

Genetic studies of quantitative traits through Hayman's approach in rice

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ABSTRACT

Genetic components of variation were estimated for yield, its components and quality traits through Hayman's approach of 8 x 8 diallel set. All the components of yield and yield except 1000 grain weight were under the influence of non-additive gene action. Kernel dimensions (length, breadth and length / breadth ratio) were largely under the control of additive gene effects. The proportion of dominant and recessive genes and genes with +ve and -ve effects were not in symmetry as per the estimates of H²/4H¹ and KD/KR. Coefficient of regression (b) was found to be significantly different from zero for plant height, panicle length and kernel breadth, which indicated that these traits satisfied the general assumptions of diallel analysis. Based on the results, progeny selection was suggested for improvement of 1000-grain weight and quality traits and for other traits only population improvement methods were the ideal approach. The parents viz., MTU 4870, JGL-1881 and white ponny were identified as good parents for hybridization.

Key words : diallel, gene action, genetic effects, rice

There is always a need to raise the rice productivity levels to meet the food requirements of the rapidly growing population and more grains have to be produced on less land as the area under agriculture is fast decreasing due to industrialization and other reasons. In Northern Telangana Zone of Andhra Pradesh state, incidence of gall midge at initial stages of the crop and blast at flowering stage is one of the main reasons of yield losses. As such, this zone needs an immediate focus to the development of high yielding cultivars with resistance to gall midge and blast in addition to good kernel quality characteristics. Choosing right parents followed by hybridization and selection of plants with desirable characters, is the commonly followed method till to day and several gall midge resistant varieties developed by such simple techniques (pedigree and back cross breeding) have become very popular. Further strengthening of these ongoing programmes very often demands the information on genetic background of parental material and also the genetic effects involved in the expression and inheritance of desirable traits. Among the different methods available to assess the nature of gene action for each character and distribution of genes in parents, the diallel cross

technique (Hayman, 1954) is a systematic method. With this view, the present study was envisaged after careful selection of the parents available from the gene bank at Regional Agricultural Research Station, Jagtial.

MATERIALS AND METHODS

The material consisted of eight divergent parents viz. Warangal Sannalu (WGL 32100)- a cross derivative of Divya/ BPT-5204 resistant to gall midge (GM), JGL 3855- derived from cross, BPT-5204/ARC 5984//Kavya is gall midge resistant Jagtial Samba (JGL 3844)- a cross derivative of BPT 5204/ ARC 5984// Kavya with resistance to GM, JGL 7046 (Pre-release)- selected from a cross, JGL 384/Vajram JGL 1881 (Pre-release)- derived from BPT-5204/ Kavya cross has multiple biotype resistance for gall midge, Deepti (MTU 4870)- derived from the cross, Sowbhagya/ ARC 6650 with resistance to, NLR 34452- selected from cross, IR 72/ BPT 5204 with resistance to blast and White ponny.

All possible 28 crosses (excluding reciprocals) were made during wet season 2005 and the resultant F₁s along with their parents were grown during subsequent dry season, 2006 in a randomized complete

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block design with three replications at Regional Agricultural Research Station, Jagtial located in Karimnagar district of Andhra Pradesh. Each parent and F1 was represented by 2 rows in each replication with a spacing of 20 x 20 cm and the crop management practices were followed as recommended by ANGR Agricultural University. Observations were recorded on ten randomly selected competitive plants in each replication for seven yield characters viz., days to 50% flowering, plant height, ear bearing tillers plant⁻¹, panicle length, panicle weight, 1000- grain weight and grain yield plant⁻¹ and other quality characters viz., kernel length, kernel breadth and length / breadth ratio. A statistical procedure as developed by Hayman (1954) was followed for genetic component analysis.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among parents, hybrids and parents vs hybrids. The estimates of genetic components and heritability (h^2) in narrow sense are furnished in table 1. Both additive (D) and non additive (H1) components were significant for the traits, plant height, panicle length, 1000-grain weight and kernel length/ breadth ratio, whereas only dominant component was significant for days to 50% flowering, ear bearing tillers, panicle weight and grain yield per plant. For remaining two characters, viz., kernel length and breadth, additive component was significant. Higher magnitude of additive component (D) indicated the greater role of additive gene action while vice versa indicated the greater importance of non-additive gene action. Similar findings were also reported earlier by Sinha *et al.* (2006) and Sanjeev kumar *et al.* (2008) for yield and yield components except for 1000-grain weight. Where as, Sanjeev kumar *et al.* (2008) stressed the importance of only non-additive gene action for this trait. Positive estimate of F for all the characters except plant height, panicle length and kernel breadth indicated the overall excess of dominant genes for the important yield and quality traits under study. The estimate of H2 component was smaller than H1 for all the traits reflecting unequal (non symmetrical) distribution of positive and negative alleles at all the loci in the parents and the same was attested by the ratios of H2/ 4H1 which were not in closer approach to the theoretical value of 0.25.

The values of mean degree of dominance as estimated by $(H1/D)^{1/2}$ in variance component were

above unity in case of days to 50% flowering, ear bearing tillers plant⁻¹, panicle weight, grain yield plant⁻¹, kernel length and length / breadth ratios which indicated existence of over dominance in these components (Verma, 1995). With respect to the remaining traits except panicle length, partial dominance was noticed. The ratios of dominant and recessive genes (KD/KR) revealed higher proportion of dominant alleles in the parents for days to 50% flowering, panicle weight, 1000 grain weight, grain yield plant⁻¹, kernel length and length / breadth ratio. This was also confirmed by positive estimates of F for these variables, whereas for the other traits viz., plant height, panicle length and kernel breadth, an excessive of recessive alleles were indicated. The distribution was highly symmetrical in case of ear bearing tillers with a KD/KR value of 1.08.

The most important parameter, which, directly represents the heritable portion of genetical variance and is estimated on the basis of additive variance is heritability in narrow sense. In the present study, estimates were observed to be low to moderate for critical yield components like days to 50% flowering, ear bearing tillers, panicle weight besides grain yield plant⁻¹, which could be attributed to more prevalence of non-additive (dominant and epistasis) gene action in these traits. But the trend was reverse in case of 1000-grain weight, which hence, permits direct selection for genetical improvement. With respect to quality traits, the values ranged from low (kernel length) to medium (breadth and length/ breadth ratio). The h^2/H^2 values were less than unity for all the characters under study including those of quality traits implied the existence of mostly one gene complex. The low magnitude of effective factors is in agreement with the earlier findings of Tripathy and Mishra (1986) and Mohanty *et al.* (1995). Hayman (1954 b) pointed out that the estimate of h^2/H^2 might indicate lower values in the event of h^2 effects of all genes being unequal in size and in the event of uncorrelated gene distribution. The value of h^2/H^2 may be depressed by the complementary gene action (Hayman, 1954 b). The correlation coefficient (r) between the parental order of dominance and parental measurement was significant for plant height, panicle length and kernel breadth which indicated the dominant genes are not equally +ve and -ve and plus signs indicated that they are showing -ve effects.

Pattern of inheritance was largely dependent on nature of parental material involved besides, the gene

Table 1. Estimates of genetic components of variation for yield, its components and kernel quality traits.

Traits/ Components	Days to flowering	Plant Height	Ear bearing tillers plant ⁻¹	Panicle length	Panicle weight	1000-grain weight	Grain yield plant ⁻¹	Kernel length	Kernel breadth	Kernel L/B Ratio
E	0.225 ±12.478	2.009** ±6.552	0.279 ±0.334	0.229* +0.110	0.030 0.077	0.015 ±0.138	1.376 ±5.031	0.027** ±0.005	0.003* ±0.001	0.008* ±0.004
D	34.217 ±37.435	261.72** ±19.56	0.286 ±1.001	2.546** ±0.331	0.228 ±0.232	7.103** ±0.413	27.610 ±15.092	0.033** ±0.016	0.009** 0.002	0.053** ±0.012
F	64.243 ±88.45	-169.470** ±46.234	0.145 ±2.364	-0.379 ±0.782	0.197 ±0.548	1.635 ±0.976	37.787 ±35.661	0.039 ±0.038	-0.001 ±0.004	0.060* ±0.028
H ₁	313.093** ±86.058	229.618** ±44.980	11.465** ±2.300	2.617** ±0.761	1.887** ±0.533	4.356** ±0.950	157.112** ±34.694	0.051 ±0.037	0.002 ±0.004	0.091** ±0.027
H ₂	197.17** ±74.870	119.839** ±39.133	9.770** ±2.001	2.175** ±0.662	1.267** ±0.464	3.201** ±0.826	131.143** ±30.184	0.018 ±0.032	0.003 ±0.004	0.048* ±0.028
h ²	0.723 ±50.211	-0.406 ±26.244	0.662 ±1.342	-0.082 0.444	0.156 0.311	2.695** ±0.554	18.031 ±20.242	-0.009 ±0.021	-0.001 ±0.003	0.000 ±0.016
(H ₁ /D) ^{1/2}	3.025	0.937	6.333	1.014	2.880	0.783	2.385	1.252	0.495	1.310
H ₂ /4H ¹	0.158	0.130	0.213	0.208	0.168	0.184	0.209	0.090	0.343	0.132
h ² (n.s)	46.1	89.4	25.2	68.5	48.4	80.2	18.8	29.7	58.4	47.9
KD/KR	1.900	0.486	1.083	0.863	1.353	1.345	1.805	2.828	0.772	2.493
h ² /H ₂	0.004	-0.003	0.068	-0.038	0.123	0.842	0.137	-0.481	-0.365	0.006
R	0.441 NS	0.865**	0.169 NS	0.739*	-0.283NS	0.575NS	0.346NS	0.240NS	0.839*	0.027NS
b	0.133	0.639	0.083	0.588	-0.086	0.381	0.184	0.195	0.647	0.022
b-o	-1.205 NS	-4.223**	-0.419NS	-2.683*	0.722 NS	-1.722NS	-0.902NS	-0.605NS	-3.771**	-0.067
1-b	7.852**	2.383 NS	4.626**	1.876NS	9.080**	2.880*	4.011**	2.471*	2.057 NS	2.958*
T ²	16.948**	2.248NS	3.648NS	0.693NS	14.356**	1.611 NS	3.109 NS	0.276 NS	1.390 NS	0.271NS

** significant at 1% level, * significant at 5% level

actions (additive/ non-additive). In general, non-additive component dominated the additive one for most of the yield traits except for 1000-grain weight. For kernel length/ breadth ratio, both the types were important. 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 (Sanjeev kumar *et al.* 2007). In the present study, regression coefficient of three traits viz., plant height, panicle length and kernel breadth was significantly different from zero suggesting the absence of epistatic gene action and non-significance of T2 values also indicated the same results earlier. Thus, the general conditions of diallel analysis were fulfilled for these traits. It reflects that these characters had a strong relationship between Vr and Wr of parental material and thus Vr, Wr was effective for genetical studies of parental material with respect to these traits. For the remaining traits the deviations of regression coefficient from zero were not significant, hence Vr, Wr graphs were not plotted. Vr, Wr graph showed that regression line intersected Wr-axis below the point of origin for plant height, panicle length and above the point of origin for kernel breadth (fig. 1-3) suggesting the role of over dominance for the first two traits and partial dominance for the third trait. All the parents except white pony (8th), possessed recessive genes for plant height, as the array points were distributed away from the point of origin. Similarly, in case of panicle length, parents 1, 2 (WGL 32100, JGL 3855) possessed recessive genes and the parent 7 (NLR

Fig 1. Vr, Wr graph for plant height

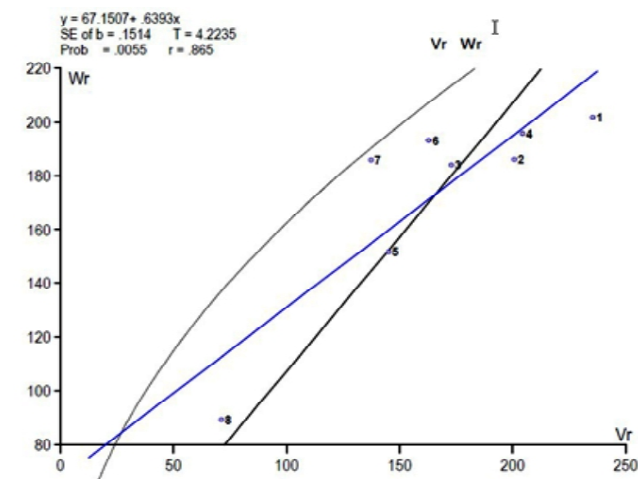


Fig 2. Vr, Wr graph for panicle length

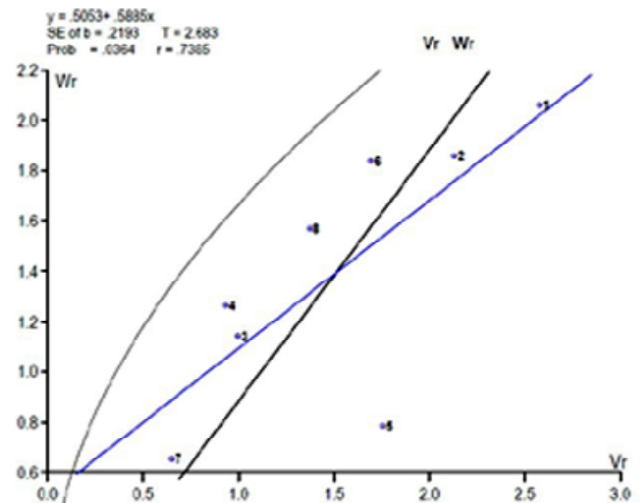
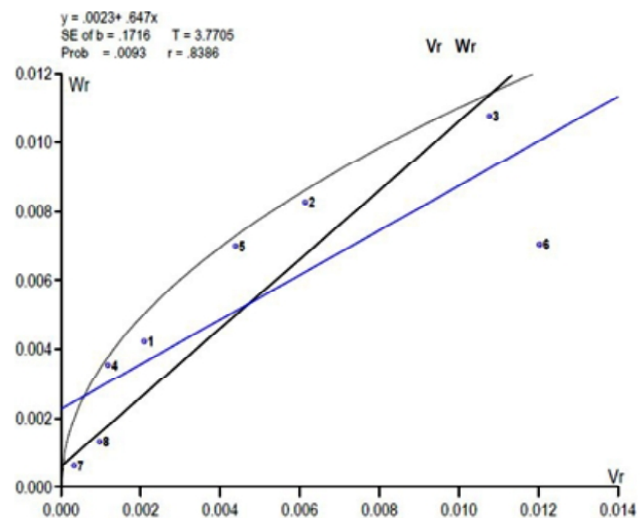


Fig 3. Vr, Wr graph for Kernel breadth



34452) had most dominant genes and the remaining ones had both types almost in equal proportion. With respect to the quality trait, kernel breadth, the parents 7, 8, 4 and 1 had dominant genes (in decreasing order), where as 3 and 6 possessed recessive genes.

As regards to the remaining traits, for which the graphs were not plotted, the values of (Vr+Wr) are presented in table 2. The lowest value corroborates with the presence of more number of dominant genes

Table 2. Estimates of Vr+Wr values for all the traits

Parents	Days to 50% flowering	Plant height	Ear bearing tillers plant ⁻¹	Panicle length	Panicle weight	1000-grams weight	Grain yield plant ⁻¹	Kernel length	Kernel breadth	Kernel length/breadth ratio
WGL-32100	94.65	437.34	4.26	4.62	0.541	5.87	61.05	0.038	0.006	0.028
JGL-3855	24.71	386.97	3.52	3.991	1.010	6.881	94.28	0.051	0.014	0.059
JGL-3844	50.02	356.98	5.80	2.13	0.327	7.06	23.29	0.052	0.022	0.053
JGL-7086	53.37	400.37	3.23	2.19	0.465	5.97	36.23	0.015	0.005	0.022
JGL- 1881	221.80	296.93	3.54	2.54	0.847	4.82	48.52	0.030	0.011	0.045
MTU-4870	38.44	356.22	2.09	3.53	0.655	4.61	39.60	0.009	0.019	0.048
NZR-34452	53.82	323.35	0.67	1.30	0.215	4.59	28.8	0.088	0.001	0.039
White Ponny	34.92	160.33	2.46	2.94	0.458	5.047	4.47	0.008	0.002	0.013

while the highest value to that of more recessive genes. More number of dominant genes were present in JGL 3855 for days to 50% flowering; NLR-34452 and MTU 4870 for ear bearing tillers and 1000 grain weight and white ponny for kernel length/breadth ratio.

The present study revealed that the pattern of inheritance was largely governed by non-additive gene action for yield and important yield components except 1000-grain weight. So, there was limited scope for improvement of yield components, except 1000-grain weight through progeny selections in early generations (Sinha *et al.*, 2006). However, Mohanty *et al.* (1995) suggested that among the three major yield components, only test weight had maximum scope to increase productivity in rice especially in early genotypes, when compared to panicle number and grain number. Nevertheless, biparental matings in early generations and delaying selection upto advance generations may be rewarding, while other traits are targeted. For improvement of kernel length and length/breadth ratio, simple pedigree method is sufficient, as the additive gene effects played greater role. Among the parents studied, MTU 4870 (BPH resistant variety), NLR 34452 (blast resistant genotype) and JGL-1881 (Gallmidge resistant genotype) for yield traits and white ponny for quality traits were identified as better ones on account of possessing most of the desirable dominant genes. Parental lines having equal proportions of

dominant and recessive genes may be exploited for getting improved populations /heterotic hybrids.

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