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Studies on heterosis, heritability and genetic advance using generation mean analysis for yield and its attributing traits in rice under saline conditions

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Abstract
The present investigation was carried out to study the nature and magnitude of gene action for yield and its attributes under saline conditions. Three crosses IR-28 × IR 55179-3B-11-3, GR-17 × IR 55179-3B-11-3 and GR-17 × Dandi were obtained by crossing the parents to produce the F_{1s} and then the F_2, BC_1 and BC_2 generations were generated by selfing and backcrossing the F_{1s} with their respective recurrent parent during *rabi* 2019-20 and *kharif* 2020. The experimental material consisting of six generations of each of the three crosses and evaluated during *kharif* 2020-21 in compact family block design with three replications at Costal Soil Salinity Research Station (CSSRC), Danti-Umbharat. The analysis of variance between families (crosses) revealed that the mean squares due to crosses were significant for all the characters. A significant difference was observed among the generations in all the characters studied for all three crosses. Highly significant and positive relative heterosis, heterobeltiosis and inbreeding depression were recorded in all the crosses for most of the traits. Significant heterosis over mid-parent and better parent, along with positive inbreeding depression, may be attributed to a major contribution from dominance (h) and additive × additive (i) gene effects, where selection will be effective only in later generations. High to moderate heritability (Narrow-sense) estimates coupled with moderate to high genetic advance was observed for most of the characters in all three crosses. High heritability coupled with a high genetic advance was most likely due to additive gene effects. So, characters having high heritability coupled with high genetic advance can be further improved by adopting selections in succeeding generations.

Keywords: Rice salinity**,** heterosis, inbreeding depression, heritability, genetic advance

Introduction
Rice (*Oryza sativa* L.; 2n = 24) is a key source of food and energy for over 2.7 billion people on a daily basis and it is grown on around one-tenth of the world's arable land. It is genetically diverse, with thousands of landraces and progenitor species, in addition to its commercial value. Rice is the princess of all grains, with twenty-four species identified in the genus Oryza and tribe Oryzeae of the Poaceae family (Gramineae) (Khush, 1997) [1]. *Oryza sativa* L. or Asian rice and *Oryza glaberrima* Steud or African rice are the only two cultivated species.

Breeding for salt tolerance is a more promising, energy-efficient, cost-effective and socially acceptable strategy for overcoming salt-stress concerns (Ray and Islam, 2008) [2]. Salinity tolerance is a complicated feature that is controlled by polygenes on both a genetic and physiological level (Baby *et al*., 2010) [3]. Understanding the genetic regulation for salt tolerance processes is required to produce novel variety with a high level of salinity tolerance. Plant breeders are primarily interested in improving features that are directly or indirectly linked to economic gains. These traits are usually quantitative in nature and are driven by a large number of genes, each of which has a little effect working cumulatively, known as polygenes. (Mather, 1943) [4]. The magnitude of heterosis aids in the discovery of suitable cross combinations for use in traditional breeding programmes to produce a wide range of variability in successive generations. Knowledge of heterosis, as well as the level of inbreeding depression in following generations, is critical for getting the most out of heterosis by using the right breeding methods.

Materials and Methods
The experimental material consisting of six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of each of the three crosses were sown during *kharif* 2021 in compact family block design with three replications.

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Each replication was divided in three compact blocks. The details of the experimental material used in the present investigation are given in Table 1. All the characters studied were recorded on randomly selected competitive plants per line. The observations recorded for days to flowering, days to maturity, productive tillers per plant, plant height (cm), 100 grain weight (g), shoot biomass (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%) were subjected to generation mean analysis.

Heterosis was estimated as percent increase or decrease in the mean value of F_1 hybrid over the mid-parent, *i.e.*, relative heterosis (Briggle, 1963) [5] and over the better parent, *i.e.*, heterobeltiosis (Fonseca and Patterson, 1968) [6], for each character as under.

$$\text{Relative heterosis (\%)} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Heterobeltiosis (\%)} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where,

$\overline{F_1}$	=	Mean performance of the F_1 hybrid
$\overline{MP}$	=	Mean value of the parents (P_1 and P_2) of a hybrid
$\overline{BP}$	=	Mean value of better parent

Inbreeding depression was computed by using the following formulae (given by):

$$\text{Inbreeding depression(\%)} = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_2}} \times 100$$

The significance of the inbreeding depression was tested by comparing the calculated 't' value with the table 't' value at 5 percent (1.96) and 1 percent (2.58) levels of significance.

The narrow-sense heritability, as suggested by Warner (1952) [7], was calculated as follows:

$$h^2_{(ns)}(\%) = \frac{\widehat{\sigma}^2_A}{\widehat{\sigma}^2_P} \times 100$$

Where,

$h^2_{(n)}$	=	Heritability in narrow sense
$\widehat{\sigma}^2_A$	=	Additive genotypic variance (d)
$\widehat{\sigma}^2_P$	=	Phenotypic variance

The expected genetic advance represents the shift in a population mean towards the superior side under some selection pressure after a single generation of selection. It was calculated using the methodology suggested by Johnson *et al.* (1955) [8].

$$\text{Expected genetic advance} = k \cdot h^2_{(ns)} \cdot \widehat{\sigma}_P$$

Where,

$h^2_{(ns)}$	=	Heritability in a narrow-sense
$\widehat{\sigma}_P$	=	Phenotypic standard deviation
K	=	Selection differential

Result and discussion
Analysis of variance

The results of the analysis of variance between the families (Crosses) and among the progenies within the families (between generations) are presented in Table 2 and 3. The mean sum of squares data revealed the significant differences between all of the three families studied for all of the characters. All of the three crosses also showed highly significant differences between populations in the mean sum of squares for most of the characters under study, except panicle length (cm) in cross GR-17 × IR 55179-3 B-11-3. Hence, the selected crosses were diverse enough to study the additive, dominance and epistatic variances that govern the traits under study.

The analysis of variance among the progenies within the family found significant for days to flowering, days to maturity, productive tillers per plant, plant height (cm), 100 grain weight (g), shoot biomass (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%) for all of the three crosses i.e., IR-28 × IR55179-3B-11-3, GR-17 × IR55179-3 B-11-3 and GR-17 × Dandi. For panicle length, the crosses, IR-28 × IR55179-3B-11-3 and GR-17 × Dandi were having significant differences among the progenies of that family while the cross GR-17 × IR55179-3B-11-3 showed non-significant results. The cross showing non-significant result was excluded from the further analysis.

Estimates of relative heterosis (RH %), Heterobeltiosis (HB %) and inbreeding depression (ID %)
The extent of heterotic effects i.e., relative heterosis (RH) and heterobeltiosis (HB) as well as inbreeding depression (ID) were estimated for all the characters under study. The relative heterosis, heterobeltiosis and inbreeding depression for various characters in three crosses are presented in Table 5 and 6.

For days to flowering, a parent having early flowering was considered the better parent. Significant and positive relative heterosis was obtained for GR-17 × IR55179-3 B-11-3 (4.86%) while the negative significant was recorded for GR-17 × Dandi (-16.80%). Similar findings were also reported by Singh and Patel (2020a) [22], Hitashi *et al.* (2020) [10] and Singh and Patel (2021) [19].

The GR-17 × Dandi (-7.02%) was also exhibiting the significant negative heterobeltiosis, a desirable trait to develop early flowering hybrid. Significant negative heterosis was also reported by Balat *et al.* (2018) [12], Makwana *et al.* (2018) [13], Patel *et al.* (2019) [14] and Hitashi *et al.* (2020) [10]. Significant positive inbreeding depression was found for IR-28 × IR55179-3 B-11-3 (8.81%) and GR-17 × IR55179-3 B-11-3 (7.36%). The significant results of inbreeding depression were also found by Makwana *et al.* (2018) [13], Patel *et al.* (2019) [14], Solanke *et al.* (2019a) [18] and Hitashi *et al.* (2020) [10].

The highest significant negative heterosis for days to maturity was found for GR-17 × Dandi (-12.64%). Similar results were also observed by Balat *et al.* (2018) [12], Hitaishi *et al.* (2020) [10] and Patel and Patel (2020b) [16]. The perusal of heterobeltiosis showed significant negative for GR-17 × Dandi (-5.00%) which is desirable to obtain early maturing hybrid. The inbreeding depression was significant for all of the crosses studied for days to maturity and the results are in parity with the findings of Balat *et al.* (2018) [12] and Hitaishi *et al.* (2020) [10].

Productive tillers per plant is one of the major grain yield contributing traits, hence heterosis in positive direction is

highly essential. For productive tillers per plant, GR-17 × IR55179-3 B-11-3 (-34.36%) showed significant relative heterosis (%). The maximum and positive significant heterobeltiosis was manifested by GR-17 × IR55179-3 B-11-3 (16.91%). The positive heterobeltiosis for productive tillers per plant was also reported by Balat et al. (2018) [12], Kumari and Senapati (2019) [17], Solanke et al. (2019a) [18] and Patel et al. (2019) [14]. Significant inbreeding depression was found for GR-17 × IR55179-3 B-11-3 (-66.49%).

The data embodied in Table 4.16 showed significant relative heterosis (%) for plant height (cm) was observed for the cross, IR-28 × IR55179-3 B-11-3 (15.84%) and GR-17 × Dandi (-2.81%). As the dwarf plant height is desirable for recording high yield in rice vigour in plant height may lead to the unfavourable source to sink ratios and harvest index (%) and below optimum yield due to lodging. The estimates of heterobeltiosis showed significant negative heterobeltiosis for GR-17 × Dandi (-6.17%), while significant positive for IR-28 × IR55179-3 B-11-3 (5.90%). The results pertaining to inbreeding depression showed significance for GR-17 × IR55179-3 B-11-3 (-3.13%), while the other two crosses were non-significant for plant height.

The data pertaining to panicle length (cm) indicated that IR-28 × IR55179-3 B-11-3 (12.08%) showed positive significant relative heterosis (%) for panicle length (cm). The maximum and positive significant heterobeltiosis was found for IR-28 × IR55179-3 B-11-3 (8.25%). The positive heterobeltiosis was also reported by Balat et al. (2018) [12], Kumari and Senapati (2019) [17], Hitaishi et al. (2020) [10] and Singh and Patel (2021) [19]. The inbreeding depression was significant for GR-17 × IR55179-3B-11-3.

A perusal of data of 100 grain weight (g) indicated the highly significant relative heterosis (%) for IR-28 × IR55179-3B-11-3 (11.90%) and GR-17 × IR55179-3 B-11-3 (7.62%). The inbreeding depression was significant for IR-28 × IR55179-3B-11-3 (11.18%) and non-significant for the other two crosses. The non-significant inbreeding depression was also observed by Kumari and Senapati (2019) [17], Patel et al. (2019) [14], Ganapati et al. (2020) [20] and Singh and Patel (2021) [19].

For shoot biomass per plant (g), relatively positive and significant relative heterosis was obtained for the IR-28 × IR55179-3 B-11-3 (8.11%) and GR-17 × IR55179-3 B-11-3 (10.17%), while GR-17 × Dandi (1.83%) resulted as non-significant. Significant inbreeding depression was found for the cross, IR-28 × IR55179-3 B-11-3 (-29.50%).

The results for grain yield per plant (g) indicated significant positive relative heterosis (%) for all of the crosses i.e., IR-28 × IR55179-3 B-11-3 (20.50%), GR-17 × IR55179-3 B-11-3 (11.92%) and GR-17 × Dandi (30.47%). Makwana et al. (2018) [13], Balat et al. (2018) [12], Kumari and Senapati (2019) [17], Patel et al. (2019) [14], Singh and Patel (2020b) [16], Ganapati et al. (2020) [20], Hitaishi et al. (2020) [10] and Singh and Patel (2021) [19] also reported similar findings for grain yield per plant (g). The inbreeding depression for the trait was non-significant for all of the three crosses and the results are in accordance with the findings of Kumari and Senapati (2019) [17], Patel and Patel (2020b) [16] and Singh and Patel (2021) [19].

A perusal of data for biological yield per plant (g) indicated highly significant positive relative heterosis (%) for all of the crosses i.e., IR-28 × IR55179-3 B-11-3 (14.13%), GR-17 × IR55179-3B-11-3 (10.99%) and GR-17 × Dandi (14.21%). Inbreeding depression for IR-28 × IR55179-3 B-11-3 (-

17.41%) was found significant.

The data of harvest index (%) revealed that IR-28 × IR55179-3B-11-3 (6.01%) and GR-17 × Dandi (13.55%) recorded positively significant relative heterosis (%). Heterobeltiosis was also found significant for all of the crosses studied. Similar results were also reported by Balat et al. (2018) [12], Kumari and Senapati (2019) [17], Solanke et al. (2019a) [18], Patel et al. (2019) [14], Singh and Patel (2020b) [16] and Hitaishi et al. (2020) [10]. Inbreeding depression was found significant for all of the crosses studied.

Heritability and genetic advance
An estimate of heritability serves as a useful guide to the breeder. The breeder can appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow-sense heritability) effects. The narrow-sense heritability for days to flowering was 142.76 percent (GR-17 × IR55179-3 B-11-3) and 140.76 percent (GR-17 × Dandi).

The value of the narrow sense heritability for days to maturity was low for IR-28 × IR55179-3 B-11-3 (18.69%), while high narrow-sense heritability was found for GR-17 × IR55179-3B-11-3 (101.81%) and GR-17 × Dandi (160.80%). Genetic advance was lower for IR-28 × IR55179-3 B-11-3 (4.16%) while high genetic advance was found for GR-17 × IR55179-3B-11-3 (14.87%) and GR-17 × Dandi (45.45%), respectively. The high heritability coupled with high genetic advance in the GR-17 × IR55179-3 B-11-3 and GR-17 × Dandi suggested the presence of additive gene action.

Narrow sense heritability for productive tillers per plant was low for GR-17 × IR55179-3 B-11-3 (12.78%) with the low genetic advance (9.05%) suggesting the role of non-additive gene action influenced by the environment. Narrow sense heritability was found high in the case of plant height (cm) for GR-17 × IR55179-3 B-11-3 (150.11%) and GR-17 × Dandi (99.25%) with a high genetic advance of 30.34 percent and 83.81 per cent, respectively. These results inferred that plant height was governed by additive gene action.

For crosses IR-28 × IR55179-3 B-11-3 and GR-17 × IR55179-3B-11-3, the genetic advance was high (23.91% and 26.49%, respectively) with high narrow-sense heritability of 60.94 percent and 68.61 percent for panicle length (cm), respectively. The results indicated the predominance of additive gene action. For cross IR-28 × IR55179-3 B-11-3, low heritability (19.05%) coupled with low genetic advance (8.99%) suggests the role of non-additive gene action with a high influence on the environment for 100 grain weight (g). The genetic advance was found to be moderate (11.79%) along with low heritability (26.60%) for GR-17 × IR55179-3B-11-3, indicating the predominance of non-additive and epistatic interactions for 100 grain weight.

Low narrow-sense heritability (16.45%) along with moderate genetic advance (15.01%) for the GR-17 × Dandi which showed the possibility of the preponderance of non-additive gene action for grain yield per plant. These results were supported by Khaled Salem et al. (2015) [21] and Patel and Patel (2020a) [22]. The other two crosses showed negative values of narrow-sense heritability and genetic advance, thus taken as zero. The value of narrow-sense heritability (87.40%) was found high coupled with moderate genetic advance (19.31%) for GR-17 × Dandi for harvest index (%) suggesting preponderance of additive gene action coupled with high influence of environment for the inheritance of the trait. The results were in parity with the findings of Singh and Patel (2020c) [23].

Table 1: Details of experimental crosses

Cross	Generation	Details
		IR-28 (S) × IR 55179-3B-11-3 (T)
1	P₁	IR-28
	P₂	IR 55179-3B-11-3
	F₁	IR-28 × IR 55179-3B-11-3
	F₂	(IR-28 × IR 55179-3B-11-3) F₁ selfed
	BC₁	(IR-28 × IR 55179-3B-11-3) × IR-28
	BC₂	(IR-28 × IR 55179-3B-11-3) × IR 55179-3B-11-3
		GR-17 (MT) × IR 55179-3B-11-3 (T)
2	P₁	GR-17
	P₂	IR 55179-3B-11-3
	F₁	GR-17 × IR 55179-3B-11-3
	F₂	(GR-17 × IR 55179-3B-11-3) F₁ selfed
	BC₁	(GR-17 × IR 55179-3B-11-3) × GR-17
	BC₂	(GR-17 × IR 55179-3B-11-3) × IR 55179-3B-11-3
		GR-17 (MT) × Dandi (MT)
3	P₁	GR-17
	P₂	Dandi
	F₁	GR-17 × Dandi
	F₂	(GR-17 × Dandi) F₁ selfed
	BC₁	(GR-17 × Dandi) × GR-17
	BC₂	(GR-17 × Dandi) × Dandi

Table 2: Analysis of variance between families for all the characters of three crosses of rice

Characters/ D.F.	Replications	Families	Error
	2	2	4
Days to flowering	0.41	106.63**	0.19
Days to maturity	0.88**	94.50**	0.01
Productive tillers per plant	0.18	4.03**	0.06
Plant height (cm)	0.14	64.70**	0.05
Panicle length (cm)	0.29	0.59*	0.08
100 grain weight (g)	0.01	0.01**	0.01
Shoot biomass per plant (g)	0.02	25.85**	0.02
Grain yield per plant (g)	0.11	2.18*	0.18
Biological yield per plant (g)	0.24	42.31**	0.28
Harvest Index (%)	0.32	8.70**	0.09

Table 3: Analysis of variance between generations within the families for Crosses I, II and III in saline soil

Characters/DF	Cross I (IR-28 × IR55179-3B-11-3)			Cross II (GR-17 × IR55179-3B-11-3)			Cross III (GR-17 × Dandi)		
	Replication	Progenies	Error	Replication	Progenies	Error	Replication	Progenies	Error
	2	5	10	2	5	10	2	5	10
Days to flowering	2.20*	169.37**	0.41	0.44	18.22**	1.41	2.21	225.10**	0.77
Days to maturity	1.18	251.42**	1.03	2.79	50.10**	0.98	1.56	228.06**	0.98
Productive tillers per plant	1.61	5.14**	0.49	0.13	19.31**	0.22	0.12	3.14**	0.25
Plant height (cm)	1.2	318.98**	1.67	0.22	8.40**	1.39	0.1	67.71**	0.59
Panicle length (cm)	0.84	12.36**	1.18	1.21	3.94	1.77	0.67	7.47**	0.55
100 grain weight (g)	0.01	0.08**	0.01	0.01	0.14**	0.01	0.01	0.06**	0.01
Shoot biomass per plant (g)	0.05	120.34**	0.9	0.02	317.99**	0.92	0.31	38.35**	0.64
Grain yield per plant (g)	0.67	33.87**	0.9	0.36	41.42**	1.05	1.85	33.46**	0.95
Biological yield per plant (g)	0.87	268.04**	2.84	0.26	565.15**	1.07	3.68	120.96**	1.16
Harvest Index (%)	0.03	21.72**	0.94	0.84	79.32**	4.36	2.21	29.91**	3.31

Table 4: Estimates of relative heterosis (RH %), Heterobeltiosis (HB %) and inbreeding depression (ID %) for different traits in three crosses of rice

	Days to flowering		Days to maturity		Productive tillers per plant		Plant height (cm)		Panicle length (cm)	
	Estimates	S. E. (±)	Estimates	S. E. (±)	Estimates	S. E. (±)	Estimates	S. E. (±)	Estimates	S. E. (±)
	Cross I (IR-28 × IR55179-3B-11-3)									
RH%	-0.05	0.73	-6.88**	0.77	-4.15	0.48	15.84**	0.58	12.08**	0.53
HB%	16.56**	0.85	6.69**	0.92	-5.46	0.57	5.90**	0.72	8.25**	0.62
ID%	8.81**	0.94	-8.34**	1.17	-3.53	0.55	-0.71	0.97	0.26	0.58
	Cross II (GR-17 × IR55179-3B-11-3)									
RH%	4.86**	1.06	1.17	1.07	-34.36**	0.36	0.26	0.65	4.02	0.54
HB%	6.61**	1.16	6.30**	1.12	-35.25**	0.41	-0.06	0.63	5.18	0.64
ID%	7.36**	1.22	4.95**	1.21	-66.49**	0.42	-3.13**	1.16	11.71**	0.56

Cross III (GR-17 × Dandi)										
RH%	-16.80**	0.97	-12.64**	0.82	9.38	0.51	-2.81**	0.76	0.46	0.51
HB%	-7.02**	1.03	-5.00**	0.90	16.91*	0.51	-6.17**	0.80	-9.49**	0.60
ID%	-6.92**	1.32	-13.12**	1.56	-11.43	0.59	-1.68	1.13	-0.49	0.52

Table 4: Contd…

	100 grain weight (g)		Shoot biomass per plant (g)		Grain yield per plant (g)		Biological yield per plant (g)		Harvest Index (%)	
	Estimates	S. E. (±)	Estimates	S. E. (±)	Estimates	S. E. (±)	Estimates	S. E. (±)	Estimates	S. E. (±)
Cross I (IR-28 × IR55179-3B-11-3)										
RH%	11.90**	0.04	8.11**	0.61	20.50**	0.56	14.13**	1.15	6.01**	0.30
HB%	2.79	0.04	1.18	0.70	6.76*	0.65	3.97	1.32	2.78**	0.36
ID%	11.18**	0.05	-29.50**	1.13	-5.93	0.99	-17.41**	2.10	9.92**	0.36
Cross II (GR-17 × IR55179-3B-11-3)										
RH%	7.62**	0.05	10.17**	0.67	11.92**	0.86	10.99**	1.44	0.09	0.70
HB%	-0.65	0.06	-8.40**	0.71	11.45*	0.91	0.36	1.75	-10.32**	0.98
ID%	3.92	0.06	-5.56	0.99	2.23	0.98	-1.89	1.94	4.03**	0.40
Cross III (GR-17 × Dandi)										
RH%	1.46	0.05	1.83	0.64	30.47**	0.73	14.21**	1.33	13.55**	0.47
HB%	-5.55*	0.05	-13.12**	0.71	20.93**	0.88	0.92	1.54	7.43**	0.60
ID%	0.15	0.06	0.60	0.87	2.72	1.02	1.65	1.84	2.74*	0.56

Table 5: Estimates of heritability and genetic advance for different traits in three crosses of rice under saline conditions.

Particulars	Estimates%									
	Days to flowering	Days to maturity	Productive tillers per plant	Plant height (cm)	Panicle length (cm)	100 grain weight (g)	Shoot biomass per plant (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest Index (%)
Cross I (IR-28 × IR55179-3B-11-3)										
Heritability% (NS)	-	18.69	-	-	60.94	19.05	-	-	-	-
Genetic Advance%	-	4.16	-	-	23.91	8.99	-	-	-	-
Cross II (GR-17 × IR55179-3B-11-3)										
Heritability% (NS)	142.76	101.81	12.78	150.11	68.61	26.60	-	-	-	-
Genetic Advance%	35.52	14.87	9.05	30.34	26.49	11.79	-	-	-	-
Cross III (GR-17 × Dandi)										
Heritability% (NS)	140.78	160.80	127.14	99.25	-	105.13	-	16.45	-	87.40
Genetic Advance%	40.17	45.45	23.08	83.81	-	44.65	-	15.01	-	19.31

Conclusion
Highly significant and positive relative heterosis, heterobeltiosis and inbreeding depression were recorded in all the crosses for most of the traits. Significant heterosis over mid-parent and better parent, along with positive inbreeding depression, may be attributed to a major contribution from dominance (h) and additive × additive (i) gene effects, where selection will be effective only in later generations. High to moderate heritability (narrow-sense) estimates coupled with moderate to high genetic advance was observed for most of the characters in all three crosses. High heritability coupled with a high genetic advance was most likely due to additive gene effects. So, characters having high heritability coupled with high genetic advance can be further improved by adopting selections in succeeding generations.

References:
1. Khush GS. Origin, dispersal, cultivation and variation of rice. Pl. Mol. Bio. 1997;35:25-34.
2. Ray P, Islam M. Genetic analysis of salinity tolerance in rice. Bangladesh J of Agric. Res. 2008;33:519-529.
3. Baby J, Jini D, Sujatha S. Biological and physiological perspectives of specificity in abiotic salt stress response from various rice plants. Asian J. Agri. Sci. 2010;2:99-105.
4. Mather K. Polygenic inheritance and natural selection. Biol. Rev. 1943;18:32-64.
5. Briggle LW. Heterosis in Wheat-A Review. Crop Sci. 1963;3:407-412.
6. Fonseca S, Patterson FL. Hybrid vigour in a seven parent diallel cross in common winter wheat (*Triticum aestivum* L.). Crop Sci. 1968;8:85-95.
7. Warner JN. A method of estimating heritability. Agron. J. 1952;44:427-430.
8. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybean and their implications in selection. Agron. J. 1955;47:477-483.
9. Singh AG, Patel PB. Generation mean analysis for yield and its components in rice (*Oryza sativa* L.). J Pharm. Innov. 2020a;9:473-477.
10. Hitaishi SK, Vimal SC, Chaudhary AK. Heterosis and inbreeding depression for yield, its contributing characters and physiological parameters in rice (*Oryza sativa* L.) under stress condition. J Pharmacogn. Phytochem. 2020;9:1216-1218.
11. Singh BS, Patel VP. Study of heterosis and inbreeding depression in F₂ generation of upland rice (*Oryza sativa* L.). J Pharm. Innov. 2021;10:655-660.
12. Balat JR, Thakor RP, Delvadiya IR, Rathva SR. Heterosis and inbreeding depression in F₂ population of rice (*Oryza sativa* L.) for yield and related traits. J Pharmacogn. Phytochem. 2018;7:3224-3226.
13. Makwana RR, Patel VP, Pandya MM, Chaudhary BA. Heterosis and inbreeding depression for morpho-physiological traits in rice [*Oryza sativa* L.]. Int. J Pure App. Biosci. 2018;6:1477-1482.

14. Patel SK, Makwana MG, Patel JM, Patel CR. Heterosis and inbreeding depression for grain yield and its component traits in rice (*Oryza sativa* L.). Int. J Genet. 2019;11:615-617.
15. Solanke AC, Patel PB, Patel PK. Study of heterosis and inbreeding depression in F_2 generation of aromatic rice. J Pharm. Innov. 2019a;8:10-15.
16. Patel HB, Patel PB. Heritability and genetic advance studies in segregating generation for yield, its components and quality traits in rice (*Oryza sativa* L.). J Pharm. Innov. 2020b;9:221-224.
17. Kumari A, Senapati BK. Studies on the genetic basis of heterosis and inbreeding depression for yield and yield attributing characters in rice (*Oryza sativa* L.). Int. J Chem. Stud. 2019;7:1887-1890.
18. Solanke AC, Patel PB and Patel PK. Study of heterosis and inbreeding depression in F_2 generation of aromatic rice. J. Pharm. Innov. 2019a;8:10-15.
19. Singh BS, Patel VP. Study of heterosis and inbreeding depression in F_2 generation of upland rice (*Oryza sativa* L.). J Pharm. Innov. 2021;10:655-660.
20. Ganapati RK, Rasul MG, Sarker U, Singha A, Faruquee M. Gene action of yield and yield contributing traits of submergence tolerant rice (*Oryza sativa* L.) in Bangladesh. Bull Natl. Res. Cent. 2020;44:8-17.
21. Khaled Salem FM, Yaseen YM, El-Abd AB, Ayoub A. Inheritance of some yield components and grain quality traits in rice (*Oryza sativa* L.). J Product and Dev. 2015;20:161-177.
22. Patel HB, Patel PB. Heritability and genetic advance studies in segregating generation for yield, its components and quality traits in rice (*Oryza sativa* L.). J Pharm. Innov. 2020a;9:221-224.
23. Singh BS, Patel VP. Study of heritability and genetic advance in segregating generations for yield and yield contributing characters in upland rice (*Oryza sativa* L.). Biosci. Trends. 2020c;13:782-788.