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Short Communication

Gene action for grain yield, its components and quality traits in hill rice (*Oryza sativa* L) varieties

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For improvement of any plant character through hybridization, it is necessary to understand the nature of gene action and genetic architecture of the donor parents for that character. In this study an attempt was made through diallel analyses to understand properly below mentioned lines for further improvement.

Five early (VLDhan221, JD8, HPR1164, HPR2047 and VL93-3613), three medium (VL93-6052, IR57893-08 and China988) and one late (VL91-1754) maturing varieties of rice (Table 1) were crossed in diallel design without reciprocals. Twenty five days old seedlings of parental lines, 36F_1's and a check (HPR2047) were transplanted during *kharif* 2003 in a randomized complete block design with three replications. Single row of the hybrids and three rows of each parent were transplanted in 3m long plots at a spacing of 20 × 15cm at the Experimental Farm of Department of Plant Breeding and Genetics of Choudhary Sarwan Kumar, Himachal Pradesh Krishi Vishvavidyalaya, Palampur (H.P.). 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 ($gcm^{-2}day^{-1}$), 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 LAB ratio. The analysis was done following the models of Hayman [2].

The analysis of variance revealed significant differences among parents, hybrids and parents vs. hybrids for all the traits. The analysis of variance revealed significant differences among parents, hybrids and parents vs. hybrids for all the traits. Both the additive (D) and non-additive(H_1) components were significant for traits like 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 narrowsense also confirmed the predominant role of additive genes. Similar results were also reported by Maurya and Singh [3] and Singh and Richharia [4] for heading duration, Borgohain and Sarma [5] for plant height and Sardana and Borthakur [6] for panicle length. The estimate of average degree of dominance was greater than unity for all the traits indicating the role of over dominance. Similar results were also reported by Kaushik and Sharma [7] and Verma *et al.* [8]. The non-symmetrical distribution of positive and negative alleles was observed for all the traits except for harvest index (Table 1) as shown by $H_2/4H_1$. The K_DK_r estimate in this study revealed that higher proportion of dominant alleles was prevalent for all the traits 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 for recessive alleles. 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 understudied. Graphical analyses are a good estimator of the prepotency of parents and thus provide a basis for choosing parental combination for selective improvements of the character concerned. Deviation of regression coefficient from zero was significant only for days to 50% flowering. It reflects that this character had a strong relationship between Vr and Wr of the parental material and thus Vr, Wr-graph was effective for the genetical studies of the parental materials with respect to this trait. For the remaining traits, deviation of regression coefficient from zero were non-significant,

Table 1. Estimates of genetic components of variation for yield, its components and grain quality traits in F_1 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
E	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
H_1	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
H_2	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	22.39* ±6.89	0.91*± 0.25	0.01± 0.01	0.27**± 0.05
h^2	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
$(H_1/D)^{1/2}$	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
$H_2/4H_1$	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
h^2(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
h^2/H_2	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**
t^2	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 and 1 percent, respectively.

LAI = Leaf area index; DM = Dry matter (g); PL = Panicle length (cm); NAR = Net-assimilation rate (gm cm^{-2} day^{-1}); GL = Grain length(mm); GB = Grain breadth (mm); - not calculated, Biological yield (g)

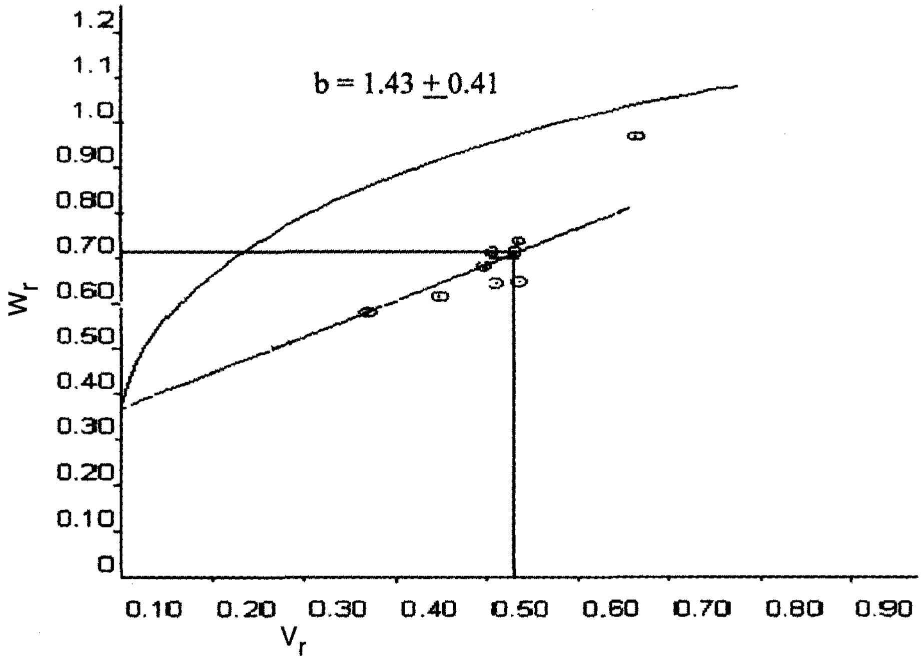

Fig. 1. Wr, Vr graph for days to 50% flowering

hence Vr, Wr-graphs were not plotted, because these traits did not have a significant relationship between Vr and Wr components. It may be due to environmental factors, genotype × environment interactions or sampling error. Vr, Wr graph showed that the regression line intersected Wr-axis below the point of origin for days to fifty percent flowering (Fig. 1) suggesting the role of over dominance for this trait. This finding reveals that this character may be improved by hybrid breeding programmes. Array points for 100-grain weight were distributed away from the point of origin revealing thereby greater proportion of recessive genes may be crossed with parental lines having greater proportion of dominant genes for developing heterotic genotypes. Parental lines having equal proportions of dominant and recessive genes may be exploited for getting improved populations.

Hence, in the present study, the predominance of additive gene action for grain length: breadth ratio suggested that a part of the heterosis can be fixed in subsequent generations to take advantage in further breeding programme. The predominance of non-additive gene action for all these traits except length : breadth ratio could be exploited in hybrid development.

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