Mode of gene action for grain yield, its components and grain quality traits in non-segregating generation (F$_1$) of rice

Sanjeev Kumar*, H.B. Singh and J.K. Sharma

Department of Plant Breading and Genetics, Choudhary Sarwan Kumar, Himachal Pradesh Krishi Vishvavidyalaya, Palampur (H.P.) India

ABSTRACT

A set of diallel crosses involving nine genotypes of rice (Oryza sativa L.) with early and medium maturity were evaluated for grain yield, morpho–physiological and some of the quality traits. Gene action estimated through Harman's (1954) approach revealed that both additive and non additive gene actions for traits viz., plant height(cm), days to 50% flowering, leaf area index(%), harvest index(%), net-assimilation rate(g cm^{-2} day^{-1}), biological yield(g), grain yield(g), panicle length(cm), 100 grain weight(g), grain length(mm), grain breadth(mm), dry matter(g) and L\B ratio. Non-additive gene action (dominance and epistasis) were predominant as compared to additive gene action except for L\B ratio, which is easily transferred through hybridization for crop improvement programme. The positive and negative genes in the parents were distributed unequally for all the traits except for harvest index (0.25). Correlation coefficient was negative and significant indicating the dominance of positive genes for days to 50% flowering, grain yield per plant, days to maturity and 100 grain weight. Significant value of F for days to 50% flowering, days to maturity, leaf area index and grain breadth indicated asymmetrical distribution of dominant and recessive genes in the parents. The high heritability in narrow sense was established for days to 50% flowering, days to maturity leaf area index and medium for plant height, length of panicle, 100 grain weight and net-assimilation rate. Consequently any selection method adopted could lead to desirable improvement in the above mentioned traits. For varietal improvement in very early group, the exploitation of parent VLDhan 221 might be useful, as it possesses more number of desirable recessive genes for earliness.

Key words: Rice, diallel, genetic components, gene action

Emphasis is being diverted towards the maximum utilization of land by producing more rice yield per unit area per unit time for which very early maturing rice varieties are one of the reliable sources. There is also an urgent need to improve different traits related to grain yield. For the improvement of any plant character through hybridization, it is necessary to understand the nature of gene actions and genetic architecture of the donor parent for that character. So, an attempt was made through diallel analysis to understand properly the nine genotypes crossed in dialed design for further improvement of early rice.

Nine rice genotypes of five early (VL Dhan221, JD8, HPR1164, HPR2047 and VL93–3613), three medium (VL93-6052, IR57893-08 and China988) and one late (VL91-1754) duration varieties (Table1) were crossed in diallel design without reciprocals.

Twenty five days old seedlings along with nine parents, 36F$_1$'S and a check (HPR2047) were transplanted during wet season 2003 in randomized block design with three replications and plot size consisted of single rows of each hybrid and three rows of each parent and a check having 3m length with 20x15cm spacing at the Experimental Farm of Department of Plant Breeding and Genetics of Choudhary Sarwan Kumar, Himachal Pradesh Krishi Vishvavidyalaya, Palampur (H.P.) India. Observations were recorded on 10 randomly selected competitive plants for days to 50% flowering, plant height(cm), leaf area index(%), dry matter(g), net-assimilation rate(g cm^{-2} day^{-1}), length of panicle(cm), days to maturity, grain yield(g), biological yield(g), harvest index(%), 100 grain weight(g), grain length(mm), grain breadth(mm) and L\B ratio. The analysis was done following the models of Hayman (1954 a).

Table 1. Mean of parental varieties for fourteen characters of rice (*Oryza sativa* L.)

Parents\traits	DFFL	PH	LAI	D M	NAR	LP	DTM	GY	BY	HI	100 GW	GL	GB	L\B ratio
HPR 1164	89.87	106.01	2.00	16.08	3.7	18.89	119.87	16.73	42.83	42.81	2.69	6.83	2.05	3.33
HPR2047	87.95	111.68	1.09	18.11	2.34	19.57	117.95	18.20	43.81	41.51	2.07	6.52	1.63	3.99
China 988	95.09	99.07	2.27	16.27	3.97	20.37	125.09	17.40	35.74	48.61	2.52	6.45	1.96	3.28
VL91-1754	100.48	121.35	3.19	20.49	4.5	25.77	130.48	19.85	44.50	44.55	2.71	6.64	1.89	3.50
VL93-3613	88.75	95.40	0.94	14.76	9.1	20.51	118.75	20.97	37.67	55.64	2.33	6.18	1.83	3.37
VL 93-6052	93.06	118.85	2.27	20.34	3.39	22.9	123.06	18.37	39.60	46.32	2.95	6.96	1.94	3.59
IR-57893-08	95.06	92.93	1.84	14.62	3.62	20.17	125.06	18.01	34.06	52.79	2.29	6.21	1.84	3.37
VL-Dhan221	71.84	111.55	0.84	15.5	0.59	20.63	106.84	14.01	33.76	41.40	2.37	6.3	1.76	3.58
JD-8	75.36	95.52	1.44	15.32	0.58	18.57	107.37	17.21	43.32	39.73	2.33	7.32	1.70	4.16

DFFL=days to 50% flowering, PH=Plant height, LAI=Leaf area index, NAR= net assimilation rate, LP=Length of panicle, DTM=days to maturity, GY =grain yield, BY =biological yield, HI =harvest index, GL =grain length, GB =grain breadth, L\B= length breadth ratio

The analysis of variance revealed significant differences among parents, hybrids and parents versus hybrids for all the traits studied. The additive component (D) and non-additive component (H$_1$) were significant for traits viz., plant height, days to 50% flowering, days to maturity , leaf area index, length of panicle and length breadth ratio whereas only dominant component was significant for grain yield, biological yield, harvest index, dry matter, 100 grain weight, net-assimilation rate, grain length and grain breadth (Table 2). Higher magnitude of additive component (D) in comparison to dominance component (H$_1$) indicated the greater importance of additive gene action while vice versa indicated the greater importance of non- additive gene action. The high value of heritability in narrow sense h² (b.s.) also confirmed the predominant role of additive nature of gene action. Similar results were also reported by Maurty and Singh (1977) and Singh and Richaria (1977) for heading duration, Brogan and Sarma (1998) for plant height and Sardana and Borthakur (1987) for panicle length. The estimate of average degree of dominance (A.D.D.) was greater than unity for all the traits indicated over dominance. Similar results were also reported by Kaushik and Sharma (1988) and Verma *et al,* (1995). The non-symmetrical distribution of positive and negative alleles was observed for all the traits except for harvest index (Table 2) as shown by H$_2$\4H$_1$. The K$_D$\K$_r$ estimate in this study revealed that higher proportion of dominant alleles was prevalent for all the traits understudied except for grain breadth. The presence of dominant and recessive alleles in the parental population was also confirmed by the estimate of F-value. The positive estimate of F indicated the overall excess of dominant alleles while negative sign for recessive alleles Regression coefficient (b) and its deviation from zero and unity was worked out. The slope of regression line was significantly different from zero suggesting the absence of epistatic gene action and providing the validity of assumption of diallel analysis for all the traits studied. Graphical analyses is a good estimator of the prepotency of parents and thus provide a basis for choosing parental combination for selective improvements of the character concerned. The values of (V$_r$ +W$_r$) are presented in Table 3. The lowest value corroborates with the presence of more number of dominant genes while highest value to that of more number of recessive genes. In the present study, more number of recessive genes were present in VLDhan221 followed by JD8 and VL93-6052, which suggested further exploitation of these varieties to obtain short duration plants. More number of dominant genes for 100 grain weight was possessed by HPR1164 followed by VL93-6052, VL91-1754 and VLDhan221, while more number of recessive genes were recorded in VL93-6052 and JD-8. More number of dominant genes for net-assimilation rate was observed in HPR2047 followed by China988 and IR57893-08, while more recessive genes were observed in VL93-3613 followed by VL93-6052 and VL91-1754. For getting longer grains, the desirable recessive genes were observed to be more in VL93-3613 and JD-8 followed by VL91-1754 and China 988, VL91-1754 (Table 3), while dominant genes were more in VL93-6052. In case of breadth of grain, VL91-1754 and IR57893-08 were having more number of dominant genes, while JD 8 had more number of recessive genes.

Table2. Estimates of genetic components of variation for yield, its components and grain quality traits in F₁ generation of rice (*Oryza sativa* L.)

Traits Components	Plant height	Days to 50% flowering	Grain yield	Biological yield	Harvest index	Days to maturity	LAI	DM	PL	100 grain weight	NAR	GL	GB	L/B ratio
EE	7.35 ±12.23	2.22 ±6.60	0.77 ±2.08	6.94 ±22.24	5.76 ±6.47	2.19 ±5.04	0.01 ±0.04	0.66 ±3.89	1.13* ±0.45	0.01 ±0.01	0.00 ±1.15	0.05 ±0.04	0.03 ±0.00	0.01 ±0.01
D	105.69** ±38.68	85.68** ±20.87	2.51 ±6.58	11.72 ±70.32	24.10 ±20.47	61.07* ±15.93	0.58* ±0.13	4.35 ±12.31	3.86* ±1.41	0.07 ±0.04	6.37 ±3.63	0.10 ±0.13	-0.02 ±0.00	0.08* ±0.03
F	121.04 ±90.23	119.02** ±48.69	-5.37 ±30.68	15.78 ±164.04	4.00 ±47.76	81.01* ±37.16	0.95** ±0.30	5.64 ±28.72	5.81 ±3.30	0.10 ±0.10	6.63 ±8.48	0.15 ±0.30	-0.03* ±0.01	0.11 ±0.07
H₁	375.58** ±85.37	247.57** ±46.06	304.64* ±58.01	526.86* ±155.20	162.66* ±45.19	205.81* ±35.16	1.77* ±0.28	181.01* ±27.17	16.43* ±3.12	0.44* ±0.10	26.9* ±8.02	1.00* ±0.29	-0.03* ±0.01	0.31** ±0.06
H₂	306.42** ±73.39	186.91** ±39.60	290.32** ±49.90	458.75* ±133.42	161.75* ±38.84	161.81* ±30.22	1.26* ±0.24	138.63* ±22.36	13.56* ±2.68	0.35* ±0.08	22.3 9* ±6.89	0.91* ±0.25	0.01 ±0.01	0.27** ±0.05
h²	176.28** ±49.161	-0.56 ±26.53	20.04* ±8.36	104.89 ±89.38	-2.06 ±26.02	1.66 ±20.25	0.02 ±0.16	142.99* ±15.69	12.96* ±1.80	0.26* ±0.06	2.28 ±4.62	-0.01 ±0.17	-0.01 ±0.01	0.00 ±0.04
(H₁/D)¹ᐟ²	1.89	1.70	11.01	6.71	2.60	1.84	1.75	6.45	2.06	2.59	2.06	3.19	1.27	1.93
H₂/4H₁	0.20	0.19	0.24	0.22	0.25	0.20	0.18	0.19	0.21	0.20	0.21	0.23	0.20	0.21
h²(n.s)	27.12	38.40	2.97	2.13	11.71	31.37	40.57	2.38	20.32	15.08	23.87	8.71	-	26.01
K_D/K_R	1.87	2.38	0.82	1.22	1.06	2.13	2.76	1.10	2.15	1.80	1.67	1.62	0.24	1.55
h²/H₂	0.58	-	0.07	0.22	-0.01	0.01	0.01	1.03	0.96	0.74	0.10	-0.01	0.50	-
R	-0.52	-0.78	-0.67*	-0.44	0.28	-0.76**	0.32	-0.29	-0.38	-0.69*	0.56	-0.0028	-0.58	-0.13
b	0.0013 ±0.33	1.43* ±0.41	0.16 ±0.13	-0.08 ±0.11	0.04 ±0.19	0.06 ±0.44	0.19 ±0.32	0.045 ±0.05	-0.20 ±0.18	-0.13 ±0.16	0.11 ±0.29	-0.070 ±0.21	0.40 ±0.27	0.38 ±0.34
1-b	3.00**	1.00*	6.13**	9.87**	4.87**	0.88	2.52**	20.16**	6.37**	6.76**	2.99**	4.93**	2.12**	1.76**
t²	0.11	0.41	9.57**	17.20*	3.51	0.72	0.14	107.36*	3.54	5.45	0.36	2.34	0.26	-

* Significant at 5 per cent probability; ** Significant at 1 percent probability; LAI = Leaf area index; DM = Dry matter; PL = Panicle length; NAR = Net-assimilation rate; GL = Grain length; GB = Grain breadth; - not calculated

Table 3. Estimates of (V$_r$+W$_r$) values for all the traits in 9 x 9 diallel of rice

Parents	DFFL	PH	LAI	DM	NAR	LP	DTM	GY	BY	HI	100 GW	GL	GB	L\B ratio
HPR 1164	86.03	200.24	0.46	15.02	5.96	6.06	65.19	7.16	63.60	44.40	0.06	0.14	0.01	0.05
HPR2047	14.42	51.82	0.71	35.71	1.13	5.22	18.12	9.18	109.62	25.62	0.15	0.31	0.03	0.08
China 988	20.03	112.28	0.47	43.33	1.59	3.73	17.79	4.18	141.54	60.93	0.11	0.28	0.01	0.22
VL91-175	20.02	66.59	0.63	38.35	11.33	3.35	24.25	6.46	103.42	70.56	0.09	0.37	0.00	0.04
VL93-3613	60.75	169.87	0.40	40.99	18.72	4.62	58.93	6.21	29.24	54.75	0.19	0.50	0.01	0.14
VL 93-6052	93.16	98.87	0.38	56.06	12.06	6.02	76.62	9.52	77.43	22.30	0.07	0.05	0.01	0.03
IR-57893-08	57.71	173.82	0.38	72.88	5.46	6.60	52.55	9.90	245.11	119.63	0.10	0.24	0.00	0.08
VL-Dhan221	150.3	104.09	0.26	57.81	10.16	2.59	115.27	10.55	245.12	64.90	0.09	0.13	0.01	0.07
JD-8	110.70	80.31	0.03	96.27	7.31	5.50	95.15	8.93	220.07	82.11	0.19	0.49	0.04	0.12

DFFL days to 50% flowering, Pl ht=Plant height, LAI=Leaf area index, NAR= net assimilation rate, LP=Length of panicle, DTM=days to maturity, GY =grain yield, BY =biological yield, H.I. =harvest index, G.L. =grain length, G.B. =grain breadth,L\B= length breadth ratio

In the present study out of fourteen characters six were observed for both additive and non-additive gene actions, and these traits can be improved through hybridization programme, while remaining traits showed only non-additive gene action. The cultivar VL Dhan 221 might be the best parent in the breeding programme for further improvement in 100 grain weight and longer grain with early duration.

REFERENCES

Brogohan R and Sarma 1988. Combining ability for grain and its components in deep water rice. Crop Research 16: 215-219

Hayman BL1954 a. The analysis of Variance of diallel table. Biometries 10: 235-244

Hayman BL 1954 b. The theory and analyses of diallel crosses. Genetics 39: 789-809

Maruty DM and Singh DP 1977. Combing ability in rice for yield and fitness. Indian J Agric Sci 47: 65-70

Sardana, S. and Borthakur, O. N. 1987. Combining ability for yield in rice. *Oryza 24*: 14-18

Singh RS and Richharia K 1977 .Combing ability for grain dimension and shape in unhulled rice. Indian J Agric Sci 47: 54-57

Kaushik RP and Sharma KD1988. Gene action and combining ability for yield and its components in rice under cold stress conditions. *Oryza* 25: 1-9

Verma YS, Singh H and Pandey MP1995. Combining ability for yield and its components in rice. *Oryza* 32: 1-5