of merit were IRSSTN-124×CSR 10 (30.54), IRSSTN-129×NDR 359 (29.84), IRSSTN 152×Improved Pusa Basmati 1 (22.47), IRSSTN-101×NDR 359 (21.84) and IRSSTN-136×Improved Pusa Basmati 1 (20.48). The negative and highly-significant sca effects were also noted for 14 crosses. Only one cross has negative and significant sca effects.

4. 16.4.7 Grains per panicle

The positive and highly-significant sca effects for spikelets per panicle were shown by fourteen crosses and two crosses recorded positive and significant sca effect. The best five crosses in order of merit were IRSSTN-129×NDR 359 (22.91), IRSSTN-124×CSR 10 (22.11), IRSSTN 152×Improved Pusa Basmati 1 (19.82), IRSSTN-142×Improved Pusa Basmati 1 (18.59) and IRSSTN-101×NDR 359 (17.96). The negative and highly-significant sca effects were also noted for fourteen crosses while one cross showed negative and significant effect.

4. 16.4.8 Spikelet fertility

Out of fifty eight crosses, only three crosses recorded positive and highly-significant sca effects for spikelet fertility while eight crosses were found with positive and significantsca effect. The best five crosses were IRSSTN-144×Improved Pusa basmati 1 (2.86), IRSSTN-117×NDR 359 (4.16), IRSSTN-135×Improved Pusa Basmati 1 (4.04), IRSSTN-143×CSR 10 (3.81) and IRSSTN-107×NDR 359 (3.76). Five crosses showed negative and highly-significant sca effects while two crosses showed negative and significant sca effect for spikelet fertility.

4. 16.4.9 1000-grain weight

The positive and highly-significant sca effects for 1000-grain weight were exhibited by fifteen crosses while one cross exhibited positive and significantscaeffect.The best five crosses among them were IRSSTN 152×Improved Pusa Basmati 1 (1.85), IRSSTN-120×CSR 10 (1.75), IRSSTN-143×NDR 359 (1.49), IRSSTN-136×CSR 10 (1.46) and IRSSTN-105×NDR 359 (1.35). The undesirable negative and highly-significant sca effects were noted for 16 crosses under salinity condition.

4. 16.4.10 L: B ratio

For L: B ratio, eighteen crosses showed positive and highly-significant sca effects, while, one cross was found with positive and significant effect. The best five crosses were IRSSTN-136×Improved Pusa Basmati 1 (0.46), IRSSTN-135×Improved Pusa Basmati 1 (0.35), IRSSTN-124×NDR 359 (0.30), IRSSTN-117×CSR 10 (0.25) and IRSSTN 152×CSR 10 (0.21). The undesirable negative and highly-significant sca effects were exhibited by sixteen crosses, while, two crosses exhibited negative and significant sca effect for L: B ratio.

4. 16.4.11 Biological yield per plant

Fifteen out of forty-eight crosses showed positive and highly significantsca effects for biological yield per plant, while, only one cross was found with positive and significant effects. The most promising five crosses among them were IRSSTN-117×Improved Pusa Basmati 1 (20.71), IRSSTN-129×CSR 10 (16.55), IRSSTN-142×CSR 10(16.19), IRSSTN-105×NDR 359 (13.84) and IRSSTN-144×Improved Pusa Basmati 1 (11.02). The undesirable negative and highly-significant sca effects for this character were exhibited by 11 crosses but five crosses having undesirable negative and significant effect under salinity condition.

4. 16.4.12 Harvest-index

For harvest-index, the positive and significant sca effects were exhibited by two hybrids *viz,*.IRSSTN 155×NDR 359 (3.37) and IRSSTN-101×CSR 10 (2.91). The negative and significant sca effects for harvest-index were also recorded by two crosses.

4. 16.4.13 Grain yield per plant

Fourteen out of forty-eight crosses emerged out with positive and highly-significant sca effects for grain yield per plant, while, only one cross showed positive and significant sca effect.The best five crosses among them were IRSSTN-117×Improved Pusa Basmati 1(7.15), IRSSTN-129×CSR 10 (5.13), IRSSTN-142×CSR 10 (4.56), IRSSTN-135×NDR 359 (4.41) and IRSSTN-144×Improved Pusa Basmati 1 (4.31). The undesirable negative and highly-significant sca effects for grain yield per plant were exhibited by twelve crosses but two crosses were found with negative and significant sca effect on grian yield per plant.

4.17 Proportional contribution of lines, testers and line × tester interactions

Proportional contribution of lines, testers and lines × testers interaction for thirteen characters have been presented in table 4.22.

The maximum contribution of females (lines) was recorded for harvest index (57.77) followed by panicle length (53.72%), biological yield per plant (52.02%), 1000- grain weight (48.72), spikelet fertility (48.62%), grains per penicle (46.97%), grain yield per plant (45.07%), spikelets per panicle (43.22%), days to 50% flowering (42.33), flag leaf area (cm^2) (33.80%), plant height (33.31%), L:B ratio (30.75%) and panicle bearing tillers per plant (23.43%), for this condition.

Maximum contribution of male (testers) was recorded for flag leaf area (41.00%) followed by L:B ratio (31.74%), plant height (27.32%), spikelet fertility (9.01%), spikelets per panicle (9.32%), panicle bearing tillers per plant (3.72%), grains per panicle (3.07%), harvest-index (2.08%), biological yield per plant (1.62%), days to 50% flowering (1.50%), 1000 grain weight (1.50), grains per panicle (1.10), panicle length (0.34%) and spikelets per panicle (0.00%).

Proportional contribution of lines × testers was found maximum for the character panicle bearing tillers per plant (72.86%) followed by spikelets per panicle (56.78%), days to 50% flowering (56.17%), grains per panicle (51.93%), grain yield per plant (51.86%), 1000-grain weight (49.78%), biological yield per plant (46.36%), panicle length (45.94%), spikelet fertility (42.36%), harvest-index (40.15%), plant height (39.75%), L:B ratio (37.51%) and flag leaf area (25.11%).

Table 4.21: Estimates of specific combining ability (SCA) effects of crosses for 13 characters in rice under salinity condition

S. N.	Line	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Plant bearing tillers per plant	Panicle length (cm)	Spikelet per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per plant (g)	Harvest index (%)	Grains yield per plant(g)
1	**IRSSTN-101×CSR 10**	0.16	-4.16*	1.26	2.32**	-0.74	-6.01	-2.49	1.41	-0.24	0.10**	1.13	2.91*	1.41
2	**IRSSTN-101×Improved Pusa Basmati 1**	3.68**	1.28	-1.88	-4.98**	-0.09	-15.83**	-15.47**	-1.24	0.06	-0.07*	2.83	-1.81	0.42
3	**IRSSTN-101×NDR 359**	-3.85**	2.88	0.63	2.67**	0.84	21.84**	17.96**	-0.17	0.19	-0.03	-3.96*	-1.10	-1.82*
4	**IRSSTN-105×CSR 10**	3.27**	-4.68*	1.46	-0.81	-1.00	1.35	6.32	2.96*	0.08	-0.04	-12.17**	1.49	-3.57**
5	**IRSSTN-105×Improved Pusa Basmati 1**	-6.54**	-1.08	-0.83	-2.91**	0.85	19.99**	14.26**	-0.34	-1.42**	0.01	-1.67	2.13	0.57
6	**IRSSTN-105xNDR 359**	3.26**	5.76**	-0.63	3.72**	0.15	-21.34**	-20.57**	-2.62	1.35**	0.03	13.84**	-3.63*	3.00**
7	**IRSSTN-107xCSR 10**	-6.23**	8.00**	0.15	2.10**	0.12	-21.54**	-16.64**	-0.62	-0.37	-0.09**	7.41**	0.36	2.87**
8	**IRSSTN-107xImproved Pusa Basmati 1**	0.63	-7.51**	0.15	-1.13	-0.38	6.85	-0.97	-3.14*	1.18**	0.11**	-17.75**	-0.05	-6.38**
9	**IRSSTN-107xNDR 359**	5.60**	-0.49	-0.29	-0.97	0.26	14.69**	17.61**	3.76*	-0.81**	-0.02	10.34**	-0.31	3.51**
10	**IRSSTN-116×CSR 10**	3.83**	4.83**	0.03	1.29	0.20	6.71	7.63	1.49	0.86**	-0.07*	0.50	1.11	0.97
11	**IRSSTN-116×Improved Pusa Basmati 1**	-3.65**	1.28	-1.53	0.99	0.27	11.80**	9.03*	0.69	-0.16	0.13**	3.47	-1.08	0.31
12	**IRSSTN-116×NDR 359**	-0.18	-6.10**	1.50	-2.27**	-0.47	-18.51**	-16.66**	-2.18	-0.70**	-0.06	-3.97*	-0.03	-1.28
13	**IRSSTN-117×CSR 10**	-3.73**	2.32	-0.54	0.01	-1.16	14.55**	12.57**	2.32	-1.03**	0.25**	-10.98**	0.17	-3.93**
14	**IRSSTN-117×Improved Pusa Basmati 1**	0.80	4.55*	-1.46	2.78**	0.55	-30.24**	-28.73**	-6.48**	0.08	-0.36**	20.71**	-1.04	7.15**

15	**IRSSTN-117×NDR 359**	2.93**	-6.87**	2.00*	-2.79**	0.62	15.69**	16.16**	4.16**	0.95**	0.11**	-9.74**	0.87	-3.22**
16	**IRSSTN-120×CSR 10**	0.05	-3.00	0.47	-0.48	1.30	6.27	4.17	-0.49	1.75**	0.11**	-1.64	1.31	0.06
17	**IRSSTN-120×Improved Pusa Basmati 1**	-0.09	0.53	2.67**	2.58**	-1.36	-8.30	-9.66*	-1.45	-1.00**	0.06	5.33**	-2.53	0.55
18	**IRSSTN-120×NDR 359**	0.04	2.47	-3.14**	-2.09**	0.05	2.04	5.49	1.94	-0.75**	-0.17**	-3.69*	1.22	-0.61
19	**IRSSTN-124×CSR 10**	-1.84*	-2.39	-0.34	-0.19	-1.85*	30.54**	22.11**	-1.13	-0.05	-0.17**	-11.96**	-2.09	-5.25**
20	**IRSSTN-124×Improved Pusa Basmati 1**	0.68	-2.88	1.74	0.37	0.02	1.23	2.53	1.01	0.98**	-0.13**	5.21**	2.10	2.88**
21	**IRSSTN-124×NDR 359**	1.15	5.27**	-1.40	-0.19	1.83*	-31.76**	-24.64**	0.13	-0.93**	0.30**	6.75**	-0.02	2.37**
22	**IRSSTN-129×CSR 10**	-0.84	0.32	2.00*	-2.03*	1.38	-9.74*	-3.47	3.49*	-1.16**	-0.02	16.55**	-0.96	5.13**
23	**IRSSTN-129×Improved Pusa Basmati 1**	0.68	0.99	-2.33*	-0.89	-0.24	-20.10**	-19.44**	-4.56**	-0.05	0.20**	6.72**	0.81	2.82**
24	**IRSSTN-129×NDR 359**	0.15	-1.31	0.33	2.93**	-1.14	29.84**	22.91**	1.07	1.21**	-0.18**	-23.27**	0.15	-7.96**
25	**IRSSTN-135×CSR 10**	0.50	1.95	0.24	1.16	0.51	14.21**	2.38	-4.95**	0.60**	-0.10**	-11.79**	1.43	-3.70**
26	**IRSSTN-135×Improved Pusa Basmati 1**	1.02	-6.28**	-0.40	-3.13**	0.78	5.34	10.76**	4.04**	0.22	0.35**	1.03	-2.68	-0.72
27	**IRSSTN-135×NDR 359**	-1.51	4.33*	0.16	1.97*	-1.29	-19.55**	-13.14**	0.92	-0.81**	-0.25**	10.76**	1.25	4.41**
28	**IRSSTN-136×CSR 10**	0.94	6.58**	-0.74	-0.84	1.70*	-18.96**	-10.87**	1.84	1.46**	-0.22**	2.17	0.55	1.29
29	**IRSSTN-136×Improved Pusa Basmati 1**	4.80**	-2.83	2.04*	0.39	-0.37	20.48**	8.19*	-3.94**	-0.96**	0.46**	-12.41**	2.22	-3.44**
30	**IRSSTN-136×NDR 359**	-5.74**	-3.75*	-1.30	0.45	-1.33	-1.52	2.69	2.10	-0.50**	-0.24**	10.24**	-2.77	2.15**
31	**IRSSTN-139×CSR 10**	0.16	-7.12**	2.20*	-2.61**	-1.46*	17.60**	12.86**	-1.03	0.58**	0.13**	-0.07	0.56	0.32
32	**IRSSTN-139×Improved Pusa Basmati 1**	-1.32	3.04	-2.51*	0.89	1.64*	-7.30	-1.46	3.28*	-0.35	-0.10**	-2.74	-0.67	-1.47

33	**IRSSTN-139×NDR 359**	1.15	4.08*	0.31	1.71*	-0.19	-10.30*	-11.40**	-2.25	-0.23	-0.03	2.82	0.11	1.15
34	**IRSSTN-142×CSR 10**	0.16	1.19	-3.22**	0.70	-0.68	-22.84**	-18.16**	-0.38	1.14**	0.21**	16.19**	-2.24	4.56**
35	**IRSSTN-142×Improved Pusa Basmati 1**	-0.32	5.10**	2.28*	-0.97	-0.83	20.22**	18.59**	1.92	0.08	-0.34**	-16.16**	0.57	-5.49**
36	**IRSSTN-142×NDR 359**	0.15	-6.29**	0.94	0.26	1.51*	2.62	-0.43	-1.54	-1.23**	0.14**	-0.03	1.68	0.92
37	**IRSSTN-143×CSR 10**	-0.50	1.45	-2.64**	-0.79	-0.42	14.29**	16.73**	3.81*	-0.22	-0.24**	-3.70*	-1.93	-2.20**
38	**IRSSTN-143×Improved Pusa Basmati 1**	2.02*	3.94*	1.46	3.76**	-1.29	-22.95**	-19.39**	-1.63	-1.27**	0.06	3.69*	1.50	2.02*
39	**IRSSTN-143×NDR 359**	-1.51	-5.39**	1.18	-2.97**	1.71*	8.66	2.67	-2.19	1.49**	0.19**	0.01	0.43	0.18
40	**IRSSTN-144×CSR 10**	-0.17	2.00	-0.90	-1.32	1.14	9.66*	-4.86	-8.30**	-0.97**	-0.16**	-3.27	-0.36	-1.33
41	**IRSSTN-144×Improved Pusa Basmati 1**	0.68	-5.93**	-0.17	2.60**	0.07	-22.17**	-5.47	8.09**	0.41*	0.16**	11.02**	0.41	4.31**
42	**IRSSTN-144×NDR 359**	-0.51	3.93*	1.07	-1.28	-1.21	12.51**	10.33**	0.21	0.56**	0.00	-7.75**	-0.05	-2.98**
43	**IRSSTN 152×CSR 10**	1.61*	1.85	1.11	0.78	0.37	-34.96**	-24.11**	2.21	-1.55**	0.21**	6.17**	0.87	2.79**
44	**IRSSTN 152×Improved Pusa Basmati 1**	-1.20	-0.02	-1.56	0.52	0.11	22.47**	19.82**	1.36	1.85**	-0.34**	-1.86	0.30	-0.69
45	**IRSSTN 152×NDR 359**	-0.40	-1.84	0.45	-1.30	-0.48	12.48**	4.30	-3.58*	-0.31	0.12**	-4.30*	-1.17	-2.10*
46	**IRSSTN 155×CSR 10**	2.61**	-9.13**	-0.55	0.71	0.57	-1.14	-4.17	-2.63	-0.88**	0.11**	5.47**	-3.17*	0.57
47	**IRSSTN 155×Improved Pusa Basmati 1**	-1.87*	5.83**	2.34*	-0.86	0.28	18.53**	17.41**	2.39	0.36	-0.19**	-7.41**	-0.19	-2.84**
48	**IRSSTN 155×NDR 359**	-0.74	3.31	-1.79	0.15	-0.85	-17.39**	-13.24**	0.24	0.52**	0.07*	1.95	3.37*	2.28**
	SE (sca Effects)	0.78	1.83	0.99	0.79	0.71	4.48	3.85	1.46	0.19	0.03	1.79	1.44	0.81
	SE (Sij -Skl)	1.11	2.58	1.40	1.12	1.01	6.33	5.45	2.06	0.27	0.04	2.53	2.04	1.15

Table 4.22: Proportional contribution of lines, testers and their interactions to total variance in a set of line × tester crosses in rice under salinity condition

Characters	**Contribution (%)**		
	Lines (Female)	**Testers (Male)**	**Lines × Testers**
Days to 50% flowering	42.33	1.50	56.17
Plant height (cm)	33.31	27.32	39.37
Flag leaf area (cm^2)	33.88	41.00	25.11
Panicle bearing tillerss per plant	23.43	3.72	72.86
Panicle length (cm)	53.72	0.34	45.94
Spikelets per panicle	43.22	0.00	56.78
Grains per panicle	46.97	1.10	51.93
Spikelet fertility (%)	48.62	9.01	42.36
1000- grains weight (g)	48.72	1.50	49.78
L:B ratio	30.75	31.74	37.51
Biological yield per plant (g)	52.02	1.62	46.36
Harvest-index (%)	57.77	2.08	40.15
Grains yield per plant(g)	45.07	3.07	51.86

4.18 Estimates of heterosis over better-parent and standard variety

Heterosis was estimated as per cent increase or decrease of F_1 value over better-parent (BP), standard variety (SV_1) and standard variety (SV_2). IR 28 and CSR 43 were used as standard variety one and two, respectively for all the characters. The estimates of heterobeltiosis and standard heterosis for thirteen characters of forty-eight crosses are presented in table 4.23. The character-wise results are described as follows:

4. 18.1 Days to 50% flowering

For days to 50% flowering, the heterosis over better-parent (BP) ranged from -9.47 (IRSSTN-136×NDR 359) to 15.94% (IRSSTN-105×CSR 10). The heterosis over standard variety (SV_1) IR 28 ranged from -4.46 (IRSSTN-107×CSR 10) to 11.90% (IRSSTN 155×CSR 10) and for standard variety (SV_2) ranged from 3.21 (IRSSTN-107×CSR 10) to 20.88 (IRSSTN 155×CSR 10). The estimates of mean heterosis were of 2.24, 5.50 and 13.98 % over BP and SV_1, $SV_{2,}$ respectively.

Out of forty-eight hybrids, five hybrids were exhibited negative and highly significant heterosis over BP. The best five hybrids were IRSSTN-136×NDR 359 (-9.47%), IRSSTN-101×NDR 359 (-7.37), IRSSTN-105×Improved pusa basmati 1 (-6.74), IRSSTN-116×Improved pusa basmati 1 (-6.64) and IRSSTN-116×NDR 359 (-2.45%). Two crosses exhibited negative and significant heterosis over SV_1 while in case of SV_2 zero cross showed negative and significant heterosis. The crosses IRSSTN-107×CSR 10 (-4.46%) and IRSSTN-136×NDR 359 (-4.09) showed significant heterosis over IR 28 (SV_1).

4. 18.2 Plant height

The mean heterosis for plant height was found to be -4.77, 0.70 and -1.39 over BP, SV_1 and $SV_{2,}$ respectively. The heterosis ranged from -19.58 (IRSSTN-107×Improved pusa basmati 1) to 9.27% (IRSSTN 152×CSR 10) over BP, whereas, it ranged from -19.89 (IRSSTN 155×CSR 10) to 12.26% (IRSSTN-135×NDR 359) over SV_1 and in case of SV_2 it ranged from -21.56 (IRSSTN 155×CSR 10) to 9.91% (IRSSTN-135×NDR 359).

Out of forty-eight hybrids, 25 hybrids exhibited negative and highly significant heterosis over BP. Among them the best five hybrids were IRSSTN-107×Improved pusa basmati 1 (-19.58%), IRSSTN-101×CSR 10 (-18.40), IRSSTN

155×CSR 10 (-17.44), IRSSTN-124×Improved pusa basmati 1 (-14.92) and IRSSTN-129×CSR 10 (-11.99%).

Eight crosses exhibited negative and significant heterosis over SV_1 and SV_2. The best five crosses were IRSSTN 155×CSR 10 (-19.89%), IRSSTN-139×CSR 10 (-14.94), IRSSTN-124×CSR 10 (-12.71), IRSSTN-107×Improved pusa basmati 1 (-12.12) and IRSSTN-120×CSR 10 (-11.44%) over SV1 and crosses IRSSTN 155×CSR 10 (-21.56), IRSSTN-139×CSR 10 (-16.72), IRSSTN-124×CSR 10 (-14.53), IRSSTN-107×Improved pusa basmati 1 (-13.95) and IRSSTN-120×CSR 10 (-13.29) over SV_2.

4. 18.3 Flag leaf area

The range of heterosis for the flag leaf area varied from -5.87 (IRSSTN-142×CSR 10) to 29.77% (IRSSTN-142×Improved pusa basmati 1) for BP and for standard variety IR 28 ranged from -8.53 (IRSSTN-120×NDR 359) to 36.20% (IRSSTN-142×Improved pusa basmati 1), while, for standard variety (CSR 43) 0.18 (IRSSTN-136×CSR 10)) to 45.89% (IRSSTN-142×Improved pusa basmati 1). The estimates of mean heterosis over BP, SV_1 and SV_2 were 10.17, 8.22 and 15.92%, respectively.

Out of forty-eight crosses, 20 crosses exhibited positive and significant heterosis over better parent and for SV_1 and SV_2, 15 and 25 crosses. The best five crosses over better parent were IRSSTN-142×Improved Pusa Basmati 1 (29.77), IRSSTN-143×Improved Pusa Basmati 1 (29.41), IRSSTN 155×Improved Pusa Basmati 1 (28.39), IRSSTN-105×CSR 10 (28.21) and IRSSTN-139×CSR 10 (25.88), while, for SV_1 the best five crosses were IRSSTN-142×Improved Pusa Basmati 1 (36.20%), IRSSTN-143×Improved Pusa Basmati 1 (30.19%), IRSSTN 155×Improved Pusa Basmati 1 (29.16%), IRSSTN-144×Improved Pusa Basmati 1 (27.62%) and IRSSTN-124×IImproved Pusa Basmati 1 (26.36%) and for SV_2 IRSSTN-142×Improved Pusa Basmati 1 (45.89), IRSSTN-143×Improved Pusa Basmati 1 (39.45), IRSSTN 155×Improved Pusa Basmati 1 (38.34), IRSSTN-144×IImproved PusaBasmati1 (36.69) and IRSSTN-124×Improved Pusa Basmati 1 (35.35).

4. 18.4 Panicle bearing tillers per plant

Heterobeltiosis for panicle bearing tillers per plant ranged from -43.38 (IRSSTN-105×Improved pusa basmati 1) to 84.31 % (IRSSTN-139×NDR 359) with mean heterosis of -19.07%. The positive and significant estimates of heterobeltiosis exhibited by 21 hybrids and the best five hybrids were IRSSTN-139×NDR 359 (84.31%), IRSSTN-139×Improved Pusa Basmati 1 (76.59%), IRSSTN-101×CSR 10 (75.76), IRSSTN-143×Improved Pusa Basmati 1 (68.48) and IRSSTN-101×NDR 359 (65.16%).

The standard heterosis (SV_1) varied from -35.02 (IRSSTN-105×Improved Pusa Basmati 1) to 69.68% (IRSSTN-120×Improved Pusa Basmati 1) with a mean heterosis of 28.28%. Twenty-seven crosses exhibited positive and significant standard heterosis and best five hybrids were IRSSTN-120×Improved Pusa Basmati 1 (69.68%), IRSSTN-139×NDR 359 (69.21%), IRSSTN-143×Improved Pusa Basmati 1 (68.48%), IRSSTN-129×NDR 359 (66.28%) and IRSSTN-116×CSR 10 (59.03%) while for SV_2 ranged from -28.91 (IRSSTN-101×Improved Pusa Basmati 1) to 85.62 (IRSSTN-120×Improved Pusa Basmati 1) with a mean heterosis of 40.34%. Thirty-five crosses showed positive and significant and the best five hybrids were IRSSTN-120×Improved PusaBasmati1 (85.62), IRSSTN-139×NDR 359 (85.11), IRSSTN-143×Improved Pusa Basmati 1 (84.32), IRSSTN-129×NDR 359 (81.91) and IRSSTN-116×CSR 10 (73.97).

4. 18.5 Panicle length

Heterobeltiosis for panicle length ranged from -22.57 (IRSSTN-116×NDR 359) to 26.05 % (IRSSTN-136×CSR 10) with mean heterosis of -5.55%. The positive and significant estimates of heterobeltiosis were exhibited by seven hybrids and best five hybrids among them were IRSSTN-136×CSR 10 (26.05%), IRSSTN 155×CSR 10 (17.78%), IRSSTN-135×CSR 10 (14.37%), IRSSTN-129×CSR 10 (13.94%) and IRSSTN-144×CSR 10 (12.56%).

The standard heterosis SV_1 varied from -1.63 (IRSSTN-120×Improved Pusa Basmati 1) to 32.09% (IRSSTN-136×CSR 10) with a mean heterosis of 13.04%.

Out of forty-eight crosses twenty-six crosses exhibited positive and significant standard heterosis and the five best crosses were IRSSTN-136×CSR 10 (32.09),IRSSTN-143×NDR 359 (26.13%), IRSSTN 155×CSR 10 (23.42), IRSSTN-124×NDR 359 (23.10) and IRSSTN 155×Improved Pusa Basmati 1 (22.26), while, for SV_2 it range from -3.67 (IRSSTN-120×Improved pusa basmati 1) to 29.35% (IRSSTN-136×CSR 10) with heretosis mean of 10.70%. Thirty-five crosses showed positive and significant and the best five crosses were IRSSTN-136×CSR 10 (29.35), IRSSTN-143×NDR 359 (23.52), IRSSTN 155×CSR 10 (20.87), IRSSTN-124×NDR 359 (20.56) and IRSSTN 155×Improved Pusa Basmati 1 (19.73).

4. 18.6 Spikelets per panicle

The mean heterosis for spikelets per panicle over better-parent, standard variety IR 28 and standard varieties CSR 43 were 9.20, 28.99 and 21.96%, respectively. The magnitude of heterobeltiosis varied from -24.64 (IRSSTN-139×NDR 359) to 50.53% (IRSSTN-120×CSR 10), Over standard heterosis SV_1 ranged from -9.73 (IRSSTN-129×Improved Pusa Basmati1) to 63.13% (IRSSTN-101×NDR 359) and for SV_2 it range from -14.65 (IRSSTN-129×Improved Pusa Basmati 1) to 54.23% (IRSSTN-101×NDR 359).

Significant and positive heterosis over BP was shown by 25 crosses. The best five crosses were IRSSTN-120×CSR 10 (50.53%), IRSSTN-124×CSR 10 (45.58%), IRSSTN-135×CSR 10 (37.43%), IRSSTN-116×CSR 10 (33.42%) and IRSSTN-105×Improved Pusa Basmati 1 (31.94%).

Significant and positive heterosis over standard variety Ir 28 was recorded by thirty-seven crosses. Based on magnitude of heterosis, the best five cross combinations were IRSSTN-101×NDR 359 (63.13%), IRSSTN-120×CSR 10 (60.05%), IRSSTN-120×NDR 359 (56.42%), IRSSTN-105×Improved Pusa Basmati 1 (55.13%) and IRSSTN-124×CSR 10 (54.80%) and for standard variety CSR 43 the significant and positive heterosis were recorded for thirty-six crosses, among them best five crosses were IRSSTN-101×NDR 359 (54.23%), IRSSTN-

120×CSR 10 (51.32%), IRSSTN-120×NDR 359 (47.88%), IRSSTN-105×Improved Pusa Basmati 1 (46.35%) and IRSSTN-124×CSR 10 (46.35%).

4. 18.7 Grains per panicle

The mean heterosis for grains per panicle over better-parent and standard variety (SV_1 and SV_2) was -1.27, -27.57 and 25.65%, respectively. The magnitude of heterobeltiosis ranged from -2.26 (IRSSTN-117×Improved Pusa Basmati 1) to 37.75% (IRSSTN-120×CSR 10). The estimates of heterosis over standard variety (SV_1) ranged from –25.93 (IRSSTN-117×Improved Pusa Basmati 1) to 77.93% (IRSSTN-101×NDR 359) and for SV_2 from -27.05 (IRSSTN-117×Improved Pusa Basmati 1) to 74.95% (IRSSTN-101×NDR 359).

Significant and positive heterosis over BP was shown by 15 crosses and best five crosses among then were IRSSTN-120×CSR 10 (37.75%), IRSSTN-124×CSR 10 (33.31%), IRSSTN-101×CSR 10 (32.49%), IRSSTN-105×CSR 10 (27.97%) and IRSSTN-101×NDR 359 (21.91%). Thirty-five crossesshowed positive and significant heterosis over each standard variety (IR 28 and CSR 43) On the basis of magnitude of heterosis, the best five cross combinations over SV 1 were IRSSTN-101×NDR 359 (77.63%), IRSSTN-120×NDR 359 (62.81%), IRSSTN-120×CSR 10 (59.51%), IRSSTN-124×CSR 10 (54.36%) and IRSSTN-101×CSR 10 (53.42%), while, in case of $SV_{2,}$ the best five combinations were IRSSTN-101×NDR 359 (74.95), IRSSTN-120×NDR 359 (60.35), IRSSTN-120×CSR 10 (57.10), IRSSTN-124×CSR 10 (52.23) and IRSSTN-101×CSR 10 (51.10).

4. 18.8 Spikelet fertility

The mean heterosis for spikelet fertility over better-parent and standard varieties (SV_1 and SV_2) was -10.58, -1.24 and 2.85%, respectively. The magnitude of heterobeltiosis varied from -28.27 (IRSSTN-117×Improved Pusa Basmati 1) to 0.75% (IRSSTN-101×CSR 10). None of the crosses showed significant and positive heterobiltiosis.

The estimates of heterosis over standard variety (SV_1) ranged from –21.76 (IRSSTN-117×Improved Pusa Basmati 1) to 9.67% (IRSSTN-101×CSR 10). Out of

48 crosses, only five cross recorded positive and significant heterosis for spikelet fertility over better-parent *i.e.* IRSSTN-101×CSR 10 (9.67), IRSSTN-101×NDR 359 (8.84), IRSSTN-139×Improved Pusa Basmati 1 (6.47), IRSSTN-105×CSR 10 (6.13) and IRSSTN-144×Improved Pusa Basmati 1 (5.87), while, for SV_2 ranged from -18.52 (IRSSTN-117×Improved Pusa Basmati 1) to 14.21% (IRSSTN-101×CSR 10). Sixteen crosses showed positive and significant heterosis over SV 2. Based on magnitude of heterosis over SV_2, best five cross combinations were IRSSTN-101×CSR 10 (14.21%), IRSSTN-101×NDR 359 (13.35%), IRSSTN-139×Improved Pusa Basmati 1 (10.88%), IRSSTN-105×CSR 10 (10.53%) and IRSSTN-144×Improved Pusa Basmati 1 (10.25%).

4. 18.9 1000-grain weight

For 1000-grain weight, the heterosis over BP ranged from -25.26 (IRSSTN-143×CSR 10) to 11.12% (IRSSTN 152×Improved Pusa Basmati 1) with the mean heterosis of –10.99%. Out of 48 crosses, only six crosses emerged with positive and significantheterosis over better parent. The five cross combinations were IRSSTN 152×Improved Pusa Basmati 1 (11.12%), IRSSTN-129×Improved Pusa Basmati 1 (9.73), IRSSTN-135×Improved Pusa Basmati 1 (9.48), IRSSTN-107×Improved Pusa Basmati 1 (9.46) and IRSSTN-142×Improved Pusa Basmati 1 (8.51%).

The heterosis over standard variety (SV_1) varied from -6.82(IRSSTN-143×Improved pusa basmati 1) to 20.14% (IRSSTN-105×NDR 359) with the mean heterosis of 8.82%. Out of 48 hybrids, thirty-seven hybrids exhibited positive and significant heterosis over SV_1 and the best five cross combinations were IRSSTN-105×NDR 359 (20.14%), IRSSTN-107×Improved PusaBasmati1 (20.07%), IRSSTN-117×NDR 359 (19.84%), IRSSTN-135×CSR 10 (19.74%), and IRSSTN-129×NDR 359 (17.52%), while for SV_2 it ranged from -21.64 (IRSSTN-143×Improved Pusa Basmati 1) to 1.03% (IRSSTN-105×NDR 359) with heterosis mean 8.49%. None of the cross was found positive and significant for SV_2.

4. 18.10 L:B ratio

For L:B ratio, the heterobeltiosis ranged from -36.87 (IRSSTN-117×Improved PusaBasmati1) to 9.37% (IRSSTN-101×CSR 10). The mean heterosis of L:B ratio was -18.63%. The positive and significant estimates of heterobeltiosis were exhibited by only five crosses and these wereIRSSTN-101×CSR 10 (9.37%), IRSSTN-101×NDR 359 (8.11%), IRSSTN-142×CSR 10 (6.87%), IRSSTN-142×NDR 359 (4.07%) and IRSSTN-136×Improved Pusa Basmati 1 (2.81%).

The standard heterosis (SV_1) ranged from -31.37 (IRSSTN-117×Improved PusaBasmati1) to 11.76% (IRSSTN-136×Improved Pusa Basmati 1) with over all mean value being -18.46%. Only one cross combination showed positive and significant heterosis over standard variety *i.e.* IRSSTN-136×Improved Pusa Basmati 1 (11.76%), while, standard heterosis (SV_2) ranged form -32.84 (IRSSTN-117×Improved Pusa Basmati 1) to 9.38% (IRSSTN-136×Improved Pusa Basmati 1) with heterosis mean -20.19%. Out of 48 cross combinations only one cross showed positive and significant heterosis over SV_2. The cross was IRSSTN-136×Improved Pusa Basmati 1 (9.38).

4. 18.11 Biological yield per plant

Theheterosis for biological yield per plant ranged from -55.48 (IRSSTN-135×CSR 10) to 85.76% (IRSSTN-116×CSR 10) over BP, standard heterosis (SV_1) ranged from -40.20 (IRSSTN-135×CSR 10) to 64.65% (IRSSTN-116×Improved Pusa Basmati 1)and for SV_2 ranged from -39.50 (IRSSTN-135×CSR 10) to 66.58% (IRSSTN-116×Improved PusaBasmati1) and with mean heterosis over BP, SV_1 and SV_2 9.94, 6.64 and 7.89%, respectively.

Out of 48 cross combinations, desirable and significant heterosis were exhibited by twenty crosses over better-parent and the best five cross combinations among them were IRSSTN-116×Improved Pusa Basmati 1 (66.58%), IRSSTN-129×CSR 10 (79.65%), IRSSTN-116×Improved Pusa Basmati 1 (78.41%), IRSSTN-139×CSR 10 (71.33%) and IRSSTN-142×CSR 10 (67.98%). Nine crosses exhibited significant and positive heterosis over SV_1 and the best five cross combinations among them were IRSSTN-116×Improved Pusa Basmati 1 (64.65%), IRSSTN-139×NDR 359 (59.30%), IRSSTN-116×CSR 10 (55.50%), IRSSTN-116×NDR 359 (54.55%) and IRSSTN-129×CSR 10 (50.38%), while, SV_2 having twenty-one positive and significant cross combinations out of them the best five were IRSSTN-116×Improved PusaBasmati1 (66.58%), IRSSTN-139×NDR 359 (61.17%), IRSSTN-116×CSR 10 (57.32%), IRSSTN-116×NDR 359 (56.37) and IRSSTN-129×CSR 10 (51.15) .

4. 18.12 Harvest-index

The heterobeltiosis for harvest-index varied from -24.92 (IRSSTN-105×NDR 359) to 12.96% (IRSSTN-143×Improved PusaBasmati1) with the mean heterosis of -7.70%. Out of forty-eight crosses only one cross exhibited positive and significant heterobeltiosis*i.e.* IRSSTN-143×Improved Pusa Basmati 1 (12.96).

The heterosis for harvest-index over standard variety (SV_1) ranged from 1.39 (IRSSTN-135×Improved PusaBasmati1) to 33.62% (IRSSTN 152×CSR 10) with the mean heterosis of 16.38%. Out of 48 hybrids, 30 cross combinations exhibited positive and significant heterosis. The best five crosses were IRSSTN 152×CSR 10 (33.62%), IRSSTN 152×Improved Pusa Basmati 1(31.31%), IRSSTN-143×Improved pusa basmati 1 (30.91%), IRSSTN 155×NDR 359(30.76%) and IRSSTN-143×NDR 359 (30.13%), while, in case of SV_2 it ranged from -17.71 (IRSSTN-135×Improved Pusa Basmati 1) to 8.45% (IRSSTN 152×CSR 10) with the total mean of heterosis -5.54%. None of the hybrid showed positive and significant heterosis over standard variety SV_2.

4. 18.13 Grain yield per plant

For grain yield per plant, the heterosis over better-parent varied from -57.64 (IRSSTN-135×CSR 10) to 91.23% (IRSSTN-116×Improved Pusa Basmati 1) with mean heterosis of 12.84%. Twenty-one crosses showed positive and significant heterosis over BP and the best five crosses among them were IRSSTN-116×Improved Pusa Basmati 1 (91.23%), IRSSTN-124×Improved Pusa Basmati 1 (74.39%), IRSSTN-116×CSR 10 (72.63%), IRSSTN-139×Improved Pusa Basmati 1 (67.44%) and IRSSTN-129×Improved Pusa Basmati 1 (61.69%).

The standard heterosis for grain yield per plant ranged from -31.30 (IRSSTN-135×CSR 10) to 78.70% (IRSSTN-139×NDR 359) over SV_1 with heterosis mean of 23.08%. twenty-seven crosses showed positive and significant heterosis over SV_1 and the best five crosses among them were IRSSTN-139×NDR 359 (78.70%), IRSSTN-116×CSR 10 (72.63%), IRSSTN-116×Improved Pusa Basmati 1 (70.42%), IRSSTN-116×NDR 359 (69.18%) and IRSSTN-117×Improved Pusa Basmati 1 (65.78%).

Standard heterosis for SV_2 ranged from -43.59 (IRSSTN-135×CSR 10) to 46.74% (IRSSTN-139×NDR 359) with heterosis mean 1.06%. Out of 48 crosses seventeen cross combinations exhibited positive and significantheterosis over standard variety CSR43 and the best five crosses were IRSSTN-139×NDR 359 (46.74%), IRSSTN-116×CSR 10 (41.75), IRSSTN-116×Improved Pusa Basmati 1 (39.94%), IRSSTN-116×NDR 359 (38.92%) and IRSSTN-117×Improved Pusa Basmati 1 (36.13%).

Table 4.23: Extent of per cent heterosis over better parent (BP) and two standard varieties (SV) for 13 characters in rice under salinity condition

S. N.	**Crosses**	**Days to 50% flowering**			**Plant height (cm)**			**Flag leaf area (cm^2)**			**Panicle bearing tillers per plant**			**Panicle length (cm)**		
		BP	**SV$_1$**	**SV$_2$**	BP	**SV$_1$**	**SV$_2$**	BP	**SV$_1$**	**SV$_2$**	BP	**SV$_1$**	**SV$_2$**	BP	**SV$_1$**	**SV$_2$**
1	**IRSSTN-101×CSR 10**	4.20**	1.49	9.64**	-18.40**	-11.23**	-13.09**	4.28	-1.98	4.99	75.76**	55.45**	70.06**	2.79	55.45**	70.06**
2	**IRSSTN-101×Improved Pusa Basmati 1**	1.06	5.95**	14.46**	-7.86**	0.69	-1.41	3.01	3.63	11.00*	-17.58	-35.02**	-28.91*	-10.84**	-35.02**	-28.91*
3	**IRSSTN-101×NDR 359**	-7.37**	-1.86	6.02**	-3.15	5.35	3.15	7.54	1.09	8.28	65.16**	51.62**	65.88**	-12.46**	51.62**	65.88**
4	**IRSSTN-105×CSR 10**	15.94**	8.18**	16.87**	-10.66**	-8.78**	-10.68**	28.21**	0.36	7.49	-15.39	3.43	13.15	2.55	3.43	13.15
5	**IRSSTN-105×Improved pusa basmati 1**	-6.74**	-2.23	5.62**	-7.39**	1.21	-0.91	8.41	9.07	16.82**	-43.38**	-30.79*	-24.29	-5.93	-30.79*	-24.29
6	**IRSSTN-105×NDR 359**	3.16**	9.29**	18.07**	4.27	11.38**	9.05**	4.77	-1.98	4.99	18.43	44.77**	58.37**	-13.98**	44.77**	58.37**
7	**IRSSTN-107×CSR 10**	2.39	-4.46**	3.21*	1.17	-1.96	-4.00	-0.42	8.53	16.24**	54.10**	53.32**	67.73**	2.38	53.32**	67.73**
8	**IRSSTN-107×Improved pusa basmati 1**	-1.06	3.72**	12.05**	-19.58**	-12.12**	-13.95**	15.33**	25.69**	34.63**	7.51	6.97	17.02	-15.83**	6.97	17.02
9	**IRSSTN-107×NDR 359**	3.68**	9.85**	18.67**	-8.01**	-1.74	-3.79	3.05	12.31*	20.29**	13.06	12.49	23.06	-18.28**	12.49	23.06
10	**IRSSTN-116×CSR 10**	0.70	7.06**	15.66**	6.44*	-0.74	-2.81	25.39**	-1.85	5.12	18.41*	59.03**	73.97**	0.84	59.03**	73.97**
11	**IRSSTN-116 ×Improved pusa basmati 1**	-6.64**	-0.74	7.23**	-6.92**	1.71	-0.41	8.90	9.56	17.35**	7.53	44.40**	57.98**	-14.84**	44.40**	57.98**
12	**IRSSTN-116×NDR 359**	-2.45*	3.72**	12.05**	-9.28**	-3.10	-5.12	16.44**	8.94	16.69**	-15.99	12.82	23.42	-22.57**	12.82	23.42
13	**IRSSTN-117×CSR 10**	1.54	-1.86	6.02**	0.25	-0.17	-2.25	-2.64	6.12	13.67*	18.65	30.69*	42.97**	-2.06	30.69*	42.97**
14	**IRSSTN-117×Improved pusa basmati 1**	-1.06	3.72**	12.05**	-0.83	8.37**	6.11*	9.96*	19.86**	28.38**	35.53**	49.28**	63.31**	-10.69**	49.28**	63.31**
15	**IRSSTN-117×NDR 359**	0.70	6.69**	15.26**	-7.03**	-0.69	-2.77	10.86*	20.84**	29.43**	-15.90	-7.36	1.34	-15.56**	-7.36	1.34

16	**IRSSTN-120×CSR 10**	2.20	3.72**	12.05**	-6.03*	-11.44**	-13.29**	12.19*	-0.63	6.44	22.41*	47.91**	61.81**	-4.63	47.91**	61.81**
17	**IRSSTN-120 ×Improved pusa basmati 1**	-0.71	4.09**	12.45**	-9.89**	-1.53	-3.59	23.90**	24.65**	33.51**	40.42**	69.68**	85.62**	-21.15**	69.68**	85.62**
18	**IRSSTN-120×NDR 359**	-1.05	4.83**	13.25**	-3.13	3.48	1.31	-2.23	-8.53	-2.02	1.64	22.82	34.36*	-20.41**	22.82	34.36*
19	**IRSSTN-124×CSR 10**	-0.70	4.83**	13.25**	-4.08	-12.71***	-14.53**	1.62	1.58	8.80	-6.65	32.17**	44.59**	0.63	32.17**	44.59**
20	**IRSSTN-124 ×Improved pusa basmati 1**	2.46*	8.18**	16.87**	-14.92**	-7.03*	-8.97**	25.61**	26.36**	35.35**	-10.40	26.86*	38.78**	-7.80	26.86*	38.78**
21	**IRSSTN-124×NDR 359**	3.16**	9.29**	18.07**	-2.14	4.53	2.35	3.09	3.05	10.38	-12.03	24.55*	36.26**	-6.20	24.55*	36.26**
22	**IRSSTN-129×CSR 10**	11.90**	4.83**	13.25**	-11.99**	2.43	0.30	22.18**	0.23	7.36	0.91	20.22	31.52*	13.94**	20.22	31.52*
23	**IRSSTN-129 ×Improved pusa basmati 1**	2.13	7.06**	15.66**	-6.06*	9.34**	7.05**	0.87	1.47	8.69	1.70	21.16	32.54*	-10.60*	21.16	32.54*
24	**IRSSTN-129×NDR 359**	1.05	7.06**	15.66**	-5.59*	9.88**	7.59**	6.33	-0.52	6.56	39.58**	66.28**	81.91**	-19.18**	66.28**	81.91**
25	**IRSSTN-135×CSR 10**	7.06**	7.06**	15.66**	-1.97	0.58	-1.52	-1.55	-0.47	6.61	7.02	52.53**	66.86**	14.37**	52.53**	66.86**
26	**IRSSTN-135 ×Improved pusa basmati 1**	3.19**	8.18**	16.87**	-10.23**	-1.90	-3.95	13.09*	14.34**	22.47**	-33.64**	-5.42	3.48	-2.67	-5.42	3.48
27	**IRSSTN-135×NDR 359**	0.00	5.95**	14.46**	5.09*	12.26**	9.91**	3.47	4.61	12.05*	7.78	53.61**	68.05**	-16.08**	53.61**	68.05**
28	**IRSSTN-136×CSR 10**	3.77**	2.23	10.44**	1.50	11.06**	8.74**	1.09	-6.47	0.18	-3.62	19.10	30.29*	26.05**	19.10	30.29*
29	**IRSSTN-136×Improved pusa basmati 1**	2.13	7.06**	15.66**	-1.90	7.34**	5.10	20.23**	20.95**	29.55**	-2.10	20.97	32.35*	-2.21	20.97	32.35*
30	**IRSSTN-136×NDR 359**	-9.47**	-4.09**	3.61**	-0.07	9.34**	7.05**	3.54	-3.13	3.76	1.52	25.45*	37.24**	-11.44**	25.45*	37.24**
31	**IRSSTN-139×CSR 10**	8.56**	3.72**	12.05**	-11.59**	-14.94**	-16.72**	25.88**	-1.47	5.53	46.70**	30.07*	42.30**	-2.39	30.07*	42.30**
32	**IRSSTN-139×Improved**	-2.13	2.60*	10.84**	-6.70**	1.95	-0.18	-2.27	-1.68	5.31	76.59**	56.57**	71.29**	-2.59	56.57**	71.29**

	pusa basmati 1															
33	**IRSSTN-139×NDR 359**	0.00	5.95**	14.46**	-0.75	6.02*	3.81	3.62	-3.05	3.84	84.31**	69.21**	85.11**	-15.11**	69.21**	85.11**
34	**IRSSTN-142×CSR 10**	11.92**	8.18**	16.87**	-7.49**	-0.08	-2.17	-5.87	-1.20	5.82	59.88**	41.41**	54.70**	0.95	41.41**	54.70**
35	**IRSSTN-142×Improved pusa basmati 1**	3.19**	8.18**	16.87**	0.87	10.23**	7.93**	29.77**	36.20**	45.89**	47.62**	11.91	22.43	-11.32**	11.91	22.43
36	**IRSSTN-142×NDR 359**	3.16**	9.29**	18.07**	-6.31*	1.19	-0.92	13.84**	19.48**	27.98**	40.46**	28.95*	41.07**	-7.54	28.95*	41.07**
37	**IRSSTN-143×CSR 10**	5.95**	5.95**	14.46**	-2.67	-2.67	-4.70	-2.06	-2.06	4.90	30.69*	30.69*	42.97**	10.92*	30.69*	42.97**
38	**IRSSTN-143 ×Improved pusa basmati 1**	4.26**	9.29**	18.07**	-2.86	6.15*	3.93	29.41**	30.19**	39.45**	68.48**	68.48**	84.32**	-10.11*	68.48**	84.32**
39	**IRSSTN-143×NDR 359**	0.00	5.95**	14.46**	-7.05**	-0.71	-2.79	17.40**	17.40**	25.74**	-0.65	-0.65	8.69	-3.89	-0.65	8.69
40	**IRSSTN-144×CSR 10**	12.94**	7.06**	15.66**	5.36	0.55	-1.55	1.97	7.79	15.45**	-3.69	24.55*	36.26**	12.56*	24.55*	36.26**
41	**IRSSTN-144×Improved pusa basmati 1**	3.55**	8.55**	17.27**	-9.97**	-1.62	-3.67	20.73**	27.62**	36.69**	20.32*	55.60**	70.22**	-9.53*	55.60**	70.22**
42	**IRSSTN-144×NDR 359**	1.75	7.81**	16.47**	4.62	11.75**	9.42**	13.90**	20.40**	28.96**	-9.30	17.29	28.32*	-19.63**	17.29	28.32*
43	**IRSSTN 152×CSR 10**	5.38**	9.29**	18.07**	9.27**	-0.56	-2.64	7.22	1.48	8.70	39.14**	23.07	34.64*	10.54*	23.07	34.64*
44	**IRSSTN 152×Improved pusa basmati 1**	1.77	6.69**	15.26**	-5.14*	3.65	1.49	8.20	8.85	16.58**	43.57**	8.84	19.08	-6.89	8.84	19.08
45	**IRSSTN 152×NDR 359**	2.11	8.18**	16.87**	-1.97	4.71	2.52	10.36	4.45	11.88*	1.22	-7.08	1.66	-14.50**	-7.08	1.66
46	**IRSSTN 155×CSR 10**	5.61**	11.90**	20.88**	-17.44**	-19.89**	-21.56**	5.05	1.36	8.57	47.59**	30.54*	42.81**	17.78**	30.54*	42.81**
47	**IRSSTN 155 ×Improved pusa basmati 1**	1.40	7.43**	16.06**	-6.59**	2.07	-0.06	28.39**	29.16**	38.34**	34.67*	2.09	11.69	-2.00	2.09	11.69
48	**IRSSTN 155×NDR 359**	3.16**	9.29**	18.07**	-4.14	2.39	0.25	5.90	2.18	9.45	27.29*	16.86	27.84*	-11.88**	16.86	27.84*

	Range of heterosis MIN	**-9.47**	**-4.46**	**3.21**	**-19.58**	**-19.89**	**-21.56**	**-5.87**	**-8.53**	**-2.02**	**-43.38**	**-35.02**	**-28.91**	**-22.57**	**-1.63**	**-3.67**
	MAX	**15.94**	**11.90**	**20.88**	**9.27**	**12.26**	**9.91**	**29.77**	**36.20**	**45.89**	**84.31**	**69.68**	**85.62**	**26.05**	**32.09**	**29.35**
	Mean heterosis(%)	2.24	**5.50**	**13.98**	-4.77	**0.70**	-1.39	10.17	**8.22**	**15.92**	19.07	**28.28**	**40.34**	-5.55	**13.04**	**10.70**
	No. of crosses with significant positive heterosis	21	**41**	**47**	**3**	**12**	9	20	**15**	25	**21**	**27**	**35**	**7**	**26**	**35**
	No. of crosses with significant negative heterosis	5	**2**	**0**	**25**	**8**	8	0	**0**	0	**2**	**2**	**1**	**22**	**2**	**1**

Cond………

S. No.	**Crosses**	**Spikelet per panicle**			**Grains per panicle**			**Spikelet fertility (%)**			**1000 seed weight (g)**		
		BP	**SV_1**	**SV_2**	**BP**	**SV_1**	**SV_2**	**BP**	**SV_1**	**SV_2**	**BP**	**SV_1**	**SV_2**
1	**IRSSTN-101×CSR 10**	31.52**	39.84**	32.21**	32.49**	53.42**	51.10**	0.75	9.67**	14.21**	-17.00**	10.78**	-6.84**
2	**IRSSTN-101×Improved Pusa Basmati 1**	11.85*	31.51**	24.34**	5.79	35.70**	33.65**	-5.43*	3.15	7.42**	1.97	10.89**	-6.75**
3	**IRSSTN-101×NDR 359**	26.98**	63.13**	54.23**	21.91**	77.63**	74.94**	-4.06	8.84**	13.35**	-11.79**	13.36**	-4.67**
4	**IRSSTN-105×CSR 10**	27.53**	39.57**	31.96**	27.97**	48.18**	45.94**	-2.50	6.13*	10.53**	-15.01**	13.43**	-4.61**
5	**IRSSTN-105×Improved Pusa Basmati 1**	31.94**	55.13**	46.67**	19.53**	53.33**	51.02**	-9.45**	-1.23	2.87	-9.38**	4.63**	-12.01**
6	**IRSSTN-105×NDR 359**	-6.26	20.44**	13.87**	-17.20**	20.64**	18.82**	-11.77**	0.10	4.24	-6.53**	20.14**	1.03
7	**IRSSTN-107×CSR 10**	11.74*	18.81**	12.33*	-1.74	13.78*	12.06*	-12.09**	-4.31	-0.34	-14.75**	13.77**	-4.32**
8	**IRSSTN-107×Improved pusa basmati 1**	21.25**	42.57**	34.79**	-0.69	27.39**	25.46**	-18.10**	-10.67**	-6.97*	9.46**	20.07**	0.97
9	**IRSSTN-107×NDR 359**	16.09**	49.14**	41.01**	5.07	53.08**	50.77**	-9.55**	2.61	6.86*	-12.79**	12.08**	-5.75**
10	**IRSSTN-116×CSR 10**	33.42**	41.87**	34.13**	17.36**	35.89**	33.84**	-12.04**	-4.25	-0.28	-19.07**	8.01**	-9.17**
11	**IRSSTN-116×Improved pusa basmati 1**	24.23**	46.06**	38.10**	4.38	33.90**	31.87**	-15.99**	-8.37**	-4.57	3.02*	1.61	-14.55**
12	**IRSSTN-116×NDR 359**	-6.12	20.61**	14.03**	-23.68**	11.20	9.52	-18.73**	-7.80**	-3.98	-21.60**	0.76	-15.27**
13	**IRSSTN-117×CSR 10**	17.31**	32.38**	25.16**	3.41	22.75**	20.90**	-14.78**	-7.23**	-3.39	-17.85**	9.64**	-7.80**
14	**IRSSTN-117×Improved pusa basmati 1**	-19.46**	-5.30	-10.46*	-42.26**	-25.93**	-27.05**	-28.27**	-21.76**	-18.52**	-2.42*	13.74**	-4.35**
15	**IRSSTN-117×NDR 359**	3.72	33.25**	25.98**	-11.78**	28.53**	26.59**	-15.04**	-3.61	0.38	-6.76**	19.84**	0.78

16	**IRSSTN-120×CSR 10**	50.53**	60.05**	51.32**	37.75**	59.51**	57.10**	-8.49**	-0.39	3.74	-15.15**	13.25**	-4.77**
17	**IRSSTN-120×Improved pusa basmati 1**	25.65**	47.74**	39.68**	9.82*	40.87**	38.74**	-12.64**	-4.71	-0.76	-17.99**	-1.73	-17.36**
18	**IRSSTN-120×NDR 359**	21.75**	56.42**	47.88**	11.75**	62.81**	60.35**	-8.32**	4.01	8.32**	-21.15**	1.33	-14.78**
19	**IRSSTN-124×CSR 10**	45.58**	54.80**	46.35**	33.31**	54.36**	52.03**	-8.43**	-0.33	3.81	-20.48**	6.13**	-10.75**
20	**IRSSTN-124×Improved pusa basmati 1**	10.66*	30.11**	23.02**	0.90	29.43**	27.48**	-8.88**	-0.61	3.51	-0.34	9.85**	-7.62**
21	**IRSSTN-124×NDR 359**	-20.29**	2.41	-3.17	-27.86**	5.11	3.52	-9.61**	2.54	6.79*	-20.45**	2.24	-14.02**
22	**IRSSTN-129×CSR 10**	-6.84	-0.95	-6.35	-14.39**	-0.87	-2.37	-8.06**	0.08	4.23	-21.04**	5.39**	-11.38**
23	**IRSSTN-129×Improved pusa basmati 1**	-23.22**	-9.73	-14.65**	-39.08**	-21.85**	-23.03**	-20.67**	-13.46**	-9.88**	9.73**	9.47**	-7.94**
24	**IRSSTN-129×NDR 359**	2.89	32.19**	24.98**	-10.89**	29.83**	27.87**	-13.47**	-1.84	2.23	-8.56**	17.52**	-1.18
25	**IRSSTN-135×CSR 10**	37.43**	49.67**	41.51**	18.87**	37.64**	35.56**	-15.51**	-8.03**	-4.22	-10.28**	19.74**	0.69
26	**IRSSTN-135×Improved pusa basmati 1**	20.89**	42.15**	34.39**	11.70*	43.28**	41.12**	-7.77**	0.60	4.77	9.48**	16.49**	-2.04
27	**IRSSTN-135×NDR 359**	-5.63	21.24**	14.63**	-15.90**	22.53**	20.68**	-11.11**	0.84	5.02	-11.91**	13.21**	-4.79**
28	**IRSSTN-136×CSR 10**	5.73	20.88**	14.29**	6.38	23.18**	21.32**	-6.51**	1.77	5.99*	-13.89**	14.93**	-3.35**
29	**IRSSTN-136×Improved pusa basmati 1**	30.89**	53.90**	45.51**	9.53*	40.50**	38.37**	-16.40**	-8.81**	-5.03	-7.71**	1.58	-14.58**
30	**IRSSTN-136×NDR 359**	5.41	35.43**	28.04**	-4.00	39.87**	37.75**	-8.91**	3.34	7.62**	-17.78**	5.67**	-11.14**
31	**IRSSTN-139×CSR 10**	-3.33	20.32**	13.76**	-2.29	24.99**	23.10**	-4.52	3.93	8.24**	-15.21**	13.17**	-4.84**
32	**IRSSTN-139×Improved pusa basmati 1**	-20.19**	-0.67	-6.08	-17.52**	5.81	4.21	-2.39	6.47*	10.88**	2.63*	7.23**	-9.82**
33	**IRSSTN-139×NDR 359**	-24.64**	-3.18	-8.47	-31.15**	0.32	-1.20	-8.71**	3.56	7.85**	-14.72**	9.61**	-7.83**
34	**IRSSTN-142×CSR 10**	-0.45	6.33	0.53	-6.92	7.78	6.15	-6.86**	1.39	5.59*	-13.93**	14.88**	-3.39**
35	**IRSSTN-142×Improved pusa basmati 1**	21.10**	42.39**	34.62**	12.59**	44.43**	42.24**	-7.12**	1.31	5.51	8.51**	8.26**	-8.96**

36	**IRSSTN-142×NDR 359**	-0.67	27.62**	20.66**	-11.46**	29.01**	27.06**	-10.88**	1.11	5.30	-19.38**	3.61**	-12.87**
37	**IRSSTN-143×CSR 10**	27.11**	35.15**	27.78**	21.42**	40.60**	38.48**	-4.41	4.05	8.36**	-25.26**	-0.25	-16.11**
38	**IRSSTN-143×Improved pusa basmati 1**	-11.71*	3.81	-1.85	-23.92**	-2.41	-3.89	-13.91**	-6.10*	-2.21	-6.82**	-6.82**	-21.64**
39	**IRSSTN-143×NDR 359**	1.45	30.33**	23.22**	-12.78**	27.09**	25.17**	-14.08**	-2.53	1.51	-15.45**	8.67**	-8.62**
40	**IRSSTN-144×CSR 10**	10.74*	30.61**	23.49**	-1.39	14.19*	12.46*	-19.51**	-12.39**	-8.76**	-24.38**	0.92	-15.13**
41	**IRSSTN-144×Improved pusa basmati 1**	-11.98**	3.81	-1.85	-14.25**	10.00	8.33	-2.94	5.87*	10.25**	-11.30**	6.36**	-10.56**
42	**IRSSTN-144×NDR 359**	3.45	32.91**	25.66**	-8.96*	32.65**	30.64**	-11.93**	-0.09	4.05	-15.27**	8.90**	-8.42**
43	**IRSSTN 152×CSR 10**	-6.05	-0.11	-5.56	-9.56	4.72	3.14	-3.59	4.94	9.29**	-25.09**	-0.02	-15.92**
44	**IRSSTN 152×Improved pusa basmati 1**	25.89**	48.02**	39.95**	16.33**	49.23**	46.97**	-7.62**	0.77	4.94	11.12**	15.44**	-2.92**
45	**IRSSTN 152×NDR 359**	8.68*	39.63**	32.01**	-5.53	37.64**	35.56**	-13.06**	-1.37	2.72	-17.08**	6.57**	-10.38**
46	**IRSSTN 155×CSR 10**	3.56	15.59**	9.28	-5.06	9.93	8.27	-12.82**	-5.10	-1.17	-23.37**	2.27	-13.99**
47	**IRSSTN 155×Improved pusa basmati 1**	12.28**	32.02**	24.81**	1.35	30.00**	28.04**	-9.82**	-1.63	2.44	0.36	7.07**	-9.96**
48	**IRSSTN 155×NDR 359**	-20.72**	1.85	-3.70	-30.08**	1.88	0.34	-11.98**	-0.14	3.99	-14.69**	9.64**	-7.80**
	Range of heterosis Min	-24.64	-9.73	-14.65	-42.26	-25.93	-27.05	-28.27	-21.76	-18.52	-25.26	-6.82	-21.64
	MAX	50.53	63.13	54.23	37.75	77.63	74.94	0.75	9.67	14.21	11.12	20.14	1.03
	Mean heterosis (%)	9.20	28.99	21.96	-1.27	27.57	25.65	-10.58	-1.24	2.85	-10.99	8.82	-8.49
	No. of crosses with significant positive heterosis	25	37	36	15	35	35	0	5	16	6	37	0
	No. of crosses with significant negative heterosis	8	0	2	16	2	2	40	10	3	38	1	42

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S. No	Crosses	L:B Ratio			Biological Yield Per Plant (g)			Harvest Index (%)			Grain Yield Per Plant (g)		
		BP	**SV$_1$**	**SV$_2$**	**BP**	**SV$_1$**	**SV$_2$**	**BP**	**SV$_1$**	**SV$_2$**	**BP**	**SV$_1$**	**SV$_2$**
1	**IRSSTN-101×CSR 10**	9.37**	-17.32**	-19.08**	-11.58	-25.99**	-25.12**	3.52	23.91**	0.57	-8.21	-8.21	-24.63**
2	**IRSSTN-101×Improved Pusa Basmati 1**	-18.34**	-11.22**	-13.11**	-13.03*	-19.73**	-18.79**	-5.24	8.38	-12.04*	-2.13	-12.77	-28.37**
3	**IRSSTN-101×NDR 359**	8.11**	-21.57**	-23.24**	-32.58**	-28.35**	-27.51**	-18.74**	13.26*	-8.07	-31.87**	-18.77*	-33.30**
4	**IRSSTN-105×CSR 10**	-33.92**	-30.61**	-32.09**	-16.79**	-23.89**	-23.00**	-0.75	18.80**	-3.58	-15.88*	-9.32	-25.54**
5	**IRSSTN-105×Improved pusa basmati 1**	-23.95**	-17.32**	-19.08**	11.04	2.48	3.68	2.41	20.32**	-2.34	14.53	23.46**	1.38
6	**IRSSTN-105×NDR 359**	-31.85**	-28.43**	-29.96**	36.30**	44.86**	46.56**	-24.92**	4.65	-15.06**	27.09**	51.53**	24.43**
7	**IRSSTN-107×CSR 10**	-33.03**	-26.91**	-28.46**	31.14**	18.96**	20.35**	-3.90	15.03*	-6.63	29.80**	37.08**	12.56
8	**IRSSTN-107×Improved pusa basmati 1**	-16.27**	-8.61**	-10.55**	-30.88**	-36.21**	-35.47**	-2.91	13.24*	-8.09	-31.52**	-27.68**	-40.62**
9	**IRSSTN-107×NDR 359**	-31.14**	-24.84**	-26.44**	26.95**	34.92**	36.50**	-17.47**	15.03*	-6.63	29.76**	54.71**	27.04**
10	**IRSSTN-116×CSR 10**	-29.85**	-24.73**	-26.33**	85.76**	55.50**	57.32**	-7.37	10.88	-10.01	72.63**	72.63**	41.75**
11	**IRSSTN-116×Improved pusa basmati 1**	-14.03**	-6.54**	-8.53**	78.41**	64.65**	66.58**	3.79	3.42	-16.06**	91.23**	70.42**	39.94**
12	**IRSSTN-116×NDR 359**	-29.54**	-24.40**	-26.01**	45.42**	54.55**	56.37**	-21.52**	9.39	-11.21*	41.89**	69.18**	38.92**
13	**IRSSTN-117×CSR 10**	-13.13**	-22.88**	-24.52**	-25.05**	-31.13**	-30.32**	-0.01	19.69**	-2.86	-22.18**	-17.53*	-32.28**
14	**IRSSTN-117×Improved pusa basmati 1**	-36.87**	-31.37**	-32.84**	55.70**	43.68**	45.37**	0.38	15.35*	-6.38	56.44**	65.78**	36.13**
15	**IRSSTN-117×NDR 359**	-18.40**	-27.56**	-29.10**	-23.81**	-19.03**	-18.08**	-10.99*	24.07**	0.70	-15.60*	0.63	-17.37*
16	**IRSSTN-120×CSR 10**	-7.71**	-15.25**	-17.06**	14.85*	7.48	8.74	0.60	20.42**	-2.26	21.91**	29.58**	6.40
17	**IRSSTN-120×Improved pusa basmati 1**	-12.73**	-5.12**	-7.14**	34.40**	25.77**	27.25**	-5.03	7.71	-12.58*	27.78**	35.82**	11.53

18	**IRSSTN-120×NDR 359**	-17.79**	-24.51**	-26.12**	5.43	12.05*	13.36*	-12.26**	22.30**	-0.74	15.48*	37.69**	13.06
19	**IRSSTN-124×CSR 10**	-22.30**	-26.36**	-27.93**	2.62	-14.09*	-13.09*	-9.17	8.73	-11.75*	-6.41	-6.41	-23.15**
20	**IRSSTN-124×Improved pusa basmati 1**	-20.54**	-13.62**	-15.46**	38.18**	27.52**	29.02**	6.17	21.54**	-1.35	74.39**	55.42**	27.62**
21	**IRSSTN-124×NDR 359**	-6.21**	-11.11**	-13.01**	29.81**	37.97**	39.59**	-15.74**	17.45**	-4.67	35.89**	62.02**	33.04**
22	**IRSSTN-129×CSR 10**	-18.59**	-17.97**	-19.72**	79.65**	50.38**	52.15**	-12.01*	5.32	-14.52**	58.31**	58.31**	29.99**
23	**IRSSTN-129×Improved pusa basmati 1**	-7.41**	0.65	-1.49	41.16**	30.27**	31.80**	-0.42	10.44	-10.36	61.69**	44.10**	18.33**
24	**IRSSTN-129×NDR 359**	-24.11**	-23.53**	-25.16**	-35.45**	-31.40**	-30.59**	-20.36**	11.01	-9.90	-36.33**	-24.09**	-37.67**
25	**IRSSTN-135×CSR 10**	-26.34**	-25.38**	-26.97**	-55.48**	-40.20**	-39.50**	-4.50	14.97*	-6.69	-57.64**	-31.30**	-43.59**
26	**IRSSTN-135×Improved pusa basmati 1**	-7.21**	0.87	-1.28	-31.90**	-8.53	-7.46	-15.78**	1.39	-17.71**	-42.64**	-6.97	-23.61**
27	**IRSSTN-135×NDR 359**	-31.61**	-30.72**	-32.20**	-10.20*	20.63**	22.04**	-16.38**	16.55*	-5.40	-13.22*	40.75**	15.57*
28	**IRSSTN-136×CSR 10**	-17.17**	-22.22**	-23.88**	6.29	22.46**	23.89**	-13.99**	17.02*	-5.03	-8.61	43.35**	17.71*
29	**IRSSTN-136×Improved pusa basmati 1**	2.81*	11.76**	9.38**	-20.61**	-8.53	-7.46	-10.47*	21.81**	-1.14	-28.92**	11.49	-8.45
30	**IRSSTN-136×NDR 359**	-17.75**	-22.77**	-24.41**	30.33**	50.16**	51.92**	-22.10**	8.59	-11.87*	3.67	62.60**	33.52**
31	**IRSSTN-139×CSR 10**	-31.26**	-25.49**	-27.08**	71.33**	43.43**	45.11**	-10.90*	11.25	-9.71	59.64**	59.64**	31.09**
32	**IRSSTN-139×Improved pusa basmati 1**	-27.56**	-21.24**	-22.92**	51.35**	39.68**	41.31**	-14.46**	6.81	-13.31*	67.44**	49.22**	22.53**
33	**IRSSTN-139×NDR 359**	-36.08**	-30.72**	-32.20**	49.89**	59.30**	61.17**	-19.69**	11.94	-9.15	49.88**	78.70**	46.74**
34	**IRSSTN-142×CSR 10**	6.87**	-8.50**	-10.45**	67.98**	40.62**	42.27**	-17.55**	6.87	-13.26*	50.73**	50.73**	23.77**
35	**IRSSTN-142×Improved pusa basmati 1**	-21.64**	-14.81**	-16.63**	-25.22**	-30.99**	-30.18**	-11.05*	15.30*	-6.42	-11.12	-19.86*	-34.20**
36	**IRSSTN-142×NDR 359**	4.07*	-10.89**	-12.79**	6.15	12.81*	14.14*	-12.85**	21.48**	-1.40	15.03*	37.15**	12.62

37	**IRSSTN-143×CSR 10**	-26.36**	-26.36**	-27.93**	-11.21	-23.55**	-22.65**	0.68	20.52**	-2.19	-7.75	-7.75	-24.25**
38	**IRSSTN-143×Improved pusa basmati 1**	-12.53**	-4.90**	-6.93**	3.70	-4.30	-3.18	12.96*	30.91**	6.25	25.59**	25.59**	3.13
39	**IRSSTN-143×NDR 359**	-12.42**	-12.42**	-14.29**	-11.36*	-5.79	-4.69	-6.64	30.13**	5.62	2.75	22.51**	0.60
40	**IRSSTN-144×CSR 10**	-16.40**	-21.13**	-22.81**	-8.85	-23.70**	-22.80**	-6.33	18.61**	-3.73	-9.32	-9.32	-25.54**
41	**IRSSTN-144×Improved pusa basmati 1**	-7.11**	0.98	-1.17	20.62**	11.32	12.62*	-4.78	20.57**	-2.14	38.28**	34.39**	10.35
42	**IRSSTN-144×NDR 359**	-10.97**	-16.01**	-17.80**	-29.13**	-24.68**	-23.80**	-12.67**	21.72**	-1.20	-23.18**	-8.40	-24.79**
43	**IRSSTN 152×CSR 10**	-23.26**	-24.51**	-26.12**	2.90	-13.87*	-12.86*	6.92	33.62**	8.45	14.96	14.96	-5.60
44	**IRSSTN 152×Improved pusa basmati 1**	-36.37**	-30.83**	-32.30**	-24.01**	-29.87**	-29.05**	5.07	31.31**	6.57	3.49	-7.77	-24.27**
45	**IRSSTN 152×NDR 359**	-26.47**	-27.67**	-29.21**	-32.76**	-28.54**	-27.70**	-7.27	29.25**	4.90	-22.57**	-7.67	-24.19**
46	**IRSSTN 155×CSR 10**	-21.21**	-20.70**	-22.39**	21.61**	1.80	2.99	-9.92	7.82	-12.49*	9.62	9.62	-9.99
47	**IRSSTN 155×Improved pusa basmati 1**	-25.35**	-18.85**	-20.58**	-19.06**	-25.30**	-24.42**	0.00	16.79*	-5.21	-1.91	-12.58	-28.22**
48	**IRSSTN 155×NDR 359**	-22.73**	-22.22**	-23.88**	-3.07	3.02	4.23	-6.19	30.76**	6.13	13.26	35.04**	10.89
	Range of heterosis MIN	**-36.87**	**-31.37**	**-32.84**	**-55.48**	**-40.20**	**-39.50**	**-24.92**	**1.39**	**-17.71**	**-57.64**	**-31.30**	**-43.59**
	MAX	**9.37**	**11.76**	**9.38**	**85.76**	**64.65**	**66.58**	**12.96**	**33.62**	**8.45**	**91.23**	**78.70**	**46.74**
	Mean heterosis (%)	**-18.63**	**-18.46**	**-20.19**	**9.94**	**6.64**	**7.89**	**-7.70**	**16.38**	**-5.54**	**12.84**	**23.08**	**1.06**
	No. of crosses with significant positive heterosis	5	1	1	20	19	21	1	30	0	21	27	17

CHAPTER-V

DISCUSSION

Recurrent genetic improvement of crops for increased yield potential is essential as the net agricultural land is fast declining due to rapid increase in population. It emphasized therefore, direct need to produce more and more on squeezing cultivable land of the country to meet the future demand.

Exploitation of semi-dwarf plant genes possessing multiple resistance/tolerance against several biotic and abiotic stresses in the early seventies helped several national programs including India to achieve higher and stable rice yields particularly under irrigated and favorable rain-fed lowland ecosystem.

Yield is a complex end product of a number of components most of which are under polygenic control. All changes in yield must be accompanied by changes in one or more of the components as have been pointed out by Grafius (1959). The ultimate goal of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic yield. It makes logical to look at the prospects of technologies which can help in quantum increase in rice yields per unit area per unit time.

Successful demonstration of hybrid rice technology on commercial basis in china during mid-eighties revealed that utilization of the phenomenon of hybrid vigor is one of the feasible options to get quantum jump in rice potential yield by 20-30 per cent over the best available inbred rice (Yuan and Virmani, 1988). China is currently having about 55 per cent of its total hectare under hybrids producing 18 million tonnes of extra paddy per annum (Virmani, 1992). Since 1979, IRRI and several countries in Asia including India have been exploring the potential and problems of commercial exploitation of heterosis.

In order to plan any breeding strategy aimed at the genetic improvement for yield and other traits of a crop it is imperative to learn the genetic architecture of the materials to be used. Information on the gene action and combining ability and nature and magnitude of heterosis could be useful to identify specific parents and crosses for further exploitation in breeding program. Therefore, the present investigation entitled

“**Genetic studies for yield and its contributing components in rice (*Oryza sativa* L.) under salt affected soil’’** was under taken with the objectives (i) to examine the genetic variability and evaluate the rice genotypes for various traits. (ii) to compute association at genotypic and phenotypic levels among different ccharacters. (iii) to assess the stability of rice genotypes. (iv) to study the combining ability variances and their effects. (v) to find out gene action involved in the inheritance of various characters. (vi) to estimate heterosis over better-parent and standard varieties, and (vii) to identify promising parents and superior hybrids for exploitation in breeding programme.

The experiment was conducted at Genetics and Plant Breeding Research Farm (GPB farm) and Student Instructional Farm of N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya. Fourty nine rice genotypes, showing wide spectrum of variation for various characters were evaluated in salinity and normal soil at GPB farm and Student Instructional Farm, respectively under irrigated condition during *Kharif* 2016 and 48 crosses were made involving 16 lines and 3 testers during *Kharif* 2016.

The combining ability experiment was based on the evaluation of a line × tester set of 48 hybrids (F_1s) and their 19 parents (16 lines and 3 testers) under salinity condition at GPB Farm in randomized block design with three replications during *Kharif*, 2017.

Thirteen characters *viz.,*days to 50% flowering, plant height (cm), flag leaf area (cm^2), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-grain weight (g), L:B ratio, biological yield per plant (g), harvest-index (%) and grain yield per plant (g) were recorded for germplasm evaluation and line×tester analysis.

The analysis of variance were done following the formulae suggested by Panse and Sukhatme (1967), the estimates of coefficients of variation by Burton and de Vane, (1953), heritability in broad sense by Hanson *et al.,*(1956) and genetic advance in per cent of mean by Johnson *et al.,* (1955), The nature of associations among different characters was studied by using genotypic and phenotypic correlation by

Searle, (1961) and path coefficient analysis by Dewey and Lu (1959), genetic divergence by D^2 statistics as suggested by Mahalanobis (1936) and Rao (1952) and stability index by Eberhart and Russell (1966). The data was subjected to line×tester analysis following Kempthorne (1957) to estimate combining ability variances and their effects and other genetic parameters. The estimates of heterosis over better parent and standard varieties were computed for the study of heterosis as suggested by Fonseca and Patterson (1968).

5.1 Germplasm Evaluation

Salient findings from these investigations are discussed under following sections

5.1.1 Analysis of variance
5.1.2 Mean performance of genotypes
5.1.3 Coefficients of variation
5.1.4 Heritability and genetic advance
5.1.5 Correlation coefficients
5.1.6 Path coefficient analysis
5.1.7 Heritbaility and gene action
5.1.8 Stability index for grain yield per plant

5.1.1 Analysis of variance

Analysis of variance revealed that mean sum of square for the treatments were highly significant for all the traits under study over both conditions. This showed that sufficient genetic variability is present in the genotypes, which can be used for the rice improvement programme.

5.1.2 Mean performance of genotypes

Forty nine entries of rice germplasm were evaluated for yield and yield components under saline and normal soil. A critical view of mean performance is given in appendix I and II. The most desirable lines for different characters are listed in Table 5.1(a) for salinity condition and in Table 5.1(b) for normal condition.

Mean performance of genotypes under saline condition

Salinity, a serious problem affecting one third of all the irrigated land in the world

(Mass and Hoffman, 1977), impairs normal growth and limits the realization of yield potential of modern cultivars. Salinity is one of the major obstacles to increase production in rice growing areas worldwide. Rice is rated as an especially salt-sensitive crop (Shannon *et al.*, 1998). Rice has enormous variability. Hence, evaluation of rice germplasm in salt affected soil is one of the important ways to identify the rice genotypes having tolerance capacity to salinity condition. Such genotypes may be used for the development of rice varieties for salt affected area.

The genotype, IRSSTN-135, produced highest grain yield per plant (20.48g) and showed highest mean performance for biological yield per plant (g).The second highest yielding genotype was IRSSTN-115 (18.56g) based on high mean performance for grain yield per plant and exhibited high mean performance for biological yield per plant (g), 1000- grains weight (g), grains per panicle, spikelets per panicle, flag leaf area (cm^2) and plant height (cm).The third ranking genotype for yield IRSSTN-131 (17.8 g) showed better mean performance for biological yield per plant (g), L:B ratio and flag leaf area (cm^2).The genotype, IRSSTN-128, which ranked fourth for grain yield per plant (17.29g) also possessed high mean performance for grains per panicle and spikelets per panicle. Line IRSSTN-125 having grain yield of 17.18g showed average mean performance for harvest-index (%).

The high yielding lines discussed above having high mean performance for grain yield and its contributing characters may be recommended for use in breeding programmes as donor or recurrent parents for developing superior genotypes for saline soil. Several lines showed very high mean performance for one or more of yield components in problematic soil conditions, but appeared average or low yielders. Such genotypes may be utilized as donors for improving yield component in a components breeding approach even if they had medium or low grain yield. In view of the above consideration, the most desirable genotypes in saline soil (Table 5.1a) were IRSSTN-105 IRSSTN-103 and IRSSTN-111 for early flowering; IRSSTN-105 IRSSTN-115 and IRSSTN-114 for plant height; IRSSTN-131 IRSSTN-125 and IRSSTN-111 for flag leaf area; IRSSTN-107, IRSSTN-109 and IRSSTN-103 for panicle length; IRSSTN-115, IRSSTN-119 and IRSSTN-134 for spikelets per panicle; IRSSTN-115, IRSSTN-119 and IRSSTN-139 for grains per panicle; IRSSTN-113 for spikelet fertility (%); IRSSTN-115, IRSSTN-138 and IRSSTN-102 for 1000- grains weight; IRSSTN-116 IRSSTN-114 and IRSSTN-108 for L:B ratio; IRSSTN-135, IRSSTN-137 and IRSSTN-139 for biological yield per plant; IRSSTN-130, IRSSTN-110 and CSR 43 for harvest-index; IRSSTN-135, IRSSTN-115 and IRSSTN-131 for grain yield per plant. Kumari *et al.* (2017), Devi *et al.* (2017) also studied mean performance of rice genotypes and reported that genotypes having high mean performance for grain yield also have mean performance for yield contributing traits.

Mean performance of genotypes under normal condition

The rice genotypes performing better in one condition not necessarily perform better in another condition. Therefore, it is necessary to test the genotypes over environments to find out the stable genotypes.

The genotype, IRSSTN-101, produced highest grain yield per plant (23.46g) and showed highest mean performance for biological yield per plant (g) and 1000- grains weight (g). The second highest yielding genotype was IRSSTN-132 (21.32g) based on high mean performance for grain yield per plant and biological yield per plant (g). The third ranking, line IRSSTN-136 (21.03g) showed better mean performance for biological yield per plant (g). The genotype, CSR 43 which ranked fourth for grain yield per plant (18.93g) also possessed high mean performance for grains per panicle and spikelets per panicle. Line IRSSTN-137 having grain yield of 18.25g showed average mean performance for L:B ratio, 1000- grains weight (g).

The most desirable genotypes in order of merit for various quantitative traits in normal soil were IRSSTN-121, IRSSTN-116 and IRSSTN-124 for early flowering; IRSSTN-126, IRSSTN-129 and IRSSTN-108 for plant height; IRSSTN-135, IRSSTN-131 and IRSSTN-111 for flag leaf area; IRSSTN-124 for panicle length; IRSSTN-146 for panicle length (cm) IRSSTN-126, IRSSTN-108 and IRSSTN-135 for spikelets per panicle; IRSSTN-108, IRSSTN-126 and IRSSTN-115 for grains per panicle; IRSSTN-117, IRSSTN-113 and IRSSTN-146 for spikelet fertility (%); IRSSTN-146, IRSSTN-101 and IRSSTN-141 for 1000- grains weight; IRSSTN-143, CSR 43 and IRSSTN-111 for L:B ratio; IRSSTN-101, IRSSTN-132 and IRSSTN-136 for biological yield per plant; CSR 43 for harvest-index; IRSSTN-101 IRSSTN-132 and IRSSTN-136 for grains yield per plant (Table 5.1b). The result revealed that IRSSTN 135 performed better over both soil conditions. These results are similar to those of Kumari *et al.* (2017) and Devi *et al.* (2017).

5.1.3 Coefficient of variation

The knowledge of genetic variability in a given crop species for characters under improvement is important in any plant breeding programme. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorized as low (0-10%), moderate (10-20%) and high (>20%) as indicated by Sivasubramanian and Madhavamenon (1973). The phenotypic and genotypic coefficients of variation were computed to assess the nature and magnitude of existing variability in the germplasm.. According to the classification high magnitude (>20%) of PCV and GCV were recorded for grain yield per plant (g) and biological yield per plant under both conditions, which indicated the possibility of getting high response to selection and inheritance of these characters are governed by the additive gene action. The existence of high variability for yield and yield contributing traits in rice has also been reported earlier by Satheesh kumar and Saravana *et aI.* (2012), Devi *et al.* (2016) and Sandeep *et al.* (2018). The moderate estimates of coefficients of variation (>10 to <20%) at genotypic and phenotypic levels were found for plant height, spikelets per panicle, grains per panicle, L:B ratio, harvest-index (%) and flag leaf area under salinity condition. Under normal condition the moderate estimates (10-20%) of PCV and GCV were recorded for flag leaf area, panicle bearing tillers per plant and L:B ratio. The characters exhibited moderate PCV and GCV values, as mentioned above, are likely to allow reasonable scope of improvement through selection in respective environment owing to their moderate genetic variability. Low estimates (<10%) of these two parameters were observed for days to days to 50% flowering, spikelet fertility and 1000-grains weight in salinity condition and days to 50% flowering, plant height, panicle length, spikelet fertility and harvest index has recorded as low estimates for PCV and GCV under normal condition, it indicates little scope of

Table 5.1 (a): The most desirable genotypes based on mean performance for 13 characters in rice under salinity condition

S.N.	Characters	Genotypes
1	Days to 50% flowering	IRSSTN-105, IRSSTN-103, IRSSTN-111, IRSSTN-113, IRSSTN-130, IRSSTN-107, CSR 43, IRSSTN-106
2	Plant height (cm)	IRSSTN-105, IRSSTN-115, IRSSTN-114, IRSSTN-134, IRSSTN-120, IRSSTN-112, IRSSTN-123, IRSSTN-110, IRSSTN-124, IRSSTN-111, IRSSTN-106, IRSSTN-107, IRSSTN-102, IRSSTN-109, IRSSTN-116
3	Flag leaf area (cm^2)	IRSSTN-131, IRSSTN-125, IRSSTN-111, IRSSTN-103, IRSSTN-114, IRSSTN-140, IRSSTN-117, IRSSTN-115, IRSSTN-144, IRSSTN-147, IRSSTN-142, IRSSTN-124, IRSSTN-130.
4	Panicle bearing tillers per plant	IRSSTN-115, IRSSTN-135, IRSSTN-119, IRSSTN-126 and IRSSTN-111.
5	Panicle length (cm)	IRSSTN-107, IRSSTN-109, IRSSTN-103, IRSSTN-112, IRSSTN-104.
6	Spikelets per panicle	IRSSTN-115, IRSSTN-119, IRSSTN-134, IRSSTN-139, IRSSTN-130, IRSSTN-145IRSSTN-147, IRSSTN-137, IRSSTN-141, IRSSTN-128
7	Grains per panicle	IRSSTN-115, IRSSTN-119, IRSSTN-139, IRSSTN-134, IRSSTN-145,IRSSTN-114IRSSTN-130, IRSSTN-142, IRSSTN-141, IRSSTN-147, IRSSTN-128
8	Spikelet fertility (%)	IRSSTN-113, IRSSTN-148, IRSSTN-114, IRSSTN-112, IRSSTN-142
9	1000- grains weight (g)	IRSSTN-115, IRSSTN-138, IRSSTN-102, IRSSTN-141, IRSSTN-104, IRSSTN-106, IRSSTN-114, IRSSTN-110, IRSSTN-121, CSR 43, IRSSTN-118, IRSSTN-105, IRSSTN-127, IRSSTN-109, IRSSTN-122, IRSSTN-108, IRSSTN-148
10	L:B ratio	IRSSTN-132, IRSSTN-116, IRSSTN-114, IRSSTN-108, IRSSTN-112, IRSSTN-117, IRSSTN-113, CSR 43, IRSSTN-131, IRSSTN-102, IRSSTN-103
11	Biological yield per plant (g)	IRSSTN-135, IRSSTN-137, IRSSTN-139, IRSSTN-129, IRSSTN-132, IRSSTN-131, IRSSTN-119, IRSSTN-121, IRSSTN-115, IRSSTN-133, IRSSTN-141
12	Harvest-index (%)	IRSSTN-130, IRSSTN-110, CSR 43, IRSSTN-108, IRSSTN-105
13	Grains yield per plant(g)	IRSSTN-135, IRSSTN-115, IRSSTN-131, IRSSTN-128, IRSSTN-125,IRSSTN-130, IRSSTN-139, IRSSTN-137, CSR 43

Table 5.1 (b): The most desirable genotypes based on mean performance for 13 characters in rice under normal condition

S.N.	Characters	Genotypes
1	**Days to 50% flowering**	IRSSTN-107, IRSSTN-106, IRSSTN-130, IRSSTN-113, IRSSTN-105
2	**Plant height (cm)**	IRSSTN-106, IRSSTN-124, IRSSTN-123, IRSSTN-121, IRSSTN-119,
3	**Flag leaf area (cm^2)**	IRSSTN-135, IRSSTN-131, IRSSTN-111, IRSSTN-114, IRSSTN-117, IRSSTN-115, IRSSTN-107, IRSSTN-140, IRSSTN-146, IRSSTN-144, IRSSTN-148, IRSSTN-125,
4	**Panicle bearing tillers per plant**	IRSSTN-135, IRSSTN-124, IRSSTN-121, IRSSTN-111, IRSSTN-132
5	**Panicle length (cm)**	IRSSTN-126, IRSSTN-107, IRSSTN-135, IRSSTN-141, IRSSTN-108, IRSSTN-146
6	**Spikelets per panicle**	IRSSTN-126, IRSSTN-108, IRSSTN-135, IRSSTN-115, IRSSTN-104, IRSSTN-114, IRSSTN-131, IRSSTN-127
7	**Grains per panicle**	IRSSTN-108, IRSSTN-125, IRSSTN-115, IRSSTN-135, IRSSTN-104, IRSSTN-114, IRSSTN-131, IRSSTN-139,IRSSTN-113
8	**Spikelet fertility (%)**	IRSSTN-117, IRSSTN-113, IRSSTN-146, IRSSTN-116, IRSSTN-123
9	**1000- grains weight (g)**	IRSSTN-146, IRSSTN-101, IRSSTN-141, 1IRSSTN-148, IRSSTN-113, IRSSTN-117, IRSSTN-137, IRSSTN-115, IRSSTN-109, CSR 43
10	**L:B ratio**	IRSSTN-143, CSR 43, IRSSTN-111, IRSSTN-114, IRSSTN-115, IRSSTN-138, IRSSTN-137, IRSSTN-141, IRSSTN-103, IRSSTN-140
11	**Biological yield per plant (g)**	IRSSTN-101, IRSSTN-132, IRSSTN-136, IRSSTN-135, IRSSTN-146, IRSSTN-125, IRSSTN-137, IRSSTN-111, IRSSTN-141, IRSSTN-115.
12	**Harvest-index (%)**	CSR 43, IRSSTN-136,
13	**Grains yield per plant(g)**	IRSSTN-101 IRSSTN-132, IRSSTN-136 CSR 43, IRSSTN-137, IRSSTN-135, IRSSTN-141, IRSSTN-146, IRSSTN-125, IRSSTN-115

improvement in these traits due to lack of requisite variability under both saline and normal conditions. In general, a high coefficient of variability indicates that there is a scope of selection and improvement of these traits. Low values indicate the need for creation of variability either by hybridization or mutation followed by selection.

The magnitude of PCV estimates in the present study was found to be slightly higher than their respective GCV for all the studied traits which might be the result of influence of environment on the development of characters period. Similar report noticed earlier by Ogunbayo *et al.* (2014) and Idris *et al.* (2012) in rice. However, the narrow magnitude of difference between PCV and GCV were recorded for characters indicating limited influence of environment in the expression of these characters. The result is in agree with Idris and Mohamed (2013) who reported small differences between PCV and GCV for plant height and panicle length. Thus selection based on phenotypic performance of these characters would be effective to bring about considerable genetic improvement. But, there were considerable difference between the PCV and GCV for panicle bearing tillers per plant and harvest index under both conditions which, indicates greater effects of environmental factors in the phenotypic expression of these characters. Thus, selection based on phenotypic performance of these characters would be ineffective to bring about considerable genetic improvement of these traits in the genotypes considered in the current study. The results of the present study in respect of genotypic and phenotypic coefficient of variation are broadly in agreement with the findings of earlier workers Souleymane *et al.* (2016), Anis *et al.* (2016), Devi *et al.* (2016), Preeti *et al.* (2018) and Dwivedi *et al.* (2015 i)

5.1.4 Heritability and genetic advance

Heritability and genetic advance are more helpful in predicting the grain under effective selection. Further, the important direct selection parameters, heritability in broad sense (h^2b) and genetic advance in per cent of mean (GA) provide index of transmissibility of traits which gives indication about the effectiveness of selection in improving the characters. Heritability was classified as low (<50%), medium (50-75%) and high (>75%) as suggested by Johanson *et al.* (1955). Considering this delineation, under salinity condition high estimates of broad sense heritability coupled with high genetic advance in per cent of mean were recorded for plant height, flag leaf area, spikelets per panicle, grains per panicle, L:B ratio, biological yield per plant and grain yield per plant (Table 4.2a). On the other hand under normal condition high heritability coupled with high genetic advance in per cent of mean were observed for flag leaf area, spikelets per panicle, grains per panicle, L:B ratio, biological yield per plant and grain yield per plant (Table 4.2b). High heritability in broad sence values indicate that the characters under study are less influenced by environment in their expression. Therefore, the rice breeder may make superior genotypes selection based on phenotypic performance for these traits.

Among above mentioned characters grains yield per plant and biological yield per plant under both conditions exhibit high h^2 and high GA also showed high GCV and PCV values, which indicated that these would be ideal traits for improvement through selection owing to their high transmissibility and variability. Thus, the germplasm evaluated and/or segregating generations derived from them may provide very high response to selection for the characters exhibiting high heritability along with high genetic advance in per cent of mean.

The occurrence of moderate heritability and moderate genetic advance in per cent of mean with moderate GCV and PCV were observed for panicle length, and harvest index under saline and for panicle bearing tillers per plant under normal conditions indicated that these traits may provide reasonable selection response in saline and normal soil conditions. The results were mostly supported by reports made earlier in rice by Krupakar and Pandey (2012) for days to heading, plant height, panicle length and biomass yield per plot in rice.

The low order of heritability coupled with low genetic advance in per cent of mean was observed for panicle bearing tillers per plant under saline and harvest index under normal condition indicated greater role of environment in the expression of the traits. Thus, direct selection for these traits will be ineffective. Therefore, methods of selection based on families and progeny testing are more effective and efficient. Similar report were also reported by other investigators Fentie *et al.* (2014), Kumari *et al.* (2018) and Sandeep, *et. al.*(2018). Akinwale *et* *al.* (2011) reported low heritability for 1000 grain weight. Tefera *et al.* (2017) reported low heritability and genetic advance in percent of mean for harvest index. In present study, medium estimates of heritability under saline and low under normal soil were reported for harvest index. The study indicated that this trait is much influenced by the environmental condition.

Heritability alone provides no an indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence, knowledge about heritability coupled with genetic advance and genotypic coefficient of variations are most useful. Thus in the present study, high heritability coupled with high GCV and high genetic advance as percentage of mean were recorded by biological yield per plant and grain yield per plant under both conditions indicated that the traits were simply inherited in nature and controlled by few major genes or possessed additive gene effects. Hence, simple selection could be effective for improving these characters. Rai *et al.* (2014) also evaluated 40 rice genotypes and observed similar results for biological yield.

Low estimates of genetic parameters were recorded for panicle length, spikelets fertility, and harvest index. This indicated these characters are governed by non-additive gene action and heterosis breeding will be useful. Similar results were reported by Tefera *et al.* (2017) for harvest index, grains per panicle and days to maturity.

5.1.5 Correlation coefficient

The grain yield, in almost all the crops, is referred to as super character, which results from multiplicative interaction of several other traits that are termed as yield components. Thus, genetic architecture of grain yield, in rice as well as other crops, is based on the balance or overall net effect produced by various yield components directly or indirectly by interacting with one another. Therefore, identification of important yield components and information about their association with yield and also with each other is very useful for developing efficient breeding strategy for evolving high yielding varieties. In this respect, the correlation coefficient, which provides symmetrical measurement of degree of association between two variables or characters, helps us in understanding the nature and magnitude of association between yield and its components.

In the present study, phenotypic and genotypic correlation under salinity and normal condition has been presented in table 4.3a, 4.3b, 4.4a and 4.4b, respectively. The genotypic correlations in general were higher than the corresponding phenotypic correlations. This is due to the modified effect of environment on character association at the genetic level.

The grain yield per plant exhibited very high positive associations with biological yield per plant followed by harvest-index (%) and panicle bearing tillers per plant at phenotypic as well as genotypic levels under salinity condition and with biological yield per plant followed by 1000-grains weight (g), harvest-index (%) and plant height (cm) under normal condition. Thus, above traits emerged as most important associates of grain yield per plant in rice. Harvest index showed significant and positive correlation with panicle bearing tillers per plant. Biological yield per plant possessed positive and highly significant correlation with grains per panicle and positive and significant correlation with spikelets per panicle and plant height (cm). Spikelet fertility (%) showed positive and high significant correlation with grains per panicle and positive and significant association with panicle bearing tillers per plant. Grains per panicle showed positive and highly significant association with spikelets per panicle. This indicated increase in one variable leads increase in second variable.

The high positive associations between grain yield with days to 50% flowering, biological yield per plant, harvest-index, spikelet fertility, spikelets per panicle, plant height and panicle bearing tillers are in agreement with earlier findings of Kumar (2015), Kumari *et al.*, (2017), Sumithra, *et al.* (2019), Saha *et al.* (2019), Sreedhar and Reddy (2019) .

5.1.6 Path-coefficient analysis

Path-coefficient analysis is a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on grain yield to provide clear picture of character associations for formulating efficient selection strategy. Path analysis differs from simple correlations in that it points out the causes and their relative importance, whereas, the latter measures simply the mutual association ignoring the causation.

In the present study, the path-coefficient analysis was carried out at genotypic as well as phenotypic levels in saline and normal soil conditions presented in table 4.5a, 4.5b, 4.6a and 4.6b.

, The highest positive direct effect on grain yield per plant at phenotypic as well as genotypic levels was exerted by biological yield per plant (0.807) followed by harvest-index (0.694), spikelets per panicle (0.495), spikelet fertility (0.201) and flag leaf area (0.039) under both conditions. The high direct effect of biological yield per plant, harvest index, spiketets per panicle, spikelet fertility and flag leaf area possessing highly significant positive association with grain yield per plant and are mostly similar highlighted the importance of this trait for rice improvement through direct selection. Dwivedi *et al.* (2012), Dwivedi *et al.* (2015), Rai *et al.* (2014), Dwivedi *et al.* (2015) and Sumithra, *et al.* (2019), have also found high direct contribution of biological yield per plant and harvest-index on grain yield per plant. Thus, biological yield per plant and harvest-index emerged as most important direct contributor towards the grain yield. Direct effects of remaining characters on grain yield per plant were moderate or too low to be considered important.

Spikelets per panicle showed maximum positive indirect effects on grain yield per plant *via* grains per panicle (0.445) followed by *via* biological yield per (g) (0.170) and days to 50% flowering (0.108). Biological yield per (g) showed highest positive indirect effects on grain yield per plant *via* grains per panicle (0.333) followed by via. spikelets per panicle (0.277), panicle bearing tillers per plant (0.269), plant height (cm) (0.261) and spikelet fertility (%) (0.203). Harvest index (%) exhibited highest positive indirect effects on grain yield per plant *via* panicle bearing tillers per plant (0.186) followed by *via* 1000-grains weight (g) (0.158) and L:B ratio (0.131). In this situation indirect traits are to be considered simultaneously for selection.

In contrast, grains per panicle showed considerable negative indirect effect on grain yield per plant *via. s*pikelets per panicle followed by *via.* spiklets fertility and biological yield per plant. The complexity arising due to contrasting negative indirect effect with positive indirect effect in case of biological yield per plant renders true role of biological yield per plant as indirect yield contributor complex in nature. On the basis of path-coefficient analysis at phenotypic and genotypic levels, the remaining estimates of indirect effects not discussed above were too low to be considered of any consequence. The high order positive direct and indirect contribution of biological yield per plant was also recorded by Jaiswal *et al*. (2007) and Yadav *et al.* (2008).

5.1.7 Genetic divergence analysis

In plant breeding programmes, genetic variability is exploited to meet the changing needs for developing improved varieties of a crop. It is also important that considerable variability for various traits exists in the breeding materials for profitable exploitation following recombination breeding or selection. Since it is not practically feasible to involve large number of lines in hybridization programme, executed for generating superior segregates for developing improved varieties. Breeder has to choose or select limited number of genotypes for exploitation in breeding programme. The existence of optimum genetic divergence between the parents is an important pre-requisite for success of any crop improvement programme based on recombination breeding, because crosses between genetically diverse parents have been found to provide superior transgressive segregants in the segregating generations. Thus, genetically diverse parents when crossed can bring together diversity of gene combinations either to exploit heterosis for developing hybrid varieties or to obtain superior recombinants for developing pure line varieties. Thus, assessment of genetic diversity existing in the breeding materials is an essential requirement for any breeding programme. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop such as rice to recover transgressive segregates has also been repeatedly emphasized by Pandey and Anurag (2010) and Padamja *et al.* (2010)

Earlier workers considered distances in place of origin as index of genetic diversity and used it for selection of parents. However, genetic diversity has not been always found to be based on factors such as geographic diversity, place of release or ploidy level in majority of crops including rice Chandra *et al.* (2007), Kumar (2008) and Raut *et al.* (2009). Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures such as D^2 statistics. These procedures characterize genetic divergence using the criterion of similarity or dissimilarity based on the aggregates of number of agronomical important characters.

In present study, Mahalanobis D^2 analysis helped in grouping 49 genotypes of rice into 8 distinct non-overlapping clusters under both salinity (Table 4.7a) and under normal conditions (Table 4.7b).

Cluster 6 contained highest numbers of 9 genotypes followed by cluster 2, 3, 4 and 5 with 7 genotypes each, cluster 8 with 5 genotypes, clusters 7 with 4 genotypes and cluster 1 with 3 genotypes under salinity condition. Under normal condition cluster 6 contained highest numbers of 14 genotypes followed by cluster 8 with 10 genotypes, cluster 2 with 8 genotypes, clusters 7 with 5 genotypes and cluster 1 with 4 genotypes

The discrimination of lines into so many discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Existence of substantial genetic divergence in rice materials have also reported by Ramya and Kumar *et al.*(2008), Ishfaq *et al.* (2009) and Rouf *et al.* (2009).

Presence of substantial genetic diversity among the lines screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed as isolating desirable segregates for developing high yielding varieties of rice suitable for saline soil.

An examination of the clustering pattern of the 49 rice genotypes into 8 clusters revealed that these genotypes originated in same place or geographic region were also found to be grouped in different clusters. This indicated lack of any definite relationship or correlation between genetic diversity and geographic origin of the rice genotypes evaluated in the present study because the lines originated at same place were grouped into different clusters. Therefore, the selection of parental materials for hybridization programme simply based on geographic diversity may not be rewarding exercise. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographic distances. This finding is in conformity with the previous reports advocating lack of parallelism between genetic and geographic diversity in rice by Chandra *et al.* (2007), Kumar (2008), Raut *et al.* (2009) and Kumari (2018). An examination of the estimates of within and between cluster, genetic diversity presented by intra-and inter-cluster D^2 values revealed that genotypes of the same cluster had little divergence form each other with respect to aggregate effect of 13 characters under both salinity (Table 4.8a) and normal conditions (Table 4.8b).

Therefore, the chances of obtaining good recombinants in segregating generations by crossing the members of the same cluster are very low. It is, therefore, suggested that crosses should be attempted between the genotypes belonging to clusters separated by large inter-cluster distances. In this respect, Under salinity condition the intra-cluster distances ranged from 115.23 (cluster 3) to 407.84 (cluster 8). The maximum inter-cluster distance was observed between cluster 3 and 8 (1188.00) followed by cluster 3 and 7 (1077.27), cluster 2 and 7 (947.08), cluster 2and 8 (935.58), cluster 1 and 8 (855.55) and cluster 3 and 6 (822.32). The minimum estimate for inter-cluster distance was recorded between cluster 2 and 3 (307.65) followed by cluster 3 and 4 (308.86) and cluster 2 and 5 (310.20).

Under normal condition the intra-cluster distances ranged from 85.32 (cluster 2) to 152.60 (cluster 7). The maximum inter-cluster distance was observed between cluster 2 and 8 (672.83) followed by cluster 2 and 6 (622.82), cluster 2 and 7 (523.82), cluster 2 and 5 (498.49) and cluster 2 and 3 (491.83). The minimum estimate for inter-cluster distance was recorded between cluster 1 and 5 (152.78) followed by cluster 6 and 7 (186.86), cluster 5 and 7 (204.04), cluster 1 and 4 (204.69) and cluster 5 and 8 (206.29). This indicated that genotypes belonging to these clusters pairs were genetically close to each other. The crosses between genotypes belonging to clusters separated by low inter-cluster distances are unlikely to throw promising recombinants in the segregating generations.

Therefore, crossing between the genotypes belonging to cluster pairs separated by larger intra-cluster distances for one or another character to be improved is likely to be more fruitful. In this context, under salinity condition cluster 8 having 5 genotypes, and under normal condition cluster 7 having 8 genotypes showed very high intra-cluster distances from other clusters.

It reflects that crosses should be made between the genotypes of two different clusters separated by long inter-cluster distance in order to get good recombinants/ trangressives ssegregates to enhance the yield potential in saline and in normal soil conditions..

5.1.8 Stability index

Germplam IRSSTN-112 was found stable in both conditions while out of 49 germplam best five genotypes found better performing for normal condition were IRSSTN-104, IRSSTN-107, IRSSTN-132 IRSSTN-111 and IRSSTN-140 and best five germplam which performed better in saline condition were IRSSTN-139, IRSSTN-123, IRSSTN-119, IRSSTN-130 and IRSSTN-122. The stable genotype IRSSTN recommended for its cultivation over environments and can be used in rice improvement programme.

5.2 Line×Tester Analysis

5.2.1 Mean performance of genotypes

52.2 Coefficients of variation, heritability and genetic advance

5.2.3 Correlation coefficients

5.2.4 Path coefficient analysis

5.2.5 Heritbaility and gene action

5.2.6 Combining ability analysis

5.2.7 Heterosis over batter parent and standard varieties

5.2.1 Mean performance of genotypes

The analysis of variance revealed highly significant mean sum of squares due to treatments, parents, crosses and line×tester for all the thirteen characters. The mean sum of squares due to parents *vs.* crosses and testers were also significant for most of the characters. This indicated presence of substantial variability in the study materials and validated further statistical and genetical analysis.

The mean performance of 69 rice genotypes for 13 characters is presented in appendix 2 and the most desirable lines for different characters are listed in table 5.2. Very wide range of variation in mean performance of genotypes was observed for all the 13 characters under study. The comparison of mean performance of rice genotypes for 13 traits using critical differences revealed existence of very high level of variability in the rice genotypes evaluated in the present study.

The genotype, IRSSTN-135 produced highest grain yield per plant (22.26g) (Table 5.3) showed desirable mean performance for days to 50% flowering, plant height, flag leaf area, panicle bearing tillers per plant, spikelet fertility, 1000 grain weight, L:B ratio, biological yield per plant and harvest index . The genotype showing second highest mean performance for grain yield per plant was IRSSTN 136 (21.53 g) showed desirable mean performance for days to 50% flowering, plant height, panicle bearing tillers per plant, spikelets per panicle, 1000 grain weight, biological yield per plant and harvest index. The other rice genotype, IRSSTN 105 (14.80 g) showed superior mean performance for days to 50% flowering, panicle bearing tillers per plant, panicle length, spikelets per panicle, grains per panicle, 1000 grain weight, L:B ratio, biological yield per plant and harvest index.

Line IRSSTN 120 (14.59 g) showed high mean performance for days to 50% flowering, panicle bearing tillers per plant, panicle length, spikelets fertility, 1000 grain weight and biological yield per plant. IRSSTN 117 (14.55g) exhibited high mean performance for days to 50% flowering, plant height, flag leaf area, panicle bearing tillers per plant, panicle length, spikelets per panicle, grains per panicle, spikelet fertility and biological yield per plant. IRSSTN 107 (14.50g) showed high mean performance for days to 50% flowering, plant height, flag leaf area, panicle length, grains per panicle, spikelet fertility, L:B ratio, biological yield per plant and harvest index. IRSSTN 143 (13.73 g) for days to 50% flowering, plant height, flag leaf area, panicle bearing tillers per plant, spikelets per panicle, grains per panicle, spikelets fertility, L:B ratio, biological yield per plant and harvest index. IRSSTN 144 (13.34) exhibited high mean performance for days to 50% flowering, flag leaf area, panicle bearing tillers per plant, panicle length, spikelets per panicle, grains per panicle, 1000 grain weight, biological yield per plant and harvest index. IRSSTN 142 (12.38) showed high mean performance for days to 50% flowering, plant height, flag leaf area, panicle length, spikelets per panicle, grains per panicle, spikelets fertility and harvest index while IRSSTN 101 (12.15g) for days to 50% flowering, plant height, flag leaf area, panicle length, spikelets fertility and biological yield per plant. Thus, the high yielding lines discussed above having high mean performance for grain yield and for several other characters may be recommended for use as parent for developing high yielding rice hybrids in stress ecosystems.

In addition to genotypes mentioned above some other genotypes showing very high mean performance for other characters may be utilized as donors for improving those characters in a component breeding approach even if they had medium or low grain yield. In view of the above consideration, the most desirable genotypes were IRSSTN-135, IRSSTN-136, IRSSTN-105, IRSSTN-120 and IRSSTN-117 for early flowering; IRSSTN-129, IRSSTN-136, IRSSTN-101, IRSSTN-142 and IRSSTN-135 for short stature; IRSSTN-117, IRSSTN-107, IRSSTN-144, IRSSTN-142 and IRSSTN-135 for flag leaf area; IRSSTN-117, IRSSTN-107, IRSSTN-144, IRSSTN-142 and IRSSTN-135 for panicle bearing tillers per plant; IRSSTN-120, IRSSTN-142, IRSSTN-139, IRSSTN-152 and IRSSTN-105 for panicle length; IRSSTN-139, IRSSTN-144, IRSSTN-136, IRSSTN-117 and IRSSTN-155for spikelets per panicle; IRSSTN-139, IRSSTN-117, IRSSTN-166, IRSSTN-144 and IRSSTN-142 for grains per panicle; IRSSTN-101, IRSSTN-117, IRSSTN-139, IRSSTN-142 and IRSSTN-107 for spikelet fertility; IRSSTN-124, IRSSTN-155, IRSSTN-144, IRSSTN-136 and IRSSTN-105 for 1000 grain weight; IRSSTN-107, IRSSTN-139, IRSSTN-116, IRSSTN-105 and IRSSTN-135for L:B ratio; IRSSTN-135, IRSSTN-136, IRSSTN-120, IRSSTN-117 and IRSSTN-105 for biological yield per plant; NIRSSTN-136, IRSSTN-142, IRSSTN-144, IRSSTN-152 and IRSSTN-139for harvest index; IRSSTN-135, IRSSTN-136, IRSSTN-105, IRSSTN-120, IRSSTN-117, IRSSTN-107, IRSSTN-143, IRSSTN-144, IRSSTN-142 and IRSSTN-101 for grain yield per plant.

5.2.2 Coefficients of variation

The success of selection in improving plant characters mainly depends on presence of substantial genetic variability and nature of heritability and genetic advance. The genetic variability is the raw material of plant breeding programme on which selection acts to evolve superior genotypes. The phenotypic and genotypic coefficients of variation can be used for assessing and comparing the nature and magnitude of variability existing for different characters in the breeding materials. Heritability in broad sense quantifies the proportion of heritable genetic variance to total phenotypic variance, while heritability in narrow sense represents the ratio of fixable additive genetic variance to total phenotypic variance. Estimates of heritability help in estimating expected progress through selection. The genetic advance in per cent of mean provides indication of expected selection response by taking into account the existing genetic variability and heritability of the character. The estimates of direct selection parameters, coefficients of variation, heritability and genetic advance in per cent of mean were computed for thirteen characters of 48 crosses and their parents (Table 4.13).

The high estimates of genotypic and phenotypic coefficient of variation, heritability in broad sense along with genetic advance in *per cent* of mean were recorded for biological yield per plant, grain yield per plant and panicle bearing tillers per plant. Grains yield per plant recorded high estimates for GCV, heritability in broad sense and genetic advance in per cent of mean, while, moderate for PCV. Flag leaf area showed high estimates for heritability while, moderate estimates for PCV, GCV and high estimate of genetic advance in per cent of mean. Grains per panicle, spikelets per panicle and L:B ratio showed moderate estimates for PCV and GCV while, high estimates for heritability and genetic advance in per cent of mean. Days to 50% flowering, plant height, spikelet fertility and 1000 grain weight recorded low estimates for PCV and GCV, moderate for genetic advance in per cent of mean while, high for heritability. Panicle length showing low estimates for PCV and GCV, moderate for heritability and genetic advance in *per cent* of mean. Harvest index showed low estimates for PCV, GCV, genetic advance in per cent for mean and heritability. The characters panicle bearing tillers per plant, biological yield per plant and grain yield per plant having high PCV, GCV, heritability and genetic advance in per cent of mean indicated that inheritance are controlled by the additive gene action and direct selection would be rewarding. The high estimates of direct selection parameters observed for the above characters are broadly in agreement with earlier reports in rice Mohammad and Deva, 2002; Yadav *et al*., 2002; Chaudhary *et al*., 2004; Shukla *et al*., 2004; Mall *et al*., 2005; Suman *et al*., 2005; Singh *et al*., 2006; Panwar *et al*., 2007; Babar *et al*., 2009; Basavaraja *et al.* 2013; Kaini, 2013 and Sathya and Jebaraj, 2013; Devi *et al*., 2016.

5.2.3 Correlation coefficient

Grain yield or economic yield, in almost all the crops, is the complex character which manifests from multiplicative interactions of several other characters that are termed as yield components. The genetic architecture of grain yield in rice as well as other crops is based on the balance or overall net effect produced by various yield components directly or indirectly by interacting with one another. Therefore, selection for yield *per se* alone would not matter much as such unless accompanied by the selection for various component characters responsible for conditioning it. Thus, identification of important components and information about their association with yield and with each other are very useful for developing efficient breeding strategy for evolving high yielding varieties/hybrids. The correlation coefficient is the measure of degree of symmetrical association between two variables or characters which helps us in understanding the nature and magnitude of association among yield and yield components.

In the present investigation, phenotypic and genotypic correlation coefficients were computed among 13 characters (Table 4.14 and 4.15). Grain yield per plant showed highly significant and positive correlation with biological yield per plant and panicle bearing tillers per plant at phenotypic and genotypic levels. Therefore, these characters emerged as most important associates of grain yield in rice. The strong positive association of grain yield with the characters mentioned above has also being reported in rice by earlier workers Ramkrishnan *et al.*, 2006, Nandan *et al.,* 2010; Akhtar *et al*., 2011, Kumar *et al.,* 2011; Bhadru *et al.,* 2011; Rangare *et al.,* 2012; Krishnamurthy and Kumar, 2012; Pankaj *et al.,* 2013; Sudhamani *et al.,*

Table 5.2: The most desirable genotypes identified for high mean performance for 13 characters in rice under salinity condition

Characters	Genotypes
Days to 50% flowering	IRSSTN-135, IRSSTN-136, IRSSTN-105, IRSSTN-120, IRSSTN-117, IRSSTN-107, IRSSTN-143, IRSSTN-144, IRSSTN-142, IRSSTN-101
Plant height (cm)	IRSSTN-129, IRSSTN-136, IRSSTN-101, IRSSTN-142, IRSSTN-135, IRSSTN-105, IRSSTN-143, IRSSTN-117, IRSSTN 155, IRSSTN-107
Flag leaf area (cm^2)	IRSSTN-117, IRSSTN-107, IRSSTN-144, IRSSTN-142, IRSSTN-135, IRSSTN-143, IRSSTN-124, IRSSTN-155, IRSSTN-152, IRSSTN-101
Panicle bearing tillers per plant	IRSSTN-135, IRSSTN-124, IRSSTN-116, IRSSTN-144, IRSSTN-136, IRSSTN-105, IRSSTN-120, IRSSTN-129, IRSSTN-117, IRSSTN-143
Panicle length (cm)	IRSSTN-120, IRSSTN-142, IRSSTN-139, IRSSTN-152, IRSSTN-105, IRSSTN-101, IRSSTN-124, IRSSTN-107, IRSSTN-117, IRSSTN-144
Spikelets per panicle	IRSSTN-139, IRSSTN-144, IRSSTN-136, IRSSTN-117, IRSSTN-155, IRSSTN-105, IRSSTN-135,IRSSTN-132, IRSSTN-142, IRSSTN-143
Grains per panicle	IRSSTN-139, IRSSTN-117, IRSSTN-166, IRSSTN-144, IRSSTN-142, IRSSTN-133, IRSSTN-105, IRSSTN-155, IRSSTN-143, IRSSTN-107
Spikelet fertility (%)	IRSSTN-101, IRSSTN-117, IRSSTN-139, IRSSTN-142, IRSSTN-107, IRSSTN-143, IRSSTN-120, IRSSTN-116, IRSSTN-135, IRSSTN-152
1000- grains weight (g)	IRSSTN-124, IRSSTN-155, IRSSTN-144, IRSSTN-136, IRSSTN-105, IRSSTN-129, IRSSTN-152, IRSSTN-135, IRSSTN-116, IRSSTN-120
L:B ratio	IRSSTN-107, IRSSTN-139, IRSSTN-116, IRSSTN-105, IRSSTN-135, IRSSTN-129, IRSSTN-155, IRSSTN-143, IRSSTN-152, IRSSTN-124
Biological yield per plant (g)	IRSSTN-135, IRSSTN-136, IRSSTN-120, IRSSTN-117, IRSSTN-105, IRSSTN-107, IRSSTN-143, IRSSTN-101, IRSSTN-144, IRSSTN-129
Harvest-index (%)	IRSSTN-136, IRSSTN-142, IRSSTN-144, IRSSTN-152, IRSSTN-139, IRSSTN-135, IRSSTN-105, IRSSTN-155, IRSSTN-107, IRSSTN-143
Grains yield per plant(g)	IRSSTN-135, IRSSTN-136, IRSSTN-105, IRSSTN-120, IRSSTN-117, IRSSTN-107, IRSSTN-143, IRSSTN-144, IRSSTN-142, IRSSTN-101

Table 5.3: The mean performance of high yielding genotypes in rice for different characters under salinity condition

S.N.	Genotypes		High mean performance for other characters
1	**IRSSTN-135**	22.26	Days to 50% flowering, plant height, flag leaf area, penicle bearing tillers per plant, spikelets fertility, 1000 grain weight, L:B ratio, biological yield per plant, harvest index and grins yield per plant
2	**IRSSTN-136**	21.53	Days to 50% flowering, plant height, penicle bearing tillers per plant, spikelets per panicle, 1000 grain weight, biological yield per plant, harvest index and grins yield per plant
3	**IRSSTN-105**	14.80	Days to 50% flowering, penicle bearing tillers per plant, penicle length, spikelets per panicle, grains per panicle, 1000 grain weight, L:B ratio, biological yield per plant, harvest index and grins yield per plant
4	**IRSSTN-120**	14.59	Days to 50% flowering, penicle bearing tillers per plant, penicle length, spikelets fertility, 1000 grain weight, biological yield per plant and grins yield per plant
5	**IRSSTN-117**	14.55	Days to 50% flowering, plant height, flag leaf area, penicle bearing tillers per plant, penicle length, spikelets per panicle, grains per panicle, spikelets fertility, biological yield per plant and grins yield per plant
6	**IRSSTN-107**	14.50	Days to 50% flowering, plant height, flag leaf area, penicle length, grains per panicle, spikelets fertility, L:B ratio, biological yield per plant, harvest index and grins yield per plant
7	**IRSSTN-143**	13.73	Days to 50% flowering, plant height, flag leaf area, penicle bearing tillers per plant, spikelets per panicle, grains per panicle, spikelets fertility, L:B ratio, biological yield per plant, harvest index and grins yield per plant
8	**IRSSTN-144**	13.34	Days to 50% flowering, flag leaf area, penicle bearing tillers per plant, penicle length, spikelets per panicle, grains per panicle, 1000 grain weight, biological yield per plant, harvest index and grins yield per plant
9	**IRSSTN-142**	12.38	Days to 50% flowering, plant height, flag leaf area, penicle length, spikelets per panicle, grains per panicle, spikelets fertility, harvest index and grins yield per plant
10	**IRSSTN-101**	12.15	Days to 50% flowering, plant height, flag leaf area, penicle length, spikelets fertility, biological yield per plant and grins yield per plant

2013; Laxmi *et al.,* 2014; Gopikannan and Ganesh 2014; Venkann *et al.,* 2014; Devi *et al*. 2016and Kumari *et al*. 2017.

Days to 50% flowering showed significant and positive association with flag leaf area and panicle length. Flag leaf area exhibited positive and significant association with spikelets per panicle. Panicle bearing tillers per plant exhibited positive and significant association with biological yield per plant. Spikelets per panicle showed positive and significant association with grains per panicle. Grains per panicle recorded positive and significant association with spikelet fertility. Days to 50% flowering, spikelets per panicle, grains per panicle and 1000 grain weight exhibited negative and significant correlation with L:B ratio. Positive associations between these characters have also been reported by Janardanam *et al.* 2002; Zahid *et al*., 2006; Kishore *et al*., 2007; Rangare *et al.,* 2012; Krishnamurthy and Kumar 2012; Laxmi *et al.,* 2014; Gopikannan and Ganesh 2014 and Venkann *et al.,* 2014, Devi *et al*. 2016 and Kumari *et al*. 2017.

In the present study, majority of significant estimates of correlations between yield and yield components were positive in nature. Out of total correlations between different character 8 estimates were positive and significant. This represents low situation for obtaining high response to selection in improving yield and yield components in rice.

The genotypes evaluated for correlation study comparing of line, tester and crosses. The testers were susceptible to salinity. Therefore, crosses not uniformly perform in the salinity conditions. Hence, most of the yield contributing traits exhibited low correlation with grain yield per plant.

5.2.4 Path coefficient analysis

Path coefficient analysis is a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on grain yield. Path analysis provides clearer picture of character associations for formulating efficient selection strategy. Path coefficient analysis differs from simple correlation in that it points out the causes and their relative importance, whereas, the later measures simply the mutual association ignoring the causation. The concept of path coefficient was developed by Wright (1921) and technique was first used for plant selection by Dewey and Lu (1959). Path analysis has emerged as a powerful and widely used technique for understanding the direct and indirect contributions of different characters to economic yield in crop plants so that the relative importance of various yield contributing characters can be assessed.

In the present study, the path coefficient analysis was carried out using correlation coefficients between thirteen characters. The high positive direct effects on grain yield per plant were exerted by biological yield per plant, spikelets per panicle and harvest-index, (Table 4.16 and 4.17). Thus, biological yield per plant, spikelets per panicle and harvest-index emerged as most important direct yield components on which emphasis should be given during simultaneous selection aimed at improving grain yield in rice. These characters have also been identified as major direct contributors towards grain yield by Nandan *et al.,* 2010; Akhtar *et al*., 2011;Kumar *et al.,* 2011; Bhadru *et al.,* 2011; Rangare *et al.,* 2012; Krishnamurthy and Kumar, 2012; Laxmi *et al.,* 2014; Gopikannan and Ganesh 2014 and Venkann *et al.,*2014; Devi *et al*. 2016 and Kumari *et al*. 2017. The direct effects of remaining characters were too low to be considered important.

High order of positive indirect effects on grain yield per plant exhibited for panicle bearing tillers per plant (0.3766) followed by plant height (cm) (0.1563) days to 50% flowering (0.0942) and panicle length (cm) (0.0898) *via* biological yield per plant. Grains per panicle *via* spikelet per panicle (0.0998). The maximum negative indirect effect on grain yield per plant possessed by harvest-index (%) *via* biological yield per plant (-0.2509). The rest of the estimates of indirect effects obtained in path analysis were negligible. The estimate of residual factors (0.090) obtained in path analysis was low. Janardanam *et al.* 2002; Mahto *et al.* 2003; Qamar *et al.* 2005; Patil and Sarawgi 2006; Zahid *et al.* 2006; Kishore *et al.* 2007 and Babar *et al.* 2009 have also identified biological yield and harvest-index as important direct and indirect yield contributing characters. The indirect effects of remaining characters were too low to be considered important.

5.2.5 Combining ability analysis

The understanding the inheritance of various characters and identification of superior parents are important pre-requisites for launching an effective and efficient breeding programme (Dhillon, 1975). It is not always necessary that parents with high mean performance for yield and other traits would produce desirable F_1s and/or segregates. The selection of a few parents having high genetic potential as per breeding objectives is essential because analyzing and handling of very large number of crosses resulting from numerous parents available in collections of a crop would be an impractical and perhaps impossible task. The concept of combining ability has assumed great importance in plant breeding as an effective means of selecting potential parents for hybridization and specific crosses for further exploitation. From the genetic view point, GCA measures additive gene effects and the SCA measures non additive gene effects including dominance and epistasis. This information on the nature of the gene action present in the population would help to determine an appropriate breeding strategy. Among the various techniques of combining ability analysis, line×tester analysis (Kempthorne, 1957) has been widely utilized for screening of germplasm to identify valuable donor parents and promising crosses in many crops including rice by Lavanya, 2000, Swamy *et al.*, 2003, Punitha *et al.*, 2004, Singh *et al.*, 2004, Dalvi and Patel, 2009; Saleem *et al.*, 2010; Saidaiah *et al.*, 2010 and Dwivedi and Pandey 2012 and Devi e*t al.*, 2017. The present study, therefore, aims to study the combining ability of parents and crosses and gene action for grain yield per plant and its components by line × tester technique. The important findings of the analysis are discussed below:

5.2.6 Gene action and components of genetic variance

The analysis of variance for combining ability for thirteen characters is presented in Table 4.18, while estimates of components of genetic variance and other genetic parameters are given in table 4.19, respectability. In the present study, the analysis of variance for combining ability revealed no significant differences among the testers for all the characters under study except flag leaf area, plant height and L:B ratio indicating absence of sufficient variations in the testers while among lines most of the characters showed no significant differences except biological yield per plant, harvest index, spikelet fertility and flag leaf area. The mean sum of squares due to lines × tester interactions was found to be highly significant for all the characters representing importance of specific combining ability and non-additive gene effects. The above results suggested importance of both additive and non-additive gene effects for majority of characters (table 4.18).

The estimates of sca variance were higher than the corresponding estimates of GCA variance for all the traits. The values of average degree of dominance were more than unity (>1) revealing over dominance for most of the characters except plant height, L:B ratio and flag leaf area. The predictability ratio was lesser than one for all the characters studied indicated importance of non-additive gene action in the inheritance of these characters except 1000 grain weight it indicates presence of additive gene action. The importance of additive as well as non-additive gene effects with predominance of non-additive gene effects in inheritance of grain yield and yield components of rice has also been reported earlier Radhidevi *et al*., 2002; Vishwakarma *et al*., 2003; Punitha *et al*., 2004; Pradhan *et al*., 2006; Rashid *et al*., 2008; Saleem *et al*., 2010; Saidaiah *et al.* 2010; Gopikannana and Ganesh; 2013; Thalapati *et al.,* 2014 and Seesang *et al.,* 2014, Dwivedi *et al.,* 1999; Koli *et al.,* 2013 and Srikrishana *et al.,* 2013, Devi *et al.,* 2018.

The predominance of non-additive gene effects representing non-fixable dominance and epistatic components of genetic variance indicated that maintenance of heterozygosity would be highly fruitful for improving the characters. Hence, the suitable breeding strategy for attaining high yield would be the full or partial exploitation of heterosis through development of hybrids. Since, the technology for development of hybrid rice varieties for commercial purposes is being widely and successfully used in different countries including India, it is recommended to explore possibility of isolating high yielding commercial hybrids utilizing the materials of the present investigation. The non-additive gene effects may also be exploited to some extent for improving the characters by resorting breeding methods such as biparental mating followed by recurrent selection and population improvement methods as suggested by Jensen (1970), Redden and Jensen (1974).

5.2.7 Heritability and genetic advance

Estimates of heritability in narrow sense reflecting the importance of fixable (additive) gene effects. Low estimate of narrow sense heritability were recorded for most of the characters except plant height, flag leaf area, spikelet fertility and L:B ratio. Low estimates of genetic advance were recorded for all the characters under study emerge as poor index for improvement through selection. Heterosis breeding is suggested to develop high yielding hybrids for these (salinity) ecosystems.

5.2.8 General combining ability effects

For illustrating genetic worth of parents for hybridization programme, the general combining ability (GCA) effects of 19 parents (16 lines + 3 testers) for thirteen characters are consolidated in table 5.4 while the parents exhibiting significant GCA effects for different characters are listed in table 5.5.

The significant and positive GCA effects for grain yield per plant were exhibited by IRSSTN 116, IRSSTN 120, IRSSTN 124, IRSSTN 136 and IRSSTN 139 among line and by NDR 359 among testers. The parent IRSSTN 116, with highest GCA effects for grain yield per plant also showed significant and desirable GCA effects for days to 50% flowering, panicle bearing tiller per plant, spikelets per panicle and biological yield per plant. Parent IRSSTN 120 recorded significant and desirable GCA effects for days to 50% flowering, plant height, panicle bearing tiller per plant, spikelets per panicle, grains per panicle and biological yield per plant. Line IRSSTN 124 emerged as good general combiner for days to 50% flowering, plant height, L:B ratio and biological yield per plant. Line IRSSTN 136 emerged as good general combiner for days to 50% flowering, spikelets per panicle, grains per panicle, L:B ratio and biological yield per plant. IRSSTN 139 was identified as good general combiner for days to 50% flowering, plant height, panicle bearing tillers per plant, spikelets fertility, 1000 grain weight and biological yield per plant. Dwivedi *et al.,* (1999) have also reported Narendra 359 and Sarjoo 52 as good general combiner for yield and its associated traits over environments.

Some other lines identified as good general combiners in desirable direction for characters other than grain yield per plant are also listed in table 5.4. These parents may also be recommended for exploitation in hybridization programme as donor of component characters for which they emerged as good general combiner in spite of being average or poor general combiner for grain yield.

It is evident from table 5.4, that most of the lines showing significant positive GCA effects for grain yield per plant also exhibited positive and significant GCA effects for some of the important yield components such as days to 50% flowering, panicle bearing tillers per plant, spikelets per panicle and biological yield per plant.

This indicated that the significant GCA effects for grain yield in positive direction resulted from similar GCA effects of some other yield components suggesting that the combining ability for grain yield was influenced by the combining ability of its component traits. Therefore, simultaneous improvement in important yield components and other associated traits along with grain yield may be better approach for raising yield potential in rice. Similar, results have also been reported by Dwivedi *et al.,* (1999), Saidaiah *et al.,* (2009), Saleem *et al.,* (2010), Bagheri and Jelodar (2010) and Saidaiah *et al.,* (2011).

5.2.9 Specific combining ability effect

The specific combining ability (SCA) effects, which are supposed to be manifestation of non-additive components of genetic variance, are highly valuable for discrimination of crosses for their genetic worth as breeding materials. The estimates of SCA effects of 48 crosses for 13 characters are given in table 4.21. The most promising specific cross combinations for different characters along with their mean performance and GCA effects of parents are listed in table 5.6.

In present study, none of the crosses showed significant SCA effects in desirable direction for all the characters. Several crosses exhibited significant and desirable SCA effects for one or more characters but none of them emerged as good specific combination for more than nine characters.

Fourteen crosses IRSSTN-105×NDR 359, IRSSTN-107×CSR 10 , IRSSTN-107×NDR 359 , IRSSTN-117×Improved Pusa Basmati 1, IRSSTN-124×Improved Pusa Basmati 1, IRSSTN-124×NDR 359, IRSSTN-124×NDR 359, IRSSTN-129×CSR 10, IRSSTN-129×Improved Pusa Basmati 1, IRSSTN-135×NDR 359, IRSSTN-136×NDR 359, IRSSTN-144×Improved Pusa Basmati 1, IRSSTN 152×CSR 10 and IRSSTN 155×NDR 359 showed highly significant and positive SCA effects for grain yield per plant while, only one cross IRSSTN-143×Improved Pusa Basmati 1 exhibited significant and positive SCA effects for grain yield per plant, as well as for some other yield components.

Table 5.4: Estimates of general combining ability (GCA) effects of parents (lines and testers) for 13 characters in rice under salinity condition

S. N.	Line	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Plant bearing tillers per plant	Panicle length (cm)	Spikelet per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield (g)	Harvest index (%)	Grains yield per plant(g)
1	IRSSTN-101	+	+	-	-	-	+	+	+	+	+	-	-	-
2	IRSSTN-105	0	-	-	-	-	+	+	+	+	-	0	-	-
3	IRSSTN-107	+	+	+	-	-	+	0	-	+	-	-	-	-
4	IRSSTN-116	+	0	-	+	-	+	-	-	-	0	+	-	+
5	IRSSTN-117	+	-	+	-	-	-	-	-	+	-	-	0	-
6	IRSSTN-120	+	+	-	+	-	+	+	0	-	+	+	0	+
7	IRSSTN-124	+	+	0	-	0	0	0	0	-	+	+	-	+
8	IRSSTN-129	-	-	-	0	-	-	-	-	+	+	+	-	0
9	IRSSTN-135	-	-	-	0	0	+	+	-	+	0	-	-	-
10	IRSSTN-136	+	-	-	-	0	+	+	0	-	+	+	-	+
11	IRSSTN-139	+	+	-	+	-	-	-	+	+	-	+	-	+
12	IRSSTN-142	-	-	+	-	0	-	-	+	0	+	0	-	-
13	IRSSTN-143	-	-	+	0	+	-	-	-	-	+	-	+	-
14	IRSSTN-144	-	-	+	0	-	-	-	-	-	+	-	0	-
15	IRSSTN 152	-	-	-	-	0	0	0	+	-	-	-	+	-
16	IRSSTN 155	-	+	0	-	+	-	-	-	-	-	-	0	-
	Tester													
1	CSR 10	+	+	-	+	0	0	0	0	0	-	-	-	-
2	Improved Pusa Basmati 1	0	-	+	-	0	-	-	-	-	+	-	-	-
3	NDR 359	-	-	-	-	-	-	+	+	+	-	+	0	+

+ = **Good combiner,** **-** = **Poor combiner,** **0** = **Average combiner**

Table 5.5: The parents exhibiting significant and desirable general combining ability effects for different characters under salinity stress condition

Characters	**Parents**
Days to 50% flowering	IRSSTN 101, IRSSTN 107, IRSSTN 116, IRSSTN 117, IRSSTN 120, IRSSTN 136, IRSSTN 139
Plant height (cm)	IRSSTN 101, IRSSTN 107, IRSSTN 120, IRSSTN 124, IRSSTN 139, CSR 10
Flag leaf area (cm^2)	IRSSTN 107, IRSSTN 117, IRSSTN 142, IR-28, IRSSTN 144
Panicle bearing tillers per plant	IRSSTN 116, IRSSTN 120, IRSSTN 139
Panicle length (cm)	IRSSTN 135, IRSSTN 144, IR-28, CSR 10
Spikelets per panicle	IRSSTN 101, IRSSTN 105, IRSSTN 107, IRSSTN 116, IRSSTN 120, IRSSTN 135, IRSSTN 136
Grains per panicle	IRSSTN 101, IRSSTN 105, IRSSTN 120, IRSSTN 135, IRSSTN 136,
Spikelet fertility (%)	IRSSTN 101, IRSSTN 105,IRSSTN 139, IRSSTN 142, IRSSTN 152
1000- grains weight (g)	IRSSTN 101, IRSSTN 105,IRSSTN 107, IRSSTN 117, IRSSTN 129, IRSSTN 135, IRSSTN 139
L:B ratio	IRSSTN 101,IRSSTN 120, IRSSTN 124, IRSSTN 129, IRSSTN 136, IRSSTN 142, IR-28
Biological yield per plant (g)	IRSSTN 116, IRSSTN 120, IRSSTN 124, IRSSTN 129, IRSSTN 136, IRSSTN 139
Harvest-index (%)	IR-28, IRSSTN 152
Grains yield per plant(g)	IRSSTN 116, IRSSTN 120, IRSSTN 124, IRSSTN 136, IRSSTN 139

The IRSSTN-117×Improved Pusa Basmati 1 having highest positive and significant SCA effects for grain yield per plant and also recorded significant SCA effects in desirable direction for panicle bearing tiller per plant and biological yield per plant. The second ranking cross IRSSTN-129×CSR 10 have desirable SCA effects for flag leaf area, panicle length, L:B ratio and biological yield per plant. The third ranking cross for significant and positive SCA effects for grain yield per plant was IRSSTN-142×CSR 10 exhibited significant and desirable SCA effects for 1000 grain weight, L:B ratio and biological yield per plant. The fourth ranking cross for significant and positive SCA effects for grain yield per plant (IRSSTN-135×NDR 359) exhibited significant and desirable SCA effects for panicle bearing tiller per plant and biological yield per plant. The fifth ranking cross in this context, IRSSTN-144×Improved Pusa Basmati 1 recorded significant SCA effects in desirable direction for panicle bearing tillers per plant, spikelets fertility, 1000 grain weight, L:B ratio and biological yield per plant. Similarly, remaining 9 crosses having highly significant and positive effects for grain yield per plant while one crosses showed positive and significant effects for grain yield per plant also possessed significant SCA effects in desirable direction for some other characters also.

In present study under saline condition, none of the crosses showed significant SCA effects in desirable direction for all the characters. Several crosses exhibited significant and desirable SCA effects for one or more characters but none of them emerged as good specific combination for more than six characters. Similar results were also reported by Koli *et al.,* (2013), Srikrishana *et al.,* (2013), Gopikannana and Ganesh (2013), Thalapati *et al.,* (2014) and Seesang *et al.,* (2014).

In general, the crosses showing significant and desirable SCA effects were associated with better *per se* performance for respective traits. However, the crosses having high SCA effects in desirable direction did not always have high mean performance for the character in question. Thus, the SCA effect of the crosses may not be directly related to their *per se* performance. This may be attributed to the fact that *per se* performance is a realized value, whereas, SCA effect is an estimate of F_1

performance over parents. Therefore, both *per se* performance along with SCA effects should be considered for evaluating the superiority of a cross although the former may be more important if development of F_1 hybrids is the ultimate objective. The most promising five crosses having significant and desirable SCA effects for different character are listed along with their mean performance and GCA effects of their parents in table 5.6. The crosses listed in table 5.6 may be considered for further utilization owing to their higher genetic worth. The crosses having high SCA effect for grain yield also were higher yielder with good agronomic performance for other quantitative traits.

The critical examination of table 5.6 would reveal that the crosses exhibiting high order of significant and desirable SCA effects for different characters involved parents having all types of combinations of GCA effects such as high × high (H × H), high × average (H × A), high × low (H × L), average × average (A × A), average × low (A × L) and low × low (L × L) general combining parents. The foregoing observations clearly indicated that there was no particular relationship between positive and significant SCA effects of crosses with GCA effects of their parents for the characters under study. Dwivedi *et. al.,* (1999), Saidaiah *et al.,* (2009), Saleem *et al.* (2010) and Dwivedi and Pandey (2012) have also reported similar findings. High × high, high × average and average × average crosses gives transgrassive segregants and selection in early generation would be advantageous for development of pure lines as there are involvement of additive gene action, whereas, crosses having high × low, average × low and low × low general combining parents are suggested for heterosis breeding as the inheritance are controlled by non additive and epistatic gene action.

Table 5.6: Most promising cross combinations for different characters along with their *per se* performance, SCA effects and GCA effects of parents under salinity condition

Characters	Crosses with significant effects	SCA effects	*Per se* performance	GCA effects of parents
Days to 50% flowering	IRSSTN-107×NDR 359	5.60	98.50	H×L
	IRSSTN-136×Improved Pusa Basmati 1	4.80	96.00	H×A
	IRSSTN-116×CSR 10	3.83	96.00	H×H
	IRSSTN-101×Improved Pusa Basmati 1	3.68	95.00	H×A
	IRSSTN-105×CSR 10	3.27	97.00	A×H
Plant height (cm)	IRSSTN-107×CSR 10	8.00	93.01	H×H
	IRSSTN-136×CSR 10	6.58	91.66	L×H
	IRSSTN 155×Improved Pusa Basmati 1	5.83	96.83	H×L
	IRSSTN-105×NDR 359	5.76	105.66	L×L
	IRSSTN-124×NDR 359	5.27	99.16	H×L
Flag leaf area (cm^2)	IRSSTN-120×Improved Pusa Basmati 1	2.67	33.86	L×H
	IRSSTN 155×Improved Pusa Basmati 1	2.34	35.09	A×H
	IRSSTN-142×Improved Pusa Basmati 1	2.28	37.00	H×H
	IRSSTN-139×CSR 10	2.20	26.77	L×L
	IRSSTN-136×Improved Pusa Basmati 1	2.04	32.86	L×H
Panicle bearing tillers per plant	IRSSTN-143×Improved Pusa Basmati 1	3.76	15.55	A×L
	IRSSTN-105×NDR 359	3.72	13.36	L×L
	IRSSTN-129×NDR 359	2.93	15.35	A×L
	IRSSTN-117×Improved Pusa Basmati 1	2.78	13.78	L×L
	IRSSTN-101×NDR 359	2.67	14.00	L×L
Panicle length (cm)	IRSSTN-124×NDR 359	1.83	24.67	A×L
	IRSSTN-143×NDR 359	1.71	25.27	H×L

	IRSSTN-136×CSR 10	1.70	26.47	A×A
	IRSSTN-139×Improved Pusa Basmati 1	1.64	24.35	L×A
	IRSSTN-142×NDR 359	1.51	24.31	A×L
Spikelets per panicle	IRSSTN-124×CSR 10	30.54	98.58	A×A
	IRSSTN-129×NDR 359	29.84	157.47	L×L
	IRSSTN 152×Improved Pusa Basmati 1	22.47	176.33	A×L
	IRSSTN-101×NDR 359	21.84	194.33	H×L
	IRSSTN-136×Improved Pusa Basmati 1	20.48	183.34	H×L
Grains per panicle	IRSSTN-129×NDR 359	22.91	118.75	L×H
	IRSSTN-124×CSR 10	22.11	141.19	A×A
	IRSSTN 152×Improved Pusa Basmati 1	19.82	136.49	A×L
	IRSSTN-142×Improved Pusa Basmati 1	18.59	132.10	L×L
	IRSSTN-101×NDR 359	17.96	162.47	H×H
Spikelet fertility (%)	IRSSTN-144×Improved Pusa Basmati 1	8.09	81.32	L×L
	IRSSTN-117×NDR 359	4.16	74.04	L×H
	IRSSTN-135×Improved Pusa Basmati 1	4.04	77.28	L×L
	IRSSTN-143×CSR 10	3.81	79.93	L×A
	IRSSTN-107×NDR 359	3.76	78.82	L×H
1000-grains weight	IRSSTN 152×Improved Pusa Basmati 1	1.85	23.35	L×L
	IRSSTN-120×CSR 10	1.75	22.91	L×A
	IRSSTN-143×NDR 359	1.49	21.98	L×H
	IRSSTN-136×CSR 10	1.46	23.25	L×A
	IRSSTN-105×NDR 359	1.35	24.30	H×H
L:B Ratio	IRSSTN-136×Improved Pusa Basmati 1	0.46	3.42	H×H

	IRSSTN-135×Improved Pusa Basmati 1	0.35	3.08	A×H
	IRSSTN-124×NDR 359	0.30	2.72	H×L
	IRSSTN-117×CSR 10	0.25	2.36	L×L
	IRSSTN 152×CSR 10	0.21	2.31	L×L
Biological yield per plant (g)	IRSSTN-117×Improved Pusa Basmati 1	20.71	62.83	L×L
	IRSSTN-129×CSR 10	16.55	65.76	H×L
	IRSSTN-142×CSR 10	16.19	61.49	A×L
	IRSSTN-105×NDR 359	13.84	63.34	A×H
	IRSSTN-144×Improved Pusa Basmati 1	11.02	48.68	L×L
Harvest-index (%)	IRSSTN 155×NDR 359	3.37	45.05	A×A
	IRSSTN-101×CSR 10	2.91	32.36	L×L
	IRSSTN-136×Improved Pusa Basmati 1	2.22	40.00	L×L
	IRSSTN-105×Improved Pusa Basmati 1	2.13	37.83	L×L
	IRSSTN-124×Improved Pusa Basmati 1	2.10	38.21	L×L
Grain yield per plant (g)	IRSSTN-117×Improved Pusa Basmati 1	7.15	22.75	L×L
	IRSSTN-129×CSR 10	5.13	21.73	A×L
	IRSSTN-142×CSR 10	4.56	20.69	L×L
	IRSSTN-135×NDR 359	4.41	19.32	L×H
	IRSSTN-144×Improved Pusa Basmati 1	4.31	18.44	L×L

H = High (significant and positive), L= Low (significant and negative) A= Average (non-significant)

5.3 Heterosis

The heterosis breeding has been used extensively in improving yield potential through development of hybrid cultivars in most of the allogamous crops and some autogamous crops like rice as well. The exploitation of heterosis for developing high yielding commercial hybrids in rice has been found highly fruitful in spite of its autogamous nature because significant heterosis is encountered in F_1 hybrids and successful and economical technology for commercial hybrid seed production is available.

The presence of high heterosis for economically important characters is not only useful for developing hybrids through exploitation of heterosis, but also helps in obtaining transgressive segregants for development of superior homozygous lines. In present study, the estimates of heterosis over better-parent and standard varieties IR 28 ($SV_{1)}$ and CSR 43(SV_2) were calculated for 48 F_1s to assess their genetic potential as breeding material in saline soils.

A wide range of variation in the estimates of heterobeltiosis and standard heterosis in positive and negative direction was observed for grain yield per plant (Table 4.23). In case of grain yield per plant, heterobeltiosis ranged -57.64 to 91.23% and standard heterosis over SV_1 (IR 28) varied from -31.30 to 78.70% and for SV_2 (CSR 43) ranged from - 43.59% to 46.74%.

Twenty one crosses showed significant positive heterobeltiosis (Table 5.8) and twenty seven crosses exhibited positive and significant standard heterosis over standard variety IR 28 (Table 5.9) and for standard variety CSR 43 (Table 5.10) seventeen cross combination exhibited positive and significant heterosis.

Among twenty one crosses the best ten crosses exhibited heterobeltiosis were IRSSTN-116×Improved Pusa Basmati 1, IRSSTN-116×CSR 10, IRSSTN-116×NDR 359, IRSSTN-124×Improved Pusa Basmati 1, IRSSTN-139×NDR 359, IRSSTN-139×CSR 10, IRSSTN-139×Improved Pusa Basmati 1, IRSSTN-129×CSR 10, IRSSTN-117×Improved Pusa Basmati 1 and IRSSTN-129×Improved Pusa Basmati 1, (Table 5.6) and among twenty seven crosses the best 10 crosses showed heterosis over standard variety IR 28, (SV_1) were IRSSTN-139×NDR 359, IRSSTN-116×CSR 10, IRSSTN-116×Improved Pusa Basmati 1, IRSSTN-116×NDR 359, IRSSTN-117×Improved Pusa Basmati 1, IRSSTN-136×NDR 359,

IRSSTN-124×NDR 359, IRSSTN-139×CSR 10, IRSSTN-129×CSR 10 and IRSSTN-124×Improved Pusa Basmati 1 (Table 5.7) while for SV_2 (CSR 23) out of seventeen the best 10 crosses were IRSSTN-120×Improved Pusa Basmati 1, IRSSTN-139×NDR 359 , IRSSTN-143×Improved Pusa Basmati 1, IRSSTN-129×NDR 359, IRSSTN-116×CSR 10, IRSSTN-139×Improved Pusa Basmati 1, IRSSTN-144×Improved Pusa Basmati 1, IRSSTN-101×CSR 10, IRSSTN-135×NDR 359 and IRSSTN-107×CSR 10.

Besides yield, substantial heterosis over better-parent and standard varieties was also observed in negative as well as in positive direction for remaining characters. However, the number of crosses showing significant estimates and the range of heterosis varied from one character to another. The mean heterosis was both positive and negative in direction for different characters. For grain yield per plant, the mean heterobeltiosis, SV_1, and SV_2 were positive. In general, some crosses showed appreciable and high heterosis for most of the characters under study. The existence of wide spectrum of heterosis in either direction with expression of high degree of desirable heterosis by some crosses for most of the characters observed in present study is in conformity with the earlier reports in rice (Dwivedi *et al*., 1998, Janardanam *et al*., 2001, Bhanumathi *et al*., 2003, Punitha *et al*., 2004, Singh *et al*., 2007, Roy *et al*., 2009, Krishna *et al.,* 2011 and Dwivedi and Pandey, 2012 and Devi *et al*., 2017).

It was also noted that higher heterosis over better-parent was found in some lower yielding crosses when compared to other crosses which have displayed high yield. This suggested that while selecting the best hybrid, besides the heterotic response over better-parent, the mean performance of the crosses should also be given due consideration. Since, heterosis estimate results from F_1-BP and depends more or less on the mean of the parents in question, there is every possibility of getting a cross with lower mean performance but high heterotic response, in case the parental performance is very poor. On the contrary, there can be a cross with high mean performance but low heterosis in case parental performance is also high. The mean performance being the realized value and the heterotic response being an estimate, the former should be given due

Table 5.7: Relationship of positive and significant heterobiltiosis for grain yield per plant with standard heterosis for other characters under Salinity condition

Characters Crosses	Grains yield per plant (g)	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000- seed weight (g)	L:B ratio	Biological yield per plant (g)	Harvest-index (%)
BP													
IRSSTN-116×Improved Pusa Basmati 1	129.83	+	+	**0**	**0**	-	+	**0**	-	+	-	+	**0**
IRSSTN-116×CSR 10	116.90	-	-	+	+	**0**	+	+	-	-	-	+	-
IRSSTN-116×NDR 359	89.66	+	+	+	-	-	-	-	-	-	-	+	-
IRSSTN-124×Improved Pusa Basmati 1	82.96	-	+	+	-	-	+	**0**	-	-	-	+	**0**
IRSSTN-139×NDR 359	78.29	-	0	**0**	+	-	-	-	-	-	-	+	-
IRSSTN-139×CSR 10	76.18	-	+	+	+	-	-	-	-	-	-	+	-
IRSSTN-139×Improved Pusa Basmati 1	75.20	**0**	+	-	+	-	-	-	-	+	-	+	-
IRSSTN-129×CSR 10	71.26	-	+	+	**0**	+	-	-	-	-	-	+	-
IRSSTN-117×Improved Pusa Basmati 1	69.95	**0**	0	+	+	-	-	-	-	-	-	+	**0**
IRSSTN-129×Improved Pusa Basmati 1	65.64	-	+	**0**	**0**	-	-	-	-	+	-	+	-

Where,
\+ = Significant and positive heterosis,
\- = Significant and negative heterosis,
0 = Non-significant heterosis

Table 5.8: Relationship of positive and significant standard heterosis over SV_1 (IR 28) for grains yield per plant with standard heterosis for other characters under salinity condition.

Characters	**Grain yield per plant (g)**	**Days to 50% flowering**	**Plant height (cm)**	**Flag leaf area (cm^2)**	**Panicle bearing tillers per plant**	**Panicle length (cm)**	**Spikelets per panicle**	**Grains per panicle**	**Spikelet fertility (%)**	**1000-seed weight (g)**	**L:B ratio**	**Biological yield per plant (g)**	**Harvest-index (%)**
Crosses	**SV_1**												
IRSSTN-139×NDR 359	78.70	-	-	-	+	+	-	**0**	**0**	+	-	+	**0**
IRSSTN-116×CSR 10	72.63	-	**0**	-	+	+	+	+	-	+	-	+	**0**
IRSSTN-116× Improved Pusa Basmati 1	70.42	**0**	-	**0**	+	+	+	+	-	**0**	-	+	**0**
IRSSTN-116×NDR 359	69.18	-	**0**	**0**	**0**	**0**	+	**0**	-	**0**	-	+	**0**
IRSSTN-117× Improved Pusa Basmati 1	65.78	-	-	+	+	+	-	-	-	+	-	+	+
IRSSTN-136×NDR 359	62.60	-	-	-	+	+	+	+	**0**	+	-	+	**0**
IRSSTN-124×NDR 359	62.02	-	-	0	+	+	**0**	**0**	**0**	**0**	-	+	+
IRSSTN-139×CSR 10	59.64	-	+	-	+	+	+	+	**0**	+	-	+	**0**
IRSSTN-129×CSR 10	58.31	-	-	**0**	**0**	**0**	-	-	**0**	+	-	+	**0**
IRSSTN-124×Improved Pusa Basmati 1	55.42	-	+	+	+	+	+	+	-	+	-	+	+

Where,
+ = Significant and positive heterosis,
- = Significant and negative heterosis,
0 = Non-significant heterosis

Table 5.9: Relationship of positive and significant standard heterosis over SV_2 (CSR 43) for grains yield per plant with standard heterosis for other characters under salinity condition.

Characters	**Grain yield per plant (g)**	**Days to 50% flowering**	**Plant height (cm)**	**Flag leaf area (cm^2)**	**Panicle bearing tillers per plant**	**Panicle length (cm)**	**Spikelets per panicle**	**Grains per panicle**	**Spikelet fertility (%)**	**1000- seed weight (g)**	**L:B ratio**	**Biological yield per plant (g)**	**Harvest-index (%)**
Crosses	**SV_2**												
IRSSTN-120×Improved Pusa Basmati 1	85.62	-	**0**	+	+	+	+	+	-	-	-	+	-
IRSSTN-139×NDR 359	85.11	-	-	0	+	+	+	-	+	-	-	+	-
IRSSTN-143×Improved Pusa Basmati 1	84.32	-	**0**	+	+	+	+	-	-	-	-	-	**0**
IRSSTN-129×NDR 359	81.91	-	-	0	+	+	+	+	**0**	-	-	-	-
IRSSTN-116×CSR 10	73.97	-	**0**	0	+	+	+	+	-	-	-	+	-
IRSSTN-139×Improved Pusa Basmati 1	71.29	-	**0**	0	+	+	-	**0**	+	-	-	+	-
IRSSTN-144×Improved Pusa Basmati 1	70.22	-	**0**	+	+	+	-	**0**	+	-	**0**	+	-
IRSSTN-101×CSR 10	70.06	-	+	0	+	+	+	+	+	-	-	-	**0**
IRSSTN-135×NDR 359	68.05	-	-	+	+	+	+	+	**0**	-	-	+	-
IRSSTN-107×CSR 10	67.73	-	**0**	+	+	+	+	+	-	-	-	+	-

Where,

+ = Significant and positive heterosis,
- = Significant and negative heterosis,
0 = Non-significant heterosis

consideration while making being an estimate, the former should be given due consideration while making selection of cross combinations especially when objective is to identify a hybrid for commercial cultivation as in present case. In this context, the most desirable crosses showing high mean performance and high and significant heterosis of one or both types for grain yield per plant were IRSSTN-139×NDR 359, IRSSTN-116×CSR 10, IRSSTN-116×Improved Pusa Basmati 1, IRSSTN-116×NDR 359, IRSSTN-117× Improved Pusa Basmati 1, IRSSTN-136×NDR 359, IRSSTN-124×NDR 359, IRSSTN-139×CSR 10, IRSSTN-129×CSR 10 and IRSSTN-124× Improved Pusa Basmati 1 (Table 5.10).

The hybrid IRSSTN-139×NDR 359 showed highest mean performance (24.53g), heterobiltiosis (49.38%), standard heterosis (SV_1) (78.70%) over IR 28, standard variety (SV_2) 46.75 over CSR 43 for grain yield per plant while SCA effect was 1.15 for this trait. The other cross IRSSTN-116×CSR 10 exhibited high mean (23.70g) performance, heterobiltiosis (72.63%), standard heterosis (SV_1) 57.54% and SV_2 (41.75) with SCA effect 0.97 for grain yield. The combination IRSSTN-116×Improved Pusa Basmati 1 showed high mean performance (23.39g) among the crosses with the heterobiltiosis of 91.23%, standard heterosis SV_1 (70.42%), standard heterosis SV_2 (39.94) and SCA effects 0.31 for grain yield per plant. The cross IRSSTN-116×NDR 359 showed high mean performance (23.22g), heterobiltiosis (41.89%), standard heterosis (SV_1) 69.18% over IR 28, standard heterosis (SV_2) 38.92% over CSR 43 and SCA effect was -1.28 for grain yield per plant. The fifth rank cross IRSSTN-117× Improved Pusa Basmati 1 showed highest mean performance (22.76g), heterobiltiosis (56.44%), standard heterosis (SV_1) 65.78% over IR 28, standard heterosis (SV_2) 36.13% over CSR 43 with SCA effect 7.15 for grain yield per plant. Similar finding were also reported by Anil *et al.,* (2013); Reddy *et al.,* (2013) and Singh *et al.,* (2013).

The crosses mentioned above also showed highly significant and positive SCA effects for grain yield per plant as well as for some other yield contributing characters. These crosses should be tested and evaluated in adaptive trails to find out their feasibility for recommendation for use as hybrid verities in the target environments.

Table 5.10: Most promising crosses based on mean performance, heterobeltiosis, standard heterosis (SV_1 and SV_2) and SCA effect for grains yield per plant in salinity condition

S. No.	**Crosses**	***per se* Performance**	**Heterosis over better-parent**	**Heterosis over SV_1**	**Heterosis over SV_2**	**SCA effect**
1	**IRSSTN-139×NDR 359**	24.53	49.38	78.70	46.75	1.15
2	**IRSSTN-116×CSR 10**	23.70	72.63	72.63	41.75	0.97
3	**IRSSTN-116× Improved Pusa Basmati 1**	23.39	91.23	70.42	39.94	0.31
4	**IRSSTN-116×NDR 359**	23.22	41.89	69.18	38.92	-1.28
5	**IRSSTN-117× Improved Pusa Basmati 1**	22.76	56.44	65.78	36.13	7.15
6	**IRSSTN-136×NDR 359**	22.32	3.67	59.64	33.52	2.15
7	**IRSSTN-124×NDR 359**	22.24	35.89	62.02	33.04	2.37
8	**IRSSTN-139×CSR 10**	21.91	59.64	59.64	31.09	0.32
9	**IRSSTN-129×CSR 10**	21.73	58.31	58.31	29.99	5.13
10	**IRSSTN-124× Improved Pusa Basmati 1**	21.33	74.39	55.42	27.62	2.88

CHAPTER-VI

SUMMARY AND CONCLUSION

The present investigation entitled "Genetic studies for yield and its contributing components in rice (*Oryza sativa* L.) under salt affected soil" was under taken with objectives (i) to examine the genetic variability and evaluate the rice genotypes for various traits. (ii) to compute association at genotypic and phenotypic levels among different characters. (iii) to assess the stability of rice genotypes. (iv) to study the combining ability variances and their effects. (v) to find out gene action involved in the inheritance of various characters. (vi) to estimate heterosis over better-parent and standard varieties, and (vii) to identify promising parents and superior hybrids for exploitation in breeding programme.

The technical programme of the present investigation was based on two sets of experiments as follows:

Experiment I:

Forty nine diverse genotypes of rice (including checks IR 28 and CRS 43) were evaluated in randomized complete block design with three replications in saline soil at GPB farm and in normal soils at Students Instructional Farm during *Kharif* 2016. Inter and intra row spacing was 20×15 cm with a 3 rows of 3 meter length. Recommended agronomical practices were adapted to raise healthy crop.

Experiment II:

A line × tester set of 48 hybrids (F_1s) were derived by crossing 16 lines (female) with three high yielding testers (male) *viz.,* Improved Pusa Basmati 1, CSR 10 and NDR 359 during *Kharif* 2016. The sixteen lines were IRSSTN 101, IRSSTN 105, IRSSTN 107, IRSSTN 116, IRSSTN 117, IRSSTN 120, IRSSTN 124, IRSSTN 129, IRSSTN 135, IRSSTN 136, IRSSTN 139, IRSSTN 142, IRSSTN 143, IRSSTN 144, IRSSTN 152 and IRSSTN 155. The experiment was conducted at Genetics and Plant Breeding

Research Farm and Student Instructional Farm of N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad. The crosses were made during *Kharif*, 2016 and the hybrids along with parental lines and check varieties were evaluated during *Kharif*, 2017. Thirteen plant characters viz., days to 50% flowering, plant height (cm), flag leaf area (cm^2), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-grain weight (g), L:B ratio, biological yield per plant (g), harvest-index (%) and grain yield per plant (g) were studied in the experiment. The data on thirteen characters was subjected to analysis of variance for randomized block design (Panse and Sukhtame, 1967), estimation of coefficients of variation (Burton and de Vane, 1953) and heritability in broad sense (Hanson *et al.,* 1956) and genetic advance in per cent of mean (Johnson *et al.,* 1955), estimation of correlation coefficients (Searle, 1961), path-coefficient analysis (Dewey and Lu, 1959), stability index (Eberhart and Russell (1966)), line × tester analysis of combining ability (Kempthorne, 1957) and computation of heterosis over better-parent and standard varieties (Fonseca and Patterson, 1968). The salient results of present study and conclusions drawn are summarized below:

1. Analysis of variance for the design of experiment indicated highly significant differences among the forty nine rice genotypes for all the thirteen characters under both conditions indicated presence of genetic variability in the study material.

2. The top five genotypes, exhibiting high mean performance for grain yield along with higher performance for other yield components were IRSSTN-135, IRSSTN-115, IRSSTN-131, IRSSTN-128 and IRSSTN-125. These lines may be used as donor parents in hybridization programme for developing high yielding genotypes for saline soil and for the normal soil condition recommended lines are IRSSTN-101, IRSSTN-132, IRSSTN-136, CSR 43 and IRSSTN-137. These lines may be used as donor parents in hybridization programme for developing high yielding genotypes.

3. The wide spectrum of variation was observed in rice germplasm for yield and yield components. High magnitude of genotypic and phenotypic coefficient of variation was observed for grains yield per plant (g). Remaining characters recorded moderate or low PCV and GCV values for salinity condition.

4. Under normal condition high magnitude of genotypic and phenotypic coefficient of variation was observed for biological yield per plant (g) and grain yield per plant.. Remaining characters recorded moderate or low PCV and GCV values.
5. Under salinity condition high estimates of broad sense heritability coupled with high genetic advance in per cent of mean were recorded for grains yield per plant (g), spikelets per panicle, flag leaf area, biological yield per plant (g), grains per panicle, plant height (cm) and L:B ratio.
6. While in normal condition high heritability coupled with high genetic advance in per cent of mean were observed for flag leaf area, spikelets grains per panicle, grains per panicle, L:B ratio, biological yield and grain yield per plant.
7. Direct selection is rewarding for the traits exhibiting high PCV, GCV, heritability and genetic advance in per cent of mean
8. The genotypic correlations coefficients were generally similar in nature and higher in magnitude than the corresponding phenotypic correlation coefficients under both the conditions. Under salinity stress condition, biological yield per plant, harvest-index (%), spikelets per panicle, grains per panicle and panicle bearing tillers per plant showed very strong significant and positive correlation of grain yield per plant at both phenotypic and genotypic levels.

9. Under normal condition biological yield per plant, 1000- grains weight (g), harvest-index (%) and plant height (cm) showed very strong significant and positive correlation of grain yield per plant at both phenotypic and genotypic correlation.
10. The highest positive direct effect on grain yield per plant was exerted by biological yield per plant followed by harvest-index, spikelets per panicle, spikelet fertility (%)

and flag leaf area (cm^2) under salinity condition, which can be taken into consideration to devise suitable breeding strategy for saline soil.

11. Path analysis under normal condition revealed that highest positive direct effect on grain yield per plant was exerted by biological yield per plant followed by harvest-index and spikelets per panicle. Yield can be improved through direct selection of these traits.
12. Forty nine genotypes of rice germplasm were grouped in to eight clusters in both saline and normal soil. Clustering pattern in both situation exhibited considerable differences.
13. Under salt stress condition major clusters in divergence analysis contained genotypes of heterogeneous origin, thereby, indicating non-parallelism between genetic and geographic diversity. Therefore, crosses between the members of clusters separated by high inter-cluster distances are likely to throw desirable segregates. High inter-cluster distances were observed between cluster 3 and 8, followed by cluster 3 and 7, cluster 2 and 7, cluster 2 and 8 and cluster 1 and 8. In this context cluster 8 having 5 genotypes, showed very high intra- cluster distance from other clusters.
14. Under normal condition high inter-cluster distances were observed between cluster 2 and 8, followed by cluster 2 and 6, cluster 2 and 6, cluster 2 and 5 and cluster 2 and3. In this context cluster 7, having 5 genotypes, showed very high intra- cluster distance from other clusters.
15. In this experiment, various clusters showed considerable differences in cluster means for 13 characters. Therefore, crosses between members of clusters having high cluster means coupled with high inter-cluster distance between them for important characters are likely to be more rewarding.
16. IRSSTN-112 showed stable performance under both conditions and all other rice genotypes showed good stability only in salinity or normal soil conditions.

17. The analysis of variance for line×tester revealed highly significant mean sum of squares due to treatments, parents, crosses and line×tester for all the thirteen characters. The mean sum of squares due to parents *vs.* crosses and testers were also

significant for most of the characters. This indicated presence of substantial variability in the study materials and validated further statistical and genetical analysis.

18. In general PCV were higher than the GCV for all characters. The high estimates of phenotypic and genotypic coefficient of variation were estimated for biological yield per plant and panicle bearing tillers per plant but GCV for grain yield per plant.

19. Genotypic correlations were high and same in magnitude as phenotypic correlation. The grain yield per plant exhibited highly significant and positive correlation with biological yield per plant and panicle bearing tillers per plant.

20. SCA variances were higher than GCA variances for all the characters indicating presence of non additive gene action. Average degree of dominance is more than one for all most all the characters except plant height, flag leaf area and L:B ratio and predictability ratio were less than one for all the characters except 1000 grain weight showed involvement of non additive gene action. Medium narrow sense heritability was reported for most of the characters.

21. For grain yield per plant parents RSSTN-116, IRSSTN-139, IRSSTN-136, IRSSTN-124 and IRSSTN-120 were recorded as good general combiner.

22. Crosses IRSSTN-117×Improved Pusa Basmati 1, IRSSTN-129×CSR 10, IRSSTN-142×CSR 10, IRSSTN-135×NDR 359 and IRSSTN-144×Improved Pusa Basmati 1 exhibited high SCA effect for grain yield per plant.

23. The contribution of line was maximum for harvest index, followed by panicle length, biological yield per plant and 1000- grain weight. Contribution of tester was maximum for flag leaf area followed by L:B ratio, plant height, spikelet fertility and spikelets per panicle. Contribution of L×T was maximum for panicle bearing tillers per plant followed by spikelets per panicle, days to 50% flowering and grains per panicle.

24. Crosses IRSSTN-116×Improved pusa basmati 1, IRSSTN-124×Improved Pusa Basmati 1, IRSSTN-116×CSR 10, IRSSTN-139×Improved Pusa Basmati 1 and IRSSTN-129×Improved Pusa Basmati1 showed high heterobeltiosis for grain yield while for standard variety (SV_1) the best crosses were IRSSTN-139×NDR 359, IRSSTN-116×CSR 10, IRSSTN-116×Improved Pusa Basmati 1, IRSSTN-116×NDR 359 and IRSSTN-117×Improved Pusa Basmati 1 and in case of standard variety (SV_2) the best five were IRSSTN-139×NDR 359, IRSSTN-116×CSR 10, IRSSTN-116×Improved Pusa Basmati 1, IRSSTN-116×NDR 359 and IRSSTN-117×Improved Pusa Basmati 1 for grain yield per plant.

25. The crosses IRSSTN-116×Improved Pusa Basmati 1 and IRSSTN-116×CSR 10 exhibited high heterosis over better parent and both check varieties.

The findings of the present investigation have been discussed considering their practical usefulness in relation to overall improvement in rice. These crosses are suggested for their cultivation in target environments after testing and release.

CHAPTER-VII

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Appendix 1 (a): Mean performance of genotypes under salinity soil

S. No.	Character	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers/ plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per (g)	Harvest index (%)	Yield/ Plant (g)
1.	**IRSSTN-101**	98.33#	97.12	24.3	7.40	23.44*#	126.62##	93.45##	73.89##	20.53##	2.19	42.00*##	22.47	9.43
2.	**IRSSTN-102**	97.67##	75.10**##	21.73	6.60	25.34**##	102.09	83.36##	81.66**##	24.50**	3.12##	29.27	36.98##	10.82##
3.	**IRSSTN-103**	93.67##	95.10	29.5**##	9.54#	25.58**##	103.82	82.97##	79.96**##	20.75##	3.11##	33.00	33.35#	10.97##
4.	**IRSSTN-104**	100.00	82.60**##	36.52**##	9.00	25.41**##	123.22##	96.15##	78.07*##	24.41**	2.27	35.33##	26.42	9.28
5.	**IRSSTN-105**	93.73##	81.50**##	19.42	10.80##	22.35*	112.69	91.17##	80.90**##	23.62##	2.90##	32.41	40.55##	13.15##
6.	**IRSSTN-106**	77.67**##	76.30**##	26.35	7.60	22.67	109.75	73.97##	67.41##	24.30##	2.83##	30.33	30.79	9.33
7.	**IRSSTN-107**	86.67##	76.10**##	28.36**##	7.20	25.68**##	106.62	80.37##	75.44##	22.38##	2.74	27.20	30.44	8.25
8.	**IRSSTN-108**	96.67##	84.15**##	16.75	8.60	23.37*#	105.62	84.43##	80.00**##	22.61##	3.22**##	32.67	41.25##	13.47##
9.	**IRSSTN-109**	102.67	74.25**##	18.27	9.20*#	25.64**##	108.42	83.84##	77.29*##	23.57##	2.19	30.33	32.89#	9.99
10.	**IRSSTN-110**	99.33	78.45**##	17.33	10.67##	21.51	112.69	84.36##	74.90##	24.27##	2.23	33.11	41.54##	13.77##
11.	**IRSSTN-111**	93.33##	77.25**##	29.58**##	11.20*	22.33	108.15	89.93##	83.16**##	22.32##	2.43	28.87	34.88##	10.08#
12.	**IRSSTN-112**	96.33##	79.20**##	23.63	10.20##	25.53**##	108.62	90.56##	83.40**##	21.29##	3.19##	33.67	30.41	10.13#
13.	**IRSSTN-113**	93.00##	87.20**##	24.52	10.80##	21.51	106.15	91.02##	85.78**##	21.77##	3.18##	32.67	33.19##	10.89##
14.	**IRSSTN-114**	104.00	80.9**##	29.12**##	9.80#	22.27	128.15##	107.10**##	83.57**##	24.28##	3.24**##	38.00##	39.54##	15.02##
15.	**IRSSTN-115**	104.00	81.40**##	28.13**#	12.50**	24.58**##	171.82**##	141.84**##	82.57**##	24.75**##	2.50	48.33**##	38.43##	18.56**##
16.	**IRSSTN-116**	96.00##	70.20**##	18.16	8.33	20.35	111.69	80.99##	72.52##	20.38##	3.28**##	30.33	34.17##	10.40#
17.	**IRSSTN-117**	97.00##	83.60**##	28.37**##	9.49#	23.39*#	110.35	81.00##	73.48##	21.21##	3.18##	39.67##	38.83##	15.35##
18.	**IRSSTN-118**	101.00	90.60**	19.48	10.51##	24.70**##	109.29	88.12##	80.61**##	23.69##	2.23	40.37##	34.04##	13.75##
19.	**IRSSTN-119**	96.00##	85.23**##	25.92	11.75*##	22.70	147.42**##	119.99**##	81.37**##	19.71	2.18	49.70**##	28.70	14.25##
20.	**IRSSTN-120**	103.00	80.56**##	22.82	8.56	23.48*#	116.35	93.76##	80.61**##	21.59##	2.17	33.49	33.10#	11.04##

21.	**IRSSTN-121**	98.53#	83.00**##	22.27	11.17*##	19.33	116.67	90.66##	77.75*##	24.15##	2.24	49.67**##	34.59##	17.15##
22.	**IRSSTN-122**	98.33#	82.59**##	18.55	10.28##	22.51	108.89	90.21##	82.85**##	22.8633	3.07##	43.33**##	29.58	12.73##
23.	**IRSSTN-123**	98.33#	79.10**##	23.03	10.23##	21.71	117.69#	96.12##	81.69**##	19.59	3.07##	42.10*##	36.34##	15.30##
24.	**IRSSTN-124**	95.00##	77.50**##	27.16	9.40#	20.02	105.29	85.29##	81.02**##	20.53##	2.20	38.33##	32.57#	12.46##
25.	**IRSSTN-125**	99.00	93.30	29.84**##	9.47#	22.12	108.02	89.68##	83.01**##	22.28##	2.52	43.00**##	39.99##	17.18##
26.	**IRSSTN-126**	99.67	92.72	17.29	11.21*##	24.25**##	118.28#	94.29##	79.72**##	21.65##	2.62	40.67##	29.76	12.12##
27.	**IRSSTN-127**	97.33##	87.52**##	22.57	7.41	19.32	122.48##	97.55##	79.63**##	23.57##	2.43	34.00	33.45#	11.39##
28.	**IRSSTN-128**	97.00##	89.52**	24.69	9.72#	19.62	129.15##	102.08**##	79.13**##	19.80	3.08##	43.00**##	40.11##	17.29##
29.	**IRSSTN-129**	99.00	106.42	21.04	9.38#	22.75	121.77##	96.17##	78.96**##	21.61##	2.95##	51.33**##	23.53	12.02##
30.	**IRSSTN-130**	89.67##	97.32	26.74	9.14	22.44	138.08**##	105.33**##	76.27##	20.61##	2.85##	41.00##	41.78##	17.11##
31.	**IRSSTN-131**	96.00##	96.52	30.77**##	9.21#	22.32	112.51	92.62##	82.30**##	18.61	3.12##	50.67**##	35.29##	17.80*##
32.	**IRSSTN-132**	96.00##	98.01	17.37	10.01#	23.64*#	118.28#	95.61##	80.88**##	21.50##	3.47**##	50.67**##	23.48	11.92##
33.	**IRSSTN-133**	97.33##	93.43	23.83	9.61#	21.34	110.75	91.62##	82.74**##	20.69##	2.19	44.00**##	25.19	11.00##
34.	**IRSSTN-134**	98.00#	80.83**##	19.43	7.94	18.78	142.15**##	113.60**##	79.92**##	20.48##	2.33	34.33#	25.78	8.83
35.	**IRSSTN-135**	101.00	91.01**	26.23	11.87*##	19.82	125.42##	100.98*##	80.55**##	22.40##	2.45	59.33**##	34.50##	20.48**##
36.	**IRSSTN-136**	99.33	91.21*	23.9	10.33##	22.25	116.42	95.55##	82.11**##	21.69##	2.20	42.33##	36.11##	15.23##
37.	**IRSSTN-137**	99.00	90.51**	22.77	10.72##	17.62	132.95	104.40**##	78.52*##	19.51	2.88##	52.33**##	31.76	16.61##
38.	**IRSSTN-138**	100.33	111.53	20.31	9.65#	21.92	112.08	87.87##	78.66**##	24.70**##	2.91##	42.67**##	34.19##	14.63##
39.	**IRSSTN-139**	99.00	95.03	18.52	9.07	21.54	141.08**	115.61**##	82.01**##	19.46	2.95##	51.33**##	33.16#	16.98##
40.	**IRSSTN-140**	98.00#	83.97**##	28.41**	7.05	20.24	116.35	95.55##	82.14**##	22.71##	2.24	38.00##	24.39	9.30
41.	**IRSSTN-141**	101.00	83.87**##	21.41	10.13##	22.33	130.08##	104.23**##	80.16**##	24.45*##	2.32	43.00**##	35.16##	15.12##
42.	**IRSSTN-142**	99.33	98.53	27.28	8.32	21.15	126.13##	105.08**##	83.34**##	18.67	2.53	30.00	32.86#	9.89
43.	**IRSSTN-143**	101.17	93.73	25.26	6.49	20.84	109.32	64.81	59.27	19.59	2.73	30.11	26.45	7.92
44.	**IRSSTN-144**	100.00	101.63	27.48	7.46	23.63*#	122.8##	91.22##	74.30##	22.17##	3.05##	31.33	34.11##	10.67#

45.	**IRSSTN-145**	101.00	96.87	23.21	9.45#	18.27	136.66*##	111.34**##	81.48**##	21.66##	2.17	32.33	36.64##	11.83##
46.	**IRSSTN-146**	102.00	87.83**##	25.73	9.56#	23.31*	104.8	82.22##	78.45**##	22.71##	2.90##	36.00##	38.09##	13.70##
47.	**IRSSTN-147**	102.67	99.63	27.40	9.25#	21.44	133.86##	103.00**##	76.88##	20.47##	2.79	27.47	32.62#	8.99
48.	**IRSSTN-148**	100.33	98.15	26.07	7.79	22.22	120.20##	100.73*##	83.80**##	22.46##	2.95##	39.05##	30.91	12.09##
49.	**CSR 43**	83.00##	96.89	25.37	8.44	20.46	126##	92.87##	73.76##	24.06##	3.13##	37.49##	41.27##	15.43##
	Mean	**97.48**	**88.06**	**24.13**	**9.38**	**22.22**	**119.46**	**94.59**	**79.14**	**21.97**	**2.71**	**38.77**	**33.38**	**12.88**
	C.V.	1.61	3.07	5.75	17.55	6.90	4.21	4.05	2.65	0.93	1.51	6.17	10.18	10.35
	F ratio	29.65	34.13	29.10	2.19	5.13	22.00	32.86	14.37	221.23	283.36	31.75	6.88	16.06
	F Prob.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	S.E.	0.91	1.56	0.80	0.95	0.89	2.90	2.21	1.21	0.12	0.02	1.38	1.96	0.77
	C.D. 5%	2.55	4.39	2.25	2.67	2.48	8.15	6.20	3.40	0.33	0.07	3.88	5.51	2.16
	C.D. 1%	3.38	5.81	2.97	3.53	3.29	10.79	8.21	4.50	0.44	0.09	5.14	7.29	2.86
	Range Lowest	77.67	70.20	16.75	6.49	17.62	102.09	64.81	59.27	18.61	2.17	27.20	22.47	7.92
	Range Highest	104.00	111.53	36.52	12.50	25.68	171.82	141.84	85.78	24.75	3.47	59.33	41.78	20.48

Significant at Check CSR 43 = *, significant at Check IR = #

Appendix 1 (b): Mean performance of genotypes under normal soil

S. No.	Character	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per (g)	Harvest index (%)	Yield/ Plant (g)
1.	**IRSSTN-101**	89.67##	97.33	26.80	11.46#	23.4	129.74##	110.00##	84.88**##	24.77##	2.87	58.74**##	39.98	23.46**
2.	**IRSSTN-102**	87.33##	103.20	25.54	7.95	24.38*	100.09	83.30	83.25**##	21.93##	2.97	33.67##	33.75	11.37
3.	**IRSSTN-103**	87.67##	90.63	24.31	10.64	24.36*	89.84	74.46	82.97**##	24.10##	3.24	33.40##	36.08	12.00
4.	**IRSSTN-104**	84.00##	94.47*	30.75**##	9.65	25.01**#	166.24**##	131.92**##	79.41	21.44##	3.08	30.33	37.69	11.45
5.	**IRSSTN-105**	80.33*##	96.87	20.67	11.29	24.00	130.37##	98.02#	75.21	24.02##	2.43	39.00##	40.10	15.66##
6.	**IRSSTN-106**	77.67**##	76.30**##	26.35	11.27	21.74	143.09##	115.13*##	80.48*	22.29##	2.39	33.23##	36.07	11.95
7.	**IRSSTN-107**	77.00**##	91.93**	29.61**#	8.52	25.55**##	118.41	100.37##	84.79**##	24.36##	3.10	39.00##	39.91	15.54##
8.	**IRSSTN-108**	84.00##	112.00	17.79	11.10	25.31**#	190.08**##	159.11**##	83.83**##	22.97##	3.05	42.67##	37.44	15.98##
9.	**IRSSTN-109**	91.67##	97.53	19.51	9.00	25.21**#	105.59	88.24	83.51**##	24.44##	2.70	32.33#	36.85	11.88
10.	**IRSSTN-110**	87.67##	91.13**	18.57	11.24	21.58	100.85	80.27	79.62	22.97##	3.18	25.67	40.03	10.30
11.	**IRSSTN-111**	82.67##	89.47**#	30.50**##	12.36**##	23.09	105.55	84.95	80.50*	23.18##	3.34	44.80##	38.29	17.14##
12.	**IRSSTN-112**	82.33##	91.40**	24.87	9.72	23.72	107.07	90.51	84.60**##	21.67##	3.18	27.52	36.72	10.12
13.	**IRSSTN-113**	78.67**##	95.60*	25.43	12.11*##	21.58	140.32##	122.61**##	87.37**##	24.61##	2.20	38.08##	35.09	13.39##
14.	**IRSSTN-114**	92.00##	95.67	30.33**##	10.16	25.03**#	153.07*##	128.02**##	83.7**##	23.57##	3.33	35.64##	35.44	12.60#
15.	**IRSSTN-115**	91.33##	98.87	30.04**##	12.07*#	25.21**#	183.66**##	156.06**##	84.93**##	24.46##	3.32	43.23##	40.40	17.46##
16.	**IRSSTN-116**	96.00##	89.03**#	20.06	11.17	21.91	93.61	80.30	85.58**##	21.54##	2.53	26.5	35.01	9.26
17.	**IRSSTN-117**	86.67##	94.47*	30.28**##	10.17	24.52*	134.43##	117.68**##	87.5**##	24.56##	2.22	40.18##	35.62	14.29##
18.	**IRSSTN-118**	86.97##	99.67	21.05	9.01	24.20*	117.15	95.37	81.28*#	21.22##	2.32	28.36	39.98	11.33
19.	**IRSSTN-119**	82.00##	83.67**##	27.49	11.38	19.05	133.58##	112.78##	84.49**##	19.30	2.45	23.73	36.18	8.55
20.	**IRSSTN-120**	91.00##	89.40**#	24.40	11.16	24.28*	104.98	85.22	81.23*#	24.08##	2.20	40.92##	35.21	14.39##

21.	**IRSSTN-121**	98.00##	83.00**##	22.27	12.37**##	20.67	96.33	77.07	79.98	23.74##	2.45	39.67##	38.33	15.20##
22.	**IRSSTN-122**	88.00##	76.08**##	20.12	11.32	23.71	102.96	84.70	82.39**##	20.37##	2.50	27.13	34.53	9.33
23.	**IRSSTN-123**	87.67##	80.27**##	23.71	8.67	23.2	127.04#	108.69##	85.54**##	18.77	2.10	25.87	35.43	9.17
24.	**IRSSTN-124**	94.67##	76.77**##	27.16	12.62**##	20.85	107.29	85.28	79.59	22.19##	2.05	30.67	37.68	11.55
25.	**IRSSTN-125**	83.00##	102.40	30.49**	11.92*#	23.83	131.12##	111.68##	85.27**##	21.57##	2.60	45.94##	38.62	17.76##
26.	**IRSSTN-126**	87.33##	114.13	18.57	10.66	26.00**##	194.37**##	158.36**##	81.63**#	21.22##	2.97	43.13##	40.20	17.31##
27.	**IRSSTN-127**	90.00##	93.93*	23.42	7.15	21.73	148.36##	115.48*##	77.83	20.62##	2.84	30.68	40.14	12.33#
28.	**IRSSTN-128**	88.67##	101.53	25.54	11.21	22.13	117.79	100.55##	85.43**##	22.17##	2.20	40.33##	38.66	15.56##
29.	**IRSSTN-129**	85.33##	110.42	21.54	11.00	25.17**#	111.72	93.70	83.90**##	21.59##	2.40	33.64##	34.41	11.60
30.	**IRSSTN-130**	77.67**##	98.07	27.52	9.00	22.68	138.03##	84.01	60.81	22.6##	2.99	33.54##	36.06	12.08
31.	**IRSSTN-131**	113.00	102.60	31.30**##	11.37	24.34*	150.90**##	127.86**##	84.73**##	23.72##	3.12	40.72##	39.60	16.13##
32.	**IRSSTN-132**	86.33##	98.67	18.62	12.30*##	25.17**#	117.09	99.31#	84.79**##	23.62##	2.80	52.77**##	40.44	21.32*##
33.	**IRSSTN-133**	86.33##	91.20**	24.40	9.00	20.81	126.21#	105.01##	83.23**##	19.95#	2.85	27.23	38.02	10.33
34.	**IRSSTN-134**	85.33##	92.00**	20.35	11.32	21.88	112.81	92.38	81.74**#	22.52##	2.41	37.21##	37.01	13.76##
35.	**IRSSTN-135**	88.67##	98.00	37.77**##	12.81**##	25.46**##	188.88**	144.01**##	76.26	24.28##	2.88	47.00##	38.56	18.10##
36.	**IRSSTN-136**	88.33##	103.80	24.96	11.41#	24.78*#	138.86##	114.49*##	82.57**##	23.62##	2.87	50.05**##	42.03#	21.03*##
37.	**IRSSTN-137**	89.00##	103.47	22.02	10.03	21.02	134.26##	114.81*##	85.54**##	24.53##	3.25	45.23##	40.38	18.25##
38.	**IRSSTN-138**	87.67##	97.13	19.55	11.00	23.14	133.83##	108.05##	80.67*	21.46##	3.28	38.49##	38.31	14.77##
39.	**IRSSTN-139**	85.67##	91.27**	20.60	8.19	23.24	148.27##	125.68*##	84.76**##	22.26##	3.22	28.35	34.25	9.75
40.	**IRSSTN-140**	84.00##	103.40	29.20**	10.00	21.84	117.74	96.16	81.82**#	23.25##	3.22	41.58##	36.46	15.12##
41.	**IRSSTN-141**	90.00##	106.07	22.66	11.45#	25.45**##	114.71	93.72	81.87**#	24.70##	3.24	43.89##	41.08	18.00##
42.	**IRSSTN-142**	86.67##	102.47	27.49	6.59	24.57*	127.23#	100.66##	79.17	20.47##	2.80	30.73	37.36	11.47
43.	**IRSSTN-143**	102.67	96.37	27.17	9.23	22.44	111.18	85.40	76.82	19.42	3.68**	27.45	36.63	10.07
44.	**IRSSTN-144**	85.00##	90.53**	28.72*	11.27	23.43	140.5##	113.33##	80.70*	23.64##	2.80	33.53##	39.67	13.31##

45.	**IRSSTN-145**	90.33##	92.93**	24.12	7.65	22.18	139.92##	108.16##	77.31	23.84##	2.89	35.82##	31.13	11.12
46.	**IRSSTN-146**	92.33##	102.67	28.48*	9.00	25.83**	135.54##	117.26**##	86.57**##	25.64**##	2.99	46.97##	38.03	17.83##
47.	**IRSSTN-147**	90.33##	104.00	26.38	7.32	21.81	126.80#	103.43##	81.58**#	23.91##	2.19	38.10##	37.59	14.31##
48.	**IRSSTN-148**	85.00##	103.27	27.98	9.00	21.17	145.98##	113.93*##	78.14	24.64##	2.69	43.18##	37.11	16.04##
49.	**CSR 43**	84.28##	102.06	26.15	9.47	21.82	135.00##	102.50##	76.01	24.42##	3.43	44.57##	42.53##	18.93##
	Mean	**87.71**	**95.86**	**25.16**	**10.32**	**23.34**	**129.97**	**106.12**	**81.75**	**22.78**	**2.81**	**37.15**	**37.68**	**14.07**
	C.V.	2.42	4.16	5.08	12.96	5.95	6.53	6.31	3.18	1.29	2.70	6.87	7.08	8.86
	F ratio	25.73	14.05	33.94	4.11	4.40	25.61	28.46	8.34	95.93	88.03	28.49	2.35	23.91
	F Prob.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	S.E.	1.22	2.30	0.74	0.77	0.80	4.90	3.87	1.50	0.17	0.04	1.47	1.54	0.72
	C.D. 5%	3.44	6.46	2.07	2.17	2.25	13.75	10.86	4.21	0.48	0.12	4.13	4.32	2.02
	C.D. 1%	4.55	8.56	2.74	2.87	2.98	18.21	14.37	5.57	0.63	0.16	5.47	5.73	2.68
	Range Lowest	77.00	76.08	17.79	6.59	19.05	89.84	74.46	60.81	18.77	2.05	23.73	31.13	8.55
	Range Highest	113.00	114.13	37.77	12.81	26.00	194.37	159.11	87.53	25.64	3.68	58.74	42.53	23.46

Significant at Check CSR 43 = *, significant at Check IR = #

Appendix 2: Mean performance, general mean, range, coefficient of variation, critical difference and standard error for 13 characters of line × tester set of 48 F_1s and their 19 parents

S.N.	Genotypes	Days to 50% flowering	Plant height (cm)	Flag leaf area (cm^2)	Panicle bearing tillers per plant (cm)	Panicle length (cm)	Spikelets per panicle	Grains per panicle	Spikelet fertility (%)	1000-grains weight (g)	L:B ratio	Biological yield per (g)	Harvest index (%)	Grains yield per plant (g)
1	**CSR 10**	83.67	86.33	21.27	8.17	21.00	126.67	105.92	83.62	27.00	2.31	36.61	37.63	13.73
2	**Improved PusaBasmati 1**	94.00	103.67	27.33	7.00	25.00	140.07	117.33	83.79	19.40	3.33	40.36	30.37	12.23
3	**NDR 359**	95.00	101.33	25.42	8.48	26.30	153.05	133.27	87.15	26.00	2.22	46.48	43.82	16.37
	Mean	**90.89**	**97.11**	**24.67**	**7.88**	**24.10**	**139.93**	**118.84**	**84.85**	**24.13**	**2.62**	**41.15**	**37.28**	**14.11**
1	**IRSSTN-101**	87.33	103.20	25.54	7.28	20.97	100.09	82.54	82.48	22.00	2.22	33.67	35.96	12.15
2	**IRSSTN-105**	80.33	96.87	20.67	11.29	21.09	130.37	98.02	75.21	23.36	3.21	40.00	36.94	14.80
3	**IRSSTN-107**	77.67	91.93	29.61	9.19	20.72	118.41	91.31	77.07	22.19	3.34	39.67	36.67	14.50
4	**IRSSTN-116**	95.33	88.47	19.40	12.40	19.98	93.61	71.35	76.00	19.95	3.28	25.93	31.33	8.12
5	**IRSSTN-117**	86.67	94.47	29.62	10.17	20.66	134.43	108.58	80.75	23.58	2.72	40.18	36.13	14.55
6	**IRSSTN-120**	91.00	89.40	24.07	11.16	23.41	104.98	80.22	76.46	24.24	2.81	40.92	35.66	14.59
7	**IRSSTN-124**	94.67	77.75	27.16	13.07	20.85	103.62	71.17	68.78	22.30	2.90	30.72	35.99	11.09
8	**IRSSTN-129**	84.00	110.42	22.29	11.00	19.59	111.72	84.19	75.51	20.18	3.08	33.31	34.87	11.65
9	**IRSSTN-135**	89.67	97.33	27.47	13.16	19.69	129.74	98.22	75.86	21.53	3.10	58.74	37.85	22.26

10	**IRSSTN-136**	88.33	103.80	25.14	11.41	19.79	136.19	102.08	74.91	22.27	2.87	50.38	42.77	21.53
11	**IRSSTN-139**	85.67	91.27	21.09	8.19	21.72	148.27	117.01	78.90	21.14	3.32	28.35	39.26	11.15
12	**IRSSTN-142**	86.67	102.47	28.52	7.00	22.06	127.23	99.19	77.98	20.18	2.62	30.40	40.75	12.38
13	**IRSSTN-143**	89.67	94.87	27.17	9.23	20.04	119.13	91.47	76.82	20.23	3.06	37.65	36.43	13.73
14	**IRSSTN-144**	85.00	90.53	28.72	11.94	20.46	140.50	101.48	72.25	24.26	2.89	33.53	39.81	13.34
15	**IRSSTN 152**	93.00	84.35	25.72	5.86	21.24	118.06	89.13	75.63	21.02	3.01	26.00	39.29	10.22
16	**IRSSTN 155**	95.00	92.05	26.22	6.41	19.82	132.96	94.64	71.31	21.58	3.08	28.93	36.72	10.58
	Mean	**88.12**	**94.32**	**25.52**	**9.92**	**20.76**	**121.83**	**92.54**	**75.99**	**21.88**	**2.97**	**36.15**	**37.28**	**13.54**
1	**IRSSTN-101×CSR 10**	91.00	84.21	26.63	14.35	21.59	166.59	140.33	84.24	22.41	2.53	32.37	38.96	12.60
2	**IRSSTN-101×Improved Pusa Basmati 1**	95.00	95.52	28.16	6.00	22.29	156.67	124.12	79.24	22.43	2.72	35.10	34.07	11.97
3	**IRSSTN-101×NDR 359**	88.00	99.95	27.47	14.00	23.02	194.33	162.48	83.61	22.93	2.40	31.33	35.61	11.15
4	**IRSSTN-105×CSR 10**	97.00	86.54	27.27	9.55	21.62	166.27	135.54	81.53	22.95	2.12	33.28	37.35	12.45
5	**IRSSTN-105×Improved Pusa Basmati 1**	87.67	96.01	29.63	6.39	23.52	184.81	140.25	75.87	21.17	2.53	44.81	37.83	16.95
6	**IRSSTN-105xNDR 359**	98.00	105.66	26.63	13.37	22.62	143.47	110.35	76.89	24.30	2.19	63.35	32.90	20.80
7	**IRSSTN-107xCSR 10**	85.67	93.01	29.49	14.16	21.50	141.54	104.07	73.51	23.02	2.24	52.02	36.17	18.82
8	**IRSSTN-107xImproved Pusa Basmati 1**	93.00	83.37	34.15	9.88	21.04	169.83	116.52	68.62	24.29	2.80	27.89	35.60	9.93

9	**IRSSTN-107xNDR 359**	98.50	93.21	30.51	10.39	21.49	177.67	140.03	78.82	22.67	2.30	59.00	36.17	21.24
10	**IRSSTN-116×CSR 10**	96.00	94.17	26.67	14.68	21.18	169.00	124.30	73.55	21.85	2.30	68.00	34.86	23.70
11	**IRSSTN-116×Improved Pusa Basmati 1**	89.00	96.49	29.77	13.33	21.29	174.00	122.48	70.39	20.56	2.86	72.00	32.52	23.39
12	**IRSSTN-116×NDR 359**	93.00	91.93	29.60	10.42	20.36	143.67	101.71	70.82	20.38	2.31	67.59	34.39	23.22
13	**IRSSTN-117×CSR 10**	88.00	94.71	28.83	12.07	20.57	157.70	112.28	71.26	22.18	2.36	30.12	37.63	11.32
14	**IRSSTN-117×Improved Pusa Basmati 1**	93.00	102.81	32.57	13.78	22.33	112.82	67.75	60.10	23.01	2.10	62.83	36.27	22.76
15	**IRSSTN-117×NDR 359**	95.67	94.21	32.83	8.55	22.21	158.74	117.57	74.04	24.24	2.22	35.41	39.01	13.81
16	**IRSSTN-120×CSR 10**	93.00	84.01	27.00	13.66	22.33	190.67	145.90	76.52	22.91	2.59	47.00	37.86	17.79
17	**IRSSTN-120×Improved Pusa Basmati 1**	93.33	93.41	33.87	15.67	19.71	176.00	128.86	73.20	19.88	2.90	55.00	33.86	18.64
18	**IRSSTN-120×NDR 359**	94.00	98.16	24.85	11.34	20.93	186.33	148.93	79.89	20.50	2.31	49.00	38.45	18.90
19	**IRSSTN-124×CSR 10**	94.00	82.81	27.60	12.20	21.13	184.41	141.19	76.57	21.47	2.25	37.57	34.18	12.85
20	**IRSSTN-124×Improved Pusa Basmati 1**	97.00	88.20	34.33	11.71	23.05	155.00	118.39	76.35	22.22	2.64	55.77	38.21	21.33
21	**IRSSTN-124×NDR 359**	98.00	99.16	28.00	11.50	24.67	122.00	96.14	78.77	20.68	2.72	60.33	36.93	22.24
22	**IRSSTN-129×CSR 10**	94.00	97.18	27.23	11.10	23.93	118.00	90.67	76.88	21.32	2.51	65.76	33.11	21.73
23	**IRSSTN-129×Improved Pusa Basmati 1**	96.00	103.72	27.57	11.19	22.35	107.54	71.48	66.47	22.15	3.08	56.97	34.72	19.78

24	**IRSSTN-129×NDR 359**	96.00	104.24	27.03	15.35	21.26	157.47	118.76	75.41	23.77	2.34	30.00	34.90	10.42
25	**IRSSTN-135×CSR 10**	96.00	95.42	27.04	14.08	24.02	178.30	125.90	70.65	24.22	2.28	26.15	36.15	9.43
26	**IRSSTN-135×Improved Pusa Basmati 1**	97.00	93.07	31.07	8.73	24.33	169.33	131.06	77.28	23.57	3.09	40.00	31.88	12.77
27	**IRSSTN-135×NDR 359**	95.00	106.49	28.42	14.18	22.07	144.43	112.08	77.46	22.90	2.12	52.75	36.64	19.32
28	**IRSSTN-136×CSR 10**	91.67	105.36	25.41	11.00	26.47	144.00	112.68	78.18	23.25	2.38	53.55	36.79	19.68
29	**IRSSTN-136×Improved Pusa Basmati 1**	96.00	101.83	32.86	11.17	24.45	183.34	128.51	70.05	20.55	3.42	40.00	38.30	15.30
30	**IRSSTN-136×NDR 359**	86.00	103.72	26.32	11.58	23.29	161.33	127.94	79.38	21.38	2.36	65.67	34.14	22.32
31	**IRSSTN-139×CSR 10**	93.00	80.69	26.77	12.01	21.20	143.33	114.33	79.84	22.89	2.28	62.72	34.98	21.91
32	**IRSSTN-139×Improved Pusa Basmati 1**	92.00	96.72	26.71	14.46	24.35	118.33	96.78	81.78	21.69	2.41	61.08	33.58	20.48
33	**IRSSTN-139×NDR 359**	95.00	100.58	26.34	15.62	22.33	115.33	91.76	79.55	22.17	2.12	69.66	35.19	24.53
34	**IRSSTN-142×CSR 10**	97.00	94.79	26.84	13.06	22.27	126.67	98.58	77.88	23.24	2.80	61.49	33.60	20.69
35	**IRSSTN-142×Improved Pusa Basmati 1**	97.00	104.57	37.01	10.33	22.17	169.63	132.11	77.83	21.90	2.61	30.18	36.25	11.00
36	**IRSSTN-142×NDR 359**	98.00	96.00	32.46	11.91	24.32	152.03	118.01	77.67	20.96	2.73	49.33	38.19	18.83
37	**IRSSTN-143×CSR 10**	95.00	92.33	26.61	12.07	23.29	161.00	128.61	79.93	20.18	2.25	33.43	37.89	12.66
38	**IRSSTN-143×Improved Pusa Basmati 1**	98.00	100.70	35.37	15.56	22.47	123.67	89.26	72.13	18.85	2.91	41.85	41.16	17.24

39	**IRSSTN-143×NDR 359**	95.00	94.19	31.90	9.17	25.28	155.26	116.25	74.87	21.98	2.68	41.20	40.91	16.82
40	**IRSSTN-144×CSR 10**	96.00	95.39	29.29	11.50	23.64	155.59	104.45	67.30	20.42	2.41	33.37	37.29	12.45
41	**IRSSTN-144×Improved Pusa Basmati 1**	97.33	93.33	34.67	14.37	22.62	123.67	100.61	81.32	21.52	3.09	48.68	37.91	18.45
42	**IRSSTN-144×NDR 359**	96.67	106.02	32.71	10.83	21.14	158.33	121.33	76.75	22.03	2.57	32.94	38.27	12.57
43	**IRSSTN 152×CSR 10**	98.00	94.33	27.57	11.36	23.48	119.00	95.79	80.61	20.23	2.31	37.67	42.01	15.78
44	**IRSSTN 152×Improved Pusa Basmati 1**	95.67	98.33	29.57	10.05	23.28	176.33	136.50	77.41	23.35	2.12	30.67	41.28	12.66
45	**IRSSTN 152×NDR 359**	97.00	99.33	28.38	8.58	22.49	166.33	125.90	75.77	21.56	2.21	31.25	40.64	12.67
46	**IRSSTN 155×CSR 10**	100.33	76.00	27.54	12.05	24.73	137.69	100.56	72.90	20.69	2.43	44.52	33.90	15.05
47	**IRSSTN 155×Improved Pusa Basmati 1**	96.33	96.83	35.09	9.43	24.50	157.27	118.91	75.56	21.66	2.48	32.67	36.72	12.00
48	**IRSSTN 155×NDR 359**	98.00	97.13	27.76	10.79	23.18	121.33	93.19	76.71	22.18	2.38	45.05	41.11	18.54
	Mean	**94.60**	**95.54**	**29.40**	**11.84**	**22.65**	**153.67**	**116.69**	**75.86**	**22.01**	**2.50**	**46.63**	**36.59**	**16.89**
	Grand Mean	**92.89**	**95.32**	**28.27**	**11.21**	**22.27**	**145.45**	**111.02**	**76.30**	**22.08**	**2.61**	**43.88**	**36.79**	**15.97**
	(Check) IRSSTN-143	89.67	94.87	27.17	9.23	20.04	119.13	91.47	76.82	20.23	3.06	43.73	31.44	13.73
	(Check) CSR 43 Ch (R)	83.00	96.89	25.37	8.44	20.46	126.00	92.87	73.76	24.06	3.13	43.22	38.74	16.72
	Range lowest	77.67	76.00	19.40	5.86	19.59	93.61	67.75	60.10	18.85	2.10	25.93	30.37	8.12
	Range highest	100.33	110.42	37.01	15.67	26.47	194.33	162.48	87.15	27.00	3.42	72.00	43.82	24.53

	C.V.	1.48	3.31	6.03	12.24	5.51	5.31	5.96	3.29	1.47	2.03	7.17	6.76	8.79
	S.E.	0.79	1.82	0.98	0.79	0.71	4.44	3.80	1.45	0.19	0.03	1.82	1.43	0.81
	C.D. 5%	2.21	5.09	2.75	2.20	1.98	12.42	10.64	4.05	0.52	0.09	5.08	4.01	2.26
	C.D. 1%	2.92	6.72	3.63	2.91	2.61	16.40	14.05	5.35	0.69	0.11	6.71	5.30	2.99

DEPARTMENT OF GENETICS AND PLANT BREEDING
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Title: “Genetic studies for yield and its contributing components in rice (*Oryza sativa* L.) under salt affected soil”

Major Advisor: **Prof. M. P. Chauhan**
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Advisory Committee

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ABSTRACT

The present investigation entitled “Genetic studies for yield and its contributing components in rice (*Oryza sativa* L.) under salt affected soil” was under taken with the objectives (i) to examine the genetic variability and evaluate the rice genotypes for various traits, (ii) to compute association at genotypic and phenotypic levels among different characters, (iii) to assess the stability of rice genotypes, (iv) to find the combining ability variances and their effects, (v) to find out gene actions involved in the inheritance of various characters, (vi) to estimate heterosis over better-parent and standard varieties and (vii) to identify promising parents and superior hybrids for exploitation in breeding programme.

The experiment was based on evaluation of forty nine rice genotypes under saline soil and normal soil conditions during *Kharif* 2016 at research farm of Genetics & Plant Breeding and Student Instructional Farm, respectively. .A set of 48 crosses were made involving 16 lines and 3 testers (line×tester) during *Kharif 2016.* The hybrids (48) along with 19 parental lines (16 lines and 3 testers) and check varieties IR 28 and CSR 43 were evaluated in randomized block design with three replications at Genetics and Plant Breeding form of N.D. University of Agriculture and Technology, Kumarganj, Ayodhya during *Kharif*, 2017. The data were recorded for days to 50% flowering, plant height (cm), flag leaf area (cm^2), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-grain weight (g), L:B ratio, biological yield per plant (g), harvest-index (%) and grain yield per plant (g). The data was subjected to analysis of variance for randomized block design, coefficients of variation, stability index, heritability and genetic advance, correlation coefficients, path coefficient analysis, combining ability analysis and heterosis analysis over batter-parent and standard varieties.

The analyses of variance due to treatments were highly significant for all the characters under both conditions indicated sufficient variation among the treatment under study. The top five genotypes, exhibiting high mean performance for grain yield along with high performance for other yield components under saline condition were IRSSTN-135, IRSSTN-115, IRSSTN-131, IRSSTN-128 and IRSSTN-125 and for the normal soil condition recommended lines were IRSSTN-101, IRSSTN-132, IRSSTN-136, CSR 43 and IRSSTN-137. These lines may be used

as donor parents in hybridization programme for developing high yielding varieties. High magnitude of phenotypic and genotypic coefficient of variation was observed for grain yield per plant (g) in saline condition, while, under normal condition high magnitude of phenotypic and genotypic coefficient of variation was observed for biological yield per plant (g), and grain yield per plant.. High estimates of broad sense heritability coupled with high genetic advance in per cent of mean were recorded for grains yield per plant (g), flag leaf area (cm^2), biological yield per plant (g), plant height (cm) and L:B ratio in salinity condition, while, for flag leaf area, spikelets grains per panicle, grains per panicle, L:B ratio, biological yield and grain yield per plant were observed for high heritability coupled with high genetic advance in per cent of mean normal conditions. Biological yield and harvest index exhibited highly significant and positive correlation with grain yield under both conditions. Path analysis revealed that the highest positive direct effect on grain yield per plant was exerted by biological yield per plant and harvest index under both situations. Forty nine genotypes of rice were grouped in to eight clusters under each condition. Under salt stress condition, major clusters in divergence analysis contained genotypes of heterogeneous origin, thereby, indicating non-parallelism between genetic and geographic diversity. Therefore, crosses between the members of clusters separated by high inter-cluster distances are likely to throw desirable segregates. Therefore, crosses between members of clusters having high cluster means coupled with high inter-cluster distance between them for important characters are likely to be more rewarding.

IRSSTN-112 showed stable performance under both conditions and all other rice genotypes showed good stability only in salinity or in normal conditions.

The analysis of variance revealed highly significant mean sum of squares due to treatments, parents, crosses and line×tester for all the thirteen characters. This indicated presence of substantial variability in the study materials and validated further statistical and genetical analysis. The high estimates of phenotypic and genotypic coefficient of variation were estimated for biological yield per plant and panicle bearing tillers per plant but GCV for grain yield per plant. The grain yield per plant exhibited highly significant and positive correlation with biological yield per plant and panicle bearing tillers per plant. Biological yield per plant, harvest-index, spikelet per panicle, spikelet fertility and panicle bearing tillers per plant showed maximum direct effect on grain yield per plant.

Specific combining ability (SCA) variances were higher than general combining ability (GCA) variances for all the characters indicating presence of non additive gene action. Average degree of dominance is more than one and predictability ratio were less than one for all most all the characters showed involvement of non additive gene action..

For grain yield per plant parents RSSTN-116, IRSSTN-139, IRSSTN-136, IRSSTN-124 and IRSSTN-120 were recorded as good general combiner. Crosses IRSSTN-

117×Improved Pusa Basmati 1, IRSSTN-129×CSR 10, IRSSTN-142×CSR 10, IRSSTN-135×NDR 359 and IRSSTN-144×Improved Pusa Basmati 1 exhibited high SCA effect for grain yield per plant.

The contribution of line, tester and L×T were maximum for harvest index, flag leaf area, panicle bearing tillers per plant, respectively.

The crosses IRSSTN-116×Improved Pusa Basmati 1, IRSSTN-124×Improved Pusa Basmati 1, IRSSTN-116×CSR 10, IRSSTN-139×Improved Pusa Basmati 1 and IRSSTN-129×Improved Pusa Basmati1 showed high heterobeltiosis for grain yield.

The crosses IRSSTN-139×NDR 359, IRSSTN-116×CSR 10, IRSSTN-116×Improved Pusa Basmati 1, IRSSTN-116×NDR 359 and IRSSTN-117×Improved Pusa Basmati 1 exhibited heterosis over SV 1 for grain yield per plant.

The best five crosses IRSSTN-139×NDR 359, IRSSTN-116×CSR 10, IRSSTN-116×Improved Pusa Basmati 1, IRSSTN-116×NDR 359 and IRSSTN-117×Improved Pusa Basmati 1 recorded high heterosis over SV 2for grain yield per plant.

The crosses IRSSTN-116×Improved Pusa Basmati 1 and IRSSTN-116×CSR 10 exhibited high heterosis over better parent and both check varieties.

The findings of the present investigation have been discussed considering their practical usefulness in relation to overall improvement in rice. These crosses are suggested for their cultivation in target environments after testing and release.

(M. P. Chauhan) **(Preeti Kumari)**