BREEDING FOR SHATTERING RESISTANCE IN RICE (*Oryza sativa* L.)

By

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THESIS

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DECLARATION

I, hereby declare that this thesis entitled **"Breeding for shattering resistance in rice (*Oryza sativa* L.)"** is a bona-fide record of research done by me during the course of research and that the thesis has not previously formed the basis for the award of any degree, diploma, fellowship or other similar title, of any other University or Society.

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Certified that this thesis, entitled **"Breeding for shattering resistance in rice (*Oryza sativa* L.)"** is a record of research work done independently by **Mrs. Anju M. Job** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to her.

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ABBREVIATIONS

%	per cent
ANOVA	Analysis of Variance
ARS	Agricultural Research Station
BTS	Break Tensile Strength
cm	Centimeter
DF	Days to Fifty per cent flowering
DM	Days to Maturity
FL	Flag Leaf Length
FW	Flag Leaf Width
g	Gram
GA	Genetic advance
GCA	General Combining Ability Variance
gca	General Combining Ability effects
GCV	Genotypic coefficient of variation
h^2	Heritability
KAU	Kerala Agricultural University
KL	Kernel Length
KW	Kernel Width
Mm	Millimetre
PCV	Phenotypic coefficient of variation
PH	Plant Height
PL	Panicle Length
PP	Number of Panicles per plant
RARS	Regional Agricultural Research Station
RBD	Randomized Block Design
SCA	Specific Combining Ability Variance
sca	Specific Combining Ability effects
SPP	Seeds per Panicle
TP	Number of Tillers per Plant
TW	Test Weight

I. INTRODUCTION

Rice (*Oryza sativa* L.) is a cereal crop, which supports almost half of the world population and it provides 21per cent of global human per capita energy and 15 per cent of per capita protein (IRRI, 2013). The year 2004 was celebrated as International year of rice with a theme - '**Rice is life'.** That was the first time in world history where an international year was devoted for a single crop.

As per archaeological studies, rice is also considered as an ancient crop species and its cultivation dates back to more than 10,000 years ago in the upstream regions of Yangtze River in southwest china from its wild ancestors (Khush, 1997). During the process of domestication ancient humans noted several important agronomical characters such as high seed yield, seed size, shape, crop duration, adaptation, reduced seed shattering etc., in the wild plant species and selected favorable plants knowingly or unknowingly.

In case of wild plant species, shattering of seeds at maturity was an important character which ensures propagation of the crop through seed dispersal at maturity and it also ensure protecting from small animals, which eat away the grains. In the early stages of domestication farmers harvested grains which was attached to the plants firmly or they could be able to collect only those grains remained after seed shattering like this way they unknowingly selected non shattering genotypes for the cultivation purpose of next season. In this way the shattering character was slowly removed from cultivated species.

Now a days in rice breeding we are using a number of wild as well as traditional land races as one of the parent to incorporate stress resistance, disease resistance, improved qualities etc., in such situations there will be a chance to get a improved rice variety with these qualities but a shattering prone one.

As per United Nations estimation, world population will increase 33 per cent by 2050, from 7.2 billion today to 9.6 billion persons (UN Dept. Economics and Social welfare, 2015). Hence in near future also rice will continue to play an important nutritional role since it is the staple crop in many of the countries that are experiencing rapid population growth now.

As far as Kerala is considered, rice is a socially and politically important crop. The wet humid tropical climate of Kerala is highly suited for the cultivation of rice and traditionally rice occupied a prime position in Kerala's agriculture. Since the Indian population continues to grow steadily food grain production is becoming a matter of concern for India as a whole and Kerala in particular. At present rice occupies 7.46 percent of the total cropped area in Kerala. However, the area under rice has been falling at an alarming rate. 8.82 lakh hectares in 1974-75, the paddy area has come down to 1.96 lakh hectares in 2015-16. The production has also concomitantly declined from 13.76 lakh MT in 1972-73, considered as peak of production to 5.49 lakh MT in 2015-16. Moreover, the productivity of the crop is very low in the State (2790 kg/ha), though it is higher than the national average (2424 kg/ha), (SPB, 2016).

Apart from the steady reduction in the land area under rice cultivation, loss of grains in the field as well as during post harvest period are considered as major reasons for reduced production in rice. The degree of shattering can be categorized into several types like easy-shattering, moderate shattering, and hard or non-shattering. The type/degree of shattering is important to consider when selecting combine machine to prevent loss of yield during harvest. For the past few years in Kerala most of the cultivation as well as harvesting operation in rice field was done using farm machines. Due to lack of farm laboures as well as high efficiency of machines, in near future the entire rice cultivation and harvesting operations will be done by farm machines. In such a situation plants with moderate or medium shattering habit may be good for combine harvester.

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In early shattering varieties, harvest loss occurs in the process of reaping and conveying the plant to the threshing section of combine apart from field loss. On the other hand, in hardy shattering varieties the grains may not be removed completely from the panicle.

In this situation even though we are having a number of high yielding varieties in rice, the post harvest loss is still a major factor in reducing yield. One of the major disadvantage of Jyothi, the most popular high yielding rice variety of Kerala is the increased shattering of grains at maturity.

Still a wide variability is observed in the response to shattering in germplasm hence; screening rice genotypes for shattering resistance and transferring shattering resistance to high yielding varieties may contribute towards saving valuable resources and lead to sustainable development of rice cultivation in Kerala.

It was in this background the present work is taken up with the following objectives

1. Screening of rice genotypes for shattering resistance and identification of donor for shattering resistance.
2. To study the gene action for shattering resistance and other yield attributing traits.
3. To study the heterosis of hybrids synthesised based on shattering resistant parents.

II. REVIEW OF LITERATURE

Developing high yielding rice varieties for different agro-climatic conditions remains as a challenge for every breeder especially when there is a huge gap between the demand and production of the same. As far as Kerala is considered we are facing some other obstacles in the way to reach the required demand of the population like steep reduction in land area accompanied with high cost of production of rice crop in the state. These problems not only lead to conversion of crop area for other purposes but also keep as barren land. Even though, through farm mechanization somehow farmers are managing the situation. But loss of grains in the field as well as after harvesting leads to reduced yield. Seed shattering is one of the major reasons for pre and post harvest yield loss in cereals

A postharvest loss study was conducted in India estimated a 10.3 per cent increase in paddy harvesting losses due to delayed harvesting because of a lack in adequate harvesting equipment (Kannan *et al.*, 2013). These data indicates the importance of shattering resistant varieties for cultivation. Another study conducted by Grover and Singh (2013) in Punjab, India, reported that due to high shattering losses, the wheat harvesting losses were found increased by about 67 per cent by delay in harvesting.

The available literature on domestication of rice, genetic variability, character association and methods to evaluate shattering are presented in this chapter.

2.1. Origin and evolution of domesticated rice germplasm in relation to grain shattering

2.2. Genetic parameters

2.3. Character association

2.4. Methods to evaluate shattering

2.1 Origin and evolution of domesticated rice germplasm in relation to grain shattering

Shedding of leaves, flowers, fruits or seeds resulting from cell expansion and separation within the abscission zones in response to the development, tissue damage, stress signals etc., are considered as a general adaptation strategy in plants (Roberts *et al.* 2002).

During ancient times when hunting and gathering was a general practice, weak shattering (but retention of the seeds in the panicle) would have been beneficial, as complete non shattering requires mechanical power to thresh the seeds. Therefore the degree of shattering could have been gradually modified in several steps, depending on the progress of harvesting styles during domestication. In particular, the degrees of seed shattering as provided by the mutations have been useful during the initial stages of domestication. In the process of domestication of rice, several important morphological changes were selected by early agriculturists. Of these reduced seed shattering was one of the most obvious phenotypic changes to enable efficient harvest (Harlan, 1975; Fuller and Allaby, 2009)

In wild rice, seed dispersal immediately by shedding seeds at maturity protects them from being eaten by small animals and guaranteeing the propagation of the same. Cereals being the world's primary food were domesticated from wild grass species. Since wild grass species naturally shed mature grain, selecting plants that could hold on to ripe grains to allow effective field harvest was a necessary early step towards cereal domestication (Harlan, 1975).

Simple changes in a single gene can cause a drastic phenotypic change during domestication. Coming to rice domestication, it is believed that the common wild rice was first domesticated before *Indica-Japonica* differentiation. There are three different hypotheses about the origin of *Indica-Japonica* differentiation of Asian cultivated rice (Oka, 1988). The first hypothesis was proposed by Ting (1957, 1961) according to this hypothesis *keng (Japonica)* rice

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was differentiated from *hsien* (*Indica*) rice, which was developed from the common wild rice in south China. Second hypothesis was made by Wang and co workers (1984), and the suggested that the common wild rice domesticated in upland fields formed *Keng* rice and that in marshy low land formed *hsien* rice. The third hypothesis was proposed by Chou (1948) and Second (1982) , a dual origin of cultivated rice, assumed that the *Indica-Japonica* differentiation had preexisted in the common wild type and *Indica*-like type and *Japonica*-like type common wild rice developed into *Indica* and *Japonica* respectively

O. sativa, the cultivated rice and its wild relatives differ for many phenotypic characters. Wild rice genotypes typically display long awns and severe shattering for seed dispersal, whereas the domesticated type have short awns if any and reduced shattering to maximize the number of seeds that can be harvested. Dormancy levels are higher in the wild forms, allowing viable seeds to persist for years before germination, but these have been reduced in cultivars to give uniform germination (Uga *et al.*, 2003).

2.2. Genetic parameters

The term 'variability' refers to the presence of differences among individuals for a particular character and it may results partly due to genotypic (heritable) and partly due to environmental (non-heritable) factors. The success of any breeding program depends mainly on two things, the amount of genetic variability among the individuals of a population and the degree to which the desirable characters are heritable. Genetic variability is fundamental for any plant breeding programme on which selection acts to evolve superior parents (Singh *et al.*, 1980; Tripathi *et al.*, 2018)

The knowledge of genetic variability in a given crop species for any characters under improvement is important in plant breeding programme. Heritability with genetic advance is more helpful in predicting the gain under effective selection from a variable population.

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Genetic variability, heritability and genetic advance studied among 150 rice genotypes for eleven characters. The analysis of variance revealed that, there are highly significant variations among all the genotypes for all the characters studied, except for leaf width and 100 seed weight. High GCV and PCV were recorded for all the characters except for panicle length and days to 50% flowering. High heritability along with high genetic advance was recorded for all the characters except for days to 50% flowering and panicle length. This indicated the involvement of additive gene action in controlling these characters (Padmaja *et al.*, 2008).

Bisne *et al.* (2009) conducted a trial with four CMS lines, eight testers and thirty-two hybrids in order to estimate genetic parameters for yield and its correspondent characters in rice for thirteen characters related to yield. They could observe low, moderate and high genotypic and phenotypic coefficient of variations. Harvest index, total number of filled spikelets per panicle, 100-grain weight and spikelet fertility percentage expressed high heritability with high genetic advance were as high heritability coupled with high genetic advance was exhibited by harvest index, total number of chaffy spikelets per panicle, grain yield per plant, total number of filled spikelets per panicle and spikelet fertility percentage indicating that direct selection may be effective for these characters.

Genetic analysis of yield and yield component traits were analyzed by evaluating a core set of germplasm (21 upland rice genotypes) grown under acid soils in hills and reported high genetic variability among the genotypes for all the traits studied. High GCV was reported for plant height, flag leaf area, number of tillers per plant, number of ear bearing tillers, number of filled grains per panicle, root length, panicle weight, straw weight and grain yield. The broad sense heritability along with high genetic advance as percentage of mean indicated that grain yield per plant and panicle weight were the two most important yield contributing traits and these traits could be used in selection criteria in upland rice grown under acid soils (Fukrei *et al.,* 2011).

Singh *et al.* (2011) to study the genetic variability, heritability and genetic advance evaluated 81 rice genotypes for 13 quantitative traits. The analysis of variance revealed that, there is a wide as well as a significant variation among all genotypes for all the characters except for width of flag leaf. High GCV and PCV were exhibited for number of spikelets per panicle followed by number of productive tillers per plant, grain yield per plant and harvest index. Highest broad sense heritability was reported for biological yield per plant and high heritability along with high genetic advance was recorded for number of spikelets per panicle.

40 rice genotypes were evaluated to study the genetic variability, heritability and genetic advance and reported high PCV and GCV values for harvest index, seed yield, number of spikelets per panicle, biological yield, plant height, flag leaf length and number of tillers per plant. High heritability along with high genetic advance was obtained for harvest index, seed yield, biological yield, numbers of spikelets per panicle and flag leaf length Yadav *et al.* (2011)

Babu *et al.* (2012) studied genetic variability in 21 rice hybrids for yield and yield contributing characters along with quality and nutritional characters. The analysis of variance revealed that, there was significant difference among all the hybrids for all the characters under study. Number of grains per panicle, number of chaffy grains per panicle and Fe content exhibited high GCV (Genotypic Coefficient of Variation) than PCV (Phenotypic Coefficient of Variation). This result indicates less influence of environmental factors on these characters.

Subudhi *et al.* (2012) collected 55 rice germplasm accessions from the tribal dominated districts of Orissa and Cuttack and evaluated to analyze variability for 16 quantitative characters according to IRRI descript for rice. They could observe that leaf length varied from 30.7 cm to 73.6 cm, culm height varied from 90.5 cm to 184.4 cm, culm number varied from 8.9 to 20.0 and panicle length varied from 22.2 cm to 32.06 cm. Based on the results, the genotypes like

Chhotbasmati, Lajkuri, Pimpudibas, Kanika, Jaigundi and Bishnubhog were selected as superior parents for rice breeding programmes.

Dhanwani *et al.* (2013) studied genetic variability, heritability and genetic advance for 19 quality traits and 13 quantitative in rice. The analysis of variance revealed that, there exist a significant and wide variability for all the traits under the study. High GCV and PCV were reported for grain yield per plant, number of grains per panicle, gel consistency, alkali spreading value and water uptake. High heritability was reported for length of kernel, length of brown rice, L/B ratio of brown rice, paddy length, alkali spreading value, plant height, days to 50% flowering, spikelet sterility percentage and grain yield per plant. A high genetic advance was reported biological yield followed by grain yield per plant, alkali spreading value and gel consistency.

Sanghera *et al.* (2013) evaluated 14 red rice ecotypes from temperate region of Kashmir to study the genetic variability for grain yield and yield contributing traits. The analysis of variance revealed a significant difference among all the ecotypes for all the traits studied and revealed a wide range of variability. High GCV and PCV were reported for the following traits, panicle weight, grain yield per plant and secondary branches per panicle. High heritability along with high to moderate genetic advance was reported for days to 50% flowering, panicle density, number of grains per panicle and plant height, indicating that additive gene action is responsible for the expression of these characters.

Soni *et al.* (2013) evaluated 45 rice lines including 30 derived hybrid lines obtained from ten tropical *Japonica*, three *Indica* and two national checks (Pusa Basmati 1121 and Sarjoo-52) to study the genetic variability, heritability and genetic advance. The analysis of variance revealed a significant difference among all the genotypes for 18 characters studied. High PCV and GCV were recorded for flag leaf area, panicle bearing tillers per plant, spikelets per panicle, grains per panicle, grain yield per plant, biological yield per plant, panicle weight, flag leaf width and flag leaf length. The highest estimates heritability along with high genetic advance was reported for plant height, spikelets per panicle followed by spikelets per panicle, L:B ratio, biological yield per plant, grains per panicle, days to 50% flowering, flag leaf area, plant height, indicating that these traits would be reliable for the effective selection of individuals for further breeding programme.

Alam *et al.* (2014) conducted screening for 76 rice genotypes with an objective to study variability, heritability and genetic advance of yield and its components. The results revealed a significant and wide range of variability among all the genotypes for all the characters. For all the characters under study, PCV was higher than GCV, indicating that to some extent environmental interaction was there for all these characters. High heritability, ranging from 78.4 to 99.1 per cent was reported for all these characters. High heritability along with high genetic advance was recorded for number of unfilled grains per panicle and number of grains per panicle.

Fifteen CMS and ten restorer lines were evaluated to study the genetic variability, heritability and genetic advance for hybrid seed production programme. High PCV and GCV were reported for effective tillers per plant followed by grain yield per plant, angle of floret and plant height. High heritability along with high genetic advance were reported for 1,000 grain weight, anther breadth, plant height, anther length, effective tillers per plant and angle of floret opening. (Bornare *et al.*, 2014).

Venkanna *et al.* (2014) evaluated F2 population obtained from 36 crosses to estimate the genetic variability, heritability and genetic advance. The analysis of variance revealed that, the PCV and GCV were low to moderate for all the characters studied. Grain quality characters *viz.,* kernel breadth, kernel length and kernel L:B ratio reported Moderate heritability along with moderate genetic advance. Low heritability along with low genetic advance was reported for harvest index, indicating that these characters were highly influenced by non-additive gene action and selection for this character was ineffective.

Perera *et al.* (2014) estimated the genetic parameters and the correlations of yield attributing characteristics of weedy rice using 370 weedy rice accessions in Sri Lanka. Analysis of variance reported significant differences among the weedy rice accessions for all the characteristics studied, implying the presence of a substantial amount of genetic variability and scope for selection. Shattering percentage, total number of spikelets per plant and the number of filled seeds per panicle reported high genotypic and phenotypic coefficients of variation. The degree of difference between phenotypic and genotypic coefficients of variation was relatively low for all the characteristics, except for the total number of spikelets per panicle, implying comparatively less environmental influence. Very high heritability values along with very high genetic advance were observed for the shattering percentage, total number of spikelets per plant and the number of filled seeds per panicle. Correlation studies revealed that simply selecting comparatively taller plants with long seeds would identify high yielding weedy rice plants, which may be used in rice improvement programmes.

Islam *et al.* (2015) screened 23 rice genotypes with an objective to study genetic variability, heritability and genetic advance (GA) for yield and yield contributing traits in rice. A significant variance for all traits studied and a wide range of variation was observed among 23 rice genotypes for plant height, number of grains per panicle, days to 50% flowering, 1000- grain weight, grain width and grain yield. They concluded that, number of grains per panicle, days to 50% flowering and days to maturity were the important yield traits and these could be used for selection in rice breeding programs.

Manjunatha *et al.* (2016) evaluated 65 rice genotypes, including traditional landraces, with the aim of identifying donor parents having organic varietal characters suited for development of organic varieties through hybridization. The results revealed that, there exists a significant and wide range of variability for all the characters studied. Based on the results, number of productive tillers per plant, straw yield per plant, number of grains per panicle, number of tillers per plant at harvest, sensory evaluation, volume expansion ratio, and pest and disease incidence were identified as organic varietal traits.

Babu *et al.* (2017) studied the genetic variability, heritability and genetic advance in segregating generations for yield and bran oil content by evaluating 200 progenies of four crosses of rice to. The analysis of variance exhibited significant and wide variations for 14 characters among the progenies. High heritability was reported in case of plant height and high genetic advance reported for number of filled grains per panicle. Whereas high heritability along with low genetic advance was reported for panicle length, number of productive tillers per plant, 1000 grain weight, kernel length and bran oil content, which indicated the predominance of non-additive gene action in controlling the traits. Hence, they concluded that improvement of these traits is not possible through simple selection and requires heterosis breeding or recurrent selection for improvement.

Mamata *et al.* (2018) evaluated two F_2 populations of rice obtained by crossing 'Rathnachoodi × BR-2655' and 'Rajamudi × BR-2655' with 500 single plants to study the genetic variability, heritability and genetic advance. High PCV and GCV values were obtained for grain yield per plant and low PCV and GCV were reported for 1000 grain weight and panicle length. High heritability along with high genetic advance was obtained for traits like spikelet fertility, plant height, grain yield per plant and harvest index. These data indicated that, these characters were controlled by additive gene action; hence improvement of these characters could be achieved through direct selection.

2.3. Character association (Correlation analysis and Path analysis)

For crop improvement through plant breeding a pre-hand Knowledge about character association between various characters especially, yield and its contributing characteristics are very important. Each character will have direct as well as indirect effect on other character; hence to develop varieties one should consider all these interactions between various characters under study. Direct and indirect effects of correlation and path coefficient analysis help to achieve the same (Priya and Joel, 2009). According to Karpagam *et al.* (2014) complete knowledge on interrelationship of plant traits is important to the rice breeders for making improvement in complex characters like grain yield for which direct selection is not much effective. From a farmer point of view, whatever qualities we incorporate in a variety like disease resistance, insect resistance, improved quality etc., but without high yielding in won't be appreciable.

Kaul and Kumar (1982), reported high genotypic coefficient of variation and high heritability in rice for plant height. Plant height is considered as an important character related to yield in rice. Plant height was found to exhibit a wide range of variability among the rice genotypes. In addition to plant height a number of other agronomic characters such as plant height, leaf area, dry-matter yield, heading date, lodging resistance and proneness to shattering influence grain yield directly or indirectly (Griffiths, 1965). According to Johnson *et al.* (1955) grain yield is the product of number of tillers per plant, thousand grain weight and number of grains per panicle when each of these characters were measured without error. It is therefore, valued to estimate the magnitude of correlations among the yield and yield component trait parameters to improve crop yield.

Oba *et al* (1990) studied the inheritance of the semidwarfness of a Chinese variety Ai-Jio-Nan Te (AJNT), two semidwarf near isogenic lines of a variety Norin 29, SC-AJNT and SC-TN1. They could find that SC-AJNT exhibit semidwarfness and shattering habit derived from the donor parent AJNT, while SC-TN1 exhibited non shattering nature along with semidwarfness of the variety TN1, which was proved to be controlled by the semidwarfing gene *sd-1*.Allelism test between the semidwarffing genes of SC-AJNT and SC-TN1revealed that AJNT has a semidwarffing gene at the same locus as that of *sd-1*. It was found that the shattering habit was controlled by a single recessive gene. In the F2 population of the cross SC-AJNT/Norin 29 and BC1of the cross SC-AJNT/Norin 29//SC-AJNTa linkage relationship between the semidwarfing gene and recessive shattering gene was observed.

Reduced seed dormancy and Non-shattering were selected consciously and unconsciously during the domestication of rice, as in other cereals. Cai and Morishima (2000) attempted to detect genomic regions associated with shattering and dormancy using 125 recombinant inbred lines obtained from a cross between cultivated and wild rice strains. A total of 147 markers were mapped on 12 rice chromosomes, and QTL analysis was done by simple interval mapping and composite interval mapping. They could found that in several chromosomal regions the shattering QTLs and dormancy QTLs are linked with each other. This redundancy of QTL associations was explained by "multifactorial linkages" followed by natural selection favoring these two co-adapted traits in rice.

Thomson *et al.* (2003) developed an advanced backcross population between an accession of *Oryza rufipogon* (IRGC 105491) and the U.S. cultivar Jefferson (*Oryza sativa* ssp. *japonica*) in order to identify quantitative trait loci (QTLs) for yield, yield components and morphological traits. Morphological traits related to the domestication process and weedy characteristics, including plant height, shattering, tiller type and awns, were found clustered on chromosomes 1 and 4.

Seed dormancy is a major adaptive trait in plants to facilitate survival as well as resistance to pre harvest sprouting. Gu *et al.* (2005) evaluated Seventeen weedy strains and 24 cultivars of rice (*Oryza sativa* L.) for germinability to screen for donors of dormancy genes. Three dormant weedy strains, LD, TKN12-2, and SS18-2, were crossed and backcrossed with the nondormant breeding line EM93-1 to find out the relationship between dormancy and the shattering, awn, hull color, and pericarp/ testa colour characteristics. They could found that all these characteristics interrelated to the covering-imposed dormancy and the interrelation and interaction reflect the importance of combined effects of dormancy and other weedy characteristics in the adaptation of weedy populations to agro-ecosystems, and suggest that domestication and breeding activities have eliminated dormancy alleles at loci near the genes for shattering and the morphological characteristics from improved cultivars.

Ji *et al.* (2006) characterized a shattering mutant line of rice, Hsh, developed by treating a non shattering *japonica* variety, Hwacheong with *N*-methyl-*N*-nitrosourea (MNU. Using a digital force gauge the breaking tensile strength (BTS) of the grain pedicel was measured at 5, 10, 15, 20, 25, 30, 35, and 40 days after heading (DAH). The BTS of Hwacheong maintained at a level of 180–240 gf through out or did not decrease with increasing DAH, , while that of Hsh decreased greatly during 10–20 DAH and finally stabilized at 50 gf. An Optical microscopy of the same revealed that Hsh had a well-developed abscission layer similar to the wild rice *Oryza nivara* (accession IRGC105706), while Hwacheong did not produce an abscission layer, indicating that the shattering of Hsh was caused by differentiation of the abscission layer.

In order to understand the genetic control on shattering habit, QTL analysis was carried out by Ishikawa *et al.* (2010) using BC_2F_1 back cross population between *Oryza sativa* cv *Nipponbare* (a recurrent parent) and *Oryza rufipogon* acc. W30 (a donor parent). They could detect two strong QTLs on chromosome 1 and 4, and they were found to be identical to the two major seed shattering loci qSH1 and sh4, respectively. Using two sets of back cross populations having reciprocal genetic background of cultivated and wild rice, further examination on allelic interaction was done at these loci. In the genetic background of cultivated rice, the wild qSH1 allele has stronger effect compared to that of sh4, While, the two alleles at both qSH1 and sh4 showed semi-dominant effect. In the genetic background of wild rice, non-shattering effects of Nipponbare allele at both loci were examined to inspect rice domestication from a view point of seed shattering. In this investigation the backcross plant individually having Nipponbare homozygous alleles at either shattering loci (qSH1 and sh4) shed all the seeds. This strongly indicates that, some other minor genes are still associated with the formation or activation of abscission layer enhancing seed shattering.

Thurber C. S. (2011) examined the abscission layer at the flower-pedicel junction in weedy individuals in comparison with wild and cultivated relatives in order to establish the morphological basis of the parallel evolution of seed shattering in weedy rice and wild rice. They could observe that shattering wild rice individuals possess clear, defined abscission layers at flowering, whereas non-shattering cultivated rice individuals do not. In all the weedy rice prior to flowering, the abscission layer has formed and by flowering it is already degrading. In contrast, wild *O. rufipogon* abscission layers have been shown not to degrade only after flowering. The timing of weedy abscission layer degradation suggests that unidentified regulatory genes may play a critical role in the reacquisition of shattering in weedy rice; this sheds light on the morphological basis of parallel evolution for shattering in weedy and wild rice.

Okubo K., (2014) investigated the grain shattering pattern and microscopic morphology of the separation zone on pedicels of five *japonica* rice cultivars, Asahi, Akebono, Omachi, Kibinohana and Setokogane. This study was performed to find an indicator for indirect selection to facilitate the selection of medium shattering habit in *japonica* rice breeding. On an average, 50% of the grains of the cultivars with hardly-shattering habit were torn off at the bent portion of pedicel. A separation pileus was observed on the terminal of the pedicel. Cultivars with easily-shattering and very easily shattering habits pose very prominent pileus, while cultivars with a medium-shattering habit had more flat pileuses than the former and the pileuses were flat in cultivars with hardly shattering habit. Also development of fibrous cell walls on theses pileus varied with degree of shattering habit. The easier the grain shattered, the poorer was the development of fibrous cell walls and vice versa. These results strongly suggest that the shape of separation pileus and the development of fibrous cell walls are related to the shattering habit in *japonica* rice.

Kwon *et al.* (2015) genetically analyzed known shattering-related loci using $F_{2:3}$ recombinant inbred lines from an interspecific cross between *Oryza sativa* cv. *Iipoombyeo* and *Oryza rufipogon*. In this study, CACTA-AG190 was significantly associated with the shattering trait CACTA-TD according to bulked segregant analysis results, and was found in the *qSH-1* region of chromosome 1.

2.4. Methods to evaluate shattering

Oba *et al.* (1990) evaluated shattering habit in rice by counting the number of grains shed when one panicle of a primary tiller was gripped tightly by the hand at about 50 days after heading and they could observe that most of the plants with shattering habit shed more than10 grains, while those without the shattering habit shed very few grains.

Gu *et al.* (2005a) evaluated seed shattering rate by bagging the panicle of each rice plant to be evaluated at the stage of heading. At maturity the shattered as well as non shattered grains were gathered. Then the rate of seed shattering was expressed by a percentage of shattered seed to the total seed weight.

Gu *et al.* (2005b) Seed shattering was quantified on the basis of air-dried weight. Panicles were cut from the plant and immediately shaken gently for about 20 s over a container to collect shattered seeds, and then hand-threshed to collect the remaining seeds from the panicle. Inert matters like chaffy grains, plant particles and dirt were removed and dried in a greenhouse for 3 days. Shattering rate was calculated as percentage of shattered seeds to the total seed weight.

Van and Jin (2010) evaluated inheritance of grain shedding and abscission layer formation in a cross combination between rice varieties. For this investigation, at maturity (about 40 to 50 after heading) the panicle of the main culm were harvested and grouped into two. The first group consist of three primary branches with 50 grains in the upper portion of each panicle and used for the measurement of BTS (Break Tensile Strength). The remainder was used for examining morphological features of the abscission layer between the grain and pedicel. The second group was used to examining the degree of seed shattering using hand grasping method. The BTS was measured by using a force gauge and the grain shedding was determined by the number of detached grains when the matured panicle was grasped by hand and a slight rolling pressure was applied with the palm and finger. To examine the morphological features of the abscission region, ten pedicels attached to the grains in each panicle were fixed and stored in a solution of F.A.A, and then the longitudinal section of pedicel was made by the paraffin technique and investigated by using a light microscope after staining with Fast Green FCF and Safranine.

Akasaka *et al.* (2011) evaluated the seed shattering degree on the basis of BTS, the force required to pull a grain away from a pedicel. The Shattering Habit Tester Model TR-II (Fuijiwara Campany, Kyoto, Japan), devised by Ichikawa *et al.* (1990) was used for this purpose. Primery tillers from the plants to be evaluated were examined every three week after heading until harvest, which is normally five week after heading.

Inoue *et al.* (2015) evaluated grain shattering by measuring the breaking tensile strength (BTS) required to detach the seeds from the panicle using a digital force gauge. From each plant 10 panicles were selected in order to get a BTS value for a plant. Average BTS value for a line is obtained by taking BTS value from three randomly selected plants of the same line. The difference in BTS values between lines were evaluated using the unpaired Student's *t*-test.

Plants to be evaluated were grown in 5 inch pots in a green house in order to reduce the environmental effect on seed shattering. Forty days after sowing, plants were allowed to be grown under 10h light followed by 14h in darkness for four weeks. After flowering, two heads having the highest number of florets in each plant were bagged to isolate auto-shattered florets. Bagged heads were harvested after 30 days of flowering. Then the harvested heads along with the bags were placed in the bottom of a 1-m wood panel slanted at 10 degrees. A concrete roller (1Kg) was then rolled twice from the top of the panel over the heads. Then the shattered grains were counted to measure shattering percentage. (Kwon *et al.*, 2015)

III. MATERIALS AND METHODS

The research work was conducted in the Department of Plant Breeding and Genetics in Kerala Agricultural University (KAU) during the academic year 2017 – 2018. The research work was mainly divided in to three experiments and carried out in two locations. Experiment 1 was the screening of rice genotypes for shattering resistance which was conducted at Agricultural Research Station (ARS), Mannuthy, Thrissur. After screening the selected rice genotypes were crossed in Line X Tester pattern and the resultant progenies were evaluated along with parents constitute second and third experiments respectively. Second and third experiments were conducted in the fields of Department of Plant Breeding and Genetics of College of Horticulture (COH) campus, Vellanikkara, Thrissur.

3.1 Materials

The experimental materials included twenty-five rice genotypes comprises of landraces as well as high yielding verities (HYVs). These rice genotypes were procured from

1. Regional Agricultural Research Station (RARS), Pattambi, Melepattambi P. O., Kerala 679306

2. Rice Research Station (RRS), Moncompu, Kerala 688502

3. Agricultural Research Station (ARS), Mannuthy, Thrissur, 680651

The salient features of twenty five rice genotypes used in this study is explained in detail below, in Table 1

Table 1. Salient features of twenty five lines of rice used in the study

Sl. No.	Variety/Line	Salient features	Source
1	Aathira	Semi-tall, non-lodging, moderate resistance to blast and blight diseases and Brown plant hopper. Suited for I and II crop seasons and also for hilly tracts.	RARS, Pattambi
2	Aiswarya	Suitable for modan cultivation. Resistant to blast and blight diseases. Resistant to Brown plant hopper. Suited for first and second crop seasons.	RARS, Pattambi
3	Vellari	Best suited to the deep ill-drained fields.	RARS, Pattambi
4	Triveni	Tolerant to Brown plant hopper. Susceptible to blast and sheath blight.	RARS, Pattambi
5	Kunjukunju	Moderately tolerant to major pests like gall fly, leaf folder, whorl maggot and stem borer.	RARS, Pattambi
6	Kurukazhuma	This variety is most suited for the *kharif* season	RARS, Pattambi
7	Ponmani	Resistant to Brown plant hopper and high yield potential.	RARS, Pattambi
8	Swarnapraba	Suited for upland (modan) and for all the three seasons in the wet lands. Resistant to blast, susceptible to sheath blight and bacterial blight. Moderately resistant to stem borer. A good component in *koottumundakan*.	ARS, Mannuthy
9	Mahsuri	Excessive shedding of grains at maturity, susceptible to blast.	RARS, Pattambi
10	Kanchana	Suitable for *Kole* and Kuttanad regions. Resistant to blight, blast, stem borer and gall midge. Suitable for all seasons.	RARS, Pattambi
11	Veluthari kayma	Suited for double cropped wet land with abundant water supply.	RARS, Pattambi
12	Aarathi	Seed dormancy up to one month. Recommended for southern regions for *virippu* season for delayed sowing and for situations were overaged seedling may have to be planted. Moderately resistant to sheath blight, sheath rot and BPH.	RARS, Pattambi
13	Thavalakkannan	Adapt to adverse soil and other conditions. It has got a good resistance to green	RARS, Pattambi

		leaf hopper, the vector for Tungro virus disease of rice.	
14	Matta Triveni	Tolerant to Brown plant hopper, susceptible to blast and sheath blight. Suitable for I and III crop seasons.	RARS, Pattambi
15	Jaya	Very high yield potential, highly susceptible to Brown plant hopper, plant hopper and other pests.	RARS, Pattambi
16	Vaishak	Suitable for direct seeding during *kharif* season in the uplands. Tolerant to moisture stress, resistant to blue beetle, moderate resistance to stem borer and whorl maggot.	RARS, Pattambi
17	Annapoorna	Suitable for direct seeding. Susceptible to blast, sheath blight and Brown plant hopper. Suited for I and III crop seasons.	RARS, Pattambi
18	Kairali	Moderately resistant to blast, blight, gall midge and leaf folder. Can be cultivated in all the three seasons.	RARS, Pattambi
19	Ponni	Fine grain quality rice.	RARS, Pattambi
20	Harsha	SuiTable for direct seeding in rainfed lowlands. Moderate resistant to blast and moisture stress.	RARS, Pattambi
21	Pavizham	Easy to thresh. Fairly resistant to Brown plant hopper. Moderately resistant to stack burn and sheath rot and fairly resistant to sheath blight.	RARS, Pattambi
22	Hraswa	Extra-short duration variety. Ideal as a contingent variety for areas where there is crop loss. Susceptible to leaf folder. Raised only as direct sown crop.	RARS, Pattambi
23	Uma	Dwarf, medium tillering, non-lodging, resistant to Brown plant hopper and GM Biotype-5. Dormancy up to 3 weeks. Suited to three seasons especially to additional *virippu* crop season of Kuttanad.	RARS, Pattambi
24	Jyothi	Moderately tolerant to Brown plant hopper and blast; susceptible to sheath blight; suitable for direct seeding, transplanting and special systems of *Kole* and Kuttanad.	RARS, Pattambi
25	Manupriya	Suitable for *kole* lands. Tolerant to sheath blight, brown spot, blast, stem borer and gall midge. Suitable for all seasons.	ARS, Mannuthy

3.2 Method

The research work was conducted as three main experiments which included, screening of rice genotypes for shattering resistance as experiment one, crossing of selected rice genotypes (three highly shattering and four shattering resistant genotypes) in Line X Tester pattern as second experiment followed by evaluation of hybrids along with parents in pots as third experiment.

3.2.1 Experiment 1: Screening of rice genotypes for shattering resistance

Twenty – five rice genotypes including both land races and HYV as presented in Table I formed the experimental material for this study. The genotypes were raised in ARS, Mannuthy in augmented design. The seedlings were raised in nursery and transplanted to the main field at twenty-fifth may of 2017 with variety Aathira as resistant check and Aiswarya as susceptible check. The main plot size was $40m^2$ and the spacing was 20 X 20 cm. with an alley row of 40 cm. after every ten lines (Plates 1 and 2). General agronomic practice was done uniformly throughout the growing season as per package of practice recommendations of KAU (2016).

. Observations including both vegetative and panicle and seed characters were recorded. Shattering was measured by Induced Random Impact (IRI) method, by using a force gauge apparatus. For measuring the shattering percentage, ten panicles from each genotype were harvested separately at physiological maturity and dried under shade in a paper bag for two to three days. After shade drying the panicles were placed in a force gauge apparatus along with 100 steel balls of 1 cm. rotated at 30 rpm for 20 seconds and the number of shattered kernels were counted. Per cent shattering was calculated using equation (Plate 3).

Observations recorded

Observations on following characters were recorded as per "Standard Evaluation System of Rice" (IRRI, 1996).

3.2.1.1 Days to 50 per cent flowering

Number of days taken from seedling to flowering of 50 per cent of the plants in each genotypes were counted.

3.2.1.2 Days to maturity

It is the duration recorded in days from seedling to 80 per cent of the grains on a panicle was fully ripened.

3.2.1.3 Plant height (cm)

Height of the plant is measured from the ground level to the tip of the flag leaf at maturity and expressed in centimeter.

3.2.1.4 Number of tillers per plant

The total number of grain bearing and non-bearing tillers per plant were counted at maturity.

3.2.1.5 Number of panicles per plant

The total number of panicles per plant was counted.

3.2.1.6 Flag leaf length (cm)

Flag leaf length was measured from the tip of top most leaf blade below the flag leaf on main culm to the joining point of the leaf blade to the culm at late vegetative stage and recorded in centimeters.

3.2.1.7 Flag leaf width (cm)

Flag leaf width was taken from the same leaf from the widest portion of the leaf and recorded in centimeters.

3.2.1.8 Panicle length (cm)

At maturity length of main axis of panicle was measured from the base to the tip of panicle and recorded in centimeters.

3.2.1.9 Number of grains per panicle

Total number of grains per panicle was recorded at maturity.

3.2.1.10 Test weight (g)

A random sample of 1000 well developed whole grains were taken at maturity after harvest and dried to 13 per cent moisture level. Using an electronic balance this 1000 dried grains were weighed and the measurements were expressed in grams.

3.2.1.11 Kernel length (mm)

After harvesting, the grain length was measured from the bottom sterile lemma to the top of the grain and recorded in millimeter.

3.2.1.12 Kernel width (mm)

Grain width was measured from the widest point of the grain and recorded in millimeter.

3.2.1.13 Grain yield per plant (g)

At maturity all productive panicles harvested and yield of individual plant were recorded in grams.

3.2.1.14 Seed shattering (%)

Shattering was measured by Induced Random Impact (IRI) method, by using a force gauge apparatus. For measuring the shattering percentage, ten panicles from each lines were harvested separately at physiological maturity and dried under shade in a paper bag for two to three days. After shade drying the panicles were placed in a force gauge apparatus along with 100 steel balls of 1 cm. rotated at 3rpm for 20 seconds and the number of shattered kernels were counted. Using the equation

Shattering percentage = (number of shattered grains/total number of grains) x 100

3.2.2 Experiment 2: Crossing of resistant ones with shattering prone high yielding varieties

Crossing of selected plants were done in L X T pattern. For this purpose a non-replicating crossing block was constructed at College of Horticulture, Vellanikkara campus under Department of Plant Breeding and Genetics. To ensure synchronization in flowering staggered sowing of parental lines were done at weekly intervals. Usual agronomical practices were done to get healthy parents and proper seed set. Crossing was done between selected lines and testers by adopting clipping method for emasculation followed by hand pollination to ensure fertilization (Plate 4).

3.2.2.1 Emasculation

Emasculation of spikelets of female parents were done to avoid self pollination and to ensure cross fertilization between selected parents. Panicles that have emerged 50 – 60 per cent out of the flag leaf were selected for emasculation and emasculated late in the afternoon, after 3 pm. For easiness in emasculation and to expose the spikelets, the leaf sheath from the panicle was slightly detached. Florets likely to open in the next day (florets having anther height more than or equal to half of the floret height) were used for emasculation. The young florets from the bottom of the panicles, in which the length of the panicle was less than half of the floret length were discarded/removed. Emasculation was done by clipping off top one third of each selected florets with the help of a clean scissors to expose the anthers and with the help of a forceps/needle the six anthers were removed without damaging the female reproductive organ. After emasculating all the selected florets, the panicles were covered with a butter paper bag to avoid contamination. Tagging and labeling of emasculated panicles were done immediately after emasculation.

3.2.2.2 Pollination

To ensure maximum seed set, the emasculated florets were pollinated on the next day of emasculation and the same panicle was pollinated continuously for 2 -3 days. Panicles of the selected male parent ready to dehisce were selected at 8 am. for getting pollen grains. Collected panicles were enclosed in a petridish and the panicles were tapped to release pollen grains sometimes a small pressure was applied for complete release of pollen grains into the water. Using a thin camel brush the pollen grains were transferred to the stigma of female plant. After hand pollination the panicles were re-bagged to avoid contamination. These panicles were checked for seed set after fifth day of hybridization and bags were removed.

A total of twelve cross combinations were made and the seeds were collected separately from each female plant. Approximately eighty to hundred seeds were obtained from each cross combination.

3.2.3 Experiment 3: Evaluation of F_1 progeny along with parents

The experiment was conducted in COH, Vellanikkara campus, under Plant Breeding and Genetic Department field. Twelve hybrids and seven parents were raised in pots with two replications. General agronomic practices were done uniformly. Morphological observations and shattering percentage was taken in the same way as done in experiment1 (Plate 5).

Sprouted seeds

Nursery preparation

Seedling nursery just before transplanting

Seedlings before transplanting

Land preparation

Plate1: Nursery and land preparation for screening of rice genotypes

Rice field at vegetative stage

Rice field at reproductive stage

Plate 2: Vegetative and reproductive stages of crop

Force gauge apparatus

Plate 3: Instrument used for the measurement of shattering

Female parents

Male parents

Clipping method of emasculation

Bagging of panicle

Harvesting matured panicle

Matured panicle

Plate 4: Hybridization

Evaluation of F_1 progeny along with parents for shattering resistance

Plate 5: Screening of progenies along with parents

IV. RESULTS AND DISCUSSION

Variability and heritability are the basis for any crop improvement programme. One can use the existing variability or can create variability through a number of ways viz., crossing of selected plants, mutation etc. any plant breeding approach aims first at exploiting the spectrum of variation present in a crop population for identification and selection of elite genotypes for further improvement. The phenotype of a plant is determined by its genetic makeup, the environmental condition in which the plant is grown, and the interaction between the genotype and environment. Identification and selection of those plants that have genotypes conferring desirable phenotype is always a challenge for a breeder. Assessment of genetic variance and parameters viz., heritability, genetic advance and genetic gain, elucidation of trait association with yield, combining ability and expression of heterosis is of immense importance in the selection process for crop improvement.

To develop shattering resistance in rice, 25 rice genotypes were evaluated in an augmented design. From this 4 resistant genotypes were selected as testers along with three susceptible genotypes as lines and used as parents in L X T mating design. During the third stage of present investigation, the F_1 progenies were evaluated along with parents in RBD with two replications. Vegetative characters, seed and panicle characters and shattering per cent were evaluated in first and third experiment. Biometrical analysis to assess the variability, association between characters, combining ability, and heterosis were done. The results are explained in the following sections.

4. Screening of rice genotypes

4.1 Variability and trait association

An insight into the magnitude of variability available in a population is of at most importance as it provides basis for selection (Singh, 1990). The extent of genetic variability present in crop species is preferable since greater the diversity, wider the scope for selection.

The total variation presents (phenotypic variation) in a population is due to the combined effects of genotypic and environmental effects. The phenotypic variance was further divided by Mather and Jinks (1971) in to three components namely heritable fixable (additive variance), heritable non-fixable (dominance and epistatic components) and non-heritable non-fixable component (environmental fraction). The genetic advance under selection was contributed by the additive component of the phenotypic variance. Hence it is necessary to split the overall variability into its heritable and non-heritable components resorting to estimation of genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic gain.

4.1.1 Analysis of variance

The analysis of variance (Table 2) revealed that, there exists a significant difference among the genotypes for most of the characters studied except for number of tillers. Very high significant difference was observed among genotypes for plant height, days to 50 per cent flowering, days to maturity, flag leaf length, panicle per plant, kernel length and shattering per cent. Were as significant difference was observed for flag leaf width, panicle length, seeds per panicle, test weight, seed yield per plant and kernel width, indicating the presence of a substantial amount of genetic variability and scope for selection to crop improvement.

Table 2. Analysis of variance calculated for different vegetative and panicle and seed character among rice genotypes

Sl. no.	Character	Treatments	Check	Germplasm	C v/s G	Error
1	Plant height (cm)	338.800	102.300**	363.100**	41.700**	4.135
2	Number of tillers per plant (no.)	9.132	0.667	7.683	49.482*	2.050
3	Days to 50 per cent flowering	355.600	170.700**	350.800**	646.100**	2.197
4	Days to maturity	332.600	0	361.800**	23.400**	1.000
5	Flag leaf width (cm)	0.108	0.18375*	0.108*	0.029	0.003
6	Flag leaf length (cm)	85.590	2.090	86.450*	150.180*	4.496
7	Number of panicle per plant (no.)	7.652	12.907**	4.894**	63.070**	1.081
8	Panicle length (cm)	3.931	4.034*	3.826*	6.150*	1.406
9	Seeds per panicle (no.)	272.000	54.000	139.800*	3399.400**	4.499
10	Test weight (g)	3.234	0.735	3.177*	6.994*	0.001
11	Seed yield per plant (g)	104.780	114.41**	60.380*	1072.060**	1.865
12	Kernel width (mm)	0.119	0.167**	0.104*	0.39145**	0.002
13	Kernel length (mm)	2.098	0.084	1.421**	19.017**	0.112
14	Shattering (per cent)	64.140	694.170**	34.070*	95.660**	1.290

***, ** significance at 5% and 1% level of significance respectively**

4.1.1.2 Mean performance of rice genotypes for vegetative characters

Mean performance of rice genotypes for the various vegetative characters are given in Table 3 and detailed below

4.1.1.3 Plant height (cm)

Plant height recorded among the genotypes varied from 82.8 cm. for Hraswa to 151.4 cm. for Mahsuri with a mean performance of 112.31 cm.

4.1.1.4 Days to 50 per cent flowering

The mean value for days to 50 per cent flowering varied from 32 days in Hraswa to 126 days in Ponmani with a mean performance of 86.28 days.

4.1.1.5 Number of tillers per plant (no.)

Among the 25 lines of rice the least number of tillers per plant was reported for Kurukayma with 5 numbers of tillers and the highest was 14 numbers of tillers in Kairali, with a mean performance of 9.37 numbers of tillers per plant.

4.1.1.6 Days to maturity

Days to maturity varied from 78 days in Hraswa to 163 days in Ponmanni, with a mean performance of 119.2 days.

4.1.1.7 Flag leaf width (cm)

Kurukayma reported the lowest flag leaf width of 1.02 cm. and Uma reported the highest flag leaf length of 2.23 among the 25 rice genotypes with a mean performance of 1.63 cm.

4.1.1.8 Flag leaf length (cm)

Among the 25 rice genotypes Veluthari kayma reported the lowest flag leaf length of 27.84 cm and the highest was for Thavalakkannan with 60.3 cm of flag leaf length. The mean performance of the 25 lines was 42.16 cm.

Table 3. Mean performance of 25 rice genotypes for vegetative characters

Sl. No.	Genotypes	Vegetative characters					
		Plant height (cm.)	Days to 50% flowering	Number of tillers (no.)	Days to maturity	Flag leaf width (cm)	Flag leaf length (cm.)
1	Aathira	119.17	102.33	12.00	117.00	1.53	47.92
2	Aiswarya	110.91	91.67	12.67	117.00	1.88	46.74
3	Vellari	142.00	111.00	6.00	138.00	1.14	57.60
4	Triveni	108.40	72.00	12.00	106.00	1.98	38.96
5	Kunjukunju	103.80	83.00	7.00	112.00	1.42	29.92
6	Kuru kayma	140.00	116.00	5.00	136.00	1.02	53.20
7	Ponmani	106.90	126.00	8.00	163.00	1.52	33.54
8	Swarnaprabha	112.80	83.00	11.00	103.00	1.52	54.36
9	Mahsuri	151.40	85.00	12.00	128.00	1.64	38.48
10	Kanchana	92.36	81.00	13.00	103.00	2.11	44.68
11	Veluthari kayama	136.78	106.00	6.00	145.00	1.42	27.84
12	Arathi	116.50	83.00	8.00	126.00	1.60	36.84
13	Thavalakkannan	125.22	101.00	6.00	127.00	1.13	60.30
14	Matta Triveni	88.60	77.00	8.00	103.00	1.65	36.00
15	Jaya	114.40	81.00	8.00	124.00	1.56	35.80
16	Vaishak	137.04	73.00	12.00	118.00	2.02	48.65
17	Annapoorna	85.60	82.00	7.00	96.00	1.44	44.60
18	Kairali	98.30	86.00	14.00	107.00	1.89	40.23
19	Ponni	110.60	96.00	8.00	145.00	1.56	36.50
20	Harsha	105.72	76.00	9.00	107.00	1.46	41.33
21	Pavizham	106.32	76.00	9.80	118.00	1.80	40.21
22	Hraswa	82.80	32.00	6.00	78.00	1.42	28.98
23	Uma	115.50	76.00	12.80	118.00	2.23	56.18
24	Jyothi	92.30	86.00	13.00	133.00	2.20	38.60
25	Manupriya	104.40	75.00	7.90	108.00	1.60	36.58

4.1.2 Mean performance of 25 rice genotypes for Panicle and seed characters

Mean performance of 25 rice genotypes for the various panicle and seed characters are given in Table 4 and detailed below

4.1.2.1 Number of panicles per plant (no.)

Among the 25 lines the least number of panicles was reported for Kuru kayma, three panicles per plant and the highest was 11.93 numbers of panicles for Aiswarya. The mean performance among the genotypes was 7.12 panicles per plant.

4.1.2.2 Panicle length (cm)

Length of panicle ranged from 20.98 cm in Manupriya to 28.9 cm in Pavizham with a mean performance of 24.4cm.

4.1.2.3 Seeds per panicle

Thavalakannan reported 82 seeds per panicle, was the least among the 25 genotypes and Aathira with 130.67 seeds per panicle was the highest. The mean performance was 103.08.

4.1.2.4 Test weight (g)

Test weight recorded among the 25 lines varied from 22.4 g. for Veluthiri to 29.0g. for Jyothi with a mean value of 26.1 g.

4.1.2.5 Seed yield per plant (g)

Among the 25 lines Veluthari reported the lowest yield of 10.04 g. and highest was 37.71 g. for Aiswarya. The mean value for seed yield per plant among the 25 lines was reported as 19.53g.

4.1.2.6 Kernel width (mm)

Hraswa reported the lowest kernel width of 2.19 cm and Kuru kayama with 3.2 cm kernel length was the highest among the 25 lines. The mean performance for kernel width was 2.63 cm.

4.1.2.7 Kernel length (mm)

Manupriya with 5.83 mm. long kernel was the lowest and Jyothi with 9.5 mm. kernel length was the highest among all the genotypes with a mean performance of 7.99mm.

4.1.2.8 Shattering (%)

Among the 25 rice genotypes Manupriya reported the lowest shattering percentage of 1.73 per cent and Jyothi with 26.92 per cent was the highest among them. The mean value for the shattering characters was 8.78 per cent.

Table 4. Mean performance of 25 rice genotypes for Panicle and seed characters

Sl. No.	genotypes	Panicle and seed characters							
		Number of panicle per plant (no.)	Panicle length (cm)	Seeds per panicle (no.)	Test weight (g)	Seed yield per plant (g)	Kernel width (mm)	Kernel length (mm)	Shattering (%)
1	Aathira	9.00	22.00	130.67	24.60	28.97	2.53	5.89	2.14
2	Aiswarya	11.93	26.53	124.67	25.30	37.71	2.20	9.38	23.66
3	Veluthiri	4.00	23.42	85.00	22.40	10.04	3.12	6.30	5.68
4	Thriveni	9.50	22.12	105.00	28.80	28.73	2.95	6.00	2.82
5	Kunjukunju	6.00	26.10	103.50	24.60	15.28	2.31	8.69	8.40
6	Kurukayma	3.00	26.26	87.00	28.00	10.75	3.20	8.98	10.70
7	Ponmani	5.30	25.90	95.60	25.80	13.07	2.34	8.64	8.36
8	Swarnapraba	8.00	24.52	96.00	26.60	20.43	2.78	8.48	7.51
9	Mahsuri	7.60	24.54	112.00	26.90	17.66	2.60	8.50	7.58
10	Kanchana	10.00	25.32	118.00	26.90	31.74	2.31	8.61	8.32
11	Veluthiri kayma	5.00	23.56	83.60	24.10	13.26	3.10	7.20	5.80
12	Arathi	5.90	24.22	106.00	26.40	16.51	2.60	8.24	7.49
13	Thavalakkannan	4.00	26.21	82.00	23.60	10.20	2.98	8.80	9.80
14	Matta Triveni	6.00	22.56	110.00	26.20	13.18	2.99	6.02	5.30
15	Jaya	6.00	21.04	104.36	26.20	16.41	2.38	5.88	1.84
16	Vaishak	10.00	23.77	128.00	28.00	29.68	2.35	7.52	7.07
17	Annapoorna	6.00	22.97	90.00	28.50	14.88	2.74	6.07	5.43
18	Kairali	9.00	24.62	98.00	25.40	22.40	2.30	8.52	8.14
19	Ponni	5.00	23.84	99.54	26.20	13.04	2.50	7.85	7.09
20	Harsha	7.00	26.20	108.00	25.10	14.69	2.67	8.69	9.60
21	Pavizham	7.30	26.56	94.00	26.80	18.39	2.96	9.45	23.80
22	Hraswa	5.40	24.10	88.00	24.40	11.20	2.19	8.15	7.48
23	Uma	10.00	23.69	112.00	28.60	32.03	2.36	7.50	6.74
24	Jyothi	11.00	28.90	110.00	29.00	35.09	2.96	9.50	26.92
25	Manupriya	6.00	20.98	106.00	26.30	12.94	2.34	5.83	1.73

4.1.3 Variability studies

Variability and genetic parameters estimated for fourteen plant characters among 25 genotypes of rice are enlisted in Table 5 and he results are explained below.

Table5. Variability and genetic parameters for fourteen characters estimated from 25 rice genotypes

Characters	Range		Mean	Coefficient of variation (%)		Heritability broad sense (%)	Genetic gain (%)
	Minimum	Maximum		GCV	PCV		
Plant height (cm)	82.80	151.40	112.31	9.74	9.91	96.66	19.73
Number of tillers per plant (no.)	5.00	14.00	9.37	14.63	21.16	47.81	20.84
Days to 50 per cent flowering	32.00	126.00	86.28	12.49	12.61	98.15	25.49
Days to maturity	78.00	163.00	119.04	8.99	9.03	99.18	18.45
Flag leaf width (cm)	1.02	2.23	1.63	11.47	12.01	91.26	22.58
Flag leaf length (cm)	27.84	60.30	42.16	11.47	12.52	83.88	21.64
Number of panicle per plant (no.)	3.00	11.93	7.12	17.93	23.13	60.11	28.64
Panicle length (cm)	20.98	28.90	24.40	5.78	7.55	58.61	9.12
Seeds per panicle (no.)	82.00	130.67	103.08	6.54	6.86	90.99	12.85
Test weight (g)	22.40	29.00	26.10	3.85	3.86	99.86	7.94
Seed yield per plant (g)	10.04	37.71	19.53	22.82	23.87	91.42	44.95
Kernel width (mm)	2.19	3.20	2.63	7.02	7.19	95.34	14.13
Kernel length (mm)	5.83	9.50	7.75	8.72	9.73	80.32	16.10
Shattering per cent	1.73	26.20	8.78	37.47	39.64	89.34	72.96

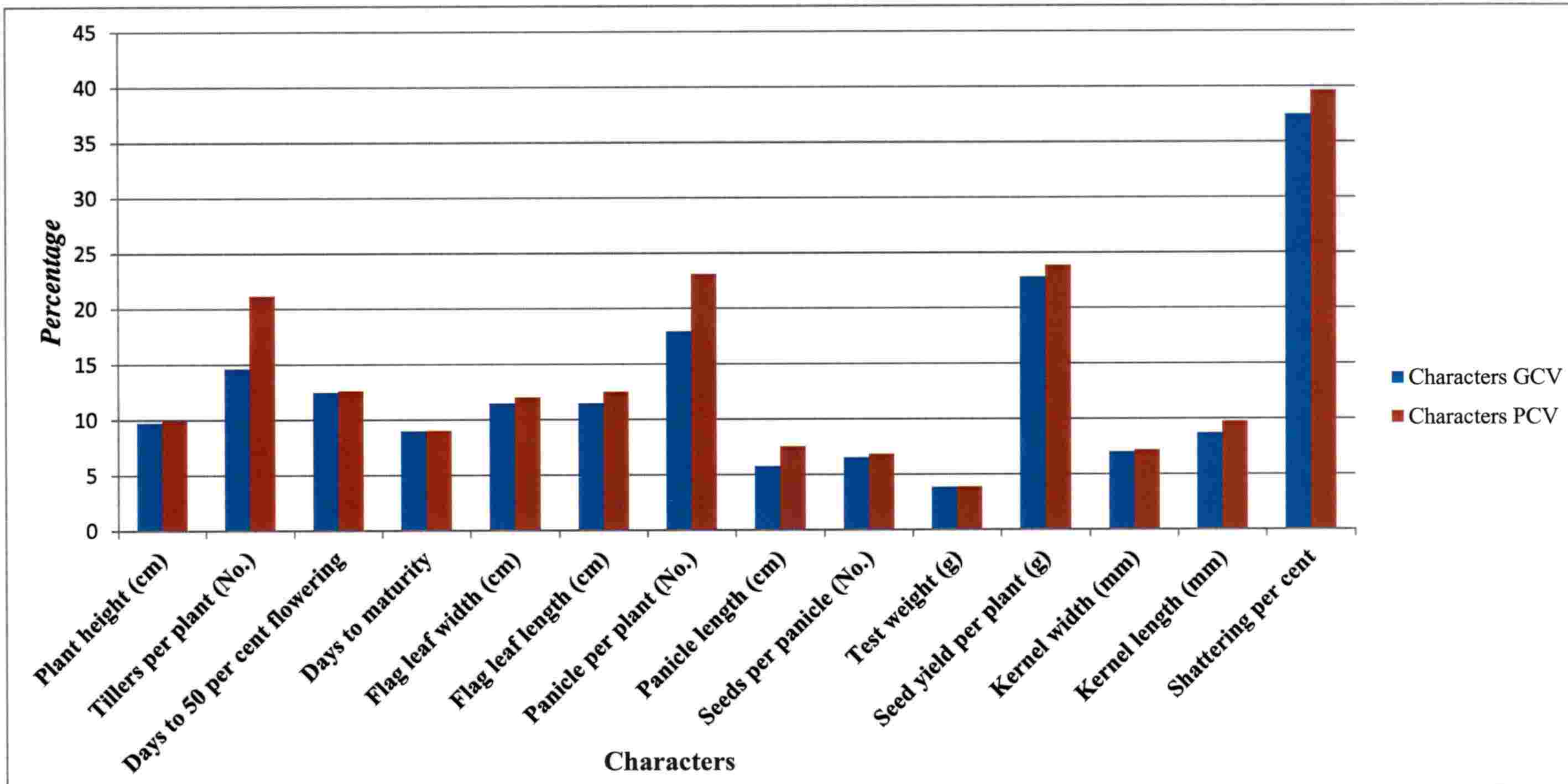
4.1.3.1 Phenotypic and genotypic coefficient of variation

Coefficient of variation provides a relative measure of variance among different traits under study. In general, the estimates phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) indicating the effect of environment on expression of genotype. The difference between PCV and GCV were highest for number of tillers per plant (6.53 per cent) followed by number of panicle per plant (5.20 per cent), and it is least for test weight (0.02 per cent) followed by days to maturity (0.04 per cent) and days to fifty per cent flowering (0.12 per cent), except for number of tillers per plant and number of panicle per plant the difference was less than five per cent indicating comparatively less influence of environment on character expression.

Phenotypic coefficient of variation ranged from 3.86 per cent to 39.64 per cent for test weight and shattering per cent respectively. Test weight (3.86 per cent), seeds per panicle (6.86 per cent), kernel width (7.19 per cent), panicle length (7.55 per cent), days to maturity (9.03 per cent), kernel length (9.73 per cent) and plant height (9.91 per cent) recorded low PCV, while flag leaf width (12.01 per cent), flag leaf length (12.52 per cent) and days to fifty per cent flowering (12.61 per cent) recorded moderate PCV. Tillers per plant (21.16 per cent), panicles per plant (23.13 per cent), seed yield per plant (23.87 per cent), and shattering per cent (39.64 per cent) have shown high PCV.

Genotypic coefficient of variation ranged from 3.85 per cent to 37.47 per cent for test weight and shattering per cent respectively. Test weight (3.85 per cent), panicle length (5.78 per cent), seeds per panicle (6.54 per cent), kernel width (7.02 per cent), kernel length (8.72 per cent), days to maturity (8.99 per cent) and plant height (9.74 per cent) recorded low GCV, while flag leaf width (11.47 per cent), flag leaf length (11.47 per cent), days to fifty per cent flowering (12.49 per cent), number of tillers per plant (14.63 per cent) and number of panicles per plant (17.93 per cent) showed moderate PCV. Only two characters; seed yield per plant (22.82 per cent) and shattering per cent (37.47 per cent) showed high GCV.

Figure 1. Comparison of PCV and GCV for vegetative and panicle and seed characters among 25 rice genotypes



Low PCV and GCV estimates in plant height were also reported by Borkakati *et al.*, (2005). Karthikeyan *et al.*, (2010) reported moderate level of PCV and GCV for days to fifty per cent flowering and low PCV and GCV for panicle length. Akhtar *et al.*, (2011) reported low GCV and PCV for test weight in rice. Borkakati *et al.*, (2005), Karim *et al.*, (2007), Sabesan *et al.*, (2009), Karthikeyan *et al.*, (2010), Jayasudha and Sharma (2010), and Fiyaz *et al.*, (2011) also reported high level of GCV and PCV for grain yield per plant. High GCV and PCV estimates in seed yield per plant and shattering per cent, indicating presence of ample variability among the genotypes for these traits and the possibility of improvement through selection. Similar findings in case of shattering per cent were reported by Perera *et al.*, (2014).

4.1.3.2 Heritability and genetic gain

The amount of genetic variation in a population alone will not be of much use to the breeder unless it is supplemented with the information on heritability estimate which is a measure of the heritable portion of the total variation. Heritability plays an important role in deciding the strategy for selection of a character since high heritability indicates high scope of genetic improvement of the character through selection.

Out of fourteen characters measured from the 25 rice genotypes, twelve characters shows high heritability. Heritability ranged from 41.87 per cent in number of tillers per plant to 99.86 per cent in test weight. Moderate heritability was observed for number of tillers per plant (47.806 per cent) and panicle length (54.039 per cent).

Findings of Jayasudha and Sharma (2010), Quatadah *et al.*, (2012) also reported high heritability for grain yield per plant. High heritability in case of 50% flowering was reported by Fiyaz *et al.*, (2011) and Singh *et al.*, (2011). Akhtar *et al.*, (2011), Fiyaz *et al.*, (2011) and Quatadeh *et al.*, (2012) reported high heritability for plant height in rice. Kumar *et al.*, (2012) also reported high heritability value for panicle length and grains per panicle similar to the findings of present study. High heritability in broad sense was noted for plant height followed by days to 50% flowering, biological yield per plant, days to maturity, grain yield per plant 1000-grain weight and spikelet per panicle by Yadav *et al.*, (2011).

Though high heritability for a character indicates the effectiveness of selection on the basis of phenotypic performance, it cannot be considered as the amount of genetic progress that can be made from selecting the best individual among the population. Panse and Sukatme (1954) reported that a high heritability value for character does not necessarily lead to a high genetic gain. If the heritability is mainly due to non-additive genetic effects (dominance and epistasis) the expected genetic gain would be low and when it is chiefly due to additive effects, a high genetic gain would be expected. Hence estimation of genetic advance as percentage mean can serve as an indication in this regards. According to Johnson *et al.*, (1955) for more effective selection heritability estimates should be considered along with genetic gain since genetic advance depends on phenotypic variability, heritability and to the selection intensity.

The genetic advance as per cent of mean estimates varied between 7.94 per cent to 72.96 per cent for test weight and shattering per cent respectively. Low genetic gain is recorded for test weight (7.94 per cent) and panicle length (9.12 per cent). Moderate estimates were recorded for Seeds per panicle (12.85 per cent), kernel width (14.13 per cent), kernel length (16.10 per cent), days to maturity (18.45 per cent) and plant height (19.73 per cent), whereas high estimates were recorded for number of tillers per plant (20.84 per cent), flag leaf length (21.64 per cent), flag leaf width (22.58 per cent), days to fifty per cent flowering (25.49 per cent) number of panicles per plant (28.64 per cent), seed yield per plant (44.95 per cent) and shattering per cent (72.96 per cent) showed high response.

Seed yield per plant and shattering per cent shown high genetic gain indicating that, judicious selection for these characters will be effective for further improvement. A high genetic gain for grain yield per plant was also reported by Fiyaz *et al.*, (2011).

4.1.4 Trait association studies

Correlation refers to the degree as well as the direction of association between two or more than two variables. It estimates the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement of yield, the value for correlation ranged between -1 to 1. A positive correlation between characters occurs due to coupling phase linkage and negative correlation occurs due to repulsion phase linkage of genes controlling two different traits.

Resistance to seed shattering and grain yield are complex traits resulting from interaction of many yield attributes. Since almost all the characters are highly influenced by the environment, selection based on knowledge of association between the dependent variables and their component traits could accentuate the progress in breeding efforts. Trait association studies could also provide information on the prediction of improvement in the expected direction for a dependent character through indirect selection. Hence the present study was undertaken to understand the inter-relation among different yield contributing characters and their association with grain yield/plant. The results are listed in Table 6 and detailed bellow.

Table 6. Simple correlation among grain yield and yield attributes influenced by seed shattering

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14
V1														
V2	-0.119^{NS}													
V3	0.500^{*}	-0.190^{NS}												
V4	0.566^{**}	-0.189^{NS}	0.825^{**}											
V5	-0.319^{NS}	0.852^{**}	-0.373^{NS}	-0.192^{NS}										
V6	0.369^{NS}	0.149^{NS}	0.284^{NS}	0.027^{NS}	-0.086^{NS}									
V7	-0.222^{NS}	0.934^{**}	-0.298^{NS}	-0.285^{NS}	0.879^{**}	0.099^{NS}								
V8	-0.054^{NS}	0.121^{NS}	0.190^{NS}	0.230^{NS}	0.081^{NS}	0.104^{NS}	0.159^{NS}							
V9	-0.045^{NS}	0.715^{**}	-0.186^{NS}	-0.170^{NS}	0.639^{**}	0.020^{NS}	0.760^{**}	-0.097^{NS}						
V10	-0.147^{NS}	0.437^{*}	-0.189^{NS}	-0.080^{NS}	0.578^{**}	0.071^{NS}	0.448^{*}	0.083^{NS}	0.270^{NS}					
V11	0.324^{NS}	-0.357^{NS}	0.367^{NS}	0.278^{NS}	-0.373^{NS}	0.266^{NS}	-0.385^{NS}	0.131^{NS}	-0.490^{*}	-0.025^{NS}				
V12	0.023^{NS}	0.179^{NS}	0.101^{NS}	0.155^{NS}	0.082^{NS}	0.031^{NS}	0.182^{NS}	0.734^{**}	0.019^{NS}	0.096^{NS}	-0.215^{NS}			
V13	-0.148^{NS}	0.269^{NS}	0.030^{NS}	0.134^{NS}	0.304^{NS}	0.054^{NS}	0.375^{NS}	0.830^{**}	0.062^{NS}	0.189^{NS}	0.126^{NS}	0.446^{*}		
V14	-0.116^{NS}	0.902^{**}	-0.235^{NS}	-0.216^{NS}	0.852^{**}	0.198^{NS}	0.978^{**}	0.157^{NS}	0.811^{**}	0.483^{*}	-0.348^{NS}	0.186^{NS}	0.358^{NS}	

*significance at 5% level; **significance at 1% level

V1 - Plant height (cm)
V2 - Number of tillers per plant (no.)
V3 - Days to 50 per cent flowering
V4 - Days to maturity
V5 - Flag leaf width (cm)
V6 - Flag leaf length (cm)
V7 - Number of panicle per plant (no.)
V8 - Panicle length (cm)
V9 - Seeds per panicle (no.)
V10 - Test weight (g)
V11 - Kernel width (cm)
V12 - Kernel length (cm)
V13 - Shattering per cent
V14 - Seed yield per plant (g)

4.1.4.1 Association of yield attributes with grain yield per plant

Seed yield per plant recorded high significant correlation with number of tillers per plant (0.902), flag leaf width (0.852), number of panicles per plant (0.978) and seeds per panicle (0.811) it also reported significant correlation with test weight (0.483).

4.1.4.2 Inter-correlation among yield attributes

Days to fifty per cent flowering shows significant inter-correlation with plant height (0.500). Days to maturity showed high significant inter-correlation with plant height (0.566) and days to fifty per cent flowering (0.825). There exist a high significant inter-correlation between flag leaf width and number of tillers per plant (0.852). Number of panicles per plant recorded a high significant inter-correlation with number of panicles per plant (0.934) and flag leaf width (0.879). Number of tillers per plant (0.715), flag leaf width (0.639) and number of panicles per plant (0.760) recorded a high significant inter-correlation with seeds per panicle. Plant height (0.437) and number of panicles per plant (0.448) exhibited significant inter-correlation with test weight and flag leaf width (0.578) recorded a high significant inter-correlation for the same. A negative significant inter-correlation was observed between kernel width and seeds per panicle (-0.490) and kernel length recorded a high significant inter-correlation with panicle length (0.734). Shattering per cent recorded a high significant inter correlation with panicle length (0.830) and significant inter-correlation with kernel length (0.446).

In this present study, grain yield per plant recorded significant correlation with number of tillers per plant, flag leaf width, number of panicles per plant, seeds per panicle and test weight. A same kind of correlation was registered by Jayasudha and Sharma (2010) and Basavaraja *et al.*, (2011) for number of tillers per plant. Shanthi *et al.*, (2011), Rangare *et al.*, (2012) and Bhadru *et al.*, (2012) reported a positive correlation among grain yield and number of panicles per plant.

After the completion of first experiment based on the performance of 25 genotypes towards seed shattering, four genotypes viz., Aathira, Triveni, Jaya and Manupriya were selected as testers since they recorded the least for seed shattering. Most shattered three genotypes viz., Aishwarya, Jyothi and Pavizham were selected as lines.

A total of twelve crosses were made among the four testers and three lines and the set seeds were collected separately. The cross combination generated is detailed in Table 7.

Table 7. Designation of genotypes resulting from LxT mating design

Line / Tester	Aathira (T1)	Triveni (T2)	Jaya (T3)	Manupriya (T4)
Pavizham (L1)	H1	H2	H3	H4
Jyothi (L2)	H5	H6	H7	H8
Aishwarya (L3)	H9	H10	H11	H12

4.2 Variability studies

After screening of twenty five genotypes including both landraces and high yielding varieties, we have selected Pavizham (L1), Jyothi (L2) and Aiswarya (L3) as females (lines) for the second experiment since they have shown high degree of shattering compared to the rest of the lines. Aathira (T1), Thriveni (T2), Jaya (T3) and Manupriya (T4) were selected as males (testers) for LxT mating design, since they reported high degree of shattering resistance compared to the rest.

4.2.1 Analysis of variance

Analysis of variance (Table 8 and 9) among parents and hybrids revealed the presence of high significant difference among all the fourteen character studied, indicating the presence of a substantial amount of genetic variability and scope for selection to improve crops.

4.2.2 Mean performance of parents and hybrids

Mean performance of parents and hybrids for fourteen characters including vegetative as well as seed and panicle characters were detailed in Table 10 and 11 and described below.

4.2.2.1 Plant height (cm)

Plant height ranged from 69.16 cm (H5) to 109.30 cm (T1) with a grand mean value 92.39 cm. Among the three lines L2 reported the least and L3 was highest with 88.10 cm and 106.00 cm respectively and in case of testers ranged from 95.10 cm (T4) to 109.30 cm (T1). In hybrids, the estimates varied from 69.16 cm (H5) to 96.19 cm (H11).

4.2.2.2 Number of tillers per plant (no.)

Number of tillers per plant varied from 10.4 (H7) to 17.50 (H9) with a grand mean value 14.04. Among lines it ranged from 13 (L1) to 16.50 (L2, L3), while it varied from11.95 (T4) to 16.00 (T1). For hybrids it ranged from10.40 (H7) to 17.50 (H9).

Table 8. Analysis of variance for vegetative characters among parents and hybrids

Source	df	Mean sum of squares					
		Plant height (cm)	Number of tillers per plant (no.)	Days to 50 per cent flowering	Days to maturity	Flag leaf width (cm)	Flag length (cm)
Replication	1	1.888	0.058	0.947	4.447	0.171*	5.784
Treatment	18	173.184**	6.4*	113.88**	117.491**	0.436**	213.753**
Error	18	7.197	2.364	1.336	2.17	0.027	7.465

*Significant at 5% ; **significant at 1%

Table 9. Analysis of variance for panicle and seed characters among parents and hybrids

Source	df	Mean sum of squares							
		Number of panicles per plant (no.)	panicle length (cm)	Seeds per panicle (no.)	Test weight (g)	Seed yield per plant (g)	Kernel width (mm)	Kernel length (mm)	shattering %
Replication	1	1.289	0.335	217.921*	0.026	111.969*	0.519*	0.006	0.096
Treatment	18	9.263**	24.978**	474.102**	3.323**	207.386**	2.125**	2.824**	139.791**
Error	18	1.987	1.223	38.754	0.243	19.702	0.074	0.003	0.327

*Significant at 5% ; **significant at 1%

Table 10. Mean performance of parents and hybrids for vegetative characters

Genotypes	Plant height (cm)	Number of tillers per plant (no.)	Days to 50 per cent flowering	Days to maturity	Flag leaf width (cm)	flag length (cm)
Lines						
L1	102.12	13.00	75.50	116.00	2.09	42.52
L2	88.10	16.50	85.00	133.50	2.49	49.62
L3	106.00	16.50	92.00	116.00	2.25	45.50
Testers						
T1	109.30	16.00	101.00	118.50	1.92	35.53
T2	99.10	15.50	71.00	107.50	2.34	39.16
T3	105.10	12.00	80.00	125.50	1.92	37.55
T4	95.10	11.95	74.00	109.50	1.96	45.69
Hybrids						
H1	83.32	13.10	82.50	110.50	1.34	24.52
H2	90.36	15.10	71.00	106.00	1.20	24.68
H3	88.01	13.90	85.00	120.00	1.21	18.97
H4	89.82	14.10	81.00	113.50	1.36	30.99
H5	69.16	13.50	88.50	127.00	1.20	24.68
H6	87.90	13.70	74.00	109.00	1.25	24.53
H7	90.63	10.40	85.50	124.50	1.31	26.57
H8	88.06	12.50	90.00	126.00	1.40	22.63
H9	87.29	12.20	80.50	111.50	1.18	19.32
H10	87.29	12.20	80.50	111.50	1.18	19.32
H11	96.19	15.10	84.00	120.50	1.18	19.03
H12	92.49	11.30	84.00	119.00	1.13	21.59

Table 11. Mean performance of parents and hybrids for panicle and seed characters

Genotypes	Number of panicles per plant (no.)	panicle length (cm)	Seeds per panicle (no.)	Test weight (g)	Seed yield per plant (g)	Kernel width (mm)	Kernel length (mm)	shattering %
Lines								
L1	10.00	24.18	104.00	26.60	27.70	2.95	6.42	24.77
L2	13.50	26.83	120.00	29.25	47.44	2.94	9.35	27.46
L3	14.50	24.46	132.00	25.40	48.63	2.15	9.39	24.76
Testers								
T1	13.50	17.34	115.50	24.70	38.45	2.61	5.72	1.78
T2	12.00	18.92	90.50	28.80	31.20	2.96	7.89	2.94
T3	10.00	20.26	89.86	26.00	23.37	2.37	7.5	2.99
T4	8.50	17.81	67.50	26.40	15.11	2.34	7.63	2.01
Hybrids								
H1	11.20	13.67	118.50	25.15	33.31	2.61	6.29	3.62
H2	12.90	15.63	111.00	27.30	34.46	2.98	5.77	3.45
H3	13.00	20.81	98.50	26.10	33.38	2.53	7.06	3.05
H4	7.70	17.75	86.50	25.65	16.87	2.57	6.66	2.79
H5	12.90	16.73	126.00	25.90	41.99	2.57	6.29	4.41
H6	11.90	15.72	109.50	28.25	36.79	2.95	7.70	2.35
H7	7.30	21.93	102.00	25.25	18.90	2.69	7.18	4.65
H8	10.50	17.30	97.00	26.75	27.06	2.52	6.79	5.99
H9	10.30	17.14	112.50	25.80	30.01	2.62	8.13	5.26
H10	10.30	17.14	112.50	25.80	30.01	2.62	8.13	5.26
H11	13.70	14.20	111.00	24.65	37.52	2.26	7.52	2.08
H12	8.80	18.30	96.50	25.95	12.95	2.30	7.11	5.79

4.2.2.3 Days to fifty per cent flowering

The estimates on days to fifty per cent flowering varied among the lines, testers and hybrids from 71 (L2, H2) to 101 (T1) with a grand mean of 83.32. It ranged from 75.50 (L1) to 92.00 (L3) among lines, 71.00 (T2) to 101.00 (T1) among testers and 71.00 (H2) to 90.00 (H8) among hybrids.

4.2.2.4 Days to maturity

Days to maturity varied from 106 (H2) to 133.50 (L2) among lines, testers and hybrids with a grand mean of 117.13. It ranged from 116.00 (LL1, L3) to 133.50 (L2) among lines, 107.00 (T2) to 125.50 (T3) among testers and 106.00 (H2) to 127.00 (H5) among hybrids.

4.2.2.5 Flag leaf width (cm)

The trait ranged among all the genotypes from 1.13 cm (H12) to 2.49 cm (L2) with a grand mean 1.71 cm. Flag leaf width varied from 2.09 cm (L1) to 2.49 cm (L2) among lines and 1.92 cm (T1, T3) to 2.34 cm (T2) among the testers. It varied from 1.13 cm (H12) to 2.63 cm (H5) among hybrids.

4.2.2.6 Flag leaf length (cm)

Among all the genotypes the estimates on flag eaf length varied from 35.53cm (T1) to 47.93 cm (H4) with a grand mean of 39.87 cm. Among lines it varied from 37.91 cm (L2) to 46.87 (L1) and among testers it ranged from 45.69 cm (T4) to 35.53 cm (T1). In case of hybrids it ranged from 35.91 cm (H3) to 47.93 cm (H4).

4.2.2.7 Number of panicles per plant (no.)

The estimates on number of panicles per plant varied among all the lines from 7.30 (H7) to 16.00 (H9) with a grand mean of 11.59. It ranged from 10.00 (L1) to 14.50 (L3) among the lines, 8.50 (T4) to 13.50 (T1) among testers and 7.30 (H7) to 16.00 (H9) among hybrids.

4.2.2.8 Panicle length (cm)

Panicle length estimated among all the genotypes varied from 13.67 cm (H1) to 26.83 cm (L2) with a grand mean of 19.58 cm. The estimates ranged from 24.46 cm (L3) to 26.83 cm (L2), 17.34 cm (T1) to 20.26 cm (T3) and 13.67 cm (H1) to 25.58 cm (H9) for lines, testers and hybrids respectively.

4.2.2.9 Seeds per panicle

Among all the genotypes, the estimates on seeds per panicle varied from 67.50 (T4) to 132.91 (H9) with a grand mean of 106.38. Among the four lines it varied from 104.00 (L1) to 132.00 (L3) and among testers it varied from 67.50 (T4) to 115.50 (T1). Among the twelve hybrids it ranged from 86.50 (H4) to 132.91 (H9).

4.2.2.10 Test weight (g)

The estimates on test weight varied from 24.65 g (H11) to 29.25 g (L2) among all the genotypes with a grand mean of 26.34 g. It varied from 25.40 g (L3) to 29.25 g (L1) among the four lines and 24.70 g (T1) to 28.80g (T2) among the three testers. Estimate reported among the hybrids ranged from 24.65 g (H11) to 28.25 g (H6).

4.2.2.11 Seed yield per plant (g)

Among all the genotypes the estimate varied from 12.95g (H12) to 54.81g (H9) with a grand mean of 32.55g. It ranged from 27.70 g (L1) to 48.63g (L3), 215.11 g (T4) to 38.45 g (T1) and 12.95g (H12) to 54.81g (H9) 12.95g (H12) to 54.81g (H9) for lines, testers and hybrids respectively.

4.2.2.12 Kernel width (mm)

Kernel width estimated among the genotypes including lines, testers and hybrids varied from 2.15 mm (L3) to 2.98 mm (H2) with a grand mean of 2.62 mm. The estimate ranged from 2.15 mm (L3) to 2.95 mm (L1), 2.34 mm (T4) to

2.96 mm (T2) and 2.26 mm (H11) to 2.98 mm (H2) for lines, testers and hybrids respectively.

4.2.2.13 Kernel length (mm)

Among the nineteen genotypes the estimate on kernel length varied from 5.72 mm (T1) to 9.39 mm (L3) with a grand mean of 7.25 mm. Among lines it ranged from 8.85mm (L1) to 9.39mm (L3), among testers it varied from 5.72mm (T1) to 5.98 mm (T3) and for hybrids it ranged from 5.77 mm (H2) to 8.29 mm (H5).

4.2.2.14 Shattering per cent

The shattering per cent was estimated among the nineteen genotypes varied from 1.78 per cent (T1) to 27.46 per cent (L2) with a grand mean of 7.12 per cent. Among the four lines it ranged from 24.77 per cent (L3) to 27.46 per cent (L2) and for testers it ranged from 1.78 per cent (T1) to 2.99 per cent (T3). Among the twelve hybrids it ranged from 2.08 per cent (H11) to 5.99 per cent (H8).

4.2.3. Evaluation of parents based on mean performance (scoring)

Scoring of parents based on the mean performance for vegetative and seed and panicle charecters were done (Table 12) by assuming 'm' as the mean performance of parents for the fourteen charecters and 's' as the standered error difference of mean based on analysis of variance. Three classes namely i) varietal mean falling above (m+s), ii) varietal mean falling between (m+s) and (m-s) and iii) varietal mean falling below (m-s) were formed with the following scores +1, 0 and 1 respectively.

According to Thirumeni (1998) the status of a parent was high if the score of a particular character was +1, moderate and low if the score equals to 0 and -1 respectively. Among the fourteen characters studied, for shattering percentage the scoring was done in a reverse order, since reduced shattering is a positive response to yield. Among the seven parents all the four testers reported a high response to reduced seed shattering and all the lines showed low response for the same. When the breeding programme is for shattering resistance, in future also these four testers can be selected as male parents since they recorded a low status for shattering percentage. For the three testers the response was high representing a need for improvement in the direction of shattering resistance.

Table12. Scoring of parents based on mean performance (X̄)

Parents	PH (cm)	TP (no.)	DF	DM	FW (cm)	FL (cm)	PP (no.)	PL (cm)	SP (no.)	TW (g)	SYP (g)	KW (mm)	KL (mm)	Shattering (%)	Total
Pavizham (L1)	-1	-1	-1	-1	0	1	0	1	0	0	-1	1	-1	-1	-4
Jyothi (L2)	1	1	1	1	1	1	1	1	1	1	1	1	1	-1	12
Aiswarya (L3)	-1	1	1	-1	1	1	1	1	1	-1	1	-1	1	-1	4
Aathira (T1)	-1	1	1	0	-1	-1	1	-1	1	-1	1	0	-1	1	0
Triveni (T2)	1	1	-1	-1	1	-1	0	-1	-1	1	-1	1	1	1	1
Jaya (T3)	-1	-1	-1	1	-1	-1	-1	-1	-1	-1	-1	-1	0	1	-9
Manupriya (T4)	1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	1	1	-8

PH – Plant height TP - Number of tillers per plant DF –Days to fifty per cent flowering DM- Days to maturity

FW – Flag leaf width FL – Flag leaf length PP – Number of panicles per plant

PL – Panicle length SP – Seeds per panicle TW – Test weight SYP –Seed yield per plant KW – Kernel width

KL – Kernel length

Table 13. Scoring of hybrids based on mean performance (X)

Hybrids	PH (cm)	TP (no.)	DF	DM	FW (cm)	FL (cm)	PP (no.)	PL (cm)	SP (no.)	TW (g)	SYP (g)	KW (mm)	KL (mm)	shattering %	Total
H1 (PaxAa)	1	0	0	-1	1	1	0	-1	1	-1	1	0	-1	1	2
H2 (PaxTr)	-1	1	-1	-1	-1	1	1	-1	1	1	1	1	-1	1	2
H3 (PaxJa)	0	1	1	1	-1	-1	1	1	-1	0	1	-1	0	1	3
H4 (PaxMa)	-1	1	0	-1	1	1	-1	0	-1	-1	-1	0	-1	1	-3
H5 (JyxAa)	1	0	1	1	-1	1	1	0	1	0	1	0	-1	0	5
H6 (JyxTr)	0	1	-1	-1	0	1	1	-1	0	1	1	1	1	1	5
H7 (JyxJa)	-1	-1	1	1	1	1	-1	1	-1	-1	-1	1	0	-1	-1
H8 (JyxMa)	0	-1	1	1	1	0	0	0	-1	1	0	-1	-1	-1	-1
H9 (AixAa)	0	-1	-1	-1	-1	-1	0	0	1	0	0	0	1	-1	-4
H10 (AixTr)	0	-1	-1	-1	-1	-1	0	0	1	0	0	0	1	-1	-4
H11 (AixJa)	-1	1	1	1	-1	-1	1	-1	1	-1	1	-1	1	1	2
H12 (AixMa)	-1	-1	1	1	-1	-1	-1	1	-1	0	-1	-1	0	-1	-6

PH – Plant height TP - Number of tillers per plant DF –Days to fifty per cent flowering DM- Days to maturity

FW – Flag leaf width FL – Flag leaf length PP – Number of panicles per plant

PL – Panicle length SP – Seeds per panicle TW – Test weight SYP –Seed yield per plant KW – Kernel width

KL – Kernel length

For seed yield per plant L2, L3 and T1recorded a high response. The response reported for panicle length and shattering per cent were exactly similar. When all the fourteen characters for the seven parents considered together, L2, L3 and T2 represented as best parents for yield and yield attributes and T1 recorded to be a moderate response.

4.2.4. Evaluation of hybrids based on mean performance (scoring)

As done in the case of parents, the scoring of hybrids also performed (Table 13) and elaborated in the following section.

Of the hybrids, H1, H2, H3, H5, H6 and H11 recorded high response for seed yield per plant and H8, H9 and H10 recorded moderate response. Out of the twelve hybrids, H1, H2, H3, H4, H6 and H11 reported a high response towards reduced shattering and H5 reported moderate response. Among the twelve hybrids HI (L1 X T1), H2 (L1 X T2), H3 (L1 X T3), H5 (L2 X T1), H6 (L2 X T2) and H11 (L3 X T3) showed a high total response compared to the rest. Gilbert, 1958 reported that parents with good performance would result in good hybrids, which was reflected in case of H6.

4.3 Studies on combining ability

Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may sometimes yield poor recombinations. Combining ability analysis provides information on additive and non-additive variance and combining ability effects, which are critical in the selection of parents and crosses in a hybridization programme. The selection of parents will be all the more effective if based on the combining ability test and mean performance (Tiwari e al., 2011). Hence, the parents were evaluated based on their mean performance along with their *gca* effects in the present study. Information on *sca* effects are associated with interaction effects which may be due to dominance and epistatic components that are non-fixable in nature and hence, worthwhile for hybrid production and commercial exploitation. A high level of heterosis along with mean performance as well as specific combining ability of the crosses are essential for breeding strategies based on hybrid production (Rahimi *et al*., 2010). In the present study, an attempt has also been made to evaluate the hybrids based on their heterosis, mean performance and *sca* effects.

4.3.1 Analysis of variance

The estimate of variance due to general and specific combining ability in the line x tester analysis for vegetative and seed and panicle character are listed in (Table 14 and 15) and elaborated bellow.

Lines registered a high significant difference for plant height, days to 50 per cent flowering, days to maturity, kernel width and kernel length and significant difference for flag leaf length, test weight and shattering per cent. Whereas testers reported high significant difference for plant height, days to 50 per cent flowering, days to maturity, panicle length, seeds per panicle, test weight, seed yield per plant, kernel width and kernel length and significant difference for panicle per plant and shattering per cent.

L x T reported high significant difference for days to 50 per cent flowering, days to maturity, panicle length, kernel width, kernel length and shattering per cent and significant difference for panicles per plant and seed yield per plant. GCA variance/SCA ratio ranged from 0.004 (shattering per cent) to 3.94 (seeds per panicle).

Apportioning of combining ability variance in to fixable and non-fixable variance indicated that, both additive and non-additive gene actions played an important role in controlling the expression of the characters studied. Higher estimates of GCA variance over SCA variance for days to maturity, flag leaf width, seeds per panicle and kernel width, pointed to be pre-ponderance of additive gene action. Additive gene action is the heritabe and fixable portion of gene action.

The magnitude of SCA variance was higher than GCA variance for plant height, number of tillers per plant, days to fifty per cent flowering, flag leaf length, number of panicles per plant, panicle length, test weight, seed yield per plant, kernel length, and shattering, indicating pre-ponderance of non-additive gene action i.e., dominance and epistatic gene action in the inheritance of these characters. Non-additive gene action is the heritable and non-fixable portion of genetic variance due to the dominance and epiststic gene action. Latha *et al.* (2013) have reported that pre-ponderance of non-additive gene action in the expression of grain yield per plant and its components.

Table 14. Analysis of variance for combining ability for vegetative characters

Source	df	Mean sum of squares					
		Plant height (cm)	Number of tillers per plant (no.)	Days to 50 per cent flowering	Days to maturity	Flag leaf width (cm)	Flag length (cm)
Lines	2	95.306**	5.571	42.792**	172.042**	0.036	63.607*
Testers	3	164.466**	1.135	133.819**	188.944**	0.008	12.993
Line X Testers	6	45.527*	5.132	27.403**	34.986**	0.011	21.646
Error	11	11.232	2.390	1.496	1.530	0.035	11.259
σ^2gca		12.051	-0.254	8.700	20.787	0.002	2.379
σ^2sca		17.147	1.371	12.953	16.728	-0.012	5.194
σ^2gca/ σ^2sca		0.703	-0.185	0.672	1.243	-0.167	0.458

*Significant at 5% ; **significant at 1%

Table 15. Analysis of variance for combining ability for seed and panicle characters

Source	df	Mean sum of squares							
		Number of panicle per plant (no.)	panicle length (cm)	Seeds per panicle (no.)	Test weight (g)	Seed yield per plant (g)	Kernel width (mm)	kernel length (mm)	shattering %
Lines	2	0.665	3.309	60.667	1.950*	25.412	0.139**	3.294**	4.261*
Testers	3	9.513*	12.845**	713.264**	3.687**	321.510**	0.183**	0.25**	3.099*
Line X Testers	6	11.630*	13.581**	62.889	1.047	124.017*	0.026**	0.79**	3.733**
Error	11	2.426	1.785	39.375	0.353	29.092	0.001	0.002	0.519
σ^2gca		-0.934	-0.786	46.297	0.288	7.063	0.019	0.14	-0.007
σ^2sca		4.602	5.898	11.757	0.347	47.463	0.012	0.394	1.607
σ^2gca/ σ^2sca		-0.203	-0.133	3.938	0.830	0.149	1.583	0.355	-0.004

*Significant at 5% ; ** significant at 1%

4.3.2. Combining ability effects

The parents were characterized for their ability to transmit desirable traits to their progenies. Information regarding general combining ability effects of parents is of at most importance in plant breeding programme as it helps in successful prediction of genetic potential of individuals to yield desirable progenies in segregating population. General combining ability effects (*gca*) of lines and testers and specific combining ability effects (*sca*) of hybrids for vegetative and seed and panicle characters are given in Table 16 and 17 respectively.

4.3.2.1 Plant height

The general combining ability effects of parents ranged from -3.61 (L2) to 3.27 (L3) for lines. L3 reported high significant *gca* effects and L2 reported a high negative significance. Among testers it varied between -7.62 (T1) to 4.07 (T3) and both these testers reported high significant *gca* effects. The *sca* effects of hybrids varied from -7.16 (H5) to 4.1 (H9).

4.3.2.2 Number of tillers per plant

The general combining ability effects among lines ranged from -0.57 (L2) to 0.96 (L1). Testers varied from -0.46 (T4) to 0.57 (T2). The *sca* effects of hybrids varied from -2.17 (H6) to 2.36 (H11).

4.3.2.3 Days to fifty per cent flowering

Among parents gca effect for lines was the minimum for L1 (-2.33) and maximum for L2 (2.29) for lines and minimum for -7.04 (T2) and maximum for 2.79 (T4) among testers n which T1, T3 and T4 reported positive significant response. The *sca* effects of hybrids varied from-3.46 (H6) to 5.29 (H1) and H10 reported a significant response to days to fifty per cent flowering.

4.3.2.4 Days to maturity

Among the parents evaluated for the general combining ability effects for days to maturity, L (-4.08) reported the minimum response and L2 (5.04) was the maximum response among the lines. It varied among the testers from -7.75 (T2) to 5.08 (T3). Among the testers T4 and T3 reported positive significant response. Minimum response among the hybrids reported by H6 (-4.88) and maximum by H5 (5.63).

4.3.2.5 Flag leaf length

Among the four lines the minimum response was reported by L3 (-3.25) and maximum for L1 (1.72) in which L3 reported a significant response among the four lines. In case of testers it ranged between -1.55 (T3) to 2.00 (T4). The *sca* effects among the hybrids varied from -4.27 (H3) to 4.2 (H4).

4.3.2.6 Number of panicles per plant

Among the parents evaluated for the general combining ability effects for days to maturity, L2 (-0.23) reported the minimum response and L1 (0.32) was the maximum response among the lines. It varied among the testers from -1.88 (T4) to 0.82 (T2). Minimum response among the hybrids reported by H7 (-3.81) and maximum by H11 (2.47).

4.3.2.7 Panicle length

Among the parents evaluated for the general combining ability effects for panicle length, L3 (-0.5) reported the minimum response and L2 (0.73) was the maximum response among the lines. It varied among the testers from -1.35 (T1) to 1.79 (T3). Minimum response among the hybrids reported by H11 (-4.28) and maximum by H7 (2.22).

4.3.2.8 Seeds per panicle

Among parents, *gca* effect for lines was the minimum for L1 (-3.17) and maximum for L2 (1.83) for lines and maximum for T4 (-13.46) and maximum for

T1 (12.21) among testers and both T4 and T3 reported significant response. The *sca* effects of hybrids varied from -7.83 (H9) to 5.83 (H11) which were reported significant response among hybrids.

4.3.2.9 Test weight

Among the parents evaluated for the general combining ability effects for days to maturity, L3 (-1.92) reported the minimum response and L4 (5.65) showed the maximum response among the lines. It varied among the testers from -1.92 (T1) to -1.86 (T2). Minimum response among the hybrids reported by H9 (-5.76) and maximum by H1 (11.23). L1, L4, H1, H6, H7, H8, H10, H11 and H912 exhibited positive significant response whereas L2, L3, T1, T2, T3, H2, H3, H4, H5 and H9 reported negative significant response.

4.3.2.10 Seed yield per plant

The general combining ability effects among lines ranged from -6.36 (L3) to 6.55 (L1) and L1 and L4 reported a positive significance for number of tillers per plant whereas L3 reported a negative significance. Testers varied from -7.86 (T3) to 2.28 (T2). The *sca* effects of hybrids varied from -9.11 (H1) to 8 (H9) and H1 and H10 reported negative significant *sca* effects and H2, H4 and H9 reported positive significance.

4.3.2.11 Kernel width

Among parents, *gca* effect for lines was the minimum for L3 (-0.17) and maximum for L2 (-0.11) for lines and maximum for T2 (--0.08) and maximum for T1 (0) among testers. The *sca* effects of hybrids varied from -0.18 (H2) to 0.20 (H4). T3, H4, H5, H10 and H11 reported significant response to combining ability effects and L3, T2, H1, H2, H3, H6, H7, H8, H9 and H12 reported negative significance.

4.3.2.12 Kernel length

Among the parents evaluated for the general combining ability effects for kernel length, L1 (-0.70) reported the minimum response and L2 (0.60) was the maximum response among the lines. It varied among the testers from -0.23 (T3) to 0.11 (T1). Minimum response among the hybrids reported by H1 (-0.18) and maximum by H6 (0.51). L2, L3, L4, T1, H1, H4, H5, H7, H8, H10, and H11 exhibited positive significant response whereas L1, T2, T3, H3, H6, H9 and H12 reported negative significant response.

4.3.2.13 Shattering per cent

Among parents *gca* effect for lines was the minimum for L4 (-1.17) and maximum for L3 (0.30) for lines and maximum for T2 (0.11) and maximum for T3 (0.77) among testers. The *sca* effects of hybrids varied from -1.69 (H10) to 1.78 (H11). T3, H1, H6, H11 and H12 reported significant response to combining ability effects and L4, H3, H4, H7, H9 and H10 reported negative significance.

Table16. General combining ability effects (*gca*) for lines and testers for vegetative and seed and panicle characters

Parents	PH (cm)	TP (no.)	DF	DM	FW (cm)	FL (cm)	PP (no.)	PL (cm)	SP (no.)	TW (g)	SYP (g)	KW (mm)	KL (mm)	Shattering (%)
Lines														
L1	0.33	0.96	-2.33*	-4.08*	0.03	1.72	0.32	-0.23	-3.17	0.00	0.07	0.07*	-0.61*	-0.83*
L2	-3.61*	-0.57	2.29*	5.04*	0.05	1.53	-0.23	0.73	1.83	0.49*	1.75	0.08*	-0.06*	0.29
L3	3.27*	-0.39	0.04	-0.96	-0.08	-3.25*	-0.10	-0.50	1.33	-0.50*	-1.82	-0.15*	0.67*	0.54
SE ± Lines	1.18	0.55	0.43	0.44	0.07	1.19	0.55	0.47	2.22	0.21	1.91	0.01	0.02	0.25
Testers														
T1	-7.62*	-0.16	1.63*	-0.25	-0.01	-0.23	0.59	-1.35*	12.21*	-0.43	5.67*	0.00	-0.15*	0.37
T2	0.97	0.57	-7.04*	-7.75*	-0.03	-0.23	0.82	-1.03	4.21	1.07*	4.31	0.25*	0.15*	-0.37
T3	4.07*	0.04	2.63*	5.08*	-0.01	-1.55	0.46	1.79*	-2.96	-0.71*	0.49	-0.11*	0.20*	-0.80*
T4	2.58	-0.46	2.79*	2.92*	0.05	2.00	-1.88*	0.59	-13.46*	0.07	-10.48*	-0.14*	-0.20*	0.80*
SE ± Tester	1.37	0.63	0.50	0.51	0.08	1.37	0.64	0.55	2.56	0.24	2.20	0.01	0.02	0.29

*Significant at 5% ; ** significant at 1%

PH – Plant height **TP - Number of tillers per plant** **DF –Days to fifty per cent flowering** **DM- Days to maturity**

FW – Flag leaf width **FL – Flag leaf length** **PP – Number of panicles per plant**

PL – Panicle length **SP – Seeds per panicle** **TW – Test weight** **SYP –Seed yield per plant** **KW – Kernel width**

KL – Kernel length

Table17. Specific combining ability effects (*sca*) for lines and testers for vegetative and seed and panicle characters

Hybrids	PH (cm)	TP (no.)	DF	DM	FW (cm)	FL (cm)	PP (no.)	PL (cm)	SP (no.)	TW (g)	SYP (g)	KW (mm)	KL (mm)	Shattering (%)
H1	3.06	-0.79	1.00	-1.75	0.06	-0.04	-0.59	-1.95	2.67	-0.47	-1.86	-0.06	-0.01	0.02
H2	1.51	0.48	-1.83	1.25	-0.04	0.12	0.88	-0.30	3.17	0.18	0.64	0.06	-0.83	0.59
H3	-3.93	-0.19	2.50	2.42	-0.06	-4.27	1.34	2.06	-2.17	0.76	3.38	-0.04	0.42	0.62
H4	-0.64	0.51	-1.67	-1.92	0.03	4.20	-1.63	0.20	-3.67	-0.47	-2.16	0.04	0.41	-1.24
H5	-7.16	1.13	2.38	5.63	-0.08	0.31	1.66	0.16	5.17	-0.21	5.14	-0.11	-0.55	-0.31
H6	2.99	0.60	-3.46	-4.88	-0.01	0.15	0.43	-1.17	-3.33	0.64	1.29	0.02	0.56	-1.63
H7	2.63	-2.17	-1.63	-2.21	0.03	3.51	-3.81	2.22	-3.67	-0.58	-12.78	0.11	-0.01	1.10
H8	1.54	0.43	2.71	1.46	0.06	-3.97	1.73	-1.21	1.83	0.14	6.35	-0.02	0.00	0.84
H9	4.10	-0.34	-3.38	-3.88	0.02	-0.27	-1.07	1.79	-7.83	0.68	-3.28	0.17	0.56	0.29
H10	-4.50	-1.08	5.29	3.63	0.05	-0.27	-1.30	1.48	0.17	-0.82	-1.93	-0.08	0.26	1.03
H11	1.31	2.36	-0.88	-0.21	0.02	0.76	2.47	-4.28	5.83	-0.19	9.40	-0.08	-0.41	-1.72
H12	-0.91	-0.94	-1.04	0.46	-0.09	-0.23	-0.10	1.01	1.83	0.33	-4.19	-0.01	-0.41	0.39
SE±Lines	2.37	1.09	0.86	0.87	0.13	2.37	1.10	0.94	4.44	0.42	3.81	0.02	0.03	0.51

PH – Plant height **TP - Number of tillers per plant** **DF –Days to fifty per cent flowering** **DM- Days to maturity**

FW – Flag leaf width **FL – Flag leaf length** **PP – Number of panicles per plant**

PL – Panicle length **SP – Seeds per panicle** **TW – Test weight** **SYP –Seed yield per plant** **KW – Kernel width**

KL – Kernel length

Table 18. Scoring of parents based on *gca* effects

Parents	PH (cm)	TP (no.)	DF	DM	FW (cm)	FL (cm)	PP (no.)	PL (cm)	SP (no.)	TW (g)	SYP (g)	KW (mm)	KL (mm)	Shattering (%)	Total
L1	0	0	-1	-1	0	0	0	0	0	0	0	1	-1	1	-1
L2	1	0	1	1	0	0	0	0	0	1	0	1	-1	0	4
L3	-1	0	0	-1	0	-1	0	0	0	-1	0	-1	1	-1	-5
T1	1	0	1	0	0	0	0	-1	1	0	1	0	-1	0	2
T2	0	0	0	-1	0	0	0	-1	0	1	1	1	1	0	2
T3	-1	0	1	1	0	0	0	1	0	-1	0	-1	1	1	2
T4	-1	0	1	1	0	0	-1	0	-1	0	-1	-1	-1	-1	-5

PH – Plant height **TP - Number of tillers per plant** **DF –Days to fifty per cent flowering** **DM- Days to maturity**

FW – Flag leaf width **FL – Flag leaf length** **PP – Number of panicles per plant**

PL – Panicle length **SP – Seeds per panicle** **TW – Test weight** **SYP –Seed yield per plant** **KW – Kernel width**

KL – Kernel length

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4.3.4 Evaluation of parents based on *gca* effects (scoring)

To get a better picture about the general combining ability effects, all the seven parents including lines and testers were scored based on their *gca* effects (Table 18), and were categorized into 3 general combiner groups. Only those parents exhibited significant *gca* effects for each trait were taken in to account as non-significant parents were statistically not different from zero. +1 (high) score was given to those parents with positive significant difference, those with negative significant effects scored as -1 (low) and those with other than the above two situations were categorized in to average or moderate combiner. The score obtained for each characters were summed up to evaluate the combining ability status of the parents.

The parents were considered as good combiner, if the total score obtained for the parent is more than +1, bad combiner if the total score is -1 or lesser and medium combiner if the total score equals to zero (Murthy and Kulkarni, 1996)

T1 was found to be better combiner for grain yield per plant and seeds per panicle. L1 and T3 recorded to be better combiner for reduced seed shattering indicating a scope for further utilization of these lines in plant breeding programmes for reduced shattering. All the seven parents recorded as a moderate combiner for tillers per plant and flag leaf width. When we consider the fourteen characters together, L2, T1, T2 and T3 reported as better combiner.

4.3.5 Evaluation of parents based on *gca* effects and mean performance

Evaluation of parents based on mean or *gca* effects alone might result in identification of different sets of parents as promising ones. However the potential of a genotype could be judged by comparing both the mean performance and combining ability effects (Table 19). Scoring based on mean performance and combining ability effects for seed yield per plant revealed that, L2, L3 and T2 proved to be promising.

Table 19. Scoring of parents based on *gca* effects and mean performance (contd...)

Parents	PH (cm)	X	TP (no.)	X	DF	X	DM	X	FW (cm)	X	FL (cm)	X
L1	0	-1	0	-1	-1	-1	-1	-1	0	0	0	1
L2	1	1	0	1	1	1	1	1	0	1	0	1
L3	-1	-1	0	1	0	1	-1	-1	0	1	-1	1
T1	1	-1	0	1	1	1	0	0	0	-1	0	-1
T2	0	1	0	1	0	-1	-1	-1	0	1	0	-1
T3	-1	-1	0	-1	1	-1	1	1	0	-1	0	-1
T4	-1	1	0	-1	1	-1	1	-1	0	-1	0	-1

Table 19. Scoring of parents based on *gca* effects and mean performance (…contd.)

Parents	PP (no.)	X	PL (cm)	X	SP (no.)	X	TW (g)	X	SYP (g)	X	KW (mm)	X	KL (mm)	X	shattering (%)	X	*gca* total	Mea n total	Total
L1	0	0	0	1	0	0	0	0	0	-1	1	1	-1	-1	1	-1	-1	-4	-5
L2	0	1	0	1	0	1	1	1	0	1	1	1	-1	1	0	-1	4	12	16
L3	0	1	0	1	0	1	-1	-1	0	1	-1	-1	1	1	-1	-1	-5	4	-1
T1	0	1	-1	-1	1	1	0	-1	1	1	0	0	-1	-1	0	1	2	0	2
T2	0	0	-1	-1	0	-1	1	1	1	-1	1	1	1	1	0	1	2	1	3
T3	0	-1	1	-1	0	-1	-1	-1	0	-1	-1	-1	1	0	1	1	2	-9	-7
T4	-1	-1	0	-1	-1	-1	0	-1	-1	-1	-1	-1	-1	1	-1	1	-5	-8	-13

Table20. Scoring of hybrids based on *sca* effects

Hybrids	PH (cm)	TP (no.)	DF	DM	FW (cm)	FL (cm)	PP (no.)	PL (cm)	SP (no.)	TW (g)	SYP (g)	KW (mm)	KL (mm)	shattering (%)	Total
H1 (PaxAa)	0	0	0	-1	0	0	0	-1	0	0	0	-1	0	0	-3
H2 (PaxTr)	0	0	-1	0	0	0	0	0	0	0	0	1	-1	-1	-2
H3 (PaxJa)	1	0	1	1	0	-1	0	1	0	1	0	-1	1	-1	3
H4 (PaxMa)	0	0	-1	-1	0	1	0	0	0	0	0	1	1	1	2
H5 (JyxAa)	1	0	1	1	0	0	1	0	0	0	0	-1	-1	1	3
H6 (JyxTr)	0	0	-1	-1	0	0	0	0	0	1	0	0	1	1	1
H7 (JyxJa)	0	-1	-1	-1	0	0	-1	1	0	0	-1	1	0	-1	-4
H8(JyxMa)	0	0	1	1	0	-1	1	0	0	0	1	0	0	-1	2
H9 (AixAa)	-1	0	-1	-1	0	0	0	1	-1	1	0	1	1	-1	-1
H10 (AixTr)	1	0	1	1	0	0	0	1	0	-1	0	-1	1	-1	2
H11 (AixJa)	0	1	0	0	0	0	1	-1	0	0	1	-1	-1	1	1
H12 (AixMa)	0	0	0	0	0	0	0	0	0	0	0	0	-1	-1	-2

T1, T2 and T3 proved to be promising parents for reduced seed shattering and T4 and L1 with a moderate response. However, the ranking of parents based on mean performance and *gca* effects showed that the parallelism between mean performance and *gca* effects does not exist always as observed by Thirumeni, (1998). Scoring based on both *gca* effects and their mean performance for all the fourteen characters revealed that L2, T1 and T2 were most promising parents. Hybridization involving these parents would there for assumed to be result in more desirable and superior recombinations in yield and yield contributing characters.

4.3.6 Evaluation of hybrids based on *sca* effects (scoring)

The *sca* effects for the 12 hybrids were done in the similar way as that of *gca* effect (Table 20). According to Sprague and Tatum (1942) the *sca* effect are the result of non additive gene action which comprises dominance and epistatic gene action.

H8 and H11 recorded high response to seed yield per panicle and except H7 remaining hybrids reported moderate response to the same. Out of the twelve hybrids, H4, H5, H6 and H11 recorded high response and H1 exhibited a moderate response for shattering per cent. When the fourteen characters considered together, H3, H4, H5, H6, H8, H10 and H 11 recorded to be better cross combination among the twelve characters.

These results indicate the possibility of combining yield with reduced seed shattering for combination breeding approaches in future. In this way it will help to produce desirable segregants in the subsequent generations as suggested by Shanthi *et al.* (2011).

It was clear that crosses exhibiting high *sca* effects did not always involve parents with high *gca* effect. The hybrids with high *sca* effects viz., H10 (L3 x T2) was a low/high cross combinations and H8 (L2 x T4) was a high/low cross combination. It clearly revealed that crosses resulted from high/poor or poor/high could be exploited for getting desirable recombinations from the segregating population.

Similarly crosses exhibiting significant desirable sca effects for different traits involved all possible combination viz., good X good, average X average, average X poor, poor X good, poor X average and poor X poor combining parents. It may be due to the inter-allelic interaction for these traits. Sharma and Mani (2008) and Hijam and Sarkar (2013) also reported similar results. Total score of mean performance and *sca* effect for all the fourteen characters (Table21) revealed that hybrids H1, H2, H3, H5, H6, and H11 reported high scores and H8 recorded moderate response.

There was no exact correspondence between mean performance and *sca* effects among the hybrids. Therefore the study indicated that the *sca* effect may not always leads to correct choice of hybrid combination. Bastian, (1999) also reported a similar kind of result and opined that such non-concordance between mean performance and *sca* effects of good progenies may be due to non additive gene action.

The top ranking hybrids involved parants with either high mean performance, high *gca* effects or combinations of both. Raghavaiah and Joshi (1986) reported that the combination of parents with high *gca* effects will be useful in the improvement of autogamous crops and for the improvement of self pollinated crops like rice, *sca* effect of a particular cross will be if it is accompanied by high *gca* of respective parents.

Best ranked hybrids may be grown in successive generations following pedigree method of selection to generate elite lines with stable yield.

Table 21. Scoring of hybrids based on mean value and *sca* effects (contd…)

Hybrids	PH (cm)	X	TP (no.)	X	DF77	X	DM	X	FW (cm)	X	FL (cm)	X
H1 (PaxAa)	0	1	0	0	0	0	0	-1	0	1	0	1
H2 (PaxTr)	0	-1	0	1	0	-1	0	-1	0	-1	0	1
H3 (PaxJa)	0	0	0	1	0	1	0	1	0	-1	0	-1
H4 (PaxMa)	0	-1	0	1	0	0	0	-1	0	1	0	1
H5 (JyxAa)	**-1**	1	0	0	0	1	1	1	0	-1	0	1
H6 (JyxTr)	0	0	0	1	0	-1	0	-1	0	0	0	1
H7 (JyxJa)	0	-1	0	-1	0	1	0	1	0	1	0	1
H8(JyxMa)	0	0	0	-1	0	1	0	1	0	1	0	0
H9 (AixAa)	0	0	0	-1	0	-1	0	-1	0	-1	0	-1
H10 (AixTr)	0	0	0	-1	**1**	-1	0	-1	0	-1	0	-1
H11 (AixJa)	0	-1	0	1	0	1	0	1	0	-1	0	-1
H12 (AixMa)	0	-1	0	-1	0	1	0	1	0	-1	0	-1

Table 21. Scoring of hybrids based on mean value and *sca* effects (…contd)

Hybrids	PP (no.)	X	PL (cm)	X	SP (no.)	X	TW (g)	X	SYP (g)	X	KW (mm)	X	KL (mm)	X	Shattering (%)	X	*sca* total	Mean total	Total
H1 (PaxAa)	0	0	0	-1	0	1	0	-1	0	1	0	0	0	-1	0	1	0	2	2
H2 (PaxTr)	0	1	0	-1	0	1	0	1	0	1	0	1	0	-1	0	1	0	2	2
H3 (PaxJa)	0	1	0	1	0	-1	0	0	0	1	0	-1	0	0	0	1	0	3	3
H4 (PaxMa)	0	-1	0	0	0	-1	0	-1	0	-1	0	0	0	-1	0	1	0	-3	-3
H5 (JyxAa)	0	1	0	0	0	1	0	0	0	1	0	0	0	-1	0	0	0	5	5
H6 (JyxTr)	0	1	0	-1	0	0	0	1	0	1	0	1	0	1	0	1	0	5	5
H7 (JyxJa)	0	-1	0	1	0	-1	0	-1	-1	-1	0	1	0	0	0	-1	-1	-1	-2
H8(JyxMa)	0	0	0	0	0	-1	0	1	1	0	0	-1	0	-1	0	-1	1	-1	0
H9 (AixAa)	0	0	0	0	-1	1	0	0	0	0	0	0	0	1	0	-1	-1	-4	-5
H10 (AixTr)	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	-1	1	-4	-3
H11 (AixJa)	0	1	0	-1	1	1	0	-1	1	1	0	-1	0	1	0	1	2	2	4
H12 (AixMa)	0	-1	0	1	0	-1	0	0	0	-1	0	-1	0	0	0	-1	0	-6	-6

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4.4 Studies on heterosis

4.4.1 Heterosis

Estimates of expression of relative heterosis (di) and heterobeltiosis (dii) detailed in Table 22 and 23 and are explained below.

4.4.1.2 Plant height

Relative heterosis for plant height ranged from H5 (-29.93) to H8 (-3.87) Nine hybrids exhibited high significant response and two hybrids recorded significant response for plant height. In case of heterobeltiosis H5 recorded the least among the twelve hybrids and H8 (-7.40) the highest. All the twelve hydrids recorded high significant response for plant height.

4.4.1.2 Number of tillers per plant

Lowest relative heterosis of this trait among hybrid was rcorded for H7 (-27.02) and highest H4 (13.03). Only four hybrids recorded significant relaive heterosis. And all of them were negatively significant. Heterobeltosis ranged from H7 (-36.97) to H4 (8.46) with 4 significant heterobeltosis among the twelve hybrids.

4.4.1.3 Days to 50% flowering

The relative heterosis for this trait ranged from H9 (-16.58) to H8 (13.21). Nine hybrids showed significant relative heterosis. Heterobeltosis varied from -20.30 (H9) to H4 (7.29). Eleven hybrids showed significant heterobeltosis in which H3, H4 and H8 registered positive significance.

4.4.1.4 Days to maturity

Out of tweleve hybrids ten registered significant relative heterosis for these traits. The value ranged from -9.54 (H6) to 5.54 (H12). Nine hybrids recorded significant heterbeltosis. The values varied between H6 (-18.35) to H12 (2.59).

4.4.1.5 Flag leaf width

The relative heterosis for flag leaf width ranged between H10 (- 48.58) to H4 (-32.84). Twelve hybrids recorded high significant relative heterosis and heterobeltosis also showed the same trend. It ranged from H5 (-51.81) to H4 (-34.93).

4.4.1.6 Flag leaf length

Among the twelve hybrids only H9 (-52.31) recorded a significant response in case pf relative heterosis for flag leaf length.

4.4.1.6 Number of panicle per plant

Lowest relative heterosis of this trait among hybrid was recorded for H7 (-37.87) and highest H3 (30.00). All the twelve hybrids recorded significant relaive heterosis in which H2, H3, and H11 recorded positive significant relative heterosis. Heterobeltosis ranged from H7 (-45.93) to H3 (30.00) and among the twelve hybrids H2 and H3 recorded positive heterobeltiosis.

4.4.1.7 Panicle length

Twelve hybrids showed significant relative heterosis and it ranged from H11 (-36.48) to H3 (-6.33). Heterobeltosis ranged from H1 (-43.48) to H3 (-13.92) and all of the recorded a negative significance for heterobeltiosis.

4.4.1.8 Seeds per panicle

Seven and two hybrids reported significant relative heterosis and heterobeltosis respectively in which H2, H5, H10 and H11 reported positive significance for relative heterosis. Relative heterosis ranged from H9 (-9.09) to H2 (14.14) and heterobeltiosis ranged from H12 (-26.89) to H2 (6.73).

Table 22. Relative heterosis and heterobeltiosis for vegetative characters

Hybrids	Plant height (cm)		Tillers per plant (No.)		Days to 50 per cent flowering		Days to maturity		Flag leaf width (cm)		flag length (cm)	
	di	dii	di	dii	di	dii	di	dii	di	dii	di	dii
H1 (PaxAa)	-21.18**	-23.77**	-9.66	-18.13	-6.52**	-18.32**	-5.76	-6.75	-33.42**	-36.12**	-37.17	-42.33
H2 (PaxTr)	-10.19**	-11.52**	5.97	-2.58	-3.07*	-5.96**	-5.15**	-8.62**	-45.82**	-48.72**	-39.57	-41.96
H3 (PaxJa)	-15.06**	-16.26**	11.20	6.92	9.33**	6.25**	-0.62**	-4.38**	-39.65**	-42.11**	-52.62	-55.39
H4 (PaxMa)	-8.91**	-12.05**	13.03	8.46	8.36**	7.29**	0.67*	-2.16*	-32.84**	-34.93**	-29.74	-32.17
H5 (JyxAa)	-29.93**	-36.73**	-16.92	-18.18	-4.84**	-12.38**	0.79**	-4.87**	-45.58**	-51.81**	-42.03	-50.26
H6 (JyxTr)	-6.09*	-11.30**	-14.38	-16.97	-5.13**	-12.94**	-9.54**	-18.35**	-48.24**	-49.80**	-44.74	-50.56
H7 (JyxJa)	-6.18*	-13.77**	-27.02**	-36.97**	3.64**	0.59	-3.86**	-6.74*	-40.59**	-47.39**	-39.04	-46.45
H8(JyxMa)	-3.87	-7.40**	-12.13	-24.24*	13.21**	5.88**	3.70**	-5.62**	-37.08**	-43.78**	-52.51	-54.39
H9 (AixAa)	-18.91**	-20.14**	-24.92**	-26.06*	-16.58**	-20.30**	-4.90	-5.91	-43.41**	-47.56**	-52.31*	-57.54
H10 (AixTr)	-14.88**	-17.65**	-23.75*	-26.06*	-1.23	-12.50**	-0.22**	-3.88**	-48.58**	-49.57**	-54.36	-57.54
H11 (AixJa)	-8.87**	-9.26**	5.97	-8.49	-2.33	-8.70**	-0.21**	-3.98**	-43.41**	-47.56**	-54.17	-58.18
H12 (AixMa)	-8.02**	-12.75**	-20.56*	-31.52**	1.21	-8.70**	5.54*	2.59	-46.32**	-49.78**	-52.65	-52.75

*Significant at 5% ; ** significant at 1%

di - relative heterosis   dii - heterobeltiosis

Table 23. Relative heterosis and heterobeltiosis for seed and panicle characters (contd…)

Hybrids	Panicle per plant (no.)		panicle length (cm)		Seeds per panicle (no.)		Test weight (g)	
	di	dii	di	dii	di	dii	di	dii
H1 (PaxAa)	-4.68**	-17.04**	-34.16**	-43.48**	7.97	2.60	-1.95**	-5.45**
H2 (PaxTr)	17.27**	7.50**	-27.45**	-35.35**	14.14*	6.73	-1.44**	-5.21**
H3 (PaxJa)	30.00**	30.00**	-6.33**	-13.92**	1.62	-5.29	-0.76**	-1.88**
H4 (PaxMa)	-16.76**	-23.00**	-15.44**	-26.58**	0.88	-16.83	-3.21**	-3.57**
H5 (JyxAa)	-4.44**	-4.44**	-24.23**	-37.63**	7.01*	5.00	-3.99**	-11.45**
H6 (JyxTr)	-6.67**	-11.85**	-31.29**	-41.42**	4.04	-8.75	-2.67**	-3.42**
H7 (JyxJa)	-37.87**	-45.93**	-6.84**	-18.25**	-2.79*	-15.00*	-8.60**	-13.68**
H8(JyxMa)	-4.55**	-22.22**	-22.47**	-35.51**	3.47	-19.17	-3.86**	-8.55**
H9 (AixAa)	-26.43**	-28.97**	-17.97**	-29.91**	-9.09**	-14.77*	2.99**	1.58**
H10 (AixTr)	-22.26**	-28.97**	-20.96**	-29.91**	1.12*	-14.77	-4.80**	-10.42**
H11 (AixJa)	11.84**	-5.52**	-36.48**	-41.93**	0.06*	-15.91	-4.09**	-5.19**
H12 (AixMa)	-23.48**	-39.31**	-13.39**	-25.17**	-3.26*	-26.89	0.19**	-1.71**

*Significant at 5% ; ** significant at 1%

Table 23. Relative heterosis and heterobeltiosis for seed and panicle characters (...contd.)

Hybrids	Seed yield per plant (g)		Kernel width (mm)		Kernel length (mm)		Shattering %	
	di	dii	di	dii	di	dii	di	dii
H1 (PaxAa)	0.72**	-13.36**	-6.03**	-11.38**	3.54**	-2.10**	-72.72**	-85.38**
H2 (PaxTr)	16.99**	10.43**	0.85**	0.68**	-19.43**	-26.93**	-75.10**	-86.07**
H3 (PaxJa)	30.71**	20.48**	-4.99**	-14.26**	1.44**	-5.87**	-78.05**	-87.70**
H4 (PaxMa)	-21.21**	-39.11**	-2.65**	-12.73**	-5.27**	-12.78**	-79.20**	-88.75**
H5 (JyxAa)	-2.23**	-11.50**	-7.57**	-12.76**	-16.59**	-32.78**	-69.87**	-83.96**
H6 (JyxTr)	-6.46**	-22.47**	-0.09**	-0.34**	-10.67**	-17.65**	-84.54**	-91.44**
H7 (JyxJa)	-46.62**	-60.16**	1.13**	-8.67**	-14.84**	-23.26**	-69.49**	-83.08**
H8(JyxMa)	-13.49**	-42.97*	-4.46**	-14.29**	-20.08**	-27.43**	-59.38**	-78.21**
H9 (AixAa)	-31.08**	-38.29**	9.87**	0.19**	7.61**	-13.42**	-60.35**	-78.75**
H10 (AixTr)	-24.82**	-38.29**	2.45**	-11.51**	-5.90**	-13.42**	-62.02**	-78.75**
H11 (AixJa)	4.21**	-22.86**	0.00**	-4.64**	-11.01**	-19.97**	-85.04**	-91.62**
H12 (AixMa)	-59.37**	-73.37**	2.34**	-1.71**	-16.51**	-24.33**	-56.77**	-76.63**

*Significant at 5% ; ** significant at 1%

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4.4.1.9 Test weight

Twelve hybrids recorded significant relative heterosis and H9 and H12 recorded positive significant relationship and it ranged from H7 (-8.60) to H9 (2.99). Heterobeltosis ranged from H7 (-13.68) to H9 (1.58) and among this twelve hybrids only H9 reported positive significance for heterobeltosis.

4.4.1.10 Seed yield per plant

Relative heterosis ranged from H12 (-59.37) to H3 (30.71) in which H1, H2, H3 and H11 reported positive significance for relative heterosis whereas heterbeltosis ranged from H12 (-73.37) to H3 (20.48) and H2 and H3 reported a positive significance for heterobeltosis.

4.4.1.11 Kernel width

The relative heterosis for this character ranged from H5 (-7.57) to H9 (9.87). H2, H7, H9, H10, H11 and H12 recorded positive significance. Heterobeltosis ranged from H8 (-14.29) to H2 (0.68) in which H2 and H9 recorded positive significance.

4.4.1.12 Kernel length

Relative heterosis for kernel length varied from H8 (-20.08) to H9 (7.61) in which H1, H2 and H9 recorded positive significance. For heterobeltosis, it ranged from H5 (-32.72) to H1 (-2.10).

4.4.1.13 Shattering

All the twelve hybrids exhibited high significant response for both relative heterosis and heterobeltiosis. Relative heterosis varied from H11 (-85.04) to H12 (-5.77) and all of them recorded negative significant relationship indicating that none of them were better than average performance of their parents. The heterobeltiosis ranged from H11 (-91.62) to H12 (-76.63) and twelve hybrids recorded negative significance indicating that all of them were better than their female parent ie., shattering prone varieties.

Study revealed that not all crosses with high heterosis effect exhibited significant *sca* effect for a particular character. There were crosses which reported high heterosis and low *sca* effect and vice versa. This revealed inconsistent relationship between heterosis and *sca* effects. This study showed that the *sca* effects may not always lead to correct choice of hybrid combination. According to Pethani and Kapoor (1984) selection of hybrids based on high mean performance and heterotic expression would be more useful than that based on *sca* effect alone.

4.4.2 Evaluation of hybrids based on mean performance and heterosis (scoring)

Exploitation of hybrid vigour needs a sound knowledge on the extent of heterosis in plants. For this poupose identification of heterotic crosses were done. In the present study the per cent heterosis varied from trait to trait and cross to cross and none of the cross combinations recorded significant heterosis for all these fourteen characters simultaneously. For every character, a cross was assigned a status 1, if its mean exceeded that of the superior parent; otherwise a status 0 was given (Bastian, 1999). Scores over all the characters could therefore be counted for each cross for heterobeltiosis (Table 24).

Based on the scoring for both mean performance and heterotic effect revealed that (Table 25), hybrids H5 recorded highest score followed by H3, H9, H11, and H1.

4.4.3 Evaluation of hybrids based on *sca* effects, mean performance and heterosis (scoring)

For having a more detailed evaluation on hybrids, mean performance, *sca* effect and heterosis considered together and hybrids ranked based on their total score for yield and yield contributing characters (Table 26).

Table 24: Scoring of hybrids for heterobeltiosis

Hybrids	PH (cm)	TP (no.)	DF	DM	FW (cm)	FL (cm)	PP (no.)	PL(cm)	SP (no.)	TW (g)	SYP (g)	KW (mm)	KL (mm)	shattering %	Total
H1 (PaxAa)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2
H2 (PaxTr)	1	0	0	0	0	0	1	0	1	0	1	1	0	0	5
H3 (PaxJa)	1	1	1	0	0	0	1	0	0	0	1	0	0	0	5
H4 (PaxMa)	1	1	1	0	0	0	0	0	0	0	0	0	0	0	3
H5 (JyxAa)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2
H6 (JyxTr)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
H7 (JyxJa)	1	0	1	0	0	0	0	0	0	0	0	0	0	0	2
H8(JyxMa)	1	0	1	0	0	0	0	0	0	0	0	0	0	0	2
H9 (AixAa)	1	0	0	0	0	0	0	0	0	1	0	1	0	0	3
H10 (AixTr)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
H11 (AixJa)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
H12 (AixMa)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1

Table 25: Comparison of hybrids for both mean performance and heterobeltiosis (contd…)

Hybrids		PH (cm)	X	TP (no.)	X	DF	X	DM	X	FW (cm)	X	FL (cm)	X
H1 (PaxAa)	H1	0	1	0	0	0	0	0	-1	0	1	0	1
H2 (PaxTr)	H2	0	-1	0	1	-1	-1	0	-1	-1	-1	0	1
H3 (PaxJa)	H3	0	0	0	1	0	1	0	1	-1	-1	0	-1
H4 (PaxMa)	H4	0	-1	0	1	0	0	0	-1	0	1	1	1
H5 (JyxAa)	H5	-1	1	1	0	0	1	0	1	1	-1	0	1
H6 (JyxTr)	H6	0	0	0	1	0	-1	0	-1	-1	0	0	1
H7 (JyxJa)	H7	0	-1	-1	-1	0	1	0	1	0	1	0	1
H8(JyxMa)	H8	0	0	0	-1	0	1	0	1	0	1	0	0
H9 (AixAa)	H9	0	0	1	-1	0	-1	0	-1	1	-1	0	-1
H10 (AixTr)	H10	0	0	-1	-1	0	-1	0	-1	-1	-1	0	-1
H11 (AixJa)	H11	0	-1	0	1	0	1	0	1	-1	-1	0	-1
H12 (AixMa)	H12	0	-1	-1	-1	0	1	0	1	-1	-1	0	-1

Table 25: Comparison of hybrids for both mean performance and heterobeltiosis (…contd.)

Hybrids	PP (no.)	X	PL (cm)	X	SP (no.)	X	TW (g)	X	SYP (g)	X	KW (mm)	X	KL (mm)	X	shattering %	X	Heterosis total	Mean total	Total
H1 (PaxAa)	0	0	0	-1	0	1	0	-1	0	1	0	0	-1	-1	0	1	-1	2	1
H2 (PaxTr)	0	1	-1	-1	0	1	0	1	0	1	1	1	-1	-1	1	1	-2	2	0
H3 (PaxJa)	1	1	1	1	0	-1	0	0	0	1	0	-1	0	0	1	1	2	3	5
H4 (PaxMa)	-1	-1	0	0	-1	-1	0	-1	-1	-1	0	0	0	-1	1	1	-1	-3	-4
H5 (JyxAa)	1	1	1	0	1	1	0	0	1	1	0	0	1	-1	0	0	6	5	11
H6 (JyxTr)	0	1	-1	-1	0	0	0	1	1	1	1	1	0	1	1	1	1	5	6
H7 (JyxJa)	-1	-1	1	1	0	-1	0	-1	-1	-1	0	1	0	0	-1	-1	-3	-1	-4
H8(JyxMa)	0	0	0	0	0	-1	0	1	-1	0	0	-1	0	-1	-1	-1	-2	-1	-3
H9 (AixAa)	1	0	1	0	1	1	0	0	1	0	0	0	1	1	-1	-1	6	-4	2
H10 (AixTr)	0	0	0	0	0	1	0	0	0	0	0	0	1	1	-1	-1	-2	-4	-6
H11 (AixJa)	1	1	-1	-1	0	1	0	-1	1	1	-1	-1	0	1	1	1	0	2	2
H12 (AixMa)	-1	-1	0	1	0	-1	0	0	-1	-1	-1	-1	0	0	-1	-1	-6	-6	-12

Table 26. Ranking of hybrids based on scoring of heterosis, mean value and *sca*

Hybrids	Scores		Total score (Heterosis + Mean + *sca*)	Final rank
	Heterosis	Mean + *sca*		
H1 (PaxAa)	-1	2	1	6
H2 (PaxTr)	-2	2	3	7
H3 (PaxJa)	2	3	7	3
H4 (PaxMa)	-1	-3	2	9
H5 (JyxAa)	6	5	8	1
H6 (JyxTr)	1	5	2	2
H7 (JyxJa)	-3	-2	-2	11
H8(JyxMa)	-2	0	1	8
H9 (AixAa)	6	-5	8	5
H10 (AixTr)	-2	-3	0	10
H11 (AixJa)	0	4	3	4
H12 (AixMa)	-6	-6	-5	12

Hybrids H5 (L3 x T1), H6 (L2 x T2) and H3 (L1 x T3) recorded the first three positions among the twelve hybrids evaluated. H5 and H6 are the cross combination with both parents as better combiners. The results also indicate that the best cross-combinations identified involved both or at least one good combiner. Hence there are more chances to have better segregants through transgressive breeding.

V. SUMMARY

The research work 'Breeding for shattering resistance in rice (*Oryza sativa* L.)' was conducted in the Department of Plant Breeding and Genetics, College of Horticulture (COH), Vellanikkara, during the academic year 2016 – 2018. The research work was mainly divided into three experiments. Experiment 1 consisted of screening of rice genotypes for shattering resistance which was conducted at Agricultural Research Station (ARS), Mannuthy. After screening, second experiment was undertaken in COH on which, four selected shattering resistant rice genotypes were crossed in Line x Tester pattern with three shattering prone high yielding varieties. In experiment 3 progenies were evaluated along with parents for shattering resistance.

Assessment of the extent of variability and genetic parameters for yield and yield attributes, understanding the degree and extent of association between grain yield and its contributing characters with special emphasis on seed shattering was envisaged in this study. In addition to the above, it also aimed at identifying potential parents and superior cross-combinations for yield and shattering resistance through the examination of heterosis and combining ability.

Salient findings of the research work are summarized below:

Variability studies

1. Wide variability was found to exist among the twenty five genotypes for yield and most yield attributes studied indicating ample scope for improvement of these traits through selection.

2. High PCV and GCV estimates were recorded for seed yield per plant and shattering per cent indicating ample variability among genotypes for these traits and the possibility of improvement through selection.

3. High heritability coupled with high genetic advance as per cent of mean indicating the influence of additive gene action in the expression of trait were observed for days to fifty per cent flowering, flag leaf width, flag leaf

length, panicle per plant, seed yield per plant and shattering per cent. Substantial improvement in the expression of these characters over base population can be expected through simple selection.

Trait association studies (simple correlation)

1. Seed yield per plant recorded high significant correlation with number of tillers per plant, flag leaf width, number of panicles per plant and seeds per panicle and significant correlation with test weight
2. Days to fifty per cent flowering shows significant inter-correlation with plant height. Days to maturity showed high significant inter-correlation with plant height and days to fifty per cent flowering. There exist a high significant inter-correlation between flag leaf width and number of tillers per plant. Number of panicles per plant recorded a high significant inter-correlation with number of panicles per plant and flag leaf width. Number of tillers per plant, flag leaf width and number of panicles per plant recorded a high significant inter-correlation with seeds per panicle. Plant height and number of panicles per plant exhibited significant inter-correlation with test weight and flag leaf width recorded a high significant inter-correlation for the same. A negative significant inter-correlation was observed between kernel width and seeds per panicle and kernel length recorded a high significant inter-correlation with panicle length
3. Shattering per cent recorded a high significant inter correlation with panicle length and significant inter-correlation with kernel length.

Studies on combining ability

1. Higher estimates of GCA variance over SCA variance for days to maturity, flag leaf width, seeds per panicle and kernel width pointed to be

pre-ponderance of additive gene action. Additive gene action is the heritable and fixable portion of gene action.

2. The magnitude of SCA variance was higher than GCA variance for plant height, tillers per plant, days to fifty per cent flowering, flag leaf length, panicle per plant, panicle length, test weight, seed yield per plant, kernel length, and shattering indicating pre-ponderance of non-additive gene action i.e., dominance and epistatic gene action in the inheritance of these characters.

3. For mean performance evaluated among parents, it was evident that for seed yield per plant L2, L3 and T1recorded a high response. The response recorded for panicle length and shattering per cent were exactly similar. When all the fourteen characters for the seven parents considered together, L2, L3 and T2 represented as best parents for yield and yield attributes and T1 recorded to be a moderate response.

4. Evaluation of hybrids based on mean performance revealed that H1, H2, H3, H5, H6 and H11 recorded high response for seed yield per plant and H8, H9 and H10 recorded moderate response. Out of the twelve hybrids, H1, H2, H3, H4, H6 and H11 recorded a high response towards reduced shattering and H5 reported moderate response. Among the twelve hybrids HI (L1 x T1), H2 (L1 x T2), H3 (L1 x T3), H5 (L2 x T1), H6 (L2 x T2) and H11 (L3 x T3) showed a high total response compared to the rest.

5. Results from *gca* effects of parents indicated that T1 recorded to be better combiner for grain yield per plant and seeds per panicle. L1 and T3 to be better combiner for reduced seed shattering indicating a scope for further utilization of these lines in plant breeding programmes for reduced shattering. When all the fourteen characters were considered, L2, T1, T2 and T3 recorded as better combiner. All the seven parents recorded to be moderate combiner for tillers per plant and flag leaf width.

6. Scoring based on mean performance and combining ability effects for seed yield per plant revealed that, L2, L3 and T2 proved to be promising. T1, T2 and T3 proved to be promising parents for reduced seed shattering and T4 and L1 with a moderate response. When all the fourteen characters considered together,L2, T1 and T2 were recorded as most promising parents.

7. Specific combining ability studied among the cross combinations indicated that H8 and H11 recorded high response to seed yield per panicle and except H7 remaining hybrids reported moderate response to the same. Out of the twelve hybrids, H4, H5, H6 and H11 recorded high response and H1 exhibited a moderate response for shattering resistance. When the fourteen characters considered together, H3, H4, H5, H6, H8, H10 and H 11 recorded to be better cross combination among the twelve characters.

8. Total score of mean performance and *sca* effect for all the fourteen characters for hybrids revealed that hybrids H1, H2, H3, H5, H6, and H11 reported high scores and H8 recorded moderate response.

Studies on Heterosis

1. All the twelve hybrids recorded high significant heterobeltiosis for plant height, flag leaf width, panicles per plant, panicle length, test weight, kernel width, kernel length and shattering per cent.

2. Based on the scoring for both mean performance and heterotic effect revealed that hybrids H5 recorded highest score followed by H3, H9, H11, and H1.

3. Evaluation of hybrids based on mean performance, *sca* effects and heterosis revealed that hybrids H5, H6 and H3 recorded the first three positions among the twelve hybrids evaluated. Among this H5 and H6 have both the parents as better combiners.

4. The remaining cross combination involving different combinations of parents viz., good x good, average x average, average x poor, poor x good, poor x average and poor x poor etc., can be used for transgressive breeding since there will be better recombinations in segregating generation.

The study revealed that seed shattering at maturity affected performance of genotypes. Existence of wide variability among genotypes for yield and other yield attributes viz., seed shattering as evident in the study indicate ample scope for improvement of yield through concerted breeding programmes.

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BREEDING FOR SHATTERING RESISTANCE IN RICE (*Oryza sativa* L.)

By

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ABSTRACT

The research work 'Breeding for shattering resistance in rice (*Oryza sativa* L.)' was conducted in the Department of Plant Breeding and Genetics, College of Horticulture (COH), Vellanikkara, during the academic year 2017 – 2018. The research work was mainly divided into three experiments. Experiment 1 consisted of screening of rice genotypes for shattering resistance which was conducted at Agricultural Research Station (ARS), Mannuthy. After screening, four selected shattering resistant rice genotypes were crossed in Line x Tester pattern with three shattering prone high yielding varieties in experiment 2. In experiment 3 progenies were evaluated along with parents for shattering resistance. Shattering was measured based on Induced Random Impact method using a force gauge apparatus.

Wide variability was found to exist among twenty five genotypes for yield and most yield attributes studied indicating ample scope for improvement through selection. High heritability coupled with high genetic advance as per cent of mean indicating the influence of additive gene action in the expression of trait were observed for days to fifty per cent flowering, flag leaf width, flag leaf length, panicle per plant, seed yield per plant and shattering per cent. Substantial improvement in the expression of these characters over base population can be expected through simple selection. Tillers per plant showed moderate heritability along with high genetic gain implying influence of both additive and non additive gene action in the expression of these characters. Improvement of these traits could be attained by following recurrent or reciprocal recurrent selection to exploit both additive and non-additive genetic components.

Seed yield per plant recorded high significant correlation with number of tillers per plant, flag leaf width, number of panicles per plant and seeds per panicle and significant correlation with test weight. Shattering per cent recorded a high significant inter correlation with panicle length and significant inter-correlation with kernel length.

High estimates of general combining ability (GCA) over specific combining ability (SCA) is indicative of preponderance of additive gene action and it was evident in the case of days to maturity, flag leaf width, seeds per panicle and kernel width. Prevalence of non-additive gene action i.e., dominance and epistatic gene action in trait expression indicated by high SCA over GCA was registered for the remaining characters.

When parents were evaluated on the basis of mean performance, it was evident that for seed yield per plant L2, L3 and T1recorded a high response. The response recorded for panicle length and shattering per cent were exactly similar. When all the fourteen characters for the seven parents considered together, L2, L3 and T2 represented as best parents for yield and yield attributes and T1 recorded to be a moderate response.

Evaluation of hybrids based on mean performance revealed that out of the twelve hybrids, H1, H2, H3, H4, H6 and H11 recorded a high response towards reduced shattering and H5 reported moderate response. Among the twelve hybrids HI (L1 x T1), H2 (L1 x T2), H3 (L1 x T3), H5 (L2 x T1), H6 (L2 x T2) and H11 (L3 x T3) showed a high total response compared to the rest.

Results from *gca* effects of parents indicated that L1 and T3 to be better combiner for reduced seed shattering indicating a scope for further utilization of these lines in plant breeding programmes for reduced shattering. When all the fourteen characters were considered, L2, T1, T2 and T3 recorded as better combiner. All the seven parents recorded to be moderate combiner for tillers per plant and flag leaf width. Scoring based on mean performance and combining ability effects for seed yield per plant revealed that, L2, L3 and T2 proved to be promising. T1, T2 and T3 proved to be promising parents for reduced seed shattering and T4 and L1 with a moderate response. When all the fourteen characters considered together L2, T1 and T2 were recorded as most promising parents.

Specific combining ability studied among the cross combinations indicated that out of the twelve hybrids, H4, H5, H6 and H11 recorded high response and H1 exhibited a moderate response for seed shattering . When the fourteen characters considered together, H3, H4, H5, H6, H8, H10 and H 11 recorded to be better cross combination among the twelve characters. When mean performance and *sca* effect for all the fourteen characters for hybrids considered, the hybrids H1, H2, H3, H5, H6, and H11 reported high scores and H8 recorded moderate response.

All the twelve hybrids recorded high significant heterobeltiosis for plant height, flag leaf width, panicles per plant, panicle length, test weight, kernel width, kernel length and shattering per cent. Based on the scoring for both mean performance and heterotic effect revealed that hybrids H5 recorded highest score followed by H3, H9, H11, and H1. Evaluation of hybrids based on mean performance, *sca* effects and heterosis revealed that hybrids H5, H6 and H3 recorded the first three positions among the twelve hybrids evaluated. Among this H5 and H6 have both the parents as better combiners. The remaining cross combination involving different combinations of parents viz., good x good, average x average, average x poor, poor x good, poor x average and poor x poor etc., can be used for transgressive breeding since there will be better recombinations in segregating generation.