

Full Length Research Paper

# Diallel analysis for salinity tolerance in rice traits at germination stage

Sharifi Peyman<sup>1\*</sup>, Mohammad Reza Safari Motlagh<sup>2</sup> and Hashem Aminpanah<sup>1</sup>

<sup>1</sup>Department of Agronomy and Plant Breeding, Rasht Branch, Islamic Azad University, Rasht, Iran.

<sup>2</sup>Department of Plant Pathology, Islamic Azad University, Rasht Branch, Rasht, Iran.

Accepted 19 December, 2011

Rice (*Oryza sativa* L.) is a medium salt-resistant crop. The present study determined the inheritance of salinity tolerance at germination stage by complete diallel crosses between six rice genotypes. Analysis of variance indicated that there were significant differences among the genotypes and specific combining ability (SCA) for all of the traits contain reduction in radicle length (RL, %), reduction in coleoptile length (PR, %), reduction in germination percentage (GP, %) and reduction in germination rate (GR, %). General combining ability (GCA) was significant for GP and RL. The reciprocal (REC) and maternal (MAT) effects were significant for GP, RL and PL. Non-maternal effect (NONMAT) were significant only for RL and PL. The significant GCA and SCA indicated the role of additive and non-additive gene actions. The higher magnitude of dominance variances showed that non-additive gene action was predominant to additive one. The perusal of GCA effects reveals that Shahpasand was an ideal general combiner for GP and RL, whereas IRFAON-215 was a good general combiner for CL. The estimates of SCA effects of crosses indicated that Shahpasand × Sepidrood and Hassani × IRFAON-215 could be regarded as the most desirable cross combination for GP and RL, respectively.

**Key words:** Combining ability, heterosis, salinity, rice, germination.

## INTRODUCTION

Rice (*Oryza sativa* L.) is a medium salt-resistant crop and its varieties exhibit variability in sensitivity to salinity conditions (IRRI, 1994). Salt stress like many other abiotic stresses can considerably suppress growth and development of a number of plants (Naz et al., 2010). Seedling was proved to be very sensitive after emergence at salinity level 10.5 ds/m (Alam et al., 2004). Salinity impairs seed germination, reduces nodule formation, retards plant development and reduces crop yield (Greenway and Munns, 1980). Earlier growth stages are more sensitive to salinity than subsequent ones (Lal, 1985). Most rice cultivars are severely injured in submerged soil cultured on EC of 8 to 10 dSm<sup>-1</sup> at 25°C, but sensitive cultivars are damaged even at 2 dSm<sup>-1</sup> (Mass and Hoffman, 1997). Under salt stress condition, the phenotypes of agronomic traits are affected not only by its salt-tolerance but also by its own genetic mechanism. In addition, improving salt tolerance of crops is necessary

for sustainable food production in different saline regions (Pitman and Lauchli, 2002).

It is necessary to understand the genetic mechanism of different germination and seedling traits to salt stress, in order to improve the accuracy of genetic evaluation and selection efficiency of salt tolerance (Gu et al., 1999). The mode of inheritance is also very important in defining the selection strategy to be applied in a breeding program. Diallel mating designs are an important tool in plant breeding programs to obtain information on the inheritance of quantitative traits. A partial diallel consisting of crosses between numbers of parents is useful when there are distinct characters (Griffing, 1956). Diallel analysis provides information on average performance of individual lines in crosses known as general combining ability (GCA). It also gives information about the performance of crosses relative to the average performance of parents involved in the cross known as specific combining ability (SCA). Heritability is defined as the ratio of variance due to hereditary difference and genotypic variance to the total phenotypic variance (Meredith, 1984). Diallel analysis leads to identification of parents

\*Corresponding author. E-mail(s): [Kadose@yahoo.com](mailto:Kadose@yahoo.com), [sharifi@iaurasht.ac.ir](mailto:sharifi@iaurasht.ac.ir).

**Table 1.** Information of some of important traits on parental varieties.

Varieties	Origin	Grain type	Stature
Shahpasand	Iran (land race)	Long	Tall
Hassani	Iran (land race)	Coarse	Tall
Deilmani	Iran (land race)	Fine	Tall
Sepidrod	Iran (Improved cultivar)	Long	Dwarf
Neda	Iran (Improved cultivar)	Medium	Dwarf
Saleh	Iran (Improved cultivar)	Long	Semi-dwarf
IRFAON-215	IRRI (line)	Coarse	Semi-dwarf

with additive and non additive effects for specific characteristics. This in turn helps in choosing parents to be included in hybridization or population breeding programs (Murtaza et al., 2005).

There are a few studies related to the genetic basis of rice salinity tolerance at the several stages. Moejopawiro and Ikehshi (1981) indicated both general and specific combining ability was significant at germination stage. The genetics of salt tolerance in rice was investigated at seed germination by Singh et al. (2008) and revealed both additive and non-additive gene effects for controlling of related traits. Gregorio and Senadhira (1993) reported both additive and dominant gene effects in controlling of rice salinity tolerance at seedling stage. Ray and Islam (2008) indicated the importance of additive effects in the inheritance of salinity tolerance at germination stage. In contrast, Lee et al. (1996) indicated that in japonica rice varieties, dominant alleles were present in salt tolerant parents. Their estimates of genetic parameters showed significant additive and nonadditive gene action for salinity tolerance score,  $K^+$  and Na/K ratio. Combining ability analysis by Griffing's (1956) method confirmed the significance of both additive and nonadditive effects, and the former showed greater importance in the inheritance of the traits (Mishra et al., 1990). The genetic basic of rice traits were studied by some of researchers at salinity condition in the other stages. El-Mouhamady et al. (2010) indicated significant general and specific combining ability effects for some of agronomic traits under normal and salinity conditions by diallel cross. Karthikeyan et al. (2009) indicated preponderance of nonadditive gene action for the characters namely, plant height, number of productive tillers, boot leaf length, panicle length, grain weight per primary panicle and grain yield per plant. Geetha et al. (2006) revealed from diallel analysis that sodicity tolerance in terms of grain yield was governed by both additive and non additive gene action. However, the predictability ratio revealed the preponderance of non additive gene action. Sankar et al. (2008) indicated the role of dominance gene action in controlling of days to 50 per cent flowering, plant height, productive tillers per plant, panicle exertion, panicle length, panicle weight, filled grains per panicle, spikelet fertility, 100 grain weight

and grain yield. In the other crops, Mano and Takeda (1997) found that salinity tolerance of barley at germination stage was controlled by over-dominant alleles, and nonadditive variance was larger than additive one; while at the seedling stage, tolerance was predominantly controlled by additive genes, with also some effects of dominance.

The objectives of this study were to determine the general and specific combining ability of six rice genotypes, the choice of best parents (between studied parents) for salinity resistance programs and the inheritance and heritability of salinity tolerance traits at the germination stage.

## MATERIALS AND METHODS

### Genetic material and crosses

The plant materials used in this study were six rice varieties containing Shahpasand ( $P_1$ ), Hassani ( $P_2$ ), Sepidrod ( $P_3$ ), Neda ( $P_4$ ), Saleh ( $P_5$ ) and IRFAON215 ( $P_6$ ). Some of traits of selected parents are shown in Table 1. Nursery was provided and the seeds of six parents were sown on the 10<sup>th</sup> of May, 2009. At 25 days after sowing the seeds in the nursery, seedlings were transplanted to the field using 25 × 25 cm spacing, in six-row plots of 3 m in length. The mating design used in this experiment was a complete diallel crosses with six parents. The experiment was carried out in the farm of Rice Research Institute of Iran (RRII) in Rasht, which is located between 49°E longitude and 37°N latitude at an altitude of 7 m below the mean sea level in north of Iran. The six parents and their  $F_1$  hybrids (overall 36 genotypes) were arranged in a randomized complete block design with three replications. Salinity tolerance evaluation was carried out in the laboratory of department of agronomy and plant breeding in Islamic Azad University of Rasht at 2010.

### Salinity tolerance evaluation

Hundred seeds of each of the six parents and their  $F_1$  hybrids (overall 36 genotypes) were surface sterilized in 5% sodium hypochlorite solution for 5 min and then carefully rinsed with distilled water to remove the sterilizing agent. Two different levels of NaCl that is, 0 and 11.2 dS/m were used. 30 seeds of each genotype were allowed to germinate in each Petri dish (diameter 9 cm) with two sheets of filter paper. The treatment solution in each Petri dish was changed every day so as to ensure the desired salt level. All Petri dishes were placed in an incubator at 25°C for 10

**Table 2.** Analysis of variance in a 6 × 6 complete diallel.

Source of variance	d. f.	Mean Square			
		GP (%)	GR (%)	RL (%)	CL (%)
Replications	2	97.69	33.48*	4.15	12.60
Genotype	35	71.39*	47.93**	384.35**	43.65**
GCA	5	42.16	58.36**	66.27	27.05*
SCA	15	76.77*	41.73**	335.23**	40.17**
REC	15	75.76	50.64**	539.50**	52.66**
MAT	5	82.05	46.51**	673.10**	84.57**
NONMAT	10	72.62	52.71**	472.70**	36.70
Error	70	34.91	6.45	53.06	9.17

\*\* and \* indicate significant at 1% and 5% levels, respectively. GCA, general combining ability; MAT, maternal effects; SCA, specific combining ability; REC, reciprocal effects; NONM, non-maternal effects. RL, radicle length reduction; CL, coleoptile length reduction; GP, germination percentage reduction; GR, germination rate reduction. d. f., Degree of freedom.

days with a 12-h light/12-h dark photoperiod. Seeds were considered to be germinated when their root length reached the seed length and shoot length half of the seed length (Wang et al., 2010). In each of these treatments the experiment was conducted in a randomized complete-block design with three replications, where the blocks corresponded to different shelves in the germination chamber. The germinated seeds were observed each day until 10 days, when almost all the seeds were germinated. The percentage of germinated seeds at 10 days was referred to as the final germination percentage (GP).

The formula used in determining germination rate (GR) values is as follows (Pieper 1952):

$$GR = \frac{n_1}{D_1} + \frac{n_2}{D_2} + \dots + \frac{n_i}{D_i}$$

Where,  $n_i$  is number of germinated seed in each counting day and  $D_i$ , number of days for each counting of germinated seed. The radicle and coleoptile length of the seedlings was measured from 10 randomly selected seedlings in each treatment from each replication on the tenth day and average of it expressed in mm. The final data were expressed as percentage of reduction in average of these traits, obtained by comparing traits in two treatments for each genotype.

### Statistical analysis

Data for percentage of reduction in radicle and plumule length and germination for the genotypes was normally distributed and were thus submitted to analysis of variance and comparison of means using LSD test ( $\alpha = 0.01$ ).

Data were analyzed using SAS (SAS, 2002). Analysis of cold tolerance parameters was conducted using the DIALLEL-SAS procedure developed by Zhang and Kang (2005). Diallel analysis was performed according to Griffing (1956), considering a fixed model (Model I) and method I that estimates the general and specific combining effects with  $p^2$  combinations. The DIALLEL-SAS program which evaluated main genotype effects contain GCA and SCA. For a diallel mating from a set of inbred lines, the generation means ( $Y_{hij}$ ) of maternal line  $i$  and paternal line  $j$  in block  $h$  can be partitioned as:

$$Y_{hij} = \mu + G_{ij} + B_h + e_{hij}$$

Where,  $\mu$  = the population mean;  $G_{ij}$  = genotypic effect,  $B_h$  = the

block effect  $e_{hij}$  = residual effect. DIALLEL-SAS program calculated the components of variances according to this formula (Zhang and Kang, 2005):

$$\sigma_{gca}^2 = \frac{[MS_{GCA} - (MS_E + p(p-1)MS_{SCA}) / (p^2 - p + 1)]}{2bp}$$

$$\sigma_{sca}^2 = \frac{p^2(MS_{SCA} - MS_E)}{2b(p^2 - p + 1)}$$

The significance of the GCA and SCA variances were carried out by DIALLEL-SAS program. Broad sense heritability ( $h_b^2$ ) and narrow sense heritability ( $h_n^2$ ) for mean values were calculated following from components of variance (Teklewold and Becker 2005):

$$h_b^2 = \frac{2\sigma_{gca}^2 + \sigma_{sca}^2}{2\sigma_{gca}^2 + \sigma_{sca}^2 + \sigma_\epsilon^2}$$

$$h_n^2 = \frac{2\sigma_{gca}^2}{2\sigma_{gca}^2 + \sigma_{sca}^2 + \sigma_\epsilon^2}$$

The following ratio was estimated to investigation of weight of additive or dominance effects (Baker, 1978):

$$\frac{2\sigma_g^2}{2\sigma_g^2 + \sigma_s^2}$$

The significance of the GCA of the parents and SCA of their hybrids was calculated, and the values of these components were estimated. These procedures were carried out by DIALLEL-SAS program (Zhang and Kang, 2005).

## RESULTS

### Analysis of variance and mean performance of salinity tolerance traits

Analysis of variance (Table 2) indicated that there were

significant differences among the genotypes and SCA for all of traits contain reduction in radicle length (RL, %), reduction in coleoptile length (PR, %), reduction in germination percentage (GP, %) and reduction in germination rate (GR, %). GCA was significant for GP and RL. The reciprocal (REC) and maternal (MAT) effects were significant for GP, RL and PL. Non-maternal effect (NONMAT) were significant only for RL and PL. The significant GCA and SCA indicated the importance of both additive and non-additive gene actions in the inheritance of the aforesaid traits (Table 2).

Reduction of GP, GR, RL and CL were inversely proportional to salinity tolerance, that is, the higher reduction in the traits revealed lower salinity tolerance or more sensitivity to salinity stress. The reduction of GP due to 11.2 ds/m NaCl concentration in comparison with control was high in the all of the parents. The highest and lowest reduction of GP in the parents was revealed in Sepidrod and Neda, respectively. Among the parents, the lowest reduction in GP, RL and CL due to salinity was revealed in Shahpasand and the highest reduction in these traits were indicated in three genotypes which contains Hassani, IRFAON215 and Sepidrod, respectively (Table 3). The hybrids presented values ranging from 73.04% (Shahpasand × Sepidrod) to 97.5% (Shahpasand × Saleh) for GP, 46.61% (Shahpasand × Sepidrod) to 74.18% (Shahpasand × Neda) for GR, 1.49% (Shahpasand × IRFAON215) to 20.13% (Sepidrod × Neda) for RL and 9.66% (Sepidrod × IRFAON215) to 44.13% (Sepidrod × Neda) for CL (Table 3). In the crosses which contain SH × H, SH × SP, H × SH, H × SP, N × SP and N × IR, the hybrids presented a lower mean for GP than the parents. Also in the crosses SH × SP, H × SP, SA × SP and IR × N, the hybrids mean for GR was lower than the lower parents (Shahpasand). Crosses which contain SH × IR and SP × IR indicated lower reduction of RL in the hybrids than their parents. Any of hybrids did not show lower reduction of CL than parents.

### Estimation of genetic parameters on appearance quality traits of rice

Estimation of genetic parameters is given in Table 4. According to the closer of genetic ratio to unity and greater GCA: SCA ratio than one can be deduce that non-additive gene effects were more important than additive gene effects in controlling the inheritance of these traits in the studied materials. The values of mean degree of dominance  $(\sigma_D^2/\sigma_A^2)^{0.5}$  were generally greater than unity indicating the existence of over-dominance for all of the traits.

The broad and narrow sense heritability is also showed in Table 4. Heritability of a trait is important to a plant breeder, because it reflects its responses to selection. The narrow sense heritability (phenotypic variance due to

additive genetic variability) differed from 0.07 (GP) to 0.17 (PL). This indicates that selection for these traits could not give a good response. Therefore, more attention should be paid to the heterosis vigor in hybrid progenies on salinity tolerance traits. The broad sense heritability (phenotypic responses for which genetic differences are responsible) based on variance of different generations were 69, 46, 78 and 80%, for GP, GR, RL and CL, respectively (Table 4). In broad sense heritability the environment plays a significant role in the expression of the phenotype.

### Estimates of GCA and SCA and genetic parameters

Negative values for the GCA and SCA effects revealed a contribution to salinity tolerance traits at germination or lower reduction in entire traits due to salinity, while positive for the GCA and SCA effects indicate tendency towards salinity sensitivity.

In controlling of GP, the GCA effects were positively significant for Saleh and IRFAON-215 and negatively for Shahpasand. Material effects were negatively significant for Shahpasand and Neda and positively for Sepidrod. The GCA effects were not significant in the any of parents for GR. The results also indicated GCA effects were negatively significant in Shahpasand and Saleh for RL. GCA effects were negatively significant in IRFAON-215 for PL. the maternal effect were negatively significant in Shahpasand and Neda for RL. The negative significant maternal effects were also revealed in Neda and Saleh (Table 5).

A negative significant SCA effect was found in SH × H and SH × SP for GP. The negative significant SCA effects were revealed in H × IR for RL. Any of hybrids did not show negative significant SCA effects for GR and CL (Table 6). All of the traits revealed low values of narrow sense heritability due to low value of additive effect.

### DISCUSSION

Since most salinity tolerance traits important for successful breeding are quantitative in nature, the estimation of the general and specific combining ability, heritabilities and mode of inheritance contributes to their better understanding thereby enabling rational and targeted combining of desirable genes into future cultivars. Similarity of parents and progenies greatly depends on the knowledge of the relationship between the additive and non-additive components of variance and mitigates the selection of the investigated materials for creating hybrids or line cultivars.

Rice salinity tolerance at the germination stage was evaluated using percentage of reduction in GP, GR, RL and PL. These traits were chosen as they proved to be the most adequate ones to differentiate salinity tolerant

**Table 3.** Averaged performance of four germination related traits in the six parents and their crosses.

CL (%)	Genotype	GP (%)	GR (%)	RL (%)	GP (%)
SH	91.25	52.10	3.23	7.56	52.10
SH × H	87.50	56.26	8.61	22.58	56.26
SH × SP	73.04	46.61	5.56	19.08	46.61
SH × N	92.94	74.18	9.00	21.29	74.18
SH × SA	97.50	73.30	6.41	14.50	73.30
SH × IR	90.00	54.43	1.49	13.74	54.43
H × SH	84.69	55.53	6.76	35.43	55.53
H	91.39	61.32	17.34	28.41	61.32
H × SP	86.50	46.71	8.40	27.12	46.71
H × N	93.50	57.19	14.95	37.68	57.19
H × SA	94.00	57.53	10.54	31.69	57.53
H × IR	96.50	56.33	9.30	30.39	56.33
SP × SH	95.39	55.37	10.62	23.98	55.37
SP × H	91.50	56.40	16.27	32.53	56.40
SP	96.50	58.62	8.94	29.04	58.62
SP × N	95.44	55.13	20.13	44.13	55.13
SP × SA	93.39	64.02	5.48	21.31	64.02
SP × IR	96.89	51.32	2.41	9.66	51.32
N × SH	96.50	61.50	13.59	19.26	61.50
N × H	91.00	53.69	9.24	15.43	53.69
N × SP	87.00	50.60	3.66	22.48	50.60
N	88.50	57.60	11.39	15.35	57.60
N × SA	90.50	53.61	4.17	22.62	53.61
N × IR	86.35	56.19	3.59	25.33	56.19
SA × SH	93.50	55.68	5.85	14.61	55.68
SA × H	93.50	58.13	8.24	13.65	58.13
SA × SP	95.00	48.36	9.26	33.83	48.36
SA × N	95.00	50.70	8.27	22.54	50.70
SA	92.50	59.18	3.39	7.63	59.18
SA × IR	89.28	61.38	5.02	15.69	61.38
IR × SH	96.33	53.71	7.08	25.13	53.71
IR × H	93.39	55.56	6.89	26.30	55.56
IR × SP	94.00	59.02	14.46	37.06	59.02
IR × N	94.27	47.84	6.69	21.46	47.84
IR × SA	92.00	52.64	6.52	29.78	52.64
IR	95.94	58.81	18.62	22.43	58.81
LSD5%	6.14	11.99	5.16	14.79	11.99
LSD1%	8.25	16.09	6.91	19.84	16.09

SH, Shahpasand; H: Hassani; SP, Sepidrod; N, Neda; SA, Saleh; IR, IRFAON-215. RL, radicle length reduction; CL, coleoptile length reduction; GP, germination percentage reduction; GR, germination rate reduction.

from salinity sensitive genotypes at the germination stage (Cruz and Milach, 2004). Analysis of variance revealed GCA effects were significant for GP and RL and SCA effects were significant for all of the traits, indicating the importance of additive gene actions for GP and RL and non-additive gene actions for all of traits. The genetic ratio and GCA: SCA ratio confirmed the role of non-additive gene actions for all of traits. The closer genetic ratio (Baker, 1987) to unity showed the predictability

based on GCA alone. Also the GCA: SCA ratios reveal that different characters show an additive or non-additive gene action. A GCA: SCA ratio with a value greater than one indicates additive gene action, whereas a GCA: SCA ratio with a value lower than one indicates dominant gene action (Hakizimana et al., 2001). This result is in agreement the report of Moejopawiro and Ikehashi (1981) which indicated both general and specific combining ability was significant at germination stage of rice. Singh

**Table 4.** Estimates of genetic parameters.

Genetic parameter	GP (%)	GR (%)	RL (%)	CL (%)
$\sigma^2D$	81.92	9	12.15	10.24
$\sigma^2A$	21.64	1	2.76	1.48
Genetic ratio	0.21	0.1	0.19	0.13
DH	1.94	3.00	2.09	2.63
$h^2n$	0.17	0.07	0.09	0.10
$h^2b$	0.80	0.69	0.46	0.78
$\sigma^2g/\sigma^2s$	0.13	0.06	0.11	0.07
$\sigma^2gca$	10.82	0.50*	1.38	0.74**
$\sigma^2sca$	81.92**	9.00**	12.15*	10.24**

$\sigma^2D$ , Dominance variance;  $\sigma^2A$ , additive variance;  $\sigma^2s$ , SCA variance;  $\sigma^2g$ , GCA variance; DH, degree of dominance;  $h^2n$ , narrow-sense heritability;  $h^2b$ , broad-sense heritability; DH,  $(\sigma^2D/\sigma^2A)^{0.5}$ .

**Table 5.** Estimates of parental general combining ability, maternal effects and their Standard error in a 6-by-6 complete diallel.

Trait	GP (%)		GR (%)		RL (%)		CL (%)		
	GCA	MAT	GCA	MAT	GCA	MAT	GCA	MAT	
Standard error	0.57	0.57	1.13	1.13	0.51	0.51	1.34	1.34	
SH	-1.18*	-2.11**	1.27	1.91	-1.30**	-1.15**	0.11	5.06**	
H	-0.77	-0.14	0.03	-0.56	2.14**	0.05	0.95	4.40**	
SP	-0.25	3.08**	-2.06	2.57*	0.66	1.29*	0.92	-0.58	
Parents	N	-0.38	-1.65**	0.02	-0.78	1.07*	-1.98**	0.39	-5.58**
SA	1.20*	-0.09	1.51	-2.23	-1.96**	0.12	0.93	-7.04**	
IR	1.39*	0.91	-0.78	-0.90	-0.61	1.65**	-3.31*	3.74**	

\*\* and \* indicate significant at 1% and 5% levels, respectively. SH, Shahpasand; H, Hassani; SP, Sepidrod; N, Neda; D, Deilmani; SA, Saleh; IR, IRFAON-215. GCA, General combining ability; MAT, maternal effects.

et al. (2008) also revealed both additive and non-additive gene effects for controlling of germination related traits. Gregorio and Senadhira (1993) reported both additive and dominant gene effects in controlling of rice salinity tolerance at seedling stage. Genetic effects were observed for all of four traits, indicating the greater importance of non-additive effects in comparison to additive effects in the studied crosses. These results are in agreement to the reports of Lee et al. (1996) which indicated that in japonica rice, more dominant alleles were present in salt tolerant parents. In contrast, Ray and Islam (2008) indicated the importance of additive effects in the inheritance of salinity tolerance at germination stage. According to the important role of GCA effects, the improvement of these characters is easy through selection. The predominance of non-additive gene action than additive gene action in controlling the inheritance of these trait denotes that non-additive gene effects were largely influencing the expression of salinity tolerance traits; hence, selection will bring no or slow genetic improvement. Therefore heterosis and use of hybrid vigor could be applied for improving of these traits. The high broad sense heritability estimates indicated that salinity

tolerance is a heritable character. The narrow sense heritability was low for all of the traits. This finding is similar to report of Ray and Islam (2008) that revealed the heritability for salinity tolerance score was very low to medium. In contrast, Zhou et al. (2010) indicated significant heritability in narrow sense for agronomic traits of rice in salt condition. The other researchers indicated low heritability for rice traits at salt condition (Akbar et al., 1986; Gregorio and Senadhira, 1993)

Consequently, for rice salinity breeding, breeders can be assisted by understanding the genetic mechanism for the traits of rice. In this study the parents with negative GCA indicated that this parent is superior variety for salinity tolerance, whereas can be distinguished inferior variety for salinity tolerance due to negative GCA effects. In some of the crosses significant negative SCA effect are indicated, demonstrating the existence of heterosis for salinity tolerance. Similarly, significance of the positive in the other crosses revealed heterosis for salinity sensitivity at germination stage. Negative and positive values of SCA effects indicate a tendency towards salinity tolerance and sensitivity of these traits, respectively. The SCA effect is an indication of the

**Table 6.** Estimates of specific combining ability, reciprocal, non-maternal effects and their standard error in the crosses.

Trait	GP (%)			GR (%)			RL (%)			CL (%)			
	SCA	REC	NONM	SCA	REC	NONM	SCA	REC	NONM	SCA	REC	NONM	
Standard error	1.29	1.52	1.24	2.57	3.03	2.47	1.14	1.34	1.09	3.05	3.59	2.93	
SH × H	-3.95**	1.40	3.38**	-1.70	0.36	-2.11	-2.16	0.92	2.13	1.84	-6.92	-7.59*	
SH × SP	-6.36**	-11.17**	-5.96**	-4.51	-4.38	-3.72	-0.28	-2.52	-0.07	-6.10*	-2.44	-8.09**	
SH × N	4.28**	-1.78	-1.31	10.24**	6.34*	3.63	4.01**	-3.79**	-4.62**	3.17	11.01**	0.37	
SH × SA	3.46*	2.00	4.02**	5.41*	8.81**	4.65	4.38**	1.27	2.55*	24.40**	34.44**	22.33**	
SH × IR	-0.67	-3.16*	-0.12	4.03	0.36	-1.70	0.36	-2.79	0.01	15.40*	-5.69	-7.01*	
H × SP	-1.98	-2.50	0.73	-2.71	-4.84	-2.46	0.51	-3.93**	-2.69	1.35	-2.70	-7.68*	
H × N	1.39	1.25	-0.25	-0.91	1.75	1.52	-0.14	2.85*	0.81	-1.39	11.12**	1.14	
Cross	H × SA	1.30	0.25	0.29	-0.01	-0.30	-1.97	0.20	1.15	1.22	-5.82	9.02*	-2.43
	H × IR	1.38	1.55	2.61*	-4.54	0.38	0.04	-6.47**	1.20	2.80*	4.21	2.04	1.38
	SP × N	-0.15	4.22**	-0.51	-1.39	2.26	-1.11	2.13	9.23**	5.95**	5.88	11.32**	6.32*
	SP × SA	1.22	-0.80	-3.98**	0.44	7.83*	3.01	-0.33	-1.89	-3.06**	-0.88	-6.25	-12.72**
	SP × IR	-2.70**	1.44	-0.73	-4.71	-3.85	-7.33**	0.78	-6.02**	-5.66**	-1.44	-13.69**	-9.37**
	N × SA	-0.08	1.44	-0.69	-5.67*	1.45	0.01	-1.90	-2.05	0.05	4.64	-1.95	-3.42
	N × IR	0.02	-3.96*	-1.39	-4.76	4.17	4.05	-4.54	-1.54	2.08	11.74*	1.93	11.26**
	SA × IR	-2.04	-1.35	-0.35	0.14	4.37	5.70*	1.04	-0.74	0.77	19.35**	-7.04	3.75

\*\* and \* indicate significant at 1% and 5% levels, respectively. SH, Shahpasand; H, Hassani, SP, Sepidro; N, Neda; D, Deilmani; SA, Saleh; IR, IRFAON-215. SCA, Specific combining ability; REC, reciprocal effects; NONM, non-maternal effects.

heterosis (interaction) for a specific trait. Although Paroda and Joshi (1970) stated that decreases in the magnitude of the SCA in the F<sub>2</sub> population were found, good results could be obtained for breeding purposes from this population. The ratio of estimated GCA to SCA variances indicated the preponderance of the latter component in controlling the expression of all the traits. The SCA variances involve both dominance and epistasis, which together constitute the non additive type of gene action, whereas the GCA variance is a reflection of additive and additive × additive type of gene action. The non additive component of gene action could be optimized in upgrading the genetic potential of the crop by adopting reciprocal recurrent selection and hybrid

technology, which has already become a field reality in rice. The better parent(s) could be selected for a breeding program by predicting the genetic merit of parents according to the breeding value of genetic main effects. The perusal of GCA effects reveals that Shahpasand was an ideal general combiner for GP and RL, whereas IRFAON-215 was a good general combiner for CL, according to their negative significant GCA effects. The estimates of SCA effects of top ranking crosses indicated that Shahpasand × Sepidro and Hassani × IRFAON-215 could be regarded as the most desirable cross combination for GP and RL, respectively. The high broad sense heritability obtained for all of the studied traits, indicates good genetic gains when selecting

for salinity tolerance at the germination stage through these traits.

### Abbreviations

**SCA**, Specific combining ability; **GCA**, General combining ability; **MAT**, Maternal effects; **NONM**, Non-maternal effects; **REC**, Reciprocal effects; **RL**, Reduction in radicle length; **PR**, Reduction in coleoptile length; **GP**, Reduction in germination percentage; **GR**, Reduction in germination rate; **SH**, Shahpasand; **H**, Hassani; **SP**, Sepidro; **N**, Neda; **SA**, Saleh; **IR**, IRFAON-215; **σ<sup>2</sup>D**, Dominance variance; **σ<sup>2</sup>A**, Additive variance; **σ<sup>2</sup>s**, SCA variance; **σ<sup>2</sup>g**, GCA variance; **DH**, Degree of

dominance;  $h^2n$ , Narrow-sense heritability;  $h^2b$ , Broad-sense heritability.

## REFERENCES

- Akbar M, Khush GS, Hilerislammers D (1986). Genetics of salt tolerance in rice. In: Manila, Philippines (Ed.): IRRI. Rice Genetics. Int. Rice Res. Institute, pp. 399-409.
- Alam MZ, Bhuiya MAA, Muttaleb, MA, Rashid, MM (2004). Effect of alternating saline and non-saline conditions on emergence and seedling growth of rice. Pak. J. Biol. Sci. 7: 883-890.
- Baker RJ (1978). Issues in Diallel Analysis. Crop Sci. 18: 533-536.
- Cruz RP, Milach SCK (2004). Cold tolerance at the germination stage of rice: Methods of evaluation and characterization of genotypes. Sci. Agric. 61: 1-8.
- El-Mouhamady AA, El-Demardash IS, Aboud KA (2010). Biochemical and Molecular Genetic Studies on Rice Tolerance to Salinity. J. Am. Sci. 6: 521-535.
- Geetha S, Shanthi P, Jebaraj S, Mohammed SEN (2006). Gene action of sodicity tolerance in rice. Indian J. Crop Sci. 1: 201-202.
- Greenway H, Munns R (1980). Mechanisms of salt tolerance in nonhalophytes. Annu. Rev. Plant Physiol. 31: 149-190.
- Gregorio GB, Senadhira D (1993). Genetic analysis of salinity tolerance in rice (*Oryza sativa* L.). Theor. Appl. Genet. 86: 333-338.
- Griffing B (1956). Concept of general and specific combining ability in relation to diallel crossing systems. Aust. J. Biol. Sci. 9: 463-493.
- Gu XY, Yan XL, Zheng SL, Lu YG (1999). Influence of salinity on genetic variation of agronomic traits in rice. Scient. Agric. Sin. Chinese, 32: 1-7
- Hakizimana F (2001). Wheat streak mosaic virus resistance studies in winter wheat (*Triticum aestivum* L.). Ph.D. Dissertation. South Dakota State Univ., Brookings.
- IRRI (1994). Rice: The Challenge of Research. (Pamphlet). Los Banos, Philippines: IRRI.
- Karthikeyan P, Anbuselvam Y, Palaniraja K, Elangaimannan R (2009). Combining ability of rice genotypes under coastal saline soils. Elect. J. Plant Breed. 1: 18-23.
- Lal RK (1985). Effect of salinity applied at different stages of growth on seed yield and its constituents in field peas (*Pisum sativum* L. var. *arvensis*). Indian J. Agron. 30: 296-299.
- Lee KS, Senadhira D, Gregorio GB, KyuSeong L (1996). Genetic analysis of salinity tolerance in japonica rice. SABRAO J. 28: 7-13.
- Mano Y, Takeda K (1997). Heritability of salt tolerance at germination based on parent-off spring correlation and selection response in barley (*Hordeum vulgare* L.). Breed. Sci. 47: 353-358.
- Mass EV, Hoffman GJ (1977). Crop salt tolerance-current assessment. J. Irrig. Drainage. Div. ASCE, 103: 115-134.
- Meredith WRJ (1984). Quantitative inheritance. In: Kohel RJ and Lewis CF (Eds.), Cotton. Agronomic Monographs, pp. 131-150. ASA, CSSA, SSSA, South Segoe, Madison, WI.
- Mishra B, Akbar M, Seshu DV (1990). Genetics studies on salinity tolerance in rice towards better productivity in salt-affected soils. Rice Research Seminar, International Rice Research Institute, Los Baños, Philippines, 12 July.
- Moejopawiro S, Ikehashi H (1981). Inheritance of salt tolerance in rice. Euphytica, 30: 291-300.
- Murtaza N, Kitaoka M, Ali GM (2005). Genetic differentiation of cotton cultivars hypolyacrylamide gel electrophoresis. J. Centr. Europe Agric. 6: 69-76.
- Naz N, Hameed M, Ashraf M (2010). Eco-morphic response to salt stress in two halophytic grasses from the Cholistan desert, Pakistan. Pak. J. Bot. 42: 1343-1351.
- Paroda RS, Joshi AB (1970). Combining ability in wheat. Indian J. Gen. Plant Breed. 30: 630-637.
- Pieper A (1952). Das Saatgut V.P. Darey Berlin, Hamburg, Germany.
- Pitman MG, Lauchli A (2002). Global impact of salinity and agricultural ecosystems. In: Salinity: Environment-Plants-Molecules. (Eds.): A. Läuchli and U. Lüttge. Dordrecht. The Netherlands, Kluwer, pp. 3-20.
- Ray PKS, Islam MA (2008). Genetic analysis of salinity tolerance in rice. Bangladesh J. Agric. Res. 33: 519-529.
- Sankar PD, Subbaraman N, Lakshmi NS (2008). Heterosis, combining ability and gene action studies in TGMS based rice hybrids under normal and salt affected environments. Indian J. Agric. Res. 42: 177 - 182.
- SAS (2002). SAS/STAT 9 user's guide. Vol. 1, 2, and 3. SAS Inst., Cary, NC.
- Singh S, Singh, AK, Singh, HP, Singh, RS (2008). Genetic analysis for seed germination, callus induction and survival of rice under salt at *in vitro* conditions. Oryza, 45: 512-520.
- Teklewold A, Becker HC (2005). Heterosis and Combining Ability in a Diallel Cross of Ethiopian Mustard Inbred Lines. Crop Sci. 45: 2629-2635.
- Wang Z, Wang J, Bao Y, Wang F, Zhang H (2010). Quantitative trait loci analysis for rice seed vigor during the germination stage. J. Zhejiang Univ. Sci. 11: 958-964.
- Zhang Y, Kang MS, Lamkey KR (2005). DIALLEL-SAS05: A Comprehensive Program for Griffing's and Gardner-Eberhart Analyses. Agron. J. 97: 1097-1106.
- Zhou HK, Hayat Y, Fang LJ, Guo RF, He JM, Xu HM (2010). Analysis of genetic and genotype  $\times$  environment interaction effects for agronomic traits of rice (*Oryza sativa* L.) in salt tolerance. Pak. J. Bot. 42(5): 3239-3246.