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Research Paper

Heritability Analysis Provide Insights into Variability for yield attributed traits in F_2 families of rice (*Oryza sativa* L.) under aerobic condition

MUTHUVIJAYARAGAVAN. R* and S. JEBARAJ
Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai, Tamil Nadu, India – 625 104
**Corresponding author MUTHUVIJAYARAGAVAN. R*

ABSTRACT
An investigation was carried out in the heterogeneous rice populations of 30 cross combinations in F_2 generation. This study was conducted with the objective of analyzing genetic variability for important economic and physiological traits. The study was conducted in the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai. The breeding nature of the segregants was investigated by their mean performance, phenotypic and genotypic variability for the traits viz., plant height, productive tillers per plant, panicle length, filled grains per panicle, 100 grain weight, spikelet fertility, days to 70% RWC, leaf rolling, leaf drying, chlorophyll stability index, root length, dry root weight, root volume, root/shoot ratio, harvest index and grain yield per plant. The variance due to phenotypic and genotypic causes is low in F_2 generation for most of the characters. The trait number of productive tillers per plant though exhibited low variability in F_2. When mean, genotypic variability, heritability and genetic advance were taken as the selection criteria, the selection will be effective in COMS 14A x IR 80286, COMS 24A x IR 79200, IR 73328A x IR 80402, IR 79128A x IR 79200 as these crosses exhibited higher mean value and high heritability along with high genetic advance for yield and its attributing traits.
***KEY WORDS**: Rice, Variability, Heritability, Heterogeneous Population, F_2 Generation*

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I. INTRODUCTION

Rice is the only crop in the world that is grown in most fragile ecosystem and hence second green revolution is possible only if rice research is undertaken vigorously and persistently to address location specific problems (Bouman *et al*., 2002). Although the production of rice has increased over time in the wake of green revolution and other technological advancements, major shortfalls caused by climatic aberrations such as drought and flooding are frequent. Drought is one of the major constraints in rice production. Nearly 10 lakh hectares of rice are prone to drought in Tamil Nadu. The success of plant breeding programme depends to a greater extent on the knowledge of the genetic architecture of the population and selection of appropriate breeding method for the improvement of traits of interest. Most breeding experiments formulated to improve drought tolerance were concentrated on yield under stress rather than selection based on secondary traits contributing to drought tolerance. Hence, the indirect selection for carefully selected secondary traits can be helpful in improving selection response (Banumathy *et al*., 2003). Understanding the target environment is critical for the success of drought tolerance research. Plants possess several morphological and physiological adaptations to overcome the deleterious effects of water stress. Drought tolerance is quantitatively inherited with a complex physiological reaction; thus its genetic basis has received limited attention and the development of drought tolerant varieties has been slow (Nadarajan and Muthuramu, 2005). Therefore, it is essential to understand the effects of the prevailing drought stress in the target environment on both yield and drought traits in order to undertake the genetic improvement of aerobic rice cultivars in this region. Hence the present investigation was undertaken in view to study the F_2 and F_3 generations with 30 crosses of rice to find out the nature and extent of variability for economic traits in each of the 30 segregating populations and also to know how far these traits are heritable and how much genetic advance can be expected for each trait.

II. MATERIALS AND METHODS

Seeds of F_2 generation of 30 cross combinations of rice, involving seven A lines, *viz.*, IR 73328A, IR 70369A, COMS 24A, COMS 14A, IR 79128A, IR 79156A and eight restorer (R) lines, *viz.*, IR 69726-29-1-2-2R, IR 79582-21-2-2-1R, IR 81178-2T-2-2-3R, IR 79200-45-2-2-1R, IR 80286-22-3-6-1R, IR 80402-88-3-1-3R, IR 7925A-428-2-1-1R, IR 05N496 and varieties *viz.*, MAS-946-1, KMP-149, MAS-26, BR-2655, KMP-105, BI-33 and KMP-148 obtained from the rice germplasm collection maintained in the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai were utilized as the experimental material in the present study. The study was conducted in the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai. The F_2 generationwas raised during *kharif* 2012.The thirty F_2 cross combinations and nineteen parents were raised in a Randomized Block Design replicated twice. Field was thoroughly prepared and each genotype was raised in a 3 m^2 plot by direct seeding in a main field at a spacing of 30cm between rows and 15cm between plants. Eighty five plants were maintained per entry per replication. Each entry consisted of four rows with twenty one hills per replication. Observations were recorded on five competitive plants from each genotype selected at random per replication. Thus, a total of one hundred and fifty plants in F_2 progenies in each cross were utilized for recording observations.

Table 1. The parents and their crosses involved in F_2 generation

Symbols	Parents involved
Cross 1	IR 73328A x IR 79200
Cross 2	COMS 24A x MAS 26
Cross 3	COMS 24A x IR 79582
Cross 4	IR 73328A x IR 69726
Cross 5	COMS 14A x BI 33
Cross 6	COMS 24A x IR 79200
Cross 7	IR 70369A x IR 80402
Cross 8	COMS 14A x IR 80286
Cross 9	IR 70369A x BI33
Cross 10	IR 70369A x IR 79200
Cross 11	IR 70369A x IR 7925
Cross 12	IR 70369A x IR 05N496
Cross 13	COMS 24A x IR05N496
Cross 14	COMS24A x KMP 105
Cross 15	COMS 24A x IR 69726
Cross 16	IR 73328A x IR 80402
Cross 17	IR 73328A x KMP 105
Cross 18	IR 73328A x IR 79200
Cross 19	IR 73328A x IR 05N496
Cross 20	IR 73328A x IR 81178
Cross 21	IR 73328A x IR 80402
Cross 22	IR 73328A x MAS 26
Cross 23	IR 79128A x IR 69726
Cross 24	IR 79128A x IR 79200
Cross 25	IR 79128A x KMP 105
Cross 26	IR 79128A x BI 33
Cross 27	IR 79156A x IR 79200
Cross 28	IR 79156A x IR 05N496
Cross 29	IR 79156A x IR 80402
Cross 30	IR 79156A x MAS 26

Observations were recorded on five competitive plants for Plant height, Productive tillers, panicle length, Filled grains, 100-grain weight, days to 70% relative water content, leaf rolling, leaf drying, Chlorophyll stability index, Root Length, Dry root weight, Root volume, Root-shoot ratio, Harvest index and grain yield per plant.

Data analysis

The Phenotypic and Genotypic coefficient of variations were calculated based on the methods advocated by Burton (1952). Heritability in broad sense was calculated using the following formula advocated by Lush (1940) and expressed in percentage. The heritability percent was categorized as suggested by Robinson *et al*. (1949). Genetic advance and also as percent of mean was estimated by the method formulated by Johnson *et al*. (1955).

III. RESULT AND DISCUSSION

Mean and variability

The mean is the foremost consideration on selecting an individual or family (Kumar *et al*., 1979). High or low mean depending upon the characters serve favourable index for selection. The genetic potential of a cross or family is measured not only by mean but also the extent of genetic variability (Allard, 1960). The existence of genetic variability is essential for exercising selection for improvement of any characters. The systematic breeding programme to improve the yield potential of a genotype demands the knowledge on the nature and magnitude of available variability and on the population (Supe and Kale, 1991). Rice possesses a wider range of variability and had a number of distinct types available all over the country. The success of an effective breeding programme depends upon the amount of genetic variability present in the materials.

In case, the variability is very much limited due to continued selection, it is warranted to plan for recombination breeding programme for further genetic amelioration (Bharadwaj *et al*., 2007). The estimate of genetic variability (GCV and PCV) helps to select potential cross. A genotypic coefficient of variation measures the range of genetic variability in traits and enables them to have a comparison of genetic variability in the quantitative traits (Allard 1960). Garner (1972) reported that the expression of the crosses in the advanced generation, following selection would depend upon the mean and genetic variation created in the population. Those crosses that attain homozygosity in earlier generations are very much amenable for further breeding work (Jennings *et al*., 1979).

Two criteria, namely mean and variability are not exclusive on deciding the selection of crosses or the families within a cross but they complement each other. Allard (1960) suggested that based on mean and variability, the segregating population may be categorized as high mean and high variability and low mean and low variability high mean and low variability and low mean and high variability. Selection would be worthwhile on the group of high mean and high variability and if necessary on the groups of high mean and low variability also because, such groups have potentiality to produce more transgressive segregants than other groups. Low mean and high variability are capable of producing more transgressive segregants, but they may be poor in performance. However, in certain characters where in low mean is desirable, as in earliness, pest and disease incidence, this group will be more promising for selection of segregants.

Mean performance of characters

The mean performance and spectrum of variation would help to identify the superior lines among the existing population. Allard (1960) has suggested that the selection should be applied mainly on the lines showing high mean and variability. In the present investigation, when the mean performance alone was taken as the criterion for selection, the crosses 26 in F_2 generation performed well comparatively than the other crosses for grain yield per plant in F_2generations. It was interesting to note that, none of the crosses showed better performance for the same trait or all the traits in F_2. The change in the superiority of the crosses for the same or different crosses from F_2 to F_3might probably be due to the change in the gene frequency as a consequence of selection exercised in the F_2 population as reported by Ganesan (1987).

Variability

The potentiality of a cross is measured not only by *per se* performance but also on the extent of variability. Knowledge on nature and magnitude of genotypic and phenotypic variability present in any crop species plays an important role in formulating successful breeding programme (Allard 1960). In case, the variability is very much limited due to continued selection, it is warranted to plan for recombination breeding programme for further genetic amelioration (Bharadwaj *et al*., 2007). The estimate of genetic variability (GCV and PCV) helps to select potential cross. A genotypic coefficient of variation measures the range of genetic diversity in traits and enables them to have a comparison of genetic variability in the quantitative traits (Allard, 1960). Garner (1972) reported that the expression of crosses in the advanced generation, following selection would depend upon the mean and genetic variation created in the population. Those crosses that attain homozygosity in earlier generations are very much amenable for further breeding work (Jennings *et al*., 1979).

In the present investigation, the variances due to phenotypic and genotypic causes were low in F_2 generation for most of the characters. The PCV and GCV values were also low in most of the characters in F_2 generations. The low variability might be due to the involvement of short duration parents which yielded early segregants in a large measure. Similar results were observed for this estimates by Sivasubramanian and Madhava menon (1973), in F_2generation of rice.

The extent of variability for plant height was low to moderate in F_2 of all the crosses, for this trait (Table 2 and Fig. 1). The findings of Manickavelu *et al*. (2006) revealed low variability with low genetic advance for plant height in F_3 generation which is similar to the findings of the current investigation. The findings of Nandeshwar *et al.* (2010) revealed moderate heritability for plant height in F_2 generation of rice genotypes which is similar to the present findings.

Number of productive tillers had low variability in F_2 generation for all crosses except the crosses 27 and 29 which showed moderate variability (Table 3). The number of productive tillers per plant exhibited high variability in F_3 generation as reported by Anbanandan *et al*. (2009) in rice genotypes. The results were in accordance with the findings of Shivani and Reddy (2000), Suresh and Reddy (2002) for moderate variability in rice genotypes. A low variability was observed in F_2 of all crosses except the crosses 3 and 17 which had moderate variability for the trait panicle length, whereas, high variability was observed for this trait in cross 29 (Table 4 and Fig. 2). Similar findings were also reported by Raju *et al*. (2004) in F_2 generation. High variability was observed for 100 grain weight in F_2 of the crosses *viz*., 25, 28, for this trait (Fig. 4). The PCV and GCV values were more than 20 per cent. These are in agreement with the findings of Sao and Motiramani (2004) for high variability; Ananda Kumar and Indubala (2005), Sanjeev Kumar *et al*. (2005) for moderate variability in F_2 generation of rice. The moderate variability was observed in the crosses 2, 16, 18 and 20 of F_2 generation as reported by Sanjeev Kumar *et al*. (2005) in F_2 generation of rice. Among the cross combinations cross 25 in F_2recorded higher variability for 100 grain weight which is in agreement with the findings of Sabesan *et al*. (2009) in rice genotypes.

For the trait spikelet fertility, low magnitude of variability was recorded by all the crosses of F_2 (less than 10 per cent) generation. None of the crosses showed high variability for this trait under study.Similar results were reported by Kole *et al*. (2008) in rice genotypes. All the crosses showed low magnitude of variability for days to 70% relative water content in F_2 generation (Fig. 5). Among the crosses studied in F_2 generation the cross 25 recorded the highest value for variability.

In the present study, the variability estimates exhibited higher magnitude of variability in F_2 of the crosses *viz*., 7 and 4 for the trait leaf rolling. Moderate variability was observed in the remaining crosses in F_2 generation. These results were in conformity with the findings of Chandra and Pradhan (2003) in rice varieties.

Leaf drying had high variability in all the crosses of F_2 generation except the crosses 13 and 18. The crosses 8, 19 and 21 showed moderate PCV and low GCV values for this trait. None of the crosses showed low PCV and GCV values in both F_2 generations.Low variability was observed for chlorophyll stability index both in F_2generation of all the crosses for this trait (Fig. 6). The CV, PCV and GCV values were less than 10 per cent. Among the cross combinations, cross 20 of F_2 recorded higher values for variability. High variability for chlorophyll stability index was recorded by Chandra and Pradhan (2003) in rice varieties.With respect to root length, low variability was observed for all the crosses in F_2 except the crosses 5 and 29. The above said crosses recorded moderate magnitude of CV, PCV and GCV values in F_2 generations. The remaining crosses showed low variability.

The extent of variability for the trait dry root weight was high in the crosses *viz*., 5 and 21 in F_2 generation. The remaining crosses showed low variability for this trait.The trait root volume showed low variability for most of the crosses in F_2 generations. The variability was high only in the crosses of 28 and 10 of F_2 generation. Padmaja *et al*. (2008) also observed high variability in rice genotypes for this trait. Whereas, the moderate variability was observed in the crosses 2 and 29 in F_2 generation. (Fig. 7)

A low variability of less than 10 per cent was observed in F_2 of all the crosses for the trait number of filled grains per panicle (Fig. 3). Low variability for number of filled grains per panicle was recorded by Vanniarajan *et al.* (1996) in F_4 generation and Abdus Salam Khan *et al.* (2009) in rice genotypes. Whereas, moderate variability was observed by Kole *et al*. (2008) in M_4 generation. Among the crosses studied in F_2 generation the cross 25 recorded the higher value of variability for number of filled grains per panicle. The findings of Ahmed Mustafa and Yassir Elsheik (2007) in rice genotypes revealed high variability for number of filled grains per panicle.

Grain yield per plant showed low variability in F_2 of all crosses as indicated by low CV, PCV and GCV values (Fig. 8).The CV, PCV and GCV values were less than 10 per cent. Among the cross combinations, the cross 18 in F_2 showed higher values for this trait. High variability for this trait was already reported by Ahmed Mustafa and Yassir Elsheik (2007) in rice genotypes, Chandra and Pradhan (2003) and Shukla Vivek *et al*., (2005) in rice varieties.

Heritability and genetic advance

The genotypic coefficient of variation alone is not sufficient for the determination of the amount of heritable variation. According to Singh *et al*. (1974), the genes cannot cause the character to develop unless they have the proper environment for expression and conversely no amount of manipulation of the environment will cause a characteristic to develop unless the necessary genes are present. Neverthless, it must be recognized that variability observed in some character is caused primarily by the difference in the genes carried by the different individual and the variability in other character is due to primary difference in the environment to which individuals have been exposed. The heritability estimate gives information on the extent to which available variation is heritable. The importance of heritability in addition to the mean performance and variability was stressed by Panse (1957).

When the character is highly heritable, the phenotype reflects the genotype very strongly. Genetic advance is an improvement in the mean genotypic value in the selected families over base population. Therefore the combination of mean, variability, heritability and genetic advance will be useful to make an efficient selection (Sivasubramanian and Madhava Menon, 1973). Johnson *et al.*, (1955) suggested that the use of heritability coupled with genetic advance in formulating evaluation suitable for selection procedures.

High heritability along with high genetic advance would indicate an additive gene action in the expression of characters (Johnson *et al.*, 1955). While high heritability with low genetic advance implied a non-additive gene action (Panse, 1957). Heritability denotes the additive genetic variance as per cent of the total variance. The additive portion of the genetic variance reflects degree to which the progenies are likely to resemble the parents (Wright, 1921).

High value of genetic advance as percent of mean together with high heritability for character indicates additive gene action and selection will be rewarding, while as high heritability along with low genetic advance indicating presence of non additive gene action, which epistasis, dominance and genotypic and environment interaction (Tikka *et al.*, 1977). Hence response to selection would be poorer.

In the present study, the estimate of heritability was high in most of the crosses for plant height in F_2 while, the genetic advance as per cent of mean was low in all the crosses of F_2generation except the crosses 7 and 28 in F_2which registered high heritability coupled with moderate genetic gain. This showed that selection criteria might be specific to a particular crosses and could not be generalized (Chauhan and Chauhan, 1994). These results are in accordance with the earlier findings of Sanjeev Kumar *et al*. (2005) and Sumathi *et al*. (2007) for high heritability along with high genetic advance; Pattanayk *et al*. (2004) for moderate heritability, Monalisa *et al*. (2006) for low genetic advance as per cent of mean.

In respect of productive tillers per plant high heritability with high GA as per cent of mean was recorded by the crosses 5, 4, 17, 27, 29 and 30 in F_2 generation. These results were in accordance with the earlier findings of Sao and Motiramani (2004), Deepa Sankar *et al*. (2006), Thirugnana Kumar *et al*. (2007) and Sumathi *et al*. (2007). High heritability coupled with high genetic advance as per cent of mean was observed for the trait number of productive tillers per plant. The aforesaid points revealed the additive gene involvement and showed the possibility of selection per se in these crosses for the improvement of productive tillers per plant. Such a possibility also exists in the crosses 1, 7, 18, 19 and 25 in F_2 since these crosses recorded high heritability with moderate GA as percent of mean.

For the trait panicle length, high heritability coupled with high genetic advance as percent of mean was recorded by the crosses 3, 17 and 29 in F_2 generation. Moderate GA with high heritability was noticed in the crosses 1, 26, and 27 in F_2 generation. These are in conformity with the findings of Pattanayk *et al*. (2004), Deepa Sankar *et al*. (2006) and Bharadwaj *et al*. (2007).

In the present study, high heritability combined with low GA as per cent of mean was recorded for number of filled grains per panicle in most of the crosses of F_2generation (Table 5). Whereas, the cross 25 of F_2 registered high heritability coupled with moderate genetic advance as per cent of mean. Mass selection procedure can be used to improve this trait (Sathish *et al*. 2004).

The findings of Sao and Motiramani (2004), Sanjeev Kumar *et al*. (2005) and Bharadwaj *et al*. (2007) revealed high heritability along with high genetic advance as per cent of mean which is similar to the present findings. Out of 30 crosses studied in the F_2 generation eight crosses (2, 4, 9, 24, 26, 27, 28 and 29) showed high values of heritability and genetic gain for 100 grain weight (Table 6). High heritability with moderate genetic gain was recorded by the crosses 12, 17 and 18 of F_2 generation.

Moderate to high magnitude of heritability with low genetic advance as per cent of mean was recorded by all crosses for spikelet fertility in F_2 except the crosses 8 and 17 which showed low heritability with low genetic advance as per cent of mean (Table 7).High heritability coupled with low genetic advance as per cent of mean was observed for days to 70% relative water content in all the crosses of F_2 except the crosses *viz.*, 2, 5, 6, 7, 12, 16, 18, 20, 25, 28 and 30 (Table 8). These results are in accordance with the findings of Chandra and Pradhan (2003) in rice varieties.

With regard to leaf rolling high heritability with high genetic advance as per cent of mean was recorded in the crosses *viz.*, cross 1, 4, 7, 9, 15, 24, 25, 26, 27, 29 and 30, in F_2 generation(Table 9). Moderate heritability coupled with moderate genetic gain was observed in the crosses 22, 23, 28, 17 and 13 in the above said generation. Padmaja *et al*. (2008) has already reported high variability for this trait in rice genotypes.

In general, the present study revealed that, the trait leaf drying showed moderate to high heritability coupled with moderate to high genetic advance for all the crosses in F_2 generation except the crosses 8 and 21 (Table 10). High values of heritability combined with high genetic advance was observed in F_2 generation for all the crosses.

With regard to chlorophyll stability index moderate heritability combined with low genetic advance was recorded in most of the crosses of F_2 generation (Table 11). But some crosses in F_2 (cross 1, 4, 5, 9, 10, 12, 21, 23, 24, 25, 26 and 27) registered high heritability with low genetic advance as per cent of mean for this

trait.This was in conformity with the earlier findings of Abd Allah (2009) for chlorophyll stability index, dry root weight, root and shoot ratio and root length.

The crosses 5 and 25 of F_2 showed high heritability coupled with high genetic advance as per cent of mean for root length (Table 12). Whereas in most of the crosses of F_2 the trend noticed for heritability and genetic advance was moderate to high heritability with low to moderate GA as per cent of mean. Abd Allah (2009) reported similar trend of high variability for root length and dry root weight.

The results of the present investigation indicated that the characters dry root weight had high heritability coupled with high genetic advance in all the crosses in F_2generation except the crosses 2, 6, 8, 9, 10, 11, 13, 14, 15, 16, 20, 22, 26 and 27 of F_2 (Table 13). The above said crosses showed low to moderate magnitude of heritability with genetic advance as per cent of mean.

For the trait root volume, the crosses *viz*., 10, 28, 29 and 30 of F_2 generation exhibited high heritability combined with high GA as per cent of mean (Table 14). In F_2, all the crosses showed moderate to high heritability except the crosses 6 and 12, which had low heritability.In light of the above, for the trait grain yield per plant, the crosses 28 and 30 of F_2 showed high heritability with moderate genetic advance. None of the crosses in F_2 had high magnitude of GA as per cent of mean(Table 15 to 17). Hence, while selection the weight-age may be given for the above said crosses (28 and 30) for the overall improvement of yield in rice.

IV. CONCLUSION

In the present study the estimates of heritability were found with an increasing trend for the traits productive tillers per plant, panicle length, 100 grain weight, leaf rolling, root length, dry root weight and grain yield per plant. Among the traits studied productive tillers per plant (IR 73328A x IR 69726); panicle length (IR 79128A x BI 33); 100 grain weight (IR 79156A x IR 79200); leaf rolling (IR 79156A x IR 79200); root length (IR 79156A x IR 79200); dry root weight (IR 79128A x KMP 105); grain yield per plant (IR 79156A x IR 05N496) had high heritability coupled with high genetic advance as percent of mean in F_2 generation. High heritability along with high genetic advance would indicate an additive gene action in the expression of the above characters.When mean, genotypic variability, heritability and genetic advance were taken as the selection criteria, the selection will be effective in COMS 14A x IR 80286, COMS 24A x IR 79200, IR 73328A x IR 80402, IR 79128A x IR 79200 as these crosses exhibited higher mean value and high heritability along with high genetic advance for yield and its attributing traits.

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Table 2. Range, mean and variability parameters for plant height in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	83.64-135.69	89.20	1.82	2.06	1.90	1.61	1.55	92.3	2.73	3.06
Cross 2	81.43-127.43	86.70	1.24	0.94	0.06	1.12	0.28	6.22	0.13	0.14
Cross 3	80.47-122.17	93.40	1.07	1.49	1.06	1.31	1.10	71.20	1.79	1.92
Cross 4	81.60-124.49	94.30	2.14	0.60	0.41	0.82	0.68	68.52	1.08	1.16
Cross 5	85.11-112.47	97.00	2.03	4.92	4.08	2.29	2.08	82.86	3.79	3.90
Cross 6	82.60-111.60	104.05	1.44	0.02	0.00	0.12	0.06	25.00	0.07	0.06
Cross 7	79.08-112.78	98.20	9.29	1.18	77.84	11.07	8.98	65.87	14.75	15.02
Cross 8	82.37-120.55	88.40	1.69	1.66	0.22	1.46	0.53	13.19	0.35	0.40
Cross 9	84.00-115.33	103.65	1.27	1.69	0.00	1.25	0.04	0.12	0.00	0.00
Cross10	96.77-128.80	112.00	0.72	0.95	0.79	0.87	0.79	83.16	1.67	1.49
Cross11	86.67-106.40	95.20	2.38	3.51	3.35	1.97	1.92	95.33	3.68	3.87
Cross12	88.97-110.53	96.05	1.32	2.23	1.38	1.55	1.22	61.65	1.90	1.97
Cross13	95.40-125.03	102.00	0.81	0.82	0.67	0.89	0.80	81.52	1.53	1.49
Cross14	83.02-125.06	98.55	1.83	4.85	4.76	2.23	2.21	98.15	4.45	4.52
Cross15	80.59-110.96	104.00	2.74	5.29	3.71	2.21	1.85	70.04	3.32	3.19

Cross16	87.67-126.79	97.10	2.18	6.09	1.26	2.54	1.15	20.62	1.05	1.08
Cross17	86.44-117.64	100.85	3.84	22.46	7.25	4.70	2.67	32.28	3.15	3.13
Cross18	85.54-118.51	90.00	1.31	2.07	0.49	1.60	0.78	23.50	0.70	0.77
Cross19	83.09-115.27	87.00	0.68	0.47	0.17	0.79	0.47	34.99	0.49	0.57
Cross20	82.13-116.14	91.30	1.11	0.03	0.00	0.2	0.05	5.88	0.02	0.02
Cross21	84.58-112.76	93.80	2.09	2.93	2.84	1.82	1.80	96.93	3.42	3.64
Cross22	95.65-121.33	114.25	2.44	11.6	0.65	2.98	0.70	5.57	0.39	0.34
Cross23	95.69-122.40	116.40	1.99	5.48	4.77	2.01	1.88	87.16	4.2	3.61
Cross24	93.86-113.80	99.75	2.54	9.32	3.07	3.06	1.76	32.94	2.07	2.08
Cross25	74.81-98.42	99.40	10.39	29.82	3.82	5.49	1.97	12.8	1.44	1.45
Cross26	92.87-130.63	121.87	4.03	33.63	14.53	4.76	3.13	43.21	5.16	4.24
Cross27	74.88-99.13	102.20	6.69	13.59	13.24	3.61	3.56	97.39	7.4	7.24
Cross28	84.54-106.29	106.30	7.6	95.19	84.37	9.18	8.64	88.63	17.81	16.76
Cross29	89.39-110.19	103.65	5.09	8.31	5.38	2.78	2.24	64.78	3.85	3.71
Cross30	88.53-107.64	109.35	6.56	9.27	9.26	2.78	2.78	99.92	6.27	5.73

CV : Coefficient of variation
PV : Phenotypic variance
GV : Genotypic variance
PCV : Phenotypic Coefficient of variation
GCV : Genotypic Coefficient of variation
H : Heritability
GA : Genetic Advance
GAM : Genetic Advance as per cent of Mean

Table 3. Range, mean and variability parameters for productive tillers/plant in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	12.77-28.20	13.96	4.85	0.68	0.66	5.91	5.84	97.54	1.66	11.88
Cross 2	15.28-27.56	17.43	5.82	1.54	0.83	7.12	5.24	54.14	1.38	7.94
Cross 3	10.62-23.74	15.86	1.99	0.15	0.08	2.41	1.83	57.32	0.45	2.85
Cross 4	9.80-23.47	11.00	14.55	3.37	3.37	16.69	16.68	99.96	3.78	34.36
Cross 5	15.63-30.98	20.45	14.41	11.24	7.3	16.39	13.21	64.93	4.48	21.93
Cross 6	16.13-27.43	21.10	5.34	1.88	0.9	6.51	4.51	47.99	1.36	6.43
Cross 7	14.55-22.44	16.05	8.72	2.52	2.17	9.89	9.17	85.95	2.81	17.51
Cross 8	11.43-24.01	13.15	8.68	1.96	0.72	10.64	6.43	36.52	1.05	8.01
Cross 9	14.88-28.39	16.65	5.35	1.18	0.4	6.52	3.78	33.6	0.75	4.51
Cross10	13.39-24.47	21.80	5.70	2.28	0.94	6.92	4.46	41.43	1.29	5.91
Cross11	11.24-21.45	12.25	3.10	0.18	0.15	3.51	3.12	79.40	0.70	5.73
Cross12	12.32-21.40	14.05	7.64	1.72	0.63	9.35	5.66	36.67	0.99	7.06
Cross13	14.43-29.44	15.95	4.17	0.66	0.15	5.08	2.39	22.09	0.37	2.31
Cross14	14.50-23.50	21.20	4.53	1.35	0.50	5.48	3.34	37.21	0.89	4.20
Cross15	16.35-29.09	17.10	11.45	4.39	0.13	12.25	2.07	2.86	0.12	0.72
Cross16	16.10-23.48	17.55	5.42	1.34	0.53	6.6	4.16	39.72	0.95	5.40
Cross17	18.25-27.71	19.25	15.25	8.31	6.63	14.97	13.38	79.82	4.74	24.62
Cross18	8.66-19.46	10.90	14.47	3.72	1.44	17.69	11.00	38.65	1.54	14.08
Cross19	6.59-17.05	8.15	11.87	1.40	0.55	14.52	9.06	38.92	0.95	11.64
Cross20	13.00-22.27	14.10	9.31	0.51	0.47	5.09	4.84	90.58	1.34	9.49
Cross21	12.99-25.18	14.45	4.86	0.72	0.37	5.85	4.19	51.3	0.89	6.18
Cross22	16.65-27.28	19.10	7.26	2.88	1.08	8.88	5.45	37.62	1.32	6.88
Cross23	15.34-29.09	17.85	8.31	3.31	1.23	10.19	6.22	37.26	1.40	7.82
Cross24	15.71-22.06	19.95	6.74	2.65	0.49	8.16	3.49	18.36	0.62	3.08
Cross25	13.65-16.89	14.95	13.53	2.17	1.92	9.84	9.26	88.45	2.68	17.93
Cross26	15.80-26.47	15.99	7.48	0.72	0.27	5.32	3.23	36.98	0.65	4.05
Cross27	6.24-14.52	7.90	16.21	1.95	1.81	17.69	17.03	92.61	2.67	33.76
Cross28	15.33-21.80	17.05	5.32	1.23	0.38	6.50	3.63	31.16	0.71	4.17
Cross29	9.10-14.25	11.44	16.12	5.01	3.31	19.57	15.90	66.03	3.05	26.61
Cross30	14.12-24.61	13.64	21.56	3.54	3.25	13.79	13.22	91.90	3.56	26.10

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GAM : Genetic Advance as per cent of Mean

Table 4. Range, mean and variability parameters for panicle length in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	18.67-29.92	20.21	4.93	1.47	1.42	6.00	5.89	96.42	2.41	11.92
Cross 2	18.22-25.03	23.10	3.40	0.89	0.19	4.09	1.88	21.05	0.41	1.77
Cross 3	18.42-26.29	22.81	9.46	6.88	6.81	11.5	11.44	99.02	5.35	23.45
Cross 4	13.95-26.04	19.41	5.28	1.57	0.20	6.46	2.31	12.75	0.33	1.70
Cross 5	17.15-26.77	24.55	4.28	1.64	0.71	5.22	3.44	43.35	1.15	4.66
Cross 6	18.43-25.01	21.80	2.07	0.29	0.04	2.46	0.89	13.04	0.14	0.66
Cross 7	17.22-25.14	19.65	8.53	4.18	1.39	10.40	6.00	33.27	1.40	7.13

Cross 8	14.94-27.89	18.90	2.16	0.25	0.12	2.65	1.84	48.37	0.50	2.64
Cross 9	21.69-27.39	24.94	5.03	0.18	0.05	1.72	0.91	27.77	0.25	0.98
Cross10	18.66-25.25	23.50	4.39	1.60	0.84	5.37	3.90	52.54	1.37	5.82
Cross11	16.61-25.66	18.55	4.34	0.97	0.33	5.31	3.10	34.00	0.69	3.72
Cross12	15.56-21.21	19.40	3.91	0.83	0.49	4.69	3.62	59.44	1.12	5.75
Cross13	18.49-27.09	25.55	2.86	0.80	0.40	3.50	2.47	49.63	0.92	3.58
Cross14	17.35-24.18	22.80	0.96	0.07	0.00	1.12	0.23	4.14	0.02	0.10
Cross15	19.61-28.96	21.95	5.98	2.50	1.18	7.21	4.95	47.20	1.54	7.01
Cross16	17.37-26.71	22.15	3.06	0.66	0.44	3.67	3.00	66.57	1.11	5.04
Cross17	18.24-25.88	24.64	10.92	8.18	8.02	11.61	11.49	98.00	5.78	23.44
Cross18	16.60-23.03	18.50	6.31	2.03	0.99	7.71	5.39	48.84	1.43	7.76
Cross19	14.69-25.85	21.30	3.62	0.55	0.53	3.48	3.42	96.41	1.47	6.92
Cross20	14.94-24.39	17.90	8.22	3.22	1.45	10.02	6.72	45.01	1.66	9.29
Cross21	18.43-26.27	20.28	5.72	1.35	0.47	5.74	3.38	34.70	0.83	4.10
Cross22	22.46-28.60	24.20	9.24	1.55	0.36	5.14	2.47	23.17	0.59	2.45
Cross23	21.32-29.31	23.80	5.15	2.18	1.10	6.20	4.40	50.36	1.53	6.43
Cross24	18.78-26.12	24.05	4.31	1.61	0.81	5.27	3.74	50.24	1.31	5.46
Cross25	15.88-23.60	20.80	9.64	1.44	0.84	5.78	4.40	57.89	1.43	6.89
Cross26	18.50-27.22	21.45	7.73	3.88	3.88	9.18	9.18	99.97	4.06	18.91
Cross27	15.96-20.51	17.90	6.12	1.80	1.59	7.49	7.04	88.24	2.44	13.62
Cross28	19.08-21.64	19.90	4.49	0.48	0.35	3.49	2.96	71.69	1.03	5.15
Cross29	19.78-23.67	17.70	29.55	35.84	33.71	33.82	32.8	94.05	11.6	65.53
Cross30	17.77-26.37	22.20	8.92	4.50	4.30	9.55	9.34	95.59	4.18	18.8

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Table 5. Range, mean and variability parameters for Filled grains/panicle in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	169.28-196.72	182.00	1.47	10.54	0.73	1.78	0.47	6.89	0.46	0.25
Cross 2	163.78-212.17	200.79	1.15	3.75	2.33	0.96	0.76	62.08	2.48	1.23
Cross 3	137.13-184.94	144.6	1.39	3.77	2.09	1.34	1.00	55.49	2.22	1.54
Cross 4	148.14-211.89	182.77	1.43	3.09	2.28	0.96	0.83	73.74	2.67	1.46
Cross 5	132.59-159.08	155.98	6.72	0.02	0.01	6.39	3.00	22.05	0.13	2.90
Cross 6	176.73-211.34	189.99	0.43	1.02	0.44	0.53	0.35	43.08	0.90	0.47
Cross 7	140.26-197.93	186.67	1.21	7.57	3.13	1.47	0.95	41.38	2.35	1.26
Cross 8	119.33-188.15	124.27	0.73	1.15	0.06	0.86	0.19	4.78	0.11	0.08
Cross 9	201.18-232.69	217.41	2.78	54.70	7.24	3.40	1.24	13.24	2.02	0.93
Cross10	158.24-188.73	166.49	0.50	1.01	0.04	0.60	0.12	4.25	0.09	0.05
Cross11	152.10-187.62	160.00	0.69	1.68	0.88	0.81	0.59	52.20	1.40	0.87
Cross12	156.89-178.03	171.01	0.76	2.00	1.91	0.83	0.81	95.32	2.78	1.63
Cross13	201.42-232.01	219.38	0.71	3.54	3.43	0.86	0.84	96.91	3.76	1.71
Cross14	181.03-227.76	219.38	0.73	3.84	3.35	0.89	0.83	87.37	3.53	1.61
Cross15	184.15-217.68	196.18	0.82	2.84	1.83	0.86	0.69	64.29	2.23	1.14
Cross16	156.88-189.55	166.08	0.90	3.37	2.41	1.10	0.94	71.69	2.71	1.63
Cross17	197.90-236.85	211.57	2.14	11.82	2.82	1.63	0.79	23.86	1.69	0.80
Cross18	126.47-156.20	135.93	1.13	2.47	0.68	1.16	0.61	27.53	0.89	0.66
Cross19	168.78-202.78	190.88	0.82	2.16	0.23	0.77	0.25	10.47	0.32	0.17
Cross20	87.88-105.81	91.36	0.92	0.99	0.18	1.09	0.46	17.95	0.37	0.40
Cross21	159.36-184.71	173.14	5.67	109.57	31.06	6.05	3.22	28.34	6.11	3.53
Cross22	177.75-211.32	189.00	2.59	31.89	27.11	2.99	2.75	85.01	9.89	5.23
Cross23	188.41-223.43	208.86	1.03	2.34	2.26	0.73	0.72	96.66	3.04	1.46
Cross24	179.17-199.96	188.97	1.17	7.33	6.66	1.43	1.37	90.83	5.07	2.68
Cross25	199.82-227.37	198.84	6.44	189.76	172.4	6.93	6.6	90.85	25.78	12.97
Cross26	175.06-212.17	205.63	1.08	5.55	4.56	1.15	1.04	82.25	3.99	1.94
Cross27	113.81-148.96	123.29	2.36	12.63	9.22	2.88	2.46	73.03	5.35	4.34
Cross28	113.03-137.99	121.41	1.25	0.45	0.42	0.55	0.54	93.1	1.29	1.06
Cross29	117.15-142.96	118.7	5.60	18.46	17.18	3.62	3.49	93.06	8.24	6.94
Cross30	117.15-143.58	123.76	2.76	17.09	4.02	3.34	1.62	23.5	2.00	1.62

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Table 6. Range, mean and variability parameters for 100 grain weight in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	1.37-4.64	1.49	4.34	0.01	0.01	4.95	4.53	83.48	0.15	8.52
Cross 2	1.42-3.49	2.13	22.68	0.12	0.10	16.47	15.00	82.95	0.6	28.14
Cross 3	1.05-4.43	2.24	3.25	0.01	0.01	4.00	3.58	80.02	0.14	6.60
Cross 4	1.05-5.42	2.29	31.06	0.47	0.45	29.87	29.41	96.92	1.37	59.65
Cross 5	1.11-3.56	2.06	41.82	1.11	0.03	51.22	8.64	2.84	0.06	3.00
Cross 6	1.65-3.83	1.76	3.11	0.01	0.00	3.86	2.89	56.22	0.09	4.47
Cross 7	0.96-2.36	2.39	27.93	0.66	0.35	34.00	24.81	53.26	0.89	37.31
Cross 8	1.00-3.21	1.07	3.68	0.00	0.00	4.40	4.17	89.86	0.09	8.14
Cross 9	2.48-3.03	2.30	25.63	0.52	0.40	31.18	27.35	76.91	1.14	49.41
Cross10	1.60-3.79	1.69	1.66	0.00	0.00	1.88	1.45	59.94	0.07	2.32
Cross11	1.04-3.69	2.28	4.4	0.02	0.01	5.43	3.72	47.05	0.12	5.26
Cross12	1.36-3.07	2.09	7.71	0.04	0.03	9.22	8.68	88.65	0.35	16.84
Cross13	2.30-4.71	2.51	2.58	0.01	0.00	3.04	2.59	72.34	0.11	4.53
Cross14	1.32-3.82	2.51	3.61	0.01	0.00	4.19	0.08	0.03	0.02	0.00
Cross15	1.67-3.90	2.11	20.98	0.09	0.01	13.97	3.64	6.77	0.04	1.95
Cross16	1.99-3.17	2.23	13.51	0.14	0.08	16.5	12.71	59.31	0.45	20.16
Cross17	1.19-4.53	2.11	11.20	0.03	0.02	8.54	6.77	62.76	0.23	11.05
Cross18	1.19-2.98	2.13	13.30	0.09	0.06	13.92	11.56	68.97	0.42	19.78
Cross19	1.38-2.30	2.44	28.31	0.49	0.04	28.77	8.42	8.56	0.12	5.07
Cross20	2.00-3.40	1.91	21.11	0.07	0.01	14.18	6.07	18.36	0.10	5.36
Cross21	1.23-3.89	1.98	22.75	0.31	0.10	27.86	15.8	32.15	0.37	18.45
Cross22	2.08-3.92	1.92	23.88	0.09	0.02	16.03	7.63	22.65	0.14	7.48
Cross23	1.05-4.03	2.03	33.99	0.21	0.08	22.61	14.02	38.46	0.36	17.91
Cross24	1.43-3.75	2.02	33.78	0.52	0.43	35.63	32.37	82.54	1.22	60.58
Cross25	1.25-2.03	1.83	44.62	0.96	0.44	53.41	36.12	45.74	0.92	50.33
Cross26	1.33-3.52	2.7	20.06	0.44	0.3	24.47	20.14	67.73	0.92	34.15
Cross27	1.59-3.81	2.16	19.76	0.05	0.05	10.66	10.64	99.57	0.47	21.87
Cross28	1.60-3.80	2.06	38.29	0.89	0.79	45.8	43.17	88.83	1.73	83.81
Cross29	1.59-2.80	1.75	41.89	0.21	0.13	26.1	20.58	62.2	0.58	33.44
Cross30	1.58-2.75	2.26	15.45	0.03	0.01	7.05	4.62	42.97	0.14	6.24

CV : Coefficient of variation
PV : Phenotypic variance
GV : Genotypic variance
PCV : Phenotypic Coefficient of variation
GCV : Genotypic Coefficient of variation
H : Heritability
GA : Genetic Advance
GAM : Genetic Advance as per cent of Mean

Table 7. Range, mean and variability parameters for Spikelet fertility in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	81.34-93.46	86.25	1.3	1.76	1.46	1.54	1.4	82.5	2.26	2.62
Cross 2	72.41-97.25	90.83	1.25	1.83	0.55	1.49	0.82	30.05	0.84	0.92
Cross 3	74.74-92.06	80.43	1.29	0.69	0.37	1.03	0.76	54.11	0.93	1.15
Cross 4	73.87-90.77	86.65	1.27	1.22	1.13	1.27	1.22	92.61	2.1	2.43
Cross 5	74.29-91.89	82.92	0.92	0.54	0.33	0.88	0.7	62.41	0.94	1.13
Cross 6	72.14-94.28	93.75	2.04	2.06	1.71	1.53	1.39	83.1	2.46	2.62
Cross 7	76.56-95.36	90.12	2.19	3.25	1.03	2.00	1.13	31.63	1.18	1.30
Cross 8	69.33-83.72	75.84	1.7	2.48	0.02	2.08	0.16	0.63	0.02	0.03
Cross 9	85.03-95.40	89.45	0.82	0.29	0.29	0.60	0.60	97.99	1.09	1.22
Cross10	63.02-96.29	89.82	1.66	1.23	1.08	1.23	1.16	88.23	2.01	2.24
Cross11	67.12-94.93	86.42	1.95	2.73	0.54	1.91	0.85	19.8	0.67	0.78
Cross12	62.69-91.28	92.55	2.15	0.31	0.29	0.61	0.58	92.55	1.07	1.16
Cross13	76.09-94.43	91.34	0.6	0.45	0.43	0.73	0.71	95.61	1.32	1.44
Cross14	68.72-92.94	91.34	0.42	0.15	0.09	0.43	0.33	58.97	0.48	0.52
Cross15	86.42-97.42	91.69	1.89	4.01	3.84	2.18	2.14	95.71	3.95	4.31
Cross16	64.43-79.02	76.85	1.86	2.71	1.19	2.14	1.42	43.84	1.49	1.94
Cross17	80.70-96.28	96.27	1.09	1.67	0.16	1.34	0.41	9.50	0.25	0.26
Cross18	59.47-72.43	77.81	1.24	1.07	0.60	1.33	1.00	56.74	1.21	1.55
Cross19	64.09-89.92	84.71	1.17	1.39	0.77	1.39	1.03	55.01	1.34	1.58
Cross20	67.22-88.72	72.81	0.79	0.4	0.17	0.87	0.57	43.00	0.56	0.77
Cross21	71.32-89.04	72.90	1.83	2.66	1.43	2.24	1.64	53.81	1.81	2.48
Cross22	81.58-97.76	83.15	2.9	8.72	2.17	3.55	1.77	24.87	1.51	1.82
Cross23	82.99-99.48	91.99	1.51	1.94	1.94	1.52	1.51	99.80	2.87	3.12
Cross24	71.15-92.35	85.01	2.88	8.86	7.86	3.5	3.30	88.70	5.44	6.40
Cross25	64.38-83.61	83.6	9.21	78.83	18.69	10.62	5.17	23.71	4.34	5.19
Cross26	76.79-99.06	92.21	1.16	1.52	1.43	1.34	1.30	94.10	2.39	2.59
Cross27	54.10-76.38	72.10	2.84	6.21	3.13	3.46	2.45	50.40	2.59	3.59
Cross28	56.85-75.21	71.98	1.74	2.15	1.27	2.04	1.56	58.8	1.78	2.47

Cross29	64.44-74.08	70.12	6.49	30.85	15.25	7.92	5.57	49.43	5.66	8.07
Cross30	61.70-76.86	74.15	1.87	0.42	0.15	0.88	0.52	35.33	0.47	0.64

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GAM : Genetic Advance as per cent of Mean

Table 8. Range, mean and variability parameters for Days to 70% RWC in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	88.16-99.70	95.49	1.77	3.37	2.45	1.92	1.64	72.72	2.75	2.88
Cross 2	64.28-92.88	85.65	3.02	9.96	4.36	3.68	2.44	43.8	2.85	3.32
Cross 3	80.90-93.07	87.06	2.33	4.94	4.48	2.55	2.43	90.64	4.15	4.77
Cross 4	79.98-90.75	86.20	0.75	0.62	0.46	0.91	0.79	74.17	1.20	1.40
Cross 5	80.87-93.90	90.50	1.39	1.18	0.95	1.20	1.07	80.55	1.80	1.99
Cross 6	81.20-92.26	87.6	2.16	3.73	1.94	2.20	1.59	51.94	2.07	2.36
Cross 7	78.89-91.38	84.73	2.76	7.82	3.94	3.3	2.34	50.4	2.90	3.43
Cross 8	81.53-90.98	87.93	1.70	3.32	2.39	2.07	1.76	72.14	2.71	3.08
Cross 9	85.21-96.52	90.37	1.83	3.37	1.78	2.03	1.48	52.84	2.00	2.21
Cross10	68.21-91.49	83.92	1.75	2.66	1.79	1.94	1.6	67.45	2.27	2.70
Cross11	81.32-95.47	89.76	1.60	3.08	0.82	1.96	1.01	26.49	0.96	1.07
Cross12	81.05-97.22	95.32	1.89	4.16	1.88	2.14	1.44	45.22	1.90	1.99
Cross13	82.64-95.86	92.11	0.63	0.35	0.32	0.64	0.62	93.26	1.13	1.23
Cross14	81.96-97.76	92.11	1.97	2.93	2.86	1.86	1.84	97.47	3.44	3.73
Cross15	80.51-95.60	83.49	0.99	0.81	0.78	1.08	1.06	96.61	1.79	2.14
Cross16	80.12-91.88	85.76	1.09	1.31	0.33	1.33	0.67	24.83	0.59	0.68
Cross17	82.49-98.69	95.26	2.43	1.27	1.28	1.18	1.19	99.99	2.34	2.45
Cross18	81.59-92.65	90.34	1.33	1.17	0.53	1.20	0.80	45.06	1.00	1.11
Cross19	81.77-97.25	94.91	2.25	6.61	4.25	2.71	2.17	64.28	3.40	3.59
Cross20	81.26-93.50	83.73	0.73	0.56	0.22	0.89	0.56	39.89	0.61	0.73
Cross21	83.80-96.43	89.60	2.07	4.52	3.71	2.37	2.15	82.04	3.60	4.01
Cross22	81.24-95.88	86.13	1.46	2.35	1.53	1.78	1.44	65.21	2.06	2.39
Cross23	80.15-95.86	90.74	1.34	2.2	1.88	1.64	1.51	85.28	2.61	2.87
Cross24	80.34-92.80	84.22	3.48	12.82	9.93	4.25	3.74	77.45	5.71	6.78
Cross25	80.58-96.25	85.8	3.5	13.49	7.03	4.28	3.09	52.15	3.95	4.6
Cross26	82.79-99.66	93.59	2.38	7.02	4.40	2.83	2.24	62.68	3.42	3.66
Cross27	81.93-92.09	88.46	1.57	2.34	2.28	1.73	1.71	97.41	3.07	3.47
Cross28	80.12-92.86	85.00	3.05	9.33	4.66	3.59	2.54	49.99	3.15	3.70
Cross29	81.03-92.18	83.7	2.87	1.7	1.61	1.56	1.51	94.38	2.54	3.03
Cross30	80.27-93.65	92.2	1.79	3.94	2.07	2.15	1.56	52.48	2.15	2.33

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Table 9. Range, mean and variability parameters for Leaf rolling in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	3.08-8.08	4.13	26.4	1.76	1.7	32.15	31.62	96.72	2.64	64.06
Cross 2	1.34-5.40	5.37	12.58	0.19	0.19	8.17	8.15	99.54	0.9	16.76
Cross 3	1.94-7.87	4.86	12.54	0.56	0.29	15.38	11.04	51.57	0.79	16.34
Cross 4	1.67-5.67	2.56	39.97	1.44	0.87	46.94	36.36	60.00	1.49	58.02
Cross 5	2.48-6.01	5.28	24.59	1.21	0.24	20.83	9.29	19.89	0.45	8.54
Cross 6	2.17-9.87	8.30	9.23	0.87	0.38	11.25	7.45	43.82	0.84	10.16
Cross 7	0.75-5.25	2.50	54.89	2.34	2.28	61.22	60.4	97.33	3.07	122.75
Cross 8	1.07-4.19	3.60	8.83	0.15	0.05	10.73	6.41	35.63	0.28	7.88
Cross 9	4.03-7.87	5.90	23.98	3.01	1.19	29.42	18.49	39.5	1.41	23.94
Cross10	0.76-5.47	1.10	23.28	0.10	0.04	28.38	18.74	43.6	0.28	25.50
Cross11	3.44-8.32	6.10	6.69	0.25	0.10	8.14	5.23	41.37	0.42	6.93
Cross12	4.02-9.79	8.65	10.00	1.01	0.19	11.61	5.04	18.83	0.39	4.50
Cross13	3.23-5.50	4.80	17.28	0.18	0.11	8.89	6.89	59.99	0.53	10.99
Cross14	0.75-6.23	1.00	16.72	0.04	0.02	20.45	13.38	42.83	0.18	18.04
Cross15	3.35-8.93	7.70	25.55	3.75	3.46	25.17	24.15	92.09	3.68	47.74
Cross16	1.54-5.34	5.00	3.18	0.04	0.02	3.88	2.47	40.32	0.16	3.23
Cross17	1.09-5.80	3.25	28.98	1.2	0.45	33.73	20.69	37.63	0.85	26.15
Cross18	2.35-6.04	4.62	9.87	0.03	0.00	3.79	0.90	5.70	0.02	0.44
Cross19	1.15-6.87	4.11	22.64	1.23	0.35	26.94	14.41	28.61	0.65	15.88
Cross20	3.12-8.72	7.30	10.02	0.8	0.20	12.23	6.18	25.56	0.47	6.44

Cross21	2.82-9.37	8.35	8.93	0.75	0.10	10.39	3.86	13.81	0.25	2.95
Cross22	2.87-5.40	4.10	16.87	0.17	0.08	9.97	7.02	49.66	0.42	10.2
Cross23	1.15-6.25	2.30	29.79	0.16	0.08	17.58	12.46	50.21	0.42	18.18
Cross24	3.52-6.94	2.70	32.56	1.16	1.08	39.85	38.52	93.45	2.07	76.71
Cross25	2.94-6.71	4.80	32.01	1.56	1.35	26.05	24.18	86.15	2.22	46.23
Cross26	3.50-7.66	6.00	19.55	1.49	1.47	20.37	20.17	98.07	2.47	41.15
Cross27	2.26-6.17	4.10	37.15	2.9	2.9	41.56	41.56	99.99	3.51	85.62
Cross28	4.15-7.26	6.95	21.91	3.37	1.21	26.41	15.82	35.88	1.36	19.53
Cross29	3.28-7.12	6.35	26.38	3.47	3.09	29.35	27.68	88.92	3.41	53.77
Cross30	2.68-9.47	8.10	14.31	1.59	1.30	15.57	14.07	81.67	2.12	26.20

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Table 10. Range, mean and variability parameters for Leaf drying in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	0.94-4.64	2.70	72.82	5.78	5.78	89.21	89.2	99.98	4.95	183.75
Cross 2	0.68-7.84	1.91	28.63	0.34	0.09	30.65	15.95	27.07	0.33	17.09
Cross 3	0.88-6.68	3.67	84.64	14.47	14.47	103.66	103.65	99.99	7.84	213.52
Cross 4	1.78-6.68	5.16	26.87	2.88	2.88	32.91	32.87	99.78	3.49	67.64
Cross 5	1.74-4.06	2.80	30.00	1.05	0.36	36.64	21.54	34.55	0.73	26.08
Cross 6	0.58-3.72	0.90	27.64	0.09	0.04	33.56	21.76	42.03	0.26	29.06
Cross 7	1.92-6.72	2.76	65.88	4.49	1.20	76.85	39.68	26.65	1.16	42.20
Cross 8	2.24-5.51	4.90	8.54	0.26	0.09	10.45	5.98	32.74	0.35	7.05
Cross 9	0.57-4.63	2.56	26.39	0.66	0.43	31.64	25.48	64.88	1.08	42.28
Cross10	0.52-7.21	2.76	97.05	10.3	10.13	116.49	115.53	98.37	6.5	236.05
Cross11	0.57-6.06	3.10	67.49	6.57	2.49	82.69	50.9	37.9	2.00	64.55
Cross12	0.77-5.49	1.68	32.6	0.44	0.21	39.40	27.4	48.35	0.66	39.24
Cross13	1.14-2.12	1.60	20.38	0.16	0.07	24.91	16.07	41.61	0.34	21.35
Cross14	0.38-4.25	0.80	41.15	0.16	0.07	50.51	32.39	41.13	0.34	42.8
Cross15	0.38-6.25	2.51	74.84	2.36	0.55	61.12	29.49	23.28	0.74	29.31
Cross16	2.29-6.53	3.71	43.04	3.57	3.14	51.01	47.8	87.8	3.42	92.27
Cross17	1.72-6.95	4.10	47.16	5.61	2.09	57.8	35.3	37.31	1.82	44.42
Cross18	3.13-7.57	5.11	17.75	1.15	0.95	21.03	19.09	82.43	1.82	35.71
Cross19	2.94-7.04	5.90	12.74	0.85	0.31	15.61	9.41	36.29	0.69	11.67
Cross20	1.96-5.96	2.90	25.95	0.85	0.33	31.79	19.67	38.27	0.73	25.06
Cross21	0.19-6.42	1.88	37.38	0.07	0.01	13.87	5.42	15.3	0.08	4.37
Cross22	1.95-7.61	3.45	30.45	1.56	0.68	36.17	23.93	43.77	1.12	32.61
Cross23	0.58-4.81	1.75	37.94	0.54	0.50	41.85	40.57	93.96	1.42	81.01
Cross24	0.19-6.54	3.05	47.20	3.02	1.91	56.93	45.35	63.44	2.27	74.4
Cross25	0.75-5.65	3.35	46.17	3.46	1.63	55.49	38.02	46.94	1.8	53.66
Cross26	2.26-8.39	2.45	32.37	0.90	0.52	38.73	29.32	57.30	1.12	45.71
Cross27	2.15-7.32	2.95	36.52	0.59	0.58	26.00	25.78	98.30	1.55	52.65
Cross28	1.35-5.06	2.25	34.51	0.50	0.22	31.48	20.88	44.01	0.64	28.54
Cross29	3.64-5.18	3.23	28.72	0.18	0.15	13.04	11.93	83.66	0.73	22.48
Cross30	1.72-6.30	1.91	39.61	0.16	0.16	20.87	20.7	98.42	0.81	42.31

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Table 11. Range, mean and variability parameters for Chlorophyll stability index in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	90.09-99.78	95.87	1.66	3.33	2.7	1.9	1.71	81.10	3.05	3.18
Cross 2	72.12-94.76	84.31	1.34	1.91	1.00	1.64	1.19	52.25	1.49	1.76
Cross 3	71.47-98.29	92	4.11	21.38	6.98	5.03	2.87	32.63	3.11	3.38
Cross 4	71.08-94.77	90.31	0.97	0.15	0.14	0.43	0.41	93.38	0.74	0.82
Cross 5	78.76-96.04	83.91	1.27	0.41	0.34	0.76	0.70	83.69	1.10	1.31
Cross 6	70.46-94.37	93.38	2.48	8.02	1.72	3.03	1.40	21.46	1.25	1.34
Cross 7	71.30-91.78	75.21	1.34	1.48	0.22	1.62	0.62	14.47	0.36	0.48
Cross 8	81.15-96.37	92.34	1.9	4.53	0.49	2.3	0.76	10.82	0.47	0.51
Cross 9	85.64-96.77	88.52	2.2	2.15	2.02	1.65	1.60	93.99	2.84	3.20
Cross10	75.88-97.77	93.54	0.76	0.72	0.66	0.91	0.87	91.85	1.60	1.71
Cross11	72.60-94.08	87.91	2.22	5.58	0.38	2.69	0.70	6.74	0.33	0.37
Cross12	71.48-93.87	88.54	1.70	3.40	2.09	2.08	1.63	61.49	2.34	2.64

Cross13	75.59-94.30	88.09	2.88	9.44	2.68	3.49	1.86	28.38	1.80	2.04
Cross14	72.34-96.75	93.51	1.68	3.08	0.26	1.88	0.55	8.42	0.31	0.33
Cross15	71.97-95.35	81.85	2.69	7.04	0.61	3.24	0.95	8.66	0.47	0.58
Cross16	71.48-96.42	92.04	1.42	2.41	1.13	1.69	1.15	46.75	1.49	1.62
Cross17	72.69-93.84	85.06	5.61	34.09	15.34	6.86	4.60	45.00	5.41	6.36
Cross18	75.63-93.05	91.92	2.66	8.94	2.48	3.25	1.71	27.8	1.71	0.28
Cross19	73.07-98.40	93.35	1.26	2.03	0.85	1.52	0.99	41.95	1.23	1.32
Cross20	71.84-92.14	92.66	5.85	44.04	19.64	7.16	4.78	44.59	6.10	6.58
Cross21	73.46-96.20	80.02	2.77	7.22	5.31	3.36	2.88	73.62	4.07	5.09
Cross22	72.58-98.92	90.01	4.31	22.52	11.83	5.27	3.82	52.53	5.14	5.70
Cross23	83.23-96.74	90.05	1.01	2.21	2.20	1.65	1.65	99.91	3.06	3.39
Cross24	78.25-97.68	88.92	2.88	9.67	6.33	3.5	2.83	65.39	4.19	4.71
Cross25	74.56-85.91	83.13	2.94	7.92	7.88	3.39	3.38	99.46	5.77	6.94
Cross26	72.28-94.95	84.78	4.31	19.75	13.2	5.24	4.29	66.82	6.12	7.22
Cross27	77.83-92.73	83.32	3.35	11.23	6.88	4.02	3.15	61.27	4.23	5.08
Cross28	79.91-93.02	13.05	3.49	13.05	3.92	4.22	2.32	30.07	2.24	2.62
Cross29	77.62-86.31	73.23	4.94	5.51	2.56	3.21	2.18	46.42	2.25	3.07
Cross30	77.50-81.70	74.18	3.61	10.44	4.77	4.36	2.95	45.75	3.04	4.10

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PV : Phenotypic variance
GV : Genotypic variance
PCV : Phenotypic Coefficient of variation
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H : Heritability
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GAM : Genetic Advance as per cent of Mean

Table 12. Range, mean and variability parameters for Root length in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	17.43-27.05	18.23	1.58	0.12	0.00	1.86	0.33	3.06	0.02	0.12
Cross 2	15.32-24.17	22.53	3.13	0.73	0.71	3.79	3.74	97.32	1.71	7.6
Cross 3	15.31-24.69	22.26	3.23	0.78	0.38	3.97	2.75	48.21	0.88	3.94
Cross 4	17.36-26.81	27.05	2.49	0.66	0.65	2.99	2.97	98.51	1.64	6.07
Cross 5	17.81-28.48	24.47	9.36	7.24	7.12	11.00	10.91	98.31	5.45	22.27
Cross 6	11.55-27.18	28.65	0.58	0.04	0.01	0.70	0.27	14.80	0.06	0.21
Cross 7	16.69-24.58	19.67	16.53	5.91	0.29	12.36	2.75	4.93	0.25	1.26
Cross 8	18.15-25.48	24.08	1.67	0.22	0.14	1.93	1.57	66.27	0.63	2.64
Cross 9	22.58-26.82	22.85	10.45	3.41	0.61	8.08	3.41	17.80	0.68	2.96
Cross10	15.93-24.38	19.67	1.37	0.10	0.01	1.60	0.49	9.45	0.06	0.31
Cross11	15.60-21.02	17.82	3.76	0.67	0.16	4.61	2.21	23.01	0.39	2.18
Cross12	19.11-28.79	19.85	9.11	4.91	2.44	11.16	7.87	49.75	2.27	11.43
Cross13	17.85-28.23	18.82	2.89	0.44	0.03	3.51	0.86	6.03	0.08	0.44
Cross14	16.49-27.77	23.03	1.02	0.08	0.02	1.25	0.61	24.15	0.14	0.62
Cross15	18.49-29.77	19.25	7.19	2.69	0.16	8.52	2.10	6.09	0.21	1.07
Cross16	18.64-24.64	26.22	2.36	0.51	0.41	2.71	2.43	80.40	1.18	4.49
Cross17	18.74-27.77	19.67	5.08	0.48	0.14	3.52	1.88	28.60	0.41	2.07
Cross18	17.31-25.47	19.31	5.26	1.26	1.19	5.82	5.64	94.01	2.18	11.27
Cross19	17.92-27.67	24.45	3.29	0.96	0.38	4.01	2.50	39.04	0.79	3.22
Cross20	15.08-26.42	20.61	4.62	1.02	0.8	4.90	4.34	78.39	1.63	7.92
Cross21	14.95-26.40	17.68	9.99	4.66	2.47	12.21	8.89	52.99	2.36	13.33
Cross22	17.68-29.51	18.75	7.34	2.66	0.42	8.70	3.47	15.9	0.53	2.85
Cross23	19.98-27.64	20.75	4.57	1.21	0.09	5.30	1.43	7.28	0.17	0.80
Cross24	18.84-28.79	19.18	7.56	2.46	2.23	8.17	7.79	90.81	2.93	15.29
Cross25	16.72-20.97	16.31	18.13	10.82	10.52	20.18	19.89	97.21	6.59	40.4
Cross26	18.94-29.67	20.85	5.34	1.86	1.39	6.55	5.66	74.81	2.10	10.09
Cross27	13.92-21.97	20.98	4.57	0.52	0.52	3.44	3.43	99.48	1.48	7.05
Cross28	18.00-24.16	20.88	6.32	1.99	1.91	6.75	6.62	96.19	2.79	13.38
Cross29	16.53-22.70	19.17	13.79	10.03	5.58	16.52	12.32	55.6	3.63	18.93
Cross30	15.26-20.95	17.68	11.97	6.72	2.52	14.67	8.98	37.48	2.00	11.33

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Table 13. Range, mean and variability parameters for Dry root weight in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	1.88-4.28	2.05	5.50	0.02	0.02	6.70	6.41	91.51	0.25	12.63
Cross 2	1.84-4.13	1.89	9.15	0.03	0.02	8.99	7.78	75.02	0.27	13.89
Cross 3	1.25-4.87	2.57	11.21	0.13	0.13	13.79	13.78	99.92	0.73	28.38
Cross 4	1.25-5.21	2.46	25.94	0.42	0.32	26.48	22.83	74.33	1.00	40.54
Cross 5	1.40-3.15	2.41	42.39	1.42	1.33	49.49	47.90	93.67	2.30	95.51
Cross 6	1.63-4.19	1.81	5.10	0.01	0.01	6.30	4.49	50.77	0.13	6.59
Cross 7	1.41-4.89	2.79	40.71	0.80	0.71	32.14	30.29	88.77	1.64	58.78
Cross 8	2.79-3.41	3.08	4.60	0.03	0.02	5.55	3.96	50.76	0.18	5.81
Cross 9	1.67-3.45	2.54	37.40	0.20	0.01	17.56	4.56	6.73	0.06	2.44
Cross10	1.27-4.54	2.41	0.45	0.01	0.01	0.46	0.40	75.57	0.21	0.72
Cross11	0.94-3.44	3.20	2.47	0.01	0.01	2.87	2.41	70.35	0.14	4.16
Cross12	1.41-4.12	2.73	27.42	0.31	0.29	20.36	19.6	92.69	1.06	38.87
Cross13	2.30-4.88	2.57	6.71	0.04	0.01	8.05	3.95	24.03	0.10	3.99
Cross14	1.77-3.05	1.90	3.01	0.01	0.00	3.83	2.78	52.82	0.09	4.17
Cross15	1.05-4.37	1.68	34.83	0.01	0.00	6.65	3.95	35.19	0.08	4.82
Cross16	1.26-3.81	2.60	4.13	0.02	0.01	5.06	2.77	30.07	0.08	3.13
Cross17	2.76-3.75	2.96	26.03	0.39	0.37	21.09	20.55	94.95	1.22	41.24
Cross18	2.08-4.56	2.95	21.7	0.61	0.61	26.5	26.43	99.51	1.60	54.31
Cross19	2.01-3.41	2.75	21.99	0.55	0.55	26.92	26.87	99.63	1.52	55.25
Cross20	1.83-4.05	2.02	4.87	0.02	0.01	5.98	5.55	86.16	0.22	10.61
Cross21	1.26-3.51	1.82	32.58	0.49	0.45	38.48	36.88	91.84	1.32	72.80
Cross22	1.58-4.96	2.09	24.17	0.21	0.07	22.12	12.53	32.09	0.30	14.62
Cross23	2.35-4.09	2.04	21.83	0.17	0.17	20.3	20.01	97.13	0.83	40.62
Cross24	2.39-4.11	1.85	23.6	0.23	0.20	26.22	24.34	86.15	0.86	46.53
Cross25	1.94-3.18	1.93	31.71	0.35	0.35	30.55	30.55	99.99	1.22	62.93
Cross26	2.07-4.27	1.87	25.36	0.11	0.02	17.72	6.88	15.07	0.11	5.50
Cross27	2.20-2.52	2.02	23.06	0.05	0.02	11.39	7.06	38.47	0.18	9.02
Cross28	1.75-3.05	2.07	36.33	0.26	0.24	24.49	23.73	93.9	0.98	47.37
Cross29	1.27-2.81	1.93	35.23	0.06	0.05	12.11	12.07	99.27	0.47	24.77
Cross30	1.40-3.90	1.73	29.96	0.37	0.26	35.31	29.51	69.84	0.88	50.81

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Table 14. Range, mean and variability parameters for Root volume in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	10.85-16.43	12.25	5.48	0.67	0.67	6.68	6.66	99.57	1.68	13.69
Cross 2	1.71-8.76	8.61	15.79	2.60	0.75	18.72	10.06	28.84	0.96	11.12
Cross 3	10.32-24.82	12.03	2.26	0.11	0.11	2.76	2.76	99.89	0.68	5.69
Cross 4	10.91-28.04	25.65	3.71	1.06	0.49	4.01	2.73	46.18	0.98	3.82
Cross 5	8.74-22.47	17.96	8.51	1.46	1.32	6.72	6.39	90.34	2.25	12.5
Cross 6	5.90-15.27	6.40	4.59	0.13	0.01	5.55	1.61	8.42	0.06	0.96
Cross 7	9.81-21.39	11.27	13.98	0.65	0.65	7.16	7.14	99.45	1.65	14.67
Cross 8	8.76-22.13	20.88	0.16	0.00	0.00	0.22	0.19	81.82	0.09	0.36
Cross 9	13.51-22.35	13.84	6.9	0.57	0.06	5.46	1.78	10.57	0.16	1.19
Cross10	8.28-21.37	14.70	25.78	19.43	15.15	30.00	26.48	77.95	7.08	48.16
Cross11	10.83-22.54	11.64	2.72	0.13	0.05	3.07	1.90	38.35	0.28	2.42
Cross12	8.19-24.11	8.55	8.84	0.86	0.01	10.82	1.13	1.08	0.02	0.24
Cross13	7.59-21.57	8.13	2.12	0.04	0.01	2.41	0.94	15.23	0.06	0.76
Cross14	7.75-19.31	8.67	3.27	0.12	0.07	4.01	3.11	60.00	0.43	4.96
Cross15	8.12-22.45	8.70	18.17	3.74	0.71	22.24	9.71	19.04	0.76	8.73
Cross16	8.90-20.18	9.64	2.48	0.08	0.06	2.91	2.42	69.49	0.40	4.16
Cross17	12.34-21.86	14.04	8.67	1.75	1.51	9.41	8.76	86.53	2.36	16.78
Cross18	8.89-18.32	14.68	7.15	1.22	1.11	7.52	7.16	90.79	2.07	14.06
Cross19	8.09-24.91	23.43	3.71	0.77	0.37	3.75	2.61	48.54	0.88	3.75
Cross20	9.20-18.27	9.62	6.86	0.47	0.06	7.14	2.58	13.08	0.19	1.92
Cross21	8.90-19.71	9.33	8.95	1.05	0.14	10.96	4.05	13.66	0.29	3.08
Cross22	6.07-19.59	7.02	9.09	0.47	0.45	9.8	9.53	94.59	1.34	19.10
Cross23	11.71-22.92	12.38	6.45	0.94	0.02	7.84	1.12	2.06	0.04	0.33
Cross24	11.98-19.30	11.43	13.19	0.47	0.09	6.02	2.61	18.82	0.27	2.33
Cross25	7.43-24.50	17.70	9.42	2.93	2.25	9.67	8.47	76.75	2.71	15.29
Cross26	9.07-27.12	25.03	4.36	0.34	0.18	2.31	1.71	54.7	0.65	2.61
Cross27	10.56-24.87	23.66	7.63	2.97	2.84	7.28	7.13	95.87	3.40	14.37
Cross28	11.71-21.51	16.29	33.15	41.85	36.65	39.71	37.16	87.58	11.67	71.64

Cross29	14.07-18.68	13.70	11.14	3.18	3.12	13.03	12.89	97.88	3.60	26.27
Cross30	10.77-19.82	12.50	17.96	6.48	6.3	20.36	20.09	97.34	5.10	40.83

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Table 15. Range, mean and variability parameters for Root/shoot ratio in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	0.05-0.12	0.07	27.76	0.00	0.00	33.99	21.08	38.46	0.00	26.93
Cross 2	0.08-0.19	0.08	27.00	0.00	0.00	19.76	15.31	60.00	0.00	24.43
Cross 3	0.04-0.15	0.06	27.33	0.00	0.00	17.89	16.00	80.00	0.00	29.48
Cross 4	0.06-0.18	0.08	31.88	0.00	0.00	36.86	20.99	32.43	0.00	24.63
Cross 5	0.07-0.22	0.09	19.52	0.00	0.00	23.56	16.16	47.06	0.00	22.84
Cross 6	0.09-0.20	0.06	36.00	0.00	0.00	26.35	20.41	60.00	0.00	32.57
Cross 7	0.12-0.21	0.16	32.53	0.00	0.00	38.23	38.10	99.31	13.00	78.20
Cross 8	0.08-0.21	0.05	32.53	0.00	0.00	21.30	19.05	80.00	0.00	35.10
Cross 9	0.10-0.19	0.11	38.26	0.00	0.00	43.88	41.60	89.89	9.20	81.25
Cross10	0.04-0.20	0.06	59.19	0.00	0.00	46.83	38.89	68.97	6.50	66.53
Cross11	0.07-0.19	0.10	36.86	0.00	0.00	37.33	27.13	52.83	0.06	40.63
Cross12	0.11-0.23	0.13	13.39	0.00	0.00	8.77	7.84	80.00	0.00	14.45
Cross13	0.09-0.18	0.11	15.18	0.00	0.00	18.32	12.58	47.06	0.00	17.76
Cross14	0.07-0.21	0.09	28.43	0.00	0.00	32.88	18.72	32.43	0.00	21.96
Cross15	0.12-0.20	0.08	31.13	0.00	0.00	37.20	28.81	60.00	0.00	45.99
Cross16	0.06-0.15	0.08	20.70	0.00	0.00	13.55	12.12	80.00	0.00	22.33
Cross17	0.04-0.15	0.06	27.33	0.00	0.00	17.89	16.00	80.00	0.00	29.49
Cross18	0.05-0.16	0.05	43.20	0.00	0.00	31.62	24.50	60.00	0.00	39.08
Cross19	0.04-0.21	0.05	47.62	0.00	0.00	47.61	46.65	96.00	0.06	94.17
Cross20	0.06-0.16	0.03	45.54	0.00	0.00	29.81	26.66	80.00	0.00	49.13
Cross21	0.02-0.13	0.04	46.68	0.00	0.00	23.53	21.05	80.00	0.00	38.79
Cross22	0.04-0.19	0.06	27.33	0.00	0.00	17.88	16.00	80.00	0.00	29.49
Cross23	0.05-0.13	0.11	20.63	0.00	0.00	23.25	22.78	96.00	0.00	45.99
Cross24	0.05-0.14	0.07	32.26	0.00	0.00	32.25	31.60	96.00	0.00	63.80
Cross25	0.08-0.14	0.11	25.62	0.00	0.00	31.20	27.90	80.00	0.00	51.42
Cross26	0.04-0.15	0.06	35.48	0.00	0.00	40.00	39.19	96.00	0.00	79.10
Cross27	0.05-0.22	0.07	28.61	0.00	0.00	14.42	12.90	80.00	0.00	23.78
Cross28	0.06-0.20	0.08	28.57	0.00	0.00	28.57	27.99	96.00	0.00	56.5
Cross29	0.08-0.18	0.10	18.26	0.00	0.00	21.21	21.21	0.00	0.00	43.69
Cross30	0.07-0.22	0.09	22.74	0.00	0.00	11.46	10.25	80.00	0.00	18.89

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Table 16. Range, mean and variability parameters for Harvest index in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	0.36-0.48	0.38	4.30	0.00	0.00	4.78	4.59	92.30	0.00	9.08
Cross 2	0.35-0.47	0.37	5.83	0.00	0.00	4.28	3.31	60.00	0.00	5.29
Cross 3	0.38-0.52	0.40	4.13	0.00	0.00	4.53	4.35	92.30	0.00	8.62
Cross 4	0.48-0.65	0.62	3.31	0.00	0.00	4.32	3.60	68.96	0.00	6.14
Cross 5	0.35-0.48	0.38	4.72	0.00	0.00	5.53	3.80	47.07	0.00	5.36
Cross 6	0.47-0.62	0.50	5.90	0.00	0.00	4.48	4.00	80.00	0.00	7.38
Cross 7	0.38-0.53	0.49	10.14	0.00	0.00	11.63	8.29	50.77	0.07	12.16
Cross 8	0.26-0.38	0.28	6.36	0.00	0.00	4.02	3.60	79.95	0.00	6.63
Cross 9	0.42-0.58	0.54	4.95	0.00	0.00	5.6	3.19	32.44	0.00	3.74
Cross10	0.38-0.54	0.50	8.59	0.00	0.00	8.5	6.89	65.75	0.04	11.51
Cross11	0.42-0.54	0.52	3.13	0.00	0.00	3.99	2.73	47.07	0.00	3.86
Cross12	0.32-0.63	0.48	28.00	0.02	0.02	30.98	30.90	99.55	0.00	63.51
Cross13	0.44-0.58	0.54	5.91	0.00	0.00	2.92	2.26	59.99	0.00	3.61
Cross14	0.42-0.54	0.52	3.28	0.00	0.00	3.99	2.73	47.08	0.00	3.87
Cross15	0.33-0.59	0.48	23.06	0.01	0.06	27.72	16.89	37.09	0.00	21.18
Cross16	0.35-0.48	0.38	6.55	0.00	0.00	8.32	6.44	60.00	0.06	10.29
Cross17	0.52-0.68	0.63	6.00	0.00	0.00	3.95	3.88	96.01	0.06	7.81
Cross18	0.39-0.48	0.41	4.29	0.00	0.00	5.18	5.18	99.99	0.00	10.65
Cross19	0.47-0.64	0.58	2.61	0.01	0.00	18.44	5.69	9.50	0.02	3.61
Cross20	0.42-0.53	0.43	2.71	0.00	0.00	3.46	0.03	0.00	0.00	0.00

Cross21	0.38-0.48	0.40	4.35	0.00	0.00	2.81	2.51	80.02	0.00	4.63
Cross22	0.52-0.67	0.60	10.3	0.00	0.00	12.66	6.48	26.20	0.00	6.83
Cross23	0.38-0.55	0.52	4.36	0.00	0.00	2.14	1.91	80.00	0.00	3.52
Cross24	0.38-0.53	0.46	15.18	0.00	0.00	17.8	17.76	99.62	0.00	36.51
Cross25	0.30-0.44	0.34	9.96	0.00	0.00	10.45	10.04	92.31	0.00	19.88
Cross26	0.47-0.59	0.53	8.48	0.00	0.00	10.16	8.43	68.97	0.07	14.43
Cross27	0.32-0.54	0.39	12.05	0.00	0.00	8.77	7.84	80.00	0.06	14.45
Cross28	0.37-0.50	0.4	10.07	0.00	0.00	7.55	4.30	32.43	0.00	5.04
Cross29	0.35-0.52	0.41	13.04	0.00	0.00	15.95	8.74	30.06	0.03	9.88
Cross30	0.36-0.54	0.41	12.52	0.00	0.00	7.02	6.59	88.24	0.00	12.78

CV : Coefficient of variation
PV : Phenotypic variance
GV : Genotypic variance
PCV : Phenotypic Coefficient of variation
GCV : Genotypic Coefficient of variation
H : Heritability
GA : Genetic Advance
GAM : Genetic Advance as per cent of Mean

Table 17. Range, mean and variability parameters for Grain yield/plant in F_2 generation

Crosses	Range (cm)	Mean (cm)	CV (%)	PV	GV	PCV (%)	GCV (%)	H (%)	GA	GAM
Cross 1	37.04-54.40	39.18	2.26	1.17	1.14	2.76	2.72	97.41	2.17	5.54
Cross 2	24.38-52.48	42.63	1.31	0.24	0.16	1.14	0.95	69.06	0.69	1.62
Cross 3	24.36-48.49	45.54	1.51	0.71	0.02	1.84	0.28	2.28	0.04	0.09
Cross 4	36.62-51.23	48.48	2.27	1.71	1.32	2.70	2.37	76.85	2.07	4.27
Cross 5	24.28-48.57	33.11	5.42	2.05	1.99	4.32	4.26	97.42	2.87	8.67
Cross 6	48.67-57.45	53.51	1.39	0.76	0.05	1.63	0.42	6.63	0.12	0.22
Cross 7	32.08-49.24	46.63	0.97	0.28	0.08	1.14	0.60	28.13	0.31	0.66
Cross 8	19.18-36.91	20.92	1.39	0.05	0.02	1.09	0.64	34.04	0.16	0.77
Cross 9	51.80-62.28	52.80	3.97	6.53	3.78	4.84	3.68	57.83	3.04	5.77
Cross10	32.43-44.28	40.13	1.28	0.16	0.16	0.99	0.99	99.07	0.81	2.02
Cross11	32.80-46.82	43.83	1.59	0.71	0.08	1.92	0.63	10.66	0.18	0.42
Cross12	41.51-46.27	43.36	2.42	0.68	0.05	1.90	0.51	7.16	0.12	0.28
Cross13	57.65-63.01	60.16	0.72	0.17	0.16	0.69	0.67	92.68	0.80	1.32
Cross14	49.39-54.20	51.80	0.39	0.04	0.04	0.39	0.37	92.77	0.39	0.74
Cross15	54.17-70.42	65.54	2.80	3.64	2.59	2.91	2.45	71.06	2.79	4.26
Cross16	30.17-38.45	32.01	1.24	0.16	0.03	1.24	0.51	17.08	0.14	0.44
Cross17	63.18-70.78	65.69	2.95	3.22	0.94	2.73	1.48	29.27	1.08	1.65
Cross18	28.89-38.83	31.82	7.87	7.05	3.22	8.34	5.64	45.76	2.50	7.86
Cross19	17.27-24.95	18.44	4.38	0.88	0.00	5.10	0.09	0.03	0.00	0.00
Cross20	22.85-28.77	24.20	1.66	0.23	0.09	1.98	1.20	36.96	0.37	1.51
Cross21	31.67-36.21	33.35	1.20	0.23	0.08	1.43	0.82	33.05	0.32	0.97
Cross22	50.16-55.98	52.85	1.13	0.32	0.04	1.07	0.40	13.72	0.16	0.30
Cross23	55.21-62.89	59.78	0.97	0.47	0.20	1.15	0.75	42.86	0.61	1.01
Cross24	46.69-50.74	48.83	1.33	0.61	0.51	1.60	1.47	84.00	1.35	2.77
Cross25	20.27-26.19	21.21	1.95	0.23	0.02	2.24	0.65	8.37	0.08	0.39
Cross26	66.57-74.13	70.28	2.32	2.88	2.83	2.41	2.39	98.44	3.44	4.89
Cross27	23.13-29.90	24.45	2.48	0.52	0.36	2.95	2.44	68.39	1.02	4.15
Cross28	23.95-28.68	25.88	5.55	2.59	2.59	6.22	6.22	99.92	3.31	12.8
Cross29	20.44-25.68	21.01	5.09	1.21	1.19	5.25	5.19	97.88	2.22	10.58
Cross30	26.72-30.83	28.47	7.11	4.32	3.21	7.3	6.29	74.26	3.18	11.17

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GCV : Genotypic Coefficient of variation
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GA : Genetic Advance
GAM : Genetic Advance as per cent of Mean

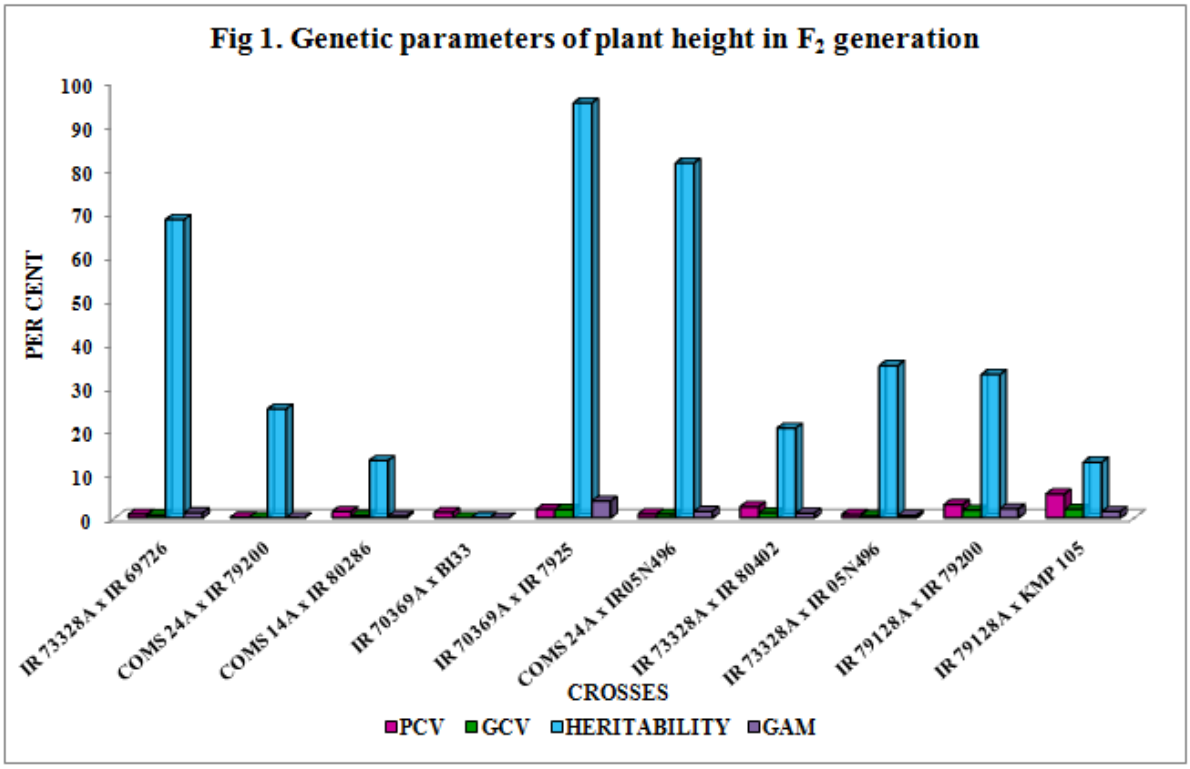
Fig 1. Genetic parameters of plant height in F2 generation
PER CENT
100
90
80
70
60
50
40
30
20
10
0
IR 73328A x IR 69726
COMS 24A x IR 79200
COMS 14A x IR 80286
IR 70369A x BI33
IR 70369A x IR 7925
COMS 24A x IR05N496
IR 73328A x IR 80402
IR 73328A x IR 05N496
IR 79128A x IR 79200
IR 79128A x KMP 105
CROSSES
PCV
GCV
HERITABILITY
GAM

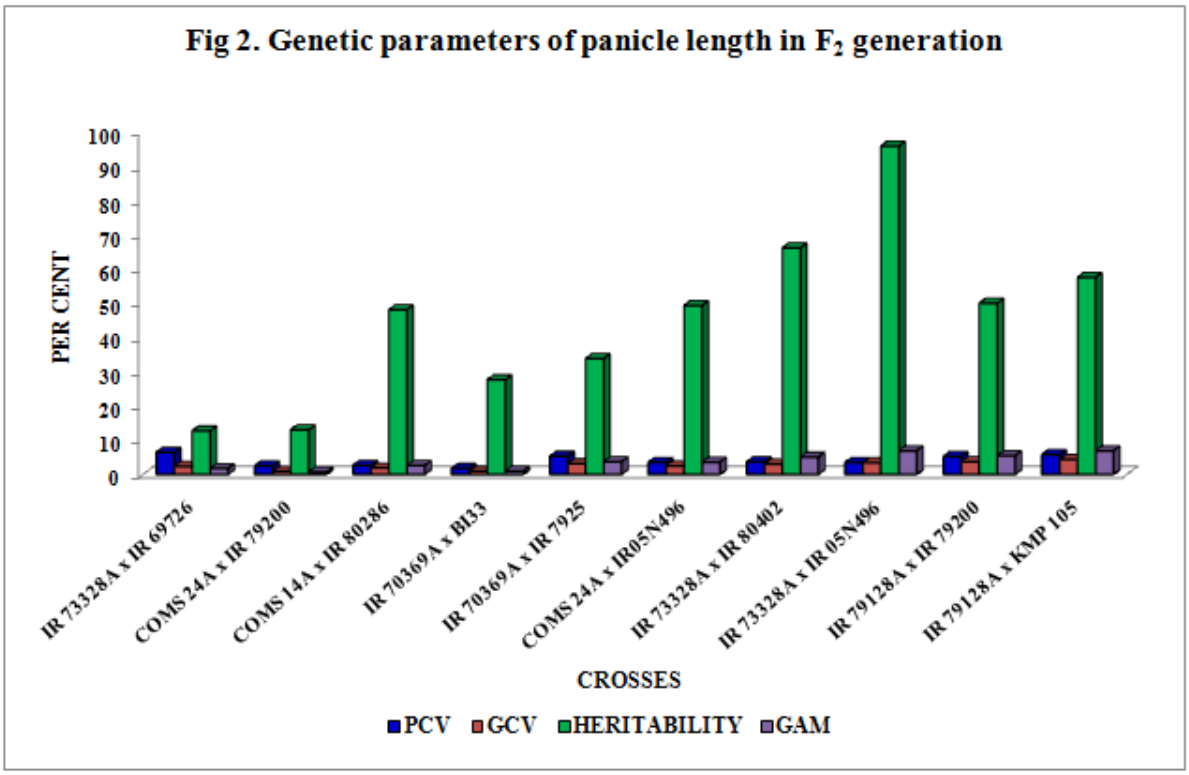
Fig 2. Genetic parameters of panicle length in F2 generation
PER CENT
100
90
80
70
60
50
40
30
20
10
0
IR 73328A x IR 69726
COMS 24A x IR 79200
COMS 14A x IR 80286
IR 70369A x BI33
IR 70369A x IR 7925
COMS 24A x IR05N496
IR 73328A x IR 80402
IR 73328A x IR 05N496
IR 79128A x IR 79200
IR 79128A x KMP 105
CROSSES
PCV
GCV
HERITABILITY
GAM

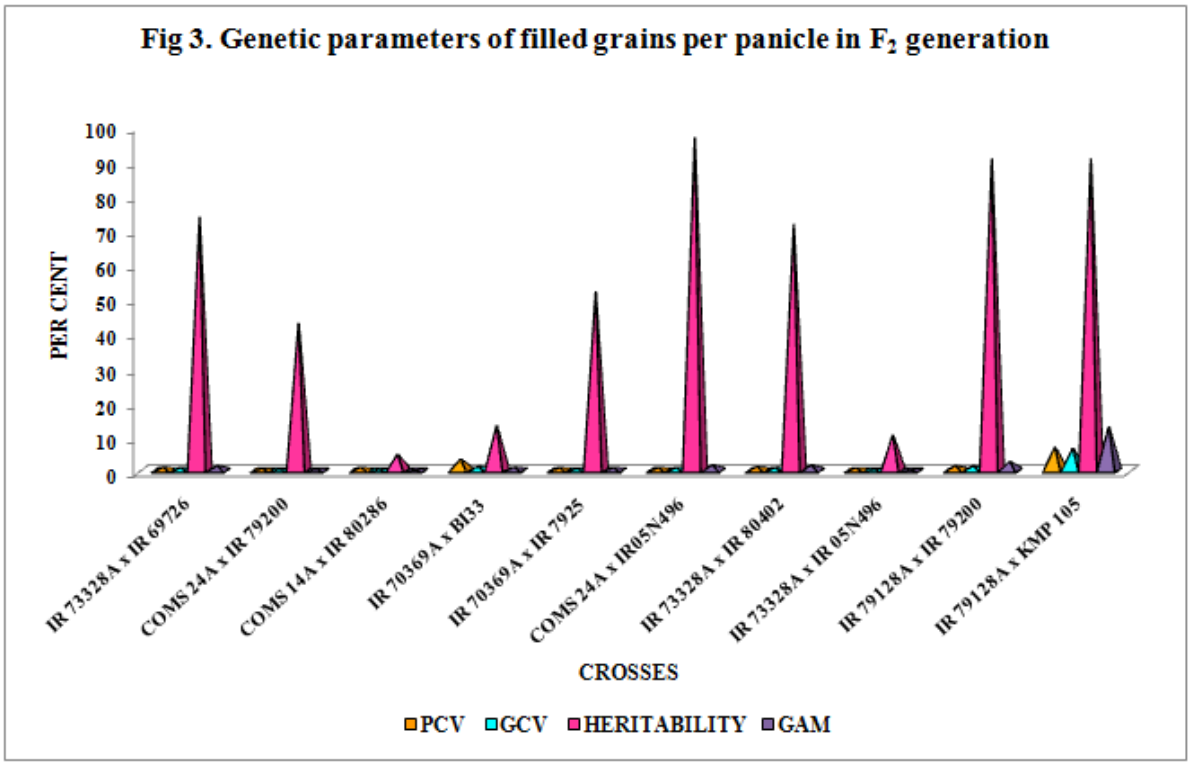
Fig 3. Genetic parameters of filled grains per panicle in F2 generation
PER CENT
100
90
80
70
60
50
40
30
20
10
0
IR 73328A x IR 69726
COMS 24A x IR 79200
COMS 14A x IR 80286
IR 70369A x BI33
IR 70369A x IR 7925
COMS 24A x IR05N496
IR 73328A x IR 80402
IR 73328A x IR 05N496
IR 79128A x IR 79200
IR 79128A x KMP 105
CROSSES
PCV
GCV
HERITABILITY
GAM

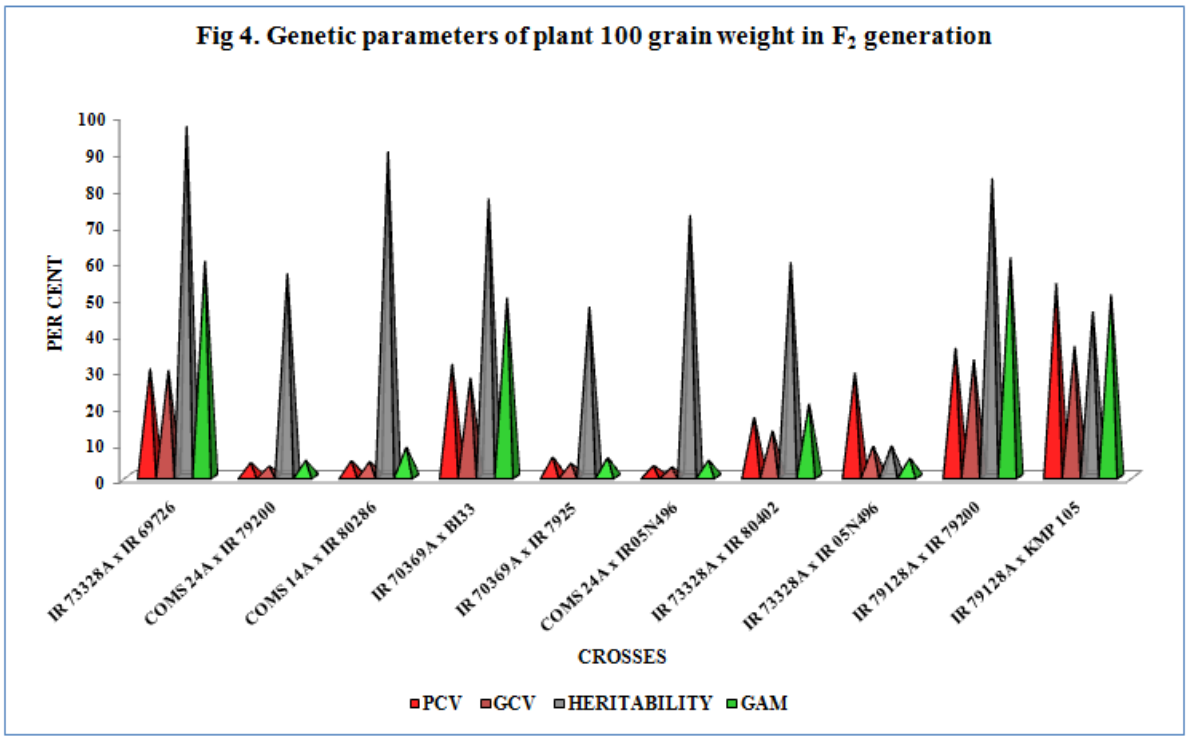
Fig 4. Genetic parameters of plant 100 grain weight in F2 generation
PER CENT
100
90
80
70
60
50
40
30
20
10
0
IR 73328A x IR 69726
COMS 24A x IR 79200
COMS 14A x IR 80286
IR 70369A x BI33
IR 70369A x IR 7925
COMS 24A x IR05N496
IR 73328A x IR 80402
IR 73328A x IR 05N496
IR 79128A x IR 79200
IR 79128A x KMP 105
CROSSES
PCV
GCV
HERITABILITY
GAM

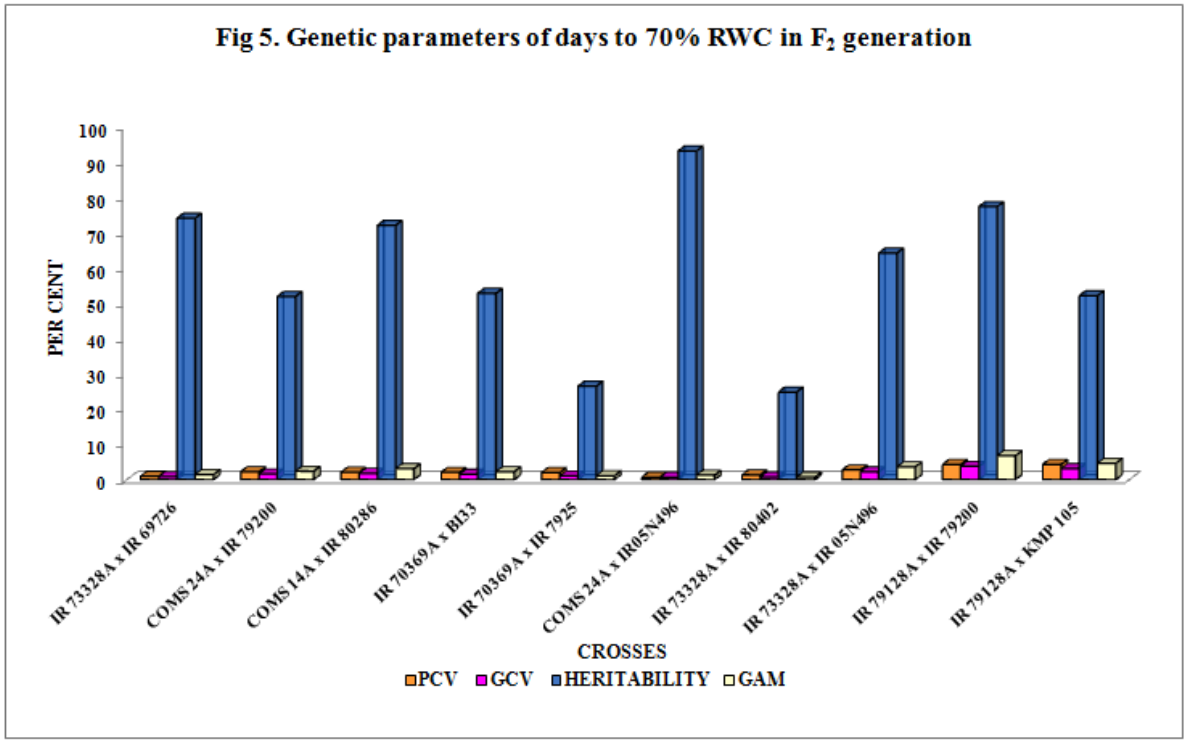
Fig 5. Genetic parameters of days to 70% RWC in F2 generation
PER CENT
100
90
80
70
60
50
40
30
20
10
0
IR 73328A x IR 69726
COMS 24A x IR 79200
COMS 14A x IR 80286
IR 70369A x BI33
IR 70369A x IR 7925
COMS 24A x IR05N496
IR 73328A x IR 80402
IR 73328A x IR 05N496
IR 79128A x IR 79200
IR 79128A x KMP 105
CROSSES
PCV
GCV
HERITABILITY
GAM

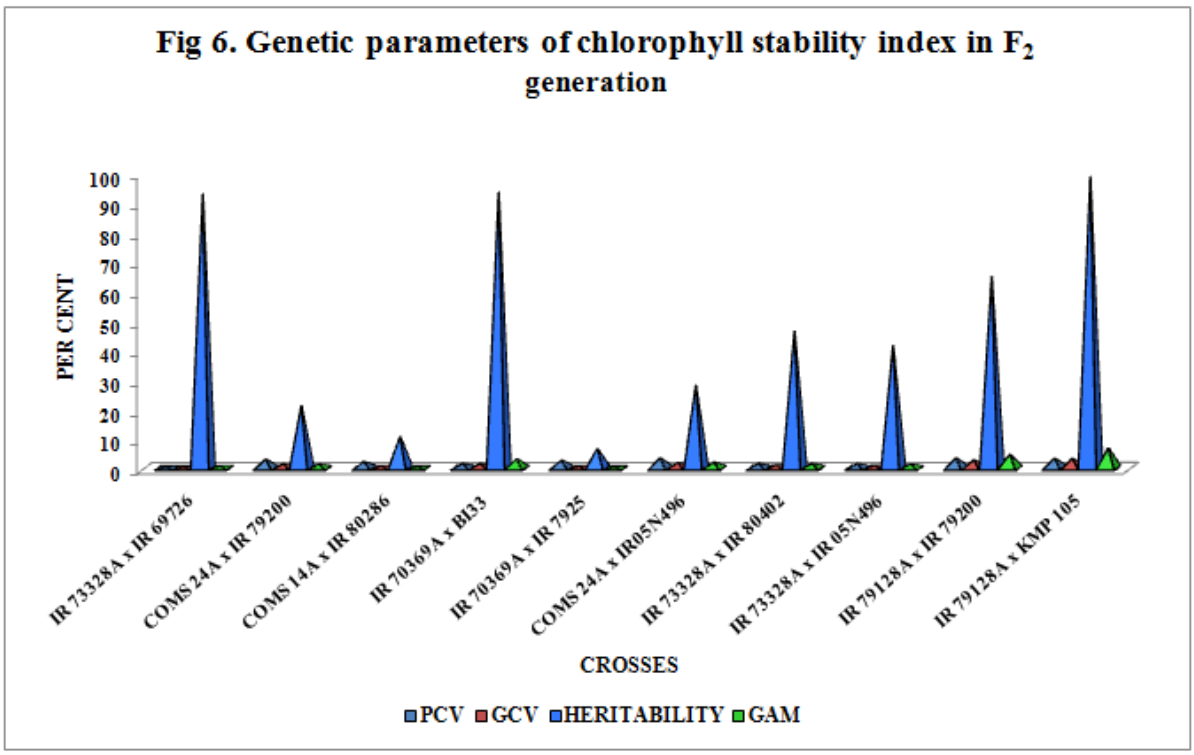
Fig 6. Genetic parameters of chlorophyll stability index in F2 generation
PER CENT
100
90
80
70
60
50
40
30
20
10
0
IR 73328A x IR 69726
COMS 24A x IR 79200
COMS 14A x IR 80286
IR 70369A x BI33
IR 70369A x IR 7925
COMS 24A x IR05N496
IR 73328A x IR 80402
IR 73328A x IR 05N496
IR 79128A x IR 79200
IR 79128A x KMP 105
CROSSES
PCV
GCV
HERITABILITY
GAM

Fig 7. Genetic parameters of root length in F_2 generation

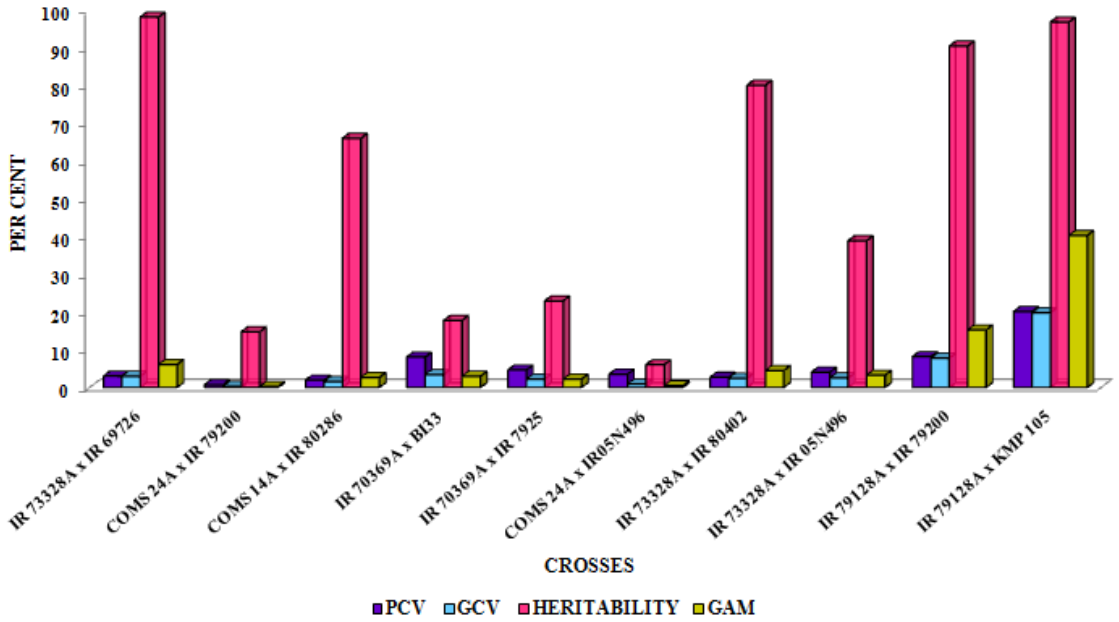

Fig 8. Genetic parameters of grain yield per plant in F_2 generation