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Original scientific paper

GENETIC PARAMETERS AND COMBINING ABILITY OF SOME IMPORTANT TRAITS IN RICE (*Oryza sativa* L.)

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In order to study the combining ability, genetic parameters and gene actions of yield, yield components and quality characters in rice, fifteen F_2 generation of a 6×6 diallel cross, excluding reciprocals, was grown in a randomized complete block design (RCBD) with three replications. The results of analysis of variance showed significant differences between the genotypes for grain yield (GY), 100-grain weight (HGW), number of panicles per plant (PN), panicle length (PL), number of full grains per panicle (FGN) and for quality characters including amylose content (AC) and gel consistency (GC). The results of combining ability analysis revealed that general combining ability (GCA) and specific combining ability (SCA) were significant for characters GY, FGN, GC, AC, HGW and PN indicating the involvement of additive and non-additive effects in their inheritance, however high amounts of Bakers ratio remarked that additive gene effect had more portion in controlling these traits. The best combiners for GY, HGW, FGN, PN and PL, were *RI18447-2, IR 50*, *Daylamani*, *RI18430-46* and *Daylamani* respectively. For AC and GC, the best combiner was *Daylamani*. Hayman's graphs showed that regression line passed below the origin cutting W_r axis in the negative region for HGW, PN, PL and GC, indicating the presence of over dominance. Estimates of genetic parameters showed significant

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amount of H1 and H2, and non-significant amount of D for the characters GY, PN, PL and GC, which confirmed the existence of dominance in the inheritance of these traits.

Key words: combining ability, diallel analysis, F_2 progenies, genetic parameters, rice.

INTRODUCTION

Rice (*Oryza sativa* L.) is the world's second most important cereal crop, belonging to the family gramineae (POEHLMAN and SLEPER,1995). Rice is the predominant staple food for at least 33 developing countries of the world, providing 27%, 20% and 3% of their dietary energy, protein and fat supply respectively (KENNEDY *et al*., *2002*).With the ever-increasing population, rice production must be increased by about 40% by 2025 to satisfy the growing demand without adversely affecting the resource base (YOGAMEENAKSHI *et al*., 2015).Breeding plants requires clear understanding of gene action and combining ability of` traits. Given that, the success of any plant breeding programs fundamentally depends not only on selection of parents but also breeding methods (TORRES and GERALDI, 2007). Therefore, appropriate breeding methodology should be devised. The knowledge of combining ability is useful to assess nicking ability among genotypes and at the same time explicate the nature and magnitude of gene actions involved (DAR *et al*., 2014). The diallel cross designs are frequently used in plant breeding research to obtain information about genetic properties of parental lines or estimates of general combining ability (GCA), specific combining ability (SCA) and heritability (BAKER, 1978; EL-MAGHRABY *et al.*, 2005; IQBAL *et al.*, 2007). Combining ability describes the breeding value of parental lines to produce hybrids. GCA refers to the average performance of a parent in hybrid combinations and SCA is the performance of a parent relatively better or worse than expected on the basis of the average performance of the other parents involved (SPRAGUE and TATUM, 1942; GRIFFING, 1956). Based on combining ability analysis of different characters, higher SCA values refer to dominance gene effects and higher GCA effects indicate a greater role of additive gene effects controlling the characters. If both the GCA and SCA values are not significant, epistatic gene effects may play an important role in the genetic of characters (SPRAGUE and TATUM, 1942).
KUMAR *et al.* (2007) in a combining ability analysis in rice revealed that the GCA and SCA variances were significant for number of productive tillers plant, number of filled grains panicle, 100-grain weight, biomass plant, grain yield plant and harvest index.

Among various diallel forms, the half diallel methods have certain advantages, giving maximum information about genetic architecture of a trait, parents and allelic frequency (FARSHADFAR *et al*., 2011). HABIB *et al.* (2012) evaluated 28 F_1s generated by crossing 8 diverse parents in a half diallel over two locations for different morpho-agronomic traits. They reported significant differences among the parents and their crosses for all the traits. They also remarked that variance due to GCA and SCA was significant which showed that additive and non-additive gene effects were important in the inheritance of the traits. ELMOGHAZY *et al.* (2015) conducted half diallel experiment to evaluate the performance of 15 rice hybrids along with their six parents. They reported highly significant for both GCA and SCA combining ability variances.

It is usually difficult to obtain sufficient F_1 seeds crops where hand emasculation must be done. Due to easiness of production of large quantity of F_2 seeds, many researchers use F_2 generation for diallel analysis to estimate combining ability and other genetic parameters, they also reported that F_2 analysis provide reliable and better information than F_1 generation (SCOTT, 2000; KAO and MC VETTY, 1987)

LENG and HONG (2004) studied the performance and inheritance of 7 quality traits using F_2 rice grain derived from 8×8 diallel crossing made by employing 8 parents of different ecological japonica rice types. They revealed that the inheritance of grain width, grain weight, chalkiness score, gelatinization temperature and gel consistency were suitable to additive-dominant model, and dominant effect contributed mainly for those traits. They also remarked that inheritance of grain length and amylose content did not fit into additive-dominant model, existing epistatic interactions. Their study expressed that dominant genes for grain width and grain weight had the efficiency of decreasing effect, and dominant genes for chalkiness score, gelatinization temperature and gel consistency had the efficiency of enhancing effect.

MALEMBA *et al*. (2017) selected four upland NERICA and two upland rice varieties were as parents for generating F_1s crosses following 6×6 diallel. The generated F_1s crosses were advanced to F_2 population for field evaluation. They reported that both GCA and SCA were significant indicating the importance of both additive and non-additive gene action in the expression of studied traits.

Keeping in view the above researches the present investigation was undertaken to get an idea of the combining ability of the used varieties, for yield and quality traits with a view to identify good combiners which may be utilized to create a population with favorable genes for grain yield and its components.

MATERIALS AND METHODS

The plant material consisted of six parent diallel cross excluding reciprocals. The experiment was conducted at Rice Research Institute of Iran (RRII), Rasht, Guilan province, during 2012-2015. Six Iranian and foreign rice varieties (Table 1) were selected as parental lines in this study. These parents had differences in origin, pedigree and some of the quality and morphological traits (Table 1). Parent lines selected among 94 rice genotypes in the first study in 2012. In the first investigation, 52 rice microsatellites RM or SSR markers were used to characterize and assess the genetic diversity among 94 pure rice cultivars from different regions and origins (ALLAHGHOLIPOUR *et al.*, 2014). These parental lines crossed in a diallel mating design in 2013. In order to produce F_2 progenies, fifteen F_1 populations from a 6×6 half diallel cross selfed in 2014.

Table 1 Name, origin of country and pedigree of rice genotypes used in this study

S.N	Genotypes	Pedigree	Origin
1	*Gilaneh*[a]	*Saleh*[a] / *Abjiboji*[b] // *Abjiboji*	RRII[c], Iran
2	*Daylamani*	Local cultivar	Mazandran, Iran
3	*IR50*	*IR50*	IRRI[d], Philippines
4	*Line 23*	*IR75479-199-3-3*	IRRI, Philippines
5	*RI18447-2*	*Sepidrood*[a] / *Gharib*[b]	RRII, Iran
6	*RI18430-46*	*Saleh*[a] / *Hashemi*[b]	RRII, Iran

[a] Improved rice variety of Iran, [b] Local rice variety of Iran, [c] Rice Research Institute of Iran, [d] International Rice Research

The plant genetic materials (parents and F_2s) were grown in a randomized complete block design with three replications in research farm of Rice Research Institute of Iran (RRII) in

2015. Each genotype was comprised of 4 rows and 10 plants per row. A composite sample of 15 plants from the middle row was used to record observations for grain yield (GY), 100-grain weight (HGW), number of panicles per plant (PN), panicle length (PL), number of full grains per panicle (FGN) and for quality characters viz.,amylose content (AC) and gel consistency (GC). AC and GC determined according to MELISSA *et al.* (2009) and CAGAMPANG *et al.* (1973), respectively.

Analysis of variance was performed by MSTATC ver 1.42 (ANOVA) and GRIFFING´s (1956) diallel analysis was conducted by Dial 98 software (UKAI, 2006) to estimate the general (GCA) and specific (SCA) combining abilities determined according to SINGH and CHAUDARY (1977). This method was calculated by following model:

$$X_{ij} = u + g_i + g_j + s_{ij} + e_{ijk}$$

where, u=the population mean, g_i=the general combining ability effect of the ith parent, g_j=the general combining ability effect of the jth parent, s_{ij}=the specific combining ability effect of the cross between ith and jth parents such that $s_{ij}=s_{ji}$ and e_{ijk} the environmental effect associated with ijkth observation. The combining ability ratio was calculated according to BAKER (1978) as follow:

$$Baker\ ratio = \frac{2MS_{GCA}}{2MS_{GCA} + MS_{SCA}}$$

F_2's genetic parameters determined according to DHELLON and MALHI (1976) and SHARMA (2006).The least square solution, on the lines of HAYMAN (1954), lead to:

$D=V_{OLO}$
$F= 4V_{OLO} – 8W_{OLO2}$
$H1= 4V_{OLO} – 16W_{OLO2} + 16V_{IL2}$
$H2= 16V_{IL2} – 16\ V_{OL2}$
$hh= (4M_{L2} – 4M_{LO})^2$

The expectations of V_{OLO}, W_{OLO2}, V_{IL2} and V_{OL2} are given by HAYMAN (1958):V_{OLO}= variances of parents, W_{OL2}= mean of W_r (covariance of array between parent progenies, where array is a group of crosses involving a special parent), V_{IL2}= mean of variances of row V_r (variances of array of parents), V_{OL2}= variances of progenies, M_{L2}= mean of progenies, M_{LO}= mean of parents, D=Additive variance, H1=Dominance variance, H2=Dominance variance, F=Relative frequency of dominant and recessive allels, hh=square of difference P vs. all. Broad sense heritability (h^2_b) determined as the ratio of genetic variance to phenotypic variance and the narrow sense heritability (h^2_n) as the ratio of additive variance to phenotypic variance.

Hayman's graph (V_r-W_r graph) is drawn with the help of variances of arrays (V_r) and covariance's (W_r) between parents and their F_2 progenies. The array refers to the crosses in which a particular parent is common. The W_{ri} values are estimated for all the arrays by the formula: $W_{ri}= (V_{ri} \times V_{OLO})^{0.5}$ where, V_{ri} is the variance of rth array and V_{OLO} is the variance of parents. The W_{ri} values are plotted against V_r values to draw the limiting parabola. The W_{ri}

values are obtained by the formula: $W_{ri} = W_r - bV_r + bV_{ri}$ for drawing regression line, where, V_{ri} is array mean of variances, W_r is array mean of covariance's and b is regression coefficient (SINGH *et al.*, 1990; SINGH and NARAYANAN, 1993).

RESULTS

Analysis of variance for all traits studied revealed significant differences among genotypes (parents and hybrids), showing the presence of genotypic variability among them (Table 2). The diallel analysis by Griffing`s method showed highly significant differences for all traits. Significant differences were also observed for SCA for all evaluated characters except PL (Table 3). The amount of Baker's ratio (Table 3) for PL and AC was closer to 1(more than 0.9) that revealed additive effects play more significant roles in controlling those traits.

Table 2. Analysis of variance for grain yield, its components and grain quality characters.

Source of variance	df	Mean Square GY	FGN	GC	AC	PL	HGW	PN
Genotypes	20	2.09**	977.65**	1929.31**	8.95**	3.94**	0.22**	21.06**
Replications	2	0.39^{ns}	1.24^{ns}	40.06^{ns}	0.09^{ns}	1.15^{ns}	0.02^{ns}	1.58^{ns}
Error	40	0.14	11.53	26.85	0.07	2.26	0.01	1.96

^{ns} and ** non-significant and significant at 1% probability level respectively.
GY=Grain Yield,FGN=Filled Grain Number, HGW=100-Grain Weight, GC=Gel Consistency, AC=Amylose Content, PL=Panicle Length, PN=Panicle Number per plant.

Table 3. Analysis of variance for combining ability.

Source of variance	df	Mean Square GY	HGW	FGN	PN	PL	AC	GC
Replication	2	0.28^{ns}	0.02^{ns}	0.12^{ns}	0.12^{ns}	1.56^{ns}	0.1^{ns}	40.47^{ns}
GCA	5	3.53**	0.21**	1292.13**	33.83**	10.49*	15.14**	2134**
SCA	15	1.97**	0.09**	1043.45**	21.27**	2.32^{ns}	2.13**	1500**
Error	40	0.18	0.01	14.66	1.37	1.82	0.06	36.94
Baker Ratio		0.78	0.82	0.71	0.76	0.9	0.93	0.74

^{ns}, * and ** non-significant and significant at 5 and 1% probability levels respectively.
GY= Grain Yield, HGW=100-Grain Weight, FGN=Filled Grain Number, PN=Panicle Number per plant, PL=Panicle Length, AC=Amylose Content,GC=Gel Consistency.

Estimate of GCA for GY of the six parental genotypes revealed that parents *RI18447-2* and *Line 23* had highest GCA, indicating that parents *RI18447-2* and *Line 23* are good combiner for GY. The best general combiners with positive effects, for improvement of HGW, FGN, PN and PL were parents *IR 50*, *Daylamani*, *RI18430-46* and *Daylamani* respectively. For AC and GC, the best combiner was *Daylamani*.

The estimates of SCA for the seven characters are presented in Table 4. The*Gilaneh×Daylamani* cross had the most SCA in GY. For HGW the *Gilaneh×IR50* was the best cross. The *Daylamani×RI18430-46,* had the highest SCA for FGN and PN. The

Gilaneh×RI18447-2, Gilaneh×IR50 and *Gilaneh×RI18447-2* were the best crosses for PL, AC and GC respectively.

Knowledge of components of genetic variation helps in formulating the most efficient breeding methodology (TIWARI and SIROHI, 2016). Estimates of genetic parameters (Table 6) showed that the parameters H1 and H2 were significant for the characters GY, PN, PL and GC, which confirmed the existence of dominance in the inheritance of these traits (Table 6). Significant amount of D, H1 and H2 for characters HGW, FGN and AC revealed that simultaneous effect of additive and dominant gene action is involved. As the ratio of average degree of dominance 0.25sqr (H1/D) was significant and greater than one for HGW, hence, over dominance is involved in the genetic of this trait.

Table 4. General combining ability (GCA) of grain yield, its components and grain quality characters

Parents	GY	HGW	FGN	PN	PL	AC	GC
Gilaneh	-0.43	-0.09	-5.37	-0.75	-0.61	0.15	17.5
Daylamani	-0.83	-0.2	15.13	1.63	1.1	-1.53	-16.08
IR50	0.21	0.18	7.79	-2.13	1.06	1.35	10.33
Line 23	0.39	0.04	-14	0.96	0.08	-0.55	-4.58
RI18447-2	0.63	-0.01	-4.75	-1.5	-0.38	1.19	-12.83
RI18430-46	0.03	0.08	1.21	1.79	-1.24	-0.62	5.67

GY=Grain Yield, HGW=100-Grain Weight, FGN=Filled Grain Number, PN=Panicle Number per plant, PL=Panicle Length, AC=Amylose Content, GC=Gel Consistency.

Table 5. Specific combining ability (SCA) of grain yield, its components and grain quality characters

Crosses	GY	HGW	FGN	PN	PL	AC	GC
1×2	1.66	-0.28	-10.03	-2.98	-0.26	0.71	25.38
1×3	-0.58	0.29	8.13	-1.89	0.45	-1.47	-1.03
1×4	-0.5	-0.01	3.18	2.53	-0.07	-0.1	13.88
1×5	-0.33	0.02	15.59	0.32	1.14	0.85	-41.87
1×6	-0.24	-0.01	-16.87	2.02	-1.26	0	3.63
2×3	-1.12	-0.01	10.22	0.4	-0.01	-0.59	-27.12
2×4	-0.14	0.18	-27.83	-0.35	0.8	0.45	2.47
2×5	-0.17	0.12	-0.33	-1.06	-0.74	-0.5	6.72
2×6	-0.23	-0.02	27.97	3.98	0.2	-0.08	-7.45
3×4	0.76	-0.22	8.42	1.23	0.18	0.6	0.38
3×5	0.42	-0.03	-8.58	0.86	-0.45	0.45	16.97
3×6	0.52	-0.03	-18.2	-0.6	-0.18	1.01	10.8
4×5	0.01	-0.06	1.22	0.94	-1.05	-0.41	4.22
4×6	-0.13	0.12	15.01	-4.35	0.14	-0.53	-20.95
5×6	0.07	-0.05	-7.91	-1.06	1.1	-0.4	13.97

GY=Grain Yield, HGW=100-Grain Weight, FGN= Filled Grain Number, PN=Panicle Number per plant, PL=Panicle Length, AC=Amylose Content, GC=Gel Consistency.

1=*Gilaneh*, 2=*Deylamani*, 3=*IR50*, 4=*line 23*, 5=*RI18447-2*, 6=*RI18430-46.*

Table 6. Estimation Genetic Parameters for studied characters

Characters Genetic Parameters	GY	HGW	FGN	PN	PL	AC	GC
D	0.29^{ns}	0.02*	210**	1.91^{ns}	-0.3^{ns}	5.43**	39.9^{ns}
H1	3.52**	0.91**	7678**	173**	8.99**	47.07**	831.7**
H2	8.32**	0.87**	5302**	113**	10.7**	18.7**	8625**
F	0.21^{ns}	0.04*	1108**	18.7**	-1.8^{ns}	9.17**	-139*
hh	1.08**	1.84**	419**	20.0**	0.20^{ns}	1.84**	1179**
E	0.05**	0.00**	4.16**	0.55**	0.67**	0.02**	10.0**
0.25sqr(H1/D)	1.42^{ns}	1.72*	1.45^{ns}	2.21^{ns}	0^{ns}	0.58**	3.86^{ns}
kd/(kd+kr)	0.52**	0.56**	0.72**	0.76**	0^{ns}	0.67**	0.43**
hh/H2	0.13^{ns}	2.09**	0.07*	0.17^{ns}	0.01^{ns}	0.09^{ns}	1.36**
h	0.26^{ns}	0.33**	5.13*	1.12^{ns}	0.16^{ns}	0.34*	27.1**
D/(D+E)	0.85**	0.90**	0.98**	0.77**	-1.0^{ns}	0.99**	0.79**
h^2_b	0.90**	0.96**	0.98**	0.93**	0.17^{ns}	0.95**	0.98**
h^2_n	0.23*	0.36*	0.13**	0.05^{ns}	-0.06^{ns}	0.42**	0.11**

^{ns}, * and ** non-significant and significant at 5 and 1% probability levels respectively.

GY=Grain Yield, HGW=100-Grain Weight, FGN=Filled Grain Number, PN=Panicle Number per plant, PL=Panicle Length, AC=Amylose Content, GC=Gel Consistency.

D=Additive variance, H1=Dominance variance, H2=Dominance variance, F=Relative frequency of dominant and recessive allels, hh=square of difference P vs. all, E Environment variance, 0.25sqr(H1/D)=Average degree of dominance, (kd/kd+kr)=Proportion of dominance genes, (hh/H2)=Number of effective factors, (h)=Average direction of dominance, (D/(D+E))=Heritability by parents, (h^2_b)=Broad-sense heritability, (h^2_n)=Narrow-sense heritability.

The position of regression line on V_r-W_r graph provides information about average degree of dominance. When the regression line passes through the origin, it indicates complete dominance. When it passes above the origin, cutting the W_r axis, it shows that there is partial dominance. But when it passes below the origin, cutting the W_r axis, it denotes the presence of over dominance. The position of parental point along the regression line indicates the dominance order of parents. The parents with more dominant genes are located closer to the origin, while those with more recessive genes fall farther from the origin. The parents with equal frequencies of dominant and recessive genes occupy the intermediate position (SINGH *et al*., 1990; SINGH and NARAYANAN, 1993). Hayman's graphs showed that regression line passed below the origin cutting W_r axis in the negative region for HGW, PN, PL and GC (Figure 2, 4, 5 and 7 respectively), indicating the presence of over dominance. Hayman's graph for GY, FGN and AC (Figure 1, 3 and 6 respectively) revealed the presence of partial dominance of gene effect due to passing regression line above the origin. However high difference between regression line and regression line with slope of one for all traits except AC, suggested the presence of non-allelic interaction. The dispersion of parents around the regression line for GY (Figure 1) showed that parents *Gilaneh*, *Deylamani* and *RI18447-2* were close to the origin of the coordinate, and accordingly had more than 75% dominant genes, parents *RI18430-46* and *line 23* had 50-75% of dominant genes, while parents *IR50* was far from the origin, therefore it had<25% of dominant genes. The dispersion of parents around the regression line for HGW (Figure 2) revealed that parent *line 23*, *RI18447-2* and *RI18430-46* were close to the origin of the coordinate, and accordingly have >75% of dominant genes parents *Deylamani* and *IR50* had 50-75% of dominant genes, while parent *Gilaneh* was far from the origin and therefore had <25% of dominant genes. Most of the dominant genes for FGN (Figure 3) were distributed in parents *Gilaneh*, *IR50*, *line 23* and *RI18447-2* while recessive genes were mostly distributed in parents *Deylamani* and *RI18430-46*. The dispersion of parents around the regression line for PN showed that parents *IR50*, *line 23* and *RI18447-2* were close to the origin of the coordinate, and accordingly had >75% of dominant genes (Figure 6), parent *Gilaneh* had 50-75% of dominant genes, while parents *RI18430-46* and *Deylamani* was far from the origin and therefore had <25% of dominant genes. Most of the dominant genes for PL and AC were distributed in parents *RI18447-2* and *Deylamani* respectively. For GC character recessive and dominant genes are equally distributed in parents *Deylamani*, *IR50*, *line 23*, *RI18447-2* and parent *Gilaneh*had most recessive genes.

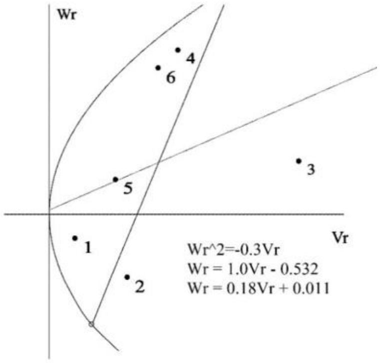

Figure 1. Regression line and dispersion of parents around origin for Grain Yield.
1=*Gilaneh*, 2=*Deylamani*, 3=*IR50*, 4=*line 23*, 5=*RI18447-2*, 6=*RI18430-46*.

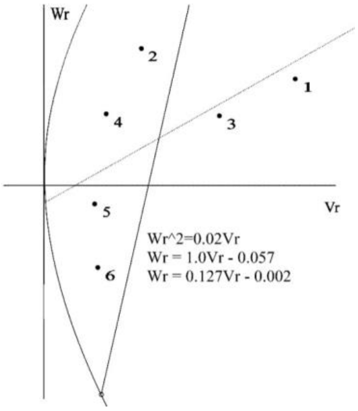

Figure 2. Regression line and dispersion of parents around origin for 100-Grain Weight.
1=*Gilaneh*, 2=*Deylamani*, 3=*IR50*, 4=*line 23*, 5=*RI18447-2*, 6=*RI18430-46*.

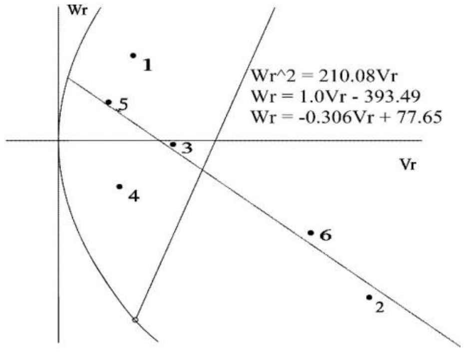

Figure 3. Regression line and dispersion of parents around origin for Filled Grain Number.
1=*Gilaneh*, 2=*Deylamani*, 3=*IR50*, 4=*line 23*, 5=*RI18447-2*, 6=*RI18430-46*.

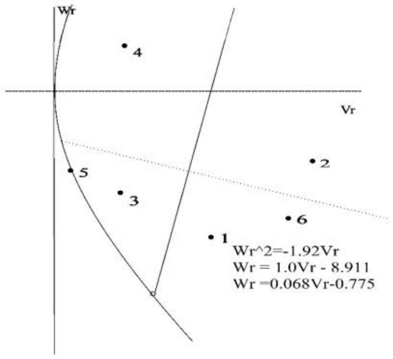

Figure 4. Regression line and dispersion of parents around origin for Panicle Number.
1=*Gilaneh*, 2=*Deylamani*, 3=*IR50*, 4=*line 23*, 5=*RI18447-2*, 6=*RI18430-46*.

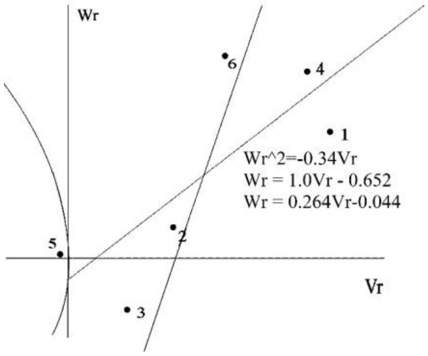

Figure 5. Regression line and dispersion of parents around origin for Panicle Length.
1=*Gilaneh*, 2=*Deylamani*, 3=*IR50*, 4=*line 23*, 5=*RI18447-2*, 6=*RI18430-46*.

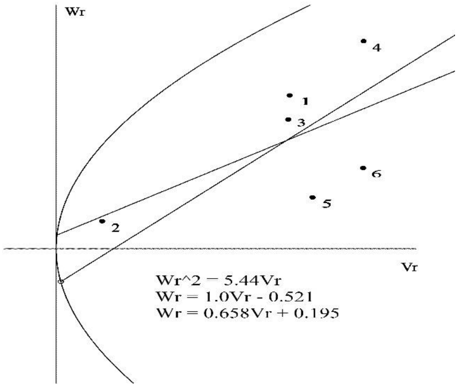

Figure 6. Regression line and dispersion of parents around origin for Amylose Content.
1=*Gilaneh*, 2=*Deylamani*, 3=*IR50*, 4=*line 23*, 5=*RI18447-2*, 6=*RI18430-46*.

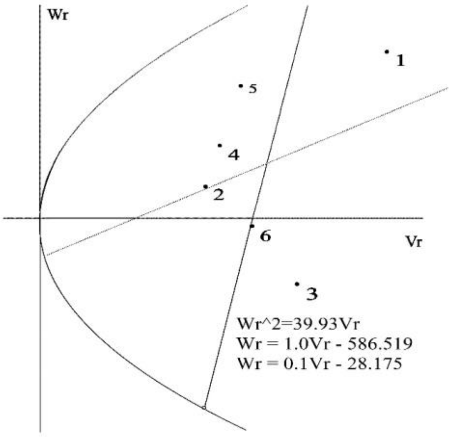

Figure 7. Regression line and dispersion of parents around origin for Gel Consistency.
1=*Gilaneh*, 2=*Deylamani*, 3=*IR50*, 4=*line 23*, 5=*RI18447-2*, 6=*RI18430-46*.

DISCUSSION

In breeding of rice high yielding varieties with good grain quality traits, the breeders frequently face the problem of selecting good parents and crosses. Combining ability analysis is one of the influential tools utilizes to estimate the combining ability effects for selecting the desirable parents and crosses (RASHID *et al.*, 2007; SARKER *et al.*, 2002).

The results of combining ability analysis exhibited that GCA and SCA were significant for characters GY, FGN, GC, AC, HGW and PN indicating the involvement of additive and non-additive effects (dominance and epistasis) in their inheritance, however high amounts of Bakers ratio remarked more portion of additive gene effect in controlling these traits. GCA was significant for PL displaying that PL is controlled by additive type of gene action, so the pedigree method of selection can be used for improvement of this trait. MALEMBA *et al.* (2017) in study of F_2 generation of diallel cross remarked significant GCA and SCA of GY.TIWARI and SIROHI (2016) reported non-additive gene action for PL, PN, HGW and GY. They also reported that parents, *IR50*, *Ratna*, *Saket 4* and *Pusa 150* had significant GCA effects for more than one desirable trait. VANAJA *et al.* (2003) investigated a half diallel of 6×6 to study combining ability for yield and yield components in rice. They suggested the importance of both additive and non-additive gene effects in governing yield and most of the yield components. Similar results were published by KUMAR *et al.* (2015), SHARMA (2006), PRADHAN *et al.*, (2006) and VERMA *et al.*, (2006).

From analysis of variance for combining ability (Table 3), it revealed that in most characters GCA as well as SCA variances founded significant and in all cases GCA variance was higher than SCA variance. Further additive genetic variances were found higher in magnitude than corresponding non-additive variance. ZHANG *et al.* (2015) investigated significant GCA for yield component traits. MOHAMMAD *et al.* (2016) reported significant role of non-additive gene actions like dominance, epistasis and other interaction effects in the expression of GC and AC.

In an overall view at estimations of GCA, it obtained that the parent *Daylamani* was the best line for improving FGN, PN, AC and GC. So, use of this line will be lead to good breeding in rice grain quality and yield components traits.

The quantitative measurement of individual character provides the basis for an interpretation of analysis of variance. The available variability in a population can be partitioned into heritable and non-heritable parts with the aid of genetic parameters (MILLER *et al.*, 1958). Estimation of narrow sense heritability showed that the FGN, PN, PL and GC had the lowest values while the other traits had either moderate or high heritability, which indicated selection in the early generations could be done to fix the favorable genes (Table 6). ALLAHGHOLIPOUR *et al.* (2015) reported that narrow sense heritability for GY and GC had the lowest values and it was high for AC and moderate for GC and PN. MOELJOPAWIRO (2015) reported high heritability estimates in the broad sense and Moderate narrow sense heritability estimates for PL and HGW, suggested that these traits can be selected with the pedigree method. Hayman's graphs revealed the parent *RI18447-2* had more dominant genes for most of traits and parent *RI18430-46* had more recessive genes for most of characters.

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GENETIČKI PARAMETERI I KOMBINACIONA SPOSOBNOST ZNAČAJNIH OSOBINA PIRINČA (*Oryza sativa* L.)

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Izvod

U cilju proučavanja kombinacione sposobnosti, genetičkih parametara za prinos, komponente prinosa i kvalitativna svojstva pirinča, 15 genotipova F_2 generacije iz 6x6 dialelnog ukrštanja, isključujući recipročna, posejano je po RCB dizajnu u tri ponavljanja. Rezultati analize varijanse pokazali su značajne razlike između genotipova za prinos zrna (GY), težinu 100 zrna (HGW), broj klasova po biljci (PN), dužinu klasa (PL), broj zrna po klasu (FGN), a za kvalitativne osobine sadržaj amiloze (AC) i koegzistenciju gela (GC). Rezultati analize kombinacione sposobnosti ukazali su da su opšta (GCA) i specifična (SCA) kombinaciona sposobnost bile značajne za osobine GY, FGN, GC, AC, HGW i PN, ukazujući na prisustvo aditivnog i neaditivnog efekta kod njihovih potomaka. Najbolji kombinatori za GY, HGW, FGN, PN i PL, bili su *RI18447-2*, *IR 50*, *Daylamani*, *RI18430-46*, a za AC i GC, najbolji kombinator bio je *Daylamani*. Regresiona linija u Hayman-ovim graficima pokazala je prisustvo super-dominantnosti. Procenjene vrednosti genetičkih parametara bile su signifikatne za H1 i H2, a nesignifikantne za D, za osobine GY, PN, PL i GC, što je potvrdilo prisustvo dominantnog efekta pri nasleđivanju ovih osobina.

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