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GENETIC BASIS OF YIELD AND SOME YIELD RELATED TRAITS IN BASMATI RICE

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Abstract

Additive, dominance and epistasis components of genetic variation for yield and some yield related traits were assessed through modified triple test cross technique in Basmati rice. Epistasis was found an important part of genetic variation for plant height, tillers per plant, secondary branches per panicle, grains per panicle, 1000-grain weight and yield per plant except primary branches per panicle and panicle length. Bifurcation of epistasis showed that additive x additive (i) type and additive x dominance + dominance x dominance (j + l) types of non-allelic interactions were involved in the expression of these traits. Additive and dominance type of gene action influenced the expression of primary branches per panicle and panicle length. No evidence of directional dominance was observed for these two traits. For plant height, tillers per plant, secondary branches per panicle, grains per panicle, 1000-grain weight and yield per plant, recurrent selection or biparental mating may be exercised in F_2 and following generations however, selection of desired plants may be postponed till F_5 or F_6 generations to permit maximum obsession of epistatic effects to develop desired cultivar(s) in Basmati rice.

Introduction

Selection of the efficient breeding method depends to large degree on understanding of the genetic scheme controlling the traits to be selected. Although simple genetic models presume additively of genetic control over loci, models (Kearsey & Jinks, 1968, Jinks *et al*., 1969; Ketata *et al*., 1976) are now accessible which detect epistasis in addition to additive and dominance components of genetic variation in self-pollinated crops. However, restricted use of these models has been made in Basmati rice where the pace of breeding work to develop high yielding and quality rice has been slow due to complex genetic nature of this crop. In order to address this issue, present study was conducted to assess the genetic basis of yield and some important yield components through triple test cross design (Kearsery & Jinks, 1968). The main reason of triple test cross analysis is to clearly detect epistasis for the characters studied. It also supplies valid test for the occurrence of additive and dominance constituents of genetic variation that are evenly accurate in the absence of epistasis (Jinks & Perkins, 1970).The theory of TTC model are not demanding and the model does not depend on allelic frequency, gene correlation and mating system (Kearsey & Jinks 1968). The information obtained through present study would help in understanding the genetic basis of the traits studied and making breeding strategy for the development of high yielding cultivar (s) or valuable germplasm in Basmati rice.

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Materials and Methods

Triple test cross (TTC) experiment was done from May, 2003 to June, 2008 at the Nuclear institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan. Ten true breeding lines of Basmati rice viz., Basmati-370, DM-2, DM-107-4, DM-16-5-1, Kashmir Basmati, Basmati-Pak, Basmati 2000, Super Basmati, Shaheen Basmati and DM-25 were crossed as male genotypes to three testers viz., L_1 (Basmati-385), L_2 (EL-30-2-1) and L_3 (Basmati-385 x EL-30-2-1). Each male had three crosses and a total of 30 crosses (20 single and 10 three-way crosses) were produced. Nursery seedlings of 43 genotypes (30 crosses + 13 parents) were grown and then transplanted into the field following randomized complete block design with three replications. Standard cultural practices were followed to grow healthy crop. Ten random plants were selected from each genotype in each replication to record various traits. A few initial results have already been published somewhere else (Saleem *el al*., 2009). In this paper, TTC analysis for plant height (cm), tillers per plant, panicle length, primary branches per panicle, secondary branches per panicle, 1000-grain weight (g) and grain yield per plant (g) is reported. The variation of sums ($L_{1i} + L_{2i}$) and differences ($L_{1i} - L_{2i}$) were used to estimate additive (D) and dominance (H) components of variation, respectively. Epistasis was estimated through variance comparison ($L_{1i} + L_{2i} – 2L_{3i}$) where L_{1i}, L2i and $2L_{3i}$ mean of traits of the i^{th} progeny in respect of their concerned testers. All TTC analysis was done following modified method (Ketata *et al*., 1976) as illustrated by Singh & Chaudhary (1985) and Khattak *et al*., (2002).

Results and Discussion

In all of the traits studied, the mean squares form the variance analysis (Table 1) showed large variation among genotypes, hybrids, parents, lines and testers. It was realized that testers L_1 and L_2 were extremely high vs low selections from the population used in current study because of the significant mean squares of L_1 vs. L_2 and $L_1 + L_2$ vs F_1 for all the characters. Therefore, the inadmissibility of testers (L_1 and L_2) to detect additive and dominance components of variation with equal precision could not be ruled out. Similar views were expressed by Kearsey & Jinks (1968). Lines vs testers and hybrids vs parents were significant for all characters except primary branches per panicle.

Analysis of variance to identify epistasis has been shown in Table 2. Except primary branches per panicle and panicle length other six parameters viz., plant height, number of tillers per plant, secondary branches per panicle, number of grains per panicle, 1000-grian weight and yield per plant were significantly controlled by non-allelic interaction. Current results were in conformity to findings of many researchers. Saleem *et al*., (2005a) reported absence of epistasis for number of primary branches per panicle and panicle length in rice. Non-allelic interactions were also documented for plant height (Vijayakumar *et al*.,1996; Saleem *et al*., 2005b); number of tillers per plant (Vijayakumar *et al*., 1996; Subbaraman & Rangaswamy, 1989; Saleem *et al*., 2005a); number of grains per spike (Gurdev & Singh, 1989) in wheat; yield per plant (Verma *et al*., 1994; Saleem *et al*., 2005a) in rice. Existence of non-allelic interactions for plant height, number of tillers per plant, 1000-grain weight and grain yield per plant were inconsistent with Ahmed *et al*., (1985) who recorded key role of additive gene action using TTC analysis and Saleem *et al*., (2010) who reported major control of dominance gene action for such traits using line x tester analysis in rice. Partition of total epistasis into i and j + l type of

epistasis indicated significant involvement of i type and j + l types of epistasis over the inheritance of plant height, number of tillers per plant, secondary branches per panicle, number of grains per panicle, 1000-grian weight and yield per plant. These results were in line with those of Saleem *et al.*, (2005b) for plant height and with Subbaraman & Rangaswamy (1989) for number of tillers per plant, number of grains per panicle and yield per plant. However, present results for plant height and number of grins per panicle were in partial agreement with Ram *et al.*, (2007) who reported presence of i type epistasis for these characters. Saleem *et al.*, (2005a) recorded j and l type epistasis for number of tillers and yield per plant.

The i type epistasis can be fixed in early generations due to its linear directional nature. Therefore, pure lines or cultivars can be developed through simple selection procedures through i type epistasis. In contrast to i type epistasis, J + l types of epistasis are considered non-directional and are unfixable under self fertilization therefore they are undesirable for the development of pure lines or cultivars (Khattak *et al.*, 2001). The j + l type epistasis have been reported to be less significant than i type epistasis in rice (Subbaraman & Rangaswamy, 1989) and in wheat (Dhiman *et al.*, 1999). The results have indicated presence of i and j + l types of epistasis for six characters including grain yield. In this situation, recurrent selection is suggested in F_2 and next generations. However, selection of desired plants must be delayed till F_6 or F_8 generations to let obsession of epistasis effects i.e., fixation of homozygosity for the most of the loci, as suggested by Subbaraman & Rangaswamy (1989) in rice and Pandey & Singh (2003) in wheat.

The epistatic deviations of individual lines have been shown in Table 3 to point out the direction, comparative magnitude and to show the lines which interacted with testers L_1 and L_2 to produce significant epistatic deviations. Lines viz., DM-2 for plant height; Basmati 2000 for number of tillers per plant; Super Basmati, Basmati 2000 and DM-16-5-1 for secondary branches per panicle; DM-107-4, Basmati-Pak, Shaheen Basmati and Super Basmati for grains per panicle; Super Basmati and Shaheen Basmati for 1000-grain weight and Basmati 2000 for yield per plant contributed significant positive role the total epistasis. The remaining lines were inert and did not played significant role to the total epistasis. The result is in partial agreement with those of Ketata *et al.*, (1976) and Khattak *et al.*, (2001) who reported various lines showing positive and negative contributions to the total epistasis. While epistasis is an integral part of genetic architecture of various characters yet it was detected for 6 characters out of 8 studied. Ketata *et al.*, (1976) stated that epistasis is determined by the nature of genotypes and to some degree by the number of lines used. Pooni *et al.*, (1980) reported that the best possible experimental size necessary to detect epistasis through TTC depends mostly on gene distribution in the tester parents. For this reason, several lines and diverse testers (L_1 and L_2) ought to be employed to detect epistasis.

The estimates of additive and dominance variance, degree of dominance and direction for those traits showing absence of epistasis has been presented in Table 4. Dominance gene effects were highly significant as compared to non-significant additive gene effects for primary branches per panicle and panicle length. Partial dominance with values of 0.68 and 0.86 was recorded for primary branches per panicle and panicle length respectively. Delayed selection of plants having more number of primary branches per panicle and panicle length would be effective. Corealtion (rs.d) between sums (L_{1i} + L_{2i}) and differences ((L_{1i} - L_{2i}) for primary branches per panicle and panicle length was non-significant showing dispersion of dominant alleles between testers; therefore no proof of directional dominance was supplied by these traits. Saleem *et al.*, (2005a) reported incomplete dominance and found no evidence of directional dominance for panicle length and number of primary branches per panicle in rice.

Table 4 Estimates of additive (D) and dominance (H) variance, degree of dominance $(H/D)^{1/2}$ and direction of dominance (rs.d) for various traits showing absence of epistasis in rice genotypes.

Traits	D	H	$(H/D)^{1/2}$	rs.d
Primary branches per panicle	2.84	1.33**	0.68	-0.81
Panicle length (cm)	21.42	16.01**	0.86	0.50

*, ** = Significant at 0.05 and 0.01 levels of probability, respectively

Conclusions

From the present study, epistasis was found as an integral part of genetic system controlling the genetic expression of 6 characters including grain yield in Basmati rice. Dominance gene effects were important for primary branches per panicle and panicle length. Recurrent selection or bi-parental mating is therefore recommended for cultivar development from present TTC population.

References

Ahmad, L., A.H. Zakri, B.S. Jalani and D.Omar. 1985. Detection of additive and dominance variation in rice. pp.555-564. *In*: *Rice Genetics-I*. *Proc*. *Int*. *Rice Genet. Symp*. IRRI, Manila, Philippines.

Dhiman, K.C., T. Dawa and T. Dawa. 1999. Genetic architecture of yield traits in bread wheat. *Crop Improv*., 26(2): 193-197.

Gurdev, S. and G.S. Singh. 1989. Estimates of gene action through triple test cross in bread wheat (*Triticum aestivum*). *Ind*. *J*. *Agric*. *Sci*., 59 (11): 700-702.

Jinks, J.L. and M.J. Perkins. 1970. A general method of detecting additive, dominance and epistatic variation for metrical traits. II. Application to inbred lines. *Heredity*, 25: 45-57.

Jinks, J.L., M.J. Perkins and E.L. Breeze. 1969. A general method of detecting additive, dominance and epistatic variation for metrical traits. II. Application to inbred lines. *Heredity*, 25: 45-57.

Kearsey, M.J. and J.L. Jinks. 1968. A general method of detecting additive, dominance and epistatic variation for biometrical traits. I. Theory. *Heredity*, 23: 403-409.

Ketata, H., E.L. Smith, L.K. Edwards and R.W. McNew. 1976. Detection of epistasis, additive and dominance variation in winter wheat. *Crop Sci*., 16: 1-4.

Khattak, G.S.S., M.A. Haq, M. Ashraf and T. McNeilly. 2001. Genetic basis of variation of yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek). *Hereditas*, 134: 211-217.

Khattak, G.S.S., M.A. Haq, M. Ashraf, A.J. Khan and R. Zamir. 2002. Genetic architecture of secondary yield components in mungbean (*Vigna radiata* (L.) Wilczek). *Breeding Sci*., 52: 235-241.

Pandey, D. P. and M. Singh. 2003. Triple test cross in bred wheat (*Triticum aestivum* L.). *Crop Res*., *Hisar*, 26(3): 473-476.

Pooni, H. S., J.L. Jinks and G.S. Pooni. 1980. A general method for the detection and estimation of additive, dominance and epistatic variation for metrical traits. IV. Triple test cross and analysis for normal families and their self. *Heredity*, 44: 177-192.

Ram, T., D. Ram, B. Mishra, G. Padmarati, A.S.R. Prasad and B.C. Viraktamath. 2007. Triple Test Cross analysis for yield and yield components in rice (*Oryza sativa*). *Ind*. *J*. *Agri*. *Sci*., 77(6): 393-395.

Saleem , M.Y., B.M. Atta, A.A. Cheema and M.A. Haq. 2005a. Genetics of panicle related traits of agronomic importance in rice through triple test cross analysis. *Spain. J. Agric. Res*., 3(4): 402-409.

Saleem , M.Y., B.M. Atta, A.A. Cheema, Z. Mukhtar and M.A. Haq. 2005b. Detection of epistasis and estimation of additive and dominance components of genetic varation using triple test cross analysis (*Oryza satva* L.). *Cademo de Pesquisa Ser Bio*., *Santa Cruz do Sul*., 17(1): 37-50.

Saleem, M.Y., J.I. Mirza and M.A. Haq. 2009. Triple test cross analysis of some physio-morphological traits in Basmati rice (*Oryza sativa* L.). *Pak. J. Bot*., 41(5): 2411-2418.

Saleem, M.Y., J.I. Mirza and M.A. Haq. 2010. Combining ability analysis of yield and yield related traits in Basmati rice (*Oryza sativa* L.). *Pak. J. Bot*., 42(1): 627-637.

Singh, R.K. and B.D. Chaudhary.1985. *Biometrical Methods in Quantitative Genetics and Analysis*. Kalyani Publ., New Delhi.

Subbaraman, N and S.S.R. Rangaswamy. 1989. Triple test cross analysis in rice. *Euphytica*, 42: 35-40.

Verma, P.K., P.C. Katoch and R.P. Kaushik. 1994. Detection of additive, dominance and epistatic variation using simplified modified triple test cross analysis in rice. *Crop Improv*., 21(1-2): 44-48.

Vijayakumar, S.B., R.S. Kulkarni and N. Murthy. 1996. Triple test cross analysis in rice. *Ind*. *J*. *Genet*., 56(2): 169-172.

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