

GENETIC ANALYSIS OF QUANTITATIVE TRAITS IN AROMATIC RICE (*Oryza sativa* L.)

Thesis

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By

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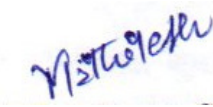
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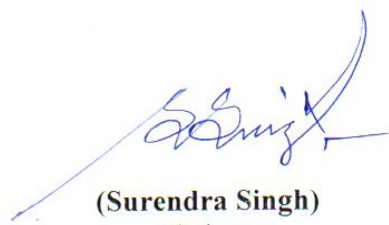

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This is to certify that the thesis entitled “**Genetic analysis of quantitative traits in aromatic rice (*Oryza sativa* L.)**” submitted in partial fulfillment of the requirements for the degree of **Doctor of Philosophy** with major in **Genetics and Plant Breeding** and minor in **Molecular Biology and Genetic Engineering**, of the college of Post-Graduate Studies, G.B. Pant University of Agriculture and Technology, Pantnagar, is a record of *bona fide* research carried out by **Mr. Mithilesh Kumar Singh, Id. No. 45841**, under my supervision and no part of the thesis has been submitted for any degree or diploma.

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

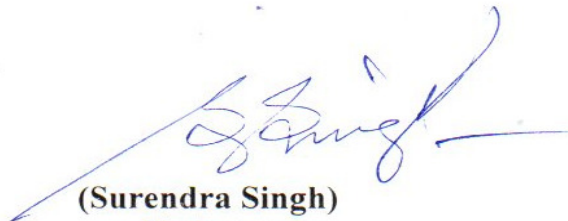
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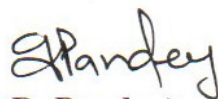
We, the undersigned, members of the Advisory Committee of **Mr. Mithilesh Kumar Singh, Id. No. 45841**, a candidate for the degree of **Doctor of Philosophy** with major in **Genetics and Plant Breeding** and minor in **Molecular Biology and Genetic Engineering**, agree that the thesis entitled **“Genetic analysis of quantitative traits in aromatic rice (*Oryza sativa* L.)”** may be submitted in partial fulfillment of the requirements for the degree.



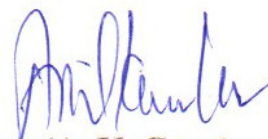
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Introduction

Rice (*Oryza sativa* L.) plant belongs to the grasses family, Gramineae (Poaceae). Rice is considered to be the world's most diverse cereal crop. The geographical distribution of rice extends from north of Manchuria in China (50°N) to as far south as Uruguay and New South Wales, Australia (Around 35°S). It is one among the three major food crops – rice, wheat and maize - of the world and serves as a staple food for about half of the global population. It provides over 21% of the calorific needs of the world's population and up to 76% of the calorific intake of the population of South East Asia (**Melissa *et al.*, 2009**). It contains 6-12% protein, 70-80% carbohydrate, 1.2-2.0% minerals and significant amount of fats and vitamins. India has a long history of rice cultivation. Rice originated in Indo-Burma region and has a domestication history of about 10,000 years. In India, its cultivation stretches from 8° N latitude to 34° N latitude. Out of world rice grown area of 155 mha, with production of 620 mt and productivity of 3750 kg ha⁻¹, India has the largest area under rice (43.8 mha) and it ranks second in production (96.70 mt) after China with an area and production of 29 mha and 178 mt, respectively. It contributes about 40.52% of the total food grain production in India.

Rice is grown in most of the states of country from J&K to Tamil Nadu. Rice production contributes 41% of total food grain production in the country (**Anonymous, 2015**). It was grown in 43.94 million hectare area with production and productivity of 106.54 million tonnes and 2424 kg/hectare, respectively, during 2013-2014 (**Ann. Rep., 2014-2015, Deptt. of Ag. & Coop., 2015**). The major rice growing Indian states are West Bengal, Uttar Pradesh, Andhra Pradesh, Punjab, Tamil Nadu, Orissa, Bihar and Chhattisgarh. Out of these states, West Bengal ranks first in area and production of rice whereas, Punjab has the highest productivity. Different states vary widely in productivity of rice. The states namely Andhra Pradesh, Haryana, Karnataka, Manipur, Punjab, Tamil Nadu and West Bengal have productivity above the national average (2424 kg/hectare).

Some rice varieties are known for their distinct texture and flavour and Basmati in particular are well known for this. Bulk of aromatic rice grown in India and Pakistan are Basmati types, while it is jasmine type in Thailand. Similarly, other aromatic rice are known by different names in their respective countries of cultivation like, Siamati in Thailand, Bahra in Afghanistan, Sadri in Iran, Della, Texamati and Kasmati in USA (Singh *et al.*, 2000). Delightful fragrance, delicious taste and its texture after cooking makes the Indian aromatic rice best among different aromatic rice of the world. The aromatic rice is being grown for centuries in the Himalayan foothill bound region of the Indian subcontinent (<http://apeda.gov.in>, APEDA, 2015). Typical agro-climatic conditions of the niche areas as well as method of harvesting, processing and aging designates this Basmati rice the “scented Pearl” that can transform even the most ordinary meal into a gourmet’s delight. Ancient texts and treatises abound such references that indicates the cultivation of diverse rice types including the scented one by farmers of Indian sub-continent from centuries (Nene, 1998). Although enormous diversity for aromatic rice exists in our country, not all of these are recognized as Basmati type. Only that aromatic rice that are aromatic, long grained, delicately curved and which elongates after cooking bearing a soft and fluffy appearance are categorized as Basmati.

The growing demand for Basmati rice in global market made India a leading exporting country. India export both, Basmati and non-basmati rice, but the revenue it receives (US\$ 800-1200 / mt) through premium Basmati type is thrice than that by non Basmati rice (US\$ 200-400 / mt). About 50-70% of basmati rice produced in India is exported to different countries like Saudi Arabia, United Arab Emirates, Iran *etc.* In year 2008-09, India exported 1556411 mt of basmati rice generating foreign exchange to the tune of Rs. 9477 crores (Rani, 2012). In export market, the traditional tall basmati varieties, Tarori Basmati, Basmati-370 and Type-3 have supremacy over other varieties. However, among the improved high yielding basmati varieties, Pusa Basmati-1121 and Pusa Basmati-1 have appropriated a special niche in the global market due to its extra long slender grains (Rani, 2012).

The varietal improvement programmes for Basmati rice were initiated long back in 1920 at Kala Shah kaku, Punjab of undivided India and at Nagina, Uttar

Pradesh. These programmes mainly relied upon pure line selections from available germplasm. These efforts yielded Basmati-370, a selection from the land races cultivated in Punjab and Type-3, T-23 and N-10B selected at Nagina. The popular Tarori Basmati is a selection from HBC-19 in late 1980's. These varieties are tall, slender stemmed, fertilizer non responsive and low yielders but were reputed for aroma, taste and cooking quality attributes (**Rani, 2012**). Out of these, Basmati 370 proved to be the major traditional basmati rice which became a standard variety for export in this category and led to export boom in Pakistan and India (**Mann, 1987**).

Further, in order to protect the monopoly of Indian basmati export in international market and to step up the overall rice production, research efforts were initiated. Two research programs initiated by Indian Council of Agricultural Research (ICAR) gave a kick-start to the basmati rice breeding in India. These programs were "Improvement of basmati rice for increased productivity and export purposes (1990-93)" and "Genetic Enhancement of Quality Rices for Higher Productivity and Export (1994-1999)". Efforts made under these programs resulted in the release of a series of aromatic/basmati varieties like Haryana Basmati-1, Taroari Basmati, Pusa Sugandh-2, Pusa Sugandh-3 and Bhogawati. Further, in year 2001, Pusa RH-10 that had significant yield advantage over Pusa Basmati 1 was released. Pusa RH-10 is the first fine grained aromatic rice hybrid released in India. In 2002, another aromatic rice variety was released as Pant Sugandh Dhan-15 by GB Pant University of Agriculture and Technology, Pantnagar. Subsequently, other aromatic rice varieties like Sugandhamati and Pusa Sugandh-5 having superiority over Pusa Basmati-1 was released in 2004. Another aromatic rice variety Pusa Sugandh-4 with unique aromatic rice qualities having extra long grains with very high kernel elongation on cooking was released. Other long slender aromatic rice variety released from GB Pant University of Agriculture and Technology, Pantnagar includes Pant Sugandh dhan-17 in 2006, Pant Sugandh dhan-21 in 2010, Pant Sugandh dhan-27 and Pant Sugandh dhan-25 in 2015. Recently Pant Basmati-1 and Pant Basmati-2 are released for commercial cultivation by this university in 2016. The variety, Improved Pusa Basmati-1 was developed using molecular marker assisted selection and released in 2007 providing moderate resistance to bacterial leaf blight without compromising the yield and quality of Pusa Basmati-1 (**Rani, 2012**).

Although, the definition of quality is not static and fixed as it is defined by the end users and their preferences may vary to a great deal (**Cruz and Khush, 2000**). However, the term quality may possess several dimensions from physical appearance to cooking and eating qualities of the grain. Super fine, long slender grained Indian Basmati rice which elongates after cooking with pleasant fragrance, soft and fluffy texture are more preferred and fetch higher price in global and domestic markets (**Kaur et al., 2011**). Indian consumer generally prefers soft, dry and flaky rice. However, consumer's preference within the country varies widely. Hence, rice quality has become an important aspect in all the breeding programmes along with classical yield and resistance features for various biotic and abiotic stresses.

Traditional Indian aromatic rice varieties are recognized as having low yielding potential. The lower yield potential of basmati rice is attributed to its tall and weak stature that causes lodging. Attempts to improve yield of basmati rice through hybridization in dwarf background has been successful to some extent. Other bottlenecks in basmati rice improvement are that these have narrow genetic base, dearth of donor parents for good grain quality, poor combiners and complex breeding behaviour of quality traits. Therefore, it is imperative to explore good combiners that can efficiently be hybridized to produce superior genotypes that have intact traditional basmati quality. Further, for achieving results towards this end, it is necessary to make proper and wise choice of parents, to understand the genetic phenomenon controlling the inheritance of yield and yield components and to adopt a suitable breeding method (**Saleem et al., 2010**) so that improvement could be made in designed way.

Diallel analysis (**Jinks and Hayman, 1953; Jink, 1954; Hayman, 1954; Griffings, 1956**) is a useful tool for evaluating several genotypes in terms of combining ability variances and effects. It also provides information on genetic components and enables the breeders to opt suitable breeding methods for hybrid variety or cultivar development programme. Plethora of literature are available on combining ability analysis in rice; however there is need to analyze combining ability in relation to mean performance, heterosis and other genetic parameters in basmati rice where the improvement has been slow due to several genetic barriers.

Keeping in view the above facts and findings, the present investigation was carried out mainly with the aim to generate heterotic F_1 's by combining premium export quality traits of Indian aromatic rice with high yielding dwarf stature plants. The objectives of the present investigation were:

- i. To estimate the extent of variability, heritability and genetic advance.
- ii. To determine the extent of heterosis for yield and quality traits and to identify the promising F_1 crosses on the basis of their heterotic response.
- iii. To study the general and specific combining ability effects in order to identify promising parents and crosses for grain yield and quality traits.
- iv. To study the nature of gene action governing the expression of yield and quality traits in aroma rice.
- v. To assess trait association among yield and yield components with direct and indirect effects of different component traits on yield.
- vi. To analyse the aroma in order to identify best aroma parents and cross combinations.

*Review
of
Literature*

The relevant scientific literature focussed to the present investigation has been reviewed under the following sub headings:

- 2.1. Genetic variability in aromatic rice
- 2.2. Components of variance
- 2.3. Heterosis
- 2.4. Combining ability
- 2.5. Graphical analysis
- 2.6. Correlation and path coefficient analysis
- 2.7. Aroma performance

2.1 Genetic variability in aromatic rice

The proportion of total phenotypic variance that is genetic was termed as “Heritability” and was symbolized as ‘ h^2 ’ by **Wright (1921)**. **Lush (1949)** classified heritability into broad sense that takes into consideration the total genetic variance and narrow sense that considers only additive genetic variance.

Saleem *et al.* (2005) while evaluating segregating generations of rice reported that highly significant differences were observed between the genotypes and their hybrids for days to flowering, plant height, panicles/plant, panicle length, spikelet fertility, 100-grain weight, number of total grains/plant and grain yield/plant. High broad sense heritability (>80%) and high genetic advance as percent of mean was observed for 100-grain weight, total number of grains/panicle and grain yield/plant that indicated the role of additive effects of genes.

Saleem *et al.* (2008) studied heritability, genetic advance and heterosis in 27 F_1 basmati rice hybrids along with parents and found that estimates of broad-sense heritability and expected genetic advance in response to selection in next generation was high for all the studied traits.

Chakraborty and Chakraborty (2010) evaluated 47 bold grained rice genotypes along with two local checks, Ranjit and Monohar Sali, to estimate genetic variability for eight morpho-physiological traits. High heritability coupled with high genetic advance was found for grain yield/hill and sterility percentage. These traits were predominantly governed by additive gene action. High heritability and moderate genetic advance was observed for plant height. Moderate heritability and moderate genetic advance was recorded for panicles/hill, flag leaf length and flag leaf breadth. High heritability with low genetic advance was found for days to 50% flowering. This indicated that these characters were mostly governed by non additive gene action.

Pandey *et al.* (2012) in an experiment conducted with 52 rice genotypes to know genetic relationship between various quantitative traits and yield reported that significant amount of variability exists for all the traits studied. High PCV and GCV was recorded for biological yield/plant, moderate for grain yield/plant, spikelets/panicle and flag leaf area. However, days to 50% flowering, days to maturity, plant height, panicle length, spikelet fertility and test weight showed lower estimate of PCV and GCV. High heritability and high genetic advance as % of mean was observed for biological yield/plant, grain yield/plant, spikelets/panicle, flag leaf area, test weight and harvest index suggesting preponderance of additive gene action.

Dutta *et al.* (2013) studied variability and genetic parameters of 68 rice genotypes for 12 agronomically important traits. High genotypic and phenotypic coefficients of variations, high heritability (broad sense) and high genetic advance as % of mean was exhibited by tillers/plant, days to 50% flowering, harvest index, spikelets/panicle, spikelet/plant, spikelet density, panicles/plant and grain yield. Thus, these characters were under the influence of additive gene action and a satisfactory improvement in these traits could be made by simple selection procedure.

Sattari *et al.* (2013) while studying gene action for cooking quality traits of rice in cross combinations of four rice varieties viz., Nada, IR36, IR65 and SHZ2 reported that the general heritability of such traits as amylose content, gelatinization temperature and gel consistency were 98%, 95% and 97%, respectively.

Allam *et al.* (2015) conducted an experiment, involving both basmati and non-basmati types, that revealed that significant differences exist for yield, its component

traits and some of the grain quality parameters among genotypes. The magnitude of differences between PCV and GCV was relatively narrow for all the traits, indicating less environmental influence. High GCV was found for alkali spread value, grain yield/per plant and panicles/plant. High heritability and high genetic advance as % of mean was recorded for days to 50% flowering, plant height, panicle length, panicles/plant, filled grains/panicle, test weight, grain yield/plant, brown rice length, brown rice L/B ratio, kernel length, kernel L/B ratio and alkali spread value indicating the additive gene effects in the genetic control of these traits.

Naseer *et al.* (2015) conducted experiment to study genetic variability for different yield attributing traits in 24 aromatic and non-aromatic rice genotypes and found that PCV was relatively greater than GCV for most of the traits, like plant height, spikelets/panicle and number of grains/panicle. Higher magnitude of phenotypic variance showed more environmental influence on trait expression. Few of the traits such as tillers/plant, spikelet fertility, filled grains weight/panicle, test weight and grain yield/plant indicated least differences between PCV and GCV. Highest GCV was observed for tillers/plant, followed by grain yield/plant, grains/panicle and filled grains weight per panicle, while spikelet fertility showed lowest value for GCV. Filled grain weight per panicle exhibited high heritability but lowest genetic advance showing non-additive type of gene control. Traits like grains/panicle, plant height and spikelets/panicle revealed high magnitudes for GCV, PCV, heritability and genetic advance. These results suggested the option for better improvement considering these traits.

Savitha and Usha (2015) evaluated six high yielding varieties *viz.* IR-72, ADT-39, ADT-43, ADT-45, ASD-16 and TPS-4 and their six F_1 's in Randomized Block Design and found that PCV was slightly higher than GCV for all the traits under study. The estimates of GCV showed a considerable range of variation for most of the traits. Observations were recorded and analysed for variability parameters and moderate values of PCV and GCV were observed for days to 50% flowering, plant height, panicles/plant, 100-grain weight and grain yield/plant. High heritability and high genetic advance were recorded for days to 50% flowering, plant height, panicles/plant and 100- grain weight indicating involvement of additive gene action for these traits and phenotypic selection for these traits would likely be more effective.

Singh et al. (2015) carried out an investigation during *kharif 2012* and 2013 at Raipur to study the genetic parameters for various quantitative traits in 83 genotypes of rice (*Oryza sativa* L.). Analysis of variance revealed significant differences for majority of the traits under study. The traits, viz. sterile spikelets/panicle, fertile spikelet/panicle, grain yield/plant, spikelet fertility, harvest index and biological yield/plant exhibited high GCV and PCV. Narrow differences were recorded between GCV and PCV for all the traits studied which indicated less influence of environment on these traits. Sterile spikelet/panicle, fertile spikelet/panicle, grain yield/plant, spikelet fertility, harvest index, biological yield/plant, spikelet/panicle, test weight and panicles/plant exhibited high heritability and high genetic advance as % of mean indicating that simple selection could be effective for improving these characters.

2.2 Components of variance

Fisher (1918) for the first time partitioned the genetic variance into 3 components that is additive genetic variance, dominance genetic variance and epistatic variance.

Cheema and Awan (1985) investigated nature of genetic control and gene action on yield and 4 yield contributing traits in basmati rice using a 6-parent diallel cross. Analysis of variance revealed significant differences among the means of all the traits in 30 F_1 's and their parents. Additive genetic variance was estimated for tillers per plant and non-additive genetic variance was estimated for grain yield/plant. All other yield components were influenced by both the additive and non-additive genetic variance.

Ichii and Takeyari (1988) conducted a study on F_2 population from a 6 x 6 diallel set of crosses and through the analysis of variance of plot means they observed significant differences between parents and their crosses in ratoon traits. Crosses involving Satominori as one parent were eliminated and reanalysis of the resulting 5 x 5 diallel set indicated the absence of non-allelic interaction in ratoon traits.

Pooni et al. (1993) studied the genetics of amylose content in rice through a diallel crosses generated from 7 elite pure lines of indica rice representing all the major rice consuming region of the globe. Analysis of data revealed additive and dominance effects as the major source of variation among 21 crosses of the 7 x 7 diallel. In

addition, cytoplasmic control of amylose content was confirmed and a large proportion of the heritable variation was shown to be controlled by a series of multiple alleles with large effects.

Bijral and Gupta (1998) investigated the inheritance of aroma in basmati rice in a cross Gold (non-aromatic) × Saanwal Basmati (aromatic). Segregation ratios in F₂ population indicated that inheritance of aroma in Saanwal Basmati was governed by a single dominant gene.

Surek and Korkut (1998) made half diallel crossed involving 8 rice cultivars to determine the pattern of inheritance of 12 quantitative characters and nature of gene action in expression of these traits in F₁ and F₂ generations. They found additive genetic variance was significantly greater than the non-additive genetic variance for all the traits except for grain yield/plant in both generations.

Sharma and Mani (2001) studied the combining ability for grain yield and some other traits in a 9 x 9 half diallel cross involving 7 basmati and 2 non-basmati genotypes following Griffing's numerical approach. They found that non-additive gene effects were predominant for plant height, flag leaf area, days to flowering, panicles/plant, panicle length, grains/panicle, test weight, grain weight/panicle, grain yield/plant, head rice recovery and amylose content. While, both additive as well as non-additive gene effects were equally important for kernel elongation ratio and harvest index.

Mahmood *et al.* (2002) studied the the combinig ability and nature of gene action in expression of various traits in a 8 x 8 diallel crossing. They found high additive effects for plant height, panicle length, panicles/plant and primary branches/panicle and non-additive effects for days to maturity, panicle fertility, shoot dry weight, paddy yield, sodium, potasium and calcium contents of the shoot and potasium/sodium ratio in the shoot.

Hasib (2005) evaluated 12 crosses of scented rice along with their 7 parents for eight important panicle traits. The values of genotypic and phenotypic coefficients of variation, heritability and genetic advance were high for panicle weight, secondary branches/panicle, spikelet number/panicle, test weight and grain yield/panicle that indicated important role of additive gene action in the expression of these traits.

Hosseini *et al.* (2005) made half diallel crosses using 8 Iranian and exotic rice cultivars and evaluated 7 quantitative traits. Analysis of variance showed that differences due to genotypes as well as GCA and SCA were significant. They found presence of overdominance for characters as maturity duration, paddy weight/plant and harvest index. The non-additive variance effect was higher than the additive variance effect for all these traits.

Kole (2005) studied inheritance of plant height using 6 x 6 diallel cross (5 gamma ray induced mutants of aromatic rice and cultivar 'Gobind bhog') and their segregation analyses. Diallel analysis revealed the presence of both, the additive and non-additive gene action with the preponderance of the latter (dominance).

Cruz *et al.* (2006), through diallel analysis, studied the inheritance and heritability of cold tolerance at germination stage in crosses involving 6 rice genotypes. Analysis of data indicated that while both additive and non-additive gene action were involved, the latter was relatively more important for percent reduction in coleoptile length as well as coleoptile growth. Generation mean analysis was also performed for coleoptile growth in 6 cold-sensitive x cold-tolerant crosses and it was shown that non-additive effects were due mainly to dominance and epistatic interactions.

Rahimi *et al.* (2010) conducted combining ability analysis for 11 traits in 15 F₁ hybrids generated through half diallel crosses of 6 diverse rice cultivars. The studied traits were growth period, reproductive period, plant height, flag leaf area, panicle length, number of panicles/plant, number of grains/panicle, test weight, grain length, grain width and grain yield,. The significance of both, the specific combining ability (SCA) and general combining ability (GCA) for all the studied traits indicated that both additive and non-additive gene effects contributed towards the inheritance of the traits.

Saleem *et al.* (2010) found additive, dominance and epistasis components of genetic variation for grain yield and yield related traits in Basmati rice using triple test cross (TTC) technique. Epistasis was found to be an important part of genetic variation for different traits like, plant height, tillers/plant, secondary branches/panicle, grains/panicle, test weight and grain yield/plant but not for traits like, primary branches/panicle and panicle length. Further splitting of epistasis showed that additive x additive, dominance x dominance and additive x dominance types of interactions were

involved in the expression of these traits. Expression of traits viz. primary branches/panicle and panicle length were influenced by additive and dominance type of gene action. Directional dominance was observed to be absent for these two traits.

Ashfaq *et al.* (2012) selected 8 parents on the basis of phenotypic and genotypic screening to generate crosses in half diallel mating design. Data were analyzed using Griffing's numerical approach to study the genetics of the traits in parents and their F₁ hybrids. Both additive and non-additive components appeared to be important in the inheritance of most of the studied traits.

Ilieva *et al.* (2013) investigated the mode of inheritance and the influence of genes on grain weight/plant in F₁ and F₂ generations of rice in a 7 x 7 half diallel cross. In both the generations most combinations had dominant mode of inheritance. The combining ability analysis showed significant activity of genes with additive and non-additive action. Data from components of genetic variance and regression analysis indicated absence of inter allelic interaction and a greater role of dominant component in the inheritance of the trait.

2.3 Heterosis

The term heterosis was coined by **Shull (1914)** for the developmental stimulus emanating from the union of different gametes and the term 'hybrid vigour' is connotation for manifested effect of heterosis. According to **Hays *et al.* (1955)** heterosis is the increased vigour of F₁'s over the better parent.

Bansal *et al.* (2000) studied heterosis and combining ability effects in 11 x 11 diallel cross. For majority of the crosses, heterosis was found significant for grain yield and its component traits. Maximum heterosis for grain yield/plant was obtained in the cross Karnal Local/Dawag.

Saxena (2000) estimated heterosis for 22 morpho-physiological characters in 88 crosses derived from 22 lines (14 elite Tropical japonica (TJ), 5 indica (I) and 3 japonica (J)) and four testers, one TJ and *aus* (A) each and two indica (I) under optimum fertility (120N: 60P:40K Kg/ha) environments and reported moderate to high heterobeltiosis and standard heterosis for grain yield and most of the components. Standard heterosis for grain yield varied from -96.71 to 259.98%. The hybrids manifesting higher heterosis for grain yield were IR-65600-77-4-2/Dullar, Akihikari/Dular and IR-65598-152-1-5-2/Pant Dhan-4.

Liao *et al.* (2003) crossed seven CMS lines with nine restorers, all belonging to indica, to generate 63 F₁s hybrids that were used to compare the eleven grain quality traits. It was revealed that for most of the F₁s, the value for different quality traits were lower than the mean of their respective parents. Apparent disparity in grain quality performance was observed among F₁s. The traits *viz.* chalky area%, chalky grain%, head rice recovery and gel consistency had great variation in all kind of heterosis estimated that suggested that a special attention should given to exercise selection for F₁ hybrids for these traits hybrid breeding. The mean value of hybrids were significantly lower than those of their better parents for all the traits except for kernel length and amylose content and the mean value of hybrids were significantly higher than those of their poor parents except for brown rice recovery, gel consistency and milled rice recovery.

Alam *et al.* (2004) pondered upon the genetic basis of heterosis in rice through mid-parent, standard check and better parent for 11 quantitative traits using 17 parental lines and 10 selective hybrids originating from them. The studied traits were days to flag leaf initiation, plant height, days to first panicle initiation, days to flowering, flag leaf length, panicle length, days to maturity, fertile spikelet/panicle, panicles/hill, grain yield/10 hill and test weight. In general, the hybrids performed significantly better than that of their respective parents. Significant heterosis was reported for most of the studied traits. Among these 10 hybrids, five hybrids *viz.*, 17A/45R, 25A/37R, 27A/39R, 35A/47R, and 31A/47R showed highest heterosis for grain yield/10 hill. Inbreeding depression in F₂ generation was also studied for 11 traits for all the 10 hybrids. Negative and positive inbreeding depression for different traits was found for different crosses but none was found to be significant. They suggested that selection of parents for developing high yielding hybrids was crucial.

Veni *et al.* (2005) studied heterosis for yield, yield contributing traits and 7 important quality parameters in 25 cross combinations of rice generated by line x tester mating design. It was revealed that in general, the magnitude of heterosis were lower for quality traits than that for yield and yield components. Nine hybrids manifested positive and significant standard heterosis for grain yield/plant, of which IR 64/Basmati-6129, IR-64/HBC 85 and PK-1379-9-1-1/Basmati-6129 were superior. IR 62874-88-2-1/PGB, PR-109/HBC-85 and IR-62874-88-2-1/Basmati-6129 recorded

significant average heterosis for all the three physical kernel traits in the desired direction. Based on yield and quality parameters, Gaurav/PGB, PR-109/PGB and PR-109/HBC-85 could be isolated for manifesting significant positive mid parent heterosis.

Faiz *et al.* (2006) estimated heterosis and combining ability effects for yield and yield contributing traits using four genotypes and hybrids originating from them using line $\times$ tester mating design. Trait studied were plant height, panicles/plant, spikelets/panicle, filled grains/panicle, sterility % and grain yield. It was observed that CMS lines reduced the plant height in their respective F_1 hybrids. The highest heterosis over better parents was recorded for grain yield (41.83%), panicles/plant (11.04%) and filled grains/ panicle (7.39%) in the cross IR69616A/Basmati-385.

Pradhan *et al.* (2007) reported highly heterotic hybrids in their hybridization programme involving 38 improved basmati lines that also included some maintainers of sterile lines. Cross combinations IR-68281A/Pusa-1235-95-73-1-1, IR-68281A/RP-3644-41-9-5, Pusa-3A/UPR-2268-4-1, IR-68281A/Pusa Basmati-1, IR-68281A/BTCE-10-98 and IR-58025A/HKR- 97-401 were found to be highly heterotic for grain yield/plant. Additionally, a direct correspondence between intra-cluster distance and magnitude of heterosis was observed that could serve as guide for prediction of heterosis.

Saleem *et al.* (2008) studied heterosis in 27 basmati rice hybrids generated in line $\times$ tester mating design. Heterosis and heterobeltiosis ranged from -21.09 to 60.13% and -33.34 to 42.99% for flag leaf area, 17.88 to 53.10% and -25.90 to 23.97% for panicle density, -3.94 to 12.28% and 3.25 to 32.21% for plant height, 7.54 to 58.77% and 12.88 to 104.37% for biological yield/plant, -8.80 to 32.43% and -24.32 to 19.29% for harvest index and 12.50 to 95.33% and -6.97 to 66.38% for yield/plant respectively. It was concluded that improvement for grain yield could be made more effective by making some compromises among some morpho-physiological traits that contribute to yield within certain limits.

Roy *et al.* (2009) generated 20 rice hybrids through line $\times$ tester mating design involving 5 high yielding lines and 4 testers having superior grain quality and evaluated them for yield and various quality traits. Significant heterosis for yield and other quality traits were observed in majority of the hybrids. Majority of the heterotic hybrids for

grain yield/plant were also heterotic for two or more component traits. The hybrids IET-5656/Kalonunia, IET-8002/Dudheswar, IET-5656/Dudheswar and IR-62/Sambamahsuri were identified for their heterotic yield and superior grain quality. Overall, heterosis for quality traits were found to be of lower magnitude than that for yield and yield component traits.

Mahalingam and Nadarajan (2010) generated 12 hybrids with normal fertility by crossing 4 aromatic rice varieties *viz.*, ADT-41, Pusa Basmati-1, Basmati-370 and Taroari Basmati with 3 TGMS lines *viz.*, TS-29, TS-6, and GD-98013 and various quality traits in search for a promising hybrid combination. Overall, two hybrids TS-29/ADT-41 and TS-29/Pusa Basmati-1 were found to be superior and could be utilized for commercial exploitation of heterosis.

Joshi (2011) studied degree and direction of hybrid vigour for various agronomic traits in rice searching for the possibilities for its commercial exploitation. They evaluated 14 crosses between rice cultivars (improved and landraces) including 3 wild aborted male sterile parents. A marked variations variation in magnitude of heterobeltiosis and standard heterosis was observed for yield and yield components. Five crosses showed significantly higher standard heterosis for grain yield. Heterobeltiosis ranging from -55% to 139%. Among component traits, panicle/plant showed highest heterosis followed by spikelet number and panicle length

Tiwari *et al.* (2011) studied heterosis for yield component traits in rice to identify the best heterotic combinations. The results indicated that the magnitude of heterobeltiosis for yield was significant in 46 hybrids that ranged from 11.63 to 113.04% and standard heterosis was significant in 43 hybrids that ranged from 10.48 to 71.56%. Majority of the hybrids superior to better parent or standard check for grain yield were also heterotic for spikelets/panicle

Kumar *et al.* (2012) estimated average heterosis, better parent heterosis and standard heterosis in 28 basmati hybrids for yield and its component traits generated by 8 x 8 diallel crosses. Hybrids pant Sugandh Dhan-15/UPR-2845-6-3-1, Pant Sugandh Dhan-15/UPR-3003-11-1-1 and Pant Sugandh Dhan-17/UPR-3003-11-1-1 showed significant standard heterosis for biological yield (158.47, 150 and 124.58%), harvest index (58.6, 37.8 and 58.4%) and grain yield (309.53, 244.45 and 255.56%).

Reddy *et al.* (2012) studied the heterosis in 7 aromatic rice hybrids for yield and quality parameters like kernel length, kernel width and kernel L/B ratio. For days to 50% flowering, 5 crosses exhibited significant negative heterosis with respect to mid parent and 6 crosses showed significant negative heterosis with respect to better parent. For panicles/plant, 2 crosses showed significant positive heterosis and 1 cross exhibited significant negative heterosis over better parent. Six cross combinations showed significant positive heterosis over better parent for grain yield. Five crosses showed significant positive heterosis over mid-parent for kernel length, among which highest (8.21%) was shown by Pusa-1121/BM-71 but none of the crosses were superior over better parent. For kernel breadth, only RNR-2354/MTU-1081 showed significant negative heterosis which was -4.27%.

Ashfaq *et al.* (2013) reported heterosis for various morphological traits *i.e.* panicles/plant, primary branches per panicle, seeds/panicle, seed weight/panicle, test weight, grain yield/plant and grain L/B ratio under different irrigated conditions in Randomized Complete Block Design (RCBD). The maximum heterosis under water stress condition for different traits are shown by different crosses as follows: i) seeds/panicle- 80.53% by Basmati-2000/CB-40, ii) panicles/plant- 16.12% by Basmati-198/CB-32, iii) test weight- 12.06% by CB-32/CB-14, iv) yield/plant- 11.10% by Basmati-198/CB-42, v) primary branches per panicle- 10.14% by Basmati-2000/Super Basmati vi) seed weight/panicle- 8.64% by Super Basmati/CB-14 and vii) grain L/B ratio- 8.04% by Basmati-2000/CB-40

Gnanamalar and Vivekanandan (2013) generated 21 rice hybrids by crossing 7 high yielding rice genotypes (AS-90033, ADT-41, ADT-46, TKM-9, CO-47, Jeeragasamba and ACM-98003) in half diallel fashion. Average heterosis, heterobeltiosis and standard heterosis were estimated for grain yield and quality parameters. High magnitude of heterosis was found for grain yield, 100-grain weight, hulling %, milling %, kernel elongation ratio, head rice recovery and amylose content but its magnitude was low for kernel length, kernel breadth, L/B ratio, alkali spreading value and kernel elongation ratio.

Venkanna *et al.* (2014) estimated extent of heterosis and inbreeding for grain yield and quality traits in rice. Significant average heterosis and heterobeltiosis in desired direction was observed for various traits in many crosses. The crosses IR-

64/NLR-34449 and MTU-1010/BPT-5204 showed highly significant heterobeltiosis for grain yield. The crosses JGL-3844/JGL-11690, Erramallelu/LGL-11690, BPT-5204/JGL-11690 and MTU-1001/JGL-1798 showed significant positive heterosis for grain yield and one or more quality traits.

Gonya *et al.* (2015) evaluated 16 hybrids developed by crossing 4 aromatic lines and 4 non-aromatic testers for yield and various grain quality traits to estimate the heterosis and to identify the best cross combinations. The estimates of standard heterosis, heterobeltiosis and average heterosis were variable among the crosses. They observed variable magnitude of average heterosis for different traits as panicles/plant (69.57%), panicle length (20.82%), filled grains/panicle (30.14%), test weight (23.12%), grain yield/plant (89.25%) and alkali spreading value (45.32%). Some of the heterotic crosses were also the best specific crosses that exhibited high per se performance.

2.4 Combining ability

While breeding for high yielding varieties or hybrids, It is common practice to perform combining ability analysis which seems to be the quickest method to understand the genetic nature of quantitative traits. Besides knowing the mean performance of parents, combining ability analysis is an important tool that helps selecting the desirable parents for the purpose of developing high yielding hybrids.

Sprague and Tatum (1942) defined general combining ability (GCA) of a line as its average performance in series of cross and specific combining ability (SCA) of a cross as certain combinations that perform relatively better/worse than that would be expected from GCA of their parents. In generally, good combining parents result in elevated frequency of heterotic hybrids than that by poor combiners. In genetic viewpoint, GCA is measure of additive gene effects whereas, SCA is a measure of non-additive gene effects that includes dominance and epistasis.

Handerson (1952) defined GCA as the average merit of a line(s) when mated with a random sample of individuals from specific populations with respect to certain traits or weighted combination of traits. And merit of progeny is measured in defined set of environment. He defined SCA as deviation of a particular cross from the value that would be expected on the basis of the GCA of the combining parents.

Griffing (1956a) and **Charnaham *et al.* (1960)** and many others suggested that GCA includes both, the additive effects as well as additive $\times$ additive epistasis. It was realized that high yielding lines may not necessarily transmit their superiority to the hybrids (**Allard, 1960**). Hence, an estimate of GCA and SCA effects may be more reliable guide as which parents to be used in crossing to develop a promising hybrid than that solely based on *per se* performance of parental lines.

With the advancement of quantitative genetics, several techniques have become available for the estimation of combining ability. Out of these, top cross technique (**Davis, 1927**), polycross (**Tysdal *et al.*, 1942**), diallel cross analysis (**Griffings, 1956**), line $\times$ tester analysis (**Kempthorne, 1957**), partial diallel cross analysis (**Kempthorne and Curnow, 1961**) and triallel cross analysis (**Rawlings and Cockerham, 1962**) are worth mentioning.

Singh and Nanda (1977) found significant SCA and GCA variances for panicle length, spikelet number, number of primary branches, test weight and grain yield/plant in a 6x6 diallel crossing. The highest SCA and GCA effects for grain yield were produced by Prasad $\times$ CH4 and CH-4 and Badshah and respectively.

Niranjana-Murthy *et al.* (1992) did combining ability analysis from data recorded on 7 parents and F_1 s originating from them in diallel fashion on yield associated and physiological traits. Significantly high values of SCA and GCA and variance of reciprocals were found that showed involvement of non-additive and additive gene effects and also the role of cytoplasmic genes.

Ganesan and Rangaswamy (1998) worked out combining ability analysis from data on 12 yield associated traits in 14 parents and 48 hybrids resulting from crossing 6 CMS lines with 8 tester in line $\times$ tester mating design. Higher GCA variance was observed than SCA variance for all traits except tillers/plant, panicles/plant, panicle length and yield/plant, that indicated the preponderance of additive gene action. The parents *viz.* IR-62829 (WA source line), White Ponni and Ponni (testers) were identified as parents having good GCA for yield and yield associated traits.

Sharma and Mani (2001) studied combining ability for yield and other traits in a 9 $\times$ 9 half diallel cross involving 7 basmati and 2 non-basmati genotypes using Griffing's numerical approach. It was found that non-additive gene effect was

predominant for plant height, days to flowering, flag leaf area, panicles/plant, panicle length, grain weight/panicle, grains/panicle, test weight, yield/plant, head rice recovery and amylose content whereas additive and non-additive gene effects were equally present for kernel elongation ratio and harvest index.

Vanaja *et al.* (2003) crossed 8 lines in half diallel fashion to study combining ability for yield and 17 other yield related traits. The analysis revealed that additive as well as non-additive gene effects were involved in governing yield and most of the yield associated traits with preponderance of non-additive gene action for majority of yield components. Additive gene action was found predominant for test weight, second upper inter-nodal length and plant height. The line *Vyttila-3* was found as good general combiner. The hybrids PK-3355-5-1-4/Hraswa, *Vyttila-3/IR-60133-184-3-2-2*, *Vyttila-3/IR-36*, *Vyttila-3/Mattatriveni* and *IR-36/Mattatriveni* have shown significant SCA effect for yield and different yield associated traits.

A study on combining ability for yield and its component traits in rice in a 6 x 6 diallel cross was carried out by **Suresh and Anbuselvam (2006)**. Analysis of variance revealed significant differences among genotypes for all the traits except for test weight. The majority of the crosses showed significant SCA effects, in which at least one parent was having high GCA effects.

Narasimman *et al.* (2007) carried out full diallel analysis aiming to work out combining ability and heterosis for grain yield and its component traits using 9 rice genotypes. It was revealed that ADT-44 was good general combiner for all the 6 traits studied. The genotype CR-1009 was also observed as good combiner for all the traits but harvest index. The cross ADT-44 x CR-1009 recorded highly significant positive SCA effects and highly significant positive heterobeltiosis and economic heterosis for filled grains/panicle, biomass production/plant and grain yield/plant.

Rashid *et al.* (2007) carried out Line x tester analysis in Basmati rice using 2 lines and 3 testers. The predictability ratio revealed the predominance of non-additive gene action in the inheritance of all studied traits. The female Super Basmati and male DM-25 and DM-107-4 were found to be good general combiners for most of the studied traits. The crosses Basmati-370/DM-25 and Super Basmati/DM-107-4 were found to be good specific combiners for grain yield/plant. However, the cross Basmati-370/EL.-30-2-1 was identified as promising specific combiner.

Ahangar *et al.* (2008) studied gene action and combining ability in 5 rice cultivars using half diallel cross. Mean squares of combining ability for all the traits showed significant additive and non-additive effects in genetic control these traits. Non-significant MS (GCA)/MS(SCA) ratio for all the traits except 1000-grain weight showed higher importance of non-additive effects. Generally, Neda, Dasht and Binam were the best parents for general combining ability and Mashhad Domsiah x Binam and Binam x IR62871-175-1-10 were the best hybrids for grain yield and its components traits.

Panwar and Ranwah (2008) studied combining ability for grain yield, yield components and some key quality traits in using 10x10 diallel crossing involving scented rice genotypes. The results revealed significant mean square differences due to GCA and SCA for all the traits in all four environments, indicating the importance of additive and non-additive gene effects in inheritance of yield, its component traits and grain quality traits. The estimates of GCA and SCA were greatly influenced by environment, indicating their inconsistency over environments. Among the parents, IET-16320, Pusa Basmati-1, IET-13549 and IET-13846 emerged as good general combiners for yield component traits and grain quality traits.

Shankar *et al.* (2009) carried out combining ability studies using 6 elite TGMS lines and 8 diverse male parents. The ratios of GCA to SCA variances revealed the predominance of non additive gene action over additive gene action in the inheritance of all the characters studied. The GCA effects of parents in the pooled analysis revealed that the lines DRR 20S and DRR 1S and the testers BCW 56R and KMR 3R were promising general combiners for grain yield and yield contributing traits. Based on the SCA effects in pooled analysis, 11 hybrids *viz.*, DRR 6S x APMS 6B, DRR 1S x IR 58025B, DRR 6S x PMS 17B, DRR 7S x EPLT 109R, DRR 17S x BCW 56R, DRR 17S x APMS 6B, DRR 17S x C 20R, DRR 20S x CRMS 32B, DRR 20S x KMR 3R, DRR 22S x KMR 3R and DRR 22S x PMS 17B were identified as promising for grain yield/plant and other traits.

Saleem *et al.* (2010) worked out combining ability analysis involving 12 parental genotypes and 27 F₁ hybrids originating from them in Basmati rice through line x tester mating design. The estimates of SCA variance, ratio of GCA to SCA variance and degree of dominance revealed preponderance of non-additive gene effects

for all the traits. Three lines *viz.*, Super Basmati, Kashmir Basmati and Basmati-2000 and one tester *i.e.* Basmati-385 were identified as good general combiners and good *per se* performers for yield and yield contributing traits. Hybrids like Basmati 2000 x EL-30-2-1, Basmati Pak x Basmati-385, Super Basmati x Basmati-385, DM-107-4 x Basmati-385, Basmati 2000 x DM-25, Kashmir Basmati x DM-25 and DM-16-5-1 x Basmati-385 showed high mean performances, SCA effects and heterobeltiosis for yield and were proposed for heterosis breeding.

Selvaraj *et al.* (2011) assessed combining ability in 26 selected rice genotypes based on reaction to blast disease and yield attributes. It was revealed that estimates of SCA variance were higher than the estimates of GCA variance for all the traits except grain yield wherein the GCA variance was higher. Among these genotypes, IR-50 was found as good general combiner for six traits. Among the testers, IR-64 showed high *per se* performance and high GCA effects for panicle length, filled grains/panicle, test weight and grain yield/palnt.

Ghara *et al.* (2012) studied the general and specific combining ability in 50 F_{1s} in rice along with 15 parents (5 CMS lines and 10 restorers). Results of analysis indicated that variances of GCA were lower than the SCA variances for traits which indicated predominance of non-additive gene action in the inheritance of the traits. Among CMS parents, NematA and among restorers, Ahlamitarom were observed to be good general combiners for most of the traitss studied. The cross NematA x IR-9 was good specific cross combinations for grain yield and most of the component traits due to highly significant SCA.

Tiwari *et al.* (2012) evaluated 60 F_{1s} along with their parents (3 CMS lines and 20 restorer variety) to work out the inheritance pattern of some morphological traits. The results indicated that the male lines (restorers) *i.e.* IET-201108, IR-35454-18-1-2R and IR-52256-9-2-2-1R were identified as good general combiner for grain yield and almost all its component traits. The lower magnitude of GCA than SCA variance, lower predictability ratio and greater value of degree of dominance in all the studied characters were suggestive of a significant role of non additive gene action. Out of 60 crosses, about 30% crosses showed significant and desirable SCA effects for grain yield along with its component traits, *viz.*, number of spikelets/panicle, number of

fertile spikelets and biological yield. High SCA effects was observed in the crosses, IR-58025A x IR-19058-107-1R, NMS4A x IR-633-76-1R, IR58025A x IR-32419-28-3-1-3-3R, NMS-4A x IR-5226-9-2-1R and NMS-4A x IR-35454-18-1-1-2R.

Ashfaq *et al.* (2013) found that genotypes Basmati-2000, CB-42, CB-17 and Basmati-198 were good general combiners for various traits particularly under water stress condition. Maximum specific combining ability was found for cross Basmati-198 x CB-17 for primary branches/panicle, Basmati-198 x CB-17 for productive tillers/plant and CB-32 x CB-14 for grain yield/plant. Some hybrids had good amount of heterosis for specific traits such as productive tillers/plant, test weight and grain yield/plant that can be used in the development of new hybrid rice varieties. They concluded that germplasm lines they studied had great potential that could be used for development of new hybrid varieties.

Kumari *et al.* (2014) estimated combining ability and heterosis for grain yield, yield attributing traits and some of the grain quality parameters in rice. The crosses were made among 3 CMS lines *i.e.* Pusa6A, IR58025A and IR68897A and 7 pollen parents *viz.* Jaya, Sarjoo-52, Sasyashree, HUR-5-2, Swetha, BPT-5204 and PR-106. 21 hybrids were generated using line x tester mating design. The superior hybrids were identified on the basis of combining ability effect and magnitude of heterosis. The higher magnitude of heterosis for all the yield and quality traits was not expressed in any one single cross combination rather it was dispersed among crosses owing to diverse genetic background of their parents. The two crosses IR68897A/BPT-5204 and IR68897A/Jaya were found to be heterotic for yield and yield contributing traits as well as the grain quality parameters.

Veeresha *et al.* (2015) worked out the extent of heterosis, general and specific combining ability for yield and yield contributing traits in rice. Higher value of specific combining ability (SCA) variance than general combining ability (GCA) variance for most of the traits indicated the preponderance of non-additive gene action in the inheritance of these traits. However, for some of the traits both the GCA and SCA variances were significant that emphasizes the significance of both additive and non-additive genetic component in trait expression. They also reported correspondence between *per se* performance and combining ability for some of the traits.

2.5 Graphical analysis

Pooni *et al.* (1993) applied the models proposed by Gale and Pooni, Kumar and Khush to study the inheritance of amylose content in a diallel set of crosses involving 7 elite inbred lines of indica rice. It was revealed that reciprocal effects could be detected unambiguously only in the F_2 diallel and the additive and non-additive effects could not be separated in the B_1 and B_2 diallel when analysed separately. Analysis of data revealed that additive and dominance effects are the main sources of variation among 21 crosses of the 7×7 diallel. Comparisons of the B_1 and B_2 diallel showed that the single dosage dominance effects differed significantly from the double dosage dominance effects. They unambiguously confirmed the cytoplasmic control of amylose content and confirmed that a large proportion of the heritable variation was controlled by a series of multiple alleles with large effects.

Lio *et al.* (2003) studied 11 grain quality traits in 63 F_1 hybrids generated through line $\times$ tester mating design involving 7 elite indica CMS line and 9 elite restorer lines. The results of the study showed that frequency of negative over dominance, dominance and partial dominance was much higher than that of the positive ones.

Leng and Hong (2004) studied the inheritance of 7 grain quality parameters *viz.* grain length, grain width, weight of 30 milled rice grains, chalkiness score, gelatinization temperature, amylose content and gel consistency using F_2 populations derived through 8×8 diallel crossing of 8 ecological types of *japonica* rice. The differences in each character were not obvious in the parents, but transgressive segregants were found for all traits in F_2 generation. This finding indicated that the genes controlling these traits were dispersed among parents.

Akram *et al.* (2007) studied the nature of gene action and inheritance of traits related to seedling vigor and grain yield in F_1 crosses of a 7 parent diallel cross. Results revealed that the seedling shoot length and rate of germination index were influenced by both additive and non-additive gene action. But, the additive component was found to be more critical in the inheritance of these traits. Wr-Vr graphic analysis indicated that the rate of germination index was under the control of complete dominance gene effect. Over dominance was shown to be more important for seedling dry weight,

seedling root length and test weight while partial dominance was found to control seedling shoot length, tillers/plant, panicle length and grain yield/plant.

Muhammad *et al.* (2007) investigated the nature of gene action for traits related to grain yield and seedling vigour in F_1 generation of a 7 parent diallel cross. They observed that the rate of germination index and seedling shoot length was influenced by both the additive and non-additive gene action. But, the additive component was more pronounced in the inheritance of these traits. Wr-Vr graphic analysis revealed that the rate of germination index was under the control of complete dominance gene effects. Over dominance was more important for seedling dry weight, seedling root length and test weight while partial dominance controlled seedling shoot length, number of tillers/plant, panicle length and grain yield/plant.

Iftekharuddaula *et al.* (2008) studied the genetic components for 8 panicle characters in rice using 8-parent half diallel cross. Hayman's analysis of variance indicated the importance of both additive and non-additive genetic components for all the panicle characters except dominance component for filled grains/secondary branches. The unidirectional dominance was observed for the traits *viz.*, primary branch length, secondary branch length, primary branches/panicle, secondary branches/panicle and filled grains/primary branch. Asymmetrical gene distribution was observed for all the panicle traits except filled grains/secondary branch. Primary branches/panicle and unfilled grains/secondary branch followed simple additive-dominance genetic model. From Vr-Wr graph partial dominance was reflected in the action of genes governing the inheritance of primary branches/panicle while, complete dominance was reflected in inheritance of unfilled grains/secondary branch. IR8 possessed most of the dominant genes, while 1R65610-38-2-4-2-6-3 possessed most of the recessive genes for unfilled grains/secondary branch. The distribution of dominant and recessive genes was unequal in the parents for these two traits. There was drastic influence of environment on these two panicle characters. Very high heritability (narrow sense) was observed for primary branches/panicle and unfilled grains/secondary branch.

Raju *et al.* (2011) estimated genetic components of variation for yield, its component traits and grain quality parameters through Hayman's approach using 8×8 diallel mating design. All the component traits of yield and yield *per se* except test weight were under the influence of non-additive gene action. Grain dimensions *viz.*

grain length, grain breadth and grain length/breadth ratio were largely under the control of additive gene action. The proportion of dominant and recessive genes and genes with positive and negative effects were not in symmetry as per the estimates of $H_2/4H_1$ and KD/KR . Coefficient of regression (b) significantly differed from zero for traits like, plant height, panicle length and grain breadth that in turn satisfied the general assumptions of diallel analysis. Based on these findings, progeny selection was suggested for improvement of test weight and grain quality parameters. And for the remaining traits population improvement methods would be the ideal approach. The parents *viz.* JGL-1881, White Ponny and MTU-4870 were classified as good parents for hybridization.

Ashfaq *et al.* (2012) analyzed experimental data using Hayman graphical approach to study the genetics of the parents and their F_1 hybrids. Based on the genetic component analysis, both additive and non-additive components were found to be important in the inheritance of most of the traits. Most of the traits showed constant gene action in both environments, but the gene action for some of the traits was affected by the environment. Morphological traits like plant height, panicles/plant and test weight were governed by over-dominance type of gene action in both the environments (control and drought) while number of grains/panicle and grain length/width ratio showed over-dominance type of gene action only in drought conditions. The grains/panicle and grain length/width ratio showed additive type of gene action with partial dominance only in control environments (irrigated condition).

Sattari *et al.* (2013) studied on how gene action controlled the traits effective in determining the cooking quality of rice. They made all cross combinations from four 4 rice varieties *viz.* IR-36, IR-65, Nada and SHZ-2. These varieties were discrete for the traits that are effective in determining the cooking quality of rice. Based on the variance of the studied parental lines along the regression line (wr to vr) it was found that the parent IR-65 which in relation to the central point was at the farthest point and hence had the highest variance and consequently it had higher number of dominant alleles. The parental lines IR-65 and Nada had the lowest variances and consequently had the lesser number of dominant alleles.

Chaturvedi *et al.* (2015) suggested that graphical analysis of a diallel cross provides useful information about average degree of dominance, dominance order of

the parents and additional information about the relationship among the parents. In their study they found that over dominance was evident for plant height, days to 50% flowering, days to maturity, panicle length, panicle weight, grains/panicle, grain filling %, length/breadth ratio and grain yield/plant; and partial dominance was recorded for panicles/plant and test weight. The parents were well scattered on the regression line indicating their diverse genetic nature.

2.6 Correlation and path analysis

Kennedy and Rangasamy (1998) carried out correlation studies on rice hybrids under low temperature conditions and found that the phenotypic and genotypic correlation coefficients had same direction but of varied magnitude. They concluded that selection for traits such as days to 50% flowering, panicles/plant, spikelet fertility and 100-grain weight may serve to increase grain yield.

Gupta *et al.* (1999) estimated character association in segregating population of basmati rice. Analysis revealed that grain yield was positively associated with panicles/plant, panicle length, grains/panicle and panicle weight. Negative correlations were observed between panicles/plant and grains/panicle, and grains/panicle and 100-grain weight. Panicle weight was positively correlated with panicles/plant, panicle length and grains/panicle. Panicle length was positively associated with grains/panicle in most of the crosses. Path analysis revealed that panicles/plant, grains/panicle and panicle weight were the important component traits of grain yield in basmati rice.

Sadhukhan and Chattopadhyay (2000) studied character association between yield attributes and grain quality parameters in aromatic rice and found that grain yield/plant had strong genotypic correlation with test weight. Test weight was positively correlated with grain length and negatively correlated with grain breadth. Elongation ratio had strong positive correlation with grain length, grain length after cooking and test weight at both the genotypic and phenotypic level. Amylose content was positively correlated with grain length and test weight at both levels.

Khedikar *et al.* (2004) carried out path coefficient analysis with 20 scented rice genotypes and found that test weight had the highest positive direct effect on grain yield per plant. It was followed by spikelet density, panicles/per plant, panicle length and days to 50% flowering, and hence direct selection through these characters is more effective.

Saleem *et al.* (2005) studied segregating generations of rice to find out a suitable trait for exercising selection to improve yield. Total number of grains/panicle and 100-grain weight showed highly significant positive genotypic correlation while panicle length showed significant positive genotypic correlation with grain yield/plant. Path analysis revealed that the improvement of yield could be easier when direct selection for total number of grain/panicle is made while indirect causal factors must be considered simultaneously to increase yield potential through panicle length and 100-grain weight.

Adesola and Omolayo (2006) studied character association and path analysis of yield components in 30 tropical cultivars of upland rice in two seasons. Leaf length, plant height, spikelet sterility, 100-grain weight and grain breadth exhibited significant negative correlation with grain yield while other characters like tillering and panicle length exhibited significant positive genotypic correlation. Primary branches per panicle had the largest direct positive effect on grain yield in both seasons (1.360, 0.894) with large indirect effects from panicle weight. Spikelets/panicle and days to 50% flowering showed the largest direct negative effect of -1.021 and -0.461 in the first and second season respectively.

Om-Vir and Singh (2006) evaluated 30 advanced aromatic rice genotypes over two years to study the nature and magnitude of character associations. In general, genotypic correlation coefficients were higher than their respective phenotypic correlation coefficients. Panicles/plant, number of fertile spikelets/plant, panicle length, panicle weight, test weight, days to 50% flowering, reproductive period, and days to maturity were positively and significantly correlated with grain yield/plant at phenotypic level. All these traits also manifested positive and larger direct effects on grain yield. Therefore, practicing selection in segregating generations for these characters may be useful in improving the yield of aromatic rice.

Kishore *et al.* (2007) studied character correlations and path analysis in aromatic and non-aromatic rice genotypes that revealed that genotypic correlation coefficients were higher than phenotypic correlation coefficients for most of the traits. A significant positive association of grains/panicle and test weight was found with grain yield/plant. Test weight, number of grains/panicle, panicles/plant, days to 50% flowering and plant height showed positive direct effects on grain yield.

Malini *et al.* (2007) carried out studies on cause and effect relationship between yield and yield contributing traits among 15 parents and their 50 crosses in rice. Grain yield had significant positive genotypic correlation with grains/panicle and spikelets/panicle. Path analysis revealed that grains/panicle had the maximum positive and direct effect on grain yield followed by panicle length and grain weight. Plant height showed highly positive indirect effect on grain yield through grains/panicle, panicle length and panicles/plant. It was concluded that genetic improvement of grain yield in rice can be made by selecting traits having high positive correlation and positive direct effect.

Chandra *et al.* (2009) carried out Correlation and path analysis for yield and yield attributing traits in rice and revealed that for most of the studied traits genotypic correlation coefficients were higher than phenotypic correlation coefficients. Significant positive association of grain yield/plant was found with panicles/plant, test weight, panicle length and number of grains/panicle. Number of grains/panicle, days to 50 per cent flowering, test weight and panicles/plant showed high positive direct effects on grain yield.

Cargnin *et al.* (2010) studied genetic correlation between several agronomic traits of rice like grain yield, plant height, days to 50% flowering, useful tillering, grains/panicle, spikelets sterility, ears per panicle, and panicle weight. They found high genotypic correlations for most of the trait pairs. The traits with strongest influence on yield were grains/panicle, spikelets sterility and panicle weight.

Chakraborty and Chakraborty (2010) studied the correlation between some of morphometric traits and grain yield in bold grained rice gene pool of Barak valley. The genotypic correlation coefficient was found to be higher than the corresponding phenotypic correlation coefficient. The results indicated strong association among grain yield/plant and other morphometric traits. Spikelet sterility, effective tillers/hill and panicle length showed significant positive genotypic correlation with grain yield/hill. Spikelet sterility, effective tillers/hill and panicle length had high co-heritability with grain yield suggesting that selection for these traits would improve grain yield.

Chakraborty *et al.* (2010) carried out quantitative genetic analysis for yield and yield components in 29 genotypes of boro rice. Significant positive genotypic correlation

of yield/plant with plant height (0.21), panicles/plant (0.53), panicle length (0.53), grains/panicle (0.57) and harvest index (0.86) was observed. Genotypic path elucidated high positive direct effect of harvest index (0.8631), panicle length (0.2560) and 100 grain weight (0.1632) on yield/plant with a residual effect of 0.33. Plant height and panicles/plant recorded high positive indirect effect on yield/plant through harvest index whereas grains/panicle on yield/plant through harvest index and panicle length. The study suggested that component traits, namely plant height, panicle length, panicles/plant, grains/plant and harvest index are critical that influence the yield of boro rice.

Laxuman *et al.* (2011) carried out correlation and path coefficients using 188 back-crossed inbred lines (BILs) from cross Swarna/NERICA-L-20 and found that days to heading, days to 50% flowering, panicles/plant and panicle length exhibited significant positive association with grain yield at both genotypic and phenotypic level. Tillers/plant (2.559), panicle weight (0.882), days to 50% flowering (0.856), shoot length at 21 days (0.378) and spikelet fertility (0.088) had high direct effect on seed yield. It was revealed from the contribution of individual traits to the variance of yield that the contribution of Tillers/plant towards variance of yield was maximum followed by panicle weight and days to 50% flowering. They concluded that selecting varieties may base on higher tiller number, more panicles/plant, long panicles, and short duration of backcross lines.

Pandey *et al.* (2012) assessed inter-character relationship through correlation coefficient and path coefficient analysis in 52 rice genotypes under salt stress environment and revealed that grain yield/plant exhibited strong positive association with biological yield/plant, flag leaf area and spikelet fertility at genotypic and phenotypic level that indicated that these traits were the strongest associates of grain yield/plant. However, significant negative association was observed between harvest index and biological yield per plant and test weight and panicles/plant. Path analysis revealed harvest-index, days to maturity, panicles plant, test weight, flag leaf area and panicle length to be the major direct contributor for grain yield/plant.

2.7 Aroma performance

Yau *et al.* (1996) tested four rice varieties *viz.* TNU-67, TNU-70, TC-189 and TC Sen-10 each served at 18°C and 60°C. In total, eight samples were evaluated by

20

trained assessors using a modified quantitative descriptive analysis. Following attributes were assessed: hot-rice aroma, cold-rice aroma and brown-rice aroma. A consensus was made among the assessors on weakest and the strongest reference samples. Intensity of each attributes was rated on a 15-point scale (1 = weakest, 7 = moderate, 15 = strongest). The 18°C and 60°C samples were significantly different in nine attributes. Assessors found that the 60°C samples were rated higher in hot-rice aroma and brown-rice aroma but lower in cold-rice aroma. TNU-70 was rated higher in hot-rice aroma and brown-rice aroma whereas, TC Sen-10 was rated higher in cold-rice aroma. Therefore, both temperatures as well as variety play role in sensory properties of cooked rice.

Buttery *et al.* (1988) compared the odour thresholds in water solution of 64 known rice volatiles and found that compound with the lowest odour thresholds (T) include (E,E)-2,4-decadienal (T=0.07ppb), (E)-2-nonenal (T=0.08ppb) and 2-acetyl-1-pyrroline (T=0.1 ppb). Data from quantitative analysis (using a tenax trap isolation method) of the major volatiles in cooked California long grain rice were used to determine the ratio of each compound's concentration in the cooked rice to its odour threshold (odour unit value) that indicated that probably major contributors to Californian long grain cooked rice odour were 2-acetyl-1-pyrroline, (E,E)-2,4-decadienal, nonanal, hexanal, (E)-2-nonenal, octanal, decanal and 4-vinyl-guaiacol.

Golam, *et al.* (2010) evaluated the expression of aroma in 55 fine rice genotypes in the tropical environment of Malaysia and found that aroma was observed in 34 rice genotypes out of which 10 were identified as superior. Out of these 10, three genotypes *viz.* E11, Sadri and Garib had strong aroma (score 4). In addition, out of these 55 aromatic genotypes, 21 did not have any aroma indicating that aroma can be highly influenced by tropical environment. However, since two genotypes (Garib and E11) perform their normal aromatic expression even in tropical Malaysian Environment, it can be concluded that this expression might be the result of the influence of dominant nature of some associated genes.

Bajpai *et al.* (2012) suggested that aroma of rice varies from very low to strong. Out of 40 varieties/lines studied, he differentiated these varieties/lines as 3 having very low aroma, 11 having low aroma, 12 having moderate aroma and 14 having strong aroma. Therefore, apart from basmati rice other non Basmati aromatic rice varieties like Kalanamak should also be promoted by scientists and adopted by more and more

farmers & traders so that consumers can get better aromatic rice at lower cost while maintaining our traditional non basmati aromatic rice germplasm.

Sarhadi *et al.* (2012) characterized 26 rice cultivars from Afghanistan, Iran, and Uzbekistan using controls from Japan, Thailand and India for various agronomic traits and aroma. F₂ populations derived from the cross Jasmine-85 aromatic/Nipponbare non-aromatic and Jasmine-85/Basmati-370 were also characterised. Individual grain test, cooking test, 1.7% KOH sensory test, and molecular marker analysis were used to distinguish between aromatic and non-aromatic rice. According to the results, 6 of 10, 2 of 7, and 0 of 6 of Afghan, Iranian, and Uzbek rice cultivars were scored as aromatic, respectively. Therefore, Afghan cultivars are a good source of aromatic rice germplasm for Central Asia. When segregation for aromatic and non-aromatic in F₂ populations of Jasmine-85 aromatic/Nipponbare non-aromatic was tested by χ^2 test a 3:1 ratio was obtained. Segregation was not been detected in F₂ populations of Jasmine-85/Basmati-370 in which both are non-aromatic. Thus, these results suggest that a single recessive gene controls aroma in all aromatic rice cultivars

Seraj *et al.* (2013) evaluated aroma of 43 rice genotypes using 1.7% KOH as a sensory test. Thirteen rice genotypes were found to have strong aroma; 10 having moderate aroma, 15 having low aroma and 5 as having no aroma. For physical appearance like grain shape, 37 genotypes had slender gains and 6 had medium grains. Aroma had significant and positive association with L/B ratio; significant and negative association with grain length, grain breadth and gelatinization temperature. Finally, it was concluded that among 43 genotypes, Basmati-370, CT19541-13-3-1-2P-1P, PSBRC18, PSB-RC2 (IR32809-26-3-3), IR64, IR50, 2001059-TR2151-6-1-1, IR64-P401 and IR72-P204 were found to have good grain quality traits having appreciable physico-chemical attributes. So, these elite lines could be readily used in breeding programmes to improve grain quality traits.

In aromatic rice, aroma volatiles are produced in aerial plant parts and then transported to mature grains. **Vidya *et al.* (2016)** reported that diverse form of aroma volatiles were synthesized during seedling stage but these were accumulated more at flowering followed by seedling stage. Distinct accumulation pattern exists for 2AP and other aroma volatiles at various developmental stages and 2AP in mature grains might be transported from leaves and stem sheath.



*Materials
and
Methods*



The present experiment was carried out during *Kharif* 2015 and 2016 at N. E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand, India. Latitude, longitude and altitude of experimental site are 29.50° N, 79.30° E and 243.84 m above the MSL. The experimental site falls in the humid sub-tropical zone in the foothills of Shivalik range of the Himalayas, popularly known as ‘Tarai’. The annual rainfall of this region is about 1700 mm with high humidity.

3.1 Experimental Materials

The experimental materials consisted of 8 parents and 28 F₁ hybrids. The parents consisted of early maturing, semi-dwarf, disease resistant, high yielding, export quality Basmati, traditional Basmati and other non basmati aromatic rice varieties. These parents chosen for hybridisation and subsequent genetic analysis were genetically diverse and exhibited wide range of variation for different quantitative traits. The present investigation was conducted to study genetics of yield and quality parameters in aromatic rice (*Oryza sativa* L.). Twenty eight F₁ hybrids were derived by crossing these 8 aromatic rice varieties in a diallel fashion excluding reciprocals. The parents that were chosen to develop F₁s in the present experiment are Pusa Basmati-1, Pusa Sugandh-4, Pusa Sugandh-6, Type-3, Basmati-370, Tarori Basmati-1 and PSD-15 (Pant Sugandh Dhann-15) and Pant Basmati-1. The details of experimental material are given in **Table 3.1a** and **Table 3.1b**.

3.2 Crossing

The crossings in half diallel fashion were made during *kharif*, 2015. The crossing work for generating the material for the genetic studies were undertaken as following schedule.

The plants selected to be used as mother parent in each cross were carefully uprooted from the nursery and transplanted in the pots in glasshouse. Plants that showed 50-60% panicle emergence were selected for emasculation. Hand emasculation was done in the afternoon. The spikelets from the top that had already undergone

anthesis and the immature spikelets from the bottom were excised with the help of scissors. Remaining spikelets were cut at slant just above the anthers ($1/3^{\text{rd}}$ to $1/2$) with the help of scissors from palea side. Anthers, in their intact form, were removed gently and neatly with the help of a pair of forceps and needle without injuring the stigma. After emasculation, the panicles were covered with wax paper bag to prevent entry of any foreign pollen. The pollination was carried out next morning with fresh pollens from male parent. Panicles were harvested from male parent and brought to the glasshouse before anthesis. Harvested panicles were kept in water to allow for exertion of anthers. When anther exertion had occurred sufficiently in most of the spikelets, the panicle was carefully lifted and tapped over the emasculated panicle after removing the wax paper bag. After pollens were dusted over the emasculated panicles, the panicles were covered again with the wax paper bag. Each pollinated panicle was carefully labelled showing the parents involved in cross and date of pollination.

The seeds were harvested from the mother plant 25-28 days after pollination, hand threshed and air dried. These seed represented the F_1 seeds. The remnants of glumes from the seeds were removed and seeds were stored safely for sowing in next *Kharif* season.

3.3. Layout and planting of experiment

In *kharif*, 2016, complete set of 28 F_1 hybrids and 8 parents were raised separately in field nursery. Twenty five day old seedlings were transplanted in the main field in randomised complete block design with three replications. Each replication consisted of 36 plots with one row gap, while each plot had only one rows of 1.5 meter length. The row to row and plant to plant distance was kept 20 cm and 15 cm, respectively. Recommended package of practices were followed to raise a healthy crop stand.

3.4 Sampling

Five randomly selected plants from each plot were tagged. Observations were recorded from these tagged plants on various parameters. Average of individual data from these plants was used for computation. Data on days to 50% flowering were recorded on whole plot basis.

Table 3.1a: Details of parentage and origin of parental aroma rice varieties

Sl. No.	Parents	Parent Number	Year of Release	Pedigree/Cross Combination	Origin
1.	Pusa Basmati-1	1	1989	Pusa-150/ Karnal Local	Delhi
2.	Pusa Sugandh-4	2	2003	Pusa 614-1-2 / Pusa 614-2-4-3	Delhi
3.	Pusa Sugandh-6	3	2008	Pusa Basmati 1/ Pusa 1121-92-8-7-1	Delhi
4.	Type-3	4	1978	Selection from Dehradun Basmati	Nagina
5.	Basmati-370	5	1933	Pureline selection from local basmati land race	Punjab
6.	Tarori Basmati-1	6	1996	Pureline selection from HBC-19	Haryana
7.	PSD-15 (Pant Sugandh Dhan-15)	7	2002	Basmati 370/Sadri// Bahral/Muskan-41	Pantnagar
8.	Pant Basmati-1	8	2016	Pusa Basmati-1/ IET-12603	Pantnagar
9.	Improved Pusa Basmati-1 (Check)	-	2007	Pusa Basmati 1 //Pusa Basmati 1/ IRBB-55	Delhi

Table 3.1b: Details of diallel crosses (excluding reciprocals)

Sl. No.	Crosses	Cross code
1	Pusa Basmati-1×Pusa Sugandh-4	(1×2)
2	Pusa Basmati-1×Pusa Sugandh-6	(1×3)
3	Pusa Basmati-1×Type-3	(1×4)
4	Pusa Basmati-1×Basmati-370	(1×5)
5	Pusa Basmati-1×Tarori Basmati-1	(1×6)
6	Pusa Basmati-1×PSD-15	(1×7)
7	Pusa Basmati-1×Pant Basmati-1	(1×8)
8	Pusa Sugandh-4×Pusa Sugandh-6	(2×3)
9	Pusa Sugandh-4×Type-3	(2×4)
10	Pusa Sugandh-4×Basmati-370	(2×5)
11	Pusa Sugandh-4×Tarori Basmati-1	(2×6)
12	Pusa Sugandh-4×PSD-15	(2×7)
13	Pusa Sugandh-4×Pant Basmati-1	(2×8)
14	Pusa Sugandh-6×Type-3	(3×4)
15	Pusa Sugandh-6×Basmati-370	(3×5)
16	Pusa Sugandh-6×Tarori Basmati-1	(3×6)
17	Pusa Sugandh-6×PSD-15	(3×7)
18	Pusa Sugandh-6×Pant Basmati-1	(3×8)
19	Type-3×Basmati-370	(4×5)
20	Type-3×Tarori Basmati-1	(4×6)
21	Type-3×PSD-15	(4×7)
22	Type-3×Pant Basmati-1	(4×8)
23	Basmati-370×Tarori Basmati-1	(5×6)
24	Basmati-370×PSD-15	(5×7)
25	Basmati-370×Pant Basmati-1	(5×8)
26	Tarori Basmati-1×PSD-15	(6×7)
27	Tarori Basmati-1×Pant Basmati-1	(6×8)
28	PSD-15×Pant Basmati-1	(7×8)

3.5 Traits/Parameters studied

3.5.1 Days to 50% flowering	3.5.2 Plant height (cm)
3.5.3 Flag leaf length (cm)	3.5.4 Panicle length (cm)
3.5.5 Number of panicles per plant	3.5.6 Number of filled grains per panicle
3.5.7 Number of unfilled grains per	3.5.8 Spikelet fertility (%)
3.5.9 Test weight (g)	3.5.10 Grain yield per plant (g)
3.5.11 Hulling recovery (%)	3.5.12 Milling recovery (%)
3.5.13 Kernel length (mm)	3.5.14 Kernel breadth (mm)
3.5.15 Kernel length/breadth ratio	3.5.16 Cooked kernel length (mm)
3.5.17 Cooked kernel breadth (mm)	3.5.18 Cooked kernel length/breadth ratio
3.5.18 Kernel elongation ratio	3.5.20 Alkali digestion value
3.5.21 Amylose content (%)	3.5.22 Aroma index

3.6 Observations recorded

The below are described the detailed procedure adopted for recording the data for various traits:

3.6.1 Days to 50% flowering

It was calculated by counting the days taken from date of sowing in the nursery to the date on which half of the plants in a plot reached the half bloom stage.

3.6.2 Plant height (cm)

Plant height was measured from ground level to the tip of the panicle at maturity stage and expressed in centimeter.

3.6.3 Flag leaf length (cm)

Length of flag leaf of primary tiller was measured and expressed in cm at the start of panicle initiation.

3.6.4 Panicle length (cm)

The length of panicle was measured from neck of the panicle to the tip of the top most spikelet (excluding awn) at maturity and expressed in cm.

3.6.5 Number of panicles per plant

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

3.6.6 Number of filled grains per panicle

Total number of filled grains in the panicle of main tiller were counted and recorded.

3.6.7 Number of unfilled grains per panicle

Total number of unfilled grains/ chaffy grains in the panicle of main tiller were counted and recorded.

3.6.8 Spikelet fertility (%)

Percent fertility was calculated by taking the percent ratio of number of filled seeds to total number of seeds per panicle and expressed in percentage.

3.6.9 Test weight (g)

The weight of 1000 seeds from each entry was recorded on an Electronic Sartorius Precision Balance and expressed in grams.

3.6.10 Grain yield per plant (g)

Total weight of all the filled grains per plant was measured on an Electronic Sartorius Precision Balance after harvest and expressed in grams.

3.6.11 Hulling recovery (%)

100 gram raw rice sample was taken from each entry at 12-14% moisture content level and was dehulled. Weight of dehulled grains was recorded in gram.

3.6.12 Milling recovery (%)

The entire dehulled rice from each entry was used for milling for 2 minutes. Weight of resulting milled rice was recorded.

3.6.13 Kernel length (mm)

Ten randomly selected kernels from each entry were dehulled to measure the kernel length. The length of these kernels was measured in millimeter with the help of graph paper and averaged.

3.6.14 Kernel breadth (mm)

Same ten dehulled kernels (as in section 3.6.11) were used to measure the breadth using graph paper as was done for length in section 3.6.11.

3.6.15 Kernel length/breadth ratio

This was recorded as the ratio of length of dehulled kernel to breadth of the same dehulled kernel.

3.6.16 Cooked kernel length (mm)

Length of ten cooked kernels was measured by keeping them over a thin glass sheet having graph paper sheet underneath. The length of ten cooked kernels was averaged and recorded in mm.

3.6.17 Cooked kernel breadth (mm)

The cooked kernel breadth was measured by placing the same ten cooked kernels breadth wise on graph paper and averaging the breadth measurement. Observations were recorded in mm.

3.6.18 Cooked kernel length/breath ratio

The cooked kernel length/breath ratio was calculated simply by dividing cooked kernel length by coked kernel breadth of the same cooked grain.

3.6.19 Kernel elongation ratio

The kernel elongation ratio was calculated according to **Azeez and Shafi (1996)** as follows:

$$\text{Kernel elongation ratio} = \frac{\text{Average length of cooked kernel (mm)}}{\text{Average length of uncooked kernel (mm)}}$$

3.6.20 Alkali digestion value

Six whole kernels from each milled sample were selected and kept evenly spaced in petri dish of 9 cm diameter containing 10 ml of 1.7% potassium hydroxide (KOH) solution and left to disintegrate for 23 hrs at room temperature ($25\pm 2^{\circ}\text{C}$). Kernels were rated for degradation on scale of 1 to 7 (**Table 3.6.20**). Average score of six kernels was taken as alkali digestion value (**Little *et al.*, 1958**).

Table 3.6.20: Numerical Scale for recording alkali digestion value

Score	Spreading pattern	Clearing pattern	Alkali digestion
1	Kernel not affected	Kernel chalky	Low
2	Kernel swollen	Kernel chalky, collar powdery	Low
3	Kernel swollen, collar incomplete and narrow	Kernel chalky, collar cottony or cloudy	Low or intermediate
4	Kernel swollen, collar complete and wide	Center cottony, collar cloudy	Intermediate
5	Kernel split or segmented, collar complete	Center cottony, collar clearing	Intermediate
6	Kernel dispersed, merging with collar	Center cottony, collar clear	High
7	All kernel dispersed and intermingled	Center cottony, collar clear	High

3.6.21 Amylose content (%)

Amylose content was determined by simplified calorimetric method as described by **Sowbhagya and Bhattacharya (1971)**.

1-2 g sample was ground with mortar and pestle. 100 mg of rice flour of 100 mesh size was oven dried at $70 \pm 5^{\circ}\text{C}$ for 24 hours. Oven dried rice flour was mixed with 1 ml of distilled ethyl alcohol thoroughly in a 100 ml volumetric flask. Then, 10 ml 1.0 N sodium hydroxide (NaOH) was added and left overnight at the room temperature ($25\pm 2^{\circ}\text{C}$). Then the volume was made up to 100 ml with boiled and cooled

distilled water. Five ml of the solution was then poured to another 100 ml volumetric flask from stock solution. Three drops of phenolphthalein was added to it. Then the volume was made up to 50 ml with boiled and cooled distilled water. One N HCl was added drop by drop in to the flask with continuous shaking till the colour disappeared. Two ml of iodine solution (0.2% iodine in 2% potassium iodide) was added in to the volumetric flask and diluted to 100 ml with boiled and cooled distilled water. Iodine blank was also prepared by diluting 2 ml iodine solution to 100 ml with distilled water. Absorbance of blue color was measured in percentage at 590 nm in a spectronic 20 spectrophotometer against the blank.

Amylose content (percent oven dried basis) was calculated as follows:

$$\text{Amylose content (\%)} = \frac{\text{Absorbance of the unknown solution}}{\text{Absorbance of the known solution}} \times \frac{\text{mg dry amylose in 1 ml standard}}{5 \times \text{dry solids in the solution}} \times 100$$

Since, undefatted rice flour was used in the amylose estimation; the results were multiplied by the correction factor 1.16 as suggested by **Sowbhagya and Bhattacharya (1971)**.

3.6.22 Aroma index

A laboratory technique to evaluate rice for presence of aroma was developed at IRRI (1971). One gram of freshly harvested milled rice was placed into centrifuge tube (50 ml round bottom). About 20 ml distilled water was added in to it and covered with aluminium foil. The samples were placed in a boiling water bath for 10 minutes. The cooked samples were allowed to cool for 20 minutes. Then the samples were smelled by random panel and scored as strongly aromatic, moderately aromatic, slightly aromatic and non aromatic in the scale of 2, 1, 0.5 and 0 respectively. A strongly scented variety was used as check for comparison.

3.7 Statistical Analysis

The trait mean values from all the 3 replications for all the 36 (28 F₁s and 8 parents) entries were subjected to the following statistical analyses:

3.7.1 Analysis of variance and mean

3.7.2 Estimation of genetic variability parameters

- 3.7.3 Estimation of heterosis
- 3.7.4 Combining ability analysis
- 3.7.5 Hayman's Graphical analysis
- 3.7.6 Correlation and path coefficient analysis
- 3.7.7 Aroma index

3.7.1 Analysis of variance (ANOVA) and mean

The analysis of variance for each trait was carried out according to randomized complete block design (RCBD) as suggested by **Fisher (1936)**. The model for analysis of variance was as follows:

$$y_{ij} = \mu + b_i + t_j + e_{ij}$$

$$i = 1, 2, 3 \dots r$$

$$j = 1, 2, 3 \dots t$$

Where,

Y_{ij} = Observed response of i^{th} genotype in the j^{th} replication.

μ = General mean of the population

b_i = Effect of i^{th} block

t_i = Effect of j^{th} treatment

e_{ij} = Random error of i^{th} block and j^{th} treatment

Table 3.7.1.1: Skeleton of ANOVA for Randomized Complete Block Design

Source of variation	d.f.	Sum of squares	Mean Sum of squares	Variance ratio (F_{cal})
Treatment	(t-1)	SS_T	MS_t	MS_t/MS_e
Replication	(r-1)	SS_R	MS_r	MS_r/MS_e
Error	(r-1) (t-1)	SS_E	MS_e	
Total	(rt-1)			

MSt , MSr and MSe are mean squares due to treatment, replication and error respectively. Significance of differences among treatment means was tested by using

the variance ratio test (F-test). Standard error of mean (SEM) and coefficient of variance (CV) were calculated as follows:

$$SEM = \frac{\sqrt{2MS_e}}{r}$$

$$CV(\%) = \frac{SD}{\bar{X}} \times 100$$

$$CD = t_0 \times SEM$$

Where,

MS_e = Error mean square

r = Number of replications

$\bar{X}$ = Trait mean

t_0 = Table value of 't' corresponding to error degree of freedom

3.7.2. Estimation of genetic variability parameters

3.7.2.1 Coefficient of variation

Genotypic, phenotypic and environmental coefficients of variation were calculated as follows:

$$\text{Genotypic coefficient of variation (GCV)\%} = \frac{\sigma G_i}{\bar{X}_i} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)\%} = \frac{\sigma P_i}{\bar{X}_i} \times 100$$

$$\text{Environmental coefficient of variation (ECV)\%} = \frac{\sigma E_i}{\bar{X}_i} \times 100$$

Where,

σG_i , σP_i , and σE_i are the genotypic, phenotypic and environmental standard deviations for i^{th} trait, respectively.

$\bar{X}_i$ = Mean of i^{th} trait

3.7.2.2 Heritability

Heritability in broad sense [$H_{(b)}$] (Allard, 1960) was estimates as follows:

$$H_b \text{ or } (h^2) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

$H_{(b)}$ or (h^2) = Heritability (%) in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.7.2.3 Expected genetic advance

The Expected genetic advance (GA) for various traits was estimated as suggested by **Allard (1960)** as follows:

$$GA = K + \sigma_p + H_{(b)}$$

Where,

GA = Expected genetic advance

K = Selection differential expressed in standard unit

σ_p = Phenotypic standard deviation

$H_{(b)}$ = Heritability in broad sense

$$GA \text{ as\% of mean } (\bar{X}) = \frac{GA}{\text{Mean } (\bar{X})}$$

3.7.3. Estimation of heterosis

Average heterosis (over mid-parental value), heterobeltiosis (over better parent) and standard heterosis (over check variety) was estimated for each trait using the following formula:

$$\text{Average heterosis} = \frac{\bar{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Heterobeltiosis} = \frac{\bar{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

$$\text{Standard heterosis} = \frac{\bar{F}_1 - \overline{CP}}{\overline{CP}} \times 100$$

Where,

$\bar{F}_1$ = Mean performance of F_1

$\bar{P}_1$ = Mean performance of parent one

$\bar{P}_2$ = Mean performance of parent two

$\overline{MP}$ = Mean performance of parents *i.e.* $(P_1+P_2)/2$

$\overline{BP}$ = Mean performance of better parent

$\overline{CP}$ = Mean performance of check variety

The significance of heterosis was tested with 't' test as follows:

(a) For average heterosis

$$t = \frac{\bar{F}_1 - \overline{MP}}{\sqrt{3M_e/2r}}$$

(b) For heterobeltiosis

$$t = \frac{\bar{F}_1 - \overline{BP}}{\sqrt{2M_e/r}}$$

(c) For standard heterosis

$$t = \frac{\bar{F}_1 - \overline{CP}}{\sqrt{2M_e/r}}$$

Where,

$\bar{F}_1$ = Mean of F_1

$\overline{MP}$ = Mean performance of parents *i.e.* $(P_1+P_2)/2$

$\overline{BP}$ = Mean performance of better parent

$\overline{CP}$ = Mean performance of check variety

M_e = Error mean square from ANOVA table and

r = Number of replications

3.7.4 Combining ability analysis

3.7.4.1 Combining ability analysis of the parents and crosses

Combining ability analysis was carried out according to Method 2 of Model I of **Griffing (1956 b)**. Model-I was chosen because only a small number of varieties have been selected on certain fixed criteria which did not represent the random sample from the population. The mathematical model for present analysis is given below:

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

$$(i, j = 1, \dots, p)$$

where,

μ = general mean (population mean)

g_i = general combining ability effect of i^{th} line

g_j = general combining ability effect of j^{th} line

s_{ij} = specific combining ability effect of $(i \times j)^{\text{th}}$ cross

e_{ij} = effect specific to the $ijkl^{\text{th}}$ observation and

p = number of parents, involved in diallel mating design

Table 3.7.4.1: Skeleton of ANOVA showing expectations of mean sum of squares for method-2 and model-I

Source	d.f.	Sum of square	Mean square	Expectations of mean sum of squares	F-value
General combining ability	$p-1$	S_g	M_g	$\sigma^2 + (p+2) \left(\frac{1}{p-1} \right) \sum_{i=1}^p g_i^2$	M_g/M_e
Specific combining ability	$p(p-1)/2$	S_s	M_s	$\sigma^2 + \frac{2}{p(p-1)} \sum_{i=1}^p \sum_{j=1}^p S_{ij}^2$	M_s/M_e
Error	m	S_e	M_e	σ_2	

Where,

$$S_g = \frac{1}{P+2} \left[\sum_{i=1}^p (X_{i.} + X_{.i})^2 - \frac{4}{P} X_{..}^2 \right]$$

$$S_s = \sum_i \sum_{j \leq i} X_{ij}^2 - \frac{1}{P+2} \sum_{i=1}^P (X_{i.} + X_{.i})^2 + \frac{2}{(P+1)(P+2)} X_{..}^2$$

$$M_e = \frac{\text{Error mean square}}{\text{Number of replications}} = \frac{Me}{r}$$

S_g = sum of squares due to general combining ability (gca)

S_s = sum of squares due to specific combining ability (sca)

P = number of parents

$X_{i.}$ = total of the array of i^{th} parent

$X_{.i}$ = mean value of the i^{th} parent

X_{ij} = mean value of $(i \times j)^{\text{th}}$ cross

$X_{..}$ = grand total of $\frac{P(P-1)}{2}$ crosses where 'P' is number of parental lines

m = error degree of freedom in analysis of variance

The following 'F' ratios were calculated to test GCA and SCA effect:

- (i) To test the differences among GCA effects:

$$F[(P-1), m] = \frac{Mg}{Me}$$

- (ii) To test the differences among SCA effects:

$$F[P(P-1)/2, m] = \frac{Ms}{Me}$$

The combining ability effects were estimated as below:

$$\hat{\mu} = \frac{2}{P(P+1)} X_{..},$$

$$\hat{g}_i = \frac{1}{(P+2)} \left[\sum (X_{i.} + X_{.i}) - \frac{2}{P} X_{..} \right]$$

$$\hat{S}_{ij} = X_{ij} - \frac{1}{(P+2)} [X_{i.} + X_{.i} + X_{.j} + X_{j.}] + \frac{2}{(P+1)(P+2)} X_{..},$$

Where,

$\hat{g}_i$ = GCA effect of i^{th} parent

$\hat{S}_{ij}$ = SCA effect of ij^{th} cross. The rest of the notations remain as described above.

The variance of any parent or F_1 mean is given as:

$$\text{var}(X_{ij}) = \hat{\sigma}^2 = M_e$$

The variance of the difference between any two mean values is calculated as:

$$\text{var}(X_{ij} - X_{kl}) = 2\sigma^2 = 2 M_e$$

Variances of effects and differences between effects were estimated as below:

$$(i) \quad \text{var}(\hat{\mu}) = \frac{2}{P(P+1)} \hat{\sigma}^2$$

$$(ii) \quad \text{var}(\hat{g}_i) = \frac{(P-1)}{P(P+2)} \hat{\sigma}^2$$

$$(iii) \quad \text{var}(\hat{S}_{ii}) = \frac{P(P-1)}{(P+1)(P+2)} \hat{\sigma}^2 \quad (i \neq j)$$

$$(iv) \quad \text{var}(\hat{S}_{ij}) = \frac{(P^2 + P + 2)}{(P+1)(P+2)} \hat{\sigma}^2 \quad (i \neq j)$$

$$(v) \quad \text{var}(\hat{g}_i - \hat{g}_j) = \frac{2}{P+2} \hat{\sigma}^2 \quad (i \neq j) \quad (i \neq j)$$

$$(vi) \quad \text{var}(\hat{S}_{ii} - \hat{S}_{jj}) = \frac{2(P-2)}{P+2} \hat{\sigma}^2 \quad (i \neq j)$$

$$(vii) \quad \text{var}(\hat{S}_{ij} - \hat{S}_{ik}) = \frac{2(P+1)}{P+2} \hat{\sigma}^2 \quad (i \neq j, k; j \neq k)$$

$$(viii) \quad \text{var}(\hat{S}_{ij} - \hat{S}_{kl}) = \frac{2P}{P+2} \hat{\sigma}^2 \quad (i \neq j, k, l; j \neq k, l; k \neq l)$$

The standard error of any parent or F_1 mean value was calculated as follows:

$$S.E.(X_{ij}) = (\hat{\sigma}^2)^{0.5} = (M_e)^{0.5}$$

The standard error of the differences between any two mean values was calculated as:

$$S.E.(X_{ij} - X_{kl}) = (2\hat{\sigma}^2)^{0.5} = (2M_e)^{0.5}$$

Standard error of effects and differences between effects were calculated as:

$$(i) \quad S.E. (\hat{\mu}) = \left[\frac{2}{P(P+1)} \hat{\sigma}^2 \right]^{0.5}$$

$$(ii) \quad S.E. (\hat{g}_i) = \left[\frac{(P-1)}{P(P+2)} \hat{\sigma}^2 \right]^{0.5}$$

$$(iii) \quad S.E. (\hat{S}_{ii}) = \left[\frac{P(P-1)}{(P+1)(P+2)} \hat{\sigma}^2 \right]^{0.5} \quad (i \neq j)$$

$$(iv) \quad S.E. (\hat{S}_{ij}) = \left[\frac{(P^2 + P + 2)}{(P+1)(P+2)} \hat{\sigma}^2 \right]^{0.5} \quad (i \neq j)$$

$$(v) \quad S.E. (\hat{g}_i - \hat{g}_j) = \left[\frac{2}{P+2} \hat{\sigma}^2 \right]^{0.5} \quad (i \neq j)$$

$$(vi) \quad S.E. (\hat{S}_{ii} - \hat{S}_{jj}) = \left[\frac{2(P-2)}{P+2} \hat{\sigma}^2 \right]^{0.5} \quad (i \neq j)$$

$$(vii) \quad S.E. (\hat{S}_{ij} - \hat{S}_{ik}) = \left[\frac{2(P+1)}{P+2} \hat{\sigma}^2 \right]^{0.5} \quad (i \neq j, k; j \neq k)$$

$$(viii) \quad S.E. (\hat{S}_{ij} - \hat{S}_{kl}) = \left[\frac{2P}{P+2} \hat{\sigma}^2 \right]^{0.5} \quad (i \neq j, k, l; j \neq k, l; k \neq l)$$

The following restrictions were imposed on the mathematical model:

$$(i) \quad \sum_{i=1}^P g_i = 0 \quad (ii) \quad \sum_{j=1}^P S_{ij} + S_{ii} = 0 \quad (\text{for each } i)$$

3.7.5 Graphical analysis

The variance (Vr), covariance (Wr) analysis of the F₁ diallel data was carried out according to as suggested by **Hayman (1954 and 1957)** and **Jink and Hayman (1953)**.

The following are the assumptions on which the graphical analysis (**Hayman, 1957**) is based:

- i. Normal diploid segregation
- ii. Lack of maternal effects
- iii. Absence of multiple alleles
- iv. Homozygosity of parents
- v. Absence of linkage
- vi. Absence of epistasis
- vii. Random mating

The different components of genetic variances were worked out according to **Lee and Kaltsikes (1952)**. The expected values of different components of genetic variance were estimated using following equations:

- (i) $D = V_0L_0 - E$
- (ii) $F = 2 V_0L_0 - 4W_0L_0I - 2(p - 2)E/p$
- (iii) $H_1 = V_0L_0 - W_0L_0I + 4VILI - 5(p - 4)E/p$
- (iv) $H_2 = 4 VILI - V_0LI - 4(p^2 - p + 1)E/p^2$
- (v) $h^2 = 4(MLI - ML_0)^2 - 4 (p - 1)E/p^2$
- (vi) $E = Me$

Table 3.7.5.1: Expectations for the statistic calculated for F₁ generation (excluding reciprocals)

Statistic	Components					
	D	F	H ₁	H ₂	h ²	E
V ₀ L ₀	1					1
W _r	1/2					1/p
W ₀ L ₀₁	1/2	-1/4				1/p
V _r	1/4		1/4			1
V ₁ L ₁	1/4	-1/4	1/4	-1/4		1
V ₀ L ₁	1/4	-1/4	1/4		1/4	(p-1)/p ²
(ML ₁ -ML ₀) ²						(p-1)/p ²

Where,

D = Component of variance that arises due to additive effect of genes

F = Relative frequency of dominant and recessive alleles in parental population and variance in the dominance level over loci

H₁ = Component of genetic variance that arises due to dominance effect of genes

H₂ = H₁ (1-(u-v))² (where, u is the proportion of the increasing alleles in the parents and v is the proportion of the decreasing alleles in the parents)

h² = Dominance effect (algebraic sum over all the loci in heterozygous phase in all crosses)

V_{0L₀} = Variance of the parents

V_r = Variance of the one array

V_{1L₁} = Mean variance of the arrays

W_r = Covariance between parents and their offspring in one array

W_{0L_{0I}} = Mean covariance between parents and arrays

V_{0L₁} = Variance of the means of the arrays

(ML₁ - ML₀) = Difference between the mean of the parents and the mean of their (p-1) crosses

E = Expected component of variation due to environment

The above parameters were calculated as follows:

$$W_r = \left(\frac{1}{b}\right)^2 \left[\frac{1}{(p-1)} \left\{ \sum xy - \frac{(\sum x)(\sum y)}{p} \right\} \right]$$

$$V_r = \left(\frac{1}{b}\right)^2 \left[\frac{1}{(p-1)} \left\{ \sum x^2 - \frac{(\sum x)^2}{p} \right\} \right]$$

Where,

x = rth array

y = parental array

The variance of the array of parents is given as:

$$V_{OL0} = \left(\frac{1}{b}\right)^2 \left[\frac{1}{(p-1)} \left\{ \sum x^2 - \frac{(\sum y)^2}{p} \right\} \right]$$

Where, b is the number of replications. The coefficient/multiplier $\left(\frac{1}{b}\right)^2$ is used to convert the variances and covariances calculated on the basis of sum over b replications, into those corresponding to the mean over b replications. The variance of the array means is given as:

$$V_{OLI} = \left(\frac{1}{b}\right)^2 \left(\frac{1}{b}\right)^2 \left[\frac{1}{(p-1)} \left\{ \sum z^2 - \frac{(\sum z)^2}{p} \right\} \right]$$

Where,

z = the array total

The coefficient/multiplier $(1/p)^2$ is used to compensate for the use of array totals instead of array means. The mean variance of the array is given as:

$$V_{ILI} = \frac{1}{p} \sum_{r=1}^p V_r$$

The mean covariance between the parents and the array is given as:

$$W_{OLI} = \frac{1}{p} \sum_{r=1}^p W_r$$

To test the validity of the assumptions underlying the graphical analysis, uniformity of W_r - V_r values was tested using the t^2 test:

$$t^2 = \frac{(p-2)}{4} \left[\frac{(\text{Var } V_r - \text{Var } W_r)^2}{(\text{Var } V_r \times \text{Var } W_r) - \text{cov}^2(V_r, W_r)} \right]$$

With (p-2) degree of freedom. The V_r and W_r graph was constructed as the pictorial representation of the genetic variance. V_r was taken along with the X-axis and W_r along the Y-axis of the graph. Limits of V_r - W_r graph are marked by parabolic curve with the equation- $W_r = (V_r \times V_{OL0})^{1/2}$ for each V_r . The observed regression line was drawn by calculating the regression coefficient for W_r on V_r . The standard error of regression coefficient was calculated using formula given below:

$$S_b = \left(\frac{S_{yy} - bS_{xy}}{S_{xx}(p-2)} \right)^2$$

Where,

$$S_{yy} = \sum y^2 - \frac{(\sum y)^2}{p}$$

$$S_{xx} = \sum x^2 - \frac{(\sum x)^2}{p}$$

$$S_{xy} = \sum xy - \frac{(\sum x)(\sum y)}{p}$$

The regression coefficient (b) was tested from 0 to 1 using following formula:

$$(i) \quad H_0: b=0, \frac{(b)}{sb}$$

$$(ii) \quad H_0: b=1, \frac{(1-b)}{sb}$$

The array values were represented on the Vr-Wr graph by plotting points against their respective values of Vr and Wr in graph.

The accuracy of the components of the genetic variance was tested using formula given below:

$$\text{Standard error (S.E.) } D = \sqrt{s^2 - CD}$$

$$\text{Standard error (S.E.) } F = \sqrt{s^2 - CF}$$

$$\text{Standard error (S.E.) } H_1 = \sqrt{s^2 - CH_1}$$

$$\text{Standard error (S.E.) } H_2 = \sqrt{s^2 - CH_2}$$

$$\text{Standard error (S.E.) } h^2 = \sqrt{s^2 - ch^2}$$

$$\text{Standard error (S.E.) } E = \sqrt{s^2 - CE}$$

Where,

$$S^2 = \frac{1}{2} \text{Var} (W_r - V_r)$$

The CD, CF, CH₁, CH₂, ch² and CE are the multipliers, the terms of main diagonal of covariance matrix as suggested by **Hayman (1954)**.

The estimates of narrow sense heritability were calculated as follows using different components of variance (**Mather and Jinks, 1971**).

$$\text{Heritability narrow sense } (h_{(ns)}^2) = \frac{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{2}H_2 - \frac{1}{2}F}{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{2}H_2 - \left(\frac{1}{2}\right)F + E}$$

The allied genetic parameters

1. Average degree of dominance = $\sqrt{\frac{H_1}{D}}$
2. Proportion of genes with increasing and decreasing effects in the parents

$$= \frac{H_2}{4H_1}$$

3. Proportion of the dominant and recessive genes in the parent

$$= \frac{(4DH_1)^{\frac{1}{2}} + F}{(4DH_1)^{\frac{1}{2}} - F}$$

4. The coefficient of correlation (r) between the parental order of dominance (Wr + Vr) and parental measurement Yr.

3.7.6 Correlation and path coefficient analysis

3.3.5.1 Correlation analysis

The genotypic and phenotypic correlation coefficients among all possible pairs of traits were estimated as suggested by **Searle (1961)** as follows:

$$r_{xy}(g) = \frac{\text{Cov}_{xy}(g)}{[\text{Var}_x(g) \cdot \text{Var}_y(g)]^{1/2}}$$

$$r_{xy}(p) = \frac{\text{Cov}_{xy}(p)}{[\text{Var}_x(p) \cdot \text{Var}_y(p)]^{1/2}}$$

Where,

$r_{xy}(g)$ and $r_{xy}(p)$ = Genotypic and phenotypic correlation coefficients between trait x and y

$\text{Cov}_{xy}(g)$ and $\text{Cov}_{xy}(p)$ = Genotypic and phenotypic covariance between trait x and y

$\text{Var}_x(g)$ and $\text{Var}_x(p)$ = genotypic and phenotypic variance of trait x

$\text{Var}_y(g)$ and $\text{Var}_y(p)$ = Genotypic and phenotypic variance of trait y

The significance of correlation coefficients (r) was tested by tested using ‘t’ test at (n-2) degree of freedom (**Snedecor and Cochran, 1967**).

$$t_{\text{cal}} = r \sqrt{\frac{n-2}{1-r^2}}$$

Where, n = Number of genotypes

3.3.5.2 Path coefficient analysis

The genotypic and phenotypic correlation coefficients obtained were partitioned into direct, indirect and residual effects using path coefficient analysis as suggested by **Wright (1921)**. Grain yield/plant was considered as dependent variable (y) and other traits assumed to influence the grain yield/plant were considered as independent variables ($x_1 \dots x_i$). The path coefficient was worked out by solving the following set of equations that describes the basic relationship between correlation and path coefficients.

$$r_{1y} = P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \dots + r_{1i} P_{iy}$$

$$r_{2y} = P_{2y} + r_{21} P_{1y} + r_{23} P_{3y} + \dots + r_{2i} P_{iy}$$

$$r_{3y} = P_{3y} + r_{31} P_{1y} + r_{32} P_{2y} + \dots + r_{3i} P_{iy}$$

$$r_{iy} = P_{iy} + r_{i1} P_{1y} + r_{i2} P_{2y} + \dots + r_{i(i-1)} P_{iy}$$

where,

r_{1y} to r_{iy} = correlation coefficients between independent variables (1...i) with dependent trait y

r_{12}, r_{i1} to $r_{i(i-1)}$ = correlation coefficients among all possible pairs of independent variables and

P_{1y} to P_{iy} = direct path effects of independent variables (1 to i) on the dependent variable y

The indirect effect of i^{th} independent variable through j^{th} independent variable on dependent variable y was computed as: $P_{1y} \times r_{ij}$

The above equation is summarised in a matrix form as follows:

$$\begin{pmatrix} \tilde{\mathbf{A}} \\ r_{1y} \\ r_{2y} \\ \vdots \\ r_{iy} \end{pmatrix} = \begin{pmatrix} \mathbf{\tilde{B}} \\ r_{11} & r_{12} & r_{13} & r_{14} \dots r_{1i} \\ r_{21} & R_{22} & r_{23} & r_{24} \dots r_{2i} \\ \vdots & \vdots & \vdots & \vdots \\ r_{i1} & r_{i2} & r_{i3} & r_{i4} \dots r_{ii} \end{pmatrix} \begin{pmatrix} \tilde{\mathbf{C}} \\ P_{1y} \\ P_{2y} \\ \vdots \\ P_{iy} \end{pmatrix}$$

Path coefficient was calculated as follows:

$$\tilde{\mathbf{C}} = \tilde{\mathbf{B}}^{-1} \tilde{\mathbf{A}}$$

The residual effect (R) that measures the contribution of rest of the traits is not considered in caused scheme. The residual effect (R) was calculated as follows:

$$R^2 = 1 - \sum_{i=1}^r P_{iy}^2 - 2 \sum_{i,j=1}^r P_{iy} P_{jy} r_{ij}$$



Results and Discussion



The improvement in grain yield and its component traits in conjunction with quality parameters is the primary objective of many plant breeders. But, the polygenic inheritance of grain yield makes its improvement rather difficult. The information on genetic variability, trait association, their direct and indirect effect on yield, heterosis, better combining parents and superior crosses have great value in plant breeding programmes for the development of high yielding varieties. The present study was, therefore, conducted with 8 aromatic rice parents and 28 hybrids originating from them in half diallel fashion. Results obtained from the present investigation have been presented and discussed under the following heads:

- 4.1. Variance and mean
- 4.2. Genetic variability parameters
- 4.3. Heterosis
- 4.4. Combining ability
- 4.5. Graphical analysis
- 4.6. Correlation and path coefficient
- 4.7. Aroma index

4.1. Variance and mean

Existence of adequate genetic variability is a basic requirement of any crop breeding programme, without which the possibility of improvement in the existing germplasm seems to be remote. Thus, before initiating any breeding programme the most important step is to confirm whether or not sufficient genetic variability for various traits exists. More the genetic variability, greater is the chance of improvement of available germplasm lines and isolation of elite lines from existing genetic stock.

Analysis of variance revealed significant differences among the means of genotypes and hybrids for all the traits (**Table 4.1.1**). These results clearly indicated wide spectrum of variations among the genotypes and hybrids for all the studied traits. This observation indicated the suitability of the experimental material chosen for the present investigation and further validated statistical and genetic analysis.

Table 4.1.1: ANOVA for grain yield and quality traits in aroma rice

Source of variation	Degree of freedom	Mean sum of squares						
		Days to 50% flowering	Plant height	Flag leaf length	Panicle length	Panicles/plant	Filled grains/panicle	Unfilled grains/panicle
Replication	2	9.03	6.83	0.10	0.13	0.17	2.23	3.93
Treatment	35	75.74**	972.38**	33.20**	28.21**	40.81**	1419.34**	157.88**
Error	70	6.24	4.66	0.38	0.62	0.42	93.55	5.99
CV (%)		2.42	1.75	1.78	2.53	3.69	5.92	4.96

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.1.1: Contd.....

Source of variation	Degree of freedom	Mean sum of squares						
		Spikelet fertility	Test weight	Grain yield/plant	Hulling recovery	Milling recovery	Kernel length	Kernel breadth
Replication	2	0.36	0.86	8.05	0.24	0.17	0.01	0.00
Treatment	35	36.49**	14.95**	292.36**	12.37**	12.37**	1.32**	0.02**
Error	70	1.54	0.67	3.41	0.23	1.12	0.01	0.00
CV (%)		1.61	3.43	5.32	0.62	1.53	1.75	2.97

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.1.1: Contd.....

Source of variation	Degree of freedom	Mean sum of squares						
		Kernel length/breadth ratio	Cooked kernel length	Cooked kernel breadth	Cooked kernel length/breadth ratio	Kernel elongation ratio	Alkali digestion value	Amylose content
Replication	2	0.02	0.02	0.01	0.02	0.01	0.05	0.18
Treatment	35	0.80**	10.00**	0.16**	3.09**	0.08**	4.49**	6.15**
Error	70	0.02	0.19	0.02	0.14	0.01	0.02	0.07
CV (%)		3.67	2.82	5.73	5.48	3.26	2.70	1.22

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

The mean performance and range of variation among all genotypes for various traits are presented in the **Table 4.1.2** and described as follows:

Days to 50% flowering ranged from 95.67days (Pusa Basmati-1×Pusa Sugandh-6) to 116.33 days (Pusa Basmati-1×Type-3) with mean value of 102.97 days and coefficient of variation of 2.42.

Plant height ranged from 95.33 cm (Pant Basmati-1) to 160.70 cm (Basmati-370 ×PSD-15) with the mean value of 123.55 cm and coefficient of variation of 1.75.

Flag leaf length ranged from 29.90 cm (Pusa Sugandh-4) to 41.20 cm (Pusa Sugandh-4×Tarori Basmati-1) with the mean value of 34.91 cm and coefficient of variation of 1.78.

Panicle length ranged from 26.03 cm (Basmati-370×Tarori Basmati-1) to 39.30 cm (Pusa Sugandh-4×Pant Basmati-1) with the mean value of 31.59 cm and coefficient of variation of 2.53.

Number of panicles per plant ranged from 11.80 (PSD-15) to 25.03(Basmati-370 ×PSD-15) with the mean value of 17.54 and coefficient of variation of 3.69.

Number of filled grains per panicle ranged from 107.93 (PSD-15) to 198.33 (Pusa Basmati-1×Pusa Sugandh-6) with the mean value of 161.30 and coefficient of variation of 5.92.

Number of unfilled grains per panicle ranged from 39.47 (Tarori Basmati-1) to 70.47 (Type-3×PSD-15) with the mean value of 49.09 and coefficient of variation of 4.96.

Spikelet fertility ranged from 66.95% (Type-3×PSD-15) to 81.95% (Pusa Sugandh-6 ×Basmati-370) with the mean value of 76.49 and coefficient of variation of 1.61.

Test weight ranged from 18.83 g. (Basmati-370) to 28.47 g. (Pusa Sugandh-4 ×PSD-15) with the mean value of 23.95 g. and coefficient of variation of 3.43.

Grain yield per plant ranged from 18.12 g. (Pant Basmati-1) to 63.58 g. (Pusa Sugandh-6×PSD-15) with the mean value of 34.37 g. and coefficient of variation of 5.32.

Hulling recovery ranged from 73.24% (Pant Basmati-1) to 80.73% (Pusa Basmati-1×Tarori Basmati-1) with the mean value of 76.44% and coefficient of variation of 0.62.

Table 4.1.2: Estimates of range, mean, critical difference and coefficients of variation for grain yield and quality traits.

Sl. No.	Traits	Range		Mean $\pm$ SE	Critical difference (C.D.)		CV
		Minimum	Maximum		1%	5%	
1.	Days to 50% flowering	95.67	116.33	102.97 $\pm$ 1.44	5.38	4.05	2.42
2.	Plant height	95.33	160.70	123.55 $\pm$ 1.25	4.66	3.51	1.75
3.	Flag leaf length	29.90	41.20	34.91 $\pm$ 0.36	1.34	1.01	1.78
4.	Panicle length	26.03	39.30	31.59 $\pm$ 0.46	1.73	1.30	2.53
5.	Panicles/plant	11.80	25.03	17.54 $\pm$ 0.37	1.40	1.05	3.69
6.	Filled grains/panicle	107.93	198.33	161.30 $\pm$ 5.51	20.63	15.54	5.92
7.	Unfilled grains/panicle	39.47	70.47	49.09 $\pm$ 1.41	5.26	3.96	4.96
8.	Spikelet fertility	66.95	81.95	76.49 $\pm$ 0.71	2.66	2.00	1.61
9.	Test weight	18.83	28.47	23.95 $\pm$ 0.47	1.77	1.34	3.43
10.	Grain yield/plant	18.12	63.58	34.37 $\pm$ 1.06	3.95	2.98	5.32
11.	Hulling recovery	73.24	80.73	76.44 $\pm$ 0.28	1.03	0.78	0.62
12.	Milling recovery	65.33	72.70	68.47 $\pm$ 0.61	2.27	1.71	1.53
13.	Kernel length	5.55	7.83	6.79 $\pm$ 0.07	0.26	0.19	1.75
14.	Kernel breadth	1.64	1.95	1.75 $\pm$ 0.03	0.11	0.08	2.97
15.	Kernel length/breadth ratio	2.88	4.76	3.90 $\pm$ 0.08	0.31	0.23	3.67
16.	Cooked kernel length	13.19	19.53	16.34 $\pm$ 0.27	1.00	0.75	2.82
17.	Cooked kernel breadth	2.25	3.35	2.48 $\pm$ 0.08	0.31	0.23	5.73
18.	Cooked kernel length/breadth ratio	4.11	8.28	6.68 $\pm$ 0.21	0.79	0.60	5.48
19.	Kernel elongation ratio	2.10	2.78	2.41 $\pm$ 0.05	0.17	0.13	3.26
20.	Alkali digestion value	3.42	7.15	5.761 $\pm$ 0.09	0.34	0.25	2.70
21.	Amylose content	18.50	24.22	21.67 $\pm$ 0.15	0.57	0.43	1.22

Milling recovery ranged from 65.33% (Tarori Basmati-1) to 72.70% (Pusa Basmati-1×Tarori Basmati-1) with the mean value of 68.47% and coefficient of variation of 1.53.

Kernel length ranged from 5.55 mm (Basmati-370) to 7.83 mm (PSD-15×Pant Basmati-1) with the mean value of 6.79 mm and coefficient of variation of 1.75.

Kernel breadth ranged from 1.64 mm (Pusa Sugandh-6×Tarori Basmati-1) to 1.95 mm (Pusa Sugandh-4×Tarori Basmati-1) with the mean value of 1.75 mm and coefficient of variation of 2.97.

Kernel length/breadth ratio ranged from 2.88 (Pusa Sugandh-4×Tarori Basmati-1) to 4.76 (Pusa Sugandh-6×Tarori Basmati-1) with the mean value of 3.90 and coefficient of variation of 3.67.

Cooked kernel length ranged from 13.19 mm (Type-3) to 19.53 mm (PSD-15×Pant Basmati-1) with the mean value of 16.34 mm and coefficient of variation of 2.82.

Cooked kernel breadth ranged from 2.25 mm (Pusa Basmati-1×Tarori Basmati-1) to 3.35 mm (Pusa Sugandh-6×Pant Basmati-1) the mean value of 2.48 mm and coefficient of variation of 5.73.

Cooked kernel length/breadth ratio ranged from 4.11 (Pusa Sugandh-6×Pant Basmati-1) to 8.28 (PSD-15×Pant Basmati-1) with the mean value of 5.48 and coefficient of variation of 3.67.

Kernel elongation ratio ranged from 2.10 (Pusa Sugandh-6) to 2.78 (Pusa Sugandh-4×Tarori Basmati-1) with the mean value of 2.41 and coefficient of variation of 3.26.

Alkali digestion value ranged from 3.42 (Pusa Sugandh-6×Tarori Basmati-1) to 7.15 (Improved Pusa Basmati-1) with the mean value of 5.761 and coefficient of variation of 2.70.

Amylose content ranged from 18.50% (Basmati-370×PSD-15) to 24.22% (Type-3×Taraori Basmati) with the mean value of 21.67% and coefficient of variation of 1.22.

The results from the analysis of variance data based on parents and crosses showed that the significant amount of variability was present in the experimental

material for all the traits studied. **Naseer *et al.* (2015), Allam *et al.* (2015), Singh *et al.* (2015)** and **Karande *et al.* (2015)** observed similar results.

4.2. Genetic variability parameters

4.2.1 Coefficient of variations

Fruition of selection and associated genetic improvement largely depends on the amount of the genetic variability present in the breeding population. The variability at phenotypic level arises due to genotype and its interaction with the environment that contribute towards phenotype development. The genetic variability present in the germplasm of a crop species and its estimation is pre-requisite in executing any effective breeding programme. These genetic variations might be either heritable or non-heritable. The magnitude of variation due to heritable component is very important because it would be a guide for selection of parents for crop improvement programme. Thus genetic variability for agronomic as well as quality traits is the key components of breeding programme for broadening the gene pool of crops. For any trait of interest, observed phenotypic differences among individuals may be due to differences in the genetic code for that trait or may be the result of variation in the environmental conditions. A large number of agronomically important traits are known to be affected by environmental factors to a great deal. Selection based on the phenotype might not be rewarding for such traits. In breeding programmes, it is often difficult to manipulate such traits, since severable factors are involved directly or indirectly in the control and expression of these traits. So, the measurement of quantitative genetic variation and understanding its components and mode of inheritance are essential steps in any crop improvement programme.

The phenotypic, genotypic and environmental coefficient of variations estimated for different traits has been presented in **Table 4.2.1**. The high estimate (>20) of phenotypic coefficient of variation (PCV) was obtained for grain yield/plant (29.33), alkali digestion value (21.45) and number of panicles/plant (21.36). Moderate estimate (10-20) of phenotypic coefficient of variation (PCV) was obtained for cooked kernel length/breadth ratio (13.41), unfilled grains/panicle (15.22), plant height (14.93), filled grains/panicle (14.53) and kernel length/breadth ratio (13.41). The low estimate of PCV was observed for panicle length (9.85), kernel length (9.74), test weight (9.79), flag leaf length (9.66) and kernel elongation ratio (7.08).

Table 4.2.1: Estimates of genetic variability parameters for grain yield and quality traits.

Sl. No.	Traits	PCV	GCV	ECV	Heritability (broad sense)	Expected genetic advance	Genetic advance as % of mean
1.	Days to 50% flowering	5.62	5.08	2.42	0.81	9.72	9.44
2.	Plant height	14.93	14.83	1.75	0.98	37.49	30.34
3.	Flag leaf length	9.66	9.50	1.78	0.96	6.71	19.23
4.	Panicle length	9.85	9.52	2.53	0.93	5.98	18.95
5.	Panicles/plant	21.36	21.03	3.69	0.97	7.49	42.68
6.	Filled grains/panicle	14.53	13.26	5.92	0.83	40.25	24.95
7.	Unfilled grains/panicle	15.22	14.39	4.96	0.89	13.76	28.03
8.	Spikelet fertility	4.70	4.42	1.61	0.88	6.54	8.55
9.	Test weight	9.79	9.17	3.43	0.87	4.24	17.70
10.	Grain yield/plant	29.33	28.84	5.32	0.96	20.08	58.43
11.	Hulling recovery	2.67	2.60	0.62	0.94	3.98	5.21
12.	Milling recovery	3.20	2.81	1.53	0.76	3.47	5.07
13.	Kernel length	9.74	9.58	1.75	0.96	1.32	19.41
14.	Kernel breadth	5.53	4.67	2.97	0.71	0.14	8.11
15.	Kernel length/breadth ratio	13.41	12.90	3.67	0.92	1.00	25.56
16.	Cooked kernel length	11.27	10.91	2.82	0.93	3.56	21.77
17.	Cooked kernel breadth	10.19	8.42	5.73	0.68	0.36	14.35
18.	Cooked kernel length/breadth ratio	15.65	14.66	5.48	0.87	1.89	28.28
19.	Kernel elongation ratio	7.08	6.29	3.26	0.78	0.28	11.50
20.	Alkali digestion value	21.45	21.27	2.70	0.98	2.50	43.48
21.	Amylose content	6.60	6.49	1.22	0.96	2.85	13.14

The high genotypic coefficient of variation (GCV) was observed for grain yield/plant (28.84) followed by alkali digestion value (21.27) and panicles/plant (21.03). Moderate estimate of genotypic coefficient of variation (GCV) was obtained for plant height (14.83) followed by cooked kernel length/breadth ratio (14.66), unfilled grains/panicle (14.39), kernel length/breadth ratio (12.90) and filled grains/panicle (13.26). Low estimate of GCV was found for kernel length (9.58) followed by panicle length (9.52), test weight (9.17), flag leaf length (9.50) and cooked kernel breadth (8.42).

Low level (< 10) of environmental coefficient of variation (ECV) was observed for all the studied traits *viz.*, filled grains/panicle (5.92), cooked kernel breadth (5.73), cooked kernel length/breadth ratio (5.48), unfilled grains/panicle (4.96) and panicles/plant (3.69).

In the present study it was observed that the PCV was higher in magnitude than the corresponding GCV for all the traits. Similar findings were reported from the study of **Allam *et al.* (2015)**, **Naseer *et al.* (2015)** and **Dutta *et al.* (2013)** for various traits.

4.2.2 Heritability, genetic advance and genetic advance as percent of mean

Heritability refers to an index of transmissibility, to measure the genetic relationship between the parent and their offspring or degree of resemblance between parent and offsprings. Heritability estimates provides authentic information about a particular genetic attribute which will be transmitted to the successive generations. A broad- sense heritability estimate provides information on the relative magnitude of genetic and environmental variation in the population and help breeders to determine the possible extent for improvement through selection. Thus, heritability infers as to how much emphasis should be placed for the selection in case of particular trait. The heritability, expected genetic advance and genetic advance as percent of mean has been presented in the **Table 4.2.1**.

Heritability estimates and genetic advance are important genetic parameters. The knowledge of heritability coupled with expected genetic advance for a trait helps breeder to anticipate extent of improvement in particular trait that could be sought through selection (**Johnson *et al.*, 1955**). Expected genetic advance indicates the expected genetic progress for a particular trait under the selection cycle and measure the extent of its stability under the selection pressure.

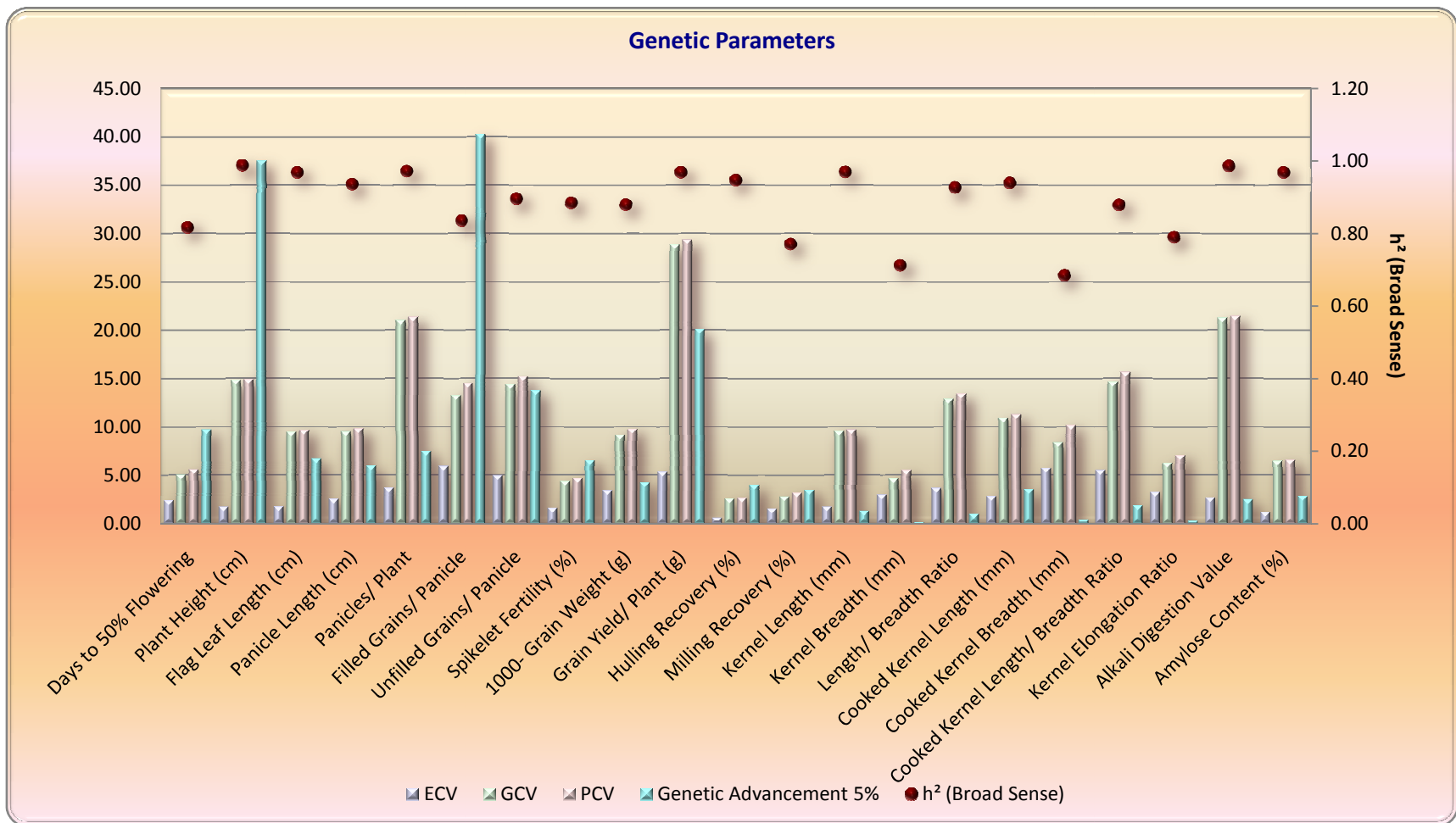


Figure 4.2: Diagrammatic representation of genetic variability parameters

Most of the traits included in the present study were highly heritable as they have shown to be associated with moderate to high estimates of broad sense heritability. High heritability was observed for plant height (0.98), alkali digestion value (0.98), flag leaf length (0.96), panicles/plant (0.97), grain yield/plant (0.96), kernel length (0.96) and amylose content (0.96). Among the studied traits the lowest heritability was observed for milling recovery (0.76), kernel breadth (0.71) and cooked kernel breadth (0.68).

The expected genetic advance varied from 0.14 (kernel breadth) to 40.25 (filled grains/panicle). Highest value of expected genetic advance was exhibited by filled grains/panicle (40.25) followed by plant height (37.49) and grain yield/plant (20.08). Lowest value of expected genetic advance was observed for kernel breadth (0.14) followed by kernel elongation ratio (0.28) and cooked kernel breadth (0.36).

Genetic advance as percent of mean recorded highest value for alkali digestion value (43.48) followed by panicles/plant (42.68), plant height (30.34), cooked kernel length/breadth ratio (28.28), unfilled grains/panicle (28.03) and kernel length/breadth ratio (25.56). Lowest value of genetic advance as percent of mean was observed for milling recovery (5.07) and hulling recovery (5.21).

High estimate of heritability for different traits were also reported earlier by **Naseer *et al.* (2015), Chakraborty and chakraborty (2010) and Saleem *et al.* (2008).** High heritability for the trait of economic importance *viz.*, plant height (0.98), alkali digestion value (0.98), flag leaf length (0.96), panicles/plant (0.97), grain yield/plant (0.96), kernel length (0.96) and amylose content (0.96) indicated that the direct selection would be effective for improvement of these traits.

High estimate of heritability does not always mean high genetic advance. **Johnson *et al.* (1955)** suggested that heritability estimates and the genetic advance as percent of mean together would provide a better way rather than heritability alone in predicting the resultant effect of selection. High heritability coupled with high genetic advance as percent of mean was observed for alkali digestion value (0.98, 43.48) followed by panicles/plant (0.97, 42.68), plant height (0.98, 30.34), cooked kernel length/breadth ratio (0.87, 28.28), unfilled grains/panicle (0.89, 28.03) and kernel length/breadth ratio (0.92, 25.56) indicating the preponderance of additive gene action

for these traits. This also suggests that selection for improvement in these traits would be effective. Similar findings have also been reported earlier by **Savitha and Usha (2015)**, **Karande *et al.* (2015)**, **Bhadru *et al.* (2012)** for various traits in rice.

High heritability with low expected genetic advance was recorded for milling recovery (0.76, 5.07) and hulling recovery (0.94, 5.21), spikelet fertility (0.88, 8.55) and days to 50% flowering (0.81, 9.44). This indicated that these traits were mostly governed by non-additive gene action. Similar results were reported by **Karande *et al.* (2015)**, **Naseer *et al.* (2015)** and **Chakraborty and Chakraborty (2010)**.

The disagreement of previous reports for some traits could be ascribed to the population and the environment in which the estimates of heritability were taken as heritability estimates are subject to environmental condition in which it is estimated (**Falconer, 1960**).

4.3 Heterosis

The superiority of F_1 over its parent is known as heterosis. The result of heterosis pertaining to heterosis for various traits in F_1 hybrids in present investigation has been presented in **Table 4.3.1**.

4.3.1 Days to 50% flowering

The range of heterosis over mid-parent varied from -14.33% (Pusa Basmati-1×Pusa Sugandh-6) to 4.18% (Pusa Basmati-1×Type-3). Among 28 crosses 15 crosses showed significant negative heterosis and only one crosses showed significant positive heterosis for days to 50% flowering over mid-parent. The maximum significant negative heterosis over mid-parent was exhibited by Pusa Basmati-1×Pusa Sugandh-6 (-14.33) followed by Basmati-370×Pant Basmati-1 (-13.74), Pusa Basmati-1×Pusa Sugandh-4(-11.34), Pusa Basmati-1×Pant Basmati-1 (-10.15), Basmati-370×PSD-15(-9.06), Pusa Sugandh-4×Basmati-370 (-8.19), Type-3×Basmati-370 (-8.19), Pusa Basmati-1×PSD-15 (-8.06), Pusa Sugandh-6×Basmati-370 (-7.89), Basmati-370×Tarori Basmati-1(-7.60), Pusa Sugandh-4×PSD-15 (-6.77), Tarori Basmati-1×Pant Basmati-1(-6.35), Tarori Basmati-1×PSD-15 (-5.40) Pusa Sugandh-4×Pusa Sugandh-6 (-4.84) and Type-3×PSD-15 (-4.44). Significant positive heterosis for days to 50% flowering over mid-parent was found in the only cross Pusa Basmati-1×Type-3 (4.18).

Table 4.3.1: Heterosis (%) over mid parent, better parent and standard variety for various traits

Sl. No	Crosses	Days to 50% flowering				Plant height (cm)			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1xPusa Sugandh-4	99.00	-11.34 **	-7.91 **	-14.66 **	112.87	6.28 **	11.60 **	17.98 **
2	Pusa Basmati-1xPusa Sugandh-6	95.67	-14.33 **	-9.75 **	-17.53 **	100.40	-2.27	1.01	4.95 **
3	Pusa Basmati-1xType-3	116.33	4.18 *	7.38 **	0.29	135.68	28.89 **	34.78 **	41.82 **
4	Pusa Basmati-1xBasmati-370	111.00	-2.63	-1.62	-4.31 *	146.53	2.21	22.40 **	53.17 **
5	Pusa Basmati-1xTarori Basmati-1	107.67	-3.58	-0.62	-7.18 **	131.27	4.18 **	18.22 **	37.21 **
6	Pusa Basmati-1xPSD-15	102.67	-8.06 **	-1.91	-11.49 **	121.40	-0.95	11.05 **	26.90 **
7	Pusa Basmati-1xPant Basmati-1	100.33	-10.15 **	-3.68 *	-13.51 **	105.73	10.06 **	10.48 **	10.52 **
8	Pusa Sugandh-4xPusa Sugandh-6	98.33	-4.84 *	-3.44	-15.23 **	117.97	11.08 **	12.92 **	23.31 **
9	Pusa Sugandh-4xType-3	103.33	-1.59	-0.80	-10.92 **	144.10	35.69 **	36.29 **	50.63 **
10	Pusa Sugandh-4xBasmati-370	104.67	-8.19 **	-3.68 *	-9.77 **	136.13	-5.05 **	9.10 **	42.30 **
11	Pusa Sugandh-4xTarori Basmati-1	103.67	-1.27	-0.48	-10.63 **	128.83	2.25	10.97 **	34.67 **
12	Pusa Sugandh-4xPSD-15	96.33	-6.77 **	-4.15 *	-16.95 **	137.13	11.88 **	19.89 **	43.34 **
13	Pusa Sugandh-4xPant Basmati-1	99.67	-3.55	-0.33	-14.08 **	100.87	5.02 **	0.10	5.44 **
14	Pusa Sugandh-6xType-3	103.33	-1.59	0.65	-10.92 **	150.33	42.81 **	44.55 **	57.14 **
15	Pusa Sugandh-6xBasmati-370	105.00	-7.89 **	-2.02	-9.48 **	151.87	5.93 **	23.42 **	58.75 **
16	Pusa Sugandh-6xTarori Basmati-1	103.33	-1.59	0.65	-10.92 **	129.82	3.03 *	13.51 **	35.70 **
17	Pusa Sugandh-6xPSD-15	97.00	-3.32	-2.02	-16.38 **	118.13	-3.62 *	4.87 **	23.48 **
18	Pusa Sugandh-6xPant Basmati-1	99.00	-1.33	0.51	-14.66 **	105.13	2.34	6.16 **	9.90 **
19	Type-3xBasmati-370	104.67	-8.19 **	-4.41 **	-9.77 **	143.67	0.21	15.57 **	50.17 **
20	Type-3xTarori Basmati-1	106.00	0.95	0.95	-8.62 **	124.37	-1.30	7.55 **	30.00 **
21	Type-3xPSD-15	100.33	-4.44 *	-0.99	-13.51 **	151.83	23.88 **	33.28 **	58.71 **
22	Type-3xPant Basmati-1	102.00	-2.86	1.16	-12.07 **	125.23	18.97 **	24.86 **	30.91 **
23	Basmati-370xTarori Basmati-1	105.33	-7.60 **	-3.81 *	-9.20 **	130.67	-8.86 **	-2.98 *	36.59 **
24	Basmati-370xPSD-15	103.67	-9.06 **	-2.05	-10.63 **	160.70	12.09 **	20.86 **	67.98 **
25	Basmati-370xPant Basmati-1	98.33	-13.74 **	-6.65 **	-15.23 **	125.00	-12.81 **	4.73 **	30.66 **
26	Tarori Basmati-1xPSD-15	99.33	-5.40 **	-1.97	-14.37 **	131.60	4.44 **	5.89 **	37.56 **
27	Tarori Basmati-1xPant Basmati-1	98.33	-6.35 **	-2.48	-15.23 **	103.68	-17.71 **	-6.31 **	8.38 **
28	PSD-15xPant Basmati-1	96.00	-1.71	-1.20	-17.24 **	107.03	-12.67 **	-1.76	11.88 **

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check) =Standard heterosis over check

The range of heterosis over better parent varied from -9.75% (Pusa Basmati-1 × Pusa Sugandh-4) to 7.38% (Pusa Basmati-1 × Type-3). Among 28 crosses, 8 crosses showed significant negative heterosis and only one cross showed significant positive heterosis for days to 50% flowering over better parent. The maximum significant negative heterosis over better parent was exhibited by Pusa Basmati-1 × Pusa Sugandh-4 (-7.91) followed by Pusa Basmati-1 × Pusa Sugandh-6 (-9.75), Pusa Basmati-1 × Pant Basmati-1 (-3.68), Pusa Sugandh-4 × Basmati-370 (-3.68), Pusa Sugandh-4 × PSD-15 (-4.15), Type-3 × Basmati-370 (-4.41), Basmati-370 × Tarori Basmati-1 (-3.81) and Basmati-370 × Pant Basmati-1 (-6.65). Significant positive heterosis for days to 50% flowering over better parent was found in the only cross Pusa Basmati-1 × Type-3 (7.38).

Range of heterosis over standard check variety (Improved Pusa Basmati-1) varied from -17.53 (Pusa Basmati-1 × Pusa Sugandh-6) to -4.31 (Pusa Basmati-1 × Basmati-370). Among 28 crosses 27 crosses showed significant negative heterosis for days to 50% flowering over standard check variety. The maximum significant negative heterosis over standard check was exhibited by Pusa Basmati-1 × Pusa Sugandh-6 (-17.53) followed by PSD-15 × Pant Basmati-1 (-17.24), Pusa Sugandh-4 × PSD-15 (-16.95), Pusa Sugandh-6 × PSD-15 (-16.38), Basmati-370 × Pant Basmati-1 (-15.23), Pusa Basmati-1 × Pusa Sugandh-4 (-14.66), Pusa Sugandh-4 × Pusa Sugandh-6 (-15.23), Tarori Basmati-1 × Pant Basmati-1 (-15.23), Pusa Sugandh-6 × Pant Basmati-1 (-14.66), Tarori Basmati-1 × PSD-15 (-14.37), Pusa Sugandh-4 × Pant Basmati-1 (-14.08), Type-3 × PSD-15 (-13.51), Pusa Basmati-1 × Pant Basmati-1 (-13.51), Type-3 × Pant Basmati-1 (-12.07), Pusa Basmati-1 × PSD-15 (-11.49), Pusa Sugandh-4 × Type-3 (-10.92), Pusa Sugandh-6 × Type-3 (-10.92), Pusa Sugandh-4 × Tarori Basmati-1 (-10.63), Basmati-370 × PSD-15 (-10.63), Pusa Sugandh-6 × Tarori Basmati-1 (-10.92), Type-3 × Basmati-370 (-9.77), Pusa Sugandh-4 × Basmati-370 (-9.77), Pusa Sugandh-6 × Basmati-370 (-9.48), Basmati-370 × Tarori Basmati-1 (-9.20), Type-3 × Tarori Basmati-1 (-8.62), Pusa Basmati-1 × Tarori Basmati-1 (-7.18), and Pusa Basmati-1 × Basmati-370 (-4.31).

4.3.2 Plant height (cm)

The range of heterosis over mid parent for plant height varied from -17.71% (Tarori Basmati-1 × Pant Basmati-1) to 42.81% (Pusa Sugandh-6 × Type-3). Among 28 crosses, 15 crosses showed significant positive heterosis and 6 crosses showed significant negative heterosis for plant height over mid parent. The maximum

significant positive heterosis for plant height over mid parent was exhibited by Pusa Sugandh-6×Type-3 (42.81) followed by Pusa Sugandh-4×Type-3 (35.69), Pusa Basmati-1×Type-3 (28.89), Type-3×PSD-15 (23.88), Type-3×Pant Basmati-1(18.97), Basmati-370×PSD-15(12.09), Pusa Sugandh-4×PSD-15 (11.88), Pusa Sugandh-4×Pusa Sugandh-6 (11.08), Pusa Basmati 1×Pant Basmati-1(10.06), Pusa Basmati-1×Pusa Sugandh-4 (6.28), Pusa Sugandh-6×Basmati-370(5.93), Pusa Sugandh-4×Pant Basmati-1 (5.02), Pusa Basmati-1×Tarori Basmati-1(4.18), Tarori Basmati-1×PSD-15 (4.44) and Pusa Sugandh-6×Tarori Basmati-1(3.03). Maximum significant negative heterosis was exhibited by Tarori Basmati-1×Pant Basmati-1 (-17.71) followed by Basmati-370×Tarori Basmati-1 (-8.86), Basmati-370×Pant Basmati-1 (-12.81), PSD-15 ×Pant Basmati-1 (-12.67), Pusa Sugandh-4×Basmati-370 (-5.05) and Pusa Sugandh-6 ×PSD-15 (-3.62).

The range of heterosis over better parent for plant height varied from -2.98% (Basmati-370×Tarori Basmati-1) to 44.55% (Pusa Sugandh-6×Type-3). Among 28 crosses 23 crosses showed significant positive heterosis and 2 crosses showed significant negative heterosis for plant height over better parent. The maximum significant positive heterosis over better parent was exhibited by Pusa Sugandh-6×Type-3 (44.55) followed by Pusa Sugandh-4×Type-3 (36.29), Pusa Basmati-1×Type-3 (34.78), Type-3×PSD-15 (33.28), Basmati-370×PSD-15 (20.86), Pusa Basmati-1 × Basmati-370 (22.40), Pusa Sugandh-6×Basmati-370 (23.42), Type-3 ×Pant Basmati-1 (24.86), Pusa Sugandh-4×PSD-15(19.89), Pusa Basmati-1×Tarori Basmati-1(18.22), Pusa Basmati-1×Pusa Sugandh-4(11.60), Pusa Basmati-1×PSD-15 (11.05), Pusa Basmati 1 × Pant Basmati-1(10.48), Pusa Sugandh-4×Pusa Sugandh-6 (12.92), Pusa Sugandh-4×Tarori Basmati-1 (10.97), Pusa Sugandh-6×Tarori Basmati-1 (13.51), Type-3×Basmati-370 (15.57), Pusa Sugandh-4×Basmati-370(9.10), Type-3 ×Tarori Basmati-1 (7.55), Pusa Sugandh-6×Pant Basmati-1 (6.16), Tarori Basmati-1 ×PSD-15 (5.89), Pusa Sugandh-6×PSD-15 (4.87) and Basmati-370×Pant Basmati-1 (4.73). The significant negative heterosis over better parent for plant height was exhibited by Tarori Basmati-1×Pant Basmati-1 (-6.31) and Basmati-370×Tarori Basmati-1 (-2.98).

Range of heterosis for plant height over standard check variety (Improved Pusa Basmati-1) varied from 4.95% (Pusa Basmati-1×Pusa Sugandh-6) to 67.98 (Basmati-370

×PSD-15). All the 28 crosses showed significant positive heterosis for plant height over standard check variety. The maximum significant positive heterosis over standard check was exhibited by Basmati-370×PSD-15 (67.98) followed by Type-3×PSD-15 (58.71), Pusa Sugandh-6×Basmati-370 (58.75), Pusa Sugandh-6×Type-3 (57.14), Pusa Sugandh-4×Type-3 (50.63), Type-3×Basmati-370 (50.17), Pusa Basmati-1×Basmati-370 (53.17), Pusa Sugandh-4×PSD-15 (43.34), Pusa Sugandh-4×Basmati-370 (42.30), Pusa Basmati-1×Type-3 (41.82), Tarori Basmati-1×PSD-15 (37.56), Pusa Basmati-1×Tarori Basmati-1 (37.21), Basmati-370×Tarori Basmati-1 (36.59), Pusa Sugandh-6×Tarori Basmati-1 (35.70), Type-3×Pant Basmati-1 (30.91), Pusa Sugandh-4×Tarori Basmati-1 (34.67), Basmati-370×Pant Basmati-1 (30.66), Type-3×Tarori Basmati-1 (30.00), Pusa Basmati-1×PSD-15 (26.90), Pusa Sugandh-6×PSD-15 (23.48), Pusa Sugandh-4×Pusa Sugandh-6 (23.31), Pusa Basmati-1×Pusa Sugandh-4 (17.98), PSD-15×Pant Basmati-1 (11.88), Pusa Basmati 1×Pant Basmati-1 (10.52), Pusa Sugandh-6×Pant Basmati-1 (9.90), Tarori Basmati-1×Pant Basmati-1(8.38), Pusa Sugandh-4×Pant Basmati-1 (5.44) and Pusa Basmati-1×Pusa Sugandh-6 (4.95)

4.3.3 Flag leaf length (cm)

The range of heterosis over mid parent for flag leaf length varied from -19.38% (Basmati-370×Pant Basmati-1) to 25.42% (Pusa Sugandh-4×Tarori Basmati-1). Among 28 crosses, 17 crosses showed significant positive heterosis and 7 crosses showed significant negative heterosis for Flag leaf length over mid-parent. The maximum significant positive heterosis over mid parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (25.42) followed by Pusa Sugandh-6×Type-3 (25.39), Type-3×PSD-15 (23.93), Pusa Sugandh-6×Basmati-370(18.50), Tarori Basmati-1×PSD-15 (18.29), Pusa Basmati-1×Pusa Sugandh-6 (15.17), Pusa Sugandh-4×Pant Basmati-1(14.34), Pusa Sugandh-4×PSD-15 (12.17), Pusa Sugandh-6×Tarori Basmati-1 (11.74), Pusa Sugandh-4×Pusa Sugandh-6 (11.07), Pusa Sugandh-4×Type-3 (9.89), Pusa Basmati-1 ×PSD-15 (8.49), Pusa Sugandh-6×Pant Basmati-1 (9.42), Pusa Sugandh-6×PSD-15 (6.35), Basmati-370×PSD-15 (4.44), Pusa Basmati 1 × Pant Basmati-1 (4.23) and Pusa Basmati-1×Tarori Basmati-1 (3.59). The maximum significant negative heterosis over mid parent was exhibited by Basmati-370×Pant Basmati-1 (-19.38) followed by PSD-15 x Pant Basmati-1 (-15.55), Type-3×Pant Basmati-1 (-8.65), Type-3×Tarori Basmati-1 (-5.48), Tarori Basmati-1×Pant Basmati-1 (-3.69), Pusa Sugandh-4×Basmati-370 (-3.39) and Pusa Basmati-1 × Basmati-370 (-3.18).

Table 4.3.1: Contd.....

Sl. No	Crosses	Flag leaf length (cm)				Panicle length (cm)			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1xPusa Sugandh-4	31.40	2.89	0.86	0.21	30.93	5.16**	5.10*	4.39
2	Pusa Basmati-1xPusa Sugandh-6	36.07	15.17**	14.50**	15.11**	30.73	5.61**	4.54*	3.71
3	Pusa Basmati-1xType-3	31.50	1.18	1.18	0.53	32.80	13.95**	11.56**	10.69**
4	Pusa Basmati-1xBasmati-370	32.97	-3.18*	-10.82**	5.21**	32.13	11.85**	9.30**	8.44**
5	Pusa Basmati-1xTarori Basmati-1	34.67	3.59**	-3.17*	10.64**	35.77	25.20**	21.66**	20.70**
6	Pusa Basmati-1xPSD-15	35.13	8.49**	4.46**	12.13**	31.60	8.59**	7.48**	6.64**
7	Pusa Basmati-1xPant Basmati-1	36.13	4.23**	-5.41**	15.32**	36.50	22.41**	20.73**	23.17**
8	Pusa Sugandh-4xPusa Sugandh-6	34.10	11.07**	8.25**	8.83**	30.83	5.90**	4.76*	4.05
9	Pusa Sugandh-4xType-3	33.53	9.89**	7.71**	7.02**	30.57	6.13**	3.85	3.15
10	Pusa Sugandh-4xBasmati-370	32.30	-3.39*	-12.62**	3.09	29.70	3.32	0.91	0.22
11	Pusa Sugandh-4xTarori Basmati-1	41.20	25.42**	15.08**	31.49**	28.07	-1.81	-4.64*	-5.29*
12	Pusa Sugandh-4xPSD-15	35.63	12.17**	5.95**	13.72**	30.33	4.18*	3.06	2.36
13	Pusa Sugandh-4xPant Basmati-1	38.93	14.34**	1.92	24.26**	39.30	31.73**	29.99**	32.62**
14	Pusa Sugandh-6xType-3	39.27	25.39**	24.66**	25.32**	34.43	20.89**	19.56**	16.20**
15	Pusa Sugandh-6xBasmati-370	40.57	18.50**	9.74**	29.47**	34.33	20.76**	19.21**	15.86**
16	Pusa Sugandh-6xTarori Basmati-1	37.60	11.74**	5.03**	20.00**	28.90	2.24	0.35	-2.47
17	Pusa Sugandh-6xPSD-15	34.63	6.35**	2.97	10.53**	31.67	9.95**	9.95**	6.86**
18	Pusa Sugandh-6xPant Basmati-1	38.13	9.42**	-0.17	21.70**	36.20	22.64**	19.74**	22.16**
19	Type-3xBasmati-370	33.43	-1.81	-9.56**	6.70**	29.07	3.39	3.20	-1.91
20	Type-3xTarori Basmati-1	31.63	-5.48**	-11.64**	0.96	30.07	7.57**	6.75**	1.46
21	Type-3xPSD-15	40.13	23.93**	19.33**	28.09**	32.70	14.80**	13.54**	10.35**
22	Type-3xPant Basmati-1	31.67	-8.65**	-17.10**	1.06	32.66	11.85**	8.03**	10.21**
23	Basmati-370xTarori Basmati-1	37.10	1.97	0.36	18.40**	26.03	-6.68**	-7.22**	-12.15**
24	Basmati-370xPSD-15	36.87	4.44**	-0.27	17.66**	33.07	16.31**	14.81**	11.59**
25	Basmati-370xPant Basmati-1	30.30	-19.38**	-20.68**	-3.30	34.47	18.25**	14.00**	16.31**
26	Tarori Basmati-1xPSD-15	41.07	18.29**	14.71**	31.06**	36.00	27.36**	25.00**	21.48**
27	Tarori Basmati-1xPant Basmati-1	35.63	-3.69**	-6.72**	13.72**	33.63	16.04**	11.25**	13.50**
28	PSD-15xPant Basmati-1	30.33	-15.55**	-20.59**	-3.19	36.07	22.19**	19.29**	21.71**

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check)=Standard heterosis over check

The range of heterosis over better parent for flag leaf length varied from -20.68% (Basmati-370×Pant Basmati-1) to 24.66% (Pusa Sugandh-6×Type-3). Among 28 crosses, 11 crosses showed significant positive heterosis and 10 crosses showed significant negative heterosis for flag leaf length over better parent. The maximum significant positive heterosis for flag leaf length over better parent was exhibited by Pusa Sugandh-6×Type-3 (24.66) followed by Type-3×PSD-15 (19.33), Tarori Basmati-1×PSD-15(14.71), Pusa Sugandh-4×Tarori Basmati-1 (15.08), Pusa Basmati-1×Pusa Sugandh-6 (14.50), Pusa Sugandh-6×Basmati-370 (9.74), Pusa Sugandh-4×Pusa Sugandh-6(8.25), Pusa Sugandh-4×Type-3 (7.71), Pusa Sugandh-6×Tarori Basmati-1 (5.03), Pusa Sugandh-4×PSD-15 (5.95) and Pusa Basmati-1×PSD-15 (4.46). The maximum significant negative heterosis for flag leaf length over better parent was exhibited by Basmati-370×Pant Basmati-1 (-20.68) followed by PSD-15×Pant Basmati-1 (-20.59), Type-3×Pant Basmati-1 (-17.10), Pusa Sugandh-4×Basmati-370 (-12.62), Type-3×Tarori Basmati-1 (-11.64), Pusa Basmati-1×Basmati-370 (-10.82), Type-3×Basmati-370 (-9.56), Tarori Basmati-1×Pant Basmati-1(-6.72), Pusa Basmati 1×Pant Basmati-1 (-5.41) and Pusa Basmati-1×Tarori Basmati-1(-3.17).

Range of heterosis for flag leaf length over standard check variety (Improved Pusa Basmati-1) varied from 5.21% (Pusa Basmati-1×Basmati-370) to 31.49% (Pusa Sugandh-4×Tarori Basmati-1). Among 28 crosses, 21 crosses showed significant positive heterosis for flag leaf length over standard check variety. The maximum significant positive heterosis over standard check was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (31.49) followed by Tarori Basmati-1×PSD-15 (31.06), Pusa Sugandh-6×Basmati-370 (29.47), Type-3×PSD-15 (28.09), Pusa Sugandh-6×Type-3 (25.32), Pusa Sugandh-4×Pant Basmati-1(24.26), Pusa Sugandh-6×Pant Basmati-1 (21.70), Pusa Sugandh-6×Tarori Basmati-1(20.00), Basmati-370×Tarori Basmati-1 (18.40), Basmati-370×PSD-15 (17.66), Pusa Basmati-1×Pant Basmati-1 (15.32), Pusa Basmati-1×Pusa Sugandh-6 (15.11), Tarori Basmati-1×Pant Basmati-1 (13.72), Pusa Sugandh-4×PSD-15 (13.72), Pusa Basmati-1×PSD-15 (12.13), Pusa Basmati-1×Tarori Basmati-1 (10.64), Pusa Sugandh-6×PSD-15 (10.53), Pusa Sugandh-4×Pusa Sugandh-6 (8.83), Pusa Sugandh-4×Type-3 (7.02), Type-3×Basmati-370 (6.70) and Pusa Basmati-1×Basmati-370 (5.21).

4.3.4 Panicle length (cm)

The range of heterosis over mid parent for panicle length varied from -6.68% (Basmati-370×Tarori Basmati-1) to 31.73% (Pusa Sugandh-4×Pant Basmati-1). Among 28 crosses 23 crosses showed significant positive heterosis while only one cross showed significant negative heterosis for panicle length over mid-parent. The maximum significant positive heterosis for panicle length over mid parent was exhibited by Pusa Sugandh-4×Pant Basmati-1 (31.73) followed by Tarori Basmati-1×PSD-15 (27.36), Pusa Basmati-1×Tarori Basmati-1 (25.20), Pusa Basmati-1×Pant Basmati-1 (22.41), Pusa Sugandh-6×Pant Basmati-1 22.64), PSD-15 x Pant Basmati-1 (22.19), Pusa Sugandh-6×Type-3 (20.89), Pusa Sugandh-6×Basmati-370 (20.76), Basmati-370×Pant Basmati-1 (18.25), Basmati-370×PSD-15 (16.31), Tarori Basmati-1×Pant Basmati-1 (16.04), Type-3×PSD-15 (14.80), Pusa Basmati-1×Type-3 (13.95), Pusa Basmati-1 × Basmati-370 (11.85), Type-3×Pant Basmati-1 (11.85), Pusa Sugandh-6×PSD-15 (9.95), Pusa Basmati-1×PSD-15 (8.59), Type-3×Tarori Basmati-1 (7.57), Pusa Sugandh-4×Type-3 (6.13), Pusa Sugandh-4×Pusa Sugandh-6 (5.90), Pusa Basmati-1×Pusa Sugandh-6 (5.61), Pusa Basmati-1×Pusa Sugandh-4 (5.16) and Pusa Sugandh-4×PSD-15 (4.18). The cross Basmati-370×Tarori Basmati-1 showed significant negative heterosis (-6.68) over mid parent for panicle length.

The range of heterosis over better parent for panicle length varied from -7.22% (Basmati-370×Tarori Basmati-1) to 29.99% (Pusa Sugandh-4×Pant Basmati-1). Among 28 crosses 21 crosses showed significant positive heterosis while 2 crosses showed significant +negative heterosis for panicle length over better parent. The maximum significant positive heterosis for panicle length over better parent was exhibited by Pusa Sugandh-4×Pant Basmati-1 (29.99) followed by Tarori Basmati-1×PSD-15 (25.00), Pusa Basmati-1×Tarori Basmati-1 (21.66), Pusa Basmati-1×Pant Basmati-1 (20.73), Pusa Sugandh-6×Pant Basmati-1(19.74), Pusa Sugandh-6×Type-3 (19.56), PSD-15 x Pant Basmati-1 (19.29), Pusa Sugandh-6×Basmati-370 (19.21), Basmati-370 ×PSD-15 (14.81), Basmati-370×Pant Basmati-1 (14.00), Type-3×PSD-15 (13.54), Pusa Basmati-1×Type-3 (11.56), Tarori Basmati-1×Pant Basmati-1 (11.25), Pusa Sugandh-6 ×PSD-15 (9.95), Pusa Basmati-1 × Basmati-370 (9.30), Type-3×Pant Basmati-1 (8.03), Pusa Basmati-1×PSD-15 (7.48), Type-3×Tarori Basmati-1 (6.75), Pusa Basmati-1 ×Pusa Sugandh-4 (5.10), Pusa Sugandh-4×Pusa Sugandh-6 (4.76) and Pusa Basmati-1

×Pusa Sugandh-6 (4.54). Maximum significant negative heterosis over better parent for panicle length was shown by cross Basmati-370×Tarori Basmati-1 (-7.22) and Pusa Sugandh-4×Tarori Basmati-1 (-4.64).

Range of heterosis for panicle length over standard check variety (Improved Pusa Basmati-1) varied from -12.15% (Basmati-370×Tarori Basmati-1) to 32.62% (Pusa Sugandh-4×Pant Basmati-1). Among 28 crosses, 17 crosses showed significant positive while 2 crosses showed significant negative heterosis for panicle length over standard check variety. The maximum significant positive heterosis for panicle length over standard check was exhibited by Pusa Sugandh-4×Pant Basmati-1 (32.62) followed by Pusa Basmati 1×Pant Basmati-1 (23.17), Pusa Sugandh-6×Pant Basmati-1 (22.16), PSD-15×Pant Basmati-1 (21.71), Tarori Basmati-1×PSD-15 (21.48), Pusa Basmati-1×Tarori Basmati-1 (20.70), Basmati-370×Pant Basmati-1 (16.31), Pusa Sugandh-6×Type-3 (16.20), Pusa Sugandh-6×Basmati-370 (15.86), Tarori Basmati-1×Pant Basmati-1 (13.50), Basmati-370×PSD-15 (11.59), Pusa Basmati-1×Type-3 (10.69), Type-3×PSD-15 (10.35), Type-3×Pant Basmati-1 (10.21), Pusa Basmati-1×Basmati-370 (8.44), Pusa Sugandh-6×PSD-15 (6.86) and Pusa Basmati-1×PSD-15 (6.64). Maximum significant negative heterosis over standard check for panicle length was shown by cross Basmati-370×Tarori Basmati-1 (-12.15) and Pusa Sugandh-4×Tarori Basmati-1 (-5.29).

4.3.5 Number of panicles per plant

The range of heterosis over mid parent for panicles/plant varied from 7.63% (Pusa Basmati-1×Tarori Basmati-1) to 100.00% (Type-3×PSD-15). Among 28 crosses, 27 crosses showed significant positive heterosis for panicles/plant over mid-parent. The maximum significant positive heterosis for panicles/plant over mid parent was exhibited by Type-3×PSD-15 (100.00) followed by Basmati-370×PSD-15 (91.09), Pusa Sugandh-6×Tarori Basmati-1 (78.64), Type-3×Pant Basmati-1 (71.17), Pusa Basmati-1×PSD-15 (63.51), Pusa Basmati-1×Pusa Sugandh-6 (61.21), Type-3×Tarori Basmati-1 (57.40), Basmati-370×Pant Basmati-1 (55.26), Basmati-370×Tarori Basmati-1 (55.29), Pusa Basmati-1×Type-3 (53.51), Pusa Sugandh-4×Pusa Sugandh-6 (52.51), Pusa Sugandh-6×PSD-15 (51.03), Pusa Sugandh-4×Type-3 (50.57), Pusa Basmati-1×Basmati-370 (49.63), PSD-15×Pant Basmati-1 (46.22), Tarori Basmati-1×PSD-15 (45.62), Pusa Sugandh-6×Basmati-370 (44.87), Pusa Basmati 1×Pant Basmati-1

Table 4.3.1: Continued.....

Sl. No	Crosses	Panicles/plant				Filled grains/panicle			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1×Pusa Sugandh-4	16.23	13.07**	2.44	22.67**	173.63	20.70**	11.02*	33.67**
2	Pusa Basmati-1×Pusa Sugandh-6	20.50	61.21**	59.33**	54.91**	198.33	37.08**	25.47**	52.68**
3	Pusa Basmati-1×Type-3	19.70	53.51**	53.11**	48.87**	166.47	20.41**	14.65**	28.15**
4	Pusa Basmati-1×Basmati-370	20.40	49.63**	41.67**	54.16**	187.53	38.10**	33.67**	44.37**
5	Pusa Basmati-1×Tarori Basmati-1	14.10	7.63**	5.75	6.55	154.23	21.92**	17.47**	18.73**
6	Pusa Basmati-1×PSD-15	20.17	63.51**	56.74**	52.39**	136.10	13.78*	3.66	4.77
7	Pusa Basmati-1×Pant Basmati-1	16.40	27.46**	27.46**	23.93**	145.33	7.07	3.69	11.88
8	Pusa Sugandh-4×Pusa Sugandh-6	21.67	52.51**	36.73**	63.73**	196.83	25.19**	24.53**	51.53**
9	Pusa Sugandh-4×Type-3	21.57	50.57**	36.10**	62.97**	177.47	17.68**	13.47**	36.62**
10	Pusa Sugandh-4×Basmati-370	18.67	23.43**	17.80**	41.06**	177.07	19.36**	13.21*	36.31**
11	Pusa Sugandh-4×Tarori Basmati-1	15.80	8.29**	-0.29	19.40**	173.93	25.09**	11.21*	33.90**
12	Pusa Sugandh-4×PSD-15	15.07	8.99*	-4.92	13.85**	187.53	41.89**	19.91**	44.37**
13	Pusa Sugandh-4×Pant Basmati-1	18.10	26.07**	14.22**	36.78*	137.81	-7.06	-11.89*	6.09
14	Pusa Sugandh-6×Type-3	15.20	19.84**	18.75**	14.86**	184.67	21.79**	16.83**	42.16**
15	Pusa Sugandh-6×Basmati-370	19.53	44.87**	35.65**	47.61**	183.40	22.94**	16.03**	41.19**
16	Pusa Sugandh-6×Tarori Basmati-1	23.13	78.64**	73.50**	74.81**	184.33	31.78**	16.62**	41.90**
17	Pusa Sugandh-6×PSD-15	18.40	51.03**	46.42**	39.04**	171.30	28.80**	8.37	31.87**
18	Pusa Sugandh-6×Pant Basmati-1	15.23	19.79**	18.39**	15.11**	148.87	-0.17	-5.82	14.60*
19	Type-3×Basmati-370	13.70	0.74	-4.86	3.53	178.57	25.09**	22.98**	37.46**
20	Type-3×Tarori Basmati-1	20.57	57.40**	54.25**	55.42**	171.77	28.71**	18.30**	32.23**
21	Type-3×PSD-15	24.60	100.00**	92.19**	85.89**	143.57	13.43*	-1.12	10.52
22	Type-3×Pant Basmati-1	21.97	71.17**	70.73*	65.99**	181.87	27.46**	25.25**	40.01**
23	Basmati-370×Tarori Basmati-1	21.53	55.29**	49.54**	62.72**	181.67	38.68**	29.48**	39.85**
24	Basmati-370×PSD-15	25.03	91.09**	73.84**	89.17**	163.60	31.81**	16.61**	25.94**
25	Basmati-370×Pant Basmati-1	21.17	55.26**	46.99**	59.95**	167.17	19.21**	19.15**	28.69**
26	Tarori Basmati-1×PSD-15	18.30	45.62**	37.25**	38.29**	158.70	38.22**	30.40**	22.17**
27	Tarori Basmati-1×Pant Basmati-1	14.57	11.20**	9.25*	10.08*	161.60	23.42**	15.29**	24.40**
28	PSD-15×Pant Basmati-1	18.03	46.22**	40.16**	36.27**	143.63	15.79**	2.47	10.57

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check)=Standard heterosis over check

(27.46), Pusa Sugandh-4×Pant Basmati-1 (26.07), Pusa Sugandh-4×Basmati-370 (23.43), Pusa Sugandh-6×Type-3 (19.84), Pusa Sugandh-6×Pant Basmati-1 (19.79), Pusa Basmati-1×Pusa Sugandh-4 (13.07), Tarori Basmati-1×Pant Basmati-1 (11.20), Pusa Sugandh-4×PSD-15 (8.99), Pusa Sugandh-4×Tarori Basmati-1 (8.29) and Pusa Basmati-1×Tarori Basmati-1 (7.63).

The range of heterosis over better parent for panicles/plant varied from 9.25% (Tarori Basmati-1×Pant Basmati-1) to 92.19% (Type-3×PSD-15). Among 28 crosses 23 crosses showed significant positive heterosis for panicles/plant over better parent. The maximum significant positive heterosis for panicles/plant over better parent was exhibited by Type-3×PSD-15 (92.19) followed by Basmati-370×PSD-15 (73.84), Pusa Sugandh-6×Tarori Basmati-1 (73.50), Type-3×Pant Basmati-1 (70.73), Pusa Basmati-1×Pusa Sugandh-6 (59.33), Pusa Basmati-1×PSD-15 (56.74), Type-3×Tarori Basmati-1 (54.25), Pusa Basmati-1×Type-3 (53.11), Basmati-370×Tarori Basmati-1 (49.54), Basmati-370×Pant Basmati-1 (46.99), Pusa Sugandh-6×PSD-15 (46.42), Pusa Basmati-1×Basmati-370 (41.67), PSD-15×Pant Basmati-1 (40.16), Tarori Basmati-1×PSD-15 (37.25), Pusa Sugandh-4×Pusa Sugandh-6 (36.73), Pusa Sugandh-4×Type-3 (36.10), Pusa Sugandh-6×Basmati-370 (35.65), Pusa Basmati 1×Pant Basmati-1 (27.46), Pusa Sugandh-6×Type-3 (18.75), Pusa Sugandh-6×Pant Basmati-1 (18.39), Pusa Sugandh-4×Basmati-370 (17.80), Pusa Sugandh-4×Pant Basmati-1 (14.22) and Tarori Basmati-1×Pant Basmati-1 (9.25).

Range of heterosis for panicles/plant over standard check variety (Improved Pusa Basmati-1) varied from 10.08% (Tarori Basmati-1×Pant Basmati-1) to 89.17% (Basmati-370×PSD-15). Among 28 crosses, 26 crosses showed significant positive heterosis for panicles/plant over standard check variety. The maximum significant positive heterosis for panicles/plant over standard check was exhibited by Basmati-370×PSD-15 (89.17) followed by Type-3×PSD-15 (85.89), Pusa Sugandh-6×Tarori Basmati-1 (74.81), Type-3×Pant Basmati-1 (65.99), Basmati-370×Tarori Basmati-1 (62.72), Pusa Sugandh-4×Pusa Sugandh-6 (63.73), Pusa Sugandh-4×Type-3 (62.97), Basmati-370×Pant Basmati-1 (59.95), Type-3×Tarori Basmati-1 (55.42), Pusa Basmati-1×Pusa Sugandh-6 (54.91), Pusa Basmati-1×Basmati-370 (54.16), Pusa Basmati-1×PSD-15 (52.39), Pusa Basmati-1×Type-3 (48.87), Pusa Sugandh-6×Basmati-370 (47.61), Pusa Sugandh-4×Basmati-370 (41.06), Pusa Sugandh-6×PSD-15 (39.04),

Tarori Basmati-1×PSD-15 (38.29), Pusa Sugandh-4×Pant Basmati-1 (36.78), PSD-15 ×Pant Basmati-1 (36.27), Pusa Basmati-1×Pant Basmati-1 (23.93), Pusa Basmati-1 ×Pusa Sugandh-4 (22.67), Pusa Sugandh-4×Tarori Basmati-1 (19.40), Pusa Sugandh-6 ×Pant Basmati-1 (15.11), Pusa Sugandh-6×Type-3 (14.86), Pusa Sugandh-4×PSD-15 (13.85) and Tarori Basmati-1×Pant Basmati-1 (10.08).

4.3.6 Number of filled grains per panicle

The range of heterosis over mid parent for filled grains/panicle varied from 13.43% (Pusa Basmati-1×Tarori Basmati-1) to 41.89% (Pusa Sugandh-4×PSD-15). Among 28 crosses 25 crosses showed significant positive heterosis for filled grains/panicle over mid-parent. The maximum significant positive heterosis for filled grains/panicle over mid parent was exhibited by Pusa Sugandh-4×PSD-15 (41.89) followed by Basmati-370×Tarori Basmati-1 (38.68), Tarori Basmati-1×PSD-15 (38.22), Pusa Basmati-1×Basmati-370 (38.10), Pusa Basmati-1×Pusa Sugandh-6 (37.08), Pusa Sugandh-6×Tarori Basmati-1 (31.78), Basmati-370×PSD-15 (31.81), Pusa Sugandh-6×PSD-15 (28.80), Type-3×Tarori Basmati-1 (28.71), Type-3×Pant Basmati-1 (27.46), Pusa Sugandh-4×Pusa Sugandh-6 (25.19), Type-3×Basmati-370 (25.09), Pusa Sugandh-4×Tarori Basmati-1 (25.09), Tarori Basmati-1×Pant Basmati-1 (23.42), Pusa Sugandh-6×Basmati-370 (22.94), Pusa Basmati-1×Tarori Basmati-1 (21.92), Pusa Sugandh-6×Type-3 (21.79), Pusa Basmati-1×Pusa Sugandh-4 (20.70), Pusa Basmati-1×Type-3 (20.41), Pusa Sugandh-4×Basmati-370 (19.36), Basmati-370 ×Pant Basmati-1 (19.21), Pusa Sugandh-4×Type-3 (17.68), PSD-15 x Pant Basmati-1 (15.79), Pusa Basmati-1×PSD-15 (13.78), and Type-3×PSD-15 (13.43).

The range of heterosis over better parent for filled grains/panicle varied from -11.89% (Pusa Sugandh-4×Pant Basmati-1) to 33.67% (Pusa Basmati-1 × Basmati-370). Among 28 crosses 21 crosses showed significant positive heterosis while one cross showed significant negative heterosis for filled grains/panicle over better parent. The maximum significant positive heterosis for filled grains/panicle over better parent was exhibited by Pusa Basmati-1×Basmati-370 (33.67) followed by Tarori Basmati-1×PSD-15 (30.40), Basmati-370×Tarori Basmati-1 (29.48), Pusa Basmati-1×Pusa Sugandh-6 (25.47), Type-3×Pant Basmati-1 (25.25), Pusa Sugandh-4×Pusa Sugandh-6 (24.53), Type-3×Basmati-370 (22.98), Pusa Sugandh-4×PSD-15 (19.91), Basmati-370×Pant Basmati-1 (19.15), Type-3×Tarori Basmati-1 (18.30), Pusa Basmati-1×Tarori Basmati-1

(17.47), Pusa Sugandh-6×Type-3 (16.83), Pusa Sugandh-6×Tarori Basmati-1 (16.62), Basmati-370×PSD-15 (16.61), Pusa Sugandh-6×Basmati-370 (16.03), Tarori Basmati-1×Pant Basmati-1 (15.29), Pusa Basmati-1×Type-3 (14.65), Pusa Sugandh-4×Type-3 (13.47), Pusa Sugandh-4×Basmati-370 (13.21), Pusa Sugandh-4×Tarori Basmati-1 (11.21) and Pusa Basmati-1×Pusa Sugandh-4 (11.02). Cross Pusa Sugandh-4×Pant Basmati-1 showed significant negative heterosis (-11.89) for grains/panicle over better parent.

Range of heterosis for filled grains/panicle over standard check variety (Improved Pusa Basmati-1) varied from 14.60% (Pusa Sugandh-6×Pant Basmati-1) to 52.68% (Pusa Basmati-1×Pusa Sugandh-6). Among 28 crosses, 23 crosses showed significant positive heterosis for filled grains/panicle over standard check variety. The maximum significant positive heterosis for filled grains/panicle over standard check was exhibited by Pusa Basmati-1×Pusa Sugandh-6 (52.68) followed by Pusa Sugandh-4×Pusa Sugandh-6 (51.53), Pusa Basmati-1×Basmati-370 (44.37), Pusa Sugandh-4×PSD-15 (44.37), Pusa Sugandh-6×Type-3 (42.16), Pusa Sugandh-6×Tarori Basmati-1 (41.90), Pusa Sugandh-6×Basmati-370 (41.19), Type-3×Pant Basmati-1 (40.01), Basmati-370×Tarori Basmati-1 (39.85), Type-3×Basmati-370 (37.46), Pusa Sugandh-4×Type-3 (36.62), Pusa Sugandh-4×Basmati-370 (36.31), Pusa Sugandh-4×Tarori Basmati-1 (33.90), Pusa Basmati-1×Pusa Sugandh-4 (33.67), Type-3×Tarori Basmati-1 (32.23), Pusa Sugandh-6×PSD-15 (31.87), Basmati-370×Pant Basmati-1 (28.69), Pusa Basmati-1×Type-3 (28.15), Basmati-370×PSD-15 (25.94), Tarori Basmati-1×Pant Basmati-1 (24.40), Tarori Basmati-1×PSD-15 (22.17), Pusa Basmati-1×Tarori Basmati-1 (18.73) and Pusa Sugandh-6×Pant Basmati-1 (14.60).

4.3.7 Number of unfilled grains per panicle

The range of heterosis over mid parent for unfilled grains/panicle varied from -36.09% (Pusa Sugandh-6×Basmati-370) to 35.86% (Type-3×PSD-15). Among 28 crosses 2 crosses showed significant positive heterosis while 23 cross showed significant negative heterosis for unfilled grains/panicle over mid parent. The maximum significant positive heterosis for unfilled grains/panicle over mid parent was exhibited by Type-3×PSD-15 (33.67) and followed by Type-3×Tarori Basmati-1 (9.90). The maximum negative heterosis for unfilled grains/panicle over mid parent was exhibited by Pusa Sugandh-6×Basmati-370 (-36.09) followed by PSD-15×

Pant Basmati-1 (-34.48), Pusa Sugandh-4×Pant Basmati-1 (-32.91), Pusa Sugandh-4×Type-3 (-32.02), Pusa Basmati 1×Pant Basmati-1 (-31.87), Pusa Sugandh-6×Pant Basmati-1 (-30.04), Pusa Sugandh-6×PSD-15(-27.92), Pusa Sugandh-6×Type-3 (-26.97), Basmati-370×Pant Basmati-1 (-24.59), Pusa Sugandh-4×Pusa Sugandh-6 (-23.54), Pusa Sugandh-6×Tarori Basmati-1 (-21.53), Pusa Sugandh-4×Basmati-370 (-19.25), Pusa Basmati-1×Pusa Sugandh-6 (-19.00), Pusa Sugandh-4×Tarori Basmati-1 (-16.71), Pusa Basmati-1×Basmati-370 (-16.69), Type-3×Pant Basmati-1(-16.33), Tarori Basmati-1×Pant Basmati-1 (-14.50), Pusa Basmati-1×Pusa Sugandh-4 (-13.11), Tarori Basmati-1×PSD-15 (-12.19), Pusa Sugandh-4×PSD-15 (-11.20), Pusa Basmati-1×PSD-15 (-10.82), Basmati-370×Tarori Basmati-1 (-9.78) and Type-3×Basmati-370 (-8.74).

The range of heterosis over better parent for unfilled grains/panicle varied from -31.41% (Pusa Sugandh-6×Basmati-370) to 45.29% (Type-3×PSD-15). Among 28 crosses, 3 crosses showed significant positive heterosis while 14 crosses showed significant negative heterosis for number of unfilled grains/panicle over better parent. The maximum significant positive heterosis for unfilled grains/panicle over better parent was exhibited by Type-3×PSD-15 (45.29) followed by Type-3×Tarori Basmati-1 (24.82) and Basmati-370×PSD-15 (7.36). The maximum negative heterosis for unfilled grains/panicle over better parent was exhibited by Pusa Sugandh-6×Basmati-370 (-31.41) followed by Pusa Sugandh-4×Pant Basmati-1 (-30.48), Pusa Sugandh-6×Pant Basmati-1 (-29.74), Pusa Sugandh-4×Type-3 (-27.51), PSD-15×Pant Basmati-1 (-23.31), Pusa Sugandh-4×Pusa Sugandh-6 (-21.08), Pusa Basmati 1×Pant Basmati-1 (-20.59), Pusa Sugandh-6×Type-3 (-19.79), Basmati-370×Pant Basmati-1(-18.75), Pusa Sugandh-6×PSD-15 (-15.91), Pusa Sugandh-4×Basmati-370 (-15.91), Pusa Basmati-1×PSD-15 (-10.36), Pusa Basmati-1×Basmati-370 (-9.25) and Type-3×Pant Basmati-1 (-7.76).

Range of heterosis for unfilled grains/panicle over standard check variety (Improved Pusa Basmati-1) varied from -10.13% (Tarori Basmati-1×PSD-15) to 59.79% (Type-3×PSD-15). Among 28 crosses, 14 crosses showed significant positive and one cross showed significant negative heterosis for unfilled grains/panicle over standard check variety. The maximum significant positive heterosis for unfilled grains/panicle over standard check was exhibited by Type-3×PSD-15 (59.79) followed

Table 4.3.1: Contd.....

Sl. No	Crosses	Unfilled grains/panicle				Spikelet fertility (%)			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1xPusa Sugandh-4	51.47	-13.11**	-1.81	16.70**	77.08	5.08**	3.89**	3.24*
2	Pusa Basmati-1xPusa Sugandh-6	51.17	-19.00**	-5.91	16.02**	79.49	9.15**	7.12**	6.46**
3	Pusa Basmati-1xType-3	51.40	-0.90	5.47	16.55**	76.39	3.32**	2.95*	2.31
4	Pusa Basmati-1xBasmati-370	45.43	-16.69**	-9.25**	3.02	80.48	10.12**	8.47**	7.79**
5	Pusa Basmati-1xTarori Basmati-1	41.57	-8.85	-2.27	-5.74	78.76	5.23**	4.32**	5.49**
6	Pusa Basmati-1xPSD-15	40.67	-10.82*	-10.36**	-7.79	77.03	6.48**	3.81**	3.17*
7	Pusa Basmati-1xPant Basmati-1	43.40	-31.87**	-20.59**	-1.59	76.98	7.73**	3.75**	3.10*
8	Pusa Sugandh-4xPusa Sugandh-6	48.30	-23.54**	-21.08**	9.52*	80.28	11.53**	10.71**	7.53**
9	Pusa Sugandh-4xType-3	40.27	-32.02**	-27.51**	-8.69	81.49	11.49**	10.62**	9.14**
10	Pusa Sugandh-4xBasmati-370	47.83	-19.25**	-15.91**	8.47	78.73	8.98**	8.57**	5.45**
11	Pusa Sugandh-4xTarori Basmati-1	49.33	-16.71**	-0.03	11.87*	77.90	5.27**	3.19*	4.34**
12	Pusa Sugandh-4xPSD-15	52.60	-11.20**	0.80	19.27**	78.01	9.11**	7.58**	4.49**
13	Pusa Sugandh-4xPant Basmati-1	42.73	-32.91**	-30.48**	-3.10	76.27	8.01**	5.18**	2.15
14	Pusa Sugandh-6xType-3	46.13	-26.97**	-19.79**	4.61	79.99	10.25**	8.59**	7.14**
15	Pusa Sugandh-6xBasmati-370	40.37	-36.09**	-31.41**	-8.47	81.95	14.27**	13.85**	9.76**
16	Pusa Sugandh-6xTarori Basmati-1	49.57	-21.53**	-3.41	12.40**	78.78	7.22**	4.35**	5.51**
17	Pusa Sugandh-6xPSD-15	45.53	-27.92**	-15.91**	3.25	78.97	11.28**	10.52**	5.77**
18	Pusa Sugandh-6xPant Basmati-1	44.57	-30.04**	-29.74**	1.06	76.93	9.78**	7.67**	3.04*
19	Type-3xBasmati-370	49.77	-8.74*	-6.45	12.85**	78.18	7.36**	6.13**	4.71**
20	Type-3xTarori Basmati-1	57.00	9.90*	24.82**	29.25**	75.12	0.72	-0.50	0.61
21	Type-3xPSD-15	70.47	35.86**	45.29**	59.79**	66.95	-7.11 **	-9.12**	-10.33**
22	Type-3xPant Basmati-1	53.30	-16.33**	-7.76*	20.86**	77.30	8.58**	4.93**	3.53*
23	Basmati-370xTarori Basmati-1	49.20	-9.78**	4.68	11.56*	78.69	6.72**	4.23**	5.39**
24	Basmati-370xPSD-15	53.50	-1.89	7.36*	21.32**	75.34	5.77**	4.67**	0.91
25	Basmati-370xPant Basmati-1	48.03	-24.59 **	-18.75**	8.92	77.64	10.36**	7.86**	3.98 **
26	Tarori Basmati-1xPSD-15	39.63	-12.19**	-6.30	-10.13*	79.99	9.59**	5.95**	7.13 **
27	Tarori Basmati-1xPant Basmati-1	54.47	-14.50**	5.59	23.51**	74.81	3.75**	-0.91	0.19
28	PSD-15xPant Basmati-1	41.73	-34.48**	-23.31**	-5.37	77.53	11.39**	10.00**	3.83 **

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check)=Standard heterosis over check

by Type-3×Tarori Basmati-1 (29.25), Tarori Basmati-1×Pant Basmati-1 (23.51), Basmati-370×PSD-15 (21.32), Type-3×Pant Basmati-1 (20.86 Pusa Sugandh-4×PSD-15 (19.27), Pusa Basmati-1×Pusa Sugandh-4 (16.70), Pusa Basmati-1×Type-3 (16.55), Pusa Basmati-1×Pusa Sugandh-6 (16.02), Type-3×Basmati-370 (12.85), Pusa Sugandh-6×Tarori Basmati-1 (12.40), Pusa Sugandh-4×Tarori Basmati-1 (11.87), Basmati-370×Tarori Basmati-1 (11.56) and Pusa Sugandh-4×Pusa Sugandh-6 (9.52). The cross Tarori Basmati-1×PSD-15 showed significant negative heterosis (-10.13) for unfilled grains/panicle over standard check variety.

4.3.8 Spikelet fertility (%)

The range of heterosis over mid parent for spikelet fertility varied from -7.11% (Type-3×PSD-15) to 14.27% (Pusa Sugandh-6×Basmati-370). Among 28 crosses 26 crosses showed significant positive heterosis while one cross showed significant negative heterosis for spikelet fertility over mid-parent. The maximum significant positive heterosis for spikelet fertility over mid parent was exhibited by Pusa Sugandh-6×Basmati-370 (14.27) followed by Pusa Sugandh-4×Pusa Sugandh-6 (11.53), Pusa Sugandh-4×Type-3 (11.49), PSD-15×Pant Basmati-1(11.39), Pusa Sugandh-6×PSD-15 (11.28), Pusa Basmati-1×Basmati-370 (10.12), Pusa Sugandh-6×Type-3 (10.25), Basmati-370×Pant Basmati-1(10.36), Pusa Sugandh-6×Pant Basmati-1 (9.78), Tarori Basmati-1×PSD-15(9.59), Pusa Sugandh-4×PSD-15 (9.11), Pusa Basmati-1×Pusa Sugandh-6 (9.15), Pusa Sugandh-4×Basmati-370 (8.98), Type-3×Pant Basmati-1 (8.58), Pusa Sugandh-4×Pant Basmati-1 (8.01), Pusa Basmati 1×Pant Basmati-1 (7.73), Type-3×Basmati-370(7.36), Pusa Sugandh-6×Tarori Basmati-1(7.22), Basmati-370×Tarori Basmati-1 (6.72), Pusa Basmati-1×PSD-15 (6.48), Basmati-370×PSD-15 (5.77), Pusa Sugandh-4×Tarori Basmati-1 (5.27), Pusa Basmati-1×Tarori Basmati-1 (5.23), Pusa Basmati-1×Pusa Sugandh-4 (5.08), Tarori Basmati-1×Pant Basmati-1 (3.75) and Pusa Basmati-1×Type-3 (3.32). The maximum significant negative heterosis for spikelet fertility over mid parent (-7.11%) was exhibited by Type-3×PSD-15.

The range of heterosis over better parent for spikelet fertility varied from -9.12% (Type-3×PSD-15) to 13.85% (Pusa Sugandh-6×Basmati-370). Among 28 crosses, 25 crosses showed significant positive heterosis while one cross showed significant negative heterosis for spikelet fertility over better parent. The maximum significant

positive heterosis for spikelet fertility over better parent was exhibited by Pusa Sugandh-6×Basmati-370 (13.85) and followed by Pusa Sugandh-4×Pusa Sugandh-6 (10.71), Pusa Sugandh-4×Type-3 (10.62), Pusa Sugandh-6×PSD-15 (10.52), PSD-15 x Pant Basmati-1 (10.00), Pusa Sugandh-6×Type-3 (8.59), Pusa Sugandh-4×Basmati-370 (8.57), Pusa Basmati-1×Basmati-370 (8.47), Basmati-370×Pant Basmati-1 (7.86), Pusa Sugandh-6×Pant Basmati-1 (7.67), Pusa Sugandh-4×PSD-15 (7.58), Pusa Basmati-1 ×Pusa Sugandh-6 (7.12), Type-3×Basmati-370 (6.13), Tarori Basmati-1×PSD-15 (5.95), Pusa Sugandh-4×Pant Basmati-1 (5.18), Type-3×Pant Basmati-1 (4.93), Basmati-370×PSD-15 (4.67), Pusa Sugandh-6×Tarori Basmati-1 (4.35), Pusa Basmati-1 ×Tarori Basmati-1 (4.32), Basmati-370×Tarori Basmati-1 (4.23), Pusa Basmati-1×Pusa Sugandh-4 (3.89), Pusa Basmati-1×PSD-15 (3.81), Pusa Basmati 1 × Pant Basmati-1 (3.75), Pusa Sugandh-4×Tarori Basmati-1 (3.19) and Pusa Basmati-1×Type-3 (2.95). The cross Type-3×PSD-15 showed significant negative heterosis (-9.12) for spikelet fertility over better parent.

Range of heterosis for spikelet fertility over standard check variety (Improved Pusa Basmati-1) varied from -10.33% (Type-3×PSD-15) to 9.76% (Type-3×PSD-15). Among 28 crosses, 22 crosses showed significant positive and one cross showed significant negative heterosis for spikelet fertility over standard check variety. The maximum significant positive heterosis for spikelet fertility over standard check was exhibited by Type-3×PSD-15 (9.76) followed by Pusa Sugandh-4×Type-3(9.14), Pusa Basmati-1×Basmati-370(7.79), Pusa Sugandh-4×Pusa Sugandh-6 (7.53), Pusa Sugandh-6×Type-3 (7.14), Tarori Basmati-1×PSD-15 (7.13), Pusa Basmati-1×Pusa Sugandh-6 (6.46), Pusa Sugandh-6×PSD-15 (5.77), Pusa Sugandh-6×Tarori Basmati-1 (5.51), Pusa Basmati-1×Tarori Basmati-1 (5.49), Pusa Sugandh-4×Basmati-370 (5.45), Basmati-370×Tarori Basmati-1(5.39), Type-3×Basmati-370 (4.71), Pusa Sugandh-4×PSD-15 (4.49), Pusa Sugandh-4×Tarori Basmati-1 (4.34), Basmati-370×Pant Basmati-1 (3.98), PSD-15×Pant Basmati-1 (3.83), Type-3×Pant Basmati-1 (3.53), Pusa Basmati-1×Pusa Sugandh-4 (3.24), Pusa Basmati-1×PSD-15 (3.17), Pusa Basmati 1×Pant Basmati-1 (3.10) and Pusa Sugandh-6×Pant Basmati-1 (3.04). The cross Type-3×PSD-15 showed significant negative heterosis (-10.33) for spikelet fertility over standard check variety.

4.3.9 Test weight (g)

The range of heterosis over mid parent for test weight varied from 5.13% (Pusa Sugandh-4×Type-3) to 26.94% (Basmati-370×Pant Basmati-1). Among 28 crosses 18 crosses showed significant positive heterosis for test weight over mid-parent. The maximum significant positive heterosis for test weight over mid parent was exhibited by Basmati-370×Pant Basmati-1 (26.94) followed by Pusa Basmati-1×PSD-15 (18.21), Pusa Sugandh-4×PSD-15 (16.42), Type-3×Pant Basmati-1 (16.40), Pusa Sugandh-6×Type-3 (14.83), Pusa Sugandh-6×Basmati-370 (14.49), Pusa Basmati-1×Basmati-370 (14.46), Basmati-370×Tarori Basmati-1 (13.38), Pusa Sugandh-4×Basmati-370 (12.56), Pusa Basmati-1×Pusa Sugandh-6 (12.47), Tarori Basmati-1×Pant Basmati-1 (11.13), Basmati-370 ×PSD-15 (10.18), Pusa Sugandh-6×PSD-15 (10.42), Pusa Basmati-1×Pusa Sugandh-4 (8.92), Type-3×Tarori Basmati-1 (8.02), PSD-15×Pant Basmati-1 (7.35), Tarori Basmati-1×PSD-15 (5.53) and Pusa Sugandh-4×Type-3 (5.13).

The range of heterosis over better parent for test weight varied from -8.88% (Pusa Sugandh-4×Tarori Basmati-1) to 17.01% (Basmati-370×Pant Basmati-1). Among 28 crosses 5 crosses showed significant positive heterosis while 3 crosses showed significant negative heterosis for test weight over better parent. The maximum significant positive heterosis for test weight over better parent was exhibited by Basmati-370×Pant Basmati-1 (17.01) and followed by Pusa Basmati-1×PSD-15 (15.24), Pusa Basmati-1×Basmati-370 (9.37), Type-3×Pant Basmati-1 (10.52) and Tarori Basmati-1×Pant Basmati-1 (6.16). The maximum significant negative heterosis for test weight over better parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-8.88) and followed by Pusa Sugandh-4×Type-3 (-8.60) and Pusa Sugandh-4×Pant Basmati-1 (-6.42).

Range of heterosis for number of test weight over standard check variety (Improved Pusa Basmati-1) varied from -8.32% (Type-3×Basmati-370) to 33.77% (Pusa Sugandh-4×PSD-15). Among 28 crosses, 22 crosses showed significant positive and one cross showed significant negative heterosis for test weight over standard check variety. The maximum significant positive heterosis for test weight over standard check was exhibited by Pusa Sugandh-4×PSD-15 (33.77) followed by Basmati-370×Pant Basmati-1 (22.71), Pusa Basmati-1×Pusa Sugandh-4 (22.35), Tarori Basmati-1×Pant Basmati-1 (22.27), Pusa Sugandh-6×Type-3 (22.16), Pusa Sugandh-6×PSD-15 (21.87),

Table 4.3.1: Contd.....

Sl. No	Crosses	Test weight (g)				Grain yield/plant (g)			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1.	Pusa Basmati-1xPusa Sugandh-4	26.04	8.92**	-4.09	22.35**	25.34	22.21**	17.14*	17.10*
2	Pusa Basmati-1xPusa Sugandh-6	25.80	12.47**	2.31	21.24**	42.38	77.79**	52.23**	95.87**
3	Pusa Basmati-1xType-3	21.32	4.72	3.19	0.20	35.64	40.01**	14.68**	64.72**
4	Pusa Basmati-1xBasmati-370	22.60	14.46**	9.37**	6.20	45.01	103.04**	83.70**	108.01**
5	Pusa Basmati-1xTarori Basmati-1	23.14	2.46	-5.58	8.76**	28.23	48.62**	42.34**	30.47**
6	Pusa Basmati-1xPSD-15	25.07	18.21**	15.24**	17.83**	54.36	123.64**	88.87**	151.26**
7	Pusa Basmati-1xPant Basmati-1	21.65	0.76	-2.97	1.75	33.11	74.48**	66.94**	53.03**
8	Pusa Sugandh-4xPusa Sugandh-6	25.93	-0.96	-4.48	21.85**	39.64	60.26**	42.39**	83.21**
9	Pusa Sugandh-4xType-3	24.81	5.13*	-8.60**	16.60**	38.71	46.90**	24.57**	78.92**
10	Pusa Sugandh-4xBasmati-370	25.87	12.56**	-4.69	21.59**	45.96	99.25**	87.58**	112.40**
11	Pusa Sugandh-4xTarori Basmati-1	24.74	-4.23	-8.88**	16.24**	35.95	80.70**	66.19**	66.14**
12	Pusa Sugandh-4xPSD-15	28.47	16.42**	4.86	33.77**	30.53	21.13**	6.08	41.12**
13	Pusa Sugandh-4xPant Basmati-1	25.40	2.72	-6.42*	19.38**	37.08	86.57**	71.43**	71.38**
14	Pusa Sugandh-6xType-3	26.00	14.83**	3.09	22.16**	46.74	58.66**	50.40**	116.02**
15	Pusa Sugandh-6xBasmati-370	25.21	14.49**	-0.01	18.48**	48.65	85.90**	74.75**	124.85**
16	Pusa Sugandh-6xTarori Basmati-1	24.56	-1.23	-2.62	15.40**	33.85	47.18**	21.59**	56.45**
17	Pusa Sugandh-6xPSD-15	25.93	10.42**	2.84	21.87**	63.58	124.58**	120.90**	193.87**
18	Pusa Sugandh-6xPant Basmati-1	24.79	4.32	-1.68	16.51**	33.88	47.43**	21.70**	56.59**
19	Type-3xBasmati-370	19.51	0.34	-2.74	-8.32*	27.60	-0.69	-11.20*	27.55**
20	Type-3xTarori Basmati-1	24.07	8.02**	-1.78	13.13**	33.30	35.26**	7.14	53.89**
21	Type-3xPSD-15	21.83	4.41	0.34	2.58	41.53	38.77**	33.65**	91.96**
22	Type-3xPant Basmati-1	24.66	16.40**	10.52**	15.90**	33.02	34.22**	6.24	52.60**
23	Basmati-370xTarori Basmati-1	24.57	13.38**	0.23	15.44**	31.85	49.33**	30.00**	47.20**
24	Basmati-370xPSD-15	22.36	10.18**	2.76	5.06	43.82	64.47**	52.23**	102.51**
25	Basmati-370xPant Basmati-1	26.11	26.94**	17.01**	22.71**	31.63	48.41**	29.09**	46.17**
26	Tarori Basmati-1xPSD-15	24.41	5.53*	-0.39	14.72**	30.98	31.98**	7.62	43.17**
27	Tarori Basmati-1xPant Basmati-1	26.02	11.13**	6.16**	22.27**	33.00	81.92**	81.73**	52.50**
28	PSD-15xPant Basmati-1	23.66	7.35**	6.00	11.17**	34.58	47.45**	20.14**	59.82**

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check)=Standard heterosis over check

Pusa Sugandh-4×Pusa Sugandh-6 (21.85), Pusa Sugandh-4×Basmati-370 (21.59), Pusa Basmati-1×Pusa Sugandh-6 (21.24), Pusa Sugandh-4×Pant Basmati-1(19.38), Pusa Sugandh-6×Basmati-370 (18.48), Pusa Basmati-1×PSD-15 (17.83), Pusa Sugandh-4×Type-3 (16.60), Pusa Sugandh-6×Pant Basmati-1(16.51), Pusa Sugandh-4×Tarori Basmati-1 (16.24), Pusa Sugandh-6×Tarori Basmati-1(15.40), Type-3×Pant Basmati-1 (15.90), Basmati-370×Tarori Basmati-1 (15.44), Tarori Basmati-1×PSD-15 (14.72), Type-3×Tarori Basmati-1 (13.13), PSD-15×Pant Basmati-1 (11.17) and Pusa Basmati-1×Tarori Basmati-1(8.76). The cross Type-3×Basmati-370 (-8.32) showed significant negative heterosis for test weight over standard check.

4.3.10 Grain yield per plant (g)

The range of heterosis over mid parent for grain yield/plant varied from 21.13% (Pusa Sugandh-4×PSD-15) to 124.58% (Pusa Sugandh-6×PSD-15). Among 28 crosses 27 crosses showed significant positive heterosis for grain yield/plant over mid-parent. The maximum significant positive heterosis for grain yield/plant over mid parent was exhibited by Pusa Sugandh-6×PSD-15 (124.58) followed by Pusa Basmati-1×PSD-15 (123.64), Pusa Basmati-1×Basmati-370 (103.04), Pusa Sugandh-4×Basmati-370 (99.25), Pusa Sugandh-4×Pant Basmati-1 (86.57), Pusa Sugandh-6×Basmati-370 (85.9), Tarori Basmati-1×Pant Basmati-1 (81.92), Pusa Sugandh-4×Tarori Basmati-1 (80.7), Pusa Basmati-1×Pusa Sugandh-6 (77.79), Pusa Basmati 1×Pant Basmati-1 (74.48), Basmati-370×PSD-15 (64.47), Pusa Sugandh-4×Pusa Sugandh-6 (60.26), Pusa Sugandh-6×Type-3 (58.66), Basmati-370×Tarori Basmati-1 (49.33), Pusa Basmati-1×Tarori Basmati-1 (48.62), Basmati-370×Pant Basmati-1 (48.41), PSD-15×Pant Basmati-1 (47.45), Pusa Sugandh-6×Pant Basmati-1 (47.43), Pusa Sugandh-6×Tarori Basmati-1 (47.18), Pusa Sugandh-4×Type-3 (46.9), Pusa Basmati-1×Type-3 (40.01), Type-3×PSD-15 (38.77), Type-3×Tarori Basmati-1 (35.26), Type-3×Pant Basmati-1 (34.22), Tarori Basmati-1×PSD-15 (31.98), Pusa Basmati-1×Pusa Sugandh-4 (22.21) and Pusa Sugandh-4×PSD-15 (21.13).

The range of heterosis over better parent for grain yield/plant varied from -11.20% (Type-3×Basmati-370) to 120.90% (Pusa Sugandh-6×PSD-15). Among 28 crosses 23 crosses showed significant positive heterosis while one cross showed significant negative heterosis for grain yield/plant over better parent. The maximum significant positive heterosis for grain yield/plant over better parent was exhibited by

Pusa Sugandh-6×PSD-15 (120.90) followed by Pusa Basmati-1×PSD-15 (88.87), Pusa Sugandh-4×Basmati-370 (87.58), Pusa basmati-1×Basmati-370 (83.70), Tarori Basmati-1×Pant Basmati-1 (81.73), Pusa Sugandh-6×Basmati-370 (74.75), Pusa Sugandh-4×Pant Basmati-1 (71.43), Pusa Basmati-1×Pant Basmati-1 (66.94), Pusa Sugandh-4×Tarori Basmati-1 (66.19), Pusa Basmati-1×Pusa Sugandh-6 (52.23), Basmati-370×PSD-15 (52.23), Pusa Sugandh-6×Type-3 (50.40), Pusa Sugandh-4×Pusa Sugandh-6 (42.39), Pusa Basmati-1×Tarori Basmati-1 (42.34), Type-3×PSD-15 (33.65), Basmati-370×Tarori Basmati-1 (30.00), Basmati-370×Pant Basmati-1 (29.09), Pusa Sugandh-4×Type-3 (24.57), Pusa Sugandh-6×Pant Basmati-1 (21.70), Pusa Sugandh-6×Tarori Basmati-1 (21.59), PSD-15×Pant Basmati-1 (20.14), Pusa Basmati-1×Pusa Sugandh-4 (17.14), Pusa Basmati-1×Type-3 (14.68) and Pusa Sugandh-6×PSD-15 (120.90). The cross Type-3×Basmati-370 showed significant negative heterosis (-11.20) for grain yield/plant over better parent.

Range of heterosis for number of grain yield/plant over standard check variety (Improved Pusa Basmati-1) varied from 17.10% (Pusa Basmati-1×Pusa Sugandh-4) to 193.87% (Pusa Sugandh-6×PSD-15). All the 28 crosses showed significant positive heterosis for grain yield/plant over standard check variety. The maximum significant positive heterosis for grain yield/plant over standard check was exhibited by Pusa Sugandh-6×PSD-15 (193.87) followed by Pusa Basmati-1×PSD-15 (151.26), Pusa Sugandh-6×Basmati-370 (124.85), Pusa Sugandh-6×Type-3 (116.02), Pusa Sugandh-4×Basmati-370 (112.4), Pusa Basmati-1×Basmati-370 (108.01), Basmati-370×PSD-15 (102.51), Pusa Basmati-1×Pusa Sugandh-6 (95.87), Type-3×PSD-15 (91.96), Pusa Sugandh-4×Pusa Sugandh-6 (83.21), Pusa Sugandh-4×Type-3 (78.92), Pusa Sugandh-4×Pant Basmati-1 (71.38), Pusa Sugandh-4×Tarori Basmati-1 (66.14), Pusa Basmati-1×Type-3 (64.72), PSD-15×Pant Basmati-1 (59.82), Pusa Sugandh-6×Pant Basmati-1 (56.59), Pusa Sugandh-6×Tarori Basmati-1 (56.45), Type-3×Tarori Basmati-1 (53.89), Pusa Basmati-1×Pant Basmati-1 (53.03), Type-3×Pant Basmati-1 (52.6), Tarori Basmati-1×Pant Basmati-1 (52.5), Basmati-370×Tarori Basmati-1 (47.2), Basmati-370×Pant Basmati-1 (46.17), Tarori Basmati-1×PSD-15 (43.17), Pusa Sugandh-4×PSD-15 (41.12), Pusa Basmati-1×Tarori Basmati-1 (30.47), Type-3×Basmati-370 (27.55) and Pusa Basmati-1×Pusa Sugandh-4 (17.1).

4.3.11 Hulling recovery (%)

The range of heterosis over mid parent for hulling recovery varied from -2.25% (Type-3×Basmati-370) to 8.28% (Pusa Basmati 1×Pant Basmati-1). Among 28 crosses 16 crosses showed significant positive heterosis while 6 cross showed significant negative heterosis for hulling recovery over mid-parent. The maximum significant positive heterosis for hulling recovery over mid parent was exhibited by Pusa Basmati 1×Pant Basmati-1 (8.28) followed by Pusa Basmati-1×Tarori Basmati-1 (8.01), Pusa Sugandh-4×Tarori Basmati-1 (8.00), PSD-15×Pant Basmati-1 (7.92), Pusa Sugandh-4×Pant Basmati-1 (7.44), Type-3×Pant Basmati-1 (6.52), Pusa Sugandh-6×Tarori Basmati-1 (5.78), Pusa Sugandh-6×Pant Basmati-1 (4.89), Tarori Basmati-1×Pant Basmati-1 (3.48), Pusa Sugandh-4×PSD-15 (3.11), Pusa Sugandh-4×Pusa Sugandh-6 (3.10), Pusa Sugandh-6×PSD-15 (3.02), Tarori Basmati-1×PSD-15 (2.98), Pusa Sugandh-6×Type-3 (1.75), Basmati-370×Tarori Basmati-1 (1.46) and Basmati-370×Pant Basmati-1 (1.05). The maximum significant negative heterosis for hulling recovery over mid parent was exhibited by Type-3×Basmati-370 (-2.25) followed by Type-3×Tarori Basmati-1 (-1.58), Pusa Basmati-1×Pusa Sugandh-6 (-1.44), Pusa Sugandh-6×Basmati-370 (-1.39), Pusa Basmati-1 × Basmati-370 (-1.18) and Pusa Basmati-1×PSD-15 (-0.95).

The range of heterosis over better parent for hulling recovery varied from -3.70% (Pusa Sugandh-6×Basmati-370) to 7.80% (PSD-15×Pant Basmati-1). Among 28 crosses 13 crosses showed significant positive heterosis while 12 cross showed significant negative heterosis for hulling recovery over better parent. The maximum significant positive heterosis for hulling recovery over better parent was exhibited by PSD-15×Pant Basmati-1 (7.80) followed by Pusa Sugandh-4×Tarori Basmati-1 (7.62), Pusa Sugandh-4×Pant Basmati-1 (6.79), Pusa Basmati-1×Tarori Basmati-1 (6.42), Pusa Basmati-1×Pant Basmati-1 (6.42), Pusa Sugandh-6×Tarori Basmati-1 (4.95), Type-3×Pant Basmati-1 (4.03), Pusa Sugandh-6×Pant Basmati-1 (3.81), Tarori Basmati-1×Pant Basmati-1 (3.22), Tarori Basmati-1×PSD-15 (2.83), Pusa Sugandh-4×Pusa Sugandh-6 (2.65), Pusa Sugandh-4×PSD-15 (2.59) and Pusa Sugandh-6×PSD-15 (2.06). The maximum significant negative heterosis for hulling recovery over better parent was exhibited by Pusa Sugandh-6×Basmati-370 (-3.70) followed by Type-3×Tarori Basmati-1 (-3.64), Pusa Sugandh-4×Basmati-370 (-3.29), Type-3×Basmati-370

Table 4.3.1: Contd.....

Sl. No	Crosses	Hulling recovery (%)				Milling recovery (%)			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1xPusa Sugandh-4	75.35	0.47	-0.67	-0.50	67.89	1.25	-0.49	1.19
2	Pusa Basmati-1xPusa Sugandh-6	74.24	-1.44**	-2.14 **	-1.97**	67.99	-0.76	-1.19	1.34
3	Pusa Basmati-1xType-3	76.41	0.08	-0.55	0.90	68.07	0.47	-0.22	1.46
4	Pusa Basmati-1xBasmati-370	76.26	-1.18**	-2.82 **	0.70	70.15	2.30*	1.78	4.56**
5	Pusa Basmati-1xTarori Basmati-1	80.73	8.01**	6.42**	6.60**	72.70	8.87**	6.56**	8.36**
6	Pusa Basmati-1xPSD-15	73.92	-0.95*	-2.56 **	-2.39**	68.71	2.90*	0.72	2.41
7	Pusa Basmati-1xPant Basmati-1	80.73	8.28**	6.42**	6.60**	72.69	8.48**	6.55**	8.35**
8	Pusa Sugandh-4xPusa Sugandh-6	76.77	3.10**	2.65**	1.38*	69.34	2.95**	0.77	3.34*
9	Pusa Sugandh-4xType-3	75.69	0.27	-1.48 **	-0.05	67.60	1.52	0.47	0.75
10	Pusa Sugandh-4xBasmati-370	75.89	-0.55	-3.29 **	0.21	68.69	1.90	-0.34	2.37
11	Pusa Sugandh-4xTarori Basmati-1	79.79	8.00**	7.62**	5.36**	71.65	9.21**	8.75**	6.79**
12	Pusa Sugandh-4xPSD-15	76.06	3.11**	2.59**	0.44	67.93	3.55**	3.11*	1.25
13	Pusa Sugandh-4xPant Basmati-1	79.18	7.44**	6.79**	4.55**	71.66	8.83**	8.76**	6.80**
14	Pusa Sugandh-6xType-3	77.14	1.75**	0.40	1.86**	66.37	-2.47*	-3.55**	-1.08
15	Pusa Sugandh-6xBasmati-370	75.56	-1.39**	-3.70 **	-0.22	68.05	-1.18	-1.26	1.43
16	Pusa Sugandh-6xTarori Basmati-1	78.50	5.78**	4.95**	3.65**	71.44	6.52**	3.83**	6.48**
17	Pusa Sugandh-6xPSD-15	76.33	3.02**	2.06**	0.80	67.76	1.03	-1.53	0.99
18	Pusa Sugandh-6xPant Basmati-1	77.64	4.89**	3.81**	2.52**	69.70	3.56**	1.29	3.89**
19	Type-3xBasmati-370	75.91	-2.25**	-3.27 **	0.23	66.86	-1.83	-3.00*	-0.35
20	Type-3xTarori Basmati-1	74.03	-1.58**	-3.64 **	-2.24**	66.07	-0.35	-1.80	-1.52
21	Type-3xPSD-15	75.20	0.12	-2.12 **	-0.70	66.84	0.81	-0.66	-0.38
22	Type-3xPant Basmati-1	79.93	6.52**	4.03**	5.55**	72.18	8.48**	7.28**	7.59**
23	Basmati-370xTarori Basmati-1	77.15	1.46**	-1.68 **	1.88**	68.99	2.77*	0.09	2.82*
24	Basmati-370xPSD-15	76.46	0.70	-2.56 **	0.97	68.07	1.41	-1.24	1.46
25	Basmati-370xPant Basmati-1	76.65	1.05*	-2.32**	1.21*	67.94	0.86	-1.42	1.27
26	Tarori Basmati-1xPSD-15	75.70	2.98**	2.83**	-0.04	66.80	2.25	2.25	-0.44
27	Tarori Basmati-1xPant Basmati-1	75.99	3.48**	3.22**	0.34	68.14	3.93 **	3.56**	1.56
28	PSD-15xPant Basmati-1	79.12	7.92**	7.80**	4.48**	70.41	7.39 **	7.00**	4.94**

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check) =Standard heterosis over check

(-3.27), Pusa Basmati-1×Basmati-370 (-2.82), Pusa Basmati-1×PSD-15 (-2.56), Basmati-370×PSD-15 (-2.56), Basmati-370×Pant Basmati-1 (-2.3), Pusa Basmati-1×Pusa Sugandh-6 (-2.14), Type-3×PSD-15 (-2.12), Basmati-370×Tarori Basmati-1 (-1.68) and Pusa Sugandh-4×Type-3 (-1.48).

Range of heterosis for number of hulling recovery over standard check variety (Improved Pusa Basmati-1) varied from -2.39% (Pusa Basmati-1×PSD-15) to 6.60% (Pusa Basmati-1×Tarori Basmati-1). Among 28 crosses, 12 crosses showed significant positive and 3 crosses showed significant negative heterosis for hulling recovery over standard check variety. The maximum significant positive heterosis for hulling recovery over standard check was exhibited by Pusa Basmati-1×Tarori Basmati-1 (6.60) followed by Pusa Basmati 1 × Pant Basmati-1 (6.60), Type-3×Pant Basmati-1 (5.55), Pusa Sugandh-4×Tarori Basmati-1 (5.36), Pusa Sugandh-4×Pant Basmati-1(4.55), PSD-15 ×Pant Basmati-1(4.48), Pusa Sugandh-6×Tarori Basmati-1(3.65), Pusa Sugandh-6×Pant Basmati-1(2.52), Basmati-370×Tarori Basmati-1(1.88), Pusa Sugandh-6×Type-3(1.86), Pusa Sugandh-4×Pusa Sugandh-6 (1.38) and Basmati-370×Pant Basmati-1(1.21). The maximum significant negative heterosis for hulling recovery over standard check was exhibited by Pusa Basmati-1×PSD-15 (-2.39) followed by Type-3×Tarori Basmati-1 (-2.24) and Pusa Basmati-1×Pusa Sugandh-6 (-1.97).

4.3.12 Milling recovery (%)

The range of heterosis over mid parent for milling recovery varied from -2.47% (Pusa Sugandh-6×Type-3) to 9.21% (Pusa Sugandh-4×Tarori Basmati-1). Among 28 crosses, 14 crosses showed significant positive heterosis while one cross showed significant negative heterosis for milling recovery over mid-parent. The maximum significant positive heterosis for milling recovery over mid parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (9.21) followed by Pusa Basmati-1×Tarori Basmati-1 (8.87), Pusa Sugandh-4×Pant Basmati-1 (8.83), Pusa Basmati 1×Pant Basmati-1 (8.48), Type-3×Pant Basmati-1 (8.48), PSD-15 x Pant Basmati-1 (7.39), Pusa Sugandh-6 ×Tarori Basmati-1 (6.52), Tarori Basmati-1×Pant Basmati-1 (3.93), Pusa Sugandh-6 ×Pant Basmati-1 (3.56), Pusa Sugandh-4×PSD-15 (3.55), Pusa Sugandh-4×Pusa Sugandh-6 (2.95), Pusa Basmati-1×PSD-15 (2.90), Basmati-370×Tarori Basmati-1 (2.77) and Pusa Basmati-1×Basmati-370 (2.30). The cross Pusa Sugandh-6×Type-3 showed significant negative heterosis (-2.47) for milling recovery over mid parent.

The range of heterosis over better parent for milling recovery varied from -3.55% (Pusa Sugandh-6×Type-3) to 8.76% (Pusa Sugandh-4×Pant Basmati-1). Among 28 crosses, 9 crosses showed significant positive heterosis while 2 crosses showed significant negative heterosis for milling recovery over better parent. The maximum significant positive heterosis for milling recovery over better parent was exhibited by Pusa Sugandh-4×Pant Basmati-1 (8.76) followed by Pusa Sugandh-4×Tarori Basmati-1 (8.75), Type-3×Pant Basmati-1 (7.28), PSD-15×Pant Basmati-1 (7.00), Pusa Basmati-1×Tarori Basmati-1 (6.56), Pusa Basmati-1×Pant Basmati-1 (6.55), Pusa Sugandh-6×Tarori Basmati-1 (3.83), Tarori Basmati-1×Pant Basmati-1 (3.56) and Pusa Sugandh-4×PSD-15 (3.11). A significant negative heterosis for milling recovery over better parent was exhibited by cross Pusa Sugandh-6×Type-3 (-3.55) and cross Type-3×Basmati-370 (-3.00).

Range of heterosis for milling recovery over standard check variety (Improved Pusa Basmati-1) varied from 2.82% (Basmati-370×Tarori Basmati-1) to 8.36% (Pusa Basmati-1×Tarori Basmati-1). Among 28 crosses, 11 crosses showed significant positive heterosis for milling recovery over standard check variety. The maximum significant positive heterosis for milling recovery over standard check was exhibited by Pusa Basmati-1×Tarori Basmati-1 (8.36) followed by Pusa Basmati 1×Pant Basmati-1 (8.35), Type-3×Pant Basmati-1 (7.59), Pusa Sugandh-4×Pant Basmati-1 (6.80), Pusa Sugandh-4×Tarori Basmati-1 (6.79), Pusa Sugandh-6×Tarori Basmati-1 (6.48), PSD-15 x Pant Basmati-1 (4.94), Pusa Basmati-1×Basmati-370 (4.56), Pusa Sugandh-6×Pant Basmati-1 (3.89), Pusa Sugandh-4×Pusa Sugandh-6 (3.34) and Basmati-370×Tarori Basmati-1 (2.82).

4.3.13 Kernel length (mm)

The range of heterosis over mid parent for kernel length varied from -21.44% (Pusa Sugandh-4×Tarori Basmati-1) to 17.92% (Type-3×Pant Basmati-1). Among 28 crosses, 21 crosses showed significant positive heterosis while 5 cross showed significant negative heterosis for kernel length over mid-parent. The maximum significant positive heterosis for kernel length over mid parent was exhibited by Type-3×Pant Basmati-1 (17.92) followed by PSD-15×Pant Basmati-1 (17.55), Pusa Basmati-1×Tarori Basmati-1 (15.49), Pusa Basmati 1×Pant Basmati-1 (15.24), Pusa Basmati-1×PSD-15 (11.62), Basmati-370×Tarori Basmati-1 (10.96), Pusa Sugandh-6×Tarori

Basmati-1 (10.24), Basmati-370×Pant Basmati-1 (7.89), Type-3×Tarori Basmati-1 (5.84), Pusa Sugandh-6×PSD-15 (5.67), Pusa Basmati-1×Pusa Sugandh-6 (5.66), Pusa Basmati-1×Basmati-370 (4.99), Pusa Basmati-1×Pusa Sugandh-4 (4.91), Type-3×PSD-15 (4.65), Pusa Sugandh-4×Basmati-370 (4.49), Pusa Sugandh-4×PSD-15 (4.29), Pusa Sugandh-6×Type-3 (4.27), Basmati-370×PSD-15 (4.00), Tarori Basmati-1×PSD-15 (3.66), Pusa Sugandh-6×Basmati-370 (3.24) and Pusa Basmati-1×Type-3 (2.70). The maximum significant negative heterosis for kernel length over mid parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-21.44) followed by Pusa Sugandh-6×Pant Basmati-1 (-18.70), Tarori Basmati-1×Pant Basmati-1 (-16.01), Pusa Sugandh-4×Pant Basmati-1 (-9.87) and Pusa Sugandh-4×Pusa Sugandh-6 (-4.69).

The range of heterosis over better parent for kernel length varied from -25.42% (Pusa Sugandh-4×Tarori Basmati-1) to 15.32% (PSD-15×Pant Basmati-1). Among 28 crosses 6 crosses showed significant positive heterosis while 12 crosses showed significant negative heterosis for kernel length over better parent. The maximum significant positive heterosis for kernel length over better parent was exhibited by PSD-15 x Pant Basmati-1 (15.32) and followed by Pusa Basmati-1×Tarori Basmati-1 (14.64), Pusa Basmati-1×Pant Basmati-1 (14.19), Pusa Basmati-1×PSD-15 (10.51), Type-3×Pant Basmati-1 (9.87) and Pusa Sugandh-6×Tarori Basmati-1 (5.5). The maximum significant negative heterosis for kernel length over better parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-25.42) followed by Pusa Sugandh-6×Pant Basmati-1 (-22.07), Tarori Basmati-1×Pant Basmati-1(-16.16), Pusa Sugandh-4×Pant Basmati-1 (-14.3), Pusa Sugandh-4×Type-3 (-12.84), Pusa Sugandh-6×Basmati-370 (-9.64), Pusa Sugandh-4×Basmati-370 (-9.21), Pusa Sugandh-6×Type-3 (-6.58), Pusa Sugandh-4×Pusa Sugandh-6 (-5.49), Basmati-370×PSD-15 (-3.78), Pusa Basmati-1×Basmati-370 (-3.75) and Pusa Basmati-1×Type-3 (-3.4).

Range of heterosis for kernel length over standard check variety (Improved Pusa Basmati-1) varied from -16.84% (Pusa Sugandh-4×Tarori Basmati-1) to 15.95% (PSD-15×Pant Basmati-1). Among 28 crosses, 11 crosses showed significant positive and 9 cross showed significant negative heterosis for kernel length over standard check variety. The maximum significant positive heterosis for kernel length over standard check was exhibited by PSD-15 x Pant Basmati-1 (15.95) followed by Pusa Sugandh-6 ×Tarori Basmati-1(15.65), Pusa Basmati-1×Tarori Basmati-1 (14.86), Pusa Basmati 1 × Pant

Table 4.3.1: Contid.....

Sl. No	Crosses	Kernel length (mm)				Kernel breadth (mm)			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1×Pusa Sugandh-4	7.44	4.91**	-1.11	10.27**	1.75	2.75	2.85	1.16
2	Pusa Basmati-1×Pusa Sugandh-6	7.43	5.66**	0.41	10.07**	1.72	1.18	1.28	-0.39
3	Pusa Basmati-1×Type-3	6.44	2.79*	-3.40*	-4.64 **	1.71	-1.91	-0.48	-0.77
4	Pusa Basmati-1×Basmati-370	6.41	4.99**	-3.75*	-4.99 **	1.73	1.96	3.28	0.19
5	Pusa Basmati-1×Tarori Basmati-1	7.75	15.49**	14.64**	14.86**	1.65	-8.32**	-5.52*	-4.25
6	Pusa Basmati-1×PSD-15	7.36	11.62**	10.51**	9.09**	1.66	-2.16	-1.29	-3.86
7	Pusa Basmati-1×Pant Basmati-1	7.75	15.24**	14.19**	14.81 **	1.66	-7.45**	-4.97*	-4.05
8	Pusa Sugandh-4×Pusa Sugandh-6	7.11	-4.69**	-5.49**	5.38**	1.72	1.37	1.37	-0.19
9	Pusa Sugandh-4×Type-3	6.56	-1.99	-12.84**	-2.81	1.83	4.77	6.19**	5.98*
10	Pusa Sugandh-4×Basmati-370	6.83	4.49**	-9.21**	1.23	1.87	10.00**	11.53**	8.30**
11	Pusa Sugandh-4×Tarori Basmati-1	5.61	-21.44**	-25.42**	-16.84 **	1.95	8.32**	11.51**	13.13**
12	Pusa Sugandh-4×PSD-15	7.33	4.29**	-2.61	8.59**	1.66	-2.55	-1.58	-4.05
13	Pusa Sugandh-4×Pant Basmati-1	6.45	-9.87**	-14.30**	-4.44 **	1.84	2.98	5.64*	6.76**
14	Pusa Sugandh-6×Type-3	6.91	4.27**	-6.58**	2.42	1.70	-2.67	-1.35	-1.54
15	Pusa Sugandh-6×Basmati-370	6.69	3.24*	-9.64**	-0.94	1.82	7.25**	8.75**	5.60*
16	Pusa Sugandh-6×Tarori Basmati-1	7.81	10.24**	5.50**	15.65**	1.64	-9.06**	-6.37**	-5.02
17	Pusa Sugandh-6×PSD-15	7.36	5.67**	-0.54	9.04**	1.70	-0.20	0.79	-1.74
18	Pusa Sugandh-6×Pant Basmati-1	5.77	-18.70**	-22.07**	-14.57 **	1.91	6.52**	9.26**	10.42**
19	Type-3×Basmati-370	5.68	-0.41	-3.01	-15.80 **	1.90	8.78**	11.76**	10.04**
20	Type-3×Tarori Basmati-1	6.68	5.84**	-1.23	-1.04	1.84	1.85	3.47	6.37*
21	Type-3×PSD-15	6.48	4.65**	-0.71	-3.95 **	1.73	-1.15	1.17	0.00
22	Type-3×Pant Basmati-1	7.46	17.92**	9.87**	10.47**	1.68	-6.15*	-5.00*	-2.70
23	Basmati-370×Tarori Basmati-1	6.83	10.96**	1.03	1.23	1.83	1.66	6.08**	6.18*
24	Basmati-370×PSD-15	6.28	4.00**	-3.78*	-6.91 **	1.74	4.40	4.82*	0.77
25	Basmati-370×Pant Basmati-1	6.66	7.89**	-1.92	-1.38	1.68	-5.96*	-2.23	-2.51
26	Tarori Basmati-1×PSD-15	6.89	3.66**	1.87	2.07	1.84	2.03	6.05**	6.56*
27	Tarori Basmati-1×Pant Basmati-1	5.69	-16.01**	-16.16**	-15.70**	1.90	5.18*	5.57**	9.85**
28	PSD-15×Pant Basmati-1	7.83	17.55 **	15.32**	15.95**	1.65	-8.01**	-4.73*	-4.63

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check) =Standard heterosis over check

Basmati-1 (14.81), Type-3×Pant Basmati-1 (10.47), Pusa Basmati-1×Pusa Sugandh-4 (10.27), Pusa Basmati-1×Pusa Sugandh-6 (10.07), Pusa Basmati-1×PSD-15 (9.09), Pusa Sugandh-6×PSD-15 (9.04), Pusa Sugandh-4×PSD-15 (8.59) and Pusa Sugandh-4×Pusa Sugandh-6 (5.38). The maximum significant negative heterosis for kernel length over standard check was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-16.84) followed by Type-3×Basmati-370 (-15.8), Tarori Basmati-1×Pant Basmati-1 (-15.7), Pusa Sugandh-6×Pant Basmati-1 (-14.57), Basmati-370×PSD-15 (-6.91), Pusa Basmati-1 × Basmati-370 (-4.99), Pusa Basmati-1×Type-3 (-4.64), Pusa Sugandh-4×Pant Basmati-1 (-4.44) and Type-3×PSD-15 (-3.95).

4.3.14 Kernel breadth (mm)

The range of heterosis over mid parent for kernel breadth varied from -9.06% (Pusa Sugandh-6×Tarori Basmati-1) to 10.00% (Pusa Sugandh-4×Basmati-370). Among 28 crosses 6 crosses showed significant positive heterosis while 6 crosses showed significant negative heterosis for kernel breadth over mid parent. The maximum significant positive heterosis for kernel breadth over mid parent was exhibited by Pusa Sugandh-4×Basmati-370 (10.00) and followed by Type-3×Basmati-370 (8.78), Pusa Sugandh-4×Tarori Basmati-1 (8.32), Pusa Sugandh-6×Basmati-370 (7.25), Pusa Sugandh-6×Pant Basmati-1 (6.52) and Tarori Basmati-1×Pant Basmati-1 (5.18). The maximum significant negative heterosis for kernel breadth over mid parent was exhibited by Pusa Sugandh-6×Tarori Basmati-1 (-9.06) and followed by Pusa Basmati-1 ×Tarori Basmati-1 (-8.32), PSD-15×Pant Basmati-1 (-8.01), Pusa Basmati-1×Pant Basmati-1 (-7.45), Type-3×Pant Basmati-1(-6.15) and Basmati-370×Pant Basmati-1 (-5.96).

The range of heterosis over better parent for kernel breadth varied from -6.37% (Pusa Sugandh-6×Tarori Basmati-1) to 11.76% (Type-3×Basmati-370). Among 28 crosses, 11 crosses showed significant positive heterosis while 5 crosses showed significant negative heterosis for kernel breadth over better parent. The maximum significant positive heterosis for kernel breadth over better parent was exhibited by Type-3×Basmati-370 (11.76) followed by Pusa Sugandh-4×Basmati-370 (11.53), Pusa Sugandh-4×Tarori Basmati-1 (11.51), Pusa Sugandh-6×Pant Basmati-1 (9.26), Pusa Sugandh-6×Basmati-370 (8.75), Pusa Sugandh-4×Type-3 (6.19), Basmati-370×Tarori Basmati-1 (6.08), Tarori Basmati-1×PSD-15 (6.05), Pusa Sugandh-4×Pant Basmati-1

(5.64), Tarori Basmati-1×Pant Basmati-1 (5.57) and Basmati-370×PSD-15 (4.82). The maximum significant negative heterosis for kernel breadth over better parent was exhibited by Pusa Sugandh-6×Tarori Basmati-1 (-6.37) followed by Pusa Basmati-1 ×Tarori Basmati-1 (-5.52), Type-3×Pant Basmati-1 (-5.00), Pusa Basmati 1×Pant Basmati-1 (-4.9) and PSD-15×Pant Basmati-1 (-4.73).

Range of heterosis for number of kernel breadth over standard check variety (Improved Pusa Basmati-1) varied from 5.6% (Pusa Sugandh-6×Basmati-370) to 13.13% (Pusa Sugandh-4×Tarori Basmati-1). Among 28 crosses, 11 crosses showed significant positive heterosis for kernel breadth over standard check variety. The maximum significant positive heterosis for kernel breadth over standard check was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (13.13) followed by Pusa Sugandh-6×Pant Basmati-1(10.42), Type-3×Basmati-370 (10.04), Tarori Basmati-1×Pant Basmati-1 (9.85), Pusa Sugandh-4×Basmati-370 (8.3), Pusa Sugandh-4×Pant Basmati-1 (6.76), Tarori Basmati-1×PSD-15 (6.56), Type-3×Tarori Basmati-1(6.37), Basmati-370×Tarori Basmati-1(6.18), Pusa Sugandh-4×Type-3 (5.98) and Pusa Sugandh-6×Basmati-370 (5.6).

4.3.15 Kernel length/breadth ratio

The range of heterosis over mid parent for kernel length/breadth ratio varied from -29.67 (Pusa Sugandh-4×Tarori Basmati-1) to 24.14% (Type-3×Pant Basmati-1). Among 28 crosses 9 crosses showed significant positive heterosis while 8 crosses showed significant negative heterosis for kernel length/breadth ratio over mid-parent. The maximum significant positive heterosis for kernel length/breadth ratio over mid parent was exhibited by Type-3×Pant Basmati-1 (24.14) followed by PSD-15×Pant Basmati-1(23.25), Pusa Basmati-1×Tarori Basmati-1(22.08), Pusa Basmati-1×Pant Basmati-1(21.05), Pusa Sugandh-6×Tarori Basmati-1(17.47), Pusa Basmati-1×PSD-15 (13.08), Basmati-370×Pant Basmati-1 (10.48), Pusa Sugandh-4×PSD-15 (6.51) and Pusa Sugandh-6×Type-3 (5.62). The maximum significant negative heterosis for kernel length/breadth ratio over mid parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-29.67) followed by Pusa Sugandh-6×Pant Basmati-1(-25.76), Tarori Basmati-1×Pant Basmati-1 (-20.53), Pusa Sugandh-4×Pant Basmati-1 (-14.88), Type-3 ×Basmati-370 (-10.87), Pusa Sugandh-4×Type-3 (-7.75), Pusa Sugandh-4×Basmati-370 (-5.99) and Pusa Sugandh-4×Pusa Sugandh-6 (-5.96).

Table 4.3.1: Contd.....

Sl. No	Crosses	Kernel length/breadth ratio				Cooked kernel length (mm)			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1xPusa Sugandh-4	4.26	2.03	-3.69	9.04**	18.73	9.72**	-0.04	19.19**
2	Pusa Basmati-1xPusa Sugandh-6	4.32	4.26	-0.84	10.49**	17.31	11.84**	11.34**	10.12**
3	Pusa Basmati-1xType-3	3.76	3.11	-4.41	-3.92	17.14	19.90**	11.27**	9.08**
4	Pusa Basmati-1xBasmati-370	3.71	1.69	-5.68	-5.20	16.61	15.77**	7.83**	5.71*
5	Pusa Basmati-1xTarori Basmati-1	4.69	22.08**	19.34**	19.95**	18.46	20.79**	19.82**	17.45**
6	Pusa Basmati-1xPSD-15	4.44	13.08**	12.89**	13.47**	17.43	15.77**	13.15**	10.92**
7	Pusa Basmati-1xPant Basmati-1	4.68	21.05**	19.00**	19.61**	18.66	22.59**	21.09**	18.71**
8	Pusa Sugandh-4xPusa Sugandh-6	4.13	-5.96*	-6.70*	5.63	17.80	3.82*	-5.03**	13.23**
9	Pusa Sugandh-4xType-3	3.59	-7.75**	-18.90**	-8.18**	15.69	-1.70	-16.26**	-0.15
10	Pusa Sugandh-4xBasmati-370	3.66	-5.99*	-17.32**	-6.39*	17.18	7.26**	-8.32**	9.31**
11	Pusa Sugandh-4xTarori Basmati-1	2.88	-29.67**	-35.02**	-26.43**	15.61	-7.93**	-16.72**	-0.70
12	Pusa Sugandh-4xPSD-15	4.44	6.51**	0.38	13.64**	18.22	8.96**	-2.76	15.95**
13	Pusa Sugandh-4xPant Basmati-1	3.50	-14.88**	-20.93**	-10.49**	17.55	3.94*	-6.35**	11.66**
14	Pusa Sugandh-6xType-3	4.07	5.62*	-6.50*	4.18	15.63	8.77**	0.54	-0.57
15	Pusa Sugandh-6xBasmati-370	3.67	-4.97	-15.84**	-6.22*	15.05	4.36	-3.20	-4.26
16	Pusa Sugandh-6xTarori Basmati-1	4.76	17.47**	9.33**	21.82**	19.47	26.80**	25.24**	23.86**
17	Pusa Sugandh-6xPSD-15	4.34	5.00	-0.31	11.08**	16.85	11.39**	8.41**	7.21**
18	Pusa Sugandh-6xPant Basmati-1	3.03	-25.76**	-30.53**	-22.59**	14.57	-4.69*	-6.26**	-7.30**
19	Type-3xBasmati-370	2.99	-10.87**	-10.91**	-23.44**	13.28	0.26	-0.13	-15.52**
20	Type-3xTarori Basmati-1	3.64	2.30	-3.11	-6.99*	15.16	6.95**	0.00	-3.54
21	Type-3xPSD-15	3.76	3.30	-4.09	-3.92	15.11	8.29**	2.70	-3.88
22	Type-3xPant Basmati-1	4.44	24.14**	16.94**	13.55**	19.02	34.77**	26.52**	21.00**
23	Basmati-370xTarori Basmati-1	3.73	4.97	-0.53	-4.52	18.24	28.23**	20.34**	16.08**
24	Basmati-370xPSD-15	3.61	-0.69	-7.74*	-7.59*	15.16	8.27**	3.06	-3.54
25	Basmati-370xPant Basmati-1	3.95	10.48**	4.13	1.11	15.16	7.05**	0.86	-3.54
26	Tarori Basmati-1xPSD-15	3.75	-2.30	-4.34	-4.18	15.04	0.70	-0.79	-4.31
27	Tarori Basmati-1xPant Basmati-1	3.00	-20.53**	-20.98**	-23.27**	14.30	-5.24*	-5.65*	-8.99**
28	PSD-15xPant Basmati-1	4.75	23.25**	21.36**	21.57**	19.53	31.36**	29.96**	24.28**

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check)=Standard heterosis over check

The range of heterosis over better parent for kernel length/breadth ratio varied from -35.02% (Pusa Sugandh-4×Tarori Basmati-1) to 21.36% (PSD-15×Pant Basmati-1). Among 28 crosses, 6 crosses showed significant positive heterosis while 11 crosses showed significant negative heterosis for kernel length/breadth ratio over better parent. The maximum significant positive heterosis for kernel length/breadth ratio over better parent was exhibited by PSD-15×Pant Basmati-1 (21.36) and followed by Pusa Basmati-1×Tarori Basmati-1 (19.34), Pusa Basmati 1×Pant Basmati-1 (19.00), Type-3×Pant Basmati-1 (16.94), Pusa Basmati-1×PSD-15 (12.89) and Pusa Sugandh-6×Tarori Basmati-1 (9.33). The maximum significant negative heterosis for kernel length/breadth ratio over better parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-35.02) and followed by Pusa Sugandh-6×Pant Basmati-1 (-30.53), Tarori Basmati-1×Pant Basmati-1 (-20.98), Pusa Sugandh-4×Pant Basmati-1 (-20.93), Pusa Sugandh-4×Type-3 (-18.90), Pusa Sugandh-4×Basmati-370 (-17.32), Pusa Sugandh-6×Basmati-370 (-15.84), Type-3×Basmati-370 (-10.91), Basmati-370×PSD-15 (-7.74), Pusa Sugandh-4×Pusa Sugandh-6 (-6.7) and Pusa Sugandh-6×Type-3 (-6.5).

Range of heterosis for number of kernel length/breadth ratio over standard check variety (Improved Pusa Basmati-1) varied from -26.43% (Pusa Sugandh-4×Tarori Basmati-1) to 21.82% (Pusa Sugandh-6×Tarori Basmati-1). Among 28 crosses, 10 crosses showed significant positive and 10 crosses showed significant negative heterosis for kernel length/breadth ratio over standard check variety. The maximum significant positive heterosis for kernel length/breadth ratio over standard check was exhibited by Pusa Sugandh-6×Tarori Basmati-1 (21.82) followed by PSD-15×Pant Basmati-1 (21.57), Pusa Basmati-1×Tarori Basmati-1 (19.95), Pusa Basmati-1×Pant Basmati-1 (19.61), Pusa Sugandh-4×PSD-15 (13.64), Type-3×Pant Basmati-1 (13.55), Pusa Basmati-1×PSD-15 (13.47), Pusa Sugandh-6×PSD-15 (11.08), Pusa Basmati-1×Pusa Sugandh-6 (10.49) and Pusa Basmati-1×Pusa Sugandh-4 (9.04). The maximum significant negative heterosis for kernel length/breadth ratio over standard check was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-26.43) followed by Type-3×Basmati-370 (-23.44), Tarori Basmati-1×Pant Basmati-1 (-23.27), Pusa Sugandh-6×Pant Basmati-1 (-22.59), Pusa Sugandh-4×Pant Basmati-1 (-10.49), Pusa Sugandh-4×Type-3 (-8.18), Basmati-370×PSD-15 (-7.59), Type-3×Tarori Basmati-1 (-6.99), Pusa Sugandh-4×Basmati-370 (-6.39) and Pusa Sugandh-6×Basmati-370 (-6.22).

4.3.16 Cooked kernel length (mm)

The range of heterosis over mid parent for cooked kernel length varied from -7.93% (Pusa Sugandh-4×Tarori Basmati-1) to 34.77% (Type-3×Pant Basmati-1). Among 28 crosses 21 crosses showed significant positive heterosis while 3 crosses showed significant negative heterosis for cooked kernel length over mid-parent. The maximum significant positive heterosis for cooked kernel length over mid parent was exhibited by Type-3×Pant Basmati-1 (34.77) followed by PSD-15×Pant Basmati-1 (31.36), Basmati-370×Tarori Basmati-1 (28.23), Pusa Sugandh-6×Tarori Basmati-1 (26.8), Pusa Basmati 1×Pant Basmati-1 (22.59), Pusa Basmati-1×Tarori Basmati-1 (20.79), Pusa Basmati-1×Type-3 (19.9), Pusa Basmati-1×Basmati-370 (15.77), Pusa Basmati-1×PSD-15 (15.77), Pusa Basmati-1×Pusa Sugandh-6 (11.84), Pusa Sugandh-6×PSD-15 (11.39), Pusa Basmati-1×Pusa Sugandh-4 (9.72), Pusa Sugandh-4×PSD-15 (8.96), Pusa Sugandh-6×Type-3 (8.77), Type-3×PSD-15 (8.29), Basmati-370×PSD-15 (8.27), Pusa Sugandh-4×Basmati-370 (7.26), Basmati-370×Pant Basmati-1 (7.05), Type-3×Tarori Basmati-1 (6.95), Pusa Sugandh-4×Pant Basmati-1 (3.94) and Pusa Sugandh-4×Pusa Sugandh-6 (3.82). The maximum significant negative heterosis for cooked kernel length over mid parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-7.93) followed by Tarori Basmati-1×Pant Basmati-1 (-5.24) and Pusa Sugandh-6×Pant Basmati-1 (-4.69).

The range of heterosis over better parent for cooked kernel length varied from -16.72% (Pusa Sugandh-4×Tarori Basmati-1) to 29.96% (PSD-15×Pant Basmati-1). Among 28 crosses, 11 crosses showed significant positive heterosis while 7 crosses showed significant negative heterosis for cooked kernel length over better parent. The maximum significant positive heterosis for cooked kernel length over better parent was exhibited by PSD-15×Pant Basmati-1 (29.96) and followed by Type-3×Pant Basmati-1 (26.52), Pusa Sugandh-6×Tarori Basmati-1 (25.24), Pusa Basmati-1×Pant Basmati-1 (21.09), Basmati-370×Tarori Basmati-1 (20.34), Pusa Basmati-1×Tarori Basmati-1 (19.82), Pusa Basmati-1×PSD-15 (13.15), Pusa Basmati-1×Pusa Sugandh-6 (11.34), Pusa Basmati-1×Type-3 (11.27), Pusa Sugandh-6×PSD-15 (8.41) and Pusa Basmati-1×Basmati-370 (7.83). The maximum significant negative heterosis for cooked kernel length over better parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (-16.72) and followed by Pusa Sugandh-4×Type-3 (-16.26), Pusa Sugandh-4×Basmati-370 (-8.32),

Pusa Sugandh-4×Pant Basmati-1 (-6.35), Pusa Sugandh-6×Pant Basmati-1 (-6.26), Tarori Basmati-1×Pant Basmati-1 (-5.65) and Pusa Sugandh-4×Pusa Sugandh-6 (-5.03).

Range of heterosis for number of cooked kernel length over standard check variety (Improved Pusa Basmati-1) varied from -15.52% (Type-3×Basmati-370) to 24.28% (PSD-15×Pant Basmati-1). Among 28 crosses, 16 crosses showed significant positive and 3 crosses showed significant negative heterosis for cooked kernel length over standard check variety. The maximum significant positive heterosis for cooked kernel length over standard check was exhibited by PSD-15×Pant Basmati-1(24.28) followed by Pusa Sugandh-6×Tarori Basmati-1(23.86), Type-3×Pant Basmati-1 (21.00), Pusa Basmati-1×Pusa Sugandh-4 (19.19), Pusa Basmati-1×Pant Basmati-1 (18.71), Pusa Basmati-1×Tarori Basmati-1 (17.45), Basmati-370×Tarori Basmati-1 (16.08), Pusa Sugandh-4×PSD-15 (15.95), Pusa Sugandh-4×Pusa Sugandh-6 (13.23), Pusa Sugandh-4×Pant Basmati-1 (11.66), Pusa Basmati-1×PSD-15 (10.92), Pusa Basmati-1×Pusa Sugandh-6 (10.12), Pusa Sugandh-4×Basmati-370 (9.31), Pusa Basmati-1×Type-3 (9.08), Pusa Sugandh-6×PSD-15 (7.21) and Pusa Basmati-1 ×Basmati-370 (5.71). The maximum significant negative heterosis for cooked kernel length over standard check was exhibited by Type-3×Basmati-370 (-15.52) followed by Tarori Basmati-1×Pant Basmati-1 (-8.99) and Pusa Sugandh-6×Pant Basmati-1 (-7.3).

4.3.17 Cooked kernel breadth (mm)

The range of heterosis over mid parent for cooked kernel breadth varied from -8.59% (Pusa Basmati-1×Tarori Basmati-1) to 38.24% (Pusa Sugandh-6×Pant Basmati-1). Among 28 crosses 6 crosses showed significant positive heterosis while one cross showed significant negative heterosis for cooked kernel breadth over mid-parent. The maximum significant positive heterosis for cooked kernel breadth over mid parent was exhibited by Pusa Sugandh-6×Pant Basmati-1 (38.24) followed by Pusa Sugandh-4 ×Tarori Basmati-1 (21.71), Tarori Basmati-1×Pant Basmati-1 (20.38), Type-3 ×Basmati-370 (17.91), Type-3×Tarori Basmati-1 (9.62) and Basmati-370×Tarori Basmati-1 (8.7). The cross Pusa Basmati-1×Tarori Basmati-1 showed significant negative heterosis (-8.59) for cooked kernel breadth over mid parent.

The range of heterosis over better parent for cooked kernel breadth varied from 16.76% (Type-3×Basmati-370) to 35.08% (Pusa Sugandh-6×Pant Basmati-1). Among

28 crosses, 4 crosses showed significant positive heterosis for cooked kernel breadth over better parent. The maximum significant positive heterosis for cooked kernel breadth over better parent was exhibited by Pusa Sugandh-6×Pant Basmati-1 (35.08) and followed by Pusa Sugandh-4×Tarori Basmati-1 (20.73), Tarori Basmati-1×Pant Basmati-1 (20.30) and Type-3×Basmati-370 (16.76).

Range of heterosis for number of cooked kernel breadth over standard check variety (Improved Pusa Basmati-1) varied from -10.11% (Pusa Basmati-1×Tarori Basmati-1) to 33.64% (Pusa Sugandh-6×Pant Basmati-1). Among 28 crosses, 4 crosses showed significant positive and 2 crosses showed significant negative heterosis for cooked kernel breadth over standard check variety. The maximum significant positive heterosis for cooked kernel breadth over standard check was exhibited by Pusa Sugandh-6×Pant Basmati-1 (33.64) followed by Pusa Sugandh-4×Tarori Basmati-1 (19.28), Tarori Basmati-1 ×Pant Basmati-1 (19.02) and Type-3×Basmati-370 (11.17). Two crosses, Pusa Basmati-1×Tarori Basmati-1 and Pusa Basmati-1 × Basmati-370 showed significant negative heterosis (-10.11 and -9.71) for cooked kernel breadth over standard check.

4.3.18 Cooked kernel length/breadth ratio

The range of heterosis over mid parent for cooked kernel length/breadth ratio varied from -35.9% (Pusa Sugandh-6×Pant Basmati-1) to 36.82% (PSD-15×Pant Basmati-1). Among 28 crosses, 16 crosses showed significant positive heterosis while 3 crosses showed significant negative heterosis for cooked kernel length/breadth ratio over mid-parent. The maximum significant positive heterosis for cooked kernel length/breadth ratio over mid parent was exhibited by PSD-15×Pant Basmati-1 (36.82) followed by Pusa Basmati-1×Tarori Basmati-1 (30.77), Pusa Basmati-1×Pant Basmati-1 (30.57), Pusa Basmati-1×Type-3(27.57), Pusa Sugandh-6×Tarori Basmati-1(27.14), Pusa Basmati-1×PSD-15(25.33), Pusa Basmati-1×Basmati-370 (23.03), Type-3×Pant Basmati-1(20.41), Basmati-370×Tarori Basmati-1(19.18), Pusa Basmati-1×Pusa Sugandh-4 (17.99), Pusa Sugandh-4×Basmati-370 (15.33), Pusa Sugandh-4×PSD-15 (14.26), Pusa Basmati-1×Pusa Sugandh-6 (13.2), Type-3×PSD-15 (11.31), Pusa Sugandh-4×Pusa Sugandh-6 (9.3) and Basmati-370×Pant Basmati-1 (9.11). The maximum significant negative heterosis for cooked kernel length/breadth ratio over mid parent was exhibited by Pusa Sugandh-6×Pant Basmati-1 (-35.9) followed by Pusa Sugandh-4×Tarori Basmati-1 (-23.15) and Tarori Basmati-1×Pant Basmati-1 (-21.93).

Table 4.3.1: Contd.....

Sl. No	Crosses	Cooked kernel breadth (mm)				Cooked kernel length/breadth ratio			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1xPusa Sugandh-4	2.31	-5.71	-5.39	-7.71	8.06	17.99**	8.92*	27.21**
2	Pusa Basmati-1xPusa Sugandh-6	2.37	-3.40	-1.66	-5.45	7.29	13.20**	10.12*	15.11**
3	Pusa Basmati-1xType-3	2.31	-5.71	-3.48	-7.71	7.58	27.57**	21.09**	19.68**
4	Pusa Basmati-1xBasmati-370	2.26	-7.74	-6.47	-9.71*	7.33	23.03**	17.04**	15.68**
5	Pusa Basmati-1xTarori Basmati-1	2.25	-9.02	-8.59*	-10.11*	8.12	30.77**	29.66**	28.16**
6	Pusa Basmati-1xPSD-15	2.29	-7.05	-6.92	-8.78	7.62	25.33**	21.73**	20.32**
7	Pusa Basmati-1xPant Basmati-1	2.33	-6.18	-5.68	-7.18	8.14	30.57**	29.98**	28.47**
8	Pusa Sugandh-4xPusa Sugandh-6	2.35	-3.69	-2.29	-6.38	7.66	9.30*	3.56	20.95**
9	Pusa Sugandh-4xType-3	2.37	-2.87	-0.91	-5.59	6.77	4.05	-8.43*	6.95
10	Pusa Sugandh-4xBasmati-370	2.35	-3.56	-2.56	-6.25	7.52	15.33**	1.71	18.79**
11	Pusa Sugandh-4xTarori Basmati-1	2.99	20.73**	21.71**	19.28**	5.21	-23.15**	-29.61**	-17.79**
12	Pusa Sugandh-4xPSD-15	2.43	-1.08	-0.61	-2.93	7.60	14.26**	2.70	19.95**
13	Pusa Sugandh-4xPant Basmati-1	2.61	5.11	6.03	3.99	6.96	2.30	-5.95	9.84*
14	Pusa Sugandh-6xType-3	2.51	6.20	6.80	0.27	6.37	4.00	-3.83	0.53
15	Pusa Sugandh-6xBasmati-370	2.39	0.14	0.56	-4.65	6.37	3.78	-3.83	0.53
16	Pusa Sugandh-6xTarori Basmati-1	2.42	-2.42	-0.21	-3.59	8.12	27.14**	22.66**	28.21**
17	Pusa Sugandh-6xPSD-15	2.55	3.79	5.80	1.86	6.65	6.28	0.50	5.05
18	Pusa Sugandh-6xPant Basmati-1	3.35	35.08**	38.24**	33.64**	4.11	-35.90**	-37.92**	-35.11**
19	Type-3xBasmati-370	2.79	16.76**	17.91**	11.17*	5.15	-8.63	-8.85	-18.68**
20	Type-3xTarori Basmati-1	2.64	6.59	9.62*	5.32	5.91	0.37	-3.95	-6.68
21	Type-3xPSD-15	2.40	-2.30	0.14	-4.12	6.41	11.31*	8.70	1.26
22	Type-3xPant Basmati-1	2.53	1.88	4.84	0.80	7.12	20.41**	14.78**	12.42*
23	Basmati-370xTarori Basmati-1	2.64	6.73	8.70*	5.45	7.03	19.18**	14.30**	11.05*
24	Basmati-370xPSD-15	2.44	-0.81	0.69	-2.66	6.02	4.24	2.03	-4.95
25	Basmati-370xPant Basmati-1	2.37	-4.44	-2.60	-5.45	6.47	9.11*	4.25	2.11
26	Tarori Basmati-1xPSD-15	2.38	-3.90	-3.58	-5.05	6.48	7.47	5.25	2.26
27	Tarori Basmati-1xPant Basmati-1	2.98	20.30**	20.38**	19.02**	4.82	-21.93**	-22.25**	-23.84 **
28	PSD-15xPant Basmati-1	2.36	-4.84	-4.45	-5.85	8.28	36.82**	33.48 **	30.74**

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check)=Standard heterosis over check

The range of heterosis over better parent for cooked kernel length/breadth ratio varied from -37.92% (Pusa Sugandh-6×Pant Basmati-1) to 33.48% (PSD-15×Pant Basmati-1). Among 28 crosses, 11 crosses showed significant positive heterosis while 4 crosses showed significant negative heterosis for cooked kernel length/breadth ratio over better parent. The maximum significant positive heterosis for cooked kernel length/breadth ratio over better parent was exhibited by PSD-15×Pant Basmati-1 (33.48) and followed by Pusa Basmati-1×Pant Basmati-1 (29.98), Pusa Basmati-1×Tarori Basmati-1 (29.66), Pusa Sugandh-6×Tarori Basmati-1 (22.66), Pusa Basmati-1×PSD-15 (21.73), Pusa Basmati-1×Type-3 (21.09), Pusa Basmati-1×Basmati-370 (17.04), Type-3×Pant Basmati-1 (14.78), Basmati-370×Tarori Basmati-1 (14.30), Pusa Basmati-1×Pusa Sugandh-6 (10.12), and Pusa Basmati-1×Pusa Sugandh-4 (8.92). The maximum significant negative heterosis for cooked kernel length/breadth ratio over better parent was exhibited by Pusa Sugandh-6×Pant Basmati-1 (-37.92) and followed by Pusa Sugandh-4×Tarori Basmati-1 (-29.61), Tarori Basmati-1×Pant Basmati-1 (-22.25) and Pusa Sugandh-4×Type-3 (-8.43).

Range of heterosis for number of cooked kernel length/breadth ratio over standard check variety (Improved Pusa Basmati-1) varied from -35.11% (Pusa Sugandh-6×Pant Basmati-1) to 30.74% (PSD-15×Pant Basmati-1). Among 28 crosses, 15 crosses showed significant positive and 4 crosses showed significant negative heterosis for cooked kernel length/breadth ratio over standard check variety. The maximum significant positive heterosis for cooked kernel length/breadth ratio over standard check was exhibited by PSD-15 x Pant Basmati-1 (30.74) followed by Pusa Basmati-1×Pant Basmati-1 (28.47), Pusa Sugandh-6×Tarori Basmati-1 (28.21), Pusa Basmati-1×Tarori Basmati-1 (28.16), Pusa Basmati-1×Pusa Sugandh-4 (27.21), Pusa Sugandh-4×Pusa Sugandh-6 (20.95), Pusa Basmati-1×PSD-15 (20.32) Pusa Sugandh-4×PSD-15 (19.95), Pusa Basmati-1×Type-3 (19.68), Pusa Sugandh-4×Basmati-370 (18.79), Pusa Basmati-1×Basmati-370 (15.68), Pusa Basmati-1×Pusa Sugandh-6 (15.11), Type-3×Pant Basmati-1 (12.42), Basmati-370×Tarori Basmati-1 (11.05) and Pusa Sugandh-4×Pant Basmati-1 (9.84). The maximum significant negative heterosis for cooked kernel length/breadth ratio over standard check was exhibited by Pusa Sugandh-6×Pant Basmati-1 (-35.11) followed by Tarori Basmati-1×Pant Basmati-1 (-23.84), Type-3×Basmati-370 (-18.68) and Pusa Sugandh-4×Tarori Basmati-1 (-17.79).

4.3.19 Kernel elongation ratio

The range of heterosis over mid parent for kernel elongation ratio varied from 4.79% (Pusa Basmati-1×Pusa Sugandh-4) to 17.46% (Pusa Sugandh-4×Tarori Basmati-1). Among 28 crosses 16 crosses showed significant positive heterosis for kernel elongation ratio over mid-parent. The maximum significant positive heterosis for kernel elongation ratio over mid parent was exhibited by Pusa Sugandh-4×Tarori Basmati-1 (17.46) followed by Pusa Sugandh-6×Pant Basmati-1(17.16), Pusa Basmati-1×Type-3 (16.73), Pusa Sugandh-4×Pant Basmati-1 (15.66), Basmati-370×Tarori Basmati-1 (15.17), Pusa Sugandh-6×Tarori Basmati-1 (14.81), Type-3×Pant Basmati-1 (14.12), Tarori Basmati-1×Pant Basmati-1 (12.79), PSD-15×Pant Basmati-1(11.73), Pusa Basmati-1×Basmati-370 (10.20), Pusa Sugandh-4×Pusa Sugandh-6 (8.93), Pusa Basmati-1×Pant Basmati-1(6.19), Pusa Basmati-1×Pusa Sugandh-6 (5.59), Pusa Sugandh-6×PSD-15(5.29), Pusa Sugandh-4×PSD-15(4.92) and Pusa Basmati-1×Pusa Sugandh-4(4.79).

The range of heterosis over better parent for kernel elongation ratio varied from -5.99% (Pusa Sugandh-6×Basmati-370) to 15.13% (Pusa Basmati-1×Type-3). Among 28 crosses 10 crosses showed significant positive heterosis while one cross showed significant negative heterosis for kernel elongation ratio over better parent. The maximum significant positive heterosis for kernel elongation ratio over better parent was exhibited by Pusa Basmati-1×Type-3 (15.13) and followed by Pusa Sugandh-6×Pant Basmati-1 (14.16), Type-3×Pant Basmati-1(13.19), Tarori Basmati-1×Pant Basmati-1 (12.04), Pusa Sugandh-4×Tarori Basmati-1 (11.65), Basmati-370×Tarori Basmati-1 (11.56), Pusa Sugandh-6×Tarori Basmati-1 (11.14), PSD-15×Pant Basmati-1 (10.81), Pusa Sugandh-4×Pant Basmati-1 (9.24) and Pusa Basmati-1×Basmati-370 (8.36). The cross Pusa Sugandh-6×Basmati-370 showed significant negative heterosis (-5.99) for kernel elongation ratio over better parent.

Range of heterosis for number of kernel elongation ratio over standard check variety (Improved Pusa Basmati-1) varied from -6.44% (Tarori Basmati-1×PSD-15) to 19.31% (Pusa Sugandh-4×Tarori Basmati-1). Among 28 crosses, 14 crosses showed significant positive and one cross showed significant negative heterosis for kernel elongation ratio over standard check variety. The maximum significant positive heterosis for kernel elongation ratio over standard check was exhibited by

Table 4.3.1: Contd.....

Sl. No	Crosses	Kernel elongation ratio				Alkali digestion value			
		F ₁ Mean	MPH	BPH	SH (Check)	F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1xPusa Sugandh-4	2.52	4.79*	1.07	8.01**	7.02	2.16	-1.08	-1.86
2	Pusa Basmati-1xPusa Sugandh-6	2.33	5.59*	0.72	0.00	7.05	3.42*	-0.61	-1.40
3	Pusa Basmati-1xType-3	2.66	16.73**	15.13**	14.31**	5.56	1.03	-21.66**	-22.28**
4	Pusa Basmati-1xBasmati-370	2.59	10.20**	8.36**	11.30**	5.51	-0.12	-22.27**	-22.89**
5	Pusa Basmati-1xTarori Basmati-1	2.38	4.61	3.03	2.29	6.81	-1.11	-4.04*	-4.80**
6	Pusa Basmati-1xPSD-15	2.37	4.02	2.59	1.86	6.46	-0.03	-8.98**	-9.70**
7	Pusa Basmati-1xPant Basmati-1	2.40	6.19**	3.89	3.15	5.65	4.57*	-20.39**	-21.03**
8	Pusa Sugandh-4xPusa Sugandh-6	2.50	8.93**	0.40	7.30**	6.93	5.18**	4.37*	-3.03
9	Pusa Sugandh-4xType-3	2.39	0.98	-3.88	2.72	5.14	-2.62	-22.68**	-28.16**
10	Pusa Sugandh-4xBasmati-370	2.51	2.94	0.94	7.87**	4.70	-11.24**	-29.25**	-34.27**
11	Pusa Sugandh-4xTarori Basmati-1	2.78	17.46**	11.65**	19.31**	6.98	4.88**	4.65*	-2.33
12	Pusa Sugandh-4xPSD-15	2.49	4.92*	-0.13	6.72*	6.28	0.75	-5.47**	-12.17**
13	Pusa Sugandh-4xPant Basmati-1	2.72	15.66**	9.24**	16.74**	6.84	32.17**	2.96	-4.34*
14	Pusa Sugandh-6xType-3	2.26	4.06	0.59	-2.86	5.02	-3.89	-23.24**	-29.79**
15	Pusa Sugandh-6xBasmati-370	2.25	0.15	-5.99*	-3.43	4.67	-10.93**	-28.59**	-34.69**
16	Pusa Sugandh-6xTarori Basmati-1	2.49	14.81**	11.14**	7.01**	3.42	-48.28**	-48.80**	-52.21**
17	Pusa Sugandh-6xPSD-15	2.29	5.29*	1.78	-1.72	6.89	11.46**	5.35**	-3.64
18	Pusa Sugandh-6xPant Basmati-1	2.53	17.16**	14.16**	8.44**	7.11	38.78**	8.72**	-0.56
19	Type-3xBasmati-370	2.34	0.65	-2.37	0.29	3.76	-4.24	-4.73	-47.41**
20	Type-3xTarori Basmati-1	2.27	1.04	0.89	-2.58	5.69	7.62**	-14.69**	-20.37**
21	Type-3xPSD-15	2.33	3.56	3.56	0.00	4.00	-17.78**	-31.31**	-44.06**
22	Type-3xPant Basmati-1	2.55	14.12**	13.19**	9.30**	4.85	27.41**	24.15**	-32.17**
23	Basmati-370xTarori Basmati-1	2.67	15.17**	11.56**	14.59**	5.45	2.70	-18.28**	-23.73**
24	Basmati-370xPSD-15	2.41	3.80	0.70	3.43	3.78	-22.62**	-35.09**	-47.13**
25	Basmati-370xPant Basmati-1	2.28	-1.01	-4.74	-2.15	6.89	80.14**	74.66**	-3.59
26	Tarori Basmati-1xPSD-15	2.18	-2.97	-3.11	-6.44*	7.02	12.30**	5.14**	-1.86
27	Tarori Basmati-1xPant Basmati-1	2.51	12.79**	12.04**	7.87**	5.28	1.80	-20.83**	-26.11**
28	PSD-15xPant Basmati-1	2.49	11.73**	10.81**	7.01**	6.93	45.51**	19.06**	-3.03

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check)=Standard heterosis over check

Pusa Sugandh-4 × Tarori Basmati-1 (19.31) followed by Pusa Sugandh-4 × Pant Basmati-1 (16.74), Basmati-370 × Tarori Basmati-1 (14.59), Pusa Basmati-1 × Type-3 (14.31), Pusa Basmati-1 × Basmati-370 (11.30), Type-3 × Pant Basmati-1 (9.3), Pusa Sugandh-6 × Pant Basmati-1 (8.44), Pusa Basmati-1 × Pusa Sugandh-4 (8.01), Pusa Sugandh-4 × Basmati-370 (7.87), Tarori Basmati-1 × Pant Basmati-1 (7.87), Pusa Sugandh-4 × Pusa Sugandh-6 (7.30), Pusa Sugandh-6 × Tarori Basmati-1 (7.01), PSD-15 × Pant Basmati-1 (7.01) and Pusa Sugandh-4 × PSD-15 (6.72). The cross Tarori Basmati-1 × PSD-15 showed significant negative heterosis (-6.44) for kernel elongation ratio over standard check.

4.3.20 Alkali digestion value

The range of heterosis over mid parent for alkali digestion value varied from -48.28% (Pusa Sugandh-6 × Tarori Basmati-1) to 80.14% (Basmati-370 × Pant Basmati-1). Among 28 crosses, 12 crosses showed significant positive heterosis while 5 crosses showed significant negative heterosis for alkali digestion value over mid-parent. The maximum significant positive heterosis for alkali digestion value over mid parent was exhibited by Basmati-370 × Pant Basmati-1 (80.14) followed by PSD-15 × Pant Basmati-1 (45.51), Pusa Sugandh-6 × Pant Basmati-1 (38.78), Pusa Sugandh-4 × Pant Basmati-1 (32.17), Type-3 × Pant Basmati-1 (27.41), Tarori Basmati-1 × PSD-15 (12.3), Pusa Sugandh-6 × PSD-15 (11.46), Type-3 × Tarori Basmati-1 (7.62), Pusa Sugandh-4 × Pusa Sugandh-6 (5.18), Pusa Sugandh-4 × Tarori Basmati-1 (4.88), Pusa Basmati 1 × Pant Basmati-1 (4.57) and Pusa Basmati-1 × Pusa Sugandh-6 (3.42). The maximum significant negative heterosis for alkali digestion value over mid parent was exhibited by Pusa Sugandh-6 × Tarori Basmati-1 (-48.28) followed by Basmati-370 × PSD-15 (-22.62), Type-3 × PSD-15 (-17.78), Pusa Sugandh-4 × Basmati-370 (-11.24) and Pusa Sugandh-6 × Basmati-370 (-10.93).

The range of heterosis over better parent for alkali digestion value varied from -48.8% (Pusa Sugandh-6 × Tarori Basmati-1) to 74.66% (Basmati-370 × Pant Basmati-1). Among 28 crosses 8 crosses showed significant positive heterosis while 16 cross showed significant negative heterosis for alkali digestion value over better parent. The maximum significant positive heterosis for alkali digestion value over better parent was exhibited by Basmati-370 × Pant Basmati-1 (74.66) and followed by Type-3 × Pant Basmati-1 (24.15), PSD-15 × Pant Basmati-1 (19.06), Pusa Sugandh-6 × Pant Basmati-1

(8.72), Pusa Sugandh-6×PSD-15(5.35), Tarori Basmati-1×PSD-15(5.14), Pusa Sugandh-4×Tarori Basmati-1(4.65) and Pusa Sugandh-4×Pusa Sugandh-6 (4.37). The maximum significant negative heterosis for alkali digestion value over better parent was exhibited by cross Pusa Sugandh-6×Tarori Basmati-1(-48.8) and followed by Basmati-370×PSD-15 (-35.09), Type-3×PSD-15(-31.31), Pusa Sugandh-4×Basmati-370 (-29.25), Pusa Sugandh-6×Basmati-370(-28.59), Pusa Sugandh-6×Type-3 (-23.24), Pusa Sugandh-4×Type-3 (-22.68), Pusa Basmati-1×Basmati-370 (-22.27), Pusa Basmati-1×Type-3 (-21.66), Tarori Basmati-1×Pant Basmati-1 (-20.83), Pusa Basmati-1×Pant Basmati-1 (-20.39), Basmati-370×Tarori Basmati-1 (-18.28), Type-3×Tarori Basmati-1 (-14.69), Pusa Basmati-1×PSD-15 (-8.98), Pusa Sugandh-4×PSD-15 (-5.47) and Pusa Basmati-1×Tarori Basmati-1 (-4.04).

Range of heterosis for number of alkali digestion value over standard check variety (Improved Pusa Basmati-1) varied from -4.34% (Pusa Sugandh-4×Pant Basmati-1) to -52.21% (Pusa Sugandh-6×Tarori Basmati-1). Among 28 crosses, 19 crosses showed significant negative heterosis for alkali digestion value over standard check variety. The maximum significant negative heterosis for alkali digestion value over standard check was exhibited by Pusa Sugandh-6×Tarori Basmati-1 (-52.21) followed by Type-3×Basmati-370 (-47.41), Basmati-370×PSD-15 (-47.13), Type-3×PSD-15 (-44.06), Pusa Sugandh-6×Basmati-370 (-34.69), Pusa Sugandh-4×Basmati-370 (-34.27), Type-3×Pant Basmati-1 (-32.17), Pusa Sugandh-6×Type-3 (-29.79), Pusa Sugandh-4×Type-3 (-28.16), Tarori Basmati-1×Pant Basmati-1 (-26.11), Basmati-370×Tarori Basmati-1 (-23.73), Pusa Basmati-1×Basmati-370 (-22.89), Pusa Basmati-1×Type-3 (-22.28), Pusa Basmati-1×Pant Basmati-1 (-21.03), Type-3×Tarori Basmati-1 (-20.37), Pusa Sugandh-4×PSD-15 (-12.17), Pusa Basmati-1×PSD-15 (-9.7), Pusa Basmati-1×Tarori Basmati-1 (-4.8) and Pusa Sugandh-4×Pant Basmati-1 (-4.34).

4.3.21 Amylose content (%)

The range of heterosis over mid parent for amylose content varied from -5.28% (Pusa Sugandh-4×Type-3) to 16.75% (Tarori Basmati-1×PSD-15). Among 28 crosses 21 crosses showed significant positive heterosis while 3 cross showed significant negative heterosis for amylose content over mid-parent. The maximum significant positive heterosis for amylose content over mid parent was exhibited by Tarori Basmati-1×PSD-15 (16.75) followed by Basmati-370×Pant Basmati-1 (16.72), Type-3

×Tarori Basmati-1 (14.59), Pusa Basmati-1×Pant Basmati-1 (12.23), Pusa Basmati-1×Tarori Basmati-1 (11.91), Pusa Sugandh-6×Pant Basmati-1 (11.49), PSD-15×Pant Basmati-1 (11.07), Basmati-370×Tarori Basmati-1 (10.67), Tarori Basmati-1×Pant Basmati-1 (8.83), Pusa Basmati-1×Basmati-370 (8.22), Pusa Sugandh-6×Basmati-370 (7.86), Pusa Sugandh-4×Tarori Basmati-1 (7.36), Pusa Basmati-1×Pusa Sugandh-6 (6.62), Pusa Sugandh-4×PSD-15 (5.09), Pusa Sugandh-4×Basmati-370 (4.93), Pusa Sugandh-6×PSD-15 (4.77), Pusa Sugandh-4×Pusa Sugandh-6 (3.96), Type-3×PSD-15 (3.81), Pusa Basmati-1×Type-3 (3.41), Pusa Sugandh-6×Tarori Basmati-1 (3.07) and Pusa Sugandh-6×Type-3 (3.01). The maximum significant negative heterosis for amylose content over mid parent was exhibited by Pusa Sugandh-4×Type-3 (-5.28) followed by Basmati-370×PSD-15 (-4.65) and Pusa Sugandh-4×Pant Basmati-1 (-3.07).

The range of heterosis over better parent for amylose content varied from -8.42% (Basmati-370×PSD-15) to 14.31% (Type-3×Tarori Basmati-1). Among 28 crosses 17 crosses showed significant positive heterosis while 6 cross showed significant negative heterosis for amylose content over better parent. The maximum significant positive heterosis for amylose content over better parent was exhibited by Type-3×Tarori Basmati-1 (14.31) and followed by Basmati-370×Pant Basmati-1 (14.26), Pusa Sugandh-6×Pant Basmati-1 (11.38), Pusa Basmati-1×Pant Basmati-1 (10.68), Pusa Basmati-1×Tarori Basmati-1 (10.62), Tarori Basmati-1×PSD-15 (9.63), Tarori Basmati-1×Pant Basmati-1 (8.57), Basmati-370×Tarori Basmati-1 (8.09), Pusa Sugandh-4×Tarori Basmati-1 (6.04), Pusa Sugandh-6×Basmati-370 (5.69), Pusa Basmati-1×Pusa Sugandh-6 (5.04), PSD-15 × Pant Basmati-1 (4.52), Pusa Basmati-1×Basmati-370 (4.5), Pusa Sugandh-4×Basmati-370 (3.74), Pusa Sugandh-4×Pusa Sugandh-6 (3.03), Pusa Sugandh-6×Type-3 (2.91) and Pusa Sugandh-6×Tarori Basmati-1 (2.72). The maximum significant negative heterosis for amylose content over better parent was exhibited by Basmati-370×PSD-15 (-8.42) and followed by Pusa Sugandh-4×Type-3 (-6.23), Pusa Basmati-1×PSD-15 (-5.89), Pusa Sugandh-4×Pant Basmati-1 (-4.03), Type-3×Basmati-370 (-2.62) and Type-3×PSD-15 (-2.31).

Range of heterosis for number of amylose content over standard check variety (Improved Pusa Basmati-1) varied from -16.8% (Basmati-370×PSD-15) to 14.31% (Type-3×Tarori Basmati-1). Among 28 crosses, 9 crosses showed significant positive and 14 crosses showed significant negative heterosis for amylose content over standard

Table 4.3.1: Contid.....

Sl. No	Crosses	Amylose content (%)			
		F ₁ Mean	MPH	BPH	SH (Check)
1	Pusa Basmati-1×Pusa Sugandh-4	21.55	1.75	-0.65	-3.09**
2	Pusa Basmati-1×Pusa Sugandh-6	22.78	6.62**	5.04**	2.46*
3	Pusa Basmati-1×Type-3	22.12	3.41**	1.98	-0.52
4	Pusa Basmati-1×Basmati-370	22.67	8.22**	4.50**	1.93
5	Pusa Basmati-1×Tarori Basmati-1	23.99	11.91**	10.62**	7.90**
6	Pusa Basmati-1×PSD-15	20.41	1.32	-5.89**	-8.20**
7	Pusa Basmati-1×Pant Basmati-1	24.01	12.23**	10.68**	7.96**
8	Pusa Sugandh-4×Pusa Sugandh-6	21.68	3.96**	3.03**	-2.49*
9	Pusa Sugandh-4×Type-3	19.78	-5.28 **	-6.23**	-11.06**
10	Pusa Sugandh-4×Basmati-370	21.44	4.93**	3.74**	-3.57**
11	Pusa Sugandh-4×Tarori Basmati-1	22.47	7.36**	6.04**	1.05
12	Pusa Sugandh-4×PSD-15	20.64	5.09**	-0.16	-7.20**
13	Pusa Sugandh-4×Pant Basmati-1	20.24	-3.07 **	-4.03**	-8.98**
14	Pusa Sugandh-6×Type-3	21.70	3.01**	2.91**	-2.40*
15	Pusa Sugandh-6×Basmati-370	22.24	7.86**	5.69**	0.03
16	Pusa Sugandh-6×Tarori Basmati-1	21.77	3.07**	2.72**	-2.11*
17	Pusa Sugandh-6×PSD-15	20.77	4.77**	-1.31	-6.60**
18	Pusa Sugandh-6×Pant Basmati-1	23.49	11.49**	11.38**	5.64**
19	Type-3×Basmati-370	20.54	-0.52	-2.62*	-7.65**
20	Type-3×Tarori Basmati-1	24.22	14.59**	14.31**	8.93**
21	Type-3×PSD-15	20.60	3.81**	-2.31*	-7.35**
22	Type-3×Pant Basmati-1	21.07	-0.08	-0.08	-5.23**
23	Basmati-370×Tarori Basmati-1	22.90	10.67**	8.09**	3.00**
24	Basmati-370×PSD-15	18.50	-4.65 **	-8.42**	-16.80 **
25	Basmati-370×Pant Basmati-1	24.10	16.72**	14.26**	8.36**
26	Tarori Basmati-1×PSD-15	23.23	16.75**	9.63**	4.47**
27	Tarori Basmati-1×Pant Basmati-1	23.01	8.83**	8.57**	3.46**
28	PSD-15×Pant Basmati-1	22.04	11.07**	4.52**	-0.87

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

MPH= Mid parent heterosis, BPH= Better parent heterosis, SH (Check) =Standard heterosis over check

check variety. The maximum significant positive heterosis for amylose content over standard check was exhibited by Type-3×Tarori Basmati-1 (8.93) followed by Basmati-370 ×Pant Basmati-1 (8.36), Pusa Basmati-1×Pant Basmati-1 (7.96), Pusa Basmati-1 ×Tarori Basmati-1 (7.9), Pusa Sugandh-6×Pant Basmati-1 (5.64), Tarori Basmati-1 ×PSD-15 (4.47), Basmati-370×Tarori Basmati-1 (3.00) and Pusa Basmati-1×Pusa Sugandh-6 (2.46). The maximum significant negative heterosis for amylose content over standard check was exhibited by Basmati-370×PSD-15 (-16.8) followed by Pusa Sugandh-4×Type-3 (-11.06), Pusa Sugandh-4×Pant Basmati-1 (-8.98), Pusa Basmati-1 ×PSD-15 (-8.2), Type-3×Basmati-370 (-7.65), Type-3×PSD-15 (-7.35), Pusa Sugandh-4 ×PSD-15 (-7.2), Pusa Sugandh-6×PSD-15 (-6.6), Type-3×Pant Basmati-1 (-5.23), Pusa Sugandh-4×Basmati-370 (-3.57), Pusa Basmati-1×Pusa Sugandh-4 (-3.09), Pusa Sugandh-4×Pusa Sugandh-6 (-2.49), Pusa Sugandh-6×Type-3(-2.4) and Pusa Sugandh-6 ×Tarori Basmati-1(-2.11).

Heterosis manifested in varietal crosses of maize encouraged other researchers to explore more about the possible benefits of varietal crosses. The heterosis concept started with the study reported by **Shull (1808)** entitled “the composition of field of maize”. The term ‘heterosis’ was coined by **Shull (1914)**. The diallel mating design has been extensively used to determine general and specific combining ability that is prerequisite for development of single and double cross hybrids. The manifestation of heterosis usually depends on: (1) degree of dominance and (2) dispersion of alleles in two parents (**Falconer, 1960**).

In the present investigation, the extent of heterosis over mid parent, better parent and over check (Improved Pusa Basmati-1) were estimated for 21 quantitative traits. For all the traits the F_1 crosses varied in magnitude and direction of heterosis. This can be ascribed to the presence of genetic diversity among parents for different traits. The results obtained for various traits are briefly discussed here:

Among 28 crosses, 15, 8 and 27 crosses exhibited significant negative heterosis over mid parent, better parent and standard check for days to 50% flowering. It was apparent from the results that the crosses Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4 ×Basmati-370, Pusa Sugandh-4×PSD-15, Type-3×Basmati-370, Basmati-370×Tarori Basmati-1 and Basmati-370×Pant Basmati-1 sowed significant negative heterosis over

mid parent, better parent and standard check for days to 50% flowering among 28 F₁ hybrid. From these crosses it is also appeared that the parents involved in these crosses contributed earliness genes responsible for reducing number of days to 50% flowering (**Virmani *et al.*, 1981; Dwivedi *et al.*, 1998; Saxena, 2000 and Alam *et al.*, 2004.**)

Among 28 crosses studied for the plant height only 6 and 2 crosses showed significant negative heterosis for plant height over mid parent and better parent respectively. None of the hybrid was dwarf than standard check. The significant positive heterosis shown by most of the crosses for plant height might produce the problem of lodging and suggests the importance of parental selection. It is apparent that in cross combination of Tarori Basmati-1×Pant Basmati-1 and Basmati-370×Tarori Basmati-1, parents produced reduced gene effect for plant height (**Pillai, 1961; Cheema *et al.*, 1999; Alam *et al.*, 2004; Saleem *et al.*, 2005 and Kumar *et al.*, 2012.**

Among 28 crosses, 17, 11 and 21 crosses exhibited significant positive heterosis over mid parent, better parent and standard check for flag leaf length, respectively. Crosses Pusa Sugandh-6×Type-3, Type-3×PSD-15, Tarori Basmati-1×PSD-15, Pusa Sugandh-4×Tarori Basmati-1, Pusa Basmati-1×Pusa Sugandh-6, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-4×PSD-15 and Pusa Basmati-1×PSD-15 had significant positive heterosis over mid parent, better parent and standard check. Similar findings were reported by **Alam *et al.* (2004) and Saleem *et al.* (2008).**

Hybrids with positive heterosis are desirable for panicle length. Results indicated that out of 28 crosses, 23, 21 and 17 crosses exhibited significant positive heterosis over mid parent, better parent and standard check, respectively. For panicle length, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1 and PSD-15×Pant Basmati-1 exhibited significant positive heterosis over mid parent, better parent and standard check. Similar findings were also reported by **Cheema *et al.* (1999), Alam *et al.* (2004) and saleem *et al.* (2005).**

Numbers of panicles/plant is generally associated with higher productivity. Therefore, the main interest is to find out the hybrids with more number of panicles/plant. For panicles/plant, out of 28 crosses, 27, 23 and 26 crosses showed significant positive heterosis over mid parent, better parent and standard check, respectively. The crosses Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1 and PSD-15×Pant Basmati-1 expressed significant positive heterosis over mid parent, better parent and standard check. Existence of significant positive heterosis for panicles/plant has been reported by **Alam *et al.* (2004)**, **Saleem *et al.* (2005)**, **Faiz *et al.* (2006)** and **Sarial *et al.* (2006)**.

Number of filled grains/panicle is closely associated with high yield. Results indicated that out of 28 crosses, 25, 21 and 23 crosses manifested significant positive heterosis over mid parent, better parent and standard check, respectively. Crosses Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Type-3×Basmati-370, Type-3×Tarori Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15 and Tarori Basmati-1×Pant Basmati-1 showed significant positive heterosis over mid parent, better parent and standard check. **Virmani *et al.* (1981)**, **Faiz *et al.* (2006)** and **Tiwari *et al.* (2011)** had reported similar findings.

Number of unfilled grains/panicle is negatively associated with grain yield. Results indicated that out of 28 crosses, 23, 14 and 01 crosses manifested significant positive heterosis over mid parent, better parent and standard check, respectively. The

only cross Tarori Basmati-1×PSD-15 showed negative heterosis over mid parent, better parent and standard check. **Virmani *et al.* (1981), Faiz *et al.* (2006) and Tiwari *et al.* (2011)** had reported similar findings.

Crosses Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15 and PSD-15×Pant Basmati-1 showed significant positive heterosis over mid parent, better parent and standard check for spikelet fertility.

Test weight is one of the most important components of grain yield that influences grain yield considerably. Out of 28 crosses, 18, 5 and 22 crosses manifested significant positive heterosis over mid parent, better parent and standard check, respectively. Crosses Basmati-370×Pant Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Basmati-370, Type-3×Pant Basmati-1 and Tarori Basmati-1×Pant Basmati-1 showed significant positive heterosis over mid parent, better parent and standard check for test weight. **Alam *et al.* (2004), Saleem *et al.* (2005) and Sarial *et al.* (2006)** also reported similar results.

Higher grain yield per plant is the main objective of any breeding programme. It is complex trait and multiplicative product of several basic component traits of grain yield. In the present study out of 28 crosses, 27, 23 and 28 crosses manifested significant positive heterosis over mid parent, better parent and standard check, respectively. Crosses Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×PSD-15, Basmati-370

×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×Pant Basmati-1 and PSD-15×Pant Basmati-1 exhibited significant positive heterosis over mid parent, better parent and standard check for grain yield/plant. **Virmani *et al.* (1881), Kaushik and Sharma (1986), Cheema *et al.* (1999), Alam *et al.* (2004), Saleem *et al.* (2005), Veni *et al.* (2005), Sarial *et al.* (2006), Rashmi *et al.* (2010), Tiwari *et al.* (2011) and Kumar *et al.* (2012)** also reported similar trend of heterosis for grain yield per plant.

Among several agronomic traits studied in the present investigation, majority of crosses for traits like panicle length, panicles/plant, filled grains/ panicle, spikelet fertility and grain yield/plant showed significant heterosis in desired direction while most of the crosses for traits like days to 50% flowering, plant height, flag leaf length and test weight exhibited significant heterosis in the direction that breeder is not interested. These findings are in agreement with the earlier reports of **Cheema *et al.* (1999), Bansal *et al.* (2000), Mahalingam and Nadarajan (2010), Rashmi *et al.* (2010), Joshi *et al.* (2011), Ashfaq *et al.* (2013), Shinde and Patel (2014), Gonya *et al.* (2015) and Veerasha *et al.* (2015).**

Out of 28 crosses, 16, 13 and 12 crosses showed significant heterosis over mid parent, better parent and standard check for hulling recovery, respectively. The crosses Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1 and PSD-15×Pant Basmati-1 exhibited significant positive heterosis over mid parent, better parent and standard check for hulling recovery. Similar findings were reported by **Saleem *et al.* (2008) and Rashmi *et al.* (2010).**

Out of 28 crosses, 14, 09 and 11 crosses showed significant positive heterosis over mid parent, better parent and standard check for milling recovery, respectively. The crosses Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Type-3×Pant Basmati-1, Tarori Basmati-1×Pant Basmati-1 and PSD-15×Pant Basmati-1 exhibited significant positive heterosis over mid parent, better parent and standard check for milling recovery. Similar findings were reported by **Pradhan *et al.* (2007).**

Among 28 crosses, 21, 06 and 11 crosses showed significant positive heterosis over mid parent, better parent and standard check, respectively, for kernel length. Six crosses viz., PSD-15×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati 1×Pant Basmati-1, Pusa Basmati-1×PSD-15, Type-3×Pant Basmati-1 and Pusa Sugandh-6×Tarori Basmati-1 showed significant positive heterosis over mid parent, better parent and standard check. Similar findings were reported by **Sarial *et al.* (2006)**.

Among 28 crosses, 06 and 05 and crosses showed significant heterosis in desired direction over mid parent and better parent for kernel breadth. Crosses Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Type-3×Pant Basmati-1, Pusa Basmati 1×Pant Basmati-1 and PSD-15×Pant Basmati-1 showed superiority for kernel breadth over both the parents. None of the crosses exhibited significant heterosis for kernel breadth over standard check. Similar findings were reported by **Alam *et al.* (2004)**.

Kernel length/ breadth ratio is an important quality parameter in basmati rice. Among 28 crosses, 09, 06 and 10 crosses showed significant positive heterosis for kernel length/ breadth ratio over mid parent, better parent and standard check, respectively. Crosses PSD-15×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati 1×Pant Basmati-1, Type-3×Pant Basmati-1, Pusa Basmati-1×PSD-15 and Pusa Sugandh-6×Tarori Basmati-1 exhibited significant positive heterosis over mid parent, better parent and standard check for length/ breadth ratio. Similar findings were reported by **Gonya *et al.* (2015)**.

For cooked kernel length, out of 28 crosses, 21, 11 and 16 crosses showed significant positive heterosis over mid parent, better parent and standard check. The crosses, PSD-15×Pant Basmati-1, Type-3×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Sugandh-6×PSD-15 and Pusa Basmati-1×Basmati-370 showed significant positive heterosis over mid parent, better parent and standard check for cooked kernel length. Similar findings were reported by **Venkanna *et al.* (2014)**.

Among 28 crosses, only one cross, Pusa Basmati-1×Tarori Basmati-1, showed heterosis for cooked kernel breadth over mid parent and two crosses, Pusa Basmati-1

×Tarori Basmati-1 and Pusa Basmati-1×Basmati-370, showed heterosis for cooked kernel breadth over standard check in desired direction for cooked kernel breadth. Similar findings were reported by **Gnanamalar and Vivekanandan (2013)**.

For cooked kernel length/breadth ratio out of 28 crosses, 16, 11 and 15 crosses exhibited significant positive heterosis over mid parent, better parent and standard check, respectively. The crosses, PSD-15×Pant Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Type-3, Pusa Basmati-1 × Basmati-370, Type-3 ×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Pusa Basmati-1×Pusa Sugandh-6 and Pusa Basmati-1×Pusa Sugandh-4 showed significant positive heterosis over mid parent, better parent and standard check. Similar findings were reported by **Kumari *et al.* (2014)**.

Among 28 crosses, 16, 10 and 14 crosses exhibited significant positive heterosis over mid parent and, better parent and standard check for elongation ratio, respectively. The crosses, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Sugandh-4 × Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Tarori Basmati-1×Pant Basmati-1 and PSD-15×Pant Basmati-1 showed significant positive heterosis over mid parent, better parent and standard check. Similar findings were reported by **Roy *et al.* (2009)**,

For alkali digestion value, 12 crosses exhibited significant positive heterosis over mid parent while 08 crosses exhibited significant positive heterosis over better parent. None of the 28 crosses showed significant positive heterosis over standard check.

For amylose content, out of 28 crosses, 21, 17 and 09 crosses showed significant heterosis over mid parent, better parent and standard check, respectively. The crosses, Type-3×Tarori Basmati-1, Type-3×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Tarori Basmati-1×PSD-15, Basmati-370×Tarori Basmati-1 and Pusa Basmati-1×Pusa Sugandh-6 showed significant positive heterosis over mid parent, better parent and standard check for amylose content.

In the present investigation, hulling recovery, milling recovery, kernel length, kernel breadth, kernel length/breadth ratio, cooked kernel length, cooked kernel breadth, cooked kernel length/breadth ratio, elongation ratio, alkali digestion value and amylose content were studied. For all the above rice grain quality parameters most of the crosses failed to register the heterosis for superior grain quality. Only few were superior either to better parent or standard check for the concerned trait. These findings are in agreement with the findings of **Lio *et al.* (2003)**, **Veni *et al.* (2005)**, **Pradhan *et al.* (2007)**, **Mahalingam and Nadarajan (2010)**, **Chougule *et al.* (2012)**, **Kumar *et al.* (2012)** and **Reddy *et al.* (2012)**.

The estimates of relative heterosis, heterobeltiosis and standard heterosis for hulling recovery, kernel length, cooked kernel length/breadth ratio and alkali digestion value were mostly negative. The crosses with negative effects indicate the reduction in performance of the trait in question. Lack of heterosis may be due to the additive effects of genes controlling the traits (**Chang *et al.*, 1973**).

Another reason for the significant negative heterosis may be assumed as the presence of dominant loci in different direction due to which there is cancellation of effects leading to absence of or negative heterosis. The crosses showing no heterosis may also be the indicative of no difference in gene frequencies in parents with respect to the trait under question (**Falconer, 1960**).

Heterosis is not a common phenomenon for all sorts of hybrids. The degree of heterosis varies greatly for different traits and among crosses for the same trait (**Cheema *et al.*, 1999**). It may, therefore, be desirable to involve a multiple crosses to incorporate such genes or gene complexes for developing improved cultivar.

A summary of promising hybrids manifesting significant heterosis for various traits over mid parent, better parent and standard check are depicted in **Table 4.3.2**, **4.3.3** and **4.3.4**, respectively. These hybrids may be exploited in breeding programme to improve yield and other rice quality parameters.

The overall mean of various traits in parental population and their hybrids with mean heterosis value is depicted in **Table 4.3.5**. The data suggested that the highest positive heterosis was observed for grain yield/plant (59.44) followed by panicles/plant (42.03), filled grains/panicle (22.92), panicle length (12.56), cooked kernel length (10.43),

Table 4.3.2: Summary of crosses showing significant mid parent heterosis in desired direction for various traits

Sl. No.	Traits	Number of crosses	Cross combinations
1	Days to 50% flowering	15	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Basmati-370, Type-3×Basmati-370, Type-3×PSD-15, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1
2	Plant height	06	Tarori Basmati-1×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Pant Sugandh Dhan-5×Pant Basmati-1, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-6×PSD-15
3	Flag leaf length	17	Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-6×Type-3, Type-3×PSD-15, Pusa Sugandh-6×Basmati-370, Tarori Basmati-1×PSD-15, Pusa Basmati-1×Pusa Sugandh-6, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Basmati-1×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Pusa Sugandh-6×PSD-15, Basmati-370×PSD-15, Pusa Basmati 1×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1
4	Panicle length	23	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant basmati-1, PSD-15×Pant Basmati-1
5	Panicles/plant	27	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant basmati-1, PSD-15×Pant Basmati-1
6	Filled grains/panicle	25	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1

7	Unfilled grains/panicle	23	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
8	Spikelet fertility	26	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant basmati-1, PSD-15×Pant Basmati-1
9	Test weight	18	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×PSD-15, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×PSD-15, Type-3×Tarori Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant basmati-1, PSD-15×Pant Basmati-1
10	Grain yield/plant	27	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4 ×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant basmati-1, PSD-15×Pant Basmati-1
11	Hulling recovery	16	Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant basmati-1, PSD-15×Pant Basmati-1
12	Milling recovery	14	Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1

13	Kernel length	21	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, PSD-15×Pant Basmati-1
14	Kernel breadth	06	Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1, PSD-15×Pant Basmati-1, Pusa Basmati 1×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Pant Basmati-1
15	Kernel length/breadth ratio	09	Type-3×Pant Basmati-1, PSD-15×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati 1×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Basmati-370×Pant Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3
16	Cooked kernel length	21	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Basmati-37, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, PSD-15×Pant Basmati-1
17	Cooked kernel breadth	01	Pusa Basmati-1×Tarori Basmati-1
18	Cooked kernel length/breadth ratio	16	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, PSD-15×Pant Basmati-1
19	Kernel elongation ratio	16	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
20	Alkali digestion value	12	Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, PSD-15×Pant Basmati-1
21	Amylose content	21	Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×PSD-15, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1

Table 4.3.3: Summary of crosses showing significant better parent heterosis in desired direction for various traits

Sl. No.	Traits	Number of crosses	Cross combinations
1.	Days to 50% flowering	08	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×PSD-15, Type-3×Basmati-370, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1
2.	Plant height	02	Tarori Basmati-1×Pant Basmati-1, Basmati-370×Tarori Basmati-1
3.	Flag leaf length	11	Pusa Sugandh-6×Type-3, Type-3×PSD-15, Tarori Basmati-1×PSD-15, Pusa Sugandh-4×Tarori Basmati-1, Pusa Basmati-1×Pusa Sugandh-6, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Basmati-1×PSD-15
4.	Panicle length	21	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
5.	Panicles/plant	23	Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
6.	Filled grains/panicle	21	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Type-3×Basmati-370, Type-3×Tarori Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1

7.	Unfilled grains/panicle	14	Pusa Basmati-1×Basmati-370, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Pant Basmati-1, PSD-15×Pant Basmati-1
8.	Spikelet fertility	25	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
9.	Test weight	05	Basmati-370×Pant Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Basmati-370, Type-3×Pant Basmati-1, Tarori Basmati-1×Pant Basmati-1
10.	Grain yield/plant	23	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×PSD-15, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
11.	Hulling recovery	13	PSD-15×Pant Basmati-1, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Type-3×Pant Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Tarori Basmati-1×Pant Basmati-1, Tarori Basmati-1×PSD-15, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×PSD-15
12.	Milling recovery	09	Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Type-3×Pant Basmati-1, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
13.	Kernel length	06	PSD-15×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati 1×Pant Basmati-1, Pusa Basmati-1×PSD-15, Type-3×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1

14.	Kernel breadth	05	Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Type-3×Pant Basmati-1, Pusa Basmati 1× Pant Basmati-1, PSD-15×Pant Basmati-1
15.	Kernel length/breadth ratio	06	PSD-15×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati 1×Pant Basmati-1, Type-3×Pant Basmati-1, Pusa Basmati-1×PSD-15, Pusa Sugandh-6×Tarori Basmati-1
16.	Cooked kernel length	11	PSD-15×Pant Basmati-1, Type-3×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Sugandh-6×PSD-15, Pusa Basmati-1×Basmati-370
17.	Cooked kernel breadth	0	-----
18.	Cooked kernel length/breadth ratio	11	PSD-15×Pant Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Type-3, Pusa Basmati-1 × Basmati-370, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Pusa Sugandh-4
19.	Kernel elongation ratio	10	Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
20.	Alkali digestion value	08	Basmati-370×Pant Basmati-1, Type-3×Pant Basmati-1, PSD-15×Pant Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Pusa Sugandh-6×PSD-15, Tarori Basmati-1×PSD-15, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6
21.	Amylose content	17	Type-3×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-6×Basmati-370, Pusa Basmati-1×Pusa Sugandh-6, PSD-15 x Pant Basmati-1, Pusa Basmati-1×Basmati-370, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Tarori Basmati-1

Table 4.3.4: Summary of crosses showing significant Standard heterosis in desired direction for various traits

Sl. No.	Traits	Number of crosses	Cross combinations
1	Days to 50% flowering	27	Pusa Basmati-1×Pusa Sugandh-6, PSD-15×Pant Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×PSD-15, Basmati-370×Pant Basmati-1, Pusa Basmati-1×Pusa Sugandh-4, Pusa Sugandh-4×Pusa Sugandh-6, Tarori Basmati-1×Pant Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Tarori Basmati-1×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Type-3×PSD-15, Pusa Basmati 1×Pant Basmati-1, Type-3×Pant Basmati-1, Pusa Basmati-1×PSD-15, Pusa Sugandh-4×Type-3, Pusa Sugandh-6×Type-3, Pusa Sugandh-4×Tarori Basmati-1, Basmati-370×PSD-15, Pusa Sugandh-6×Tarori Basmati-1, Type-3×Basmati-370, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-6×Basmati-370, Basmati-370×Tarori Basmati-1, Type-3×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Basmati-370
2	Plant height	0	
3	Flag leaf length	21	Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×PSD-15, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1
4	Panicle length	17	Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
5	Panicles/plant	26	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
6	Filled grains/panicle	23	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Tarori Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1

7	Unfilled grains/panicle	01	Tarori Basmati-1×PSD-15
8	Spikelet fertility	22	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, PSD-15×Pant Basmati-1
9	Test weight	22	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1 × Pusa Sugandh-6, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4 × Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Tarori Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
10	Grain yield/plant	28	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×PSD-15, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
11	Hulling recovery	12	Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×Pant Basmati-1, PSD-15×Pant Basmati-1
12	Milling recovery	11	Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, PSD-15 × Pant Basmati-1
13	Kernel length	11	PSD-15×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati 1×Pant Basmati-1, Type-3×Pant Basmati-1, Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×PSD-15, Pusa Sugandh-6×PSD-15, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pusa Sugandh-6

14	Kernel breadth	0	
15	Kernel length/breadth ratio	10	Pusa Sugandh-6×Tarori Basmati-1, PSD-15×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×PSD-15, Type-3×Pant Basmati-1, Pusa Basmati-1×PSD-15, Pusa Sugandh-6×PSD-15, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Pusa Sugandh-4
16	Cooked kernel length	16	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, PSD-15×Pant Basmati-1
17	Cooked kernel breadth	02	Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Basmati-370
18	Cooked kernel length/breadth ratio	15	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, PSD-15×Pant Basmati-1
19	Kernel elongation ratio	14	Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Pusa Sugandh-6×Pant Basmati-1, Type-3×Basmati-370, Type-3×Tarori Basmati-1, Type-3×PSD-15, Type-3×Pant Basmati-1, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Basmati-370×Pant Basmati-1, Tarori Basmati-1×Pant Basmati-1, PSD-15×Pant Basmati-1
20	Alkali digestion value	0	
21	Amylose content	09	Type-3×Tarori Basmati-1, Type-3×Tarori Basmati-1, Basmati-370×Pant Basmati-1, Pusa Basmati-1×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Tarori Basmati-1×PSD-15, Basmati-370×Tarori Basmati-1, Pusa Basmati-1×Pusa Sugandh-6

Table 4.3.5: Mean performance of parents and hybrids and mean heterosis for various traits

Sl. No.	Traits	Mean of hybrids	Parents	Mean heterosis (%)
1	Days to 50% flowering	102.15	104.21	-1.97
2	Plant height (cm)	127.78	112.19	13.90
3	Flag leaf length (cm)	35.43	33.53	5.64
4	Panicle length (cm)	32.45	28.83	12.56
5	Panicles/plant	18.90	13.31	42.03
6	Filled grains/panicle	169.18	137.63	22.92
7	Unfilled grains/panicle	48.19	52.84	-8.79
8	Spikelet fertility (%)	77.75	72.31	7.52
9	Test weight (g)	24.45	22.56	8.36
10	Grain yield/plant (g)	37.85	23.74	59.44
11	Hulling recovery (%)	76.87	75.04	2.43
12	Milling recovery (%)	68.95	66.95	3.00
13	Kernel length (mm)	6.84	6.64	3.08
14	Kernel breadth (mm)	1.76	1.72	2.41
15	Kernel length/breadth ratio	3.91	3.86	1.31
16	Cooked kernel length (mm)	16.71	15.13	10.43
17	Cooked kernel breadth (mm)	2.50	2.43	3.06
18	Cooked kernel length/breadth ratio	6.83	6.23	9.65
19	Kernel elongation ratio	2.45	2.28	7.24
20	Alkali digestion value	5.77	5.54	4.20
21	Amylose content (%)	21.93	20.70	5.94

cooked kernel length/breadth ratio (9.65), test weight (8.36), spikelet fertility (7.52), kernel elongation ratio (7.24), amylose content (5.94), flag leaf length (5.64), alkali digestion value (4.20), kernel length (3.08), cooked kernel breadth (2.41), milling recovery (3.00), hulling recovery (2.43), kernel breadth (2.41) and kernel length/breadth ratio (1.31). Overall negative heterosis was found for unfilled grains/panicle (-8.79) and days to 50% flowering (-1.97). These findings are in agreement with the earlier reports of **Alam *et al.* (2004)**, **Sarial *et al.* (2006)**, **Pradhan *et al.* (2007)**, **Saleem *et al.* (2008)** and **Rahimi *et al.* (2010)**.

4.4. Combining ability

Combining ability analysis as an effective tool for identifying superior parents for hybrid development has been divided into two categories by **Sprague and Tatum (1942)**, *i.e.*, general combining ability and specific combining ability. General combining ability (GCA) denotes the average performance of the lines in a series of cross combinations while the specific combining ability (SCA) is the deviation of a specific cross combination from expectation on the basis of GCA of combining parents. Both GCA and SCA variances have been determined and related to the possible types of gene action involved. The variance of GCA includes additive genetic component while SCA variance usually includes non-additive genetic component of the total genetic variance arising largely from dominance and epistatic deviations.

4.4.1. Analysis of variance

In the present investigation, an 8 × 8 half diallel set of crosses along with the parents were evaluated for twenty one traits. The ANOVA for various traits is presented in **Table 4.4.1.1**.

The perusal of ANOVA indicated highly significant variance for all the traits included under investigation. The sum of squares due to treatments was further partitioned in to three component *viz.*, among parents, among hybrids and parents vs. hybrids.

The differences were highly significant among parents for days to 50% flowering, plant height, flag leaf length, panicles/plant, filled grains/panicle, unfilled grains/panicle, spikelet fertility, test weight, grain yield/plant, hulling recovery, milling recovery, kernel length, kernel length/breadth ratio, cooked kernel length, cooked kernel length/breadth ratio, kernel elongation ratio, alkali digestion value and amylose content while significant

Table 4.4.1.1: ANOVA of diallel set for various traits

Source of variation	Degree of freedom	Mean sum of squares						
		Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/plant	Filled grains/panicle	Unfilled grains/panicle
Replication	2	9.03	6.83	0.10	0.13	0.17	2.23	3.93
Treatment	35	75.74**	972.38**	33.20**	28.21**	40.81**	1419.34**	157.88**
Parents	7	114.95**	851.88**	28.96**	2.10*	4.76**	864.24**	239.97**
Hybrids	27	65.47**	871.53**	33.06**	26.96**	30.02**	927.89**	127.54**
Parent vs. Hybrids	1	78.72**	4538.77**	66.88**	244.65**	584.29**	18574.26**	402.48**
Error	70	6.24	4.66	0.38	0.62	0.42	93.55	5.99
Total	107	29.02	321.24	11.11	9.64	13.63	525.51	55.64
CV (%)		2.417	1.746	1.779	2.530	3.685	5.919	4.960

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.4.1.1: Contd.....

Source of variation	Degree of freedom	Mean sum of squares						
		Spikelet fertility (%)	Test weight (g)	Grain yield/plant (g)	Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel breadth (mm)
Replication	2	0.36	0.86	8.05	0.24	0.17	0.01	0.00
Treatment	35	36.49**	14.95**	292.36**	12.37**	12.37**	1.32**	0.02**
Parents	7	14.03**	24.17**	76.77**	10.49**	7.20**	1.37**	0.01*
Hybrids	27	23.21**	10.66**	221.40**	11.01**	11.39**	1.33**	0.03**
Parent vs. Hybrids	1	552.31**	66.41**	3717.51**	62.16**	75.07**	0.78**	0.03*
Error	70	1.54	0.69	3.41	0.23	1.12	0.01	0.00
Total	107	12.95	5.36	98.01	4.20	4.78	0.44	0.01
CV (%)		1.609	3.425	5.322	0.624	1.534	1.750	2.971

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.4.1.1: Contd.....

Source of variation	Degree of freedom	Mean sum of squares						
		Kernel length/breadth ratio	Cooked kernel length (mm)	Cooked kernel breadth (mm)	Cooked kernel length/breadth ratio	Kernel elongation ratio	Alkali digestion value	Amylose content (%)
Replication	2	0.02	0.02	0.01	0.02	0.01	0.05	0.17
Treatment	35	0.80**	10.00**	0.16**	3.09**	0.08**	4.49**	6.15**
Parents	7	0.47**	8.83**	0.01	1.00**	0.04**	6.24**	2.70**
Hybrids	27	0.92**	8.96**	0.20**	3.50**	0.07**	4.17**	6.22**
Parent vs. Hybrids	1	0.05	46.52**	0.10	6.74**	0.51**	1.01**	28.25**
Error	70	0.02	0.19	0.02	0.14	0.01	0.02	0.07
Total	107	0.28	3.40	0.06	1.10	0.03	1.49	2.06
CV (%)		3.667	2.823	5.731	5.480	3.257	2.704	1.215

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

for panicle length and kernel breadth. The differences for cooked kernel breadth among parents was insignificant. Among hybrids the differences were highly significant for all the studied traits. The group mean comparison of parents vs. hybrids were highly significant for days to 50% flowering, plant height, flag leaf length, panicle length, panicles/plant, filled grains/panicle, unfilled grains/panicle, spikelet fertility, test weight, grain yield/plant, hulling recovery, milling recovery, kernel length, cooked kernel length, cooked kernel length/breadth ratio, kernel elongation ratio, alkali digestion value and amylose content; significant for kernel breadth and insignificant for kernel length/breadth ratio and cooked kernel breadth.

4.4.2. Analysis of variance for combining ability

The analysis of variance for combining ability for twenty one traits included under investigation is presented in **Table 4.4.2.1**. ANOVA for combining ability revealed highly significant general combining ability (GCA) variance and specific combining ability (SCA) variance for all the traits studied. It showed that both additive and non-additive genetic variance were important for expression of these traits. The results are in agreement with the findings of **Ceng (1977)**, **Singh and Nanda (1997)**, **Cheema and Awan (1985)**, **Geetha (1998)** and **Kumar *et al.* (2007)** for most of the traits.

The magnitude of mean square due to GCA was greater than SCA for days to 50% flowering, plant height, flag leaf length, panicle length, filled grains/panicle, test weight, grain yield/plant, kernel length, kernel length/breadth ratio, cooked kernel length, cooked kernel breadth, cooked kernel length/breadth ratio, kernel elongation ratio, alkali digestion value and amylose content. Whereas, for panicles/plant, unfilled grains/panicle, spikelet fertility, hulling recovery and milling recovery, magnitude of mean square due to SCA was greater than GCA.

The estimate of GCA variance (σ^2 GCA) was greater than SCA variance (σ^2 SCA) for days to 50% flowering and therefore the ratio of variance of GCA to that of SCA was greater than unity (1.07). All the remaining traits (except days to 50% flowering) had lower GCA variance (σ^2 GCA) than SCA variance (σ^2 SCA) and hence the ratio of variance of GCA to that of SCA was lesser than unity.

Table 4.4.2.1: ANOVA for general combining ability (GCA) and specific combining ability (SCA) for various traits

Source of variation	Degree of freedom	Mean sum of squares						
		Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/plant	Filled grains/panicle	Unfilled grains/panicle
GCA	7.00	86.37**	940.75**	11.14**	13.29**	3.46**	806.88**	35.41**
SCA	28.00	9.97**	169.97**	11.05**	8.43**	16.14**	389.67**	56.93**
Error	70.00	2.08	1.55	0.13	0.21	0.14	31.18	2.00
Components of variance								
σ^2_g		8.43	93.92	1.10	1.31	0.33	77.57	3.34
σ^2_s		7.89	168.42	10.92	8.22	16.00	358.49	54.94
σ^2_e		2.08	1.55	0.13	0.21	0.14	31.18	2.00
σ^2_a		16.86	187.84	2.20	2.62	0.66	155.14	6.68
σ^2_D		7.89	168.42	10.92	8.22	16.00	358.49	54.94
σ^2_P		26.83	357.81	13.25	11.05	16.80	544.81	63.61
h^2 (narrow sense)		0.63	0.52	0.17	0.24	0.04	0.28	0.11
σ^2_g / σ^2_s		1.07	0.56	0.10	0.16	0.02	0.22	0.06
Predictability		0.68	0.53	0.17	0.24	0.04	0.30	0.11

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.4.2.1: Continued.....

Source of variation	Degree of freedom	Mean sum of squares						
		Spikelet fertility (%)	Test weight (g)	Grain yield/plant (g)	Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel breadth (mm)
GCA	7.00	9.77**	13.99**	130.94**	2.10**	4.01**	0.73**	0.01**
SCA	28.00	12.76**	2.73**	89.08**	4.63**	4.15**	0.37**	0.01**
Error	70.00	0.51	0.23	1.14	0.08	0.37	0.00	0.00
Components of variance								
σ^2_g		0.93	1.38	12.98	0.20	0.36	0.07	0.00
σ^2_s		12.25	2.50	87.94	4.55	3.78	0.36	0.01
σ^2_e		0.51	0.23	1.14	0.08	0.37	0.00	0.00
σ^2_a		1.85	2.75	25.96	0.40	0.73	0.14	0.00
σ^2_D		12.25	2.50	87.94	4.55	3.78	0.36	0.01
σ^2_P		14.61	5.49	115.04	5.03	4.88	0.51	0.01
h^2 (narrow sense)		0.13	0.50	0.23	0.08	0.15	0.28	0.25
σ^2_g / σ^2_s		0.08	0.55	0.15	0.04	0.10	0.20	0.19
Predictability		0.13	0.52	0.23	0.08	0.16	0.28	0.28

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.4.2.1: Contd.....

Source of variation	Degree of freedom	Mean sum of squares						
		Kernel length/breadth ratio	Cooked kernel length (mm)	Cooked kernel breadth (mm)	Cooked kernel length/breadth ratio	Kernel elongation ratio	Alkali digestion value	Amylose content (%)
GCA	7.00	0.42**	5.49**	0.06**	1.31**	0.04**	3.79**	4.65**
SCA	28.00	0.23**	2.80**	0.05**	0.96**	0.02**	0.92**	1.40**
Error	70.00	0.01	0.06	0.01	0.05	0.00	0.01	0.02
Components of variance								
σ^2_g		0.04	0.54	0.01	0.13	0.00	0.38	0.46
σ^2_s		0.22	2.73	0.04	0.91	0.02	0.92	1.38
σ^2_e		0.01	0.06	0.01	0.05	0.00	0.01	0.02
σ^2_a		0.08	1.08	0.01	0.25	0.01	0.76	0.93
σ^2_D		0.22	2.73	0.04	0.91	0.02	0.92	1.38
σ^2_P		0.31	3.88	0.06	1.21	0.03	1.68	2.32
h^2 (narrow sense)		0.26	0.28	0.19	0.21	0.26	0.45	0.40
σ^2_g / σ^2_s		0.18	0.20	0.13	0.14	0.19	0.41	0.34
Predictability		0.27	0.28	0.21	0.22	0.28	0.45	0.40

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

The highest estimates of predictability ratio were observed for days to 50% flowering (0.68), plant height (0.53) and test weight (0.52). The lowest value estimates of predictability ratio were observed for filled grains/panicle (0.3), kernel length (0.28), kernel breadth (0.28) cooked kernel length (0.28), kernel elongation ratio (0.28), kernel length/breadth ratio (0.27), Panicle length (0.24), grain yield/plant (0.23), cooked kernel length/breadth ratio (0.22), cooked kernel breadth (0.21), flag leaf length (0.17), milling recovery (0.16), spikelet fertility (0.13), unfilled grains/panicle (0.11), hulling recovery (0.08) and panicles/plant (0.04). The moderate estimates of predictability ratio were observed for alkali digestion value (0.45) and amylose content (0.4) (**Table 4.4.2.1**).

Estimates of GCA variance (σ^2_{GCA}) and SCA variance (σ^2_{SCA}) were used to determine the additive (σ^2_A) and non additive (σ^2_D) components of population variance and predictability ratio $\sigma^2_A/(\sigma^2_A + \sigma^2_D)$. A high predictability ratio (>0.5) indicates preponderance of additive gene action, low predictability ratio (< 0.5) indicates non additive gene action and predictability ratio equal to or near to 0.5 indicates equivalence of both additive and non-additive gene action in the expression of the traits.

The variance due to GCA was higher than SCA as evidenced by the $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio being greater than unity along with high predictability ratio suggesting major role of additive gene action in the expression of the trait days to 50% flowering. The variance due to GCA was lower than SCA as indicated by the $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratio being less than unity with low predictability ratio suggesting significant role of non-additive gene action (dominance, epistasis and other interaction effects) in the expression of traits filled grains/panicle, kernel length, kernel breadth cooked kernel length, kernel elongation ratio, kernel length/breadth ratio, Panicle length, grain yield/plant, cooked kernel length/breadth ratio, cooked kernel breadth, flag leaf length, milling recovery, spikelet fertility, unfilled grains/panicle, hulling recovery and panicles/plant. The lower estimates of GCA variance than SCA variance along with moderate predictability ratio was observed for plant height, test weight, alkali digestion value and amylose content, indicating equivalence of both additive and non-additive gene action in the expression of these traits. The present observations are in agreement with the finding of **Hosseini *et al.* (2005), Shankar *et al.* (2009), Saleem *et al.* (2010), Dwivedi and Pandey (2012), Ghara *et al.* (2012), Roy and Senapati (2012) and**

Prasad *et al.* (2013). Tiwari *et al.* (2011) reported the higher magnitude of SCA than GCA variance and lower values of predictability ratio for various yield and yield contributing traits suggesting the role of non-additive gene action.

4.4.3. Estimates of general and specific combining ability effects

The estimates of GCA effects of parents and SCA effects of crosses for all the studied traits have been presented in **Table 4.4.3.1** and **Table 4.4.3.2**, respectively. The result for each of the individual traits is described below:

4.4.3.1. Days to 50% flowering

The result indicated that significantly negative GCA effect estimates were observed for Pant Basmati-1 (-3.65) followed by PSD-15 (-3.28), Pusa Sugandh-6 (-2.12) and Pusa Sugandh-4 (-1.18). This indicated that these parents were good general combiners for earliness. The significant positive GCA effect was recorded for Basmati-370 (3.72) followed by Pusa Basmati-1 (3.25) and Type-3 (2.25). Thus, these parents were good general combiner for lateness.

The SCA effect for days to 50% flowering ranged from -8.08 (Pusa Basmati-1×Pusa Sugandh-6) to 8.22 (Pusa Basmati-1×Type-3). Out of 28 crosses, 4 crosses exhibited significant negative SCA effect while only one cross exhibited significant positive SCA effects. The best specific combiner for early flowering was Pusa Basmati-1 ×Pusa Sugandh-6 (-8.08) followed by Pusa Basmati-1×Pusa Sugandh-4 (-5.68), Basmati-370×Pant Basmati-1 (-4.34) and Type-3×Basmati-370 (-3.91).

4.4.3.2. Plant height (cm)

Significantly negative estimates of GCA effect was observed for Pant Basmati-1 (-15.55) followed by Pusa Basmati-1 (-7.29), Pusa Sugandh-6 (-3.98) and Pusa Sugandh-4 (-2.86). This indicated that these parents were good general combiners for reduced plant height. The significant positive GCA effect was recorded for Basmati-370 (16.24) followed by Type-3 (6.69), PSD-15 (5.41) and Tarori Basmati-1 (1.34). Thus, these parents were good general combiner for tall plant stature.

The SCA effect for plant height ranged from -12.66 (Pusa Basmati-1×Pusa Sugandh-6) to 23.30 (Pusa Sugandh-6×Type-3). Out of 28 crosses, 8 crosses exhibited significant negative SCA effect while 13 crosses exhibited significant positive SCA

effects. The best specific combiner for reduced plant height were Pusa Basmati-1×Pusa Sugandh-6 (-12.66) followed by Basmati-370×Tarori Basmati-1 (-11.23), Type-3×Tarori Basmati-1 (-7.98), Pusa Sugandh-6×PSD-15 (-7.62), PSD-15×Pant Basmati-1 (-7.14), Tarori Basmati-1×Pant Basmati-1 (-6.42), Pusa Sugandh-4×Pant Basmati-1 (-5.04) and Type-3×Basmati-370 (-3.58).

4.4.3.3. Flag leaf length (cm)

Significantly positive estimates of GCA effect for flag leaf length was observed for Tarori Basmati-1 (1.55) followed by Pusa Sugandh-6 (0.83) and PSD-15 (0.60). Hence, these parents were good general combiners for longer flag leaf. The significant negative GCA effect was recorded for Pusa Basmati-1 (-1.49) followed by Type-3 (-1.16) and Pusa Sugandh-4 (-0.82). Thus, these parents were good general combiner for shorter flag leaf.

The SCA effect for flag leaf length among crosses ranged from -5.52 (PSD-15×Pant Basmati-1) to 5.69 (Type-3×PSD-15). Out of 28 crosses, 11 crosses exhibited significant positive SCA effect while 9 crosses exhibited significant negative SCA effects. The best specific combiner for longer flag leaf were Type-3×PSD-15 (5.69) followed by Pusa Sugandh-4×Tarori Basmati-1 (5.46), Pusa Sugandh-6×Type-3 (4.59), Pusa Sugandh-4×Pant Basmati-1 (4.49) and Pusa Sugandh-6×Basmati-370 (4.49).

4.4.3.4. Panicle length (cm)

Significantly positive estimates of GCA effect for panicle length was observed for Pant Basmati-1 (2.45) followed by Pusa Basmati-1 (0.45) and PSD-15 (0.42). Hence, these parents were good general combiners for longer panicles. The significant negative GCA effect was recorded for Tarori Basmati-1 (-1.09) followed by Basmati-370 (-0.99), Type-3 (-0.62) and Pusa Sugandh-4 (-0.62). Thus, these parents were good general combiner for smaller panicles.

The SCA effect for panicle length among crosses ranged from -3.54 (Basmati-370×Tarori Basmati-1) to 5.83 (Pusa Sugandh-4×Pant Basmati-1). Out of 28 crosses, 12 crosses exhibited significant positive SCA effect while 4 crosses exhibited significant negative SCA effects. The best specific combiner for longer panicle were Pusa Sugandh-4×Pant Basmati-1 (5.83) followed by Tarori Basmati-1×PSD-15 (5.02), Pusa Basmati-1×Tarori Basmati-1 (4.76), Pusa Sugandh-6×Basmati-370 (3.69) and Pusa Sugandh-6×Type-3 (3.42).

Table 4.4.3.1: Estimates of general combining ability (GCA) effect of parents for various traits

Sl. No.	Parents	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/plant	Filled/panicle	Unfilled grains/panicle
1.	Pusa Basmati-1	3.25**	-7.29**	-1.49**	0.45*	-0.57**	-3.53	-2.67**
2.	Pusa Sugandh-4	-1.18*	-2.86**	-0.82**	-0.62**	-0.02	7.76**	0.80
3.	Pusa Sugandh-6	-2.12**	-3.98**	0.83**	-0.01	-0.02	12.44**	0.89
4.	Type-3	2.25**	6.69**	-1.16**	-0.62**	0.39**	3.53	2.90**
5.	Basmati-370	3.72**	16.24**	0.24	-0.99**	0.99**	6.01**	0.02
6.	Tarori Basmati-1	1.02	1.34**	1.55**	-1.09**	-0.43**	-2.99	-2.33**
7.	PSD-15	-3.28**	5.41**	0.60**	0.42*	0.42**	-13.92**	-0.86
8.	Pant Basmati-1	-3.65**	-15.55**	0.25	2.45**	-0.78**	-9.29**	1.26*
	SE (g _i)	1.01	0.87	0.25	0.32	0.26	3.91	0.99
	SE (g _i - g _j)	1.52	1.32	0.38	0.48	0.40	5.91	1.49

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.4.3.2: Estimates of specific combining ability (SCA) effect of hybrids for various traits

Sl. No	Crosses	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/plant	Filled grains/panicle	Unfilled grains/panicle
1	Pusa Basmati-1xPusa Sugandh-4	-5.68**	-1.31	-1.30**	-0.54	-0.84	7.24	4.12*
2	Pusa Basmati-1xPusa Sugandh-6	-8.08**	-12.66**	1.72**	-1.35*	3.43**	27.26**	3.72*
3	Pusa Basmati-1xType-3	8.22**	11.96**	-0.85	1.33*	2.22**	4.30	1.94
4	Pusa Basmati-1xBasmati-370	1.42	13.26**	-0.79	1.03	2.32**	22.88**	-1.14
5	Pusa Basmati-1xTarori Basmati-1	0.79	12.90**	-0.39	4.76**	-2.56**	-1.42	-2.65
6	Pusa Basmati-1xPSD-15	0.09	-1.04	1.02*	-0.91	2.65**	-8.62	-5.02**
7	Pusa Basmati-1xPant Basmati-1	-1.88	4.25**	2.37**	1.96**	0.09	-4.02	-4.41*
8	Pusa Sugandh-4xPusa Sugandh-6	-0.98	0.48	-0.92*	-0.18	4.04**	14.47*	-2.62
9	Pusa Sugandh-4xType-3	-0.34	15.95**	0.50	0.16	3.53**	4.02	-12.66**
10	Pusa Sugandh-4xBasmati-370	-0.48	-1.57	-2.13**	-0.34	0.03	1.13	-2.21
11	Pusa Sugandh-4xTarori Basmati-1	1.22	6.04**	5.46**	-1.87**	-1.42**	7.00	1.64
12	Pusa Sugandh-4xPSD-15	-1.81	10.26**	0.84	-1.11	-3.00**	31.53**	3.44
13	Pusa Sugandh-4xPant Basmati-1	1.89	-5.04**	4.49**	5.83**	1.23*	-22.82**	-8.55**
14	Pusa Sugandh-6xType-3	0.59	23.30**	4.59**	3.42**	-2.84**	6.54	-6.89**
15	Pusa Sugandh-6xBasmati-370	0.79	15.28**	4.49**	3.69**	0.90	2.79	-9.77**
16	Pusa Sugandh-6xTarori Basmati-1	1.82	8.14**	0.22	-1.65**	5.92**	12.72	1.78
17	Pusa Sugandh-6xPSD-15	-0.21	-7.62**	-1.81**	-0.39	0.33	10.62	-3.72*
18	Pusa Sugandh-6xPant Basmati-1	2.16	0.34	2.05**	2.12**	-1.64**	-16.45*	-6.81
19	Type-3xBasmati-370	-3.91*	-3.58*	-0.65	-0.97	-5.34**	6.86	-2.38
20	Type-3xTarori Basmati-1	0.12	-7.98**	-3.76**	0.13	2.94**	9.06	7.20**
21	Type-3xPSD-15	-1.24	15.42**	5.69**	1.25*	6.12**	-8.21	19.20**
22	Type-3xPant Basmati-1	0.79	9.78**	-2.43**	-0.82	4.69**	25.46**	-0.09
23	Basmati-370xTarori Basmati-1	-2.01	-11.23**	0.31	-3.54**	3.31**	16.48*	2.29
24	Basmati-370xPSD-15	0.62	14.73**	1.02*	1.99**	5.96**	9.34	5.12**
25	Basmati-370xPant Basmati-1	-4.34*	-0.01	-5.20**	1.36*	3.29**	8.28	-2.47
26	Tarori Basmati-1xPSD-15	-1.01	0.54	3.91**	5.02**	0.64	13.44	-6.40**
27	Tarori Basmati-1xPant Basmati-1	-1.64	-6.42**	-1.17*	0.63	-1.89**	11.71	6.31**
28	PSD-15xPant Basmati-1	0.32	-7.14**	-5.52**	1.55**	0.72	4.68	-7.89**
	SE (S_{ij})	2.68	2.32	0.66	0.85	0.70	10.39	2.63
	SE ($S_{ij} - S_{ik}$)	3.97	3.43	0.98	1.25	1.04	15.37	3.89
	SE ($S_{ij} - S_{kl}$)	3.74	3.23	0.92	1.18	0.98	14.49	3.67

4.4.3.5. Number of panicles per plant

Significantly positive estimates of GCA effect for panicles/plant was observed for Basmati-370 (0.99) followed by PSD-15 (0.42) and Type-3 (0.39). Hence, these parents were good general combiners for panicles/plant. The significant negative GCA effect was recorded for Pant Basmati-1 (-0.78) followed by Pusa Basmati-1 (-0.57) and Tarori Basmati-1 (-0.43). Thus, these parents were good general combiner for fewer panicles/plant.

The SCA effect for panicles/plant among crosses ranged from -5.34 (Type-3 × Basmati-370) to 6.12 (Type-3 × PSD-15). Out of 28 crosses, 14 crosses exhibited significant positive SCA effect while 7 crosses exhibited significant negative SCA effects. The best specific combiner for panicles/plant were Type-3 × PSD-15 (6.12) followed by Basmati-370 × PSD-15 (5.96), Pusa Sugandh-6 × Tarori Basmati-1 (5.92) Type-3 × Pant Basmati-1 (4.69) and Pusa Sugandh-4 × Pusa Sugandh-6 (4.04).

4.4.3.6. Number of filled grains per panicle

Significantly positive estimates of GCA effect for filled grains/panicle was observed for Pusa Sugandh-6 (12.44) followed by Pusa Sugandh-4 (7.76) and Basmati-370 (6.01). Hence, these parents were good general combiners for filled grains/panicle. The significant negative GCA effect was recorded for PSD-15 (-13.92) and Pant Basmati-1 (-9.29). Thus, these parents were good general combiner for fewer number of filled grains/panicle.

The SCA effect for number of filled grains/panicle among crosses ranged from -22.82 (Pusa Sugandh-4 × Pant Basmati-1) to 31.53 (Pusa Sugandh-4 × PSD-15). Out of 28 crosses, 6 crosses exhibited significant positive SCA effect while 2 crosses exhibited significant negative SCA effects. The best specific combiner for filled grains/panicle were Pusa Sugandh-4 × PSD-15 (31.53) followed by Pusa Basmati-1 × Pusa Sugandh-6 (27.26), Type-3 × Pant Basmati-1 (25.46) Pusa Basmati-1 × Basmati-370 (22.88) and Basmati-370 × Tarori Basmati-1 (16.48).

4.4.3.7. Number of unfilled grains per panicle

Significantly negative estimates of GCA effect for unfilled grains/panicle were observed for Pusa Basmati-1 and Tarori Basmati-1 (-2.67, -2.33). This indicated that

these two parents were good general combiners for fewer unfilled grains/panicle. The significant positive GCA effect was recorded for Type-3 and Pant Basmati-1 (2.90, 1.26). This indicated that these two parents were good general combiners for more of unfilled grains/panicle.

The SCA effect for unfilled grains/panicle among crosses ranged from -12.66 (Pusa Sugandh-4×Type-3) to 19.20 (Type-3×PSD-15). Out of 28 crosses, 9 crosses exhibited significant negative SCA effect while 6 crosses exhibited significant positive SCA effects. The best specific combiner for unfilled grains/panicle were Pusa Sugandh-4×Type-3 (-12.66) followed by Pusa Sugandh-6×Basmati-370 (-9.77), Pusa Sugandh-4×Pant Basmati-1 (-8.55), PSD-15×Pant Basmati-1 (-7.89) and Tarori Basmati-1×PSD-15 (-6.40).

4.4.3.8. Spikelet fertility (%)

Significantly positive estimates of GCA effect for spikelet fertility was observed for Pusa Sugandh-6 (1.04), Basmati-370 (0.61), Basmati-370 (0.61), Pusa Sugandh-4 (0.59) and Pusa Basmati-1 (0.57), indicating these as a good general combiner for higher spikelet fertility. The significant negative GCA effect was recorded for PSD-15 (-1.41), Pant Basmati-1 (-1.40) and Type-3 (-0.61), indicating these as a good general combiner for lower spikelet fertility.

The SCA effect for spikelet fertility among crosses ranged from -7.57 (Type-3 ×PSD-15) to 4.97 (Pusa Sugandh-4×Type-3). Out of 28 crosses, 11 crosses exhibited significant positive SCA effect while only one cross exhibited significant negative SCA effects. The best specific combiner for number of spikelet fertility were Pusa Sugandh-4 ×Type-3 (4.97) followed by Tarori Basmati-1×PSD-15 (4.24), PSD-15×Pant Basmati-1 (3.80), Pusa Sugandh-6×Basmati-370 (3.76) and Pusa Sugandh-6×Type-3 (3.02).

4.4.3.9. Test weight (g)

Significantly positive estimates of GCA effect for test weight was observed for Pusa Sugandh-4 (1.93) followed by Pusa Sugandh-6 (1.24) and Tarori Basmati-1 (0.43), indicating these as a good general combiner for heavier test weight. The significant negative GCA effect was recorded for Type-3 (-1.39), Basmati-370 (-1.24) and Pusa Basmati-1 (-0.93), indicating these as a good general combiner for lower test weight.

Table 4.4.3.1: Contd.....

Sl. No.	Parents	Spikelet fertility (%)	Test weight (g)	Grain yield/plant (g)	Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel breadth (mm)
1.	Pusa Basmati-1	0.57*	-0.93**	-0.87*	0.12	0.81**	0.28**	-0.05**
2.	Pusa Sugandh-4	0.59*	1.93**	-1.60**	-0.12	0.00	0.12**	0.03*
3.	Pusa Sugandh-6	1.04**	1.24**	5.19**	-0.24*	0.17	0.27**	-0.02
4.	Type-3	-0.61*	-1.39**	0.62	-0.02	-0.80**	-0.32**	0.01
5.	Basmati-370	0.61*	-1.24**	1.10**	0.26*	0.00	-0.47**	0.01
6.	Taraori Basmati-1	0.61*	0.43*	-4.90**	0.09	-0.01	-0.04	0.05**
7.	PSD-15	-1.41**	-0.10	4.45**	-0.86**	-0.94**	0.14**	-0.05**
8.	Pant Basmati-1	-1.40**	0.07	-3.99**	0.76**	0.78**	0.00	0.01
	SE (g _i)	0.50	0.33	0.75	0.20	0.43	0.05	0.02
	SE (g _i - g _j)	0.76	0.51	1.13	0.30	0.65	0.07	0.03

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.4.3.2: Contd.....

Sl. No	Crosses	Spikelet fertility (%)	Test weight (g)	Grain yield/plant (g)	Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel breadth (mm)
1	Pusa Basmati-1xPusa Sugandh-4	-0.62	1.01	-6.91**	-1.12**	-1.42	0.25**	0.02
2	Pusa Basmati-1xPusa Sugandh-6	1.33	1.46*	3.34*	-2.10**	-1.49	0.09	0.03
3	Pusa Basmati-1xType-3	-0.11	-0.38	1.17	-0.15	-0.44	-0.31**	0.00
4	Pusa Basmati-1xBasmati-370	2.76**	0.74	10.06**	-0.59	0.83	-0.19*	0.02
5	Pusa Basmati-1xTarori Basmati-1	1.03	-0.38	-0.71	4.05**	3.40**	0.72**	-0.10*
6	Pusa Basmati-1xPSD-15	1.33	2.08**	16.07**	-1.81**	0.34	0.15	0.00
7	Pusa Basmati-1xPant Basmati-1	1.27	-1.51*	3.26*	3.39**	2.60 **	0.68**	-0.06
8	Pusa Sugandh-4xPusa Sugandh-6	2.11*	-1.27*	1.33	0.67	0.66	-0.08	-0.04
9	Pusa Sugandh-4xType-3	4.97**	0.25	4.97**	-0.64	-0.10	-0.04	0.04
10	Pusa Sugandh-4xBasmati-370	0.99	1.15	11.73**	-0.73*	0.18	0.38**	0.08*
11	Pusa Sugandh-4xTarori Basmati-1	0.15	-1.65**	7.73**	3.35**	3.16 **	-1.27**	0.13**
12	Pusa Sugandh-4xPSD-15	2.29*	2.61**	-7.03**	0.57	0.37	0.27**	-0.07
13	Pusa Sugandh-4xPant Basmati-1	0.54	-0.62	7.96**	2.07**	2.38 **	-0.47**	0.05
14	Pusa Sugandh-6xType-3	3.02**	2.12**	6.21**	0.93**	-1.51	0.17	-0.05
15	Pusa Sugandh-6xBasmati-370	3.76**	1.18	7.63**	-0.92*	-0.63	0.08	0.08
16	Pusa Sugandh-6xTarori Basmati-1	0.58	-1.14	-1.16	2.18**	2.78 **	0.77**	-0.15**
17	Pusa Sugandh-6xPSD-15	2.80**	0.77	19.22**	0.97**	0.02	0.15	0.01
18	Pusa Sugandh-6xPant Basmati-1	0.75	-0.54	-2.04	0.66	0.25	-1.30**	0.16**
19	Type-3xBasmati-370	1.65	-1.89**	-8.85**	-0.80*	-0.85	-0.32**	0.12
20	Type-3xTarori Basmati-1	-1.43	1.01	2.86*	-2.51**	-1.62 *	0.24**	0.02
21	Type-3xPSD-15	-7.57**	-0.70	1.74	-0.38	0.07	-0.13	0.01
22	Type-3xPant Basmati-1	2.77**	1.96**	1.67	2.73**	3.70**	0.98**	-0.10*
23	Basmati-370xTarori Basmati-1	0.92	1.35*	0.93	0.33	0.49	0.54**	0.02
24	Basmati-370xPSD-15	-0.40	-0.33	3.55*	0.59	0.50	-0.19*	0.02
25	Basmati-370xPant Basmati-1	1.89*	3.25**	-0.20	-0.83*	-1.34	0.33**	-0.09*
26	Tarori Basmati-1xPSD-15	4.24**	0.06	-3.29*	0.00	-0.76	-0.01	0.09*
27	Tarori Basmati-1xPant Basmati-1	-0.95	1.50*	7.17**	-1.33**	-1.13	-1.07**	0.08*
28	PSD-15xPant Basmati-1	3.80**	-0.34	-0.59	2.76**	2.06 **	0.89**	-0.07
	SE (S _{ij})	1.33	0.89	1.98	0.52	1.14	0.13	0.06
	SE (S _{ij} - S _{ik})	1.97	1.32	2.94	0.77	1.68	0.19	0.08
	SE (S _{ij} - S _{kl})	1.86	1.24	2.77	0.72	1.59	0.18	0.08

The SCA effect for test weight among crosses ranged from -1.89 (Type-3 × Basmati-370) to 3.25 (Basmati-370 × Pant Basmati-1). Out of 28 crosses, 8 crosses exhibited significant positive SCA effect while 4 crosses exhibited significant negative SCA effects. The best specific combiner for test weight were Basmati-370 × Pant Basmati-1 (3.25) followed by Pusa Sugandh-4 × PSD-15 (2.61), Pusa Sugandh-6 × Type-3 (2.12), Pusa Basmati-1 × PSD-15 (2.08) and Type-3 × Pant Basmati-1 (1.96).

4.4.3.10. Grain yield per plant (g)

Significantly positive estimates of GCA effect for grain yield/plant was observed for Pusa Sugandh-6 (5.19) followed by PSD-15 (4.45) and Basmati-370 (1.10). So, these parents were good general combiner for grain yield/plant. The significant negative GCA effect was recorded for Tarori Basmati-1 (-4.90), Pant Basmati-1 (-3.99), Pusa Sugandh-4 (-1.60) and Pusa Basmati-1 (-0.87). Therefore, these parents were poor general combiner for grain yield/plant.

The SCA effect for grain yield/plant among crosses ranged from -8.85 (Type-3 × Basmati-370) to 19.22 (Pusa Sugandh-6 × PSD-15). Out of 28 crosses, 14 crosses exhibited significant positive SCA effect while 4 crosses exhibited significant negative SCA effects. The best specific combiner for grain yield/plant were Pusa Sugandh-6 × PSD-15 (19.22) followed by Pusa Basmati-1 × PSD-15 (16.07), Pusa Sugandh-4 × Basmati-370 (11.73), Pusa Basmati-1 × Basmati-370 (10.06) and Pusa Sugandh-4 × Pant Basmati-1 (7.96).

4.4.3.11. Hulling recovery (%)

Significantly positive estimates of GCA effect for hulling recovery was observed for Basmati-370 (0.26) whereas significantly negative estimates of GCA effect was recorded by PSD-15 (-0.86) and Pusa Sugandh-6 (-0.24). So, Basmati-370 was good general combiner for high hulling recovery and PSD-15 and Pusa Sugandh-6 was poor general combiner for hulling recovery.

The SCA effect for hulling recovery among crosses ranged from -2.51 (Type-3 × Tarori Basmati-1) to 4.05 (Pusa Basmati-1 × Tarori Basmati-1). Out of 28 crosses, 9 crosses exhibited significant positive SCA effect while 9 crosses exhibited significant negative SCA effects. The best specific combiner for hulling recovery was Pusa Basmati-1 × Tarori Basmati-1 (4.05) followed by Pusa Basmati-1 × Pant Basmati-1 (3.39),

Pusa Sugandh-4×Tarori Basmati-1 (3.35), PSD-15×Pant Basmati-1 (2.76) and Type-3×Pant Basmati-1 (2.73).

4.4.3.12. Milling recovery (%)

Significantly positive estimates of GCA effect for milling recovery was observed for Pusa Basmati-1 (0.78) and Pusa Basmati-1 (0.81) whereas, significantly negative estimates of GCA effect was recorded by PSD-15 (-0.94) and Type-3 (-0.80). So, Pusa Basmati-1 and Pusa Basmati-1 was good general combiner for high milling recovery and PSD-15 and Type-3 was poor general combiner for milling recovery.

The SCA effect for milling recovery among crosses ranged from -1.62 (Type-3×Tarori Basmati-1) to 3.70 (Type-3×Pant Basmati-1). Out of 28 crosses, 7 crosses exhibited significant positive SCA effect while only one crosses exhibited significant negative SCA effects. The best specific combiner for milling recovery was Type-3×Pant Basmati-1 (3.70) followed by Pusa Basmati-1×Tarori Basmati-1 (3.40), Pusa Sugandh-4×Tarori Basmati-1 (3.16), Pusa Sugandh-6×Tarori Basmati-1 (2.78) and Pusa Basmati-1×Pant Basmati-1 (2.60).

4.4.3.13. Kernel length (mm)

Significantly positive estimates of GCA effect for kernel length were observed for Pusa Basmati-1 (0.28), Pusa Sugandh-6 (0.27), PSD-15 (0.14) and Pusa Sugandh-4 (0.12). Significantly negative estimates of GCA effect was recorded by Basmati-370 (-0.47) and Type-3 (-0.32). So, Pusa Basmati-1, Pusa Sugandh-6, PSD-15 and Pusa Sugandh-4 were good general combiner for long kernel. Basmati-370 and Type-3 was poor general combiner for long kernel.

The SCA effect for kernel length among crosses ranged from -1.30 (Pusa Sugandh-6×Pant Basmati-1) to 0.98 (Type-3×Pant Basmati-1). Out of 28 crosses, 11 crosses exhibited significant positive SCA effect while 8 crosses exhibited significant negative SCA effects. The best specific combiner for kernel length was Type-3×Pant Basmati-1 (0.98) followed by PSD-15×Pant Basmati-1 (0.89), Pusa Sugandh-6×Tarori Basmati-1 (0.77), Pusa Basmati-1×Tarori Basmati-1 (0.72) and Pusa Basmati-1×Pant Basmati-1 (0.68).

4.4.3.14. Kernel breadth (mm)

Significantly negative estimates of GCA effect for kernel breadth were observed for Pusa Basmati-1 (-0.05) and PSD-15 (-0.05). This indicated that these two parents were good general combiners for superfine quality of aromatic rice. The significant positive GCA effect was recorded for Tarori Basmati-1 (0.05) and Pusa Sugandh-4 (0.03).

The SCA effect for Kernel breadth among crosses ranged from -0.15 (Pusa Sugandh-6×Tarori Basmati-1) to 0.16 (Pusa Sugandh-6×Pant Basmati-1). Out of 28 crosses, 4 crosses exhibited significant negative SCA effect while 5 crosses exhibited significant positive SCA effects. The best specific combiner for superfine quality of aromatic rice was Pusa Sugandh-6×Tarori Basmati-1 (-0.15) followed by Pusa Basmati-1×Tarori Basmati-1 (-0.10), Type-3×Pant Basmati-1 (-0.10) and Basmati-370×Pant Basmati-1 (-0.09).

4.4.3.15. Kernel length/breadth ratio

Significant positive estimates of GCA effect for kernel length/breadth ratio was found for Pusa Basmati-1 (0.26) followed by Pusa Sugandh-6 (0.19) and PSD-15 (0.18). This indicated that these parents are good general combiner for superfine quality of aromatic rice. However, significant negative estimates of GCA effect was recorded by Basmati-370 (-0.31) and followed by Type-3 (-0.22) and Tarori Basmati-1 (-0.12).

The SCA effect for kernel length/breadth ratio among crosses ranged from -1.05 (Pusa Sugandh-6×Pant Basmati-1) to 0.79 (Pusa Sugandh-6×Tarori Basmati-1). Out of 28 crosses, 8 crosses exhibited significant positive SCA effect while 6 crosses exhibited significant negative SCA effects. The best specific combiner for superfine quality of aromatic rice was Pusa Sugandh-6×Tarori Basmati-1 (0.79) followed by Type-3×Pant Basmati-1 (0.77), PSD-15×Pant Basmati-1 (0.69), Pusa Basmati-1×Tarori Basmati-1 (0.64) and Pusa Basmati-1×Pant Basmati-1 (0.53).

4.4.3.16. Cooked kernel length (mm)

Significantly positive estimates of GCA effect for cooked kernel length were observed for Pusa Sugandh-4 (1.10), Pusa Basmati-1 (0.79) hence these were good general combiner for cooked kernel length. However, Basmati-370 (-1.00) and Type-3 (-0.99) showed significantly negative estimates of GCA effect for cooked kernel length.

Table 4.4.3.1: Contd.....

Sl. No.	Parents	Kernel length/breadth ratio	Cooked kernel length (mm)	Cooked kernel breadth (mm)	Cooked kernel length/breadth ratio	Kernel elongation ratio	Alkali digestion value	Amylose content (%)
1.	Pusa Basmati-1	0.26**	0.79**	-0.13**	0.64**	0.02	0.67**	0.60**
2.	Pusa Sugandh-4	0.02	1.10**	-0.01	0.43**	0.12**	0.57**	-0.57**
3.	Pusa Sugandh-6	0.19**	0.05	0.03	-0.04	-0.08**	0.27**	0.16**
4.	Type-3	-0.22**	-0.99**	-0.01	-0.37**	-0.04*	-0.97**	-0.27**
5.	Basmati-370	-0.31**	-1.00**	-0.03	-0.31**	0.01	-0.88**	-0.21**
6.	Taraori Basmati-1	-0.12**	-0.07	0.09**	-0.22**	0.01	0.25**	0.91**
7.	PSD-15	0.18**	-0.05	-0.06	0.06	-0.06**	0.15**	-1.15**
8.	Pant Basmati-1	-0.02	0.16	0.11**	-0.19*	0.02	-0.05	0.52**
	SE (g _i)	0.06	0.18	0.06	0.15	0.03	0.06	0.11
	SE (g _i - g _j)	0.09	0.27	0.09	0.23	0.05	0.10	0.16

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.4.3.2: Contd.....

Sl. No	Crosses	Kernel length/breadth ratio	Cooked kernel length (mm)	Cooked kernel breadth (mm)	Cooked kernel length/breadth ratio	Kernel elongation ratio	Alkali digestion value	Amylose content (%)
1	Pusa Basmati-1xPusa Sugandh-4	0.08	0.48	-0.03	0.29	-0.03	0.05	-0.13
2	Pusa Basmati-1xPusa Sugandh-6	-0.03	0.11	-0.01	0.00	-0.02	0.39**	0.36
3	Pusa Basmati-1xType-3	-0.19	0.98**	-0.03	0.61*	0.27**	0.13	0.13
4	Pusa Basmati-1xBasmati-370	-0.15	0.46	-0.06	0.30	0.15**	0.00	0.62**
5	Pusa Basmati-1xTarori Basmati-1	0.64**	1.37**	-0.19	1.01**	-0.06	0.16	0.83**
6	Pusa Basmati-1xPSD-15	0.09	0.33	-0.01	0.22	0.01	-0.09	-0.69**
7	Pusa Basmati-1xPant Basmati-1	0.53**	1.35**	-0.14	1.00**	-0.05	-0.70**	1.23**
8	Pusa Sugandh-4xPusa Sugandh-6	0.02	0.28	-0.16	0.58*	0.05	0.38**	0.44*
9	Pusa Sugandh-4xType-3	-0.12	-0.78*	-0.10	0.02	-0.10	-0.19	-1.04**
10	Pusa Sugandh-4xBasmati-370	0.04	0.72*	-0.09	0.70*	-0.03	-0.71**	0.57**
11	Pusa Sugandh-4xTarori Basmati-1	-0.93**	-1.79**	0.42**	-1.69**	0.24**	0.44**	0.48*
12	Pusa Sugandh-4xPSD-15	0.34**	0.81*	0.01	0.41	0.02	-0.16	0.71**
13	Pusa Sugandh-4xPant Basmati-1	-0.40**	-0.07	0.02	0.02	0.17**	0.60**	-1.36**
14	Pusa Sugandh-6xType-3	0.19	0.20	0.01	0.08	-0.02	0.00	0.15
15	Pusa Sugandh-6xBasmati-370	-0.12	-0.37	-0.09	0.02	-0.09	-0.44**	0.63**
16	Pusa Sugandh-6xTarori Basmati-1	0.79**	3.12**	-0.19	1.69**	0.16**	-2.82**	-0.96**
17	Pusa Sugandh-6xPSD-15	0.07	0.49	0.09	-0.06	0.03	0.75**	0.10
18	Pusa Sugandh-6xPant Basmati-1	-1.05**	-2.00**	0.72**	-2.35**	0.18**	1.17**	1.15**
19	Type-3xBasmati-370	-0.39**	-1.10**	0.35**	-0.87**	-0.05	-0.11	-0.64**
20	Type-3xTarori Basmati-1	0.07	-0.15	0.08	-0.19	-0.11*	0.69**	1.93**
21	Type-3xPSD-15	-0.11	-0.22	-0.01	0.03	0.02	-0.91**	0.36
22	Type-3xPant Basmati-1	0.77**	3.48**	-0.06	0.99**	0.15**	0.15	-0.84**
23	Basmati-370xTarori Basmati-1	0.25*	2.95**	0.10	0.87**	0.24**	0.37**	0.55**
24	Basmati-370xPSD-15	-0.16	-0.15	0.05	-0.43	0.05	-1.21**	-1.80**
25	Basmati-370xPant Basmati-1	0.38**	-0.36	-0.19	0.27	-0.17**	2.11**	2.13**
26	Tarori Basmati-1xPSD-15	-0.22*	-1.21**	-0.14	-0.05	-0.18**	0.89**	1.82**
27	Tarori Basmati-1xPant Basmati-1	-0.77**	-2.15**	0.30**	-1.45**	0.07	-0.64**	-0.08
28	PSD-15xPant Basmati-1	0.69**	3.06**	-0.18	1.72**	0.12*	1.11**	1.01**
	SE (S _{ij})	0.16	0.47	0.15	0.40	0.08	0.17	0.28
	SE (S _{ij} - S _{ik})	0.23	0.69	0.23	0.59	0.12	0.25	0.42
	SE (S _{ij} - S _{kl})	0.22	0.65	0.22	0.56	0.11	0.24	0.39

The SCA effect for cooked kernel length among crosses ranged from -2.15 (Tarori Basmati-1×Pant Basmati-1) to 3.48 (Type-3×Pant Basmati-1). Out of 28 crosses, 9 crosses exhibited significant positive SCA effect while 6 crosses exhibited significant negative SCA effects. The best specific combiner for cooked kernel length was Type-3×Pant Basmati-1 (3.48) followed by Pusa Sugandh-6×Tarori Basmati-1 (3.12), PSD-15×Pant Basmati-1 (3.06), Basmati-370×Tarori Basmati-1 (2.95) and Pusa Basmati-1×Tarori Basmati-1 (1.37).

4.4.3.17. Cooked kernel breadth (mm)

Significant negative estimates of GCA effect for cooked kernel breadth was observed for the only parent, Pusa Basmati-1 (-0.13) and hence was good general combiner for this trait. Tarori Basmati-1 and Pant Basmati-1 showed significant positive estimates of GCA effect (0.09, 0.11) for cooked kernel breadth.

The SCA effect for cooked kernel breadth among crosses ranged from 0.30 (Tarori Basmati-1×Pant Basmati-1) to 0.72 (Pusa Sugandh-6×Pant Basmati-1). Out of 28 crosses, 4 crosses exhibited significant positive SCA effect while none of the crosses exhibited significant negative SCA effects. Crosses showing significant positive SCA effects for cooked kernel breadth are: Pusa Sugandh-6×Pant Basmati-1 (0.72), Pusa Sugandh-4×Tarori Basmati-1 (0.42), Type-3×Basmati-370 (0.35) and Tarori Basmati-1×Pant Basmati-1 (0.30).

4.4.3.18. Cooked kernel length/breadth ratio

Significantly positive estimates of GCA effect for cooked kernel length were observed for Pusa Basmati-1(0.64) and Pusa Sugandh-4 (0.43). Hence, these parents were good general combiner for cooked kernel length/breadth ratio. However, parents Type-3 (-0.37), Basmati-370 (-0.31), Tarori Basmati-1 (-0.22) and Pant Basmati-1 (-0.19) showed significantly negative estimates of GCA effect for cooked kernel length/breadth ratio.

The SCA effect for cooked kernel length/breadth ratio among crosses ranged from -2.35 (Pusa Sugandh-6×Pant Basmati-1) to 1.72 (PSD-15×Pant Basmati-1). Out of 28 crosses, 9 crosses exhibited significant positive SCA effect while 5 crosses exhibited significant negative SCA effects for cooked kernel length/breadth ratio. The best specific combiner for cooked kernel length/breadth was PSD-15×Pant Basmati-1

(1.72) followed by Pusa Sugandh-6×Tarori Basmati-1 (1.69), Pusa Basmati-1×Tarori Basmati-1 (1.01), Pusa Basmati-1×Pant Basmati-1 (1.00) and Type-3×Pant Basmati-1 (0.99).

4.4.3.19. Kernel elongation ratio

The significant positive estimates of GCA effect for kernel elongation ratio were observed for the only parent Pusa Sugandh-4 (0.12) and hence, it is good general combiner for improved kernel elongation ratio. However, Pusa Sugandh-6 (-0.08), PSD-15 (-0.06) and Type-3 (-0.04) showed significantly negative estimates of GCA effect and were poor general combiner for improvement in kernel elongation ratio.

The SCA effect for kernel elongation ratio among crosses ranged from -0.18 (Tarori Basmati-1×PSD-15) to 0.27 (Pusa Basmati-1×Type-3). Out of 28 crosses, 9 crosses exhibited significant positive SCA effect while 3 crosses exhibited significant negative SCA effects. The best specific combiner for kernel elongation ratio was Pusa Basmati-1×Type-3 (0.27) followed by Pusa Sugandh-4×Tarori Basmati-1 (0.24), Basmati-370×Tarori Basmati-1 (0.24), Pusa Sugandh-6×Pant Basmati-1 (0.18) and Pusa Sugandh-4×Pant Basmati-1 (0.17).

4.4.3.20. Alkali digestion value

The highest significant positive estimates of GCA effect for alkali digestion value were observed for Pusa Basmati-1 (0.67) followed by Pusa Sugandh-4 (0.57), Pusa Sugandh-6 (0.27), Tarori Basmati-1 (0.25) and PSD-15 (0.15). Therefore these parents were good general combiner for alkali digestion value. However, Type-3 (-0.97) and Basmati-370 (-0.88) showed significant negative estimates of GCA effect for alkali digestion value.

The estimate of SCA effect for alkali digestion value among crosses ranged from -2.82 (Pusa Sugandh-6×Tarori Basmati-1) to 2.11 (Basmati-370×Pant Basmati-1). Out of 28 crosses, 11 crosses exhibited significant positive SCA effect while 7 crosses exhibited significant negative SCA effects. The best specific combiner for alkali digestion value was Basmati-370×Pant Basmati-1 (2.11) followed by Pusa Sugandh-6×Pant Basmati-1 (1.17), PSD-15×Pant Basmati-1 (1.11), Tarori Basmati-1×PSD-15 (0.89) and Pusa Sugandh-6×PSD-15 (0.75).

4.4.3.21. Amylose content (%)

The highest significant positive estimates of GCA effect for amylose content was observed for Tarori Basmati-1 (0.91) followed by Pusa Basmati-1 (0.60), Pant Basmati-1 (0.52) and Pusa Sugandh-6 (0.16). Therefore these parents were good general combiner for amylose content. However, PSD-15 (-1.15), Pusa Sugandh-4 (-0.57), Type-3 (-0.27) and Basmati-370 (-0.21) showed significantly negative estimates of GCA effect for amylose content.

The estimate of SCA effect for amylose content among crosses ranged from - 1.80 (Basmati-370×PSD-15) to 2.13 (Basmati-370×Pant Basmati-1). Out of 28 crosses, 14 crosses exhibited significant positive SCA effect while 7 crosses exhibited significant negative SCA effects. The promising specific combiner for amylose content was Basmati-370×Pant Basmati-1 (2.13) followed by Type-3×Tarori Basmati-1 (1.93), Tarori Basmati-1×PSD-15 (1.82), Pusa Basmati-1×Pant Basmati-1 (1.23) and Pusa Sugandh-6×Pant Basmati-1 (1.15).

Selection is much effective and progress in bringing up the improvement in economic traits is much faster when genetic variance is attributable to additive genetic variance. Under such situation mean of generation remain unchanged and genetic variance is readily transmittable from one generation to the next. However, preponderance of both GCA and SCA effects for the prime trait 'yield' suggests that the breeding methods aimed to exploit both the additive as well as non additive gene action are likely to be more effective. SCA effect represents dominance and epistatic effects that are correlated with heterosis. However in autogamous crops - like rice - additive × additive type of interaction component is also fixable in later generation.

The GCA effects of parents for different traits are represented in **Table 4.4.3.3**. The perusal of **Table 4.4.3.3** revealed that none of the parent was excellent general combiner for all the traits studied. This suggested use of multiple parents through multiple crossing to effect substantial improvement in yield, its component traits and quality traits. The general combining ability effects of the parents indicated Pusa Basmati-1 to be the best general combiner among parents as evident from significant GCA effect for maximum of 13 traits viz. plant height, panicle length, unfilled grains/panicle, spikelet fertility, milling recovery, kernel length, kernel breadth, kernel

length/breadth ratio, cooked kernel length, cooked kernel breadth, cooked kernel length/breadth ratio, alkali digestion value and amylose content. General combining ability of parent Pusa Basmati-1 was followed by Pusa Sugandh-6, Pusa Sugandh-4, PSD-15, Tarori Basmati-1, Pant Basmati-1, Basmati-370 and Type-3 for significant GCA effects for 11, 10, 09, 06, 06, 05 and 01 traits respectively, each were the next best general combiner with significant GCA effects for respective number of traits.

Parental line Pusa Sugandh-6 was found good general combiner for days to 50% flowering, plant height, flag leaf length, filled grains/panicle, spikelet fertility, test weight, grain yield/plant, kernel length, kernel length/breadth ratio, alkali digestion value and amylose content. Parental line Pusa Sugandh-4 was found good general combiner for days to 50% flowering, plant height, filled grains/panicle, spikelet fertility, test weight, kernel length, cooked kernel length, cooked kernel length/breadth ratio, kernel elongation ratio and alkali digestion value. Parental line PSD-15 was found good general combiner for days to 50% flowering, flag leaf length, panicle length, panicles/plant, grain yield/plant, kernel length, kernel breadth, kernel length/breadth ratio and alkali digestion value. Parental line Tarori Basmati-1 was found good general combiner for flag leaf length, unfilled grains/panicle, spikelet fertility, test weight, alkali digestion value and amylose content. Parental line Pant Basmati-1 was found good general combiner for days to 50% flowering, plant height, panicle length, hulling recovery, milling recovery and amylose content. Parental line Basmati-370 was found good general combiner for panicles/plant, filled grains/panicle, spikelet fertility, grain yield/plant and hulling recovery. Parental line and Type-3 was found good general combiner for only one trait *i.e.* panicles/ plant.

Per se parental performance has been suggested as a useful index for selecting parents for hybridisation in rice breeding (Singh and Nanda, 1977; Saxena *et al.*, 2000). But, the parents showing the best *per se* performance were not always the best general combiner for various traits. Therefore, *per se* performance should not be the sole criteria in selecting the parents for hybridisation. There was some good *per se* performers and good general combiners. Higher mean performance of these parents maybe primarily due to the preponderance of non additive gene action (dominance, additive $\times$ dominance and dominance $\times$ dominance) effects, therefore, high performance of parents could not be transferred in to hybrid superiority in such case

(Allard, 1960). The relationship between GCA effects and parental performances for various traits are presented in **Table 4.4.3.5**.

The SCA effect of crosses are summarised in **Table 4.4.3.4**. Crosses are ranked as G=Good, A=Average and P=Poor specific combiner for the concerned trait. Crosses with significant SCA effects towards desired direction are ranked as good specific combiner (G), those having significant SCA effects towards undesired direction are ranked as poor specific combiner (P) while those showing non significant SCA effect were labelled as average specific combiner (A). The SCA effects represent mainly dominance, additive $\times$ dominance and dominance $\times$ dominance effects. Those crosses that show high SCA effect and involve parents with good general combining ability could be exploited through recombination breeding. The crosses showing high SCA effect and involving one parent as good general combiner and other as poor or average general combiner are likely to yield transgressive segregants if additive genetic system is present in good general combiner and epistatic effects in the cross act in the same direction so as to maximize the desired expression of the trait (Whitehouse, 1958; Lonnquist, 1961).

The top three hybrids expressing highest SCA effects for different traits that combined parents that were either good general combiner - good general combiner, good general combiner - average general combiner, good general combiner - poor general combiner, average general combiner - average general combiner, average general combiner - poor general combiner, poor general combiner - poor general combiner is presented in **Table 4.3.3.5**. High SCA effect crosses Pusa Basmati-1 $\times$ Pusa Sugandh-6, Pusa Basmati-1 $\times$ Pusa Sugandh-4 and Basmati-370 $\times$ Pant Basmati-1 for days to 50% flowering were P/G, P/G and P/G combinations, respectively. High SCA effect crosses Pusa Basmati-1 $\times$ Pusa Sugandh-6, Basmati-370 $\times$ Tarori Basmati-1 and Type-3 $\times$ Tarori Basmati-1 for Plant height were G/G, P/P and P/P combinations, respectively. High SCA effect crosses Type-3 $\times$ PSD-15, Pusa Sugandh-4 $\times$ Tarori Basmati-1 and Pusa Sugandh-6 $\times$ Type-3 for Flag leaf length were P/G, P/G and G/P combinations, respectively. High SCA effect crosses Pusa Sugandh-4 $\times$ Pant Basmati-1, Tarori Basmati-1 $\times$ PSD-15 and Pusa Basmati-1 $\times$ Tarori Basmati-1 for Panicle length were P/G, P/G and G/P combinations, respectively. High SCA effect crosses Type-3 $\times$ PSD-15, Basmati-370 $\times$ PSD-15 and Pusa Sugandh-6 $\times$ Tarori Basmati-1 for Panicles/plant were G/G, G/G and A/P combinations, respectively. High SCA effect crosses Pusa Sugandh-4 $\times$ PSD-15,

Table 4.4.3.3: Summary of general combining ability (GCA) effects of parents for various traits

Sl. No.	Parents Traits	Pusa Basmati-1	Pusa Sugandh-4	Pusa Sugandh-6	Type-3	Basmati-370	Tarori Basmati-1	PSD-15	Pant Basmati-1
1	Days to 50% flowering	P	G	G	P	P	A	G	G
2	Plant height (cm)	G	G	G	P	P	P	P	G
3	Flag leaf length (cm)	P	P	G	P	A	G	G	A
4	Panicle length (cm)	G	P	A	P	P	P	G	G
5	Panicles/plant	P	A	A	G	G	P	G	P
6	Filled grains/panicle	A	G	G	A	G	A	P	P
7	Unfilled grains/panicle	G	A	A	P	A	G	A	P
8	Spikelet fertility (%)	G	G	G	P	G	G	P	P
9	Test weight (g)	P	G	G	P	P	G	A	A
10	Grain yield/plant (g)	P	P	G	A	G	P	G	P
11	Hulling recovery (%)	A	A	P	A	G	A	P	G
12	Milling recovery (%)	G	A	A	P	A	A	P	G
13	Kernel length (mm)	G	G	G	P	P	A	G	A
14	Kernel breadth (mm)	G	P	A	A	A	P	G	A
15	Kernel length/breadth ratio	G	A	G	P	P	P	G	A
16	Cooked kernel length (mm)	G	G	A	P	P	A	A	A
17	Cooked kernel breadth (mm)	G	A	A	A	A	P	A	P
18	Cooked kernel length/breadth ratio	G	G	A	P	P	P	A	P
19	Kernel elongation ratio	A	G	P	P	A	A	P	A
20	Alkali digestion value	G	G	G	P	P	G	G	A
21	Amylose content (%)	G	P	G	P	P	G	P	G

Table 4.4.3.4: Summary of specific combining ability (SCA) effects of crosses for various traits

Sl. No	Crosses	Days to 50% flowering	Plant Height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/ plant	Filled grains/panicle	Unfilled grains/panicle
1	Pusa Basmati-1xPusa Sugandh-4	G	A	P	A	A	A	P
2	Pusa Basmati-1xPusa Sugandh-6	G	G	G	P	G	G	P
3	Pusa Basmati-1xType-3	P	P	A	G	G	A	A
4	Pusa Basmati-1xBasmati-370	A	P	A	A	G	G	A
5	Pusa Basmati-1xTarori Basmati-1	A	P	A	G	P	A	A
6	Pusa Basmati-1xPSD-15	A	A	G	A	G	A	G
7	Pusa Basmati-1xPant Basmati-1	A	P	G	G	A	A	G
8	Pusa Sugandh-4xPusa Sugandh-6	A	A	P	A	G	G	A
9	Pusa Sugandh-4xType-3	A	P	A	A	G	A	G
10	Pusa Sugandh-4xBasmati-370	A	A	P	A	A	A	A
11	Pusa Sugandh-4xTarori Basmati-1	A	P	G	P	P	A	A
12	Pusa Sugandh-4xPSD-15	A	P	A	A	P	G	A
13	Pusa Sugandh-4xPant Basmati-1	A	G	G	G	G	P	G
14	Pusa Sugandh-6xType-3	A	P	G	G	P	A	G
15	Pusa Sugandh-6xBasmati-370	A	P	G	G	A	A	G
16	Pusa Sugandh-6xTarori Basmati-1	A	P	A	P	G	A	A
17	Pusa Sugandh-6xPSD-15	A	G	P	A	A	A	G
18	Pusa Sugandh-6xPant Basmati-1	A	A	G	G	P	G	A
19	Type-3xBasmati-370	G	G	A	A	P	A	A
20	Type-3xTarori Basmati-1	A	G	P	A	G	A	P
21	Type-3xPSD-15	A	P	G	G	G	A	P
22	Type-3xPant Basmati-1	A	P	P	A	G	G	A
23	Basmati-370xTarori Basmati-1	A	G	A	P	G	G	A
24	Basmati-370xPSD-15	A	P	G	G	G	A	P
25	Basmati-370xPant Basmati-1	G	A	P	G	G	A	A
26	Tarori Basmati-1xPSD-15	A	A	G	G	A	A	G
27	Tarori Basmati-1xPant Basmati-1	A	G	P	A	P	A	P
28	PSD-15xPant Basmati-1	A	G	P	G	A	A	G

Table 4.4.3.4: Contd.....

Sl. No	Crosses	Spikelet fertility (%)	Test weight (g)	Grain yield/ plant (g)	Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel breadth (mm)
1	Pusa Basmati-1xPusa Sugandh-4	A	A	P	P	A	G	A
2	Pusa Basmati-1xPusa Sugandh-6	A	G	G	P	A	A	A
3	Pusa Basmati-1xType-3	A	A	A	A	A	P	A
4	Pusa Basmati-1xBasmati-370	G	A	G	A	A	P	A
5	Pusa Basmati-1xTarori Basmati-1	A	A	A	G	G	G	G
6	Pusa Basmati-1xPSD-15	A	G	G	P	A	A	A
7	Pusa Basmati-1xPant Basmati-1	A	P	G	G	G	G	A
8	Pusa Sugandh-4xPusa Sugandh-6	G	P	A	A	A	A	A
9	Pusa Sugandh-4xType-3	G	A	G	A	A	A	A
10	Pusa Sugandh-4xBasmati-370	A	A	G	P	A	G	P
11	Pusa Sugandh-4xTarori Basmati-1	A	P	G	G	G	P	P
12	Pusa Sugandh-4xPSD-15	G	G	P	A	A	G	A
13	Pusa Sugandh-4xPant Basmati-1	A	A	G	G	G	P	A
14	Pusa Sugandh-6xType-3	G	G	G	G	A	A	A
15	Pusa Sugandh-6xBasmati-370	G	A	G	P	A	A	A
16	Pusa Sugandh-6xTarori Basmati-1	A	A	A	G	G	G	G
17	Pusa Sugandh-6xPSD-15	G	A	G	G	A	A	A
18	Pusa Sugandh-6xPant Basmati-1	A	A	A	A	A	P	P
19	Type-3xBasmati-370	A	P	P	P	A	P	A
20	Type-3xTarori Basmati-1	A	A	G	P	P	G	A
21	Type-3xPSD-15	P	A	A	A	A	A	A
22	Type-3xPant Basmati-1	G	G	A	G	G	G	G
23	Basmati-370xTarori Basmati-1	A	G	A	A	A	G	A
24	Basmati-370xPSD-15	A	A	G	A	A	P	A
25	Basmati-370xPant Basmati-1	G	G	A	P	A	G	G
26	Tarori Basmati-1xPSD-15	G	A	P	A	A	A	P
27	Tarori Basmati-1xPant Basmati-1	A	G	G	P	A	P	P
28	PSD-15xPant Basmati-1	G	A	A	G	G	G	A

Table 4.4.3.4: Contd.....

Sl. No	Crosses	Kernel length/breadth ratio	Cooked kernel length (mm)	Cooked kernel breadth (mm)	Cooked kernel length/breadth ratio	Kernel elongation ratio	Alkali digestion value	Amylose content (%)
1	Pusa Basmati-1×Pusa Sugandh-4	A	A	A	A	A	A	A
2	Pusa Basmati-1×Pusa Sugandh-6	A	A	A	A	A	G	A
3	Pusa Basmati-1×Type-3	A	G	A	G	G	A	A
4	Pusa Basmati-1×Basmati-370	A	A	A	A	G	A	G
5	Pusa Basmati-1×Tarori Basmati-1	G	G	A	G	A	A	G
6	Pusa Basmati-1×PSD-15	A	A	A	A	A	A	P
7	Pusa Basmati-1×Pant Basmati-1	G	G	A	G	A	P	G
8	Pusa Sugandh-4×Pusa Sugandh-6	A	A	A	G	A	G	G
9	Pusa Sugandh-4×Type-3	A	P	A	A	A	A	P
10	Pusa Sugandh-4×Basmati-370	A	G	A	G	A	P	G
11	Pusa Sugandh-4×Tarori Basmati-1	P	P	p	P	G	G	G
12	Pusa Sugandh-4×PSD-15	G	G	A	A	A	A	G
13	Pusa Sugandh-4×Pant Basmati-1	P	A	A	A	G	G	P
14	Pusa Sugandh-6×Type-3	A	A	A	A	A	A	A
15	Pusa Sugandh-6×Basmati-370	A	A	A	A	A	P	G
16	Pusa Sugandh-6×Tarori Basmati-1	G	G	A	G	G	P	P
17	Pusa Sugandh-6×PSD-15	A	A	A	A	A	G	A
18	Pusa Sugandh-6×Pant Basmati-1	P	P	p	P	G	G	G
19	Type-3×Basmati-370	P	P	p	P	A	A	P
20	Type-3×Tarori Basmati-1	A	A	A	A	P	G	G
21	Type-3×PSD-15	A	A	A	A	A	P	A
22	Type-3×Pant Basmati-1	G	G	A	G	G	A	P
23	Basmati-370×Tarori Basmati-1	G	G	A	G	G	G	G
24	Basmati-370×PSD-15	A	A	A	A	A	P	P
25	Basmati-370×Pant Basmati-1	G	A	A	A	P	G	G
26	Tarori Basmati-1×PSD-15	P	P	A	A	P	G	G
27	Tarori Basmati-1×Pant Basmati-1	P	P	P	P	A	P	A
28	PSD-15×Pant Basmati-1	G	G	A	G	G	G	G

Table 4.3.3.5: Best three parents and crosses for various traits

Sl. No.	Trait	Parents		crosses		GCA of parents in crosses
		<i>Per se</i> Performance	GCA	<i>Per se</i> Performance	SCA	
1	Days to 50% flowering	Pant Basmati-1	Pant Basmati-1	Pusa Basmati-1 × Pusa Sugandh-6	Pusa Basmati-1 × Pusa Sugandh-6	P/G
		PSD-15	PSD-15	PSD-15 × Pant Basmati-1	Pusa Basmati-1 × Pusa Sugandh-4	P/G
		Pusa Sugandh-6	Pusa Sugandh-6	Pusa Sugandh-4 × PSD-15	Basmati-370 × Pant Basmati-1	P/G
2	Plant height (cm)	Pant Basmati-1	Pant Basmati-1	Pusa Basmati-1 × Pusa Sugandh-6	Pusa Basmati-1 × Pusa Sugandh-6	G/G
		Pusa Basmati-1	Pusa Basmati-1	Pusa Sugandh-4 × Pant Basmati-1	Basmati-370 × Tarori Basmati-1	P/P
		Pusa Sugandh-6	Pusa Sugandh-6	Tarori Basmati-1 × Pant Basmati-1	Type-3 × Tarori Basmati-1	P/P
3	Flag leaf length (cm)	Pant Basmati-1	Tarori Basmati-1	Pusa Sugandh-4 × Tarori Basmati-1	Type-3 × PSD-15	P/G
		Basmati-370	Pusa Sugandh-6	Tarori Basmati-1 × PSD-15	Pusa Sugandh-4 × Tarori Basmati-1	P/G
		Tarori Basmati-1	PSD-15	Pusa Sugandh-6 × Basmati-370	Pusa Sugandh-6 × Type-3	G/P
4	Panicle length (cm)	Pant Basmati-1	Pant Basmati-1	Pusa Sugandh-4 × Pant Basmati-1	Pusa Sugandh-4 × Pant Basmati-1	P/G
		Pusa Sugandh-4	Pusa Basmati-1	Pusa Basmati 1 × Pant Basmati-1	Tarori Basmati-1 × PSD-15	P/G
		Pusa Basmati-1	PSD-15	Pusa Sugandh-6 × Pant Basmati-1	Pusa Basmati-1 × Tarori Basmati-1	G/P
5	Panicles/plant	Pusa Sugandh-4	Basmati-370	Basmati-370 × PSD-15	Type-3 × PSD-15	G/G
		Basmati-370	PSD-15	Type-3 × PSD-15	Basmati-370 × PSD-15	G/G
		Tarori Basmati-1	Type-3	Pusa Sugandh-6 × Tarori Basmati-1	Pusa Sugandh-6 × Tarori Basmati-1	A/P
6	Filled grains /panicle	Pusa Sugandh-6	Pusa Sugandh-6	Pusa Basmati-1 × Pusa Sugandh-6	Pusa Sugandh-4 × PSD-15	G/P
		Pusa Sugandh-4	Pusa Sugandh-4	Pusa Sugandh-4 × Pusa Sugandh-6	Pusa Basmati-1 × Pusa Sugandh-6	A/G
		Type-3	Basmati-370	Pusa Basmati-1 × Basmati-370	Type-3 × Pant Basmati-1	A/P
7	Unfilled grains/ panicle	Tarori Basmati-1	Pusa Basmati-1	Tarori Basmati-1 × PSD-15	Pusa Sugandh-4 × Type-3	A/P
		PSD-15	Tarori Basmati-1	Pusa Sugandh-4 × Type-3	Pusa Sugandh-6 × Basmati-370	A/A
		Pusa Basmati-1	PSD-15	Pusa Sugandh-6 × Basmati-370	Pusa Sugandh-4 × Pant Basmati-1	A/P

Table 4.3.3.5: Contd.....

Sl. No.	Trait	Parents		Crosses		GCA of parents in crosses
		<i>Per se Performance</i>	GCA	<i>Per se Performance</i>	SCA	
8	Spikelet fertility (%)	Tarori Basmati-1	Pusa Sugandh-6	Pusa Sugandh-6×Basmati-370	Pusa Sugandh-4×Type-3	G/P
		Pusa Basmati-1	Basmati-370	Pusa Sugandh-4×Type-3	Tarori Basmati-1×PSD-15	G/P
		Type-3	Tarori Basmati-1	Pusa Basmati-1×Basmati-370	PSD-15×Pant Basmati-1	P/P
9	Test weight (g)	Pusa Sugandh-4	Pusa Sugandh-4	Pusa Sugandh-4×PSD-15	Basmati-370×Pant Basmati-1	P/A
		Pusa Sugandh-6	Pusa Sugandh-6	Basmati-370×Pant Basmati-1	Pusa Sugandh-4×PSD-15	G/A
		Tarori Basmati-1	Tarori Basmati-1	Pusa Basmati-1×Pusa Sugandh-4	Pusa Sugandh-6×Type-3	G/P
10	Grain yield/plant (g)	Type-3	Pusa Sugandh-6	Pusa Sugandh-6×PSD-15	Pusa Sugandh-6×PSD-15	G/G
		PSD-15	PSD-15	Pusa Basmati-1×PSD-15	Pusa Basmati-1×PSD-15	P/G
		Pusa Sugandh-6	Basmati-370	Pusa Sugandh-6×Basmati-370	Pusa Sugandh-4×Basmati-370	P/G
11	Hulling recovery (%)	Basmati-370	Pant Basmati-1	Pusa Basmati-1×Tarori Basmati-1	Pusa Basmati-1×Tarori Basmati-1	A/A
		Type-3	Basmati-370	Pusa Basmati 1×Pant Basmati-1	Pusa Basmati-1×Pant Basmati-1	A/G
		Pusa Basmati-1	Pusa Basmati-1	Type-3×Pant Basmati-1	Pusa Sugandh-4×Tarori Basmati-1	A/A
12	Milling recovery (%)	Basmati-370	Pusa Basmati-1	Pusa Basmati-1×Tarori Basmati-1	Pusa Sugandh-4×Tarori Basmati-1	A/A
		Pusa Sugandh-6	Pant Basmati-1	Pusa Basmati 1×Pant Basmati-1	Pusa Sugandh-6×Tarori Basmati-1	A/A
		Pusa Basmati-1	Pusa Sugandh-6	Type-3×Pant Basmati-1	Pusa Basmati-1×Pant Basmati-1	G/G
13	Kernel length (mm)	Pusa Sugandh-4	Pusa Basmati-1	PSD-15×Pant Basmati-1	Type-3×Pant Basmati-1	P/A
		Pusa Sugandh-6	Pusa Sugandh-6	Pusa Sugandh-6×Tarori Basmati-1	PSD-15×Pant Basmati-1	G/A
		Pant Basmati-1	PSD-15	Pusa Basmati-1×Tarori Basmati-1	Pusa Sugandh-6×Tarori Basmati-1	G/A
14	Kernel breadth (mm)	Basmati-370	Pusa Basmati-1	Pusa Sugandh-6×Tarori Basmati-1	Pusa Sugandh-6×Tarori Basmati-1	A/P
		PSD-15	PSD-15	Pusa Basmati-1×Tarori Basmati-1	Pusa Basmati-1×Tarori Basmati-1	G/P
		Pusa Basmati-1	Pusa Sugandh-6	PSD-15×Pant Basmati-1	Type-3×Pant Basmati-1	A/A

Table 4.3.3.5: Contd.....

Sl. No.	Trait	Parents		Crosses		GCA of parents in crosses
		<i>Per se Performance</i>	GCA	<i>Per se Performance</i>	SCA	
15	Kernel length/breadth ratio	Pusa Sugandh-4	Pusa Basmati-1	Pusa Sugandh-6×Tarori Basmati-1	Pusa Sugandh-6×Tarori Basmati-1	G/P
		Pusa Sugandh-6	Pusa Sugandh-6	PSD-15×Pant Basmati-1	Type-3×Pant Basmati-1	P/A
		Pusa Basmati-1	PSD-15	Pusa Basmati-1×Tarori Basmati-1	PSD-15×Pant Basmati-1	G/A
16	Cooked kernel length (mm)	Pusa Sugandh-4	Pusa Sugandh-4	PSD-15×Pant Basmati-1	Type-3×Pant Basmati-1	P/A
		Pusa Sugandh-6	Pusa Basmati-1	Pusa Sugandh-6× Tarori Basmati-1	Pusa Sugandh-6×Tarori Basmati-1	A/A
		Pusa Basmati-1	Pant Basmati-1	Type-3×Pant Basmati-1	Pant Sugandh Dhan-1× Pant Basmati-1	A/A
17	Cooked kernel breadth (mm)	Type-3	Pusa Basmati-1	Pusa Basmati-1×Tarori Basmati-1	Pusa Basmati-1×Tarori Basmati-1	G/P
		Pusa Sugandh-6	PSD-15	Pusa Basmati-1×Basmati-370	Pusa Sugandh-6×Tarori Basmati-1	A/P
		Basmati-370	Basmati-370	Pusa Basmati-1×PSD-15	Basmati-370× Pant Basmati-1	A/P
18	Cooked kernel length/breadth ratio	Pusa Sugandh-4	Pusa Basmati-1	PSD-15×Pant Basmati-1	PSD-15×Pant Basmati-1	A/P
		Pusa Sugandh-6	Pusa Sugandh-4	Pusa Basmati 1×Pant Basmati-1	Pusa Sugandh-6×Tarori Basmati-1	A/P
		Pusa Basmati-1	PSD-15	Pusa Basmati-1×Tarori Basmati-1	Pusa Basmati-1×Tarori Basmati-1	G/P
19	Kernel elongation ratio	Pusa Sugandh-4	Pusa Sugandh-4	Pusa Sugandh-4×Tarori Basmati-1	Pusa Basmati-1×Type-3	A/P
		Basmati-370	Pusa Basmati-1	Pusa Sugandh-4×Pant Basmati-1	Pusa Sugandh-4×Tarori Basmati-1	G/A
		Pusa Basmati-1	Pant Basmati-1	Basmati-370×Tarori Basmati-1	Basmati-370× Tarori Basmati-1	A/A
20	Alkali digestion value	Pusa Basmati-1	Pusa Basmati-1	Pusa Sugandh-6×Pant Basmati-1	Basmati-370×Pant Basmati-1	P/A
		Tarori Basmati-1	Pusa Sugandh-4	Pusa Basmati-1×Pusa Sugandh-6	Pusa Sugandh-6×Pant Basmati-1	G/A
		Pusa Sugandh-4	Pusa Sugandh-6	Pusa Basmati-1×Pusa Sugandh-4	PSD-15×Pant Basmati-1	G/A
21	Amylose content (%)	Pusa Basmati-1	Tarori Basmati-1	Type-3×Tarori Basmati-1	Basmati-370×Pant Basmati-1	P/G
		Tarori Basmati-1	Pusa Basmati-1	Basmati-370×Pant Basmati-1	Type-3×Tarori Basmati-1	P/G
		Type-3	Pant Basmati-1	Pusa Basmati 1×Pant Basmati-1	Tarori Basmati-1×PSD-15	G/P

Pusa Basmati-1×Pusa Sugandh-6 and Type-3×Pant Basmati-1 for Filled grains/panicle were G/P, A/G and A/P combinations, respectively. High SCA effect crosses Pusa Sugandh-4×Type-3, Pusa Sugandh-6×Basmati-370 and Pusa Sugandh-4×Pant Basmati-1 for unfilled grains/panicle were A/P, A/A and A/P combinations respectively. High SCA effect crosses Pusa Sugandh-4×Type-3, Tarori Basmati-1×PSD-15 and PSD-15×Pant Basmati-1 for Spikelet fertility were G/P, G/P and P/P combinations, respectively. High SCA effect crosses Basmati-370×Pant Basmati-1, Pusa Sugandh-4×PSD-15 and Pusa Sugandh-6×Type-3 for days to Test weight were P/A, G/A and G/P combinations, respectively. High SCA effect crosses Pusa Sugandh-6×PSD-15, Pusa Basmati-1×PSD-15 and Pusa Sugandh-4×Basmati-370 for Grain yield/plant were G/G, P/G and P/G combinations, respectively. High SCA effect crosses Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1 and Pusa Sugandh-4×Tarori Basmati-1 for hulling recovery were A/A, A/G and A/A combinations, respectively. High SCA effect crosses Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-6×Tarori Basmati-1 and Pusa Basmati-1×Pant Basmati-1 for milling recovery were A/A, A/A and G/G combinations, respectively. High SCA effect crosses Type-3×Pant Basmati-1, PSD-15×Pant Basmati-1 and Pusa Sugandh-6×Tarori Basmati-1 for Kernel length were P/A, G/A and G/A combinations, respectively. High SCA effect crosses Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1 and Type-3×Pant Basmati-1 for Kernel breadth were A/P, G/P and A/A combinations, respectively. High SCA effect crosses Pusa Sugandh-6×Tarori Basmati-1, Type-3×Pant Basmati-1 and PSD-15×Pant Basmati-1 for Kernel length/breadth ratio were G/P, P/A and G/A combinations, respectively. High SCA effect crosses Type-3×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1 and PSD-15×Pant Basmati-1 for cooked kernel length were P/A, A/A and A/A combinations, respectively. High SCA effect crosses Pusa Basmati-1×Tarori Basmati-1, Pusa Sugandh-6×Tarori Basmati-1 and Basmati-370×Pant Basmati-1 for cooked kernel breadth were G/P, A/P and A/P combinations, respectively. High SCA effect crosses PSD-15×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1 and Pusa Basmati-1×Tarori Basmati-1 for cooked kernel length/breadth ratio were A/P, A/P and G/P combinations, respectively. High SCA effect crosses Pusa Basmati-1×Type-3, Pusa Sugandh-4×Tarori Basmati-1 and Basmati-370 ×Tarori Basmati-1 for Kernel elongation ratio were A/P, G/A and A/A combinations, respectively. High SCA effect crosses Basmati-370×Pant Basmati-1, Pusa

Sugandh-6×Pant Basmati-1 and PSD-15×Pant Basmati-1 for Alkali digestion value were P/A, G/A and G/A combinations respectively. High SCA effect crosses Basmati-370×Pant Basmati-1, Type-3×Tarori Basmati-1 and Tarori Basmati-1×PSD-15 for Amylose content were P/G, P/G and G/P combinations, respectively.

The findings of the present study are in conformity with the findings of several workers in rice crop **Roy and Senapati (2012)**, **Dwivedi and Pandey (2012)**, **Tiwari et al. (2011)**, **Selvaraj et al. (2011)**, **Ahangar et al. (2008)**, **Saleem et al. (2010)**, **Kumar (2009)**, **Sharma and Mani (2005)**, **Shankar et al. (2009)**, **Pradhan et al. (2006)**, **Sharma and Mani (2005)** and **Vanaja et al. (2003)**.

Perusal of **Table 4.3.3.5** revealed that none of top three hybrids that showed high SCA effect for grain yield/plant expressed high SCA falling within top three for any of the quality parameters. Also, none of the top three cross combinations in terms of *per se* performance for grain yield/plant were included among top three crosses for better performance in any of the quality parameters. More or less similar findings were also reported by **Roy and Senapati (2012)**, **Saleem et al. (2010)**, **Shankar et al. (2009)**, **Pradhan et al. (2006)** and **Vanaja et al. (2003)**.

Thus, a look at the SCA effects and *per se* performance of the hybrids indicated that the hybrids recording high SCA effect may not always have high *per se* performance. Therefore, identification of heterotic crosses based on *per se* performance would be more realistic than that on the basis of SCA effects. This supports the conclusion of **Chaudhary et al. (1974)**, that although the relative amount of GCA and SCA play a vital role in planning appropriate breeding strategy, that if often fulfilled by the analysis of variance of combining ability itself. It is therefore, advisable to lay more emphasis on the mean performance of the hybrids rather than specific combining ability.

4.5. Graphical analysis

The data for 21 traits obtained from 28 F₁ and 8 parental populations were subjected to graphical and component of variance analysis. The t^2 value was significant for 11 traits viz., days to 50% flowering, panicle length, panicles/plant, spikelet fertility, grain yield/plant, kernel breadth, kernel length/breadth ratio, cooked kernel breadth, cooked kernel length/breadth ratio, kernel elongation ratio and amylose content. For rest of the 10 traits t^2 values were non-significant that justifies the assumptions underlying diallel analysis (**Table 4.5.1**). The trait wise results are discussed below:

4.5.1. Days to 50% flowering

The slope of regression line of W_r (covariance) on V_r (variance) (0.477 ± 0.132) deviating significantly from zero as well as from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r -axis above the origin indicating the presence of partial dominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.1**) showed that the parents Pant Basmati-1, Pusa Sugandh-6 and Pusa Sugandh-4 had more dominant genes and occupied position nearest to the origin whereas, Pusa Basmati-1, Basmati-370 and Type-3 had more number of recessive genes and occupied position farthest from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pant Basmati-1, Pusa Sugandh-6 and Pusa Sugandh-4 had more dominant genes and Pusa Basmati-1, Basmati-370 and Type-3 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that D (36.210 ± 7.151), H_1 (35.683 ± 16.440) and H_2 (31.863 ± 14.302), were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci [$(H_1/D)^{1/2}$] was 0.993 that indicated the presence of partial dominance for this trait. The proportion of dominant to recessive genes [$(4DH_1)^{1/2} + F$] / [$(4DH_1)^{1/2} - F$], was 1.178 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci [$H_2/4H_1$] was 0.223 indicating thereby, asymmetry at loci showing dominance. The positive correlation (0.823) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests days to 50% flowering to be primarily conditioned by dominant genes.

4.5.2. Plant height (cm)

The slope of regression line of W_r (covariance) on V_r (variance) (0.612 ± 0.154) deviating significantly from zero as well as from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r -axis below the origin indicating the presence of partial dominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.2**) showed that the parents Tarori Basmati-1, Basmati-370 and Pant Basmati-1 had more dominant genes and occupied the position

Table 4.5.1: Estimates of regression coefficient of Wr on Vr, deviation from zero and unity and t^2 value for various traits

Sl. No.	Traits	F_1			
		b	b/SE_b	(1-b)/SE_b	t^2
1	Days to 50% flowering	0.477 ± 0.132	-3.603**	3.957**	6.374*
2	Plant height (cm)	0.612 ± 0.154	-3.970**	2.517*	2.453
3	Flag leaf length (cm)	-0.238 ± 0.503	0.473	2.460*	0.328
4	Panicle length (cm)	0.204 ± 0.083	-2.464*	9.615**	30.688**
5	Panicles/plant	0.026 ± 0.120	-0.214	8.105**	14.412**
6	Filled grains/panicle	0.835 ± 0.236	-3.534**	0.700	0.004
7	Unfilled grains/panicle	-0.126 ± 0.389	0.325	2.894*	0.009
8	Spikelet fertility (%)	0.030 ± 0.080	-0.379	12.194**	36.505**
9	Test weight (g)	1.010 ± 0.101	-10.001**	-0.094	0.158
10	Grain yield/plant (g)	0.119 ± 0.082	-1.462	10.779**	33.499**
11	Hulling recovery (%)	0.041 ± 0.195	-0.212	4.918**	3.905
12	Milling recovery (%)	0.296 ± 0.191	-1.550	3.695**	3.318
13	Kernel length (mm)	-1.143 ± 0.120	9.560**	17.926**	2.683
14	Kernel breadth (mm)	0.303 ± 0.131	-2.315	5.327**	9.472**
15	Kernel length/breadth ratio	-0.331 ± 0.151	2.202	8.847**	6.282*
16	Cooked kernel length (mm)	-0.262 ± 0.258	1.015	4.890**	1.063
17	Cooked kernel breadth (mm)	0.017 ± 0.037	-0.447	26.600**	179.799**
18	Cooked kernel length/breadth ratio	-0.207 ± 0.095	2.184	12.736**	22.713**
19	Kernel elongation ratio	0.325 ± 0.154	-2.111	4.384**	5.966*
20	Alkali digestion value	-0.209 ± 0.263	0.794	4.591**	1.052
21	Amylose content (%)	0.419 ± 0.143	-2.932*	4.064**	6.025*

*Significant @ 5% level of significance; ** Significant @ 1% level of significance

Table 4.5.2: Components of variance for various traits

Sl. No.	Genetic parameters and ratios	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/plant	Filled grains/panicle	Unfilled grains/panicle
1	D	36.210 ±7.151*	282.388 ±47.371*	9.528 ±4.137*	0.496 ±2.048	1.447 ±3.406	257.743 ±65.933*	78.011 ±32.040*
2	F	5.873 ±16.898	15.380 ±111.935	14.524 ±9.776	-2.604 ±4.841	3.192 ±8.049	30.244 ±155.795	138.137 ±75.708
3	H ₁	35.683 ±16.440*	680.880 ±108.901*	48.621 ±9.511*	30.671 ±4.709*	54.356 ±7.831*	1177.614 ±151.571*	258.022 ±73.656*
4	H ₂	31.863 ±14.302*	515.609 ±94.743*	38.444 ±8.274*	26.487 ±4.097*	50.523 ±6.813*	1051.504 ±131.867*	185.978 ±64.081*
5	h ²	11.994 ±9.592	743.954 ±63.539*	10.918 ±5.549*	40.048 ±2.748*	95.799 ±4.569*	3034.060 ±88.435*	65.167 ±42.975
6	E	2.104 ±2.383	1.572 ±15.790	0.124 ±1.379	0.202 ±0.682	0.139 ±1.135	30.337 ±21.977	1.977 ±10.680
7	(H ₁ /D) ^{1/2}	0.993	1.553	2.259	7.860	6.127	2.138	1.819
8	H ₂ /4H ₁	0.223	0.189	0.198	0.216	0.232	0.223	0.180
9	[(4DH ₁) ^{1/2} +F]/ [(4DH ₁) ^{1/2} - F]	1.178	1.036	2.018	0.500	1.439	1.056	2.897
10	‘r’ between Yr and Wr+Vr	0.823	-0.490	-0.475	-0.360	-0.742	-0.810	-0.385

Table 4.5.3: Order of dominance (Wr + Vr) for various traits in F₁ generation

Traits	Pusa Basmati-1	Pusa Sugandh-4	Pusa Sugandh-6	Type-3	Basmati-370	Tarori Basmati-1	PSD-15	Pant Basmati-1
Days to 50% flowering	82.20	19.99	18.23	44.13	50.02	27.46	24.95	9.73
Plant height (cm)	574.38	418.13	650.16	318.20	163.93	150.98	514.69	212.74
Flag leaf length (cm)	8.27	22.59	14.24	11.10	10.80	9.36	9.71	10.93
Panicle length (cm)	6.05	13.904	8.071	5.72	11.54	16.58	6.30	7.67
Panicles/plant	8.60	6.217	15.575	18.13	12.03	13.44	20.45	10.96
Filled grains/panicle	883.62	287.14	296.98	412.17	272.71	627.99	922.65	244.3
Unfilled grains/panicle	42.47	26.84	57.81	30.43	4.23	89.19	120.07	71.41
Spikelet fertility (%)	3.35	8.15	12.23	20.61	11.17	3.49	21.20	12.09
Test weight (g)	8.77	2.13	0.10	11.90	14.61	1.25	10.73	3.89
Grain yield/plant (g)	167.02	75.77	150.90	45.93	91.13	43.46	170.89	45.29
Hulling recovery (%)	5.68	2.12	0.89	2.79	1.59	7.29	2.71	7.41
Milling recovery (%)	2.93	3.42	1.24	3.07	1.21	10.02	2.79	6.43
Kernel length (mm)	0.60	0.53	0.49	0.59	0.56	0.60	0.57	0.45
Kernel breadth (mm)	0	0.013	0.007	0.005	0.01	0.013	0.006	0.015
Kernel length/breadth ratio	0.22	0.43	0.34	0.28	0.15	0.49	0.28	0.37
Cooked kernel length (mm)	2.17	2.75	3.97	5.03	5.24	3.68	4.92	4.76
Cooked kernel breadth (mm)	0.004	0.058	0.12	0.027	0.027	0.075	0.004	0.125
Cooked kernel length/breadth ratio	0.46	0.85	1.67	0.87	1.05	1.40	1.00	1.99
Kernel elongation ratio	0.024	0.014	0.03	0.026	0.03	0.059	0.019	0.03
Alkali digestion value	1.51	1.72	2.27	1.37	1.25	2.02	2.85	2.34
Amylose content (%)	2.20	0.96	1.26	2.42	4.56	1.02	3.49	2.36

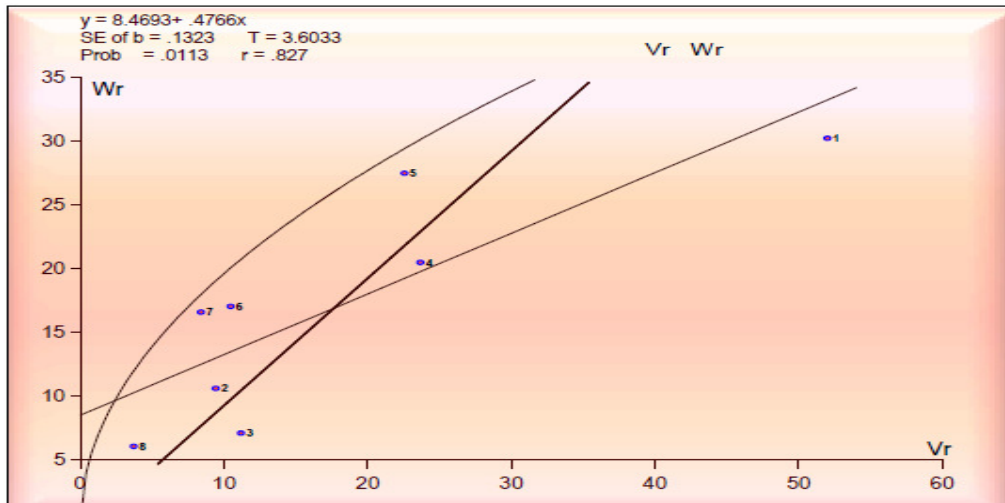


Figure 4.5.1: V_r - W_r graph for days to 50% flowering

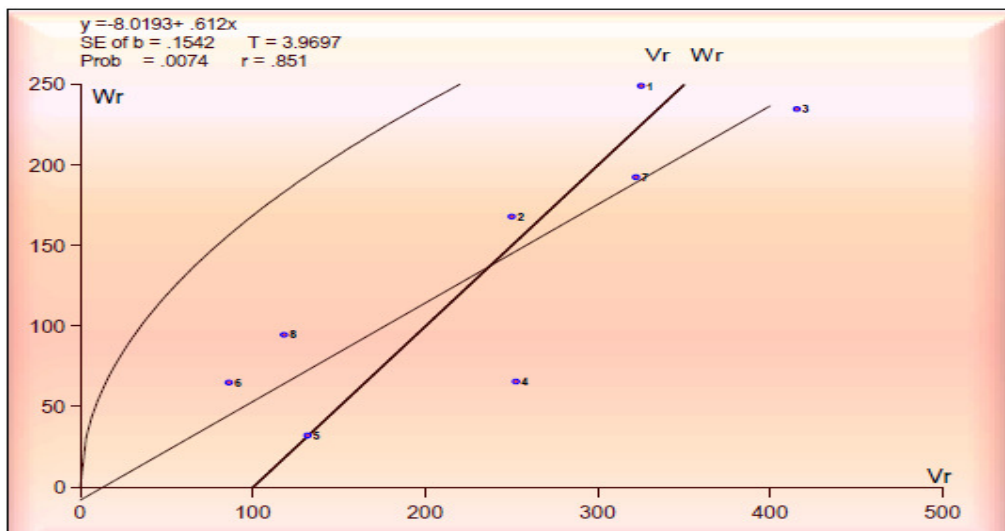


Figure 4.5.2: V_r - W_r graph for plant height (cm)

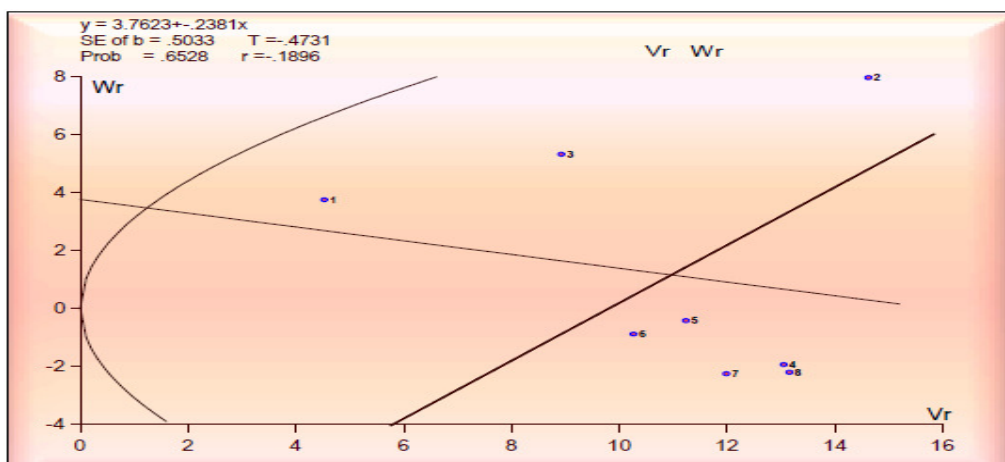


Figure 4.5.3: V_r - W_r graph for flag leaf length (cm)

nearest to the origin whereas, Pusa Sugandh-6, Pusa Basmati-1 and PSD-15 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Tarori Basmati-1, Basmati-370 and Pant Basmati-1 had more dominant genes and Sugandh-6, Pusa Basmati-1 and PSD-15 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that D (282.388 ± 47.371), H_1 (680.88 ± 108.90) and H_2 (515.609 ± 94.743) were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 1.553 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 1.036 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.189 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.49) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests plant height was primarily conditioned by dominant genes.

4.5.3. Flag leaf length (cm)

The slope of regression line of W_r (covariance) on V_r (variance) (-0.238 ± 0.503) deviating significantly from unity but not from zero indicated presence of inter allelic interaction. The regression line intercepted the W_r - axis above the origin indicating the presence of partial dominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.3**) showed that the parents Pusa Basmati-1, Tarori Basmati-1, PSD-15 and Basmati-370 had more dominant genes and occupied the position nearest to the origin whereas, Pusa Sugandh-4 and Pusa Sugandh-6 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Basmati-1, Tarori Basmati-1, PSD-15 and Basmati-370 had more dominant genes and Pusa Sugandh-4 and Pusa Sugandh-6 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that D (9.528 ± 4.137), H_1 (48.621 ± 9.511) and H_2 (38.444 ± 8.274) were significant. This

suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 2.259 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2}-F]$, was 2.018 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.198 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.475) between parental performance (Yr) and order of dominance (Vr + Wr) suggests flag leaf length was primarily conditioned by dominant genes.

4.5.4. Panicle length (cm)

The slope of regression line of Wr (covariance) on Vr (variance) (0.204 ± 0.083) deviating significantly from zero as well as from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the Wr - axis below the origin indicating the presence of overdominance type of gene action. A perusal of Wr- Vr graph (**Figure 4.5.4**) showed that the parents Type-3, Pusa Basmati-1 and PSD-15 had more dominant genes and occupied the position nearest to the origin whereas, Tarori Basmati-1, Pusa Sugandh-4 and Basmati-370 had more number of recessive genes and occupied farthest position from the origin. The order of dominance (Vr + Wr) also revealed that the Type-3, Pusa Basmati-1 and PSD-15 had more dominant genes and Tarori Basmati-1, Pusa Sugandh-4 and Basmati-370 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (30.671 ± 4.709) and H_2 (26.487 ± 4.097) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 7.86 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2}-F]$, was 0.5 suggesting that the recessive genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.216 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.36) between parental performance (Yr) and order of dominance (Vr + Wr) suggests that panicle length was primarily conditioned by dominant genes.

4.5.5. Number of panicles per plant

The slope of regression line of W_r (covariance) on V_r (variance) (0.026 ± 0.120) deviating significantly from unity but not from zero indicated presence of inter allelic interaction. The regression line intercepted the W_r - axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.5**) showed that the parents Pusa Sugandh-4, Pusa Basmati-1 and Pant Basmati-1 had more dominant genes and occupied the position nearest to the origin. Whereas, PSD-15, Type-3 and Pusa Sugandh-6 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Sugandh-4, Pusa Basmati-1 and Pant Basmati-1 had more dominant genes and PSD-15, Type-3 and Pusa Sugandh-6 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (54.356 ± 7.831) and H_2 (50.523 ± 6.813) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 6.127 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F]/[(4DH_1)^{1/2} - F]$, was 1.439 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.232 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.742) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests that panicles/plant was primarily conditioned by dominant genes.

4.5.6. Number of filled grains per panicle

The slope of regression line of W_r (covariance) on V_r (variance) (0.835 ± 0.236) deviating significantly from zero but not from unity indicating close fit to theoretical slope of unity and significantly different from zero. The deviation of regression coefficient from zero suggested additive gene action to be involved in expression of the trait. The regression line intercepted the W_r -axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.6**) showed that the parents Pant Basmati-1, Basmati-370 and Pusa Sugandh-4 had

more dominant genes and occupied the position nearest to the origin. Whereas, PSD-15, Pusa Basmati-1 and Tarori Basmati-1 had excess of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pant Basmati-1, Basmati-370 and Pusa Sugandh-4 had more dominant genes and PSD-15, Pusa Basmati-1 and Tarori Basmati-1 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that D (257.743 ± 65.933), H_1 (1177.614 ± 151.571) and H_2 (1051.504 ± 131.867) were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 2.138 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F]/[(4DH_1)^{1/2} - F]$, was 1.056 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.223 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.81) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests that filled grains/panicle was primarily conditioned by dominant genes.

4.5.7. Number of unfilled grains per panicle

The slope of regression line of W_r (covariance) on V_r (variance) (-0.126 ± 0.389) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r - axis above the origin indicating the presence of partial dominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.7**) showed that the parents Basmati-370, Pusa Sugandh-4 and Type-3 had more dominant genes and occupied the position nearest to the origin. Whereas, PSD-15, Tarori Basmati-1 and Pant Basmati-1 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Basmati-370, Pusa Sugandh-4 and Type-3 had more dominant genes and PSD-15, Tarori Basmati-1 and Pant Basmati-1 had more number of recessive genes (**Table 4.5.3**).

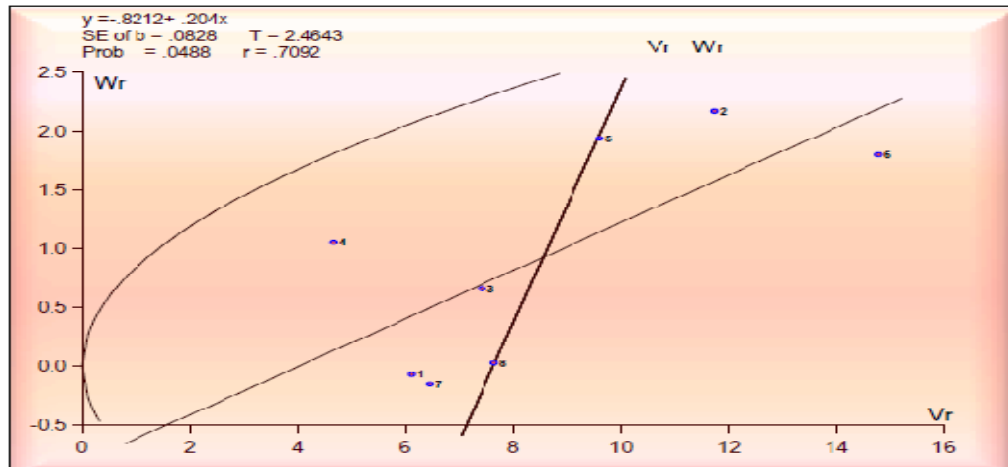


Figure 4.5.4: Vr - Wr graph for panicle length (cm)

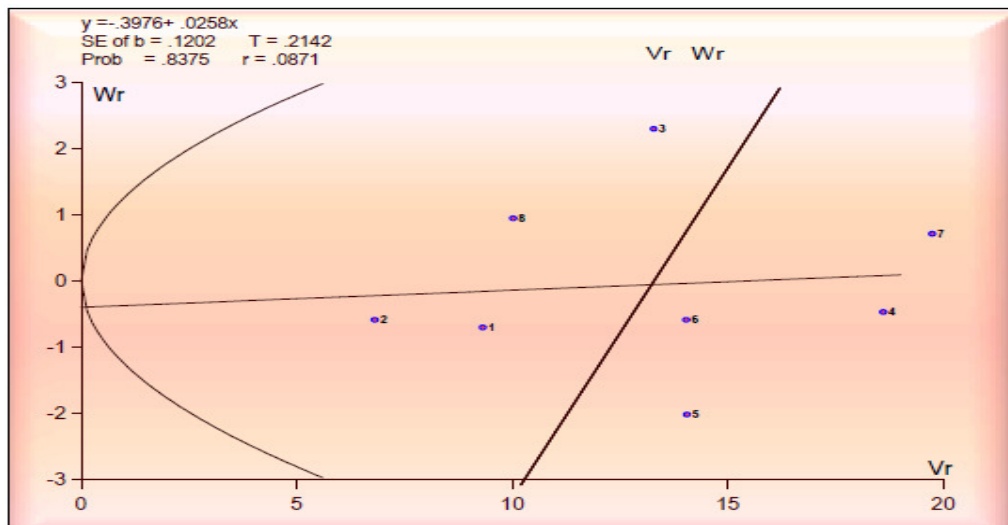


Figure 4.5.5: Vr - Wr graph for number of panicles per plant

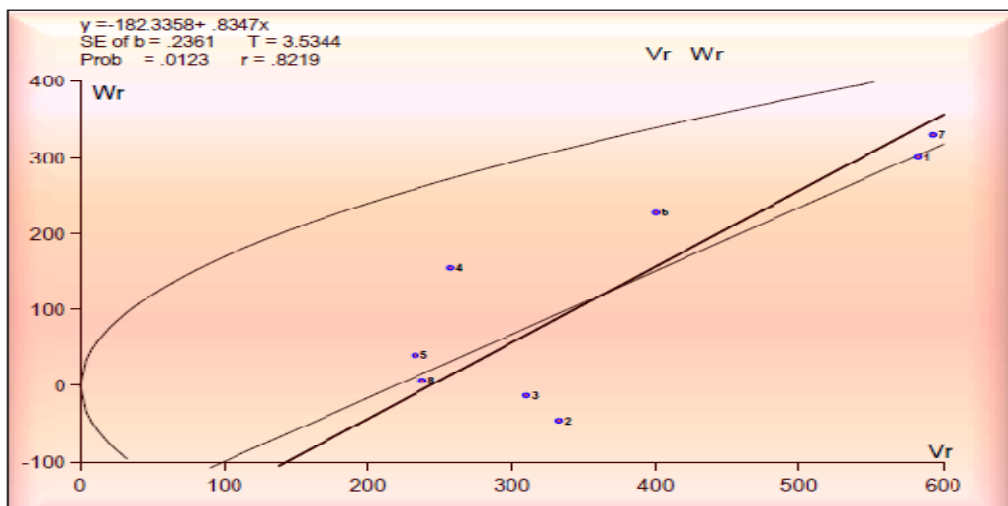


Figure 4.5.6: Vr - Wr graph for number of filled grains per panicle

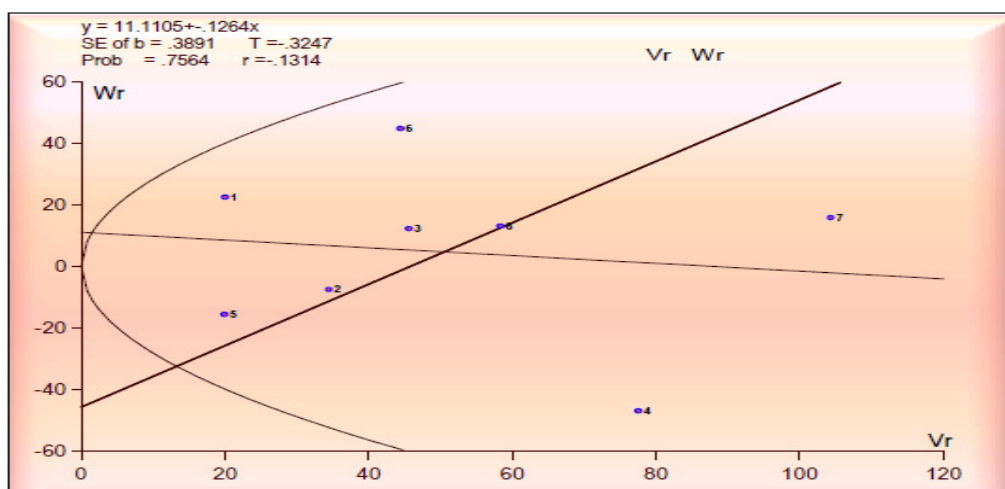


Figure 4.5.7: V_r - W_r graph for number of unfilled grains per panicle

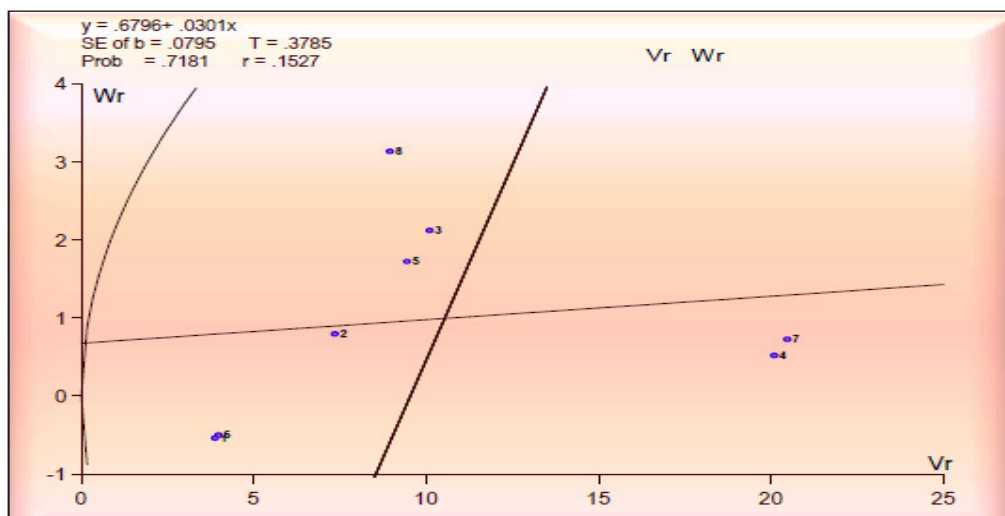


Figure 4.5.8: V_r - W_r graph for spikelet fertility (%)

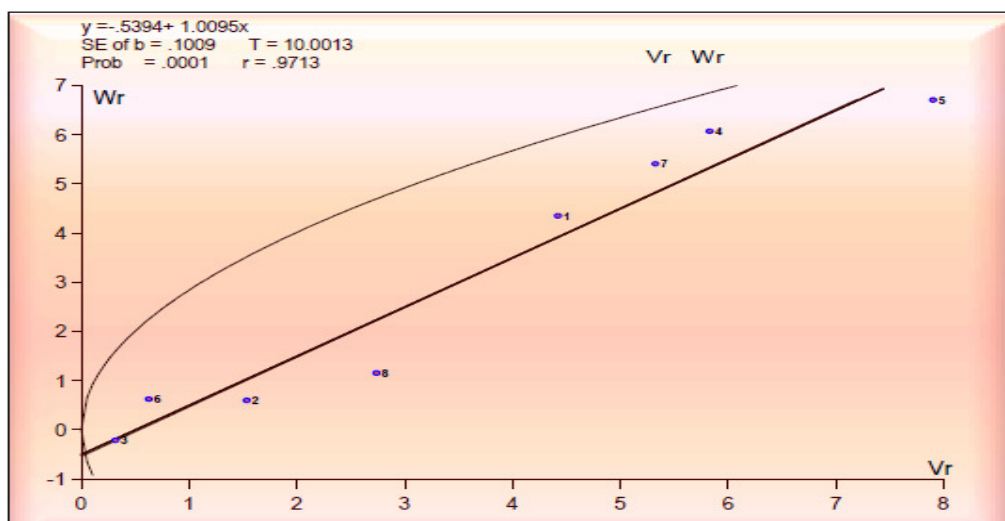


Figure 4.5.9: V_r - W_r graph for test weight (g)

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that D (78.011 ± 32.040), H_1 (258.022 ± 73.656) and H_2 (185.978 ± 64.081) were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 1.819 that indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 2.897 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.18 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.385) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests that unfilled grains/panicle was primarily conditioned by dominant genes.

4.5.8. Spikelet fertility (%)

The slope of regression line of W_r (covariance) on V_r (variance) (0.030 ± 0.080) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r - axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.8**) showed that the parents Pusa Basmati-1, Tarori Basmati-1 and Pusa Sugandh-4 had more dominant genes and occupied the position nearest to the origin. Whereas, PSD-15, Type-3 and Pusa Sugandh-6 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Basmati-1, Tarori Basmati-1 and Pusa Sugandh-4 had more dominant genes and PSD-15, Type-3 and Pusa Sugandh-6 had more number of recessive genes (Table 4.5.3).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (41.459 ± 10.999) and H_2 (36.328 ± 9.569) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 3.151 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 1.425 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$

Table 4.5.2: Contd.....

Sl. No.	Genetic parameters and ratios	Spikelet fertility (%)	Test weight (g)	Grain yield/ plant (g)	Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel breadth (mm)
1	D	4.175 ±4.785	7.824 ±0.505*	24.409 ±33.295	3.419 ±1.818	2.035 ±1.362	0.453 ±0.270	0.002 ±0.002
2	F	4.613 ±11.306	3.430 ±1.192*	-13.318 ±78.672	7.874 ±4.296	4.209 ±3.218	0.379 ±0.637	0.001 ±0.005
3	H ₁	41.459 ±10.999*	9.442 ±1.160*	292.085 ±76.540*	20.508 ±4.180*	16.861 ±3.131*	1.576 ±0.620*	0.027 ±0.005*
4	H ₂	36.328 ±9.569*	8.737 ±1.009*	265.550 ±66.589*	14.730 ±3.637*	12.430 ±2.724*	1.359 ±0.539*	0.022 ±0.004*
5	h ²	90.392 ±6.418*	10.794 ±0.677*	609.389 ±44.658*	10.165 ±2.439*	12.157 ±1.827*	0.125 ±0.362	0.005 ±0.003
6	E	0.503 ±1.595	0.231 ±0.168	1.180 ±11.098	0.078 ±0.606	0.365 ±0.454	0.005 ±0.090	0.001 ±0.001
7	(H ₁ /D) ^{1/2}	3.151	1.099	3.459	2.449	2.878	1.867	3.559
8	H ₂ /4H ₁	0.219	0.231	0.227	0.180	0.184	0.215	0.209
9	[(4DH ₁) ^{1/2} +F]/ [(4DH ₁) ^{1/2} - F]	1.425	1.499	0.854	2.775	2.121	1.578	1.073
10	‘r’ between Yr and Wr+Vr	-0.485	-0.897	0.290	-0.450	-0.695	-0.471	0.490

was 0.219 indicating thereby, asymmetry at loci showing dominance. The negative correlation between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests spikelet fertility was primarily conditioned by dominant genes.

4.5.9. Test weight (g)

The slope of regression line of W_r (covariance) on V_r (variance) (1.010 ± 0.101) deviating significantly from zero suggesting additive gene action to be involved in expression of the trait. The regression line intercepted the W_r - axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.9**) showed that the parents Pusa Sugandh-6, Tarori Basmati-1 and Pusa Sugandh-4 had more dominant genes and occupied the position nearest to the origin. Whereas, Basmati-370, PSD-15 and Type-3 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Sugandh-6, Tarori Basmati-1 and Pusa Sugandh-4 had more dominant genes and Basmati-370, PSD-15 and Type-3 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in Table 4.5.2 revealed that D (7.824 ± 0.505), H_1 (9.442 ± 1.160) and H_2 (8.737 ± 1.009) were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci [$(H_1/D)^{1/2}$] was 1.099 that indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes [$(4DH_1)^{1/2} + F$] / [$(4DH_1)^{1/2} - F$], was 1.499 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci [$H_2/4H_1$] was 0.231 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.897) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests test weight was primarily conditioned by dominant genes.

4.5.10. Grain yield per plant (g)

The slope of regression line of W_r (covariance) on V_r (variance) (0.119 ± 0.082) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r - axis below the origin indicating the

presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.10**) showed that the parents Tarori Basmati-1, Pant Basmati-1 and Type-3 had more dominant genes and occupied the position nearest to the origin. Whereas, PSD-15, Pusa Basmati-1 and Pusa Sugandh-6 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Tarori Basmati-1, Pant Basmati-1 and Type-3 had more dominant genes and PSD-15, Pusa Basmati-1 and Pusa Sugandh-6 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (292.085 ± 76.540) and H_2 (265.55 ± 66.589), were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 3.459 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 0.854 suggesting that the recessive genes were in excess. The same information was provided by the negative F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.227 indicating thereby, asymmetry at loci showing dominance. The positive correlation (0.29) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests grain yield/plant was primarily conditioned by dominant genes.

4.5.11. Hulling recovery (%)

The slope of regression line of W_r (covariance) on V_r (variance) (0.041 ± 0.195) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r -axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.11**) showed that the parents Pusa Sugandh-6, Basmati-370 and Pusa Sugandh-4 had more dominant genes and occupied the position nearest to the origin. Whereas, Pant Basmati-1, Tarori Basmati-1 and Pusa Basmati-1 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Sugandh-6, Basmati-370 and Pusa Sugandh-4 had more dominant genes and Pant Basmati-1, Tarori Basmati-1 and Pusa Basmati-1 had more number of recessive genes (**Table 4.5.3**).

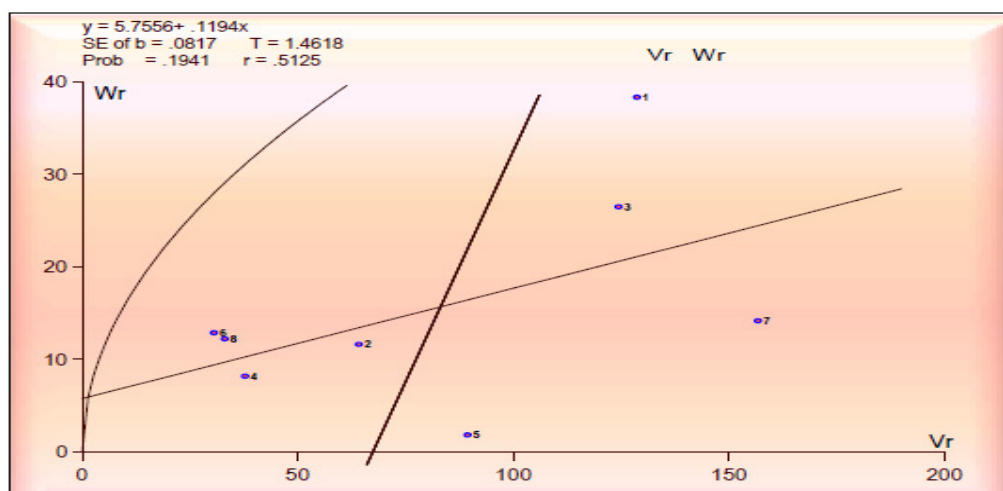


Figure 4.5.10: Vr - Wr graph for grain yield per plant (g)

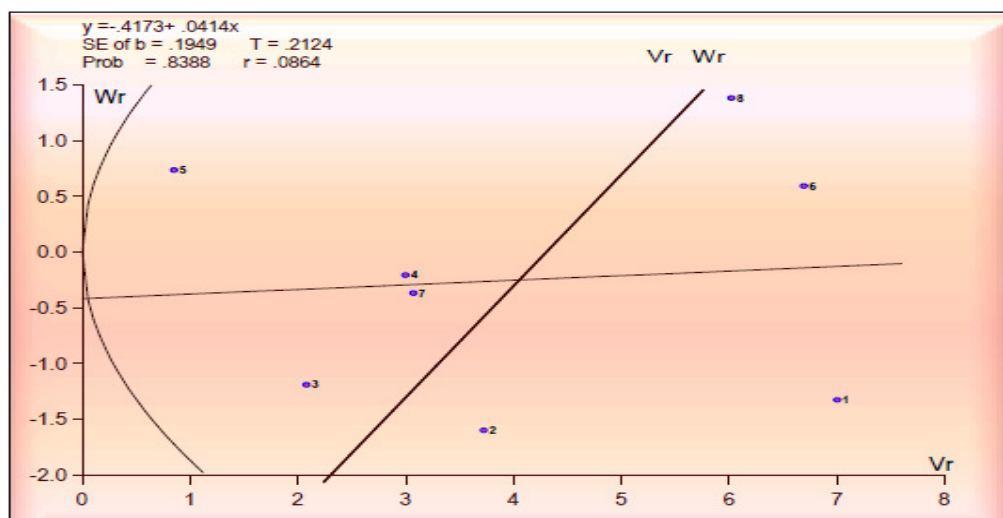


Figure 4.5.11: Vr - Wr graph for hulling recovery (%)

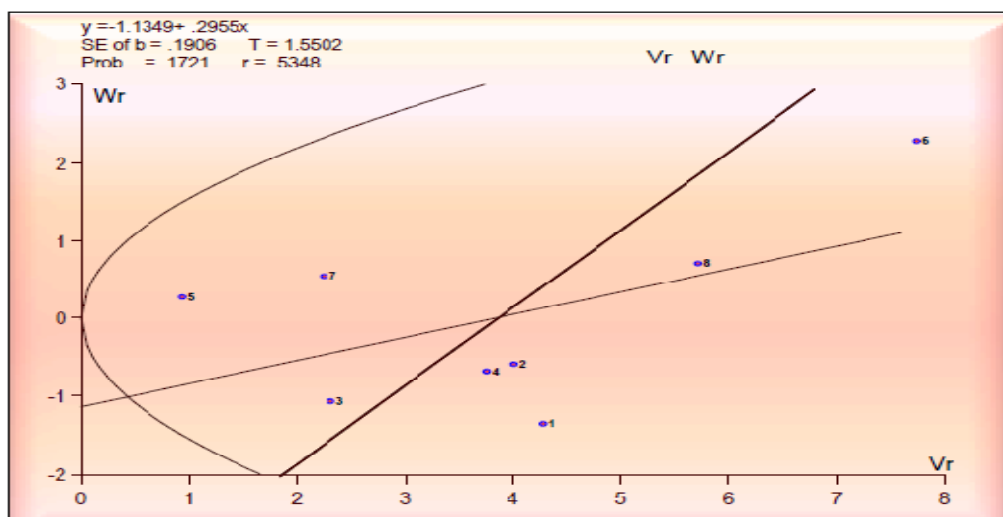


Figure 4.5.12: Vr - Wr graph for milling recovery (%)

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that, H_1 (20.508 ± 4.180) and H_2 (14.73 ± 3.637) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 2.449 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 2.775 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.18 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.45) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests hulling recovery was primarily conditioned by dominant genes.

4.5.12. Milling recovery (%)

The slope of regression line of W_r (covariance) on V_r (variance) (0.296 ± 0.191) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r - axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.12**) showed that the parents Basmati-370, Pusa Sugandh-6 and PSD-15 had more dominant genes and occupied the position nearest to the origin. Whereas, Tarori Basmati-1, Pant Basmati-1 and Type-3 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Basmati-370, Pusa Sugandh-6 and PSD-15 had more dominant genes and Tarori Basmati-1, Pant Basmati-1 and Type-3 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (16.861 ± 3.131) and H_2 (12.43 ± 2.724) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 2.878 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 2.121 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.184 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.695) between

parental performance (Yr) and order of dominance (Vr + Wr) suggests milling recovery was primarily conditioned by dominant genes.

4.5.13. Kernel length (mm)

The slope of regression line of Wr (covariance) on Vr (variance) (-1.143 ± 0.120) deviating significantly from zero as well as from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the Wr-axis below the origin indicating the presence of overdominance type of gene action. A perusal of Wr - Vr graph (**Figure 4.5.13**) showed that all the 8 parents had almost equal proportion of dominant and recessive genes as they occupied intermediate position on Wr- Vr graph. The order of dominance (Vr + Wr) also revealed the similar result (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that, H_1 (1.576 ± 0.620) and H_2 (1.359 ± 0.539) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 1.867 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 1.578 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.215 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.471) between parental performance (Yr) and order of dominance (Vr + Wr) suggests kernel length was primarily conditioned by dominant genes.

4.5.14. Kernel breadth (mm)

The slope of regression line of Wr (covariance) on Vr (variance) (0.303 ± 0.131) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the Wr-axis below the origin indicating the presence of overdominance type of gene action. A perusal of Wr- Vr graph (**Figure 4.5.14**) showed that the parents Pusa Basmati-1, Type-3 and PSD-15 had more dominant genes and occupied the position nearest to the origin. Whereas, Pant Basmati-1, Pusa Sugandh-4 and Tarori Basmati-1 had more number of recessive genes and occupied farthest position from the origin. The order of dominance (Vr + Wr) also revealed that the Pusa Basmati-1, Type-3 and PSD-15 had more dominant genes and Pant Basmati-1, Pusa Sugandh-4 and Tarori Basmati-1 had more number of recessive genes (**Table 4.5.3**).

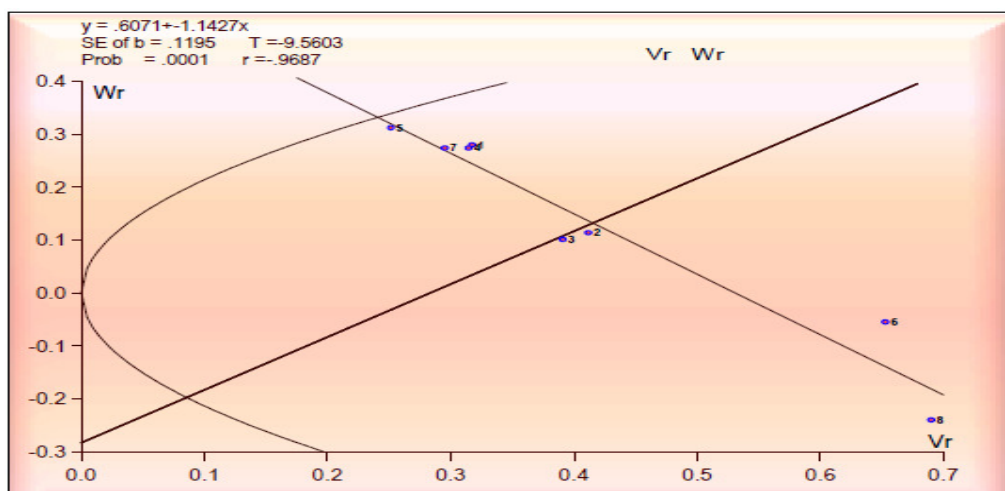


Figure 4.5.13: Vr - Wr graph for kernel length (mm)

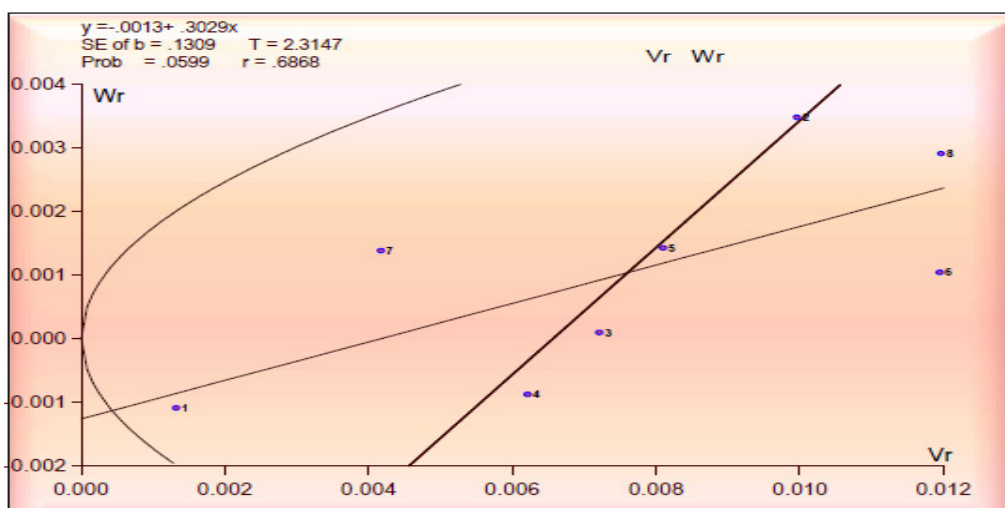


Figure 4.5.14: Vr - Wr graph for kernel breadth (mm)

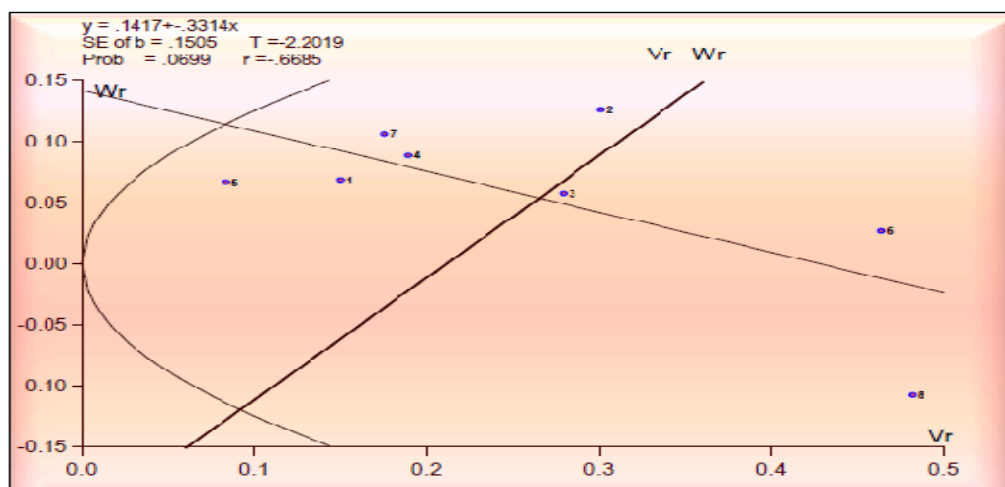


Figure 4.5.15: Vr - Wr graph for kernel length/breadth ratio

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (0.027 ± 0.005) and H_2 (0.022 ± 0.004) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 3.559 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 1.073 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.209 indicating thereby, asymmetry at loci showing dominance. The positive correlation (0.49) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests kernel breadth was primarily conditioned by dominant genes.

4.5.15. Kernel length/breadth ratio

The slope of regression line of W_r (covariance) on V_r (variance) (-0.331 ± 0.151) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r - axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.15**) showed that the parents Basmati-370, Pusa Basmati-1, Type-3 and PSD-15 had more dominant genes and occupied the position nearest to the origin whereas, Tarori Basmati-1, Pusa Sugandh-4 and Pant Basmati-1 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Basmati-370, Pusa Basmati-1, Type-3 and PSD-15 had more dominant genes and Tarori Basmati-1, Pusa Sugandh-4 and Pant Basmati-1 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (0.983 ± 0.346) and H_2 (0.85 ± 0.301) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 2.566 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 1.256 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.216 indicating thereby, asymmetry at loci showing dominance. The positive correlation (0.469) between

Table 4.5.2: Contd.....

Sl. No.	Genetic parameters and ratios	Kernel length/breadth ratio	Cooked kernel length (mm)	Cooked kernel breadth (mm)	Cooked kernel length/breadth ratio	Kernel elongation ratio	Alkali digestion value	Amylose content (%)
1	D	0.149 ±0.150	2.882 ±1.236*	-0.004 ±0.035	0.289 ±0.5500	0.012 ±0.006*	2.072 ±0.556*	0.875 ±0.437*
2	F	0.087 ±0.355	1.579 ±2.921	-0.007 ±0.083	0.117 ±1.300	0.001 ±0.014	1.367 ±1.314	-0.453 ±1.033
3	H ₁	0.983 ±0.346*	10.600 ±2.841*	0.199 ±0.081*	3.889 ±1.265*	0.076 ±0.013*	4.158 ±1.279*	5.527 ±1.005*
4	H ₂	0.850 ±0.301*	9.728 ±2.472*	0.165 ±0.070*	3.392 ±1.100*	0.070 ±0.011*	3.324 ±1.113*	4.563 ±0.874*
5	h ²	0.005 ±0.202	7.604 ±1.658*	0.014 ±0.047	1.087 ±0.738	0.083 ±0.008*	0.163 ±0.746	4.624 ±0.586*
6	E	0.007 ±0.050	0.062 ±0.412	0.007 ±0.011	0.045 ±0.183	0.002 ±0.002	0.008 ±0.185	0.024 ±0.146
7	(H ₁ /D) ^{1/2}	2.566	1.918	7.091	3.670	2.508	1.417	2.513
8	H ₂ /4H ₁	0.216	0.229	0.208	0.218	0.229	0.200	0.206
9	[(4DH ₁) ^{1/2} +F]/ [(4DH ₁) ^{1/2} - F]	1.256	1.333	0.777	1.117	1.029	1.607	0.813
10	‘r’ between Yr and (Wr+Vr)	0.469	-0.717	0.077	0.03	-0.372	0.193	-0.552

parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests kernel length/breadth ratio was primarily conditioned by dominant genes.

4.5.16. Cooked kernel length (mm)

The slope of regression line of W_r (covariance) on V_r (variance) (-0.262 ± 0.258) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r -axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.16**) showed that the parents Pusa Basmati-1, Pusa Sugandh-4 and Tarori Basmati-1 had more dominant genes and occupied the position nearest to the origin whereas, Basmati-370, Type-3, PSD-15 and Pant Basmati-1 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Basmati-1, Pusa Sugandh-4 and Tarori Basmati-1 had more dominant genes and Basmati-370, Type-3, PSD-15 and Pant Basmati-1 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that D (2.882 ± 1.236), H_1 (10.6 ± 2.841) and H_2 (9.728 ± 2.472) were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci [$(H_1/D)^{1/2}$] was 1.918 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes [$(4DH_1)^{1/2} + F$] / [$(4DH_1)^{1/2} - F$], was 1.333 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci [$H_2/4H_1$] was 0.229 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.717) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests cooked kernel length was primarily conditioned by dominant genes.

4.5.17. Cooked kernel breadth (mm)

The slope of regression line of W_r (covariance) on V_r (variance) (0.017 ± 0.037) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r - axis below the origin indicating the presence of partial dominance type of gene action. A perusal of W_r - V_r graph

(**Figure 4.5.17**) showed that the parents Pusa Basmati-1, PSD-15, Type-3 and Basmati-370 had more dominant genes and occupied the position nearest to the origin. Whereas, Pant Basmati-1, Pusa Sugandh-6, Tarori Basmati-1 and Pusa Sugandh-4 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Basmati-1, PSD-15, Type-3 and Basmati-370 had more dominant genes and Pant Basmati-1, Pusa Sugandh-6, Tarori Basmati-1 and Pusa Sugandh-4 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (0.199 ± 0.081) and H_2 (0.165 ± 0.070) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 7.091 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 0.777 suggesting that the recessive genes were in excess. The same information was provided by the negative F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.208 indicating thereby, asymmetry at loci showing dominance. The positive correlation (0.077) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests cooked kernel breadth was primarily conditioned by dominant genes.

4.5.18. Cooked kernel length/breadth ratio

The slope of regression line of W_r (covariance) on V_r (variance) (-0.207 ± 0.095) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r - axis below the origin indicating the presence of partial dominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.18**) showed that the parents Pusa Basmati-1, Pusa Sugandh-4 and Type-3 had more number of dominant genes and occupied position near to the origin whereas Pusa Sugandh-6 and Tarori Basmati-1 had more number of recessive genes and occupied position farther from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Basmati-1, Pusa Sugandh-4 and Type-3 had more dominant genes and Pusa Sugandh-6 and Tarori Basmati-1 had more number of recessive genes (**Table 4.5.3**).

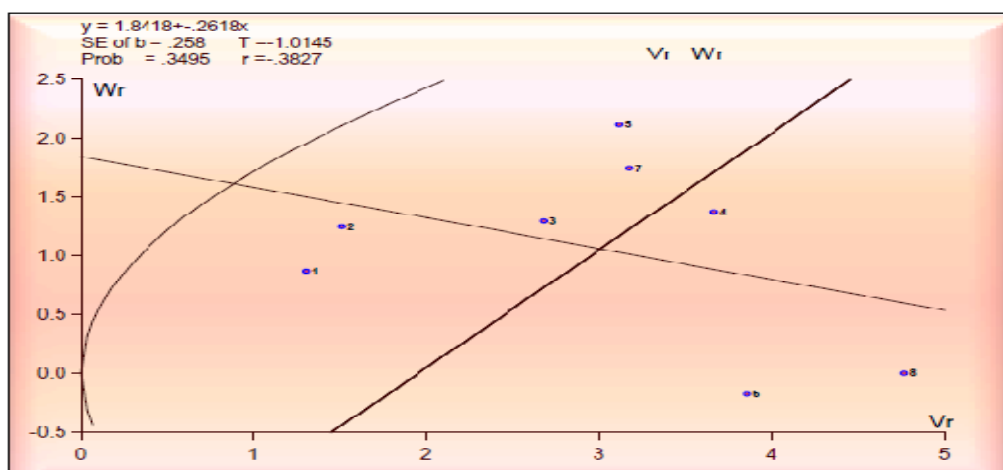


Figure 4.5.16: Vr - Wr graph for cooked kernel length (mm)

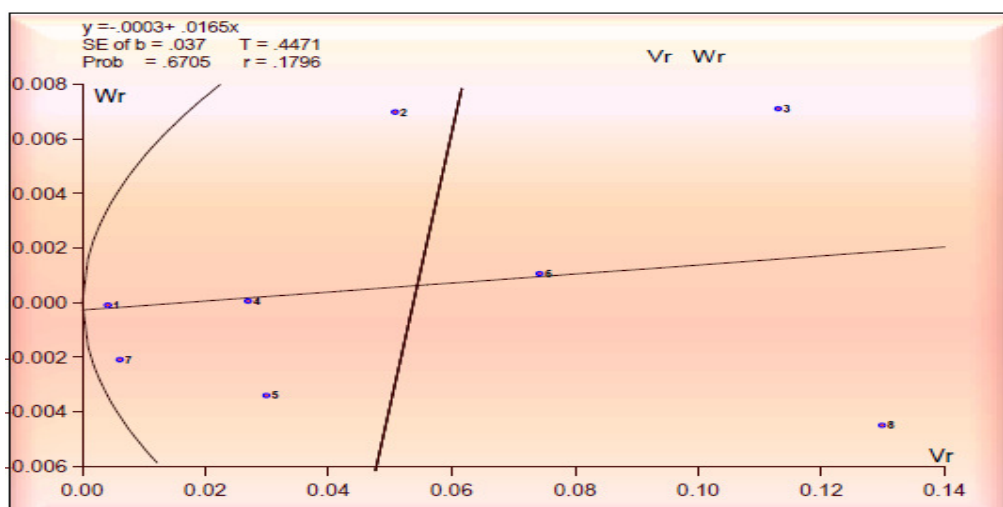


Figure 4.5.17: Vr - Wr graph for cooked kernel breadth (mm)

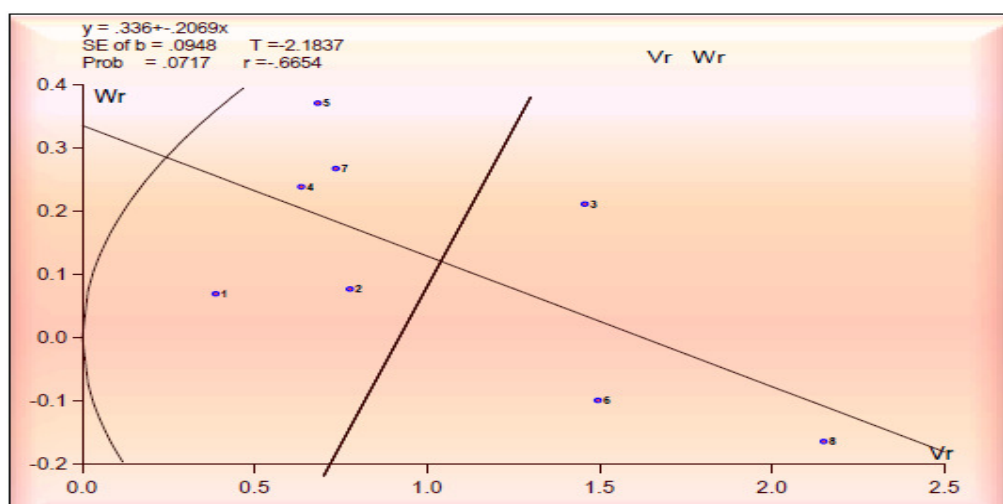


Figure 4.5.18: Vr - Wr graph for cooked kernel length/breadth ratio

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that H_1 (3.889 ± 1.265) and H_2 (3.392 ± 1.100) were significant. This suggests that non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 3.67 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 1.117 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.218 indicating thereby, asymmetry at loci showing dominance. The positive correlation (0.03) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests cooked kernel length/breadth ratio was primarily conditioned by dominant genes.

4.5.19. Kernel elongation ratio

The slope of regression line of W_r (covariance) on V_r (variance) (0.325 ± 0.154) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the W_r - axis below the origin indicating the presence of overdominance type of gene action. A perusal of W_r - V_r graph (**Figure 4.5.19**) showed that the parents Pusa Sugandh-4, PSD-15 and Pusa Basmati-1 had more dominant genes and occupied the position nearest to the origin whereas, Tarori Basmati-1, Basmati-370, Pusa Sugandh-6 and Pant Basmati-1 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Sugandh-4, PSD-15 and Pusa Basmati-1 had more dominant genes and Tarori Basmati-1, Basmati-370, Pusa Sugandh-6 and Pant Basmati-1 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that D (0.012 ± 0.006), H_1 (0.076 ± 0.013) and H_2 (0.070 ± 0.011) were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 2.508 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 1.029 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.229 indicating thereby, asymmetry at loci showing dominance. The negative

correlation (-0.372) between parental performance (Yr) and order of dominance (Vr + Wr) suggests kernel elongation ratio was primarily conditioned by dominant genes.

4.5.20. Alkali digestion value

The slope of regression line of Wr (covariance) on Vr (variance) (-0.209 ± 0.263) deviating significantly from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the Wr - axis below the origin indicating the presence of overdominance type of gene action. A perusal of Wr- Vr graph (**Figure 4.5.20**) showed that the parents Basmati-370, Type-3 and Pusa Basmati-1 had more dominant genes and occupied the position nearest to the origin. Whereas, PSD-15, Pant Basmati-1 and Pusa Sugandh-6 had more number of recessive genes and occupied farthest position from the origin. The order of dominance (Vr + Wr) also revealed that the Basmati-370, Type-3 and Pusa Basmati-1 had more dominant genes and PSD-15, Pant Basmati-1 and Pusa Sugandh-6 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that D (2.072 ± 0.556), H_1 (4.158 ± 1.279) and H_2 (3.324 ± 1.113) were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 1.417 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 1.607 suggesting that the dominant genes were in excess. The same information was provided by the positive F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.2 indicating thereby, asymmetry at loci showing dominance. The positive correlation (0.193) between parental performance (Yr) and order of dominance (Vr + Wr) suggests alkali digestion value was primarily conditioned by dominant genes.

4.5.21. Amylose content (%)

The slope of regression line of Wr (covariance) on Vr (variance) (0.419 ± 0.143) deviating significantly from zero as well as from unity indicated epistasis to be involved in the expression of the trait. The regression line intercepted the Wr - axis below the origin indicating the presence of overdominance type of gene action. A

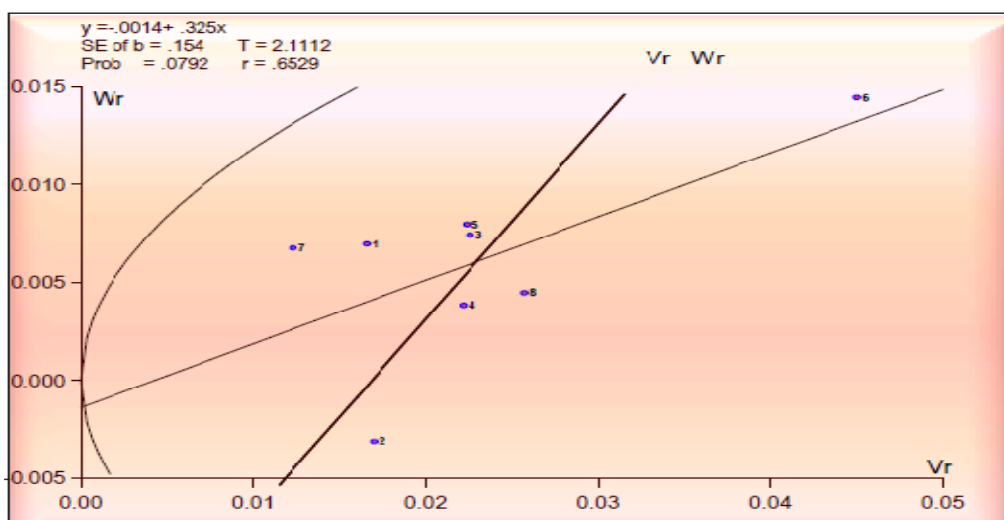


Figure 4.5.19: Vr - Wr graph for kernel elongation ratio

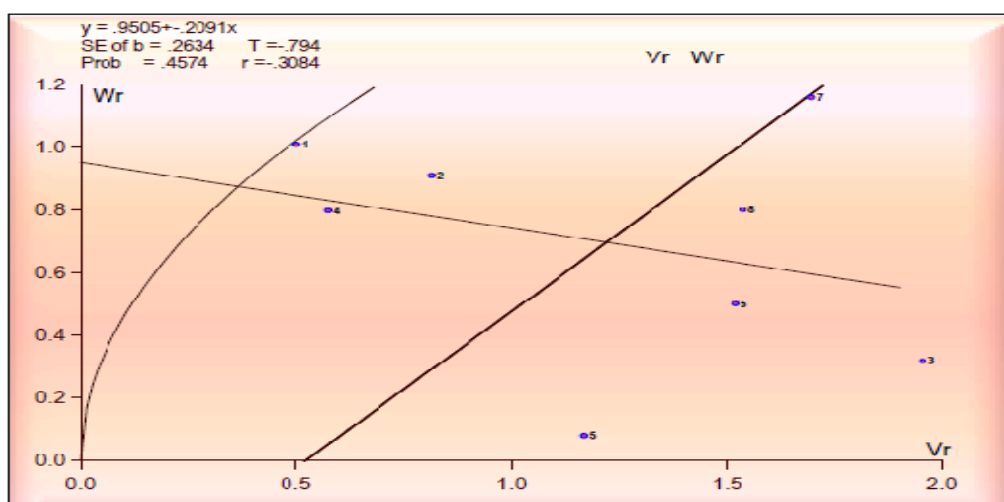


Figure 4.5.20: Vr - Wr graph for alkali digestion value

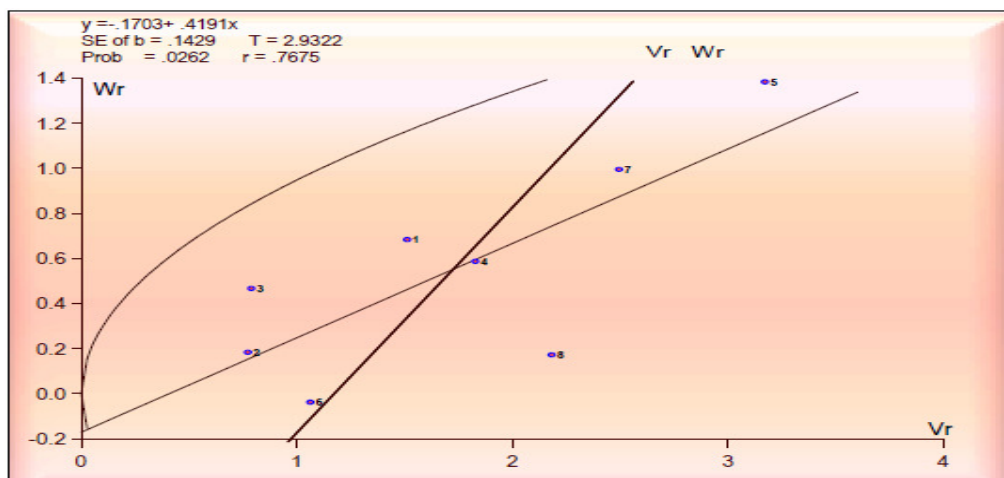


Figure 4.5.21: Vr - Wr graph for amylose content (%)

perusal of W_r - V_r graph (**Figure 4.5.21**) showed that the parents Pusa Sugandh-4, Tarori Basmati-1 and Pusa Sugandh-6 had more dominant genes and occupied the position nearest to the origin. Whereas, Basmati-370, PSD-15 and Type-3 had more number of recessive genes and occupied farthest position from the origin. The order of dominance ($V_r + W_r$) also revealed that the Pusa Sugandh-4, Tarori Basmati-1 and Pusa Sugandh-6 had more dominant genes and Basmati-370, PSD-15 and Type-3 had more number of recessive genes (**Table 4.5.3**).

The estimate of genetic component of variance as given in **Table 4.5.2** revealed that the both additive and non-additive genetic variances as D (0.875 ± 0.437), H_1 (5.527 ± 1.005) and H_2 (4.563 ± 0.874) were significant. This suggests that additive as well as non-additive genes have important role in the expression of the trait. The mean degree of dominance over all loci $[(H_1/D)^{1/2}]$ was 2.513 indicated the presence of overdominance for this trait. The proportion of dominant to recessive genes $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, was 0.813 suggesting that the recessive genes were in excess. The same information was provided by the negative F value. The mean value of proportion of dominant genes with positive/negative effect (UV) over all loci $[H_2/4H_1]$ was 0.206 indicating thereby, asymmetry at loci showing dominance. The negative correlation (-0.552) between parental performance (Y_r) and order of dominance ($V_r + W_r$) suggests amylose content was primarily conditioned by dominant genes.

In breeding for high yielding varieties, the breeder is confronted with the problem of choice of parents. Elimination of poor yielding hybrids on the basis of their performance in early generations has been recommended that would become relatively easy when genetic architecture of yield and its components are known. Diallel analysis is the quickest method of understanding the genetic nature of quantitatively inherited traits and to ascertain the prepotency of parents. The graphical analysis provides useful information by the means of indicating the nature of inheritance of various traits. This analysis is based on some genetic assumption such as normal diploid segregation, absence of reciprocal difference, absence of multiple allelism, uncorrelated distribution of genes among parents and lack of epistasis. This poses restriction on the material to be used for the study and the reliability of various estimates. In case of non-fulfilment of any of these assumptions, **Hayman (1954)** suggested suitable modification which is

helpful in obtaining fairly reliable estimates. The graphical analysis helps in understanding:

1. Genetic architecture of parents.
2. Types of gene action controlling the traits.
3. Genetic diversity among parents.

In the present analysis the graphical analysis indicated that the general assumptions of diallel analysis was valid for all the traits except these 11 traits viz., days to 50% flowering, panicle length, panicles/plant, spikelet fertility, grain yield/plant, kernel breadth, kernel length/breadth ratio, cooked kernel breadth, cooked kernel length/breadth ratio, kernel elongation ratio and amylose content. The regression of W_r on V_r was not significant from unity for traits filled grains/panicle and test weight. The regression line of unit slope intercepted the W_r -axis well near the origin for filled grains/panicle and test weight. This suggested that these traits are predominantly controlled by additive gene effects.

A perusal of the **Table 4.5.1** revealed that both additive as well as non-additive gene action were important for the traits days to 50% flowering, plant height, flag leaf length, panicle length, panicles/plant, unfilled grains/panicle, spikelet fertility, grain yield/plant, hulling recovery, milling recovery, kernel length, kernel breadth, kernel length/breadth ratio, cooked kernel length, cooked kernel breadth, cooked kernel length/breadth ratio, kernel elongation ratio, alkali digestion value and amylose content. For these traits, the regression coefficient deviated significantly from unity, indicating the presence of epistasis. The observation that non-allelic interaction is encountered frequently in the inheritance of qualitative traits, provide presumptive evidence that it (epistasis) could be an important factor in the expression of quantitative traits as well. Further, presence of epistasis has been shown to be an important component of total genetic variance. For this reason, reservations have been expressed on the validity of conclusion derived from quantitative genetic experiments ignoring epistatic parental arrays (**Yermanos and Allard, 1961**).

Further, genetic component of variance provides detailed information about the nature and magnitude of various genetic components that helps in calculating the allied

statistics. The genetic improvement in the population depends largely upon the composition of components of genetic variance and their relative magnitude.

In the present study, a critical perusal of Table 4.5.2 constructed following analysis of genetic component of variance revealed significance of both additive genetic variance (D) non-additive genetic variance (H_1 and H_2) for all the traits days to 50% flowering, plant height, flag leaf length, filled grains/panicle, unfilled grains/panicle, test weight, cooked kernel length, kernel elongation ratio, alkali digestion value and amylose content. Whereas, only non-additive genetic variance (H_1 and H_2) found significance for traits Panicle length, panicles/plant, spikelet fertility, grain yield/plant, hulling recovery, milling recovery, kernel length, kernel breadth, kernel length/breadth ratio, cooked kernel breadth and cooked kernel length/breadth ratio. Thus, the non-significant additive component of variance (D) towards expression of these traits indicated the preponderance of non-additive gene action.

The average degree of dominance $[(H_1/D)^{1/2}]$ was calculated for all the studied traits. It was found that for days to 50% flowering and test weight, the value for average degree of dominance $[(H_1/D)^{1/2}]$ was very much close to unity that indicates complete dominance and hence, preponderance of non-additive gene action. The value for average degree of dominance $[(H_1/D)^{1/2}]$ for traits viz., plant height, flag leaf length, panicle length, panicles/plant, filled grains/panicle, unfilled grains/panicle, spikelet fertility, grain yield/plant, hulling recovery, milling recovery, kernel length, kernel breadth, kernel length/breadth ratio, cooked kernel length, cooked kernel breadth, cooked kernel length/breadth ratio, kernel elongation ratio, alkali digestion value and amylose content were clearly above unity and therefore, these traits showed the case of overdominance.

The estimates of proportion of dominant to recessive genes, $[(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2}-F]$, suggested that dominant and recessive alleles were in equal proportion for the traits plant height, filled grains/panicle, kernel breadth and kernel elongation ratio. Excess of dominant allele was found for the traits days to 50% flowering, flag leaf length, panicles/plant, unfilled grains/panicle, spikelet fertility, test weight, hulling recovery, milling recovery, kernel length, kernel length/breadth ratio, cooked kernel length, cooked kernel length/breadth ratio and alkali digestion value. On the contrary, it

was indicated that traits panicle length, grain yield/plant, cooked kernel breadth and amylose content had excess of recessive alleles in the parents.

The mean value of proportion of genes with positive and negative effects over all loci in the parent [$H_2/4H_1$] was less than 0.25 for all the studied traits that indicated asymmetry of distribution of dominant gene in parents.

The similar findings was reported by **Chaturvedi *et al.* (2015)**, **Sattari *et al.* (2013)**, **Ilieva *et al.* (2013)**, **Ashfaq *et al.* (2012)**, **Raju *et al.* (2011)**, **Kimani *et al.* (2011)**, **Iftekharuddaula *et al.* (2008)**, **Kumar *et al.* (2007a)**, **Kumar *et al.* (2007b)**, **Akram *et al.* (2007)**, **Yan and Lin (2004)**, **Pooni *et al.* (1993)** and **Thattil and Perara (1991)**. The results of the present study are in close agreement with these results.

4.6 Correlation and path coefficient

4.6.1. Correlation

The grain yield is a highly variable and complex trait and hence, direct selection for grain yield may not be yield fruitful result. Further, yield components are not always independent rather in interlinked in their action. The selection practised for one component trait may simultaneously bring correlated change in other associated traits. Thus, the information on degree and direction of association between component traits are essential for indirect selection for yield. This information may be useful in prediction of correlated response to directional selection in the construction of selection indices and in the detection of such traits that have no role in themselves but being indication of the more important ones under consideration (**Johnson *et al.*, 1955**).

Phenotypic correlation arises from observed association between two traits that include effect of genetic association and environmental influence for trait expression modulation. This kind of correlation is not stable and hence, of little practical use in plant breeding unless genetic and environmental correlations between a pair of traits are in the same direction when estimated separately. Genetic correlations provide a stable association between trait pairs and are heritable. This kind of correlation may be accounted for either due to linkage or pleiotropy. This can be used reliably for indirect selection. Genotypic correlation in the true essence may be interpreted as the correlation of breeding value. The environmental correlation includes both environmental and non-additive genetic deviations.

Many a time, phenotypic correlations were smaller than the genotypic correlations. The probable reason may be that the genes that govern two traits are similar and the environmental conditions pertaining to the expression of these traits has small and similar effect on both the traits. The phenotypic and genotypic correlations among yield component traits are presented in **Table 4.6.1.1** and **4.6.1.2**, respectively and are described as below:

4.6.1.1. Days to 50% flowering

Days to 50% flowering showed significant positive correlation with plant height at phenotypic ($r_{ph}=0.220$) and genotypic ($r_g=0.247$) level. While, significant negative correlation was found with flag leaf length, panicle length, test weight at phenotypic level ($r_{ph} = -0.188, -0.245, -0.507$) and with flag leaf length, panicle length, test weight and grain yield/plant at genotypic level ($r_g = -0.208, -0.284, -0.590, -0.201$).

4.6.1.2. Plant height (cm)

Plant height showed significant positive correlation with flag leaf length, panicles/plant, filled grains/panicle, spikelet fertility and grain yield/plant at phenotypic ($r_{ph} = 0.321, 0.459, 0.350, 0.276, 0.382$) and genotypic level ($r_g = 0.326, 0.471, 0.391, 0.298, 0.395$).

4.6.1.3. Flag leaf length (cm)

Flag leaf length showed significant positive correlation with panicle length and grain yield/ plant at phenotypic ($r_{ph} = 0.232, 0.241$) and genotypic level ($r_g = 0.233, 0.253$).

4.6.1.4. Panicle length (cm)

Panicle length showed significant positive correlation with panicles/plant, spikelet fertility and grain yield/plant at phenotypic ($r_{ph} = 0.188, 0.243, 0.281$) and genotypic level ($r_g = 0.196, 0.249, 0.296$). While, significant negative correlation was found with unfilled grains/panicle at phenotypic ($r_{ph} = -0.295$) and genotypic level ($r_g = -0.328$).

4.6.1.5. Number of panicles per plant

Number of panicles per plant showed significant positive correlation with filled grains/panicle, spikelet fertility, test weight and grain yield/plant at phenotypic ($r_{ph} = 0.470, 0.314, 0.220, 0.550$) and genotypic level ($r_g = 0.527, 0.338, 0.241, 0.566$).

Table 4.6.1.1: Phenotypic correlation coefficient among grain yield and its component traits

Traits	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/ plant	Filled grains /panicle	Unfilled grains/ panicle	Spikelet fertility (%)	Test weight (g)
Plant height (cm)	0.220*	1.000							
Flag leaf length (cm)	-0.188*	0.321**	1.000						
Panicle length (cm)	-0.245**	-0.019	0.232*	1.000					
Panicles/plant	-0.076	0.459**	0.141	0.188*	1.000				
Filled grains/panicle	-0.080	0.350**	0.058	-0.017	0.470**	1.000			
Unfilled grains/panicle	-0.093	-0.033	-0.054	-0.295**	0.058	0.092	1.0000		
Spikelet fertility (%)	0.017	0.276**	0.082	0.243*	0.314**	0.667**	-0.668**	1.0000	
Test weight (g)	-0.507**	-0.062	0.081	0.163	0.220*	0.423**	-0.091	0.390**	1.000
Grain yield/plant (g)	-0.177	0.382**	0.241*	0.281**	0.550**	0.397**	-0.197*	0.444**	0.289**

Table 4.6.1.2: Genotypic correlation coefficient among grain yield and its component traits

Character	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/ plant	Filled grains/ panicle	Unfilled grains/ panicle	Spikelet fertility (%)	Test weight (g)
Plant height (cm)	0.247**	1.000							
Flag leaf length (cm)	-0.208*	0.326**	1.000						
Panicle length (cm)	-0.284**	-0.024	0.233*	1.000					
Panicles/plant	-0.095	0.471**	0.147	0.196*	1.000				
Filled grains/panicle	-0.154	0.391**	0.070	-0.045	0.527**	1.000			
Unfilled grains/ Panicle	-0.108	-0.035	-0.063	-0.328**	0.070	0.073	1.0000		
Spikelet fertility (%)	-0.025	0.298**	0.096	0.249**	0.338**	0.661**	-0.698**	1.000	
Test weight (g)	-0.590**	-0.064	0.074	0.171	0.241*	0.491**	-0.067	0.414**	1.000
Grain yield/plant (g)	-0.201*	0.395**	0.253**	0.296**	0.566**	0.438**	-0.211*	0.474**	0.314**

Table 4.6.2.1: Phenotypic path coefficient of grain yield component traits towards grain yield

Traits	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/ plant	Filled grains/ panicle	Unfilled grains/ panicle	Spikelet fertility (%)	Test weight (g)
Days to 50% flowering		-0.010	0.008	0.011	0.003	0.004	0.004	0.006	0.023
Plant height (cm)	0.012		0.018	-0.001	0.026	0.020	-0.002	-0.005	-0.003
Flag leaf length (cm)	-0.014	0.024		0.017	0.010	0.004	-0.004	0.015	0.006
Panicle length (cm)	-0.046	-0.003	0.043		0.035	-0.003	-0.055	0.020	0.030
Panicles/plant	-0.031	0.187	0.058	0.077		0.192	0.024	0.038	0.090
Filled grains/panicle	-0.022	0.095	0.016	-0.005	0.127		0.025	-0.009	0.115
Unfilled grains/panicle	-0.021	0.007	0.012	0.068	-0.013	-0.021		-0.025	0.021
Spikelet fertility (%)	-0.002	0.027	0.022	-0.004	-0.006	0.025	-0.015		0.05
Test weight (g)	-0.044	-0.005	0.007	0.014	0.019	0.037	-0.008	-0.006	
Grain yield/plant (g)	-0.177	0.382**	0.241*	0.281**	0.550**	0.397**	-0.197*	0.444**	0.289**
Partial R ²	0.008	0.022	0.018	0.052	0.225	0.108	0.045	0.125	0.025

R² = 0.5001; Residual effect = 0.7071

Table 4.6.2.2: Genotypic path coefficient of grain yield component traits towards grain yield

Character	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/ plant	Filled grains/ panicle	Unfilled grains/ panicle	Spikelet fertility (%)	Test weight (g)
Days to 50% flowering		-0.000	0.000	0.000	0.000	0.000	0.000	-0.000	0.000
Plant height (cm)	0.055		0.072	-0.005	0.104	0.086	-0.008	0.158	-0.014
Flag leaf length (cm)	-0.014	0.023		0.016	0.010	0.005	-0.004	-0.024	0.005
Panicle length (cm)	-0.081	-0.007	0.066		0.056	-0.013	-0.094	0.014	0.049
Panicles/plant	-0.024	0.122	0.038	0.051		0.136	0.018	0.000	0.062
Filled grains/panicle	-0.083	0.211	0.038	-0.024	0.284		0.039	0.087	0.264
Unfilled grains/panicle	0.052	0.017	0.030	0.158	-0.034	-0.035		0.005	0.032
Spikelet fertility (%)	-0.083	0.211	0.038	-0.024	0.056	-0.013	-0.014		0.055
Test weight (g)	-0.049	-0.005	0.006	0.014	0.020	0.041	-0.005	0.136	
Grain yield/plant (g)	-0.201*	0.395**	0.253**	0.296**	0.566**	0.438**	-0.211*	0.474**	0.314**
Partial R ²	0.0003	0.0874	0.0175	0.0844	0.1461	0.2361	0.1017	0.1423	0.0261

R² = 0.7303; Residual effect = 0.5193

4.6.1.6. Number of filled grains per panicle

Number of filled grains per panicle showed significant positive correlation with spikelet fertility, test weight and grain yield/plant at phenotypic ($r_{ph} = 0.667, 0.423, 0.397$) and genotypic level ($r_g = 0.661, 0.491, 0.438$).

4.6.1.7. Number of unfilled grains per panicle

Number of unfilled grains/panicle showed significant negative correlation with spikelet fertility and grain yield/plant at phenotypic ($r_{ph} = -0.668, -0.197$) and genotypic level ($r_g = -0.698, -0.211$)

4.6.1.8. Spikelet fertility (%)

Spikelet fertility showed significant positive correlation with test weight and grain yield/plant at phenotypic ($r_{ph} = 0.390, 0.444$) and genotypic level ($r_g = 0.414, 0.474$).

4.6.1.9. Test weight (g)

Test weight showed significant positive correlation with grain yield/plant at phenotypic ($r_{ph}=0.289$) and genotypic level ($r_g=0.314$).

Out of ten, seven traits *viz.*, plant height, flag leaf length, panicle length, panicles/ plant, filled grains/panicle, spikelet fertility and test weight exhibited significant positive correlation with grain yield/plant whereas, two traits *viz.*, days to 50% flowering and unfilled grains/panicle exhibited significant negative correlation with grain yield/plant at both, phenotypic and genotypic level. Similar results were also reported by **Laxuman *et al.* (2011), Chandra *et al.* (2009), Kishore *et al.* (2007), Om-Vir and Singh (2006) and Kennedy and Rangasamy (1998).**

Test weight showed significant positive association with spikelet fertility, filled grains/panicle, panicles/plant at both, phenotypic and genotypic level and significant negative association with days to 50% flowering at both, phenotypic and genotypic level. Spikelet fertility showed significant positive association with filled grains/panicle, panicle/plant, panicle length and plant height at both, phenotypic and genotypic level whereas significant negative association with unfilled grains/panicle at both, phenotypic and genotypic level. These findings are in agreement with the earlier findings of **Chakraborty *et al.* (2010)., Chandra *et al.* (2009), Malini *et al.* (2007), Zahid *et al.* (2006), Khedikar *et al.* (2004) and Cheema *et al.* (1998).**

4.6.2 Path coefficient

An extensive stockpile of literature on yield has now developed but the major problem remains intriguing that yield component traits are interrelated. Physiological and genetic aspects of this interdependence are still debatable. Under such circumstances, the value of yield analysis in breeding programme must be called in question. However, a few plant breeders appear to turn to statistical procedures such as factor analysis or path coefficient analysis.

The path coefficient analysis was carried out by taking grain yield/plant as dependent variable and rest of the traits as independent variable. Phenotypic and genotypic direct effects in F_1 and their parents are presented in **Table 4.6.2.1** and **Table 4.6.2.2**, respectively.

A critical observation of phenotypic path coefficient presented in **Table 4.6.2.1** revealed that the plant height exhibited significant positive phenotypic correlation with grain yield/plant (0.382) and positive direct effect on grain yield/plant (0.022). It (Plant height) exerts positive indirect effect through flag leaf length (0.024), panicles/plant (0.187), filled grains/panicle (0.095), unfilled grains/panicle (0.007), spikelet fertility (0.027) and negative indirect effect through days to 50% flowering (-0.010), panicle length (-0.003) and test weight (-0.005).

Flag leaf length exhibited significant positive phenotypic correlation with grain yield/plant (0.241) and positive direct effect on grain yield (0.018). It exerts positive indirect effect through days to 50% flowering (0.008), plant height (0.018), panicle length (0.043), panicles/plant (0.058), filled grains/panicle (0.016), unfilled grains/panicle (0.012), spikelet fertility (0.022) and test weight (0.007).

Panicle length exhibited significant positive phenotypic correlation with grain yield/plant (0.281) and positive direct effect on grain yield (0.052). It exerts positive indirect effect through days to 50% flowering (0.011), flag leaf length (0.017), panicles/plant (0.077), unfilled grains/panicle (0.068), and test weight (0.007) and negative indirect effect through plant height (-0.001), filled grains/panicle (-0.005) and spikelet fertility (-0.004).

Number of panicles/plant exhibited significant positive phenotypic correlation with grain yield/plant (0.550) and positive direct effect on grain yield/plant (0.225). It

exerts positive indirect effect through days to 50% flowering (0.003), plant height (0.026), flag leaf length (0.010), panicle length (0.035), filled grains/panicle (0.127) and test weight (0.019) and negative indirect effect through unfilled grains/panicle (-0.013) and spikelet fertility (-0.006).

Number of filled grains/panicle exhibited significant positive phenotypic correlation with grain yield/plant (0.397) and positive direct effect on grain yield (0.108). It exerts positive indirect effect through days to 50% flowering (0.004), plant height (0.020), flag leaf length (0.004), panicles/plant (0.192), spikelet fertility (0.025) and test weight (0.037) and negative indirect effect through panicle length (-0.003) and unfilled grains/panicle (-0.021).

Number of unfilled grains/panicle exhibited significant negative phenotypic correlation with grain yield/plant (-0.197) and positive direct effect on grain yield (0.045). It exerts positive indirect effect through days to 50% flowering (0.004), panicles/plant (0.024) and filled grains/panicle (0.025) and negative indirect effect through plant height (-0.002), flag leaf length (-0.004), panicle length (-0.055), spikelet fertility (-0.015) and test weight (-0.008).

Spikelet fertility exhibited significant positive phenotypic correlation with grain yield/plant (0.444) and positive direct effect on grain yield (0.125). It exerts positive indirect effect through days to 50% flowering (0.006), flag leaf length (0.015), panicle length (0.020) and panicles/plant (0.038) and negative indirect effect through plant height (-0.005), filled grains/panicle (-0.009), unfilled grains/panicle (-0.025) and test weight (-0.006).

Test weight exhibited significant positive phenotypic correlation with grain yield/plant (0.289) and positive direct effect on grain yield/plant (0.025). It exerts positive indirect effect through days to 50% flowering (0.023), flag leaf length (0.006), panicle length (0.030) and panicles/plant (0.090), filled grains/panicle (0.115), unfilled grains/panicle (0.021) and spikelet fertility (0.05) and negative indirect effect through plant height (-0.003) and test weight (-0.006).

A critical observation of genotypic path coefficient presented in **Table 4.6.2.1** revealed that the days to 50% flowering exhibited significant negative genotypic correlation with grain yield/plant (-0.201) and positive direct effect on grain yield/plant

(0.0003). It (days to 50% flowering) exerts positive indirect effect through plant height (0.055) and unfilled grains/panicle (0.052) and negative indirect effect through flag leaf length (- 0.014), panicle length (- 0.081), panicles/plant (- 0.024), filled grains/panicle (- 0.083), spikelet fertility (- 0.083) and test weight (- 0.049).

Plant height exhibited significant positive genotypic correlation with grain yield/plant (0.395) and positive direct effect on grain yield (0.0874). It (Plant height) exerts positive indirect effect through flag leaf length (0.023), panicles/plant (0.122), filled grains/panicle (0.211), unfilled grains/panicle (0.017) and spikelet fertility (0.211) and negative indirect effect through days to 50% flowering (- 0.000), panicle length (- 0.007) and test weight (- 0.005).

Flag leaf length exhibited significant positive genotypic correlation with grain yield/plant (0.253) and positive direct effect on grain yield/plant (0.0175). It exerts positive indirect effect through plant height (0.072), panicle length (0.066), panicles/plant (0.038), filled grains/panicle (0.038), unfilled grains/panicle (0.030), spikelet fertility (0.038) and test weight (0.006).

Panicle length exhibited significant positive genotypic correlation with grain yield/plant (0.296) and positive direct effect on grain yield (0.0844). It exerts positive indirect effect through flag leaf length (0.016), panicles/plant (0.051), unfilled grains/panicle (0.158), and test weight (0.014) and negative indirect effect through plant height (-0.005), filled grains/panicle (-0.024) and spikelet fertility (-0.024).

Number of panicles/plant exhibited significant positive genotypic correlation with grain yield/plant (0.566) and positive direct effect on grain yield/plant (0.1461). It exerts positive indirect effect through plant height (0.104), flag leaf length (0.010), panicle length (0.056), filled grains/panicle (0.284), spikelet fertility (0.056) and test weight (0.020) and negative indirect effect through unfilled grains/panicle (-0.034).

Number of filled grains/panicle exhibited significant positive genotypic correlation with grain yield/plant (0.438) and positive direct effect on grain yield/plant (0.2361). It exerts positive indirect effect through plant height (0.086), flag leaf length (0.005), panicles/plant (0.136) and test weight (0.041) and negative indirect effect through panicle length (- 0.013), spikelet fertility (- 0.013) and unfilled grains/panicle (- 0.035).

Number of unfilled grains/panicle exhibited significant negative genotypic correlation with grain yield/plant (- 0.211) and positive direct effect on grain yield/plant (0.102). It exerts positive indirect effect through panicles/plant (0.018) and filled grains/panicle (0.039) and negative indirect effect through plant height (-0.008), flag leaf length (-0.004), panicle length (- 0.094), spikelet fertility (- 0.014) and test weight (-0.005).

Spikelet fertility exhibited significant positive genotypic correlation with grain yield/plant (0.474) and positive direct effect on grain yield/plant (0.1423). It exerts positive indirect effect through plant height (0.158), panicle length (0.014), filled grains/panicle (0.087), unfilled grains/panicle (0.005) and test weight (0.136) and negative indirect effect through flag leaf length (-0.024).

Test weight exhibited significant positive genotypic correlation with grain yield/plant (0.314) and positive direct effect on grain yield/plant (0.0261). It exerts positive indirect effect through flag leaf length (0.005), panicle length (0.049) and panicles/plant (0.062), filled grains/panicle (0.264), unfilled grains/panicle (0.032) and spikelet fertility (0.055) and negative indirect effect through plant height (-0.014).

Contrary to correlation coefficient that measures the degree and direction of association between two variables, path coefficient measures the magnitude of direct and indirect effects of independent variable on dependent variable, say yield. This enable breeder to judge the most relevant component trait that affect the yield and helps in indirect selection. The concept of path analysis was developed by **Wright (1921)**, and this was used for the first time for plant selection by **Dewey and Lu (1959)**.

Path coefficient analysis enables one to thoroughly understand various traits by partitioning the correlation coefficient into measures of direct and indirect effects. Path coefficient analysis was worked out considering grain yield as dependent trait and all other traits as independent variables.

Present study revealed direct positive effects of traits *viz.*, plant height, flag leaf length, panicle length, number of panicles/plant, number of filled grains/panicle, spikelet fertility and test weight along with their significant positive association with grain yield at both genotypic and phenotypic level. Thus, there is true relationship between these traits and grain yield and direct selection for these traits can bring an

indirect improvement for the dependent trait, the grain yield/plant. The findings of **Malini *et al.* (2007)** and **Khedikar *et al.* (2004)** on trait association and path coefficient confirmed the findings of the present study.

The perusal of path coefficient analysis at genotypic level revealed that filled grains/panicle ($r_g=0.438$, partial $R^2=0.2361$) was the most important positive direct contributor towards the grain yield/plant followed by panicles/plant ($r_g=0.566$, partial $R^2=0.1461$) and spikelet fertility ($r_g=0.474$, partial $R^2=0.1423$). Similar information was reported by **Ramakrishna *et al.* (2006)**, **Gupta *et al.* (1999)** and **Cheema *et al.* (1998)**.

At both phenotypic and genotypic level, plant height despite having positive direct effect on grain yield had negative association with grain yield/plant that seems evident from its (Plant height) negative indirect effect through several traits like flag leaf length, panicle length, panicles/plant, filled grains/panicle, spikelet fertility and test weight. Similarly, number of unfilled grains/panicle had direct positive effect on grain yield/plant but association was negative that may be due to its unfavorable negative indirect effect through plant height, flag leaf length, panicle length, spikelet fertility and test weight. A similar result was also reported by **Zahid *et al.* (2006)**.

Thus, path coefficient analysis identified filled grains/panicle, panicles/plant and spikelet fertility as the chief contributor towards grain yield/plant. Therefore, these traits should be given emphasis while making selection for genetic improvement of grain yield/plant in aromatic rice cultivars. More or less similar observations were made by earlier researchers while working on rice like **Chakraborty *et al.* (2010)**, **Chandra *et al.* (2009)** and **Kishore *et al.* (2007)**.

4.7. Aroma index

The aroma is an economically important trait of rice. Indian aromatic rice is a small group of premium aromatic rice from India, prized in international trade. It is praised for its unique quality aroma, is a connoisseur's delight, a nature gift to Indian sub-continent. The aromatic trait differentiates the highly valued aromatic rice from the other rice types. In the present study 28 F_1 hybrids generated from diallel mating and their 8 parents were evaluated for the aroma strength as per laboratory techniques developed at IRRI (1971) to evaluate presence of aroma in rice cultivars (**Cruz and Khush, 2000**).

The perusal of Table 4.7.1 revealed that aroma strength ranged from 0.050 (weak aroma) to 2.00 (strong aroma) among 8 parents and their 28 crosses, all parents and their 22 crosses had strong aroma. Whereas, four crosses had moderate aroma and two crosses had weak aroma.

The crosses viz., Pusa Basmati-1×Pusa Sugandh-4, Pusa Basmati-1×Pusa Sugandh-6, Pusa Basmati-1×Type-3, Pusa Basmati-1×Basmati-370, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×PSD-15, Pusa Basmati-1×Pant Basmati-1, Pusa Sugandh-4×Pusa Sugandh-6, Pusa Sugandh-4×Type-3, Pusa Sugandh-4×Basmati-370, Pusa Sugandh-4×PSD-15, Pusa Sugandh-4×Pant Basmati-1, Pusa Sugandh-6×Type-3, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Tarori Basmati-1, Pusa Sugandh-6×PSD-15, Type-3×Basmati-370, Type-3×PSD-15, Basmati-370×Tarori Basmati-1, Basmati-370×PSD-15, Tarori Basmati-1×PSD-15 and Tarori Basmati-1×Pant Basmati-1 showed strong aroma.

Crosses, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-6×Pant Basmati-1, Type-3×Pant Basmati-1 and Basmati-370×Pant Basmati-1 showed moderate aroma while, the crosses, Type-3×Tarori Basmati-1 and PSD-15×Pant Basmati-1 had weak aroma.

The similar findings had also been reported by the Seraj *et al.* (2013), Bajpai *et al.* (2012), Bhonsle and Sellappan (2010), Golam *et al.* (2011) and Yau *et al.* (1996) in different rice varieties and land races.

Aroma is the unique feature of aroma rice varieties caused by an extremely small amount of volatile compounds, which are contained as complex mixture. The number of compounds that constitutes aroma as reported by different researchers varies considerably and no individual compound has been identified or can be attributed responsible for the aroma of cooked scented rice. Rather, a blend of a number of volatile compounds is believed to impart the characteristic aroma and flavour to such rice varieties. Among these 2-Acetyl-1-pyrroline (2-AP) is considered by some researchers to be the most important (Weber *et al.*, 2000 and Buttery *et al.*, 1988).

Table 4.7.1: Aroma index of parents and their crosses based on aroma strength score

Sl. No.	Crosses/parents	Score	Aroma strength
1	Pusa Basmati-1×Pusa Sugandh-4	2.00	Strong aroma
2	Pusa Basmati-1×Pusa Sugandh-6	2.00	Strong aroma
3	Pusa Basmati-1×Type-3	2.00	Strong aroma
4	Pusa Basmati-1×Basmati-370	2.00	Strong aroma
5	Pusa Basmati-1×Tarori Basmati-1	2.00	Strong aroma
6	Pusa Basmati-1×PSD-15	2.00	Strong aroma
7	Pusa Basmati-1×Pant Basmati-1	2.00	Strong aroma
8	Pusa Sugandh-4×Pusa Sugandh-6	2.00	Strong aroma
9	Pusa Sugandh-4×Type-3	2.00	Strong aroma
10	Pusa Sugandh-4×Basmati-370	2.00	Strong aroma
11	Pusa Sugandh-4×Tarori Basmati-1	1.00	Moderate aroma
12	Pusa Sugandh-4×PSD-15	2.00	Strong aroma
13	Pusa Sugandh-4×Pant Basmati-1	2.00	Strong aroma
14	Pusa Sugandh-6×Type-3	2.00	Strong aroma
15	Pusa Sugandh-6×Basmati-370	2.00	Strong aroma
16	Pusa Sugandh-6×Tarori Basmati-1	2.00	Strong aroma
17	Pusa Sugandh-6×PSD-15	2.00	Strong aroma
18	Pusa Sugandh-6×Pant Basmati-1	1.00	Moderate aroma
19	Type-3×Basmati-370	2.00	Strong aroma
20	Type-3×Tarori Basmati-1	0.50	Weak aroma
21	Type-3×PSD-15	2.00	Strong aroma
22	Type-3×Pant Basmati-1	1.00	Moderate aroma
23	Basmati-370×Tarori Basmati-1	2.00	Strong aroma
24	Basmati-370×PSD-15	2.00	Strong aroma
25	Basmati-370×Pant Basmati-1	1.00	Moderate aroma
26	Tarori Basmati-1×PSD-15	2.00	Strong aroma
27	Tarori Basmati-1×Pant Basmati-1	2.00	Strong aroma
28	PSD-15×Pant Basmati-1	0.50	Weak aroma
29	Pusa Basmati-1	2.00	Strong aroma
30	Pusa Sugandh-4	2.00	Strong aroma
31	Pusa Sugandh-6	2.00	Strong aroma
32	Type-3	2.00	Strong aroma
33	Basmati-370	2.00	Strong aroma
34	Tarori Basmati-1	2.00	Strong aroma
35	PSD-15	2.00	Strong aroma
36	Pant Basmati-1	2.00	Strong aroma

*Summary
and
Conclusions*

The present study entitled “Genetic analysis of quantitative traits in aromatic rice (*Oryza sativa* L.)” was carried out with following objectives:

- i. To estimate the extent of variability, heritability and genetic advance.
- ii. To determine the extent of heterosis for yield and quality traits and to identify the promising F₁ crosses on the basis of their heterotic response.
- iii. To study the general and specific combining ability effects in order to identify promising parents and crosses for grain yield and quality traits.
- iv. To study the nature of gene action governing the expression of yield and quality traits in aroma rice.
- v. To assess trait association among yield and yield components with direct and indirect effects of different component traits on yield.
- vi. To analyse the aroma in order to identify best aroma parents and cross combinations.

The present experiment was carried out during *Kharif*, 2015 and 2016 at N. E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India.

Eight genetically diverse cultivars of aromatic rice *viz.*, Pusa Basmati-1, Pusa Sugandh-4, Pusa Sugandh-6, Type-3, Basmati-370, Tarori Basmati-1, PSD-15 and Pant Basmati-1 were crossed in half diallel fashion to generate 28 F₁s during *Kharif*, 2015. All the 28 hybrids along with 8 parents and 1 check (Improved Pusa Basmati-1) were evaluated during *Kharif*, 2016 in randomized complete block design with 3 replications.

The observations were recorded on 22 traits namely, days to 50% flowering, plant height, flag leaf length, panicle length, number of panicles per plant, number of filled grains per panicle, number of unfilled grains per panicle, spikelet fertility, test weight, grain yield per plant, hulling recovery, milling recovery, kernel length, kernel breadth, kernel length/breadth ratio, cooked kernel length, cooked kernel breadth, cooked

kernel length/breadth ratio, kernel elongation ratio, alkali digestion value, amylose content and aroma index. Mean data for each trait was used for statistical analysis.

The major outcomes of present investigation that became evident from statistical analysis are summarised below:

- Analysis of variance for grain yield, yield components and quality traits revealed significant differences among the means of parental genotypes and hybrids for all the traits.
- The magnitude of phenotypic coefficient of variation (PCV) was higher than that of genotypic coefficient of variation (GCV) for all the traits. High PCV as well as high GCV was observed for number of panicles per plant, grain yield per plant and alkali digestion value. Low PCV and GCV was found for days to 50% flowering, flag leaf length, panicle length, spikelet fertility, test weight, hulling recovery, milling recovery, kernel length, kernel breadth, kernel elongation ratio and amylose content.
- High heritability (>60%) was observed for all the studied traits, among which highest was recorded by plant height, alkali digestion value and number of panicles per plant and lowest was recorded by cooked kernel breadth, kernel breadth and milling recovery.
- High heritability coupled with high genetic advance as percent of mean was observed for alkali digestion value followed by number of panicles per plant, plant height, cooked kernel length/breadth ratio, number of unfilled grains per panicle and kernel length/breadth ratio.
- For grain yield/plant, average heterosis ranged from 21.13% (Pusa Sugandh-4×PSD-15) to 124.58% (Pusa Sugandh-6×PSD-15); heterobeltiosis ranged from -11.20% (Type-3×Basmati-370) to 88.87% (Pusa Basmati-1×PSD-15) and standard heterosis ranged from 17.10% (Pusa Basmati-1×Pusa Sugandh-4) to 193.87% (Pusa Sugandh-6×PSD-15).
- Out of 28 crosses, 27, 23 and 28 crosses showed significant average heterosis, heterobeltiosis and standard heterosis for grain yield per plant, respectively. Twenty three crosses exhibited significant average heterosis, heterobeltiosis and standard heterosis simultaneously.

- On the basis of per se performance, five best crosses for grain yield per plant were Pusa Sugandh-6×PSD-15, Pusa Basmati-1×PSD-15, Pusa Sugandh-6×Basmati-370, Pusa Sugandh-6×Type-3 and Pusa Sugandh-4×Basmati-370.
- Crosses possessing superfine rice quality parameters: kernel length, kernel breadth and kernel length/breadth ratio are the major determinants of superfine rice quality. Best 5 crosses having long kernel length were PSD-15×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1 and Type-3×Pant Basmati-1. None of the crosses showed significant reduction in kernel breadth. Top 5 crosses having high kernel length/breadth ratio were Pusa Sugandh-6×Tarori Basmati-1, PSD-15×Pant Basmati-1, Pusa Basmati-1×Tarori Basmati-1, Pusa Basmati-1×Pant Basmati-1 and Pusa Basmati-1×PSD-15.
- The highest percentage of heterosis with respect to standard check in desired direction was observed for grain yield per plant followed by number of panicles per plant, number of filled grains per panicle, test weight, panicle length, flag leaf length and days to 50% flowering. Rest of the traits showed less than 10 % heterosis in desired direction. Thus, highest manifestation of heterosis for grain yield per plant may have arose due to heterosis for its component traits *viz.* number of panicles per plant, number of filled grain per panicle, test weight, panicle length, flag leaf length and days to 50% flowering.
- Best performing cross (Pusa Sugandh-6×PSD-15) for grain yield/plant also exhibited highest SCA effect (Pusa Sugandh-6×PSD-15) indicating that manifestation of heterosis has intrinsic role of SCA effect.
- The analysis of variance for combining ability revealed that GCA and SCA variance was significant for all the traits. Thus, additive as well as non-additive genetic variances were important for expression of these traits.
- GCA variance was higher than SCA variance ($\sigma^2_{GCA}/\sigma^2_{SCA} = 1.07$) with high predictability ratio (0.68) for days to 50% flowering suggesting major role of additive gene action in the expression of trait. The $\sigma^2_{GCA}/\sigma^2_{SCA} < 1.00$ with low value of predictability ratio for filled grains/panicle, kernel length, kernel breadth *etc.*, suggests major role of non-additive gene action in expression of

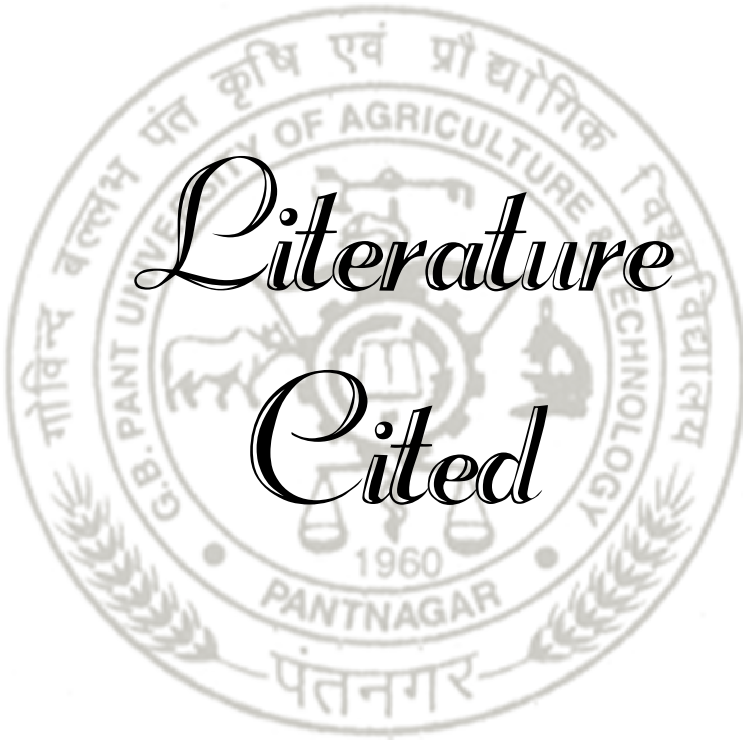
these traits. The $\sigma^2_{GCA}/\sigma^2_{SCA} < 1.00$ with moderate value of predictability ratio for alkali digestion value and amylose content suggest the role of both additive and non additive gene actions in trait expression.

- Pusa Basmati-1 was the best general combiner among parents as it had significant GCA effect for maximum of 13 traits *viz.* plant height, panicle length, number of unfilled grains/panicle, spikelet fertility, milling recovery, kernel length, kernel breadth, kernel length/breadth ratio, cooked kernel length, cooked kernel breadth, cooked kernel length/breadth ratio, alkali digestion value and amylose content. Second best general combiner was Pusa Sugandh-6 having significant GCA effect for 11 traits *viz.*, days to 50% flowering, plant height, flag leaf length, number of filled grains per panicle, spikelet fertility, test weight, grain yield per plant, kernel length, kernel length/breadth ratio, alkali digestion value and amylose content. Third best general combiner was Pusa Sugandh-6 that showed significant GCA effect for 10 traits *viz.*, days to 50% flowering, plant height, number of filled grains per panicle, spikelet fertility, test weight, kernel length, cooked kernel length, cooked kernel length/breadth ratio, kernel elongation ratio and alkali digestion value. None of the parents were good general combiner for all the studied traits.
- The cross Pusa Sugandh-6×Pant Sugandh had highest SCA effect and involved both parents having high GCA effect hence, can be exploited through recombination breeding. The second and third highest SCA effect crosses for grain yield per plant *viz.*, Pusa Basmati-1×PSD-15 and Pusa Sugandh-4×Basmati-370 involved one parent that had good GCA effect and hence, can be exploited through conventional breeding method.
- Lack of consistent relationship was found between SCA effect of crosses and GCA effect of parents involved in crosses. Many of the crosses with high SCA effect for various traits were derived from two parents that were either, good/average, average/average, average/poor or even poor/poor general combiner for respective traits. Therefore, high SCA effect should not be the sole criteria for selection of hybrid rather in many case per se performance of cross may serve as better guide to select the promising hybrid.

- None of the top three hybrids that showed high SCA effect for grain yield per plant expressed high SCA falling within top three for any of the quality parameters. Also, none of the top three cross combinations in terms of *per se* performance for grain yield/plant were included among top three crosses for better performance in any of the quality parameters.
- Mean performance of the hybrids indicated that the hybrids recording high SCA effects were not always having high mean value.
- The graphical analysis revealed partial dominance for days to 50% flowering while overdominance of rest of the traits.
- A significant deviation of regression line from unity indicated the presence of epistasis to be involved in expression of all the traits except test weight and number of filled grains per panicle.
- Array of parental points scattered in Wr-Vr graph for most of the traits indicated that the parents were genetically diverse.
- The analysis of component of variance indicated the preponderance of non-additive genetic variance for panicle length, number of panicles per plant, spikelet fertility, grain yield per plant, hulling recovery, milling recovery, kernel length, kernel breadth, kernel length/breadth ratio and cooked kernel length while preponderance of both additive and non-additive genetic variance was found for days to 50% flowering, plant height, flag leaf length, number of filled grains per panicle, number of unfilled grains per panicle, test weight, cooked kernel breadth, cooked kernel length/breadth ratio, kernel elongation ratio, alkali digestion value and amylose content.
- The proportion of dominant to recessive genes $[(4DH_1)^{1/2}+F]/[(4DH_1)^{1/2}-F]$ suggested that dominant and recessive alleles were in equal proportion for the traits plant height, number of filled grains per panicle, kernel breadth and kernel elongation ratio while they are skewed in parents for rest of the traits.
- The mean value of proportion of genes with positive and negative effects over all loci in the parent $[H_2/4H_1]$ was less than 0.25 for all the studied traits that indicated asymmetry in distribution of genes with positive and negative effects in parents.

- Trait association study indicated significant positive association of plant height, flag leaf length, panicle length, number of panicles per plant, number of filled grains per panicle, spikelet fertility and test weight with grain yield per plant at both, genotypic and phenotypic level.
- Path coefficient analysis identified number of filled grains per panicle, number of panicles per plant and spikelet fertility as the chief contributor towards grain yield/plant and these traits should be given emphasis while making selection for genetic improvement of grain yield in aromatic rice cultivars.
- Aroma index of genotypes ranged from weakly aromatic to strongly aromatic and classified all the parents and 22 hybrids as strongly aromatic, 4 hybrids as moderately aromatic and 2 hybrids as weakly aromatic.

Considering the overall results from the present study, it is apparent that both additive as well as non-additive genetic effects has role in expression of most of the traits that may be utilized through selection in early segregating generation exploiting the fixable effects. Diallel selective mating (**Jensen, 1970**), multiple crossing and early generation selection followed by inter-mating among segregating generation following F₂ generation of selected plants (**Redden and Jensen, 1974**) may be useful for further genetic improvement of various economic quantitative traits. Multiple crossing and biparental mating may ensure rational utilization of both additive and non-additive gene actions with the present set of lines.



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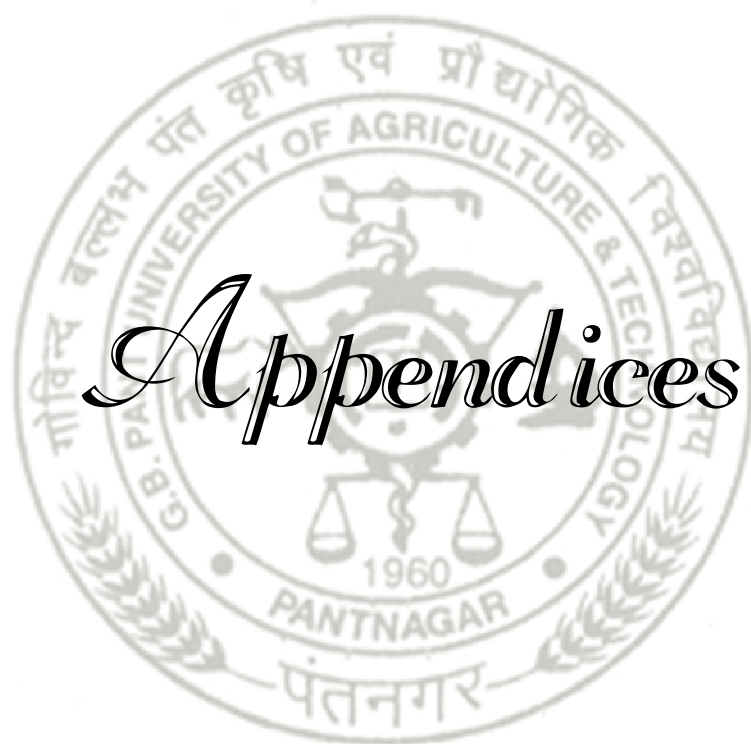
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Appendices

APPENDIX I

Monthly meteorological data at the crop research centre, Pantnagar, during experimental period (June 2015 to November, 2015)

Sl. No.	Month	Average temperature (°C)		Average relative humidity (%)		Average sunshine hours
		Maximum	Minimum	Maximum	Minimum	
1.	June	40.31	25.89	62.06	30.50	7.33
2.	July	33.19	26.39	84.96	66.12	3.82
3.	August	31.90	25.46	89.38	73.38	3.90
4.	September	31.86	23.90	89.36	68.43	6.43
5.	October	31.12	16.16	88.06	44.22	8.67
6.	November	26.98	09.83	90.87	37.61	6.97

APPENDIX II

Crossing plan in half diallel fashion among eight aromatic rice varieties

	Pusa Basmati-1 (1)	Pusa Sugandh-4 (2)	Pusa Sugandh-6 (3)	Type-3 (4)	Basmati-370 (5)	Tarori Basmati-1 (6)	Pant Sugandh Dhan-15 (7)	Pant Basmati-1 (8)
Pusa Basmati-1 (1)		(1×2)	(1×3)	(1×4)	(1×5)	(1×6)	(1×7)	(1×8)
Pusa Sugandh-4 (2)			(2×3)	(2×4)	(2×5)	(2×6)	(2×7)	(2×8)
Pusa Sugandh-6 (3)				(3×4)	(3×5)	(3×6)	(3×7)	(3×8)
Type-3 (4)					(4×5)	(4×6)	(4×7)	(4×8)
Basmati-370 (5)						(5×6)	(5×7)	(5×8)
Tarori Basmati-1 (6)							(6×7)	(6×8)
Pant Sugandh Dhan-15 (7)								(7×8)
Pant Basmati-1 (8)								

APPENDIX III

Mean of various traits for parents and their hybrids in aromatic rice (*Oryza sativa* L.)

Sl. No.	Cross/ Parents	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Panicle length (cm)	Panicles/plant
1.	Pusa Basmati-1 × Pusa Sugandh-4	99.00	112.87	31.40	30.93	16.23
2.	Pusa Basmati-1 × Pusa Sugandh-6	95.67	100.40	36.07	30.73	20.50
3.	Pusa Basmati-1 × Type-3	116.33	135.68	31.50	32.80	19.70
4.	Pusa Basmati-1 × Basmati-370	111.00	146.53	32.97	32.13	20.40
5.	Pusa Basmati-1 × Tarori Basmati-1	107.67	131.27	34.67	35.77	14.10
6.	Pusa Basmati-1 × Pant Sugandh Dhan-15	102.67	121.40	35.13	31.60	20.17
7.	Pusa Basmati 1 × Pant Basmati-1	100.33	105.73	36.13	36.50	16.40
8.	Pusa Sugandh-4 × Pusa Sugandh-6	98.33	117.97	34.10	30.83	21.67
9.	Pusa Sugandh-4 × Type-3	103.33	144.10	33.53	30.57	21.57
10.	Pusa Sugandh-4 × Basmati-370	104.67	136.13	32.30	29.70	18.67
11.	Pusa Sugandh-4 × Tarori Basmati-1	103.67	128.83	41.20	28.07	15.80
12.	Pusa Sugandh-4 × Pant Sugandh Dhan-15	96.33	137.13	35.63	30.33	15.07
13.	Pusa Sugandh-4 × Pant Basmati-1	99.67	100.87	38.93	39.30	18.10
14.	Pusa Sugandh-6 × Type-3	103.33	150.33	39.27	34.43	15.20
15.	Pusa Sugandh-6 × Basmati-370	105.00	151.87	40.57	34.33	19.53
16.	Pusa Sugandh-6 × Tarori Basmati-1	103.33	129.82	37.60	28.90	23.13
17.	Pusa Sugandh-6 × Pant Sugandh Dhan-15	97.00	118.13	34.63	31.67	18.40
18.	Pusa Sugandh-6 × Pant Basmati-1	99.00	105.13	38.13	36.20	15.23
19.	Type-3 × Basmati-370	104.67	143.67	33.43	29.07	13.70
20.	Type-3 × Tarori Basmati-1	106.00	124.37	31.63	30.07	20.57
21.	Type-3 × Pant Sugandh Dhan-15	100.33	151.83	40.13	32.70	24.60
22.	Type-3 × Pant Basmati-1	102.00	125.23	31.67	32.66	21.97
23.	Basmati-370 × Tarori Basmati-1	105.33	130.67	37.10	26.03	21.53
24.	Basmati-370 × Pant Sugandh Dhan-15	103.67	160.70	36.87	33.07	25.03
25.	Basmati-370 × Pant Basmati-1	98.33	125.00	30.30	34.47	21.17
26.	Tarori Basmati-1 × Pant Sugandh Dhan-15	99.33	131.60	41.07	36.00	18.30
27.	Tarori Basmati-1 × Pant Basmati-1	98.33	103.68	35.63	33.63	14.57
28.	Pant Sugandh Dhan-15 × Pant Basmati-1	96.00	107.03	30.33	36.07	18.03
29.	Pusa Basmati-1	111.67	96.07	31.13	29.40	12.87
30.	Pusa Sugandh-4	103.33	106.20	29.90	29.43	15.85
31.	Pusa Sugandh-6	100.33	102.73	31.50	28.80	12.57
32.	Type-3	105.00	105.27	31.13	28.17	12.80
33.	Basmati-370	114.00	143.37	36.97	28.06	14.40
34.	Tarori Basmati-1	105.00	126.00	35.80	27.73	13.33
35.	Pant Sugandh Dhan-15	97.67	122.57	33.63	28.80	11.80
36.	Pant Basmati-1	96.67	95.33	38.20	30.23	12.87
37.	Imp. Pusa Basmati-1 ©	116.00	95.67	31.33	29.63	13.23
38.	Mean	102.97	123.55	34.91	31.59	17.54
39.	C.V.	2.42	1.75	1.78	2.53	3.69
40.	S.E.M	1.44	1.25	0.36	0.46	0.37
41.	C.D. @ 5%	4.05	3.51	1.01	1.30	1.05

Appendix III: Contd.....

Sl. No.	Cross/ Parents	Filled grains/panic le	Unfilled grains/panic le	Spikelet fertility (%)	Test weight (g)	Grain yield/plant (g)
1.	Pusa Basmati-1 × Pusa Sugandh-4	173.63	51.47	77.08	26.04	25.34
2.	Pusa Basmati-1 × Pusa Sugandh-6	198.33	51.17	79.49	25.80	42.38
3.	Pusa Basmati-1 × Type-3	166.47	51.40	76.39	21.32	35.64
4.	Pusa Basmati-1 × Basmati-370	187.53	45.43	80.48	22.60	45.01
5.	Pusa Basmati-1 × Tarori Basmati-1	154.23	41.57	78.76	23.14	28.23
6.	Pusa Basmati-1 × Pant Sugandh Dhan-15	136.10	40.67	77.03	25.07	54.36
7.	Pusa Basmati 1 × Pant Basmati-1	145.33	43.40	76.98	21.65	33.11
8.	Pusa Sugandh-4 × Pusa Sugandh-6	196.83	48.30	80.28	25.93	39.64
9.	Pusa Sugandh-4 × Type-3	177.47	40.27	81.49	24.81	38.71
10.	Pusa Sugandh-4 × Basmati-370	177.07	47.83	78.73	25.87	45.96
11.	Pusa Sugandh-4 × Tarori Basmati-1	173.93	49.33	77.90	24.74	35.95
12.	Pusa Sugandh-4 × Pant Sugandh Dhan-15	187.53	52.60	78.01	28.47	30.53
13.	Pusa Sugandh-4 × Pant Basmati-1	137.81	42.73	76.27	25.40	37.08
14.	Pusa Sugandh-6 × Type-3	184.67	46.13	79.99	26.00	46.74
15.	Pusa Sugandh-6 × Basmati-370	183.40	40.37	81.95	25.21	48.65
16.	Pusa Sugandh-6 × Tarori Basmati-1	184.33	49.57	78.78	24.56	33.85
17.	Pusa Sugandh-6 × Pant Sugandh Dhan-15	171.30	45.53	78.97	25.93	63.58
18.	Pusa Sugandh-6 × Pant Basmati-1	148.87	44.57	76.93	24.79	33.88
19.	Type-3 × Basmati-370	178.57	49.77	78.18	19.51	27.60
20.	Type-3 × Tarori Basmati-1	171.77	57.00	75.12	24.07	33.30
21.	Type-3 × Pant Sugandh Dhan-15	143.57	70.47	66.95	21.83	41.53
22.	Type-3 × Pant Basmati-1	181.87	53.30	77.30	24.66	33.02
23.	Basmati-370 × Tarori Basmati-1	181.67	49.20	78.69	24.57	31.85
24.	Basmati-370 × Pant Sugandh Dhan-15	163.60	53.50	75.34	22.36	43.82
25.	Basmati-370 × Pant Basmati-1	167.17	48.03	77.64	26.11	31.63
26.	Tarori Basmati-1 × Pant Sugandh Dhan-15	158.70	39.63	79.99	24.41	30.98
27.	Tarori Basmati-1 × Pant Basmati-1	161.60	54.47	74.81	26.02	33.00
28.	Pant Sugandh Dhan-15 × Pant Basmati-1	143.63	41.73	77.53	23.66	34.58
29.	Pusa Basmati-1	131.30	45.60	74.20	20.66	19.83
30.	Pusa Sugandh-4	156.40	59.23	72.52	27.15	21.63
31.	Pusa Sugandh-6	158.07	63.17	71.45	25.22	27.84
32.	Type-3	145.20	51.87	73.67	20.06	31.08
33.	Basmati-370	140.30	54.53	71.98	18.83	24.50
34.	Tarori Basmati-1	121.70	39.47	75.50	24.51	18.16
35.	Pant Sugandh Dhan-15	107.93	45.13	70.48	21.76	28.78
36.	Pant Basmati-1	140.17	63.70	68.71	22.32	18.12
37.	Improved Pusa Basmati-1 ©	129.90	44.10	74.66	21.28	21.64
38.	Mean	161.30	49.09	76.49	23.95	34.37
39.	C.V.	5.92	4.96	1.61	3.43	5.32
40.	S.E.M	5.51	1.41	0.71	0.47	1.06
41.	C.D. @ 5%	15.54	3.96	2.00	1.34	2.98

Appendix III: Contd.....

Sl. No.	Cross/ Parents	Hulling recovery (%)	Milling recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel length/breadth ratio
1.	Pusa Basmati-1 × Pusa Sugandh-4	75.35	67.89	7.44	1.75	4.26
2.	Pusa Basmati-1 × Pusa Sugandh-6	74.24	67.99	7.43	1.72	4.32
3.	Pusa Basmati-1 × Type-3	76.41	68.07	6.44	1.71	3.76
4.	Pusa Basmati-1 × Basmati-370	76.26	70.15	6.41	1.73	3.71
5.	Pusa Basmati-1 × Tarori Basmati-1	80.73	72.70	7.75	1.65	4.69
6.	Pusa Basmati-1 × Pant Sugandh Dhan-15	73.92	68.71	7.36	1.66	4.44
7.	Pusa Basmati 1 × Pant Basmati-1	80.73	72.69	7.75	1.66	4.68
8.	Pusa Sugandh-4 × Pusa Sugandh-6	76.77	69.34	7.11	1.72	4.13
9.	Pusa Sugandh-4 × Type-3	75.69	67.60	6.56	1.83	3.59
10.	Pusa Sugandh-4 × Basmati-370	75.89	68.69	6.83	1.87	3.66
11.	Pusa Sugandh-4 × Tarori Basmati-1	79.79	71.65	5.61	1.95	2.88
12.	Pusa Sugandh-4 × Pant Sugandh Dhan-15	76.06	67.93	7.33	1.66	4.44
13.	Pusa Sugandh-4 × Pant Basmati-1	79.18	71.66	6.45	1.84	3.50
14.	Pusa Sugandh-6 × Type-3	77.14	66.37	6.91	1.70	4.07
15.	Pusa Sugandh-6 × Basmati-370	75.56	68.05	6.69	1.82	3.67
16.	Pusa Sugandh-6 × Tarori Basmati-1	78.50	71.44	7.81	1.64	4.76
17.	Pusa Sugandh-6 × Pant Sugandh Dhan-15	76.33	67.76	7.36	1.70	4.34
18.	Pusa Sugandh-6 × Pant Basmati-1	77.64	69.70	5.77	1.91	3.03
19.	Type-3 × Basmati-370	75.91	66.86	5.68	1.90	2.99
20.	Type-3 × Tarori Basmati-1	74.03	66.07	6.68	1.84	3.64
21.	Type-3 × Pant Sugandh Dhan-15	75.20	66.84	6.48	1.73	3.76
22.	Type-3 × Pant Basmati-1	79.93	72.18	7.46	1.68	4.44
23.	Basmati-370 × Tarori Basmati-1	77.15	68.99	6.83	1.83	3.73
24.	Basmati-370 × Pant Sugandh Dhan-15	76.46	68.07	6.28	1.74	3.61
25.	Basmati-370 × Pant Basmati-1	76.65	67.94	6.66	1.68	3.95
26.	Tarori Basmati-1 × Pant Sugandh Dhan-15	75.70	66.80	6.89	1.84	3.75
27.	Tarori Basmati-1 × Pant Basmati-1	75.99	68.14	5.69	1.90	3.00
28.	Pant Sugandh Dhan-15 × Pant Basmati-1	79.12	70.41	7.83	1.65	4.75
29.	Pusa Basmati-1	75.86	68.22	6.66	1.70	3.93
30.	Pusa Sugandh-4	74.14	65.89	7.53	1.70	4.43
31.	Pusa Sugandh-6	74.79	68.81	7.40	1.70	4.36
32.	Type-3	76.83	67.28	5.86	1.75	3.36
33.	Basmati-370	78.47	68.92	5.55	1.65	3.36
34.	Tarori Basmati-1	73.62	65.33	6.76	1.80	3.75
35.	Pant Sugandh Dhan-15	73.40	65.33	6.53	1.67	3.92
36.	Pant Basmati-1	73.24	65.80	6.79	1.79	3.80
37.	Imp. Pusa Basmati-1 ©	75.73	67.09	6.75	1.73	3.91
38.	Mean	76.44	68.47	6.79	1.75	3.90
39.	C.V.	0.62	1.53	1.75	2.97	3.67
40.	S.E.M	0.28	0.61	0.07	0.03	0.08
41.	C.D. @ 5%	0.78	1.71	0.19	0.08	0.23

Appendix III: Contd.....

Sl. No.	Cross/ Parents	Cooked kernel length (mm)	Cooked kernel breadth (mm)	Cooked kernel length/breadth ratio	Kernel elongation ratio	Alkali digestion value	Amylose content (%)
1.	Pusa Basmati-1 × Pusa Sugandh-4	18.73	2.31	8.06	2.52	7.02	21.55
2.	Pusa Basmati-1 × Pusa Sugandh-6	17.31	2.37	7.29	2.33	7.05	22.78
3.	Pusa Basmati-1 × Type-3	17.14	2.31	7.58	2.66	5.56	22.12
4.	Pusa Basmati-1 × Basmati-370	16.61	2.26	7.33	2.59	5.51	22.67
5.	Pusa Basmati-1 × Tarori Basmati-1	18.46	2.25	8.12	2.38	6.81	23.99
6.	Pusa Basmati-1 × Pant Sugandh Dhan-15	17.43	2.29	7.62	2.37	6.46	20.41
7.	Pusa Basmati 1 × Pant Basmati-1	18.66	2.33	8.14	2.40	5.65	24.01
8.	Pusa Sugandh-4 × Pusa Sugandh-6	17.80	2.35	7.66	2.50	6.93	21.68
9.	Pusa Sugandh-4 × Type-3	15.69	2.37	6.77	2.39	5.14	19.78
10.	Pusa Sugandh-4 × Basmati-370	17.18	2.35	7.52	2.51	4.70	21.44
11.	Pusa Sugandh-4 × Tarori Basmati-1	15.61	2.99	5.21	2.78	6.98	22.47
12.	Pusa Sugandh-4 × Pant Sugandh Dhan-15	18.22	2.43	7.60	2.49	6.28	20.64
13.	Pusa Sugandh-4 × Pant Basmati-1	17.55	2.61	6.96	2.72	6.84	20.24
14.	Pusa Sugandh-6 × Type-3	15.63	2.51	6.37	2.26	5.02	21.70
15.	Pusa Sugandh-6 × Basmati-370	15.05	2.39	6.37	2.25	4.67	22.24
16.	Pusa Sugandh-6 × Tarori Basmati-1	19.47	2.42	8.12	2.49	3.42	21.77
17.	Pusa Sugandh-6 × Pant Sugandh Dhan-15	16.85	2.55	6.65	2.29	6.89	20.77
18.	Pusa Sugandh-6 × Pant Basmati-1	14.57	3.35	4.11	2.53	7.11	23.49
19.	Type-3 × Basmati-370	13.28	2.79	5.15	2.34	3.76	20.54
20.	Type-3 × Tarori Basmati-1	15.16	2.64	5.91	2.27	5.69	24.22
21.	Type-3 × Pant Sugandh Dhan-15	15.11	2.40	6.41	2.33	4.00	20.60
22.	Type-3 × Pant Basmati-1	19.02	2.53	7.12	2.55	4.85	21.07
23.	Basmati-370 × Tarori Basmati-1	18.24	2.64	7.03	2.67	5.45	22.90
24.	Basmati-370 × Pant Sugandh Dhan-15	15.16	2.44	6.02	2.41	3.78	18.50
25.	Basmati-370 × Pant Basmati-1	15.16	2.37	6.47	2.28	6.89	24.10
26.	Tarori Basmati-1 × Pant Sugandh Dhan-15	15.04	2.38	6.48	2.18	7.02	23.23
27.	Tarori Basmati-1 × Pant Basmati-1	14.30	2.98	4.82	2.51	5.28	23.01
28.	Pant Sugandh Dhan-15 × Pant Basmati-1	19.53	2.36	8.28	2.49	6.93	22.04
29.	Pusa Basmati-1	15.41	2.45	6.26	2.31	7.09	21.69
30.	Pusa Sugandh-4	18.74	2.44	7.40	2.49	6.64	20.67
31.	Pusa Sugandh-6	15.54	2.37	6.62	2.10	6.54	21.05
32.	Type-3	13.19	2.34	5.62	2.25	3.91	21.09
33.	Basmati-370	13.29	2.39	5.65	2.39	3.95	20.20
34.	Tarori Basmati-1	15.16	2.48	6.15	2.24	6.67	21.19
35.	Pant Sugandh Dhan-15	14.71	2.46	5.90	2.25	5.82	18.60
36.	Pant Basmati-1	15.03	2.48	6.20	2.21	3.71	21.09
37.	Imp. Pusa Basmati-1 ©	15.72	2.51	6.33	2.33	7.15	22.24
38.	Mean	16.34	2.48	6.68	2.41	5.76	21.67
39.	C.V.	2.82	5.73	5.48	3.26	2.70	1.22
40.	S.E.	0.27	0.08	0.21	0.05	0.09	0.15
41.	C.D. 5%	0.75	0.23	0.60	0.13	0.25	0.43

Mithilesh Kumar Singh, the author of this manuscript, was born on 25th January 1989 at Aurangabad (Bihar). He passed his Secondary School Examination in year 2003 from Saraswati Shishu Mandir, Aurangabad (Bihar) and Intermediate Examination in year 2006 from B.N. College, Patna (Bihar). He earned his degree of Bachelor of Science (Agriculture) from Banaras Hindu University, Varanasi (Uttar Pradesh) in year 2011. He completed his degree of Master of Science (Agriculture) in Genetics and Plant Breeding from University of Agricultural Sciences, Bangalore (Karnataka) in year 2013. He joined Govind Ballabh Pant University of Agriculture and Technology, Pantnagar (Uttarakhand) in year 2014 as Ph.D. Scholar with Major in Genetics and Plant Breeding and Minor in Molecular Biology and Genetic Engineering. The author was recipient of ICAR - Junior Research Fellowship during his Master of Science degree programme and ICAR - Senior Research Fellowship during Ph.D. degree programme.

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ABSTRACT

Name : Mithilesh Kumar Singh **Id. No.** : 45841
Sem. & year of admission : IInd, Sem, 2013-2014 **Degree** : Ph.D.
Department : Genetics and Plant Breeding
Major : Genetics and Plant Breeding **Minor** : Molecular Biology & Biotechnology
Thesis Title : “Genetic analysis of quantitative traits in aromatic rice (*Oryza sativa* L.)”
Advisor : Dr. Surendra Singh

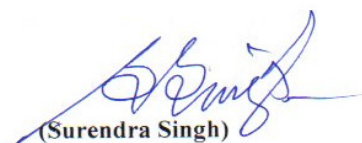
The present investigation was conducted with 28 F₁ hybrids, 8 parents and one check variety (Improved Pusa Basmati-1) during *kharif*, 2016 at Norman E. Borlaug Crop Research Centre, Pantnagar to study the combining abilities, gene action and their genetic parameters for yield and quality traits.

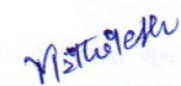
Analysis of variance revealed significant differences among genotypes for all the traits indicating the presence of ample amount of variability. The magnitude of the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits. The highest estimates of broad sense heritability were observed for plant height. High heritability estimates coupled with high genetic advance as percent of mean was recorded for alkali digestion value and number of panicles per plant.

The standard heterosis for grain yield per plant varied from 17.10% (Pusa Basmati-1×Pusa Sugandh-4) to 193.87% (Pusa Sugandh-6×PSD-15). The top three promising hybrids for grain yield per plant were Pusa Sugandh-6×PSD-15, Pusa Basmati-1×PSD-15 and Pusa Sugandh-6×Basmati-370. For superfine aromatic rice quality traits; top three promising hybrids for kernel length were PSD-15×Pant Basmati-1, Pusa Sugandh-6×Tarori Basmati-1 and Pusa Basmati-1×Tarori Basmati-1 whereas, Pusa Sugandh-6×Tarori Basmati-1, PSD-15×Pant Basmati-1 and Pusa Basmati-1×Tarori Basmati-1 were top three hybrids for kernel length/breadth ratio. Top three promising hybrids, Pusa Sugandh-4×Tarori Basmati-1, Pusa Sugandh-4×Pant Basmati-1 and Basmati-370×Tarori Basmati-1 expressed highest estimates of positive heterosis over standard check for kernel elongation ratio. Combining ability analysis revealed that the GCA and SCA variance were significant for all the traits indicating importance of both additive and non-additive genetic variance in trait expression. The GCA effects of the parents indicated Pusa Basmati-1 as best general combiner for 13 traits followed by Pusa Sugandh-6 for 11 traits. The top 3 specific combiners for grain yield/plant were Pusa Sugandh-6×PSD-15, Pusa Basmati-1×PSD-15 and Pusa Sugandh-4×Basmati-370. The hybrids Pusa Sugandh-6×Tarori Basmati-1, PSD-15×Pant Basmati-1 and Pusa Basmati-1×Tarori Basmati-1 were top three per se performer for super fine aroma rice quality traits like kernel length, kernel length/breadth ratio and kernel elongation ratio, among which the cross Pusa Sugandh-6×Tarori Basmati-1 also had high SCA effect for all these three traits.

The graphical analysis revealed partial dominance for days to 50% flowering while overdominance of rest of the traits. A significant deviation of regression line from unity indicated the presence of epistasis to be involved in expression of all the traits except test weight and number of filled grains per panicle. Array of parental points scattered in Wr-Vr graph for most of the traits indicated that the parents were genetically diverse. The estimates of genetic component of variance indicated preponderance of non-additive gene action for some traits while preponderance of both additive as well as non additive gene action for rest of the traits. The proportion of dominant to recessive genes was not in equal proportion for most of traits in parents. The genes showing positive and negative were asymmetrically distributed among parents for all the traits.

Grain yield per plant showed positive and significant correlation with plant height, flag leaf length, panicle length, number of panicles per plant, number of filled grains per panicle, spikelet fertility and test at both, genotypic and phenotypic level. Most of the genotypes were strong in aroma as suggested by aroma index.


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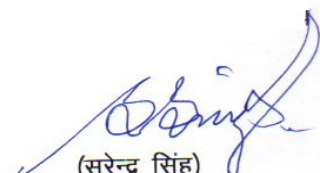
सारांश

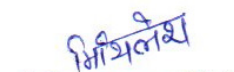
नाम : मिथिलेश कुमार सिंह परिचयांक : 45841
षट्मास एवं प्रवेश का वर्ष : द्वितीय, 2013-14 उपाधि : पीएच.डी.
मुख्य विषय : आनुवंशिकी एवं पादप प्रजनन विभाग : आनुवंशिकी एवं पादप प्रजनन
गौण विषय : आणविक जीव विज्ञान एवं जैव प्रौद्योगिकी
पोष षीर्षक : "सुगंधित धान (ओराईजा सटाइवा एल.) में मात्रात्मक लक्षणों का आनुवंशिक विश्लेषण"
सलाहकार : डा. सुरेन्द्र सिंह

प्रस्तुत शोध में 28 संकर, 8 पैतृक एवं एक जाँच प्रविष्टि (उन्नत पूसा बासमती-1) के साथ वर्ष 2016 खरीफ में नॉर्मन ई0 बोरलॉग फसल अनुसंधान केन्द्र, पन्तनगर में सुगंधित धान में मात्रात्मक लक्षणों का आनुवंशिक विश्लेषण का अध्ययन किया गया। विभिन्नता विश्लेषण से सभी लक्षणों के लिए पर्याप्त विभिन्नता का पता चलता है। अभिलिखित भिन्नता गुणांक (पी0सी0वी0) आनुवंशिक भिन्नता गुणांक (जी0सी0वी0) से अधिक पाया गया। पौध लम्बाई की विस्तृत आनुवंशिकता सबसे अधिक पायी गयी। क्षारीय पाचनांक एवं प्रति पौध बालियों की संख्या के लिये उच्च आनुवंशिकता के साथ-साथ अधिक आनुवंशिक प्रगति पाया गया। मानक आनुवंशिक उच्चता 17.10% (पूसा बासमती-1 × पूसा सुगंध-4) से 193.87% (पूसा सुगंध-6 × पी0एस0डी0-15) तक परिवर्तित हुये। दानों की उपज के लिए उच्च 3 प्रतिज्ञाता संकर पूसा सुगंध-6 × पी0एस0डी0-15, पूसा बासमती-1 × पी0एस0डी0-15 एवं पूसा सुगंध-6 × बासमती-370 सिद्ध हुये। सुगंधित धान गुणवत्ता लक्षणों में 3 उच्च संकर पी0एस0डी0-15 × पंत बासमती-1, पूसा सुगंध-6 × तरोरी बासमती-1 एवं पूसा बासमती-1 × तरोरी बासमती-1 में उच्चतम सकारात्मक आनुवंशिक उच्चता मापक जाँच प्रविष्टि की दाने की लम्बाई से उच्च पायी गयी, जबकि संकर पूसा सुगंध-6 × तरोरी बासमती-1, पी0एस0डी0-15 × पंत बासमती-1 एवं पूसा बासमती-1 × तरोरी बासमती-1 द्वारा सकारात्मक आनुवंशिक उच्चता मापक जाँच के लम्बाई/चौड़ाई के अनुपात के लिए प्रदर्शित हुआ। वृद्धिकरण अनुपात के लिये 3 उच्च संकर पूसा सुगंध-4 × तरोरी बासमती-1, पूसा सुगंध-4 × पंत बासमती-1 एवं बासमती-370 × तरोरी बासमती-1 द्वारा उच्चतम सकारात्मक आनुवंशिक उच्चता प्रदर्शित हुई।

संयोजक क्षमता अध्ययन द्वारा जी0सी0ए0 (सामान्य संयोजक क्षमता) एवं एस0सी0ए0 (विशिष्ट संयोजक क्षमता) भिन्नता से सभी लक्षणों के लिए दोनों, योजक एवं गैर-योजक जीन एक्सन के उपस्थित होने का पता चला। पैतृक जी0सी0ए0 प्रभाव से पूसा बासमती-1 को 13 लक्षणों के लिए एवं पूसा सुगंध-6 को 11 लक्षणों के लिए श्रेष्ठ सामान्य संयोजक पाया गया। प्रति पौध उपज के लिए उच्च 3 विशिष्ट संयोजक पूसा सुगंध-6 × पी0एस0डी0-15, पूसा बासमती-1 × पी0एस0डी0-15 एवं पूसा सुगंध-4 × बासमती-370 पाये गये। उत्कृष्ट सुगंधित धान गुणवत्ता लक्षणों, जैसे कि दाने की लम्बाई, लम्बाई/चौड़ाई अनुपात एवं दीर्घीकरण अनुपात में उच्च प्रदर्शन वाले 3 संकर पूसा सुगंध-6 × तरोरी बासमती-1, पी0एस0डी0-15 × पंत बासमती-1 एवं पूसा बासमती-1 × तरोरी बासमती-1 पाये गये, जिनमें पूसा सुगंध-6 × तरोरी बासमती-1 का एस0सी0ए0 प्रभाव भी तीनों लक्षणों के लिए ज्यादा था।

आलेखी विश्लेषण से 50% फूल खिलने के दिन के लिए आंशिक प्रधानता एवं शेष सभी लक्षणों के लिए अधिकतम प्रधानता पायी गयी। प्रति बाली भरे हुये दानों को छोड़कर शेष सभी लक्षणों के लिए गैर एलिलिक अंतः क्रिया स्पष्ट पायी गयी। वी0आर0-डब्ल्यू0आर0 आलेखी में पैतृक शृंखला बिन्दुओं के फैलाव से सभी लक्षणों के लिए पैतृक प्रविष्टियों के आनुवंशिक भिन्नता का पता चलता है। आनुवंशिक भिन्नता से सभी लक्षणों में योजक एवं गैर-योजक अनुपात से सभी लक्षणों के लिए प्रधान एवं अप्रभावी वंशाणु बराबर अनुपात में नहीं पाये गये। प्रति पौध उपज का पौध लम्बाई, पताका पर्ण की लम्बाई, बाली की लम्बाई, प्रति पौध बालियों की संख्या, प्रति बाली भरे हुए दानों की संख्या एवं 100-बीज भार से दोनों स्तर पर अभिलिखित एवं आनुवंशिक, अति सकारात्मक सह-संबंध पाये गये। सुगंध सूचकांक द्वारा सर्वाधिक प्रविष्टियों में विशिष्ट सुगंध पाये गये।


(सुरेन्द्र सिंह)
सलाहकार


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लेखक