(RESEARCH ARTICLE)

Estimation of general combining ability, specific combining ability and heterosis among selected rice (*Oryza sativa* L.) genotypes

Pritika Neupane *

Department of Plant Breeding and Genetics, Institute of Agriculture and Animal Science, Tribhuvan University, Nepal.

Abstract

Rice is the most important cereal crop and is primary source of calorie for Nepalese. Though, few rice varieties have been released for cultivation among farmers, most of them are low yielding so are not preferred by the farmers. So, broadening the genetic base of rice is an important intervention that can be done to increase productivity. Thus, an experiment was conducted to estimate general combining ability, specific combining ability, and heterosis from three sets of crosses to find out best parents and their cross combinations. The set1 consists 2 lines and 4 testers, set2 consists 3 lines and 2 testers and set3 consists 2 lines and 2 testers respectively. Each set of parents were crossed in line X tester mating design with two replications to produce 18 F1. The analyzed data showed that all genotypic values were significant and showed maximum variations among the traits. When fertile grain number was considered Sukhadhan-2 was best parents and cross of Manjushree 2 X Samba Mahsuri Sub-1 and Himali X Taichung-176 were the best cross and for panicle length IR775- 39-80-2- 2-2 was obtained as best parent and the best cross was Khumal 8 X Sugandha- 2. Maximum heterosis was observed in Khumal 8 X Sukhadhan-2 for fertile grain number and Khumal -4 X Sugandha-2 for panicle length. Therefore, best parents could be utilized for creating best lines through hybridization and best cross combinations would work as best lines for further selection and evaluation. These lines might work as promising varieties for Nepal.

1. Introduction

Rice is the most important cereal in Nepal. It is primary source of livelihood and income for more than two-thirds of farm households and it is deeply embedded in the country's culture. It contributes to 15% to the Agricultural Gross Domestic Product (AGDP) and more than 5 % to the total GDP. It is cultivated in Nepal from the plain of terai to the foot of the Himalayas. It is cultivated in nearly 43% of the total cropped area with the total contribution of 53 % of the cereal grain production (MOALD,2021). Rice's importance to Nepalese diet is also tremendous. More than 35% of the calorie requirement of Nepalese is provided by Rice (MOALD, 2021), most people consume rice daily as staple food with per capita consumption of 137.5 kg/year (Joshi,2020).

Though few rice varieties have been released for general cultivation among farmers in Nepal, most of the varieties are low yielding, disease and pest susceptible and lodging in nature. Therefore, they are not preferred by the farmers. So, broadening the genetic base of rice is an important intervention that can be done to increase lower productivity of rice which is 3.8 ton/ha as per MOALD, 2021.To meet the demand, among the available genetic resources to increase rice productivity, superior rice genotype with high yielding trait can be of great benefit.

* Corresponding author: Pritika Neupane
Department of Plant Breeding and Genetics, Institute of Agriculture and Animal Science, Tribhuvan University, Nepal.

Plant breeding strategies leading to the selection of superior genotypes need the expected level of heterosis as well as the specific combining ability. The prime initiative of rice breeders for developing superior hybrid rice cultivars is to choose suitable mating parents (Cao and Zhan, 2014). These parental characteristics are heritable and are able to appear in the F1 generation. Combining ability analysis is one of the valuable tools available to ascertain the combining ability effects and helps in selecting the desirable parents and crosses for the exploitation of heterosis.

The parental lines are considered to be the backbone of rice breeding since the performance of the progenies mainly depends on the genetic potential of the parents. Breeders are therefore constantly facing a challenge when attempting to select, breed, develop, and improve superior parental lines. This selection cannot be based solely on per se performance, requiring, therefore, selection for gene actions. So, the aim of combining ability analysis is to investigate the ability of a specific parental line to pass down genetic information to its progenies (Sprague and Tatum, 1942). A line X tester mating design screens parents for their genetic effects and enables the investigation of general combining ability (GCA) and specific combining ability (SCA) even in small sample sizes (Kempthorne, 1957; Tiwari et al., 2011). The GCA is the average performance of a line in a series of crosses, and this mean performance can be used to identify and improve superior parental lines by helping breeders identify the appropriate parents, crosses and breeding procedures required to select desirable progenies. It is mainly associated with additive gene action. In comparison, SCA refers to the positive/negative genetic value added to the expected average performance of the lines involved due to the interaction between those particular genotypes which may help identify good hybrid combinations. SCA is mainly associated with non-additive gene action resulting from dominance, overdominance and epistatic effects (Griffing, 1956; Latha et al., 2013; Sprague and Tatum 1942)

So, this research was conducted with the aim to select the best parents, which can further be utilized for creating best lines through hybridization and the best cross combination would work as best lines for further selection and evaluation to be released as a variety with high yielding traits that help in increasing productivity and production of rice.

2. Material and methods

To find out the best parents and best cross combinations in rice, three sets of crosses were produced following Line X Tester mating design developed by Kempthorne 1957. To facilitate the experiment easily with a limited number of F1 genotypes, the available genotypes were categorized into three sets where set1 consisted two lines and four testers, set2 consisted three lines and two testers and set3 consisted two lines and two testers. The parents were crossed in Line X Tester mating fashion developed in 2020 and 18 F1 were produced and planted in 2021. RCBD design was used with 2 replications.

The materials for the parents and their crosses were made available by National Plant Breeding and Genetics Research Center, Khumaltar, Lalitpur, Nepal.

Table 1 Parents and crosses used in the experimentation during 2020

Parents and their crosses	
Set 1	Khumal 4 (Line)
Khumal 8 (Line)	
Sukhadhan-2 (Tester)	
Purple rice (Tester)	
Sugandha 2 (Tester)	
IR775-39-80-2-2-2 (Tester)	
Khumal4 X Sukhadhan-2(NR11832)	
Khumal 4 X Purple rice (NR11847)	
Khumal 4 X Sugandha 2 (NR11850)	
Khumal 4 X IR775-39-80-2-2-2 (NR11851)	
Khumal 8 X Sukhadhan-2(NR11833)	
Khumal 8 X Purple rice (NR11839)	
Khumal 8 X Sugandha- 2 (NR11846)	

Khumal 8 X IR775-39-80-2-2-2 (NR11829)	
Set2	Aanga (Line)
IR775-39-80-2-2-2 (Line)	
IR67017 (Line)	
Khumal 4(Tester)	
Khumal 10(Tester)	
Aanga X Khumal 4 (NR11836)	
Aanga X Khumal 10 (NR11849)	
IR775-39-80-2-2-2 X Khumal 4 (NR11835)	
IR775-39-80-2-2-2 X Khumal 10 (NR11853)	
IR67017 X Khumal 4(NR11845)	
IR67017 X Khumal 10 (NR11869)	
Set 3	Manjushree 2 (Line)
Himali (Line)	
Samba Mahsuri Sub-1 (Tester)	
Taichung-176 (Tester)	
Manjushree 2 X Samba Mahsuri Sub- 1(NR11828)	
Manjushree 2 X Taichung 176(NR11856)	
Himali X Samba Mahsuri Sub-1(NR11859)	
Himali X Taichung-176(NR11862)	

For estimation of genetic parameters, characters such as days to flowering, days to maturity, plant height, panicle length, fertile grain number, sterile grain number and thousand grain weight were taken. For statistical analysis AGRISTAT developed by Dr. N. Manivannan was used.

3. Results and discussion

3.1. GCA, SCA values of parents and their crosses

GCA and SCA values of parents and crosses from set1, set2 and set3 are presented in table 2, 3 and 4 respectively.

3.2. GCA and SCA values for days to flowering

In set1, a total of 4 genotypes had negative values of GCA and SCA. Sugandha-2 had highest negative GCA value of -1.4 among the parents and Khumal 8 X Sugandha 2 had highest negative SCA value of -7.19. While in set2, a total of 3 genotypes had negative values. Khumal 4 had the highest negative GCA value for DTF (-4) and the cross of IR67017 X Khumal 4 had highest negative SCA (-1.25). On set3, a total of 4 genotypes had negative values for DTF, Himali had the highest negative GCA for DTF (-9.63) and Manjushree X Samba Mahsuri Sub -1 with the value of -4.88 had the highest negative SCA value. Finally, while taking all sets, Himali is the best parent and Khumal 8 X Sugandha 2 is the best cross for DTF. The results are compatible with the findings of Chakraborty et al. (2009), Ariful Islam et al. (2015), Thakor and Mistry (2018), Deepika et al. (2019) and Salah et al. (2020). So, the identified lines and testers will be effective for developing early maturing rice hybrids

3.3. GCA and SCA values for days to maturity

In set1, a total of six genotypes had negative GCA and SCA values. Sugandha-2 was the best parent (GCA: -11.81) and Khumal 8 X Sugandha-2 with the value of 14.69 had the highest SCA value. While in set2, Khumal 4 had highest GCA value (11.92) and IR 775- 3980-2-2-2 X Khumal 4 had highest SCA (-4.08). In set3, Himali had the highest GCA value (-4) but none of the crosses had significant SCA values. So, taking all the sets into consideration, Khumal 4 was best parent and Khumal8 X Sugandha 2 was best cross for DTM.

This result implies that the maturity days for the hybrids might fluctuate maximum from the parents and there would be maximum effect on the environment for deciding the date of maturation of the variety.

3.4. GCA and SCA values for effective tillers

In set1, 4 genotypes had positive GCA and SCA values. Sukhadhan-2 had 7.69 GCA value and the cross of Khumal 8 X IR775-39-80-2-2-2 had SCA value of 6.31 which is the highest value. In set2, none of the parents and crosses had positive GCA value for ET. On the third set, 4 genotypes had positive GCA and SCA values, Manjushree 2 had the highest GCA value (8) and among crosses, Manjushree 2 X Samba Mahsuri Sub-1 and Himali X Taichung-176 both had highest SCA value of 5. So, overall Manjushree 2 has the highest GCA and Khumal 8 X IR775-39-80-2-2-2 has SCA value for ET.These findings are in akin with earlier reports of Kumar et al. (2007), Hasan et al.(2014), Sharma et al. (2013), Veeresha et al. (2015) and Salah et al. (2020).

3.5. GCA and SCA values for plant height

In set1, neither parents nor crosses had negative GCA or SCA value for PHT, while in set 2, Khumal 10 had highest negative GCA value of -9.08 but none of the crosses had significant SCA values. In set3, 4 genotypes had negative values, Himali had the highest negative GCA value of -19.13 and Manjushree 2 X Samba Mahsuri Sub- 1 and Himali X Taichung-176 had the highest SCA value of -7.38. So, overall, Himal is the best parent. Manjushree 2 X Samba Mahsuri Sub- 1 and the Himali and Taichung-176 are best crosses for plant height.

These results are in agreement with the findings of Sharma et al. (2013), Hasan et al. (2014), Ariful Islam et al. (2015), Upadhyay and Jaiswal (2015) and Salah et al. (2020)

3.6. GCA and SCA values for panicle length

In set1, only 2 crosses had positive SCA values for PANL. Khumal 8 X Sugandha- 2 had the highest SCA value of 4.13. In set2, only 2 parents had positive significant GCA values for PANL. IR775-39-80-2-2-2 had highest GCA value (2.83**) and finally in set3, Manjushree 2 had the highest GCA value of 2.50. So, the best parent for PANL is IR775- 39-80-2-2-2 and best cross is Khumal 8 X Sugandha- 2. The results are in consonance with the findings of Bagheri (2010), Vieria et al. (2013), Hasan et al. (2015) and Shukla et al. (2020).

3.7. GCA and SCA values fertile grain number

In set1, a total of 5 genotypes had positive values, Sukhadhan-2 had 57.19 GCA value and Khumal 8 X Sugandha- 2 had 40.75 SCA value which were the highest values. While in set2 none of the parents and crosses had positive GCA or SCA values for FGN. In set3, 4 genotypes had positive s GCA and SCA values for FGN. Samba Mahsuri Sub-1 had highest GCA value of 44.50 and Manjushree 2 X Samba Mahsuri Sub-1 and Himali X Taichung-176 had highest SCA value of 47. Hence, Sukhadhan-2 is the best parent and of Manjushree 2 X Samba Mahsuri Sub-1 and Himali X Taichung-176 are best crosses for FGN. The results are in agreement with the findings of Faiz et al. (2006), Verica et al. (2013), Ariful Islam et al. (2015) and Patel et al. (2019).

3.8. GCA, SCA values for sterile grain number

In the set1,5 genotypes had negative values of GCA and SCA for SGN. Purple rice had highest negative GCA value of -35.81 and Khumal 4 X Purple rice had highest negative SCA value of -45.06. In set2 only IR67017 had negative GCA value with the value of 1.58. In set3, 4 genotypes had negative values of GCA and SCA. Manjushree-2 had the highest negative GCA value (-28.63) and the Manjushree-2X Samba Mahsuri Sub- 1 and HimaliTaichung-176 had the highest SCA value of -29.88. Hence, the best parent for SGN is purple rice and the best cross is Khumal 4 X Purple rice.

3.9. GCA and SCA values for thousand grain weight

In set1, 4 genotypes had positive GCA and SCA values, Sugandha 2 had highest GCA value of 4.11 and Khumal 4 X Sukhadhan- 2 had highest SCA value of 1.2. In set2, Khumal 4 had highest GCA value of 1.66, whereas Anga X Khumal 10 had highest SCA value (1.76). In set3, only Manjushree 2 had positive GCA for TGW which was 3.52 respectively. So, Sugandha -2 is the best parent and Khumal 8 X Sugandha-2 is the best cross for TGW. These results are in agreement with the findings of Chakraborty et al. (2009), Hasan et al. (2014).

Table 2 GCA, SCA of parents and crosses in set 1

Parents and their crosses	DTF	DTM	ET	PHT	PANL	FGN	SGN	TGW
Khumal 4	-0.19ns	2.31 **	-1.69 **	-8.25 ns	-0.38 ns	5.69 **	5.69 **	-0.66 **
Khumal 8	0.19ns	-2.31 **	1.69 **	8.25 ns	0.38 ns	-5.69 **	-5.69 **	0.66 **
Sukhadhan-2	-1.44	6.94 **	7.69 **	-3.00 ns	-0.38 ns	57.19 **	57.19 **	-2.85 **
Purple rice	-0.44ns	1.19 ns	-4.06 **	9.00 ns	-0.38 ns	-35.81 **	-35.81 **	-0.39 ns
Sugandha 2	-3.94**	-11.81 **	-4.31 **	-7.75 ns	0.63 ns	-12.31 **	-12.31 **	4.11 **
IR775-39-80-2-2-2	5.81**	3.69 **	0.69 ns	1.75 ns	0.13 ns	-9.06 **	-9.06 **	-0.87 *
Khumal4 X Sukhadhan-2	0.19ns	-3.56*	-0.31ns	-5.50ns	0.88ns	7.75**	19.81**	1.25**
Khumal 4 X Purple rice	-0.81ns	-4.31*	5.94**	7.50ns	0.88ns	14.75**	-34.19**	0.86*
Khumal 4 X Sugandha 2	7.19**	14.69**	0.69ns	19.75ns	-4.13**	-40.75**	30.69**	-2.24**
Khumal 4 X IR775-39-80-2-2-2	-6.56**	-6.81**	-6.31**	-21.75ns	2.38**	18.25**	45.06**	0.13ns
Khumal 8 X Sukhadhan-2	-0.19ns	3.56*	0.31ns	5.50ns	-0.88ns	-7.75**	-19.81**	-1.25**
Khumal 8 X Purple rice	0.81ns	4.31*	-5.94**	-7.50ns	-0.88ns	-14.75**	34.19**	-0.86*
.Khumal 8 X Sugandha- 2	-7.19**	-14.69**	-0.69ns	-19.75ns	4.13**	40.75**	-30.69**	2.24**
Khumal 8 X IR775-39-80-2-2-2	6.56**	6.81**	6.31**	21.75ns	-2.38**	-18.25**	-45.06**	-0.13ns

'**'= significant at p-value < 0.01, '*'= significant at p value 0.05, 'ns'= non-significant; DTF= Days to flowering, DTM= Days to maturity, ET= Effective tillers, PHT= Plant height, PANL= Panicle length, FGN= Fertile grain number, SGN= Sterile Grain number, TGW= Thousand grain weight

Table 3 GCA, SCA of parents and crosses in set2

Parents and their crosses	DTF	DTM	ET	PHT	PANL	FGN	SGN	TGW
Aanga	0.67 *	4.58 **	-1.75 ns	0.42 ns	-2.17 **	15.17 ns	-10.50 ns	-1.17 *
IR775-39-80-2-2-2	0.92 **	4.08 **	5.00 ns	17.42 ns	2.83 **	22.17 ns	21.50 ns	0.27 ns
IR67017	-1.58 **	-1.58 **	-1.58 **	-1.58 **	-1.58 **	-1.58 **	-1.58 **	-1.58 **
Khumal 4	-4.00 **	-11.92 **	2.92 ns	19.08 *	1.58 **	19.42 ns	-2.58 ns	1.66 **
Khumal 10	4.00 **	11.92 **	-2.92 ns	-19.08 *	-1.58 **	-19.42 ns	2.58 ns	-1.66 **
Aanga X Khumal 4	0.50ns	2.42ns	-1.92ns	-12.08ns	-0.33ns	-22.67ns	10.83ns	-1.76*
Aanga X Khumal 10	-0.50ns	-2.42ns	1.92ns	12.08ns	0.33ns	22.67ns	-10.83ns	1.76*
IR775-39-80-2-2-2 X Khumal 4	0.75ns	-4.08*	4.33ns	9.92ns	0.67ns	23.83ns	-20.67ns	-20.67ns
IR775-39-80-2-2-2 X Khumal 10	-0.75ns	4.08*	-4.33ns	-9.92ns	-0.67ns	-23.83ns	20.67ns	20.67ns
IR67017 X Khumal 4	-1.25*	1.67ns	-2.42ns	2.17ns	-0.33ns	-1.17ns	9.83ns	9.83ns
IR67017 X Khumal 10	1.25*	-1.67ns	2.42ns	-2.17ns	0.33ns	1.17ns	-9.83ns	-9.83ns

'**'= significant at p-value < 0.01, '*'= significant at p value 0.05, 'ns'= non-significant DTF= Days to flowering, DTM= Days to maturity; ET= Effective tillers, PHT= Plant height, PANL= Panicle length, FGN= Fertile Grain Number, SGN= Sterile Grain Number, TGW= Thousand grain weight

Table 4 GCA, SCA of parents and crosses in set3

Parents and their crosses	DTF	DTM	ET	PHT	PANL	FGN	SGN	TGW
Manjushree 2	9.63**	4.00*	8.00**	19.13**	2.50**	32.50**	-28.63**	3.52**
Himali	-9.63**	-4.00*	-8.0**	-19.13**	-2.50**	-32.50**	28.63**	-3.52**
Samba mahsuri Sub-1	5.88**	1.25 ns	4.25**	-7.63**	1.00 ns	44.50**	-26.88**	0.13 ns
Taichung-176	-5.88**	-1.25 ns	-4.25**	7.63**	-1.00 ns	-44.50**	26.88**	-0.13 ns
Manjushree 2 X Samba Mahsuri Sub-1	4.88*	2.75 ns	5.0**	-7.38**	0.50 ns	47.00**	-29.88**	0.27ns
Manjushree 2 X Taichung 176	-4.88*	-2.75 ns	-5.0**	7.38**	-0.50 ns	-47.00**	29.88**	-0.27ns
Himali X Samba Mahsuri Sub-1	-4.88**	-2.75 ns	-5.0**	7.38**	-0.50 ns	-47.00**	29.88**	-0.27ns
Himali X Taichung-176	4.88**	2.75 ns	5.0**	-7.38**	0.50 ns	47.00**	-29.88**	0.27ns

'**'= significant at p-value < 0.01, '*'= significant at p value 0.05, 'ns'= non-significant; DTF= Days to flowering, DTM= Days to maturity, ET= Effective tillers, PHT= Plant height, PANL= Panicle length, FGN= Fertile grain number, SGN= Sterile grain number, TGW= Thousand grain weight

4. Heterosis

Heterosis for a trait could be both positive and negative while the desired value of heterosis is dependent on the nature of the particular trait. The positive heterosis in general is used for yield whereas heterosis in the negative direction is desired for earliness. The exploitation of heterosis can enhance yield from 30 to 40 % and can also enrich the domesticated crops with most important traits of qualitative and quantitative nature. In the present study heterosis over better parent (heterobeltiosis) and mid parents heterosis were estimated in 18 hybrids for eight characters to find out the best combination of parents for their prospects for future use in breeding programs. A large characterization of parents for their prospects for future use in breeding programs. A large number of hybrids had significant desired heterosis over the better parent as well could be isolated for further evaluation at different locations and seasons. The character wise performance of hybrids is presented in table 5, 6 7 and 8.

4.1. Heterosis values for days to flowering

Negative heterosis is considered suitable for DTF. None of the crosses had negative heterosis for DTF when better parents were considered but only one cross of Khumal 4 X Sukhadhan-2 had negative mid parent heterosis value which is desirable.

Similar finding was reported by Tiwari *et al.* (2011), Latha *et al.* (2013), Thorat *et al.* (2017), Gokulakrishnan (2018) and Shukla *et al.* (2020) indicating the possibility of exploiting heterosis for earliness.

4.2. Heterosis value for days to maturity

Negative heterosis is considered suitable for DTM. None of the crosses had negative heterosis for DTM while considering better parent heterosis and mid parent heterosis suggesting the crosses were not early maturing.

4.3. Heterosis value for effective tillers

Six of the genotypes were significant for effective tillers.NR11835 (IR775-39- 80- 2-2-2X Khumal-4) had highest heterobeltiosis value of 195.24. But, when mid- parent heterosis was considered 6 genotypes had positive significant value with NR11835 (IR775-39-80-2-2-2 X Khumal-4) also had highest mid parent heterosis value of 244.44.

4.4. Heterosis value for plant height

6 crosses had significant negative value considering better parent whereas 3 crosses had negative mid- parent heterosis value which is desirable for plant height as short stature plants are desirable**.** NR11862 (HimaliXTaiching-176) had the highest negative value of -53.02 for plant height for heterobeltiosis and NR11869 (IR67017 X Khumal-10) had highest negative value of -49.81 for mid- parent heterosis.

Tiwari *et al.* (2011b), Thorat *et al.* (2017), Bano and Singh (2018), Vartika and Karanwal (2018), Gokulakrishnan (2018), Sari *et al.* (2019) and Shukla *et al.* (2020) also emphasized the importance of negative significant heterosis for plant height to develop dwarf plant types.

4.5. Heterosis value for panicle length

With regard to panicle length, heterosis in a positive direction is desirable. Out of 18 crosses, only one cross had significant positive heterosis over better parent and three cross had significant values for mid parent heterosis. NR11850 (Khumal-4 X Sugandha -2) with the value of 21.82 had higher heterobeltiosis for PANL.

Panicle length is one of the main attributes to higher yields and the results are in with the findings of Tiwari *et al.* (2011 b), Thakor *et al.* (2018), Patel *et al.* (2018) and Shukla *et al.* (2020)

4.6. Heterosis value for fertile grain number

NR11833 (Khumal -8 X Sukhadhan-2) had highest heterobeltiosis value of 70.90 for FGN and NR1135 (IR775-39-80-2-2-2 X Khumal-4) had highest mid parent heterosis of 54.49* These two are only significant positive values for FGN among 18 crosses.

Similar kind of heterotic pattern was observed by Vennila *et al.* (2011) Mistry *et al.* (2015), Thakor *et al.* (2018) and Sari *et al.* (2019) who reported high heterotic effects for the number of grains per panicle.

4.7. Heterosis value for sterile grain number

Only one cross had negative significant value for sterile grain number considering heterobeltiosis which is desirable for sterile grain number.NR11850(Khumal-4 X Sugandha-2) with the value of -45.96 had the highest or only negative significant value of heterobeltiosis. And none cross had negative significant mid parent heterosis value for SGN.

4.8. Heterosis value for thousand grain weight

None of the crosses had significant heterosis value for TGW while considering heterobeltiosis. However, five crosses had significant values for mid parent heterosis. NR11835(IR775-39-80-2-2-2 X Khumal-4) with the value of 20.8 had highest mid parent heterosis for TGW.

The results are in akin with the findings of Bedi and Sharma (2016), Priyanka and Jaiswal (2017), Thorat *et al.* (2017), Sari *et al. (*2019) and Shukla *et al.* (2020).

Table 5 Heterobeltiosis value for crosses

	NR11836	NR11849	NR11835	NR11853	NR11845	NR11869	NR11828	NR11856	NR11859
DTF	3.64**	10.00**	4.09**	10**	0 ns	9.55**	29.09**	14.22**	2.73**
DTM	16.33**	29.25**	11.56**	33.33**	8.28**	22.41**	33.10**	33.10**	21.81**
ET	16.13ns	3.23ns	195.24**	57.14 ns	52.38 ns	42.86 ns	141.38**	22.22ns	-37.93 ns
PHT	-7.41 ns	-29.89*	24.69 ns	-33.45 *	-11.43 ns	-53.02**	-28.09**	-2.55ns	-49.38**
PANL	-10.91 ns	-22.81*	10.91ns	-8.77 ns	-5.45 ns	-17.54 ns	10.04 ns	-1.54 ns	-12.79*
FGN	-22.25 ns	-32.31*	5.76 ns	-49.56**	-38.48*	-64.63**	57.55 ns	-92.82**	-72.45*
SGN	-37.18 ns	-79.49 ns	-10.71 ns	155.36 ns	-53.06 ns	-82.65 ns	-54.26ns	400.00**	199.68**
TGW	-6.53 ns	-11.15*	5.78 ns	-17.23 **	5.17 ns	-11.88*	10.74ns	0.39 ns	-15.78*

'**'= significant at p-value < 0.01, '*'= significant at p value 0.05, 'ns'= non-significant; DTF= Days to flowering, DTM= Days to maturity, ET= Effective tillers, PHT= Plant height, PANL= Panicle length, FGN= Fertile Grain Number, SGN= Sterile Grain number, TW= TGW= Thousand grain weight

Table 6 Heterobeltiosis value for crosses contd**...**

	NR11862	NR11832	NR11847	NR11850	NR11851	NR11833	NR11839	NR11846	NR11829
DTF	1.83*	9.55**	9.55**	13.64**	10.00**	9.55**	11.36**	0.19ns	22.27**
DTM	25.94**	33.10**	30.42**	32.76**	26.87**	31.21**	27.85**	6.38**	31.21**
ET	-22.22 ns	133.33**	80.95**	17.39ns	9.52ns	96.55**	-27.59ns	6.90 ns	89.66**
PHT	-48.96**	-16.87 ns	-12.20 ns	0 ns	-26.34 ns	-5.51 ns	-11.15 ns	-27.57ns	9.93 ns
PANL	-16.67*	-7.27 ns	-8.93 ns	21.82**	0 ns	-18.33**	-18.33**	1.67ns	-21.67**
FGN	-75.16ns	-58.12**	14.40ns	-46.86**	-20.16 ns	70.90**	-8.96 ns	-11.94ns	-45.27**
SGN	301.52**	954.84**	-42.11ns	-45.96**	337.50**	400**	157.89**	16.15 ns	-25 ns
TGW	-25.20**	-20.54**	-4.75 ns	5.65 ns	-19.36 **	-25.21**	-9.60**	-22.13**	-15.30**

'**'= significant at p-value < 0.01, '*'= significant at p value 0.05, 'ns'= non-significant; DTF= Days to flowering, DTM= Days to maturity, ET= Effective tillers, PHT= Plant height, PANL= Panicle length, FGN= Fertile Grain   Number, SGN= Sterile Grain number, TGW= Thousand grain weight

Table 7 Mid parent heterosis value of crosses

	NR11832	NR11847	NR11850	NR11851	NR11833	NR11839	NR11846	NR11829	NR11836
DTF	-11.57**	11.57**	15.74**	12.04**	9.55**	11.36**	0.19ns	22.27**	5.56**
DTM	34.03**	32.74**	33.68**	28.62**	32.99**	32.75**	7.82**	32.09**	17.93**
ET	151.28**	85.37**	22.73ns	27.78ns	142.55**	-14.29ns	19.23ns	150**	38.46 ns
PHT	-10.62ns	-4.91 ns	-5.42 ns	-19.00 ns	6.86 ns	-8.77 ns	19.59ns	26.96 ns	-3.02ns
PANL	-3.77 ns	-8.11 ns	-17.31*	5.77 ns	-11.71 ns	15.52*	11.92 ns	-13.76*	-6.67ns
FGN	-46.67**	24.68ns	-27.76ns	16.63ns	-62.26**	1.53ns	21.65ns	-18.97ns	-13.10 ns
SGN	-1089.09	-25 ns	-9.38ns	463.22*	552.12**	188.24**	81.55**	-16.33ns	-10.09 ns
TGW	-10.28**	3.64 ns	12.75**	-7.86**	-23.38**	-8.07**	26.77**	-12.06**	4.33 ns

'**'= significant at p-value < 0.01, '*'= significant at p value 0.05, 'ns'= non-significant; DTF= Days to flowering, DTM= Days to maturity, ET= Effective tillers, PHT= Plant height, PANL= Panicle length, FGN= Fertile Grain   Number, SGN= Sterile Grain number, TGW= Thousand grain weight

Table 8 Mid parent heterosis value of crosses contd...

	NR11849	NR11835	NR11853	NR11845	NR11869	NR11828	NR11856	NR11859	NR11862
DTF	10.00**	6.02**	10 **	1.85**	9.55**	31.79**	22.03**	3.20**	10.45**
DTM	33.33**	13.10**	37.54**	9.03**	25.44**	34.72**	34.77**	22.84**	36.16**
ET	23.08 ns	244.44**	83.33 ns	52.38 ns	42.86 ns	180.00**	37.50 ns	-28.00ns	-12.50 ns
PHT	-21.51 ns	37.10*	22.08 ns	-11.07 ns	-49.81**	-13.33 ns	2.92 ns	-38.38**	-45.45 **
PANL	-17.76*	17.3*	-1.89 ns	-5,45 ns	-16.07*	45.38*	8.74ns	-8.72ns	-8.12 ns
FGN	-18.42 ns	54.49*	-22.87 ns	-24.92 ns	-53.85**	50.97 ns	-91.84 **	-71.81*	-72.92**
SGN	-70.09 ns	14.94 ns	236.47*	-28.68 ns	-73.23 ns	-41.89ns	414.29**	246.25**	352.99**
TGW	-8.51 ns	20.87**	-17.00 **	20.26**	-11.71 *	16.50**	3.76 ns	-14.14*	-20.25**

'**'= significant at p-value < 0.01, '*'= significant at p value 0.05, 'ns'= non-significant; DTF= Days to flowering, DTM= Days to maturity, ET= Effective tillers, PHT= Plant height, PANL= Panicle length, FGN= Fertile Grain   Number, SGN= Sterile Grain number, TW= TGW= Thousand grain weight

Table 9 Contribution of Lines, Testers and Line X Tester for set1, set2 and set 3

	set1			set2			set3		
	Contribution of lines	Contribution of testers	Contribution of LxT	Contribution of lines	Contribution of testers	Contribution of LxT	Contribution of lines	Contribution of testers	Contribution of LxT
DTF	0.10	35.04	64.86	7.00	88.62	4.38	61.38	22.87	15.75
DTM	4.13	39.16	56.70	19.99	75.52	4.48	63.68	6.22	30.1
ET	6.27	52.09	41.64	41.78	27.61	30.61	59.78	16.87	23.35
PHT	19.80	11.14	69.06	31.66	55.65	12.69	76.47	12.16	11.37
PANL	-1.55	5.63	-1.55	61.66	35.22	3.12	83.33	13.33	3.33
FGN	0.33	79.00	20.68	48.86	26.12	25.02	20.14	37.75	42.11
SGN	1.37	50.65	47.98	51.19	1.48	47.33	33.66	29.67	36.67
TGW	4.98	74.04	20.98	14.61	53.5	31.89	99.29	0.15	0.56

DTF= Days to flowering, DTM= Days to maturity, ET= Effective tillers, PHT= Plant height, PANL= Panicle length, FGN= Fertile Grain   Number, SGN= Sterile Grain number, TGW= Thousand grain weight, LxT= Line X Tester

4.9. Contribution of Lines, Testers and Line X Tester for set1, set2 and set 3

As seen in table 9 In set1, Line had no contribution to any of the traits, contribution of tester was on effective tillers, panicle length, fertile grain number, sterile grain number and thousand grain weight. Similar result was reporter by Faiz et al,2006 who showed that tester had more contribution to the various characters of rice. While Line X Tester had contributions on days to flowering, days to maturity and plant height. Smaller contribution of line x testers than the testers indicate higher estimates of variances due to general combining ability. Rissi et al. (1991) also reported higher estimates of GCA variances due to testers in rice.

In set2, contribution of Line was on characters such as effective tillers, panicle length, fertile grain number and sterile grain number, while days to flowering, days to maturity, plant height and thousand grain weight were contributed by tester. No contribution of Line X Tester on any of the characters. This shows cross had no contribution of hybrid to the variation in the characters. This is in accordance with the research of Dinesh et al. (2016) whose study showed more contribution of Lines for the variance in the characters.

And while considering set3, Line contributed to the characters such as days to flowering, days to maturity, effective tillers, plant height, panicle length and thousand grain weight and Line X Tester contributed to fertile grain number and sterile grain number. Testers had no contribution to any of the characters.

5. Conclusion

Out of all characters when panicle length and fertile grain number- which are the yield determining characters - were considered Sukhadhan-2 was found to be the best parent for fertile grain number and cross between Himali X Taichung-176 and Manjushree-2 X Samba Mahsuri Sub-1 were found to be best cross due to high GCA and SCA values respectively. When panicle length was considered, IR775- 39-80-2-2-2 was the best parent and cross of Khumal 8 X Sugandha-2 were the best cross having highest GCA and SCA value respectively. When fertile grain number was considered cross of Khumal 8 X Sukhadhan-2 had highest heterobeltiosis value and when panicle length was considered cross of Khumal 4 X Sugandha-2 had highest heterotic value.

So, those parents which had the highest GCA value for a certain trait are good combiners for that character, that can be further utilized to produce offspring   with desirable character.

Compliance with ethical standards

References

[1]   Ali Q., A. Ali, Awan, M. Tariq, S. Ali. 2014. Combining ability analysis for various physiological, grain yield and quality traits of Zea mays L. Life Science Journal, 11:540-551.

[2]   Allard, RW.1960. Principles of plant breeding. John Wiley and Sons Inc, New York, USA. Alumira, J. and J.Rusike. 2005.The green revolution in Zimbabwe. Electronic Journal of Agricultural and Development Economics, 2:50–66.

[3]   Ariful Islam, M.D., M.A. Khaleque Mian, G. Rasul, Q.A. Khaliq and M.A. Mannan Akanda. 2015. Estimation of gene action and variance components of some reproductive traits of rice (*Oryza sativa* L.) through line x tester analysis. Journal of Rice Research,3:1-9.

[4]   Bao, Y., S. Wang and X. Wang.2009. Heterosis and combining ability for major yield traits bed combinations. J Ann Sci Agron.24:523–530.

[5]   Bedi,S. and D. Sharma. 2016. Heterosis studies in hybrid rice (*Oryza sativa* L.). International Journal of Forestry and Crop Improvement, 7: 1-6.

[6]   Bernardo, R.2014.Breeding for quantitative traits in plants. Woodbury, MN: Stemma press   1: 369.

[7]   Bhateris, S., S.P. Sood and A. Pathania.2006. Genetic analysis of quantitative traits across crossing system. Australian Journal of Biological Sciences, 9:463–493.

[8]   Bicer, B.T. and D. Sakar.2008. Heritability and gene effects for yield and yield components. Plant Science, 55:78-100.

[9]   Blank, A.F., Y.R.Rosa, J.L. Carvalho Filho.2012. A diallel study of yield components and ability effects for grain yield in elite Iranian maize inbred lines. Journal of Crop improvements, 27:137-152.

[10]   Blum, A., BIG. Haussmann, A.B. Obilana, P.O. Ayiecho, W. Schipprack. 2006.Hybrid performance of sorghum and its relationship to morphological and physiological traits under variable drought stress in Kenya. Plant Breeding, 117: .223-229.

[11]   Bruce, *A*. B.1910.The Mendelian theory of heredity and the augmentation of vigor. Science, 32: 627- 628.

[12]   Charlesworth, D. and J.H. Willis JH. 2009.The genetics of inbreeding depression. Nature Review Genetics, 10: 783-796.

[13]   Collins, G.N.1921.Dominance and the vigor of first-generation hybrids. Am Natural, 55: 116-133.

[14]   Comstock, R.E. and H.F. Robinson. 1948. The components of genetic variance in rice.Nature Review, 55:99-120.

[15]   Dao, A., J. Sanou, V. Gracen and E.Y. Danquah. 2014.Heterotic relationship among earliness, plant growth, yield and fruit attributes in hot pepper (Capsicum annuum L). Euphytica,150:185- 194

[16] Davenport, C.B. 1908.Determination of dominance in Mendelian inheritance. Proceedings of the American philosophical Society, 47: 59-63.

[17] Deepika, C., R.P. Gnanamalar, K. Thangaraj and N. Revathy. 2019. Combining ability analysis for yield and yield contributing traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding, 10:440-445.

[18] Deglene, L., G. Alibert and P. Lesigne. 1999. Inheritance of resistance to stem canker. Plant science, 87-97-110.

[19] Dehghanpour, Z., N. Singh and R. Bhaatia.2014. Stability of general and specific combining ability, variance estimation and heterotic group classification. Crop Science.54: 89-100.

[20] Dey, S.S., N. Singh and R. Bhaatia. 2014. Genetic combining ability and heterosis for maize. Horticulture Science,99:116-128.

[21] Dhekale. 2019. Correlation studies in hybrid rice (*Oryza sativa* L.). International Journal of Ethopia Field Crops Research,153: 86-93.

[22] Duvick, D.N. 2001.Biotechnology in the 1930s: the development of hybrid maize. Nature Review Genetics, 2: 69-74.

[23] El-Gabry, MAH., TIH. Solieman and AIA. Abido.2014. Combining ability and heritability of some tomato (Solanum lycopersicum L.) cultivars. International Society of Ethopia, 67-88.

[24] Faiz, F.A., M. Sabar, T.H. Awan, M. Ijaz and Z. Manzoor. 2006. Heterosis and combining ability analysis in basmati rice hybrids. Journal of Animal and Plant Science, 16:1-2

[25] FAOSTAT. 2020. Agricultural production statistics agricultural production statistics 2000- 2020. Website: https://www.fao.org/faostat/en/#data/QCL (Retrieved on June 29, 2022)

[26] Fasahat, P., A. Rajabi,J.M. Rad, J. Derera .2016. Principles and utilization of combining ability in plant breeding.Intern ational Journal of Biostatics and Biometrics, 4: 1-24.

[27] Fato,P., J. Derera, P. Tongoona, I. Makanda and J.Sibiya .2012. Heterotic orientation of tropical maize inbred lines towards populations ZM523 and Suwan-1 under downy mildew infestation. Euphytica,187: 381- 392.

[28] Fehr, WR.1993. Principles of cultivar development: development of hybrid cultivars. Biomet Biostatist Int Journal, 4: 1-24.

[29] Fisher, R.A.1926. The arrangement of field experiments. Journal of Ministry of Agriculture, for yield and yield contributing traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding, 10:440-445.

[30] Gaurav, K., P. Kumar and D. Singh. 2017. Estimates of combining ability and standard heterosis for grain yield and various Agro-morphological traits in rice (*Oryza sativa* L.). Journal of Applied and Natural Science. 9:526-532.

[31] Gokulakrishnan, H. 2018. Heterosis for yield and yield attributed traits in rice (*Oryza sativa* L.).Horticultural Biotechnology Research, 4: 26-29.

[32] Griffing, B. 1956a. A generalized treatment of the use of diallel crosses, in quantitative traits in rice(*Oryza sativa*). Heredity, 67-98-110.

[33] Gupta, DK., Acharya S, Patel JB.2011.Combining ability and heterosis studies in pigeon pea using A2 cytoplasm from Cajanus scarabaeoides as source of male sterility. Food Legumes, 24: 58-64.

[34] Hallauer, A. R and J.B. Miranda. 1988.Testers and combining ability, in Quantitative traits. Bangladesh Journal of Plant Breeding and Genetics,24:45-51.

[35] Hasan, M.J., M.U. Kulsum, A. Akter, A.S.M. Masuduzzaman and M.S. Ramesha. 2011.Genetic variability and character association for agronomic traits in hybrid rice (*Oryza sativa* L.). Bangladesh Journal of Plant Breeding and Genetics,24:45- 51.

[36] Jenkins, M.T. and A..M Brunaon.1932. A method of testing inbred line of maize. Agromical Science, 23:77-90

[37] Jones, D.F. 1917.Dominance of linked factors as a means of accounting for heterosis. Genetics, 2: 466-479.

[38] Joshi, S.K., S.N. Sharma and D.L. Singhania. 2004. Combining ability in F1 and F2. various physiological, grain yield and quality traits of Zea mays L. Life Science Journal, 11: 540- 551.

[39] Kagoda, F., J.Derera and P.Tongoona. 2011. Genetic analysis of resistance to nematodes in inbred maize (Zea mays L.) and maize hybrids. Euphytica, 377-393.

[40] Kempthorne, D. and R.N. Curnow.1961. The partial diallel cross. Biometrics,17:229–240. Kempthorne O. An introduction of genetics statistics. John Wiley and Sons, New York,

[41] USA. Kenga, R., S.O. Alabi and S.C. Gupta.2004. Combining ability studies in tropical maize. Crop Science,49: 1165-1176.

[42] Khaled, AGA., K.A. Hamam, MH Motawea. 2013.. Genetic studies on tissue culture response and some agronomical traits in Egyptian bread wheat. Journal of Genetic Engineering and Biotechnology,11:79–86

[43] Kulembeka HP, Ferguson M, Herselman L, *et al.* Diallel analysis of field resistance to brown streak disease in cassava (Manihot esculenta Crantz) landraces from Tanzania. Euphytica. 2012;187(2):277–288.

[44] Kumar, S., N.K. Singh, R. Kumar, S.K. Singh, C. Kumar and A. Kumar. 2017. Heterosis studies for various morphological traits of rice under drought conditions. International Journal of Current Microbiology and Applied Sciences, 6:507-521.

[45] Latha, S., D. Sharma and G.S. Sanghera. 2013. Combining Ability and Heterosis for grain yield and its component traits in rice (*Oryza sativa* L.). Notulae Scientia Biologicae, 5:90-97.

[46] Machida L, J. Derera, P. Tongoona. 2010. Combining ability and reciprocal cross effects of elite quality protein maize inbred lines in subtropical environments. Crop Science, 210:1708–1717.

[47] Makanda, I., P. Tongoona and J. Derera J. 2010.Combining ability and cultivar superiority of sorghum germplasm for grain yield across tropical low- and mid-altitude environments. Field Crops Research,116:75–85.

[48] Makumbi, D., FJ Betran, M. Banziger M. 2011.Combining ability, heterosis and genetic diversity in tropical maize (Zeamays L.) under stress and non-stress conditions. Euphytica, 118:143–162.

[49] Matzinger, DF.1953. Comparison of three types of testers for the evaluation of inbred lines of corn. Agronomy Journal,45:493–495.

[50] Melchinger, A., W. Schmit, H.H. Geiger.1998. Comparison of testcrosses from F2 and first backcross populations in maize. Crop Science, 28:743–749.

[51] Milić, D., S. Katić, D. Karagić.2011. Genetic control of agronomic traits in alfalfa (M sativassp. sativaL.). Euphytica, 182:25–33.

[52] Mistry, P.M., V.J. Patel, N.M. Desai. and M.H. Chaudhari. 2015. Relative heterosis and combining ability of rice. Crop science, 34:32-46.

[53] MOALD. (2021). Statistical information on Nepalese Agriculture 2076/77. 2019/20). Singh durbar, Kathmandu, Nepal.

[54] Moterle, L.M., A.L. Braccini, C.A. Scapio.2012. Combining ability of popcorn lines for seed quality and agronomic traits. Euphytica, 2012;185(3):337–347.

[55] Mukankusi, C., J. Derera and Melis R.2011. Genetic analysis of resistance to Fusarium root rot in common bean. Euphytica,182:11–23.

[56] Bagheri, N. 2010. Heterosis and combining ability analysis for yield and related-traits in pigeonpea using A2 cytoplasm from Cajanus scarabaeoides as source of male sterility. J Food Legumes,24: 58-64.

[57] Nyaligwa,L .2016.Genetic diversity analysis of elite maize inbred lines of diverse sources using SSR markers. Maydica,60: 1-8.

[58] Oakey. H., A. Verbyla and W. Pitchford.2016. Joint modeling of additive and non-additive action.Journal of Crop science, 62:17-18.

[59] OEC. (2022). Rice in Nepal.Website:https://oec.world/en/profile/bilateral- product/wheat/reporter/npl (Retrieved on June 29, 2022).

[60] Patel, A., K. Rathava, P.D. Gajjar, C.G. Intwala. and P. Patel. 2018. Study of heterosis for grain yield and its components in aerobic rice (*Oryza sativa* L.) International Journal of Pure and Applied Biosciences, 6:358-368.

[61] Piepho, H. P 2009.Ridge regression and extensions for genomewide selection in populations of biparental progenies and their uses in estimating the average degree of dominance. Biometrics, 4: 254-266.

[62] Priyanka, K., H.K. Jaiswal. and S.A. Waza. 2014. Combining ability and heterosis for yield, its component traits and some grain quality parameters in rice (*Oryza sativa* L.). Journal of Applied and Natural Science, 6:495-506.

[63] Pswarayi, A., B.Vivek B. 2008.Combining ability amongst CIMMYT's early maturing maize (Zea mays L.) germplasm under stress and non-stress conditions and identification of testers. Euphytica, 162:353–362.

[64] Qu, Z., L. Li and J. Luo.2012. QTL mapping of combining ability and heterosis of rice(*Oryza sativa* l.)Plant Science, 76:667-700.

[65] Ramesh, C., C.D. Raju, C.S Raju. and N.R. Varma. 2018. Combining ability and gene action in hybrid rice. International Journal of Pure and Applied Biosciences,6:497- 510.

[66] Ramu, P., C. Billot, J.F. Rami, S. Senthilvel and H.D. Updahyaya. 2013.Assessment of genetic diversity in the sorghum reference using EST-SSR markers. Theoretical and Applied Genetics,126: 2051-2064.

[67] Reif, J.C., A. E Melchinger, X.C. Xia, M.L. Warburton and D.A. Hoisington .2003.Use of SSRs for establishing heterotic groups in subtropical maize. Theoretical and Applied Genetics, 107: 947-957.

[68] Reif, JC., S. Hamrit,M. Heckenberger, W. Schipprack and H.P. Maurer. 2005. Trends in genetic diversity among European maize cultivars and their parental components during the past50 years. Theoretical and Applied Genetics, 111: 838-845.

[69] Salah, G.M.H., A.E.M. Diaa, M.M.R. Ehab and E.M.M. Mohamed. 2020.Combining ability and gene action studies for horticultural traits in garden pea: A review. Afr J Agric Res. 8: 4718- 4725.

[70] Sari, W.K., C. Nualsri, N.Junsawang. and W. Soonsuwon. 2019. Heterosis studies for yield and agronomic traits in Thai upland rice. Indian Journal of Agricultural Research, 53:255-262.

[71] Sharma, B.B., V.K.Sharma, M.K. Dhakar and S. Punetha. 2013.Combining ability and gene action studies for horticultural traits in garden pea: A review. African Journal of Agricultural Research, 8: 4718-4725.

[72] Shukla, D.K., S.N. Singh, S.C. Gaur and A. Kumar. 2020. Effects of heterosis for yield components in two-line hybrids involving thermosensitive genic male sterile lines in rice (*Oryza sativa* L.). Plant Breeding,22:28–32.

[73] Sibiya, J., P. Tongoona, P and J. Derera.2013. Combining ability and GGE biplot analysisforesistance to to northern leaf blight in tropical and subtropical elite maize inbredlines. Euphytica, 191:245–257.

[74] Singh, A.K., R.S, Pan and P Bhavana. 2013.Heterosis and combining ability analysis in bittergourd (Momordica charantia L.). Bioscan, 8: 1533-1536.

[75] Smith, JSC., T. Hussain and ES. Jones. 2008. Use of doubled haploids in maize breeding. American journal of Agronomy.55:66-89.

[76] Sprague, G.F. and L.A. Tatum.1942. General versus specific combining ability in single crosses in corn. Agronomy Journal, 34:923-932.

[77] Stephens, JC. And P.F Holland PF .1954. Cytoplasmic male sterility for hybrid sorghum seed production. Agronomy Journal, 46: 20-23.

[78] Sukla, S.K. and M.P. Pandey.2008. Combining ability and heterosis over environments for yield and yield components in two-line hybrids involving thermosensitive genic male sterile lines in rice (*Oryza sativa* L.). Plant Breeding,127:28–32.

[79] Thakor, R.P., J.R. Balat, I.R. Delvadiya. and S.R. Rathva. 2018. Heterosis and heterobeltosis studies for grain yield and yield attributing traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding, 9:1286-1294.

[80] Thorat, B.S., R.L. Kunkerkar, S.M. Raut, Desai S.S. Gavai, M,P, M.H. Keluskar. and J.S. Dhekale. 2019. Correlation studies in hybrid rice (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences, 8:1158-1164.

[81] Tiwari, D.K., P. Pandey, S.P. Giri. and J.L. Dwivedi. 2011. Prediction of gene action, heterosis and combining ability to identify superior rice hybrids. International Journal of Botany,7:126- 144.

[82] Townsend, T., V. Segura and G. Chigeza.2013. The use of combining ability analysis to Trends in Biosciences, 8:74-81.

[83] Tyagi, A.P.and P. Lal.2005. Line × tester analysis in sugar cane (Saccharum officinarum). South Pacific Journal of Natural Science, 23:30–36.

[84] Umakanth, A.V., J.V. Patiln and Ch. Rani. 2012. Combining ability and heterosis over mid- parent.Plant breeding, 32-55-67.

[85] Upadhyay, M.N. and H.K. Jaiswal. 2015. Combining ability analysis for yield and earliness in hybrid rice (*Oryza sativa* L.). Asian Journal of Crop Science, 7:81-86.

[86] Updahyaya.2013. Assessment of genetic combining ability of rice. Plant Breeding, 76:92- 104.

[87] Vartika, B. and M.K. Karanwal. 2018. Studies on economic heterosis for grain yield under irrigated and timely transplanted condition in rice (*Oryza sativa* L.). International Journal of Genetics, 10:552-555.

[88] Vasal SK, Cordova H, Pandey S, *et al.* Tropical maize and heterosis. CIMMYT research highlights,Mexico, DF, CIMMYT. 1986.

[89] Veeresha, B.A., N.G. Hanamaratti. and P.M. Salimath. 2015. Heterosis and combining ability studies for yield and productivity traits in rice. International Journal of Current Agricultural Research, 4:120-126.

[90] Vennila, S., Y.Anbuselvam. and K. Palaniraja.2011. Heterosis studies for yield and its components in rice (*Oryza sativa* L.). International Journal of Recent Scientific Research, 2: 261-262.

[91] Verica, I., M. Natalija, D. Andov. and A. Danica.2013. Combining ability analysis of some yield components in rice (*Oryza sativa* L.). Food Science Engineering and Technologies., 9:1005- 1009.

[92] Virmani, S.S. 1994. Prospects of hybrid rice in the tropics and subtropics. Hybrid rice,32- 45-56.

[93] Wassimi,N.N., T.G. Isleib and G.L. Hosfield.1986. Fixed effect genetic analysis of a diallel cross in dry beans (Phaseolus vulgaris L.). Theoretical and Applieded Genetics.88:55-78.

[94] Wilson, N.D., D.E. Weibel and R.W McNew RW.1978. Diallel analyses of grain yield, percent protein, and protein yield in grain Sorghum 1. Crop Science, 18: 491-495.

[95] Yallou, C.G., A. Menkir and V.O. Adetimirin. 2009. Combining ability of maize inbred lines containing genes from Zea diploperennis for resistance to Striga. Plant Breeding, 32:55-67.

[96] Yates, F.1935. Complex experiments. Supplement to the Journal of the Royal Statistical Society, 2:181– 223.

[97] Yucel, C., F.S. Baloch and H. Ozkan. 2009. Genetic analysis of some physical properties of bread wheat ((Triticum aestivum L. em Thell). Turkish Journal of Agriculture, 92:156-167.

[98] Zhang, X., L. Lv, C. Lv, B. Guo and R. Xu R .2015. Combining ability of different agronomic traits and yield components in hybrid barley. PloS One, 10: e0126828.