

INHERITANCE OF TRAITS RELATED TO SEEDLING VIGOR AND GRAIN YIELD IN RICE (*ORYZA SATIVA L.*)

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Abstract

Nature of gene action and inheritance of traits related to seedling vigor and grain yield was determined in F_1 generation of a 7 parent diallel cross. Genetic component analysis revealed that rate of germination index and seedling shoot length were influenced by both additive and non-additive gene action, however, the additive component was found to be more pronounced in the inheritance of these two traits.

Wr-Vr graphic analysis indicated that rate of germination index was under the control of complete dominance gene effects. Over dominance appeared to be more important for seedling root length, seedling dry weight and 100 seed weight while partial dominance was found controlling seedling shoot length, number of tillers per plant, panicle length and grain yield per plant.

Introduction

Rice occupies about 10% of total cropped area in Pakistan. It is cultivated in all the four provinces of the country but Punjab and Sindh are the major producers. Basmati rice of Pakistan fetches a premium price in the international market due to its excellent grain quality. Rice is playing an important role as a staple food as well as an export commodity. Pakistan is one of the major rice exporter country. In spite of the prime position of rice in the national economy, the average paddy yield (3000 kg/ha) is much lower than other rice growing countries of the world. Many factors such as seed quality, seedling age, land preparation, plant density, nutrient management and pest management contribute towards yield.

In Pakistan, almost all the rice crop is established by transplanting 25-30 days old seedlings in the puddled field manually by the hired labour through contract made on area basis. The labourers transplant the seedlings at wider distance resulting lower number of plants than the required. Labour shortage due to industrialization is also a big issue that hinders the rice transplanting well in time. Delayed transplanting also causes reduction in yield. Rice cultivation by direct seeding can be an alternate of transplanting. Direct seeding of rice is practiced in USA, Italy and several other countries. Under direct seeded rice culture, varieties with high seedling vigor are required for better competitive ability against weeds (Mackill & Redona, 1997). Seed and seedling vigor is genetically controlled and modified by the environment (Perry, 1972) and it is possible to incorporate this trait in high yielding varieties (Seshu & Krishnasamy, 1987). Seed and seedling vigor in rice is associated with several quantitative characters (Petersen *et al.*, 1978).

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Materials and Methods

The present study was conducted during 2001-02 at National Agricultural Research Centre, Islamabad. Seven rice genotypes (IR50, IR25924-92-1-3, TNAU (AD)103, IR31779-19-3-3-2-2, IR21820-154-3-2-2-3, IR9764-45-2-2 and MI48) were selected from a set of 57 rice genotypes after evaluation for rate of germination, seedling root length, seedling shoot length and seedling dry weight (Akram *et al.*, 2001). These selected genotypes were crossed in all possible combinations excluding the reciprocals. Half of the F_1 seeds, after breaking the dormancy by dry heat treatment (Datta *et al.*, 1997) were subjected to vigor tests, viz., rate of germination index, seedling root length, seedling shoot length and seedling dry weight. Rate of germination (RG index) was determined following the procedure of (Seshu *et al.*, 1988). Root and shoot length and dry weight of seedling were recorded following Krishnasamy & Seshu (1989).

The remaining F_1 seeds were used for field experiment conducted at Rice Research Institute, Kala Shah Kaku, Pakistan. Twenty one days old seedlings were transplanted in the field following randomized complete block design with three replications during 2002. Each replication comprised of 28 entries (21 F_1 s + 7 parents). Each entry was planted in two rows of 2 meter length. Single seedling per hill were planted by keeping 20 cm distance between rows and hills. Fertilizer was applied at 120-60-0 NPK (kg/ha). The crop was fully protected from pest attack. Data on tillers per plant, panicle length, and 100 seed weight were recorded on five randomly selected normal plants from each plot. Two adequacy tests were carried out to validate the data set for estimation of genetic parameters. The diallel cross technique as developed by (Hayman, 1954) and elaborated by Singh & Chaudhry (1985) was used for genetic analysis. Graphic analysis was conducted to establish the genetic behaviour of parental lines and gene effects.

Results and Discussion

The estimates of components of variance from a diallel cross are unbiased, only if certain assumptions are met (Hayman, 1954). These assumptions are: Diploid segregation, no reciprocal differences, homozygous parents, no multiple allelism, uncorrelated gene distributions and absence of non allelic interaction. Two adequacy tests were used to validate these assumptions. The first test was t^2 test (a significant t^2 would indicate the failure of hypothesis), and the second test was analysis of the regression (W_r , V_r). In this test the regression coefficient (b) for each trait is expected to be significantly different from zero but not from unity. According to these tests, the traits other than RG index seedling dry weight, panicle sterility and grain yield per plant fulfilled all the assumptions (Table 1). Estimates of genetic parameters in the present context are given in Table 2. The inferences regarding present studies based on estimates of genetic parameters and W_r , V_r graphic analysis for the characters studied are discussed.

Rate of germination index: Significant values D , H_1 and h^2 indicted the importance of both additive and non additive types of gene action involved in the inheritance of this trait. However, the additive gene effects seemed to be more important than dominance ones. This was supported by positive value of D/H_1 . A low value (0.20) of the proportion $H_2/4H_1$ indicated that the positive and negative alleles are unequally distributed at the loci exhibiting dominance in the parental genotypes. This again is substantiated by H_1 being greater than H_2 in this case. The ratio (2.52) for proportion of dominant and recessive genes among the parents suggested that more dominant alleles than the recessive ones are controlling the character. Unequal frequency of alleles with positive and negative effects

Table 1. Validity of hypothesis through homogeneity tests.

Characters	Statistics				
	t ²	B	S.E.(b)	Ho:b=1	Ho:b=0
RG Index	6.68*	1.116	0.050	22.38**	-2.33
Seedling root length	0.357	0.750	0.200	3.753*	1.254
Seedling shoot length	4.376	0.360	0.173	2.086	3.711*
Seedling dry weight	11.214*	0.297	0.125	2.381	5.646**
Tillers per plant	0.292	0.735	0.214	3.438*	1.239
Panicle length	0.000	0.828	0.247	3.358*	0.697
Grain yield per plant	14.596*	0.176	0.118	1.498	6.996**
100-seed weight	2.151	0.593	0.171	3.467*	2.378

**, * significant at 1% and 5% probability level respectively.

has already been established by low $H_2/4H_1$ ratio. Correlation between Wr + Vr and Yr was close to unity thus indicating the direction of dominance towards high RG index.

The assumption of the absence of non-allelic interaction appears to be satisfied as the regression coefficient did not differ significantly from unity. The regression line passed the Wr-axis through the origin (Fig. 1). There appeared to be predominant influence of dominance gene effects. Parents IRSO, IR25924-921-3, TNAU (AD) 103 and IR31779-19-3-3-2-2 were having most of the dominant genes while M2148 with the most recessive genes.

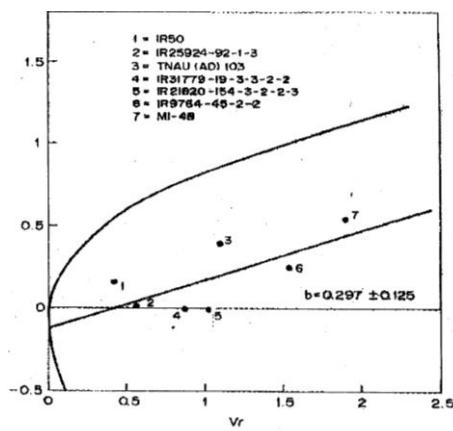
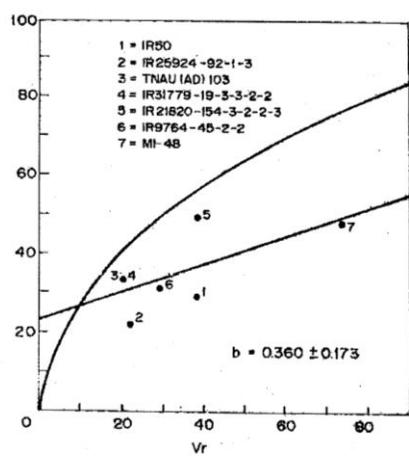
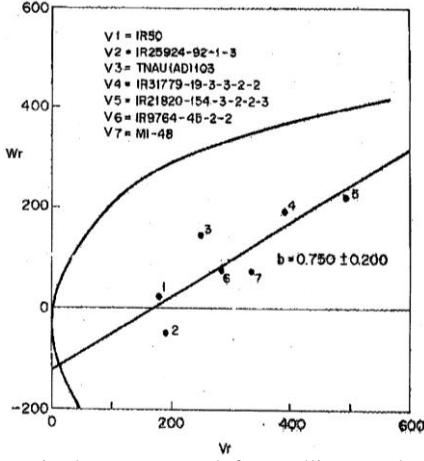
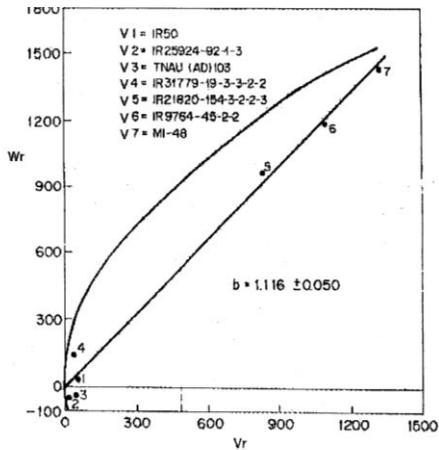
Seedling root length: Both D and H components were significant indicating the role of additive and dominance effects for this trait. However dominant gene effects seem to be more important as supported by low heritability and negative value of D/H₁. Significant value of F and high KD/KR indicated that most of the parents carried mainly dominant genes. The positive and negative alleles were not in equal distribution as indicated by low $H_2/4H_1$ value. Over-dominance was operating because $(H_1/D)^{1/2}$ was greater than one. Relationship of Wr+Vr and Yr suggested the direction of dominance towards lower side.

The regression coefficient did not differ significantly from unity. The regression line cuts the Wr-axis below the point of origin (Fig. 2) indicating the control of over dominance for this trait which is also shown by $(H_1/D)^{1/2}$ value greater than unity (Table 2). The position of the varietal array on the graph showed that IR50 and IR25924-92-13 contained the maximum number of dominant genes while IR21820-154-3-3-3-3 the most recessive genes. The spread of array points projected considerable genetic diversity present among the parents.

Seedling shoot length: Additive and non-additive types of gene action were found to be involved in the inheritance of seedling shoot length as indicated by significant D, H₁ and H₂ values. Additive gene effects seem to be more important than dominance gene effects unlike in case of root length. This is evidenced by positive value of D-H₁ and relatively high estimates of narrow sense heritability. The value of $H_2/4H_1$ ratio was <0.25 indicating unequal distribution of positive and negative alleles among the parents. The ratio KD/KR was greater than 1 which revealed the preponderance of dominant genes. The positive correlation of Wr+Vr with Yr provided evidence that most of the dominant alleles act in the direction of shorter shoot length. Partial dominance was evidenced by the $(H_1/D)^{1/2}$ value which was < 1. Li and Rutger (1980) reported that under cool temperature conditions (18°C) shoot length of seedlings grown for 14 days (expressed as seedling vigor) was regulated by additive and dominance effects in F₁ and F₂ generations,

and the additive effects being consistent over both the generations. Their results are in close agreement with the present findings, although the test material was grown under a different temperature (25°C).

The regression coefficient is significantly different from unity and non-significant from zero showing the involvement of some non-allelic interactions controlling this trait, meaning by partial failure of assumptions but in such cases, estimates of the genetic parameters of that trait is still possible (Hayman, 1954). The regression line intercepted the Wr-axis above the origin (Fig. 3), which indicated partial dominance. Partial dominance was also indicated by the estimates i.e. $D > H_1$ and the ratio $(H_1/D)^{1/2} < 1$ (Table 2). Among the parents IR25924-92-1-3 had the most dominant genes, whereas MI48 possessed the most recessive genes. TNAU(AD)103 and IR3177-19-3-3-2-2 had exactly equal number of dominant genes as both of them overlapped. The position of array points along the regression line showed almost complete dispersion suggesting sufficient genotypic variability among the parents.



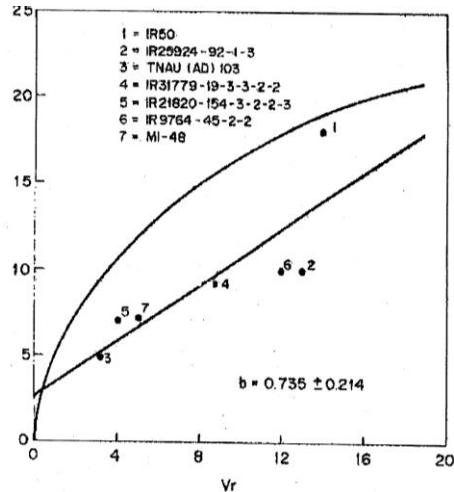


Fig. 5. Wr, Vr-graph for tillers per plant.

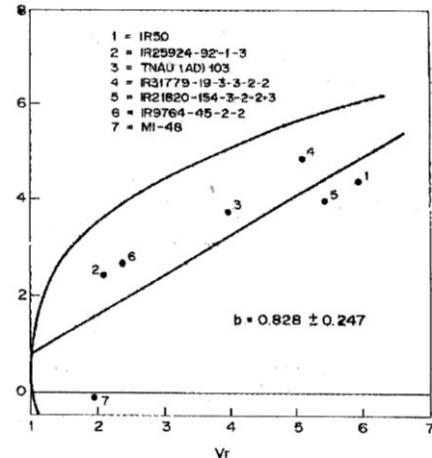


Fig. 6. Wr, Vr-graph for panicle length.

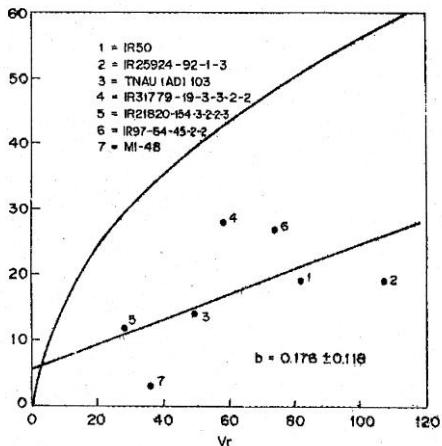


Fig. 7. Wr, Vr-graph for grain yield per plant.

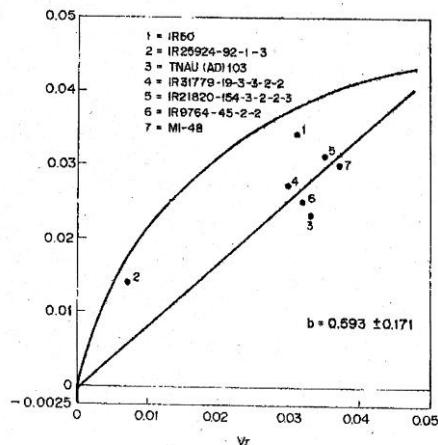


Fig. 8. Wr, Vr-graph for 100-seed weight.

Seedling dry weight: Like many other traits seedling dry weight was also under the influence of both additive and non-additive gene effects. The non-additive gene effects were found to be playing more important role as indicated by higher H_1 value than D . Most of the parents were carrying dominant genes as indicated by positive value of F and higher KD/KR ratio (1.403). The positive and negative alleles were not in equal distribution at all the loci showing dominance ($H_2/4H_1=0.22$). Since $D < H_1$, the genetic system can be classified as mainly of dominance type. This is further supported by the value of $(H_1/D)^{1/2}$ which is greater than 1 indicating the effects of over dominance. Lee *et al.*, (1986) reported that dry weight of 12 day-old rice seedling was under the control of additive and dominance effects, the additive effects being more important. As far as the involvement of both additive and dominance effects was concerned, present study is in agreement with their findings.

The regression coefficient for this trait is significantly different from unity indicating the presence of non-allelic interactions. The point of interception was below the origin (Fig. 4) showing over dominance for this trait. This is in accordance with the estimates $D < H_1$ and $(H_1/D)^{1/2}$ ratio higher than unity (Table 2). IR50 contained the most dominant genes whereas MI48 the most recessive genes. The others fall between these in the following order: IR25924-92-1-3, IR31779-19-3-3-2-2, IR1820-154-3-2-2-3, TNAU (AD)103 and IR9764-45-2-2

Tillers per plant: This trait was found to be controlled by additive and dominance gene action with the additive effects playing greater role. This was indicated by positive $D-H_1$ value and high heritability. Significantly positive F value and higher KD/KR ratio suggested that most parents carried mainly dominant genes. Unequal distribution of positive and negative genes were found at all the loci across parents as indicated by low $H_2/4H_1$ value of 0.16.

The regression coefficient did not differ significantly from unity hence the assumptions of the absence of non-allelic interaction appears to be satisfied. The regression line intercepted the Wr -axis above the point of origin (Fig. 5) indicating partial dominance for the trait under study. The distribution of Wr , Vr points showed the concentration of dominant alleles in TAN U (AD) 1 03, followed by IR21820-154-3-2-23 and M148, and the recessive alleles in IR31779-19-3-3-2-2, IR9764-45-2-2 and IR25924-92-1-3. Present results agree with the findings of Li & Chang (1970). However, these results contradict with those reported by Singh *et al.* (1970) and Kaushik (1984).

Panicle length: The additive (D) and dominant components (H_1 , H_2 and h^2) were significant indicating the involvement of both of the two types of gene action for this trait. Higher value of H_1 than D suggests that the dominant gene effects play amore important role. A symmetry of positive and negative genes was indicated by low $H_2/4H_1$ and the ratio KD/KR which was almost equal to unity. The $(H_1/D)^{1/2}$ value was greater than 1 indicating over dominance. Li & Chang (1970) reported the involvement of both types of gene action for panicle length as indicated from the present studies. These results also confirm the earlier results of Kaushik (1984) that additive and dominance gene effects were involved in inheritance of panicle length in rice but dominance effects were more important. Contrary to the present investigation, Nematzadeh (1987) reported that panicle length was fully under the control of non-additive gene effects.

The assumption of the absence of non-allelic interaction seems valid as the regression coefficient is not significantly different from unity. The regression line intercepted the Wr -axis above the point of origin showing partial dominance (Fig. 6) while the ratio $(H_1/D)^{1/2}$ suggested over-dominance for panicle length. Thus, the results of graphic analysis and that of genetic component analysis did not agree for this trait. The position of the arrays on the graph indicated that MI48 followed by IR2592492-1-3 and IR9764-45-2-2 had the most dominant genes for longer panicle, while IR50, IR31779-19-3-3-2-2, IR21820-154-3-2-2-3 seemed to form a group with most recessive genes.

Grain yield per plant: Non significant value of D and significant values of H_1 and H_2 indicated that this important economic trait was under the control of non-additive gene effects. High value of $(H_1/D)^{1/2}$ indicated over-dominance effects. The positive and negative alleles were present in unequal proportions in the parents as indicated by the value of $H_2/4H_1$ which was equal to 0.17.

Presence of non-allelic interaction was evident as the regression coefficient "b" was significantly different from unity. The regression line intercepted the Wr-axis above the point of origin (Fig. 8) indicating partial dominance. The estimates of D, H_1 components showed that $D < H_1$ and $(H_1/D)^{1/2}$ ratio is greater than unity, indicating that the regression line should pass below the origin. Fig. 7 did not agree with the estimates given in table-2 for grain yield per plant. The position of the arrays on the graph showed that IR21820-154-3-2-2-3 had the most dominant genes followed by MI48. IR25924-92-1-3 had the most recessive genes while other parents fall in between these. Results of the present study are in conformity with those reported by Singh *et al.*, (1970), Kaushik (1984) and Nematzadeh (1987). However, the findings of this study are contrary to those of Li & Chang (1970).

100-Seed weight: Both additive and dominance gene effects played role in this trait. However, the dominance gene effects seemed more important as evident from the fact $D < H_1$. Greater than 1 value of $(H_1/D)^{1/2}$ indicated over-dominance. Positive and negative alleles were present in unequal proportions as indicated by the value of $H_2/4H_1$ which was less than 0.25. Negative F value and low value of KD/KR suggested that most parents carried mainly recessive genes. Kaushik (1984) and Nematzadeh (1987) reported similar findings on seed weight, however, Haque *et al.*, (1981) reported major role of additive gene effects in controlling the inheritance of seed weight in rice. Non-significance of regressions coefficient from unity showed that Wr is related to Vr by a straight regression line of unit slope. The regression line of the Wr, Vr-graph touched the Wr-axis below the point of origin (Fig. 8) showing over dominance which was also indicated by $(H_1/D)^{1/2}$ ratio (Table 1). So both graphic analysis and component analysis showed similar trend for 100-seed weight. There was a big cluster based on the distribution of points along the regression line from the point of origin, which included all the parents except IR25924-92-1-3. The latter had the most dominant genes as it was very near to the point of origin whereas all others seemed to contain the most recessive genes. The proximity of array points except IR25924-92-1-3 may be an indication of their genotypic similarity and their differences may be due to some genes with small effects on the trait.

Genetic component analysis revealed that two important traits of seed and seedling vigor viz., rate of germination and seedling shoot length, were although influenced by both additive and non-additive gene action, the additive component was more important in controlling the inheritance of these two traits. An overall review of the Wr, Vr-graphic analysis for the different traits indicated over-dominance for seedling root length, seedling dry weight and 100-seed weight; complete dominance for RG index, and partial dominance for seedling shoot length, tillers per plant, panicle length and grain yield per plant.

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