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Genetic Analysis for Yield Components and Yield in Rice (*Oryza sativa* L.)

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Abstract

Component analysis indicated importance of both additive and dominance gene action for the characters days to 50% flowering, 50% flowering to maturity, plant height, panicle length, grain filling percentage and length-breadth ratio, while only the dominance component was important for the characters like effective tillers per plant, panicle weight, grains panicle^{-1}, 1000 grains weight and yield plant^{-1}. Dominant genes were more frequent in the parents than the recessive genes for the characters days to 50% flowering, 50% flowering to maturity, plant height, panicle length and length-breadth ratio. Unequal gene frequencies for positive and negative alleles in the parents were observed for all the characters except grains panicle^{-1} for which equal gene frequencies were evident. The estimates of degree of dominance were more than unity for all the characters including yield plant^{-1}, which indicated prevalence of over-dominance.

1. Introduction

For more than half of humanity, rice is life. It is the grain that has shaped the cultures, diets and economies of billions of people. Given the fact that rice consuming population will increase by additional 80-100 million every year, it is estimated that the world's un-milled rice production has to increase by about 65% by 2030 to keep pace with the population growth. Therefore, there is a need to enhance the productivity potential of rice by evolving high yielding genotypes. In the pursuit of rendering a permanent genetic improvement in crop plants, an adequate knowledge of gene action, especially components of genetic variance and allied parameters (such as heritability, degree of dominance and genetic correlations between relatives, etc.) are necessary. Numerous reports like Joshi (1979), Mehla et al. (2000), Pradhan et al. (2006) and Raju et al (2006) are available in rice for gene action on various characters including yield. Since local genotypes are valuable with reference to many rare physiological and quantitative traits, therefore, the present investigation was carried out to study the nature of gene action among three local genotypes viz. *Malong*, *Mehuru*, *Teke* of Nagaland and three improved genotypes, viz. *Piolee*, *Ranjit* and *Bahadur* of Assam for yield and its components in 6 x 6 diallel cross.

2. Materials and Methods

The present investigation was conducted at the experimental farm of ICAR Research Complex for NEH Region (Jharnapani) located at 25^{0}45'49" N latitude and 93^0 33'04"E longitudes at an altitude of 304.80 msl above sea level bearing sub-tropical climate during the period 2003-2004. The hybridization work was carried out in wet season 2003. In 2004 wet season, six parents (*Malong*, *Mehuru*, *Teke*, *Piolee*, *Ranjit* and *Bahadur*) along with 15 F$_1$ hybrids (*Malong* x *Mehuru*, *Malong* x *Teke*, *Malong* x *Piolee*, *Malong* x *Ranjit*, *Malong* x *Bahadur*, *Mehuru* x *Teke*, *Mehuru* x *Piolee*, *Mehuru* x *Ranjit*, *Mehuru* x *Bahadur*, *Teke* x *Piolee*, *Teke* x *Ranjit*, *Teke* x *Bahadur*, *Piolee* x *Ranjit*, *Piolee* x *Bahadur and Ranjit* x *Bahadur*) of a 6 x 6 diallel cross (excluding reciprocals) were grown in randomized complete block design with three replications. Thirty days old single seedling hill^{-1} was planted at a spacing of 20 x 15 cm^2 with three-meter length row having three rows in each entry. The experiment was conducted with normal package of practices and need based plant protection measures. Observations were recorded on ten sampled plants of the middle row of each plot avoiding the border rows and border plants for days to 50% flowering, 50% flowering to maturity, effective tillers plant^{-1}, plant height, panicle weight, panicle length, grains panicle^{-1}, grain filling percentage, length-breadth ratio, 1000 grains weight and yield plant^{-1}. Data pertaining to the parents and F$_1$'s of 6 x 6 diallel cross (excluding reciprocals) were analyzed according to Hayman-Jinks method (Jinks and Hayman, 1953; Hayman, 1954; Jinks, 1954).

3. Results and Discussion

The estimates of components of variance as obtained from Vr-Wr statistics are presented in Table 1. The genetic proportions derived from these components are presented in table 2. The relative magnitude of dominance components H_1 and H_2 were observed to be higher than additive component D for all the characters. For the characters like effective tillers hill^{-1}, panicle weight, grains panicle^{-1}, 1000 grains weight and yield plant^{-1} only dominance components H_1, H_2 and h^2 (except 1000 grains weight) were significant which indicated the involvement of only dominance component of variation in their expression. All the components D, H and H_2 were significant for the characters days to 50% flowering, 50% flowering to maturity, plant height, panicle length, grain filling percentage and length-breadth ratio. These results are in conformity with those of Mehla et al. (2000), Pradhan et al. (2006) and Raju et al. (2006). As involvement of both additive and non- additive components were observed in the control of yield attributing characters, viz. days to 50% flowering, 50% flowering to maturity, plant height, panicle length, grain filling percentage and length-breadth ratio, with pre-dominance of non- additive component, simple pedigree selection for these characters will not be effective. In such situations, population improvement program which may bring about the accumulation of fixable gene effects as well as which will maintain considerable variability and heterozygosity for exploiting non-fixable gene effects will prove to be the most effective method (Joshi, 1979).

The value of ‘F’ was positively significant for days to 50% flowering, 50% flowering to maturity, plant height, panicle length and length-breadth ratio. This indicates that dominant genes were more frequent in the parents than the recessive genes for these characters.

The estimates of degree of dominance were to be more than unity for all the characters including yield plant^{-1} which indicated prevalence of over-dominance. The proportion of alleles in the parents with positive and negative effects ($H_2/4H_1$) were below the expected value of 0.25 for all the characters except grains panicle^{-1}, where it was almost 0.25. This indicated the unequal allelic frequencies for all other characters and equal allelic frequency for grains panicle^{-1}.

As indicated by KD/KR, the parents might contain more number of dominant genes than recessives for the characters like days to 50% flowering, 50% flowering to maturity, effective tillers plant^{-1}, plant height, panicle weight, panicle length, grain filling percentage and 1000 grains weight whereas recessives might be more than dominants for grains panicle^{-1}. These findings corroborated the findings from values of ‘F’. The value of KD/KR for the characters length-breadth ratio and yield plant^{-1} almost equals to unity which indicates equality of dominance and recessive genes.

The value of h^2/H_2 indicated that one to two gene groups might be involved in the control of days to 50% flowering, 50% flowering to maturity, effective tillers plant^{-1} and length-breadth ratio; two to three gene groups for plant height, grains panicle^{-1} and grain filling percentage and four gene groups for panicle weight. However, the very low values of the parameters for panicle length and 1000 grains weight did not reflect any conclusive inference regarding the number of gene groups controlling these two characters.

The negative correlation between the mean values of the parents ‘Yr’ and the parental order of the dominance (Wr + Vr) for all the characters except 50% flowering to maturity, plant height, panicle length and 1000 grains weight suggested that the dominant genes were associated with high mean expression. It clearly indicated that early flowering was controlled mostly by recessive genes. The positive correlation for 50% flowering to maturity, plant height, panicle length and 1000 grains weight suggested high mean expression to be associated with more recessive genes. The association of recessive genes with high mean expression is an advantage in breeding program as it might facilitate fixation of the trait in the early generation (Subramanium and Rathinum, 1984).

4. Conclusion

The relative magnitude of dominance components H_1 and H_2 were observed to be higher than additive component D for all the characters studied. The estimates of degree of dominance were found to be more than unity for all the characters including yield plant^{-1} which indicated prevalence of over-dominance. The ratio of KD/KR corroborated the findings from values of ‘F’. The values of h^2/H_2 indicated one to four gene groups controlling different characters.

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Table 1: Estimates of genetic components of variance for seed yield and its components in rice

Genetic parameter	Days to 50% flowering	50% flowering to maturity	Effective tillers plant^{-1}	Plant height (cm)	Panicle weight (g)	Panicle length (cm)	Grains panicle^{-1}	Grain filling percentage	Length-breadth ratio (mm)	1000 grains weight (g)	Yield plant^{-1} (g)
D	220.72** ±22.51	25.86** ±2.92	1.44 ±1.81	523.68** ±82.57	0.59 ±0.35	3.82** ±1.10	101.99 ±163.29	51.14** ±17.19	0.09** ±0.02	9.53 ±5.37	35.00 ±40.52
H_1	308.85** ±57.15	47.20** ±7.41	23.38** ±4.59	1052.61** ±209.60	7.42** ±0.89	9.51** ±2.79	3056.08** ±414.53	233.72** ±45.51	0.32** ±0.05	51.40** ±13.62	384.80** ±102.87
H_2	225.91** ±51.06	36.14** ±6.62	20.62** ±4.10	862.82** ±187.24	6.57** ±0.79	5.88* ±2.49	2886.50** ±370.31	202.44** ±40.65	0.22** ±0.05	32.96** ±12.17	309.90** ±91.90
h^2	127.57** ±34.36	63.78** ±4.46	31.78** ±2.76	2563.90** ±126.02	23.24** ±0.53	0.62 ±1.68	6447.30** ±249.24	451.89** ±24.36	0.28** ±0.03	5.01 ±8.19	228.17** ±61.85
F	213.82** ±55.00	33.09** ±7.13	3.09 ±4.42	612.75** ±201.71	0.95 ±0.85	6.55* ±2.69	-148.09 ±398.92	58.78 ±43.80	0.11* ±0.05	24.30 ±13.11	35.98 ±99.00
E	2.32 ±8.51	0.40 ±1.10	0.17 ±0.68	2.39 ±31.21	0.02 ±0.13	0.63 ±0.42	21.78 ±61.72	4.50 ±6.78	0.01 ±0.01	0.56 ±2.03	0.42 ±15.32

Table 2: Proportion of genetic components of variance for 11 characters

Components	Days to 50% flowering	50% flowering to maturity	Effective tillers plant^{-1}	Plant height (cm)	Panicle weight (g)	Panicle length (cm)	Grains panicle^{-1}	Grain Filling %	Length-breadth ratio (mm)	1000 grains weight (g)	Yield plant^{-1} (g)
$(H_1/D)^{1/2}$	1.18	1.35	4.03	1.42	3.53	1.58	5.47	2.14	1.86	2.32	3.32
$H_2/4H_1$	0.18	0.19	0.22	0.20	0.22	0.15	0.24	0.22	0.18	0.16	0.20
KD/KR	2.38	2.79	1.72	2.40	1.04	3.38	0.76	1.73	1.05	3.43	1.01
h^2/H_2	0.56	1.35	1.54	2.97	3.53	0.10	2.23	2.23	1.27	0.15	0.73
Heritability (ns)	67.90	62.21	6.41	53.81	8.30	41.10	3.00	20.95	28.08	24.53	9.08