RESEARCH ARTICLE Indian Journal of Agricultural Research, Volume 58 Issue 2: 188-194 (April 2024)

Revelation of Epistasis through Triple Test Cross (TTC) Analysis in Rice (*Oryza sativa* L.)

J. Johnny Subakar Ivin[1], Y. Anbuselvam[1], Maddi Sivakumar[1], M. Surendhar[1], S. Keerthana[1]

10.18805/IJARe.A-5688

ABSTRACT

Background: An investigation was performed to identify epistasis, additive, dominance components of genetic variation and yield and yield variability attributing characteristics by triple test cross testing involving three testers (P1, P2 and F_1) and ten rice lines.

Methods: The study materials consisted of F_1 seeds of three crosses, involving six parents namely, ASD16, ADT47, ASD18, CO51, TKM9 and MTU 7029. They are evaluated in randomized complete block design with three replications. Observations were reported for seven traits, namely plant height, number of tillers per plant, number of productive tillers per plant, length of panicle, number of grains per panicle, weight of 1000 grains and yield of grain per plant on five randomly selected plants per replication.

Result: The segregating population of three crosses exhibited wide range of variability for most of the traits. The difference between GCV and PCV was low for most of the characters indicated less influence of environment. Among the three crosses ASD18 × CO15 recorded high percent of heritability and genetic advance for grain yield per plant. The estimate of total epistasis revealed that i type of epistasis (additive × additive) was highly significant for number of tillers per plant, number of productive tillers per plant, panicle length and 1000 grain weight. The effect of the additive (D) variance was very important for all the traits except the number of grains per panicle. Across all traits, the degree of dominance $(H/D)^{1/2}$ was less than unity (< 1) suggesting, partial of dominance. Since, the pre dominance component of epistasis in autogamous crop is additive × additive (i type), it was suggested that the selection may be post ponded to later generation until all the non-additive components of variance has been mitigated to additive components.

Key words: Additive, Dominance, Epistasis, Gene action, Heritability, Rice, Trible text cross.

INTRODUCTION

Rice (*Oryza sativa* L.) is a valuable plant which belongs to the grass family Poaceae and it is important cereal and economically essential staple food crop for all over the world population relied on rice to fulfill their daily nutritional requirements (Serba *et al*., 2020).

India ranks second among rice-growing countries with a total area of approximately 44.6 million hectares, comprising 42% of food grain production and 55% of irrigated cereal production (52.6%), rain-fed (32.4%), upland (12%) and flooded regions (3%) (Kumar *et al.,* 2020). According to FAO, the productivity level of rice in India is very low (117.5 million tonnes) as compared to the average productivity level of China (207 million tonnes) and world (769.7 million tonnes) from this it could be understood that the production of rice could not able to meet the burgeoning population. Also, it is a well-known fact that the area under the cultivation of rice has almost reached the plateau. Hence it becomes necessary to increase the production of the crop (Elbasiouny *et al*., 2020). India will grow 135-140 million tons of rice by 2030, in order to ensure self-sufficiency and fulfill potential food grain requirements in future. (Messerli *et al*., 2019). This could be achieved only through genetic manipulation.

The success in the selection programme of a plant breeding programme largely depends on the availability of reliable information about the nature and magnitude of gene action present in the material being handled by the breeder (Boopathi, 2020). Among the existing genetical models used to detect and estimate different components of variation, the triple test cross analysis is the most efficient estimates of dominance but also an unambiguous test for epistasis (Marwa and Elmahas, 2015). It has also the widest applicability, as the design with its modified forms can be used to investigate both segregating and non-segregating populations arising from different generations (Parvez *et al*., 2007).

Among the different biometrical methods available, triple test cross analysis is one of the most efficient designs currently available for investigating the genetical structure of populations (Drewek *et al*., 1981). It provides a test of epistasis and its absence gives independent and equally precise estimates of additive and dominance genetic components (Monnahan and Kelly, 2015).

[1]Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar-608 002, Tamil Nadu, India.

Corresponding Author: Y. Anbuselvam, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar-608 002, Tamil Nadu, India.
Email: yanbuselvam@gmail.com

How to cite this article: Ivin, J.J.S., Anbuselvam, Y., Sivakumar, M., Surendhar, M. and Keerthana, S. (2024). Revelation of Epistasis through Triple Test Cross (TTC) Analysis in Rice (*Oryza sativa* L.). Indian Journal of Agricultural Research. 58(2): 188-194. doi: 10.18805/IJARe.A-5688.

Submitted: 30-09-2020 **Accepted:** 16-03-2021 **Online:** 10-04-2021

Hence in the present study triple test cross analysis was employed to get information on the presence of epistasis and allow for orthogonal estimation of additive and dominance components of genetic variance.

MATERIALS AND METHODS

The experimental materials consist of F_1 seeds of three cross combinations and their parents which were obtained from the germplasm collection of Department of Genetics and Plant Breeding, Annamalai University. The present study was conducted during January 2017 to April 2018 at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar which was located at 11°24′N latitude and 79°41′E longitude at an altitude of 5.79 m above sea level. Experimental site was totally irrigated and the soil type was found to be clay loam with pH of 7.5.

From each of the three cross combinations (Table 1) 200 F_2 plants were raised in non-replicated trial during January (2017) to April (2017) with a spacing of 60 cm between rows and 45 cm between plants. The triple test cross progenies were obtained by mating randomly selected F_2 plants with the parents (P1 and P2) and F_1. Recommended agronomic practices and need based plant protection measures were carried out. Ten F_2 plants selected randomly were designated as female (f1-f10).

Triple test cross progenies were developed by crossing each of these females with both parents (P1 and P2) and F_1. The plants used as female were chosen as random for the development of TTC progenies and no seed pollen parent was used in more than one mating. Each set contains three groups *i.e.*, 30 crosses. Thus, three sets per cross were maintained.

Seeds of F_2 generation were sown in raised nursery beds during the next season of August 2017. Three seedlings per hill were transplanted at age of 25 days old, with the spacing of 20 cm between rows and 15 cm between plants in 3 m long rows. The experiment with three replications was performed in randomized block design. A uniform population of 20 plants in a row was maintained.

Triple test cross generation

Ten plants were randomly chosen from the F2's of cross I (ASD 16 × ADT 47) and were back crossed as female to P1, P2 and F_1 (P1×P2) and L1i, L2i and L3i families receptively were generated.

Where:
P1 = ASD 16.
P2 = ADT 47.
F1 = ASD 16 × ADT 47.

Thirty families L1(10) +L2(10) +L3(10) (from cross I) thus obtained were raised in randomized complete block design with three replications during January 2018. Five plants were randomly tagged for each replication and were analyzed on the method reported by (Mather and Jinks, 1982). The data were collected from 10 randomly selected plants per replication for the following traits. Plant height (cm), number of tillers per plant, number of productive tillers per plant, panicle length (cm), number of grains per panicle, 1000 seed weight (g), grain yield/plant (g).

Statistical analysis

Analysis of variance

The analysis of variance was carried out using the approach defined by (Singh and Chaudhary, 1999) to assess the importance of the treatments and to separate the impact of the treatment in order to determine the meaning differences between the hybrids, parents, lines, testers, P1 + P2 vs. F1, P1 vs. P2, lines vs. testers and hybrids vs. parents for each trait using the TTC approach.

Unit analysis

For each genotype the mean values were based on three replications. The variance of the mean and the related standard errors is determined from the difference in the individual values (Panse and Sukhatme, 1985).

Variability analysis and association analysis

The parameters of genetic variation, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were established as suggested by (Burton and Devane, 1953); (Lush, 1949); (Sivasubramanian and Madhavamenon, 1973) (Robinson *et al.*, 1949), as well as broad sense heritability (h^2) and average genetic advance (AGA).

Additive-dominance model

It has been calculated that additive and dominance elements do not presume epistasis. The family twenty sums of means yielded a variation of amounts for 19 degrees of freedom. Similarly, for 19 degrees of freedom the variance of differences was further obtained, the additive-dominance

Table 1: Details of the rice accessions and the cross combination of the parentage.

Parentage	Crosses	Name of the genotype	Origin
ADT 31/CO 39	Cross 1	ASD 16	RRS, Ambasamudram, TN, India.
ADT 43/Jeeraga samba		ADT 47	Tamil Nadu Rice Research Institute (TRRI), Aduthurai, TN, India.
ADT 31/IR 50	Cross 2	ASD 18	RRS, Ambasamudram, TN, India.
ADT43/RR272-1745		CO 51	Tamil Nadu Agricultural University, Coimbatore.
TKM 7/IR 8	Cross 3	TKM 9	Rice Research Station, Thirurkuppam.
IARI-5901-2/IR-8.		MTU 7029	Andhra Pradesh Rice Research Institute, Maruteru.

model was carried out on the data as illustrated by the (Kearsey and Jinks, 1968).

Test for epistasis

Epistasis detection was performed using the system outlined by (Kearsey and Jinks, 1968) and is based on the genetic model.

$$L_{ijk} = M + G_{ij} + R_k + E_{ijk}$$

RESULTS AND DISCUSSION

The progress in the breeding for economic traits depends on the magnitude and the nature of their genetic variability. In the present investigation, an attempt has been made to study the variability and its components in six parents and their F_2 generations of rice, the result obtained are discussed below:

Analysis of variance

In the present study, triple test cross analysis was conducted in rice with three crosses involving the parents of different plant habits. The analysis of variance for all the characters is shown in (Table 2).

Test for epistasis

The analysis of variance describes for evaluating the existence of epistasis in (Table 3) the inheritance of all of the traits tested. The mean square for the L1i + L2i 2L3i deviations revealed that significant epistasis is present for all traits.

Mean performance

Parent selection was based on the general principle that selected parents should have high performance per se for desirable traits. In this contrast a high order of mean performance of the important yield attributes Thus, in the present study six parents and their F2 generations were studied (Table 4).

Variability

The analysis of variance for various characters gave a clear picture of the existence of wide genetic variability among the genotype chosen for the study. A high estimate of PCV and GCV was recorded by the number of grains per panicle (Table 5).

Heritability

Heritability value alone provides no indication of the amount of genetic progress. According to (Hanson, 1961), heritability and genetic advance are complementary aspects. Ramanujam and Tirumalachar, (1967) discussed the limitation of estimating heritability in broad sense and suggested that heritability in broad sense will be reliable, when if accompanied by high genetic advance.

Genetic analysis

In the present investigation, high heritability was seen in all the segregating generations in almost all the three crosses for the plant height, number of tillers per plant, number of

Table 2: Analysis of variance of agronomic traits in rice genotypes.

Source of variance	Df	Mean squares						
		Plant height	Number of tillers per plant	Number of productive tillers per plant	Panicle length	Number of grains per panicle	1000 seed weight	Grain yield per plant
Replicates	2	231.142	105.937**	147.137**	103.225**	161.644	82.010**	17.255
Parents (Lines)	2	1100.622**	79.3439**	155.916**	241.310**	26437.01**	786.563**	2741.51**
Parents (testers)	9	206.635*	9.2135	6.5815	11.4523	435.4272	13.7007*	32.0955*
Crosses	18	129.806	6.6411	5.0528	7.4957	311.616	8.1729	18.2097
Errors	58	83.6994	5.3226	5.0387	10.263	256.7364	6.4859	12.7058

*, ** Significant at 5% and 1% level of probability.

Table 3: Analysis of variance for detection of epistasis for yield and its components.

Source of variance	Df	Mean squares						
		Plant height	Number of tillers per plant	Number of productive tillers per plant	Panicle length	Number of grains per panicle	1000 seed weight	Grain yield per plant
I Type of epistasis	1	0.0088	136.068**	257.18**	288.29**	126.672	234.56**	42.719
J+L Type epistasis	9	137.118	-1.101	-10.628	-4.9689	348.672	-5.1013	16.255
Total epistasis (I+J+L)	10	123.407	12.6155	16.153*	24.357**	326.472	18.824*	18.902

*, ** Significant at 5% and 1% level of probability.

Table 4: Mean performance in rice crosses.

Characters	Mean								
	Cross-1			Cross-2			Cross-3		
Generation	P1	P2	F_2	P1	P2	F2	P1	P2	F_2
Plant height (cm)	10.84	88.83	90.239	75.32	14.73	98.20	100.76	93.60	93.155
Number of tillers per plant	18.33	20.66	18.3675	21.07	23.88	24.90	18.23	15.95	17.13
Number of productive tillers per plant	15.66	16.66	14.91	11.165	17.07	16.77	9.82	12.11	11.46
Panicle length (cm)	26.96	23.36	23.1357	20.10	23.10	23.59	19.65	14.69	21.05
Number of grains per panicle	207	263	161.64	125.96	250.78	183.29	105.21	165.77	113.13
1000 grain weight (g)	2.433	1.533	2.376	2.1049	1.4784	1.8207	2.33	3.06	1.8769
Grain yield per plant (g)	45.13	23.33	23.95	29.91	25.53	23.99	17.03	19.77	17.73

Table 5: Variability studies of rice crosses.

Characters	Cross-1					Cross-2					Cross-3				
Parameters	V_g	V_e	V_p	PCV	GCV	V_g	V_e	V_p	PCV	GCV	V_g	V_e	V_p	PCV	GCV
Plant height (cm)	87.52	1.07	88.57	10.42	10.36	222.76	5.57	228.34	15.38	15.19	157.17	5.61	162.79	13.69	13.45
Number of tillers per plant	15.49	2.33	17.82	22.98	21.42	81.51	0.33	81.85	36.32	36.24	11.83	1.93	13.77	21.65	20.07
Number of productive tillers	13.01	3.33	16.34	27.10	24.18	40.43	0.14	40.57	37.97	37.91	6.78	0.93	7.72	24.24	22.72
Panicle length	8.82	0.53	9.35	13.22	12.83	6.98	0.30	7.2	11.44	11.19	10.94	1.84	12.78	16.98	15.71
Number of grains per panicle	586.02	22.00	608.02	15.25	14.97	536.90	27.23	5064.13	38.82	38.72	802.73	161.78	964.51	27.45	25.04
1000 grain weight (g)	0.06	0.08	0.15	16.33	10.92	0.10	0.00	0.10	17.64	17.46	0.23	0.05	0.29	28.91	25.89
Grain yield per plant(g)	48.99	0.47	49.46	29.35	29.21	148.98	0.49	149.47	51.07	50.99	39.08	2.55	41.64	36.38	35.25

PCV-Phenotypic coefficient variation; GCV-Genotypic coefficient variation .

Table 6: Heritability genetic advance and genetic advance as percentage of mean.

Parameters	Heritability			Genetic advance			GA % of mean		
Characters	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Plant height	98.78	97.55	96.55	19.15	30.36	25.37	21.22	30.92	27.24
Number of tillers per plant	86.91	7.55	41.15	99.59	18.56	74.52	85.93	6.56	38.33
Number of productive tillers per plant	79.61	99.65	87.88	6.63	13.07	5.03	44.46	77.96	43.89
Panicle length	94.30	95.77	85.6	5.94	5.32	6.3	25.68	22.57	29.94
Number of grains per panicle	88..02	92.14	90.10	12.15	15.07	13.18	51.89	98.57	60.21
1000 grain weight	44.69	98.01	80.2	0.35	0.64	0.89	15.04	35.62	47.77
Grain yield per plant	99..04	99.67	93.85	14.35	25.10	12.47	59.89	104.87	70.35

productive tillers per plant, panicle length, number of grains per panicle, 1000 grain weight and yield per plant. All the crosses recorded low to moderate genetic advance was recorded for plant height, number of tillers per plant, number of productive tillers per plant, panicle length. 1000 grain weight and yield per plant (Table 6).

Additive and Dominance

The estimates of the genetic components additive and dominance, degrees of freedom and path of dominance for these traits are studied and given in Table 7. It could be concluded, therefore, that selection criteria based on buildup of additive effects would be helpful in enhancing all the traits studied. The results for grain yield per plant, amount of grain per panicle, 1000 grains weight were highly significantly to significant additives. For all these characteristics, the magnitude of the additive variance was greater than that of the dominance variance. For the number of grains per panicle, the dominance effect was highly significant for the yield of grain per plant and plant height respectively. The degree of dominance $[(H/D)^{1/2}]$ was less than unity for all these traits. It ranged from 0.42 for Number of productive tillers per plant to 0.64 for grain yield per plant (Table 8).

Gene action

Several procedures have been outlined for the prediction of gene action using either the mean values of different generations or the variance calculated for various types of populations.

The triple test cross analysis has been found to be the most efficient method (Mather and Jinks, 1971), since it provides an unambiguous test to predict the epistatic components and also precisely estimates the additive and dominance components. It was reported that only diallel, North Carolina design III and the Triple test cross can give unbiased estimates of the dominance ratio when the gene frequencies are unequal (Jinks *et al.*, 1969). Triple test cross has also the widest applicability as it can be used to investigate segregating population arising from the different generation such as F2, back cross and homozygous lines. (Jinks and Perkins, 1970); (Singh and Singh, 1976); (Jinks and Virk, 1977); Snape (1982); (Tapsell and Thomas, 1983); (Subbaraman and Sree Rangasamy, 1989).

Triple test cross analysis

The triple test cross analysis revealed the presence of epistasis for almost all the characters except the number of grains per panicle. Significant additive × additive (i type) epistasis can be used for the evolving elite genotypes through pedigree breeding while significant j and i type epistasis are useful in the development on hybrids. In a self-pollinated crop such as rice, where the production of commercial hybrids become popular might be due to j and i type of interactions. The absence of i type epistasis for characters like plant height, number of grains per panicle and yield per plant indicated i type epistasis is relatively minor components of epistasis. The estimate of additive

Table 7: Estimates of additive and dominance components, degree of dominance and heritability for yield and its components.

Parameters	Plant height	Numbers of tillers per plant	Number of productive tillers per plant	Panicle length	Number of grains per panicle	1000 seed weight	Grain yield per plant
(D)	67.12**	2.92*	2.04*	3.75**	104.8**	4.70**	11.13**
(H)	10.22**	0.29	0.18*	0.76*	19.44**	0.74**	2.30**
$(H/D)^{1/2}$	0.55	0.45	0.42	0.63	0.60	0.56	0.64
rs.d	0.50	0.49	0.48	0.49	0.32	0.54	0.54

Additive (D) Dominance (H) Degree of dominance $(H/D)^{1/2}$ rs.d- direction of dominance.

component is independent of dominance but still it will be biased by due to epistasis. Nevertheless, it is skill likely to provide the best source for the prediction of variance of recombinant homozygous population (Jinks, 1981).

The additive gene effects were significant for almost all the traits. We have to follow a breeding methodology such as reciprocal recurrent selection for make use of both additive and non-additive gene actions.

The degree of dominance further reveled the predominant nature of additive genetic component in almost all the characters. For plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of grains per panicle, 1000 grain weight and yield per plant where the degree of dominance is less than the unity, indicated less predominant role of dominance action similar results were obtained by Ranjana patial *et al.* (2020) in their studies on Urdbean.

Simple selection procedure in the early generation may not help much in achieving improvement for these characters. In rice epistatic components play an improvement role in governing all the characters. Therefore, epistasis cannot be ignored when one is formulating breeding plans to improve rice population for economic traits (Koli *et al*., 2014). The D component was highly significant for almost all characters. This is in agreement with the studies of Saravanan *et al.,* (2005); in bhendi. This can be exploited in the later generations when homozygosity sets in and therefore selection has to be postponed to later generations. The presence of epistasis for almost all the traits expect the number of grains per panicle can be exploited by recurrent selection techniques. Since j and i type of epistasis interaction cannot be fixed and hence selection in the early segregating generation has to be avoided, similar results are obtained by Vijaykumar *et al*. (1996) Saleem *et al*. (2009) in their studies in rice and Bhor *et al*. (2014) in soybean. The selection procedures have to be postponed to F_6 or F_8 generations when the homozygosity would have set in for most of the loci.

However, since the present experiments was conducted at one location for a season, the estimates of additive and dominance components are confounded with environmental effects (locations, seasons *etc*.). The characters which showed absence of epistasis may give the evidence of epistasis under other environmental conditions. Similarly, the characters which showed presence of significant epistasis may not do so if it is tested in other environments. Therefore, more elaborate experiments are to be conducted to get a clear picture about the genetic system controlling these characters and for in developing more efficient breeding procedures.

Table 8: Genetic components for seven characters in rice.

Characters	Components	Cross 1
Plant height	D	67.12**
	H	10.22
	$(H/D)^{1/2}$	0.55
Numbers of tillers per plant	D	2.92**
	H	0.29
	$(H/D)^{1/2}$	0.45
Number of productive tillers per plant	D	2.04*
	H	0.18
	$(H/D)^{1/2}$	0.42
Panicle length	D	3.75**
	H	0.766
	$(H/D)^{1/2}$	0.63
Numbers of grains per panicle	D	104.80
	H	19.44
	$(H/D)^{1/2}$	0.609
1000 seed weight	D	4.70**
	H	0.743
	$(H/D)^{1/2}$	0.562
Grain yield per plant	D	11.34**
	H	2.30
	$(H/D)^{1/2}$	0.6427

*, ** Significant at 5% and 1% level of probability.

ACKNOWLEDGEMENT

Authors are thankful to the department of Genetics and Plant Breeding, Faculty of agriculture, Annamalai University, Tamil Nadu, India for providing the laboratory facilities for the conduct of present study.

Conflict of interest

All authors declare that they have no conflict of interest.

REFERENCES

Bhor, T.J., Chimote, V.P. and Deshmukh, M.P. (2014). Genetic analysis of yield and yield components in soybean [*Glycine max* (L.) Merrill]. Indian Journal of Agricultural Research. 48(6): 446-452. doi: 10.5958/0976-058X.2014.01328.6.

Boopathi, N.M. (2020). Marker-assisted selection (MAS). In genetic mapping and marker assisted selection springer. Singapore. pp. 343-388.

Burton, G.W. and Devane, D.E. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. Agronomy Journal. 45(10): 478-481.

Drewek, K.J. and Broadhurst, P.L. (1981). A simplified triple-test cross analysis of alcohol preference in the rat. Behavior Genetics. 11(5): 517-531.

Elbasiouny, H. and Elbehiry, F. (2020). Rice Production in Egypt: The Challenges of Climate Change and Water Deficiency. In: Climate Change Impacts on Agriculture and Food Security in Egypt. Springer. Cham. pp 295-319.

Hanson, W.D. (1961). Heritabilities in Statistical Genetics Plant Breeding. Nat. Acad. Sci, Nat. Res. Coun. Washington. pp. 125-140.

Jinks, I.L. and Perkins J.M. (1970). A general method for the detection of additive, dominance and epistatic components of variation. III. F2 and backcross populations. Heredity. 25: 419-429.

Jinks, J.L. and Virk, D.S. (1977). A modified triple test cross analysis to test and allow for in adequate testers, Heredity. 38: 165-170.

Jinks, J.L. (1981). The genetic frame work of plant breeding Phil Trans R. Soc, (Lond) B. 292: 407-419.

Jinks, J.L., Perkins, J.M. and Breeze, E.L. (1969). A general method of detecting additive, dominance and epistatic components of variation for metrical traits II. Application to inbred lines. Heredity. 24: 45-57.

Kearsey, M.J. and Jinks, J.L. (1968). A general method of detecting additive, dominance and epistatic variation for metrical traits I, Theory Heredity. 23: 403-409.

Koli, N.R., Prakash, C., Mahawar, R.K., Kumhar, B.L. and Punia, S.S. (2014). Detection of epitasis, additive and dominance variation in rice (*Oryza sativa* L.) using triple test cross analysis. Electronic Journal of Plant Breeding. 5(4): 632-635.

Kumar, P., Garg, A. and Gupta, N.C. (2020). Mitigating CH4 and N2O Emissions from the Rice Crop System in IGP Region in India. Environmental Claims Journal. 32(2): 125-138.

Lush, J.L. (1949). Heritability of quantitative characters in farm animals. Hereditas. 35: 356-375.

Marwa, M. and El-Nahas (2015). Using triple test cross analysis to estimates genetic components, prediction and genetic correlation in bread wheat. International journal of Current Microbiology and Applied Sciences. 4(11): 79-87.

Mather, K. and Jinks, J.L. (1982). Biometrical Genetics. Chapman and Hall, London.

Mather, K. and Jinks, J.L. (1971). Biometrical Genetics. Chapman and Hall, London.

Messerli, P., Murniningtyas, E., Eloundou-Enyegue, P., Foli, E.G., Furman, E., Glassman, A. and Moatti, J.P. (2019). The Future is Now-Science for Achieving Sustainable Development. Irrigated and Integrated Agro Production Systems Help Mozambique Adapt to Climate Change, Republic of Indonesia.

Monnahan, P.J. and Kelly, J.K. (2015). Epistasis Is a Major Determinant of the Additive Genetic Variance in Mimulus guttatus. PLOS Genet. 11(5): e1005201.

Panse, V.G. and Sukhatme. (1985). Statistical Methods for Agricultural Workers. ICAR, New Delhi.

Parvez, A., Sofi, A.G., Rather, M.Z.K. and Warsi. (2007). Implications of epistasis in maize breeding. International Journal of Plant Breeding and Genetics. 1: 1-11.

Ramanujam and Thirumalachar (1963). Genetic variability of certain characters in red pepper. Mysore J. Agric Sci. 1: 30-36.

Ranjana patial, Mittak, R.K., Sood, V.K., Nimit Kumar (2020). Detection of epistasis for biometrical traits in urdbean [*Vigna mungo* (L) Hepper] under mid hill conditions of Northwestern Himalayas. Indian Journal of Agricultural Research. doi: 10.18805/LR-4426.

Robinson, H.F., Comstock, R.E. and Harvey, P.H. (1955). Genetic variances in open pollinated varieties of corn. Genetics. 40(1): 45-60.

Saleem, M.Y., Asghar, M., Haq, M.A., Rafique, T., Kamran, A. and Khan A.A. (2009). Genetic analysis to identify suitable parents for hybrid seed production in tomato (*Lycopersicon esculentum Mill.*). Pak. J. Bot. 41(3): 1107-1116.

Saravanan, K., Sabesan, T., Kumar, N.S. and Ganesan, J. (2005). Triple test cross analysis in Bhendi [*Abelmoschus esculentus* (L.) Moench]. Indian Journal of Agricultural Research. 39(4): 242-248.

Serba, D.D., Yadav, R.S., Varshney, R.K., Gupta, S.K., Mahalingam, G., Srivastava, R.K., and Tesso, T.T. (2020). Genomic Designing of Pearl Millet: A Resilient Crop for Arid and Semi-arid Environments. In Genomic Designing of Climate-Smart Cereal Crops Springer. Cham. pp. 221-286.

Singh, R.K. and Chaudhary B.D. (1999). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Pub. Ludhina, New Delhi, Revised Ed. p. 92-101.

Singh, S. and Singh, R.B. (1976). Triple test cross analysis in two wheat crosses. Heredity. 37: 173-177.

Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. Madras Agric. 60: (9-13): 1093-1096.

Smith, G.R. and Archer, R. (2020). Climate, population, food security: adapting and evolving in times of global change. International Journal of Sustainable Development and World Ecology. 1-5.

Snape, J.W. (1982). Predicting the frequencies of transgressive segregants for yield and yield components in wheat. Theoretical and Applied Genetics. 62(2): 127-134.

Subbaraman, N. and Rangasamy, S.S. (1989). Triple test cross analysis in rice. Euphytica. 42(1-2). 35-40.

Tapsell, C.R and Thomas, W.T.B. (1983). Cross prediction studies on spring barley. Theoretical and Applied Genetics. 64(4): 353-358.

Vijaykumar, S.B., Kulkarni, R.S. and Murthy, N. (1996). Trible test cross analysis in rice. Indian J. Genet. 56(2): 169-17.