



Full Length Article

Studying the Genetic Mechanism of Some Yield Contributing Traits in Wheat (*Triticum aestivum*)

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ABSTRACT

Diallel mating system was used to evaluate seven wheat varieties including five cultivars from Pakistan viz. Inqilab-91, Shalimar-88, Chenab-2000, Uqab-2000, Punjab-85 and two from CIMMYT naming Weebli-1 and Maya/Pavon. These were crossed in diallel fashion to get 42 cross combinations including direct and reciprocals. Significant differences were observed among genotypes for all the traits. Scaling tests were used to test the adequacy of the data for analyzing additive-dominance model, which showed that additive-dominance model was fully adequate for plant traits like number of grains per spike and grain yield, but characters like tillers per plant, spike length and 100-grain weight showed partial adequacy of the data. The D component for all the traits was significant showed that all the characters are additively controlled. The Vr-Wr graphs showed over dominance for number of grains per spike, while partial dominance was observed in traits like plant height, tillers per plant, 100-grains weight and grain yield per plant. © 2010 Friends Science Publishers

Key Words: Gene action; Genetic components; Regression co-efficient; Narrow sense heritability

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important grain crop and a staple food for a large part of the world population including Pakistan. It is a dietary mainstay for millions of people as it provides 50% caloric and protein requirements to a major population of the world. It also plays a significant role in critical areas of food security and economic stability of our country, when self sufficiency in wheat production is a far cry. It is grown on an area of 8.41 million hectares in the country with a production of 21.83 million tones of wheat grain (Government of Pakistan, 2007-2008). This is far below than that of most of the leading wheat producers in the world especially Germany (7.9 t ha⁻¹), France (6.6 t ha⁻¹) and Egypt (6.4 t ha⁻¹). This yield is generally insufficient to fulfill the domestic requirements. Sometimes we have to import large amount of wheat to fulfill the domestic needs and considerable amount of foreign exchange is spent on it. There is continuous increase in area, but the average yield is trailing far behind the average yield produced by the rival countries in wheat. Its production can be enhanced through the development of improved cultivars having wider genetic base capable of producing better yield under various agro-climatic conditions. The diallel mating system developed and advocated by Hayman (1954) and Mather and Jinks (1982) provides fairly reliable mechanism especially in self fertilized crops like wheat to assess the genetic system and gene action involved in the expression of important plant

attributes right in the F₁ generation. Genetic studies of different characters showed different pattern of inheritance. For plant height some researchers found additive type of gene action (Chowdhry *et al.*, 1997). Mishra *et al.* (1996) and Iqbal (2004) reported partial dominance in controlling plant height. Number of tillers per plant is among one of the important yield components. Tillers per plant in wheat is controlled by additive genetic effects (Chowdhry *et al.*, 2005), additive type of gene action controlling this trait with partial dominance in the absence of epistasis has been reported by Khan *et al.* (1982) and Chowdhry *et al.* (2001), so early generations selection for this trait is desirable. However, over-dominance gene effects are much preferred than additive effects for controlling this trait (Khaliq & Chowdhry, 2001). Khan *et al.* (2003) reported over dominance for number of grains per spike. In another study Rahman *et al.* (2003) found partial dominance for number of grains per spike. Asif *et al.* (1999) found over dominance for 1000-grain weight.

In wheat breeding programmes, higher yield is the ultimate objective. It is a polygenic character and is greatly influenced by the varying environments. Over dominance for grain yield per plant was reported by (Khan *et al.*, 2003). Wheat varieties with better genetic potentials perform better in conducive and non-conducive ecosystems (Calenderini & Slafer, 1999; Reynolds & Borlaug, 2006). The objectives of the present investigations were to create variability, expose genetic effects and to determine appropriate parents for yield related traits by employing diallel cross technique. The

genetic information thus obtained would be utilized in wheat breeding program for the evolution of new wheat cultivars with wider adaptability and higher yield potential.

MATERIALS AND METHODS

The experimental material comprised of seven wheat cultivars including five locals Shalimar-88, Chenab-2000, Inqilab-91, Uqab-2000 and Punjab-85 and two exotic CIMMYT originated cultivars Weebli-1 and Maya/Pavon were sown in the field on 5th of November, 2006 in the Department of Plant Breeding and Genetics and later hybridized in all possible combinations including reciprocals.

During next crop season, seven wheat varieties/lines (parents) and their hybrids (F_1) were planted in field on 10th of November, 2007 following a triplicated randomized complete block design. Thirty plants of each genotype were grown in a 5 m long row in each replication. The plants were spaced 15 and 30 cm apart within and between the rows, respectively. To keep uniformity in the distance and depth of the seeds, a template was used. Two seeds were dibbled per hole and after germination one healthy seedling was retained at each hole after thinning. All standard agronomic practices i.e., hoeing, weeding and irrigation etc. were adopted uniformly. For data collection ten guarded plants for each parent and cross were tagged at random for each replication and data were recorded for plant height (cm) from base of plant to the tip of spike excluding awns of mother shoot. Number of tillers per plants were counted at maturity and number of grains per spike was counted after thrashing the spike of the mother shoot. 100-grains (g) were counted randomly from bulk of the selected plants and weighed on electric balance (Compax- Cx-600) and for grain yield (g) all spikes of individual selected plants were thrashed manually and weighed using electric balance (Compax- Cx-600).

The collected data were analyzed to determine significant varietal differences among the 42 genotypes following Steel *et al.* (1997). The simple additive-dominance (AD) model as suggested by Hayman (1954) and Jinks (1954) modified by Mather and Jinks (1982) for diallel analysis was employed for further investigations.

RESULTS

Genotypic variation among the parents: Preliminary analysis of variance indicated significant differences ($P < 0.01$) for all the traits among genotypes. The mean squares for the traits are represented in Table I describing high significance of the 'F' test for all the characters under study. Array means showed that seven parents (e.g., Inqilab-91, Shalimar-88, Chenab-2000, Uqab-2000, Punjab-85, Maya/Pavon & Weebli-1) used in this study varied considerably for each component of yield (Table II).

Assessment of the data for additive-dominance model: The data were assessed for Additive-Dominance model by

exploiting various adequacy parameters given in Table III. According to Mather and Jinks (1982) the data will be only valid for genetic interpretation if the value of regression coefficient (b) must deviate significantly from zero, but not from the unity. The value of b was significantly varying from zero, but not from one for all the characters under study to fulfill this criterion. The test for 't' square indicated its non-significance value, which proved the absence of non-allelic interactions in genetic behavior of all traits, which in turn attested the data valid for AD model for all the characters. The appropriateness of the model data analysis was also verified by the analysis of variance of ($W_r + V_r$) and ($W_r - V_r$). In this test the mean squares for ($W_r + V_r$) should be significantly different between the arrays, while the mean squares for ($W_r - V_r$) should be non-significant (Mather & Jinks, 1982). The lack of significant variation in the ($W_r - V_r$) arrays over replications for all the characters suggested that any kind of epistasis was not involved in the phenotypic expression of the traits. Although the value of regression coefficient (b) proved the fitness of the data of plant height (1.02), tillers per plant (0.76), 100-grain weight (1.08) and for AD model, mean square value of ($W_r + V_r$) for the traits indicated no significant deviation, thus emphasizing partial validity of these characters for further genetic analysis (Table III). The value of b (0.78 ± 0.27) in case of number of grains per spike was significantly differed from zero and not from one, highly significant value of mean squares for ($W_r + V_r$) between the arrays (477.42) and non-significance of ($W_r - V_r$) mean squares (53.22) revealed full fitness of the data for further genetic elaboration. Similarly in case of grain yield per plant the value of b was (1.23 ± 0.12) and highly significant value of mean squares for ($W_r + V_r$) between the arrays (26.46) and non-significance of ($W_r - V_r$) mean squares (0.83) revealed full fitness of the data for further genetic estimation (Table III).

Estimation of genetic components and graphical representation of the results: Genetics of yield related traits was evaluated by the calculation of genetic components of variation D , H_1 , H_2 and F (Table IV). Components of variation given in Table-IV showed that for plant height D , H_1 and H_2 are positive, but only the D component is significant and its value is more than H_1 and H_2 , which shows that the additive effects were more important in controlling plant height than non-additive effects. The values of H_1 and H_2 were not equal to each other indicating that un-equal distribution of dominant genes in the parents. Positive value of 'F' indicated the presence of more dominant genes in the parents and it was supported by high value of $\sqrt{4DH_1 + F}/\sqrt{4DH_1 - F}$. The value of ' h^2 ' was negative, which indicated unequal contribution of dominant genes for plant height. The mean degree of dominance was less than one, indicated the presence of partial dominance with heritability of 65%.

The V_r/W_r graph shows that the regression line cuts the W_r axis above the origin showing additive gene action with partial dominance revealed that Weebli-1 and

Table I: Mean squares for various yield related parameters

Source of variation	Plant height (cm)	Tillers per plant	No. of grains/spike	100-grain weight (g)	Grain yield (g)
Replications	11.57*	0.63 ^{NS}	1.32 ^{NS}	0.019 ^{NS}	1.44 ^{NS}
Genotypes	10.53**	1.45**	83.82**	0.12**	10.65**
Error	2.82	0.26	1.76	0.03	1.37

**, Significant at $P \leq 0.01$; *Significant at $P \leq 0.05$; NS, Non-significant at $P > 0.05$

Table II: Array means for various yield related parameters

Parents	Plant height (cm)	Tillers per plant	No. of grains per spike	100-grain weight (g)	Grain yield (g)
Inqilab-91	87.19	7.07	46.38	4.27	18.81
Shalimar-88	91.29	6.40	51.73	4.68	19.14
Chenab-2000	94.76	6.17	45.20	4.25	14.93
Uqab-2000	94.95	7.73	56.80	4.29	19.45
Punjab-85	92.27	8.00	46.50	4.07	15.49
Maya/Pavon	93.07	8.30	49.82	4.75	19.56
Weebli-1	92.08	7.60	58.37	4.63	24.14

Maya/Pavon possess maximum dominant genes as they are close to the origin. However, the maximum recessive genes were shown by the Uqab-2000 and Inqilab-91 as they are farthest from the origin.

For tillers per plant the relative value of components of H_1 and H_2 were un-equal in magnitude and D was positive and significant Table IV, which indicates the importance of additive effects for the control of this trait. As H_1 and H_2 are un-equal indicating the un-equal distribution of genes. The value of $H_2/4H_1$ ratio was more than 0.25, which indicated equal distribution of genes for the trait among the parents. Negative F value signified the important role of recessive genes. The negative value of ' h^2 ' was noted. The degree of dominance was less than one suggesting the presence of partial dominance in F_1 hybrid, which was supported by the slope on the regression line in Fig. 2. The estimate of narrow sense heritability was 75%.

The inheritance pattern for this trait was found to be additive with partial dominance type as the regression line intercepted the Wr axis above the origin. The graphical representation of this trait in Fig. 2 also indicated that Inqilab- 91 and Chenab-2000 contains maximum number of dominant genes for this trait. Punjab-85 and Weebli-1 possess maximum recessive genes for controlling this trait.

The significant value of D for number of grains per spike showed that this trait was under the control of additive gene effects. However, it was less than H_1 and H_2 , which shows that non-additive effects are equally important. The values of H_1 were greater than H_2 revealed un-equal contribution of dominant genes for transmission of number of grains per spike confirmed by the low value of $H_2/4H_1$ (0.20). Negative and non-significant value of 'F' indicated the absence of dominant genes in parents and it was supported by high value of $\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F} = 0.96$. The value of ' h^2 ' was positive, which indicated that

dominance effect of genes is considerable and it is towards the parent with increasing number of grains per spike. The degree of dominance was greater than one, indicated the presence of over-dominance type of gene action with heritability 63%.

The Vr/Wr graph (Fig. 3) indicated that both the varieties Maya/Pavon possessed the maximum dominant genes responsible for inheritance of number of grains per spike. However, maximum recessive genes were exhibited by the variety Uqab-2000, followed by Punjab-85. Since the regression line intercepted the Wr axis below the point of origin, showing the presence of over-dominance type of gene action in case of number of grains per spike along with an effective additive control for this character. The deviation of the regression line from unit slope was found non-significant thus indicated the absence of non-allelic interactions.

The relative value of components of H_1 and H_2 were un-equal in magnitude and D was positive and significant for 100-grain weight. Positive and significant value of D indicates the importance of additive effects for the control of this trait. As H_1 and H_2 are un-equal indicating the un-equal distribution of genes. The value of $H_2/4H_1$ ratio was less than 0.25, which indicated un-equal distribution of genes for the trait among the parents. Negative F value signified the important role of recessive genes, which was supported by high value of $\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F}$. The negative value of ' h^2 ' was noted. The degree of dominance was less than one suggesting the presence of partial dominance in F_1 hybrid, which was supported by the slope on the regression line in Fig. 4. The estimate of narrow sense heritability was 71%.

The regression line in case of 100-grain weight intercepted above the point of origin showed the involvement of partial dominance. The graphical representation of this trait in Fig. 4 indicated that Maya/Pavon and Weebli-1 contains maximum number of dominant genes for the trait. Genotypes Punjab-85 and Chenab-2000 possess maximum recessive genes for controlling this trait.

The genetic components for grain yield per plant showed that H_1 , H_2 and D component were positive and significant. The component D is more than H_1 and H_2 showing the presence of additive genetic effects in controlling grain yield. The value of $H_2/4H_1$ ratio was less than 0.25, which indicated un-equal distribution of genes for the trait among the parents. Positive F value signified the important role of dominant genes, which was supported by high value of $\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F} = 2.09$. The negative value of ' h^2 ' was noted. The degree of dominance was less than one suggesting the presence of partial dominance in F_1 hybrid, which was supported by the regression slope in Fig. 5. The estimate of narrow sense heritability was 74%.

Placement of array points displayed that Maya/Pavon and Uqab-2000 had maximum number of dominant genes for grain yield per plant. However, Chenab-2000 and Weebli-1 had maximum recessive genes for controlling

Table III: Adequacy test of additive dominance-model for yield related traits

Parameters	Plant height (cm)	Tillers per plant	No. of grains/spike	100-grain weight (g)	Grain yield (g)
Joint regression (b)	1.02±0.25	0.76±0.21	0.78±0.27	1.08±0.30	1.23±0.12
Test for b=0	4.02*	3.57*	2.92*	3.63*	10.28*
Test for b=1	-9.50 ^{NS}	1.10 ^{NS}	0.80 ^{NS}	-2.81 ^{NS}	-1.92 ^{NS}
Mean squares of Wr+Vr between arrays	28.96 ^{NS}	0.12 ^{NS}	477.42**	0.0015 ^{NS}	26.46**
Mean squares of Wr-Vr between arrays	2.62 ^{NS}	0.031 ^{NS}	53.22 ^{NS}	0.0003 ^{NS}	0.83 ^{NS}
Fitness of the data	Partial	Partial	Full	Partial	Full

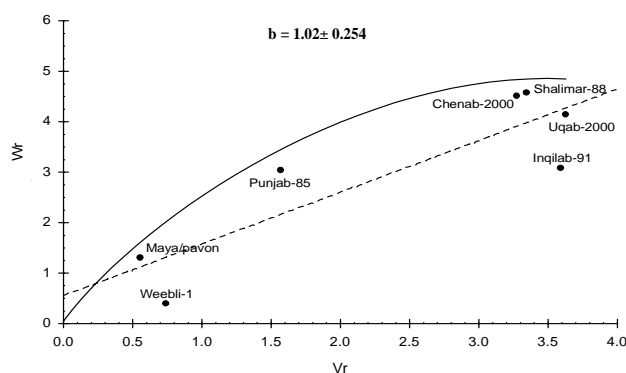
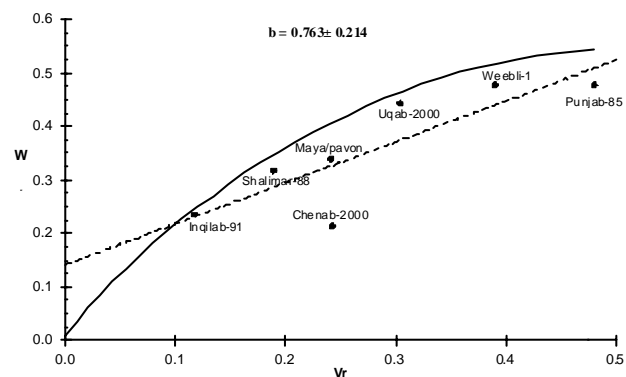
**, Significant at $P \leq 0.01$; *Significant at $P \leq 0.05$; NS, Non-significant at $P > 0.05$

Table IV: Estimation of the components of genetic variation

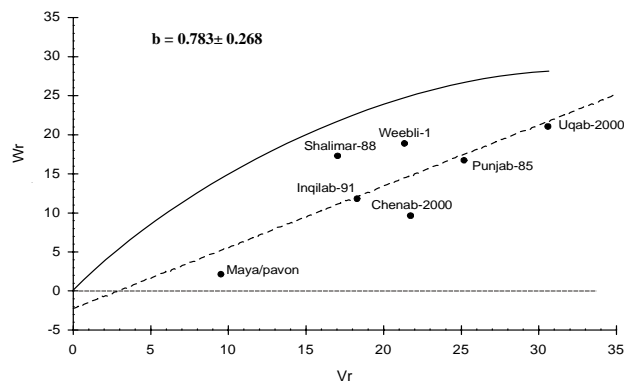
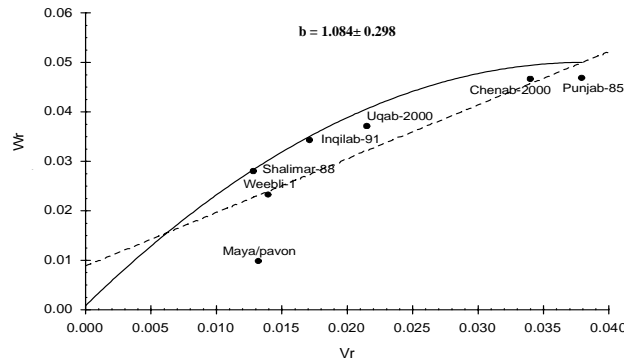
Components of variation	Plant height (cm)	Tillers per plant	Number of grains/spike	100-grain weight (g)	Grain yield (g)
D	5.73±0.59	0.55±0.049	26.77±3.20	0.05±0.005	8.78±0.34
H ₁	1.45±1.43	0.093±0.11	52.46±7.70	-0.006±0.012	2.71±0.83
H ₂	1.69±1.26	0.14±0.11	42.79±6.78	0.001±0.011	2.09±0.73
F	0.065±1.43	-0.26±0.12	-1.61±7.67	-0.007±0.012	3.45±0.82
h ²	-0.49±0.84	0.13±0.070	44.10±4.56	-0.004±0.007	-0.15±0.49
E	1.06±0.21	0.094±0.01	0.62±1.13	0.011±0.0018	0.49±0.12
(H ₁ /D) ^{0.5}	0.50	0.41	1.40	0.32	0.55
H ₂ /4H ₁	0.29	0.36	0.20	-0.030	0.19
(4DH ₁) ^{0.5} +F/(4DH ₁) ^{0.5} -F	1.02	0.28	0.96	0.65	2.09
h ² (n.s)	0.65	0.75	0.63	0.71	0.74

*The value is significant when it exceeds 1.96 after dividing with its standard error

E = environmental variance, D = additive variance, H₁ = dominance variance, H₂ = proportion of positive and negative genes in the parents, F = Relative frequency of dominant and recessive alleles in the parent, h² = dominance effect (over all loci in heterozygous phase), $\sqrt{H_1/D}$ = mean degree of dominance, H₂ / 4H₁ = proportion of genes with positive and negative effects in the parents, $\sqrt{4DH_1 + F} / \sqrt{4DH_1 - F}$ = proportion of dominant and recessive genes in the parents, Heritability h² (n.s).

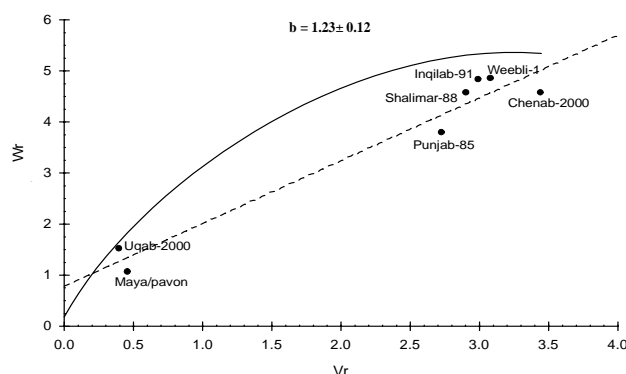
Fig. 1: Vr-Wr graph for plant height**Fig. 2: Vr-Wr graph for tillers per plant**

grain yield. The regression line for this trait also cuts the Wr axis above the origin showing partial dominance for this trait.

Fig. 3: Vr-Wr graph for number of grains per spike**Fig. 4: Vr-Wr graph for 100-grain weight**

DISCUSSION

Development of wheat varieties possessing improved yield related characters had been the major objective of

Fig. 5: Vr-Wr graph for grain yield

wheat breeders. Thus availability of genetically based variation for traits like plant height, tillers per plant, number of grains per spike, 100-grain weight and grain yield in breeding population is essential. Present sample of genetic material used here to generate information on genetic mechanism of these traits. The genotypic differences were significant for all the traits. Significant variation among genotypes for grain yield and related traits in different varieties of wheat were also reported by (Ambreen *et al.*, 2002). Assessment of data for additive dominance model revealed full fitness of the data for number of grains per spike and grain yield, but was partially fit for plant height, tillers per plant and 100-grain weight. The partially adequate models for these plant characters may be because of the presence of non-allelic interaction, linkage and non-independent distribution of the genes in the parents as suggested by Mather and Jinks (1982). However, several partial adequacy of the simple genetic model to the data set, never the less analyzed the diallel cross data in wheat (Hussain, 1991).

Significant differences for genetic components; additive and dominant for all the traits studied indicated the efficient creation of genetic variability. The breeding value of a line is a function of the additive gene action. The traits like plant height, tillers per plant, 100-grain weight and grain yield are under the control of additive genetic effects, which were evident from the significant and higher value of D than the dominance variance H_1 and H_2 , which shows the proportion of positive and negative genes in the parents. However, the significant value of D for number of grains per spike was less than the values of H_1 and H_2 showing the involvement of both additive and non-additive effects. The values of H_1 and H_2 were un-equal in all the traits studied thus indicating un-equal distribution of dominant alleles. F which indicates the relative frequency of dominant and recessive alleles in the parents was negative for tillers per plant, number of grains per spike and grain yield thus showed the importance of recessive alleles in these characters. But positive values of F in traits like plant height and grain yield showed the important role of dominant genes in the parents.

Degree of dominance was less than one for plant

height, tillers per plant, 100-grain weight and grain yield so, Partial dominance type of gene action was predominated for these traits, which was confirmed from the regression line, which cuts the Wr axis above the origin. Preponderance of partial dominance in these traits revealed the importance of early generation selection, which would be helpful in future breeding endeavors. Partial dominance with additive effects for these traits was also reported (Khan *et al.*, 1982; Mishra *et al.*, 1996; Chowdhry *et al.*, 2001; Joshi *et al.*, 2002; Hakizimana *et al.*, 2004). Over dominance was observed for number of grains per spike, which revealed the manifestation of this trait in later generation selections. Similar findings were observed (Aziz & Chowdhry, 1999; Khan *et al.*, 2003).

The value of ' h^2 ', which shows net dominance effect was positive for tillers per plant and number of grains per spike, which indicated that dominance effect of genes is considerable and it is towards the parent with increasing number of tillers and number of grains. But for plant height, 100-grain weight and grain yield the value of ' h^2 ' was negative. The narrow sense heritability estimates were high for tillers per plant, 100-grain weight and grain yield, but for plant height and number of grains per spike it was moderate. Gene action following diallel cross analysis was also reported for yield and related parameters in wheat (Lonts, 1986; Chowdhry *et al.*, 2001; Mahmood & Chowdhry, 2002; Rahim *et al.*, 2006). Thus this genetic umbrella of different yield related traits would be proceeded further in order to achieve high yield potential.

CONCLUSION

The results revealed that there was significant genotypic variation among the genotypes. The data for the characters like plant height, tillers per plant and 100-grain weight was partially adequate and for number of grains per spike and grain yield per plant was fully adequate for genetic interpretation. Additive genes coupled with moderate to high narrow sense heritability were involved in the heritage of almost all the traits with the exception of number of grain per spike, which showed dominance properties along with additive effects. Heterosis breeding might be fruitful for progress in number of grains per spike. But for all other traits selection in early generations would be very useful.

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