# COMBINING ABILITY STUDIES FOR YIELD AND QUALITY PARAMETERS IN WHEAT (*Triticum Aestivum* L.)

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## ABSTRACT

Combining ability studies on yield components and quality parameters were carried out in *aestivum* wheat by using 12 lines and 4 testers, in a line x tester mating design. The study indicated that both GCA and SCA variances were important for most of the yield components and also for protein content and pelshenke value which can be improved by breeding methods that can exploit both additive and nonadditive gene systems like biparental mating. Nonadditive gence effects were of great importance in the genetic control of single plant yield and trytophan content. The line, p932 was proved to be the best general combiner among the lines with high gca effects for many yield components. For plant yield, Pusa5-3 and WLR154 showed high gca. p104, p608 and Pusa5-3 among lines and HD2329 and DL 153-2 among testers were found to be suitable for the improvement of gluten quality. The cross HD2329 x P1035 was found to be the best cross with desirable sca effects for many characters, viz. tiller number per plant. spikelets/ spike. spike length. grains/spike, 1000 grain weight, yield/plant and protein percentage.

KEY WORDS: Wheat, Combining ability, Yield, Quality, Gene effects.

The knowledge on combining ability is important to the breeder in the choice of parents in any breeding programme. This analysis has been extensively used to study the genetics of quantitative characters in wheat (Paroda and Joshi, 1970, Iqbal Singh and Paroda, 1987, Mann and Sharma, 1995 and Rasal *et al.*1991), but very few reports are available on the use of this technique for the understanding of genetic architecture of quality parameters. Therefore, the present investigation was undertaken to derive information on combining ability and inheritance of some quality attributes along with yield and its components.

## MATERIAL AND METHODS

The experimental material included four testers viz. HD2285, HD2329, HD2428 and DL153-2 and twelve strains were selected as lines on the basis of their high protein content from three different maturity groups. Of these, P38-15, P118-2, KLM26 and P104 belong to early maturity group, P608, P769, P925 and Pusa5-3 belong to medium maturity group and P768, P932, WLR154 and P1035 to late maturity group.

The crossing programme was taken up in a line x tester design and 49 cross combinations were obtained. These hybrids along with their parents were grown in a randomised block design with four replications at IARI, New Delhi during 1990-91. Five plants each cross and per replications were selected randomly to record data on various observations viz. days to 50% flowering, number of days to maturity, plant height, tiller number/ plant, spike length, spikelest/spike, grains/spike, grain weight per spike, 1000 grain weight and grain yield/plant. Quality analysis was carried out for protein content, pelshenke value. tryptophan content and Dye Binding Capacity (DBC) value. Protein content was determined by NIR analyser and for Pelshenke Value, the method modified by Austin and Ram(1971) was followed. The method of Spies and Chambers(1949) was used for the estimation of tryptophan and for DBC value, modified method by Kaul, Dhar and Raghavaiah(1970) was used. Combining ability analysis was done by the method developed by Kempthorne(1957).

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Table 1. Analysis of variance for combining ability from line x tester experiment

| S.No. | Characters | Mean Sum of Squares | | | |
|---|---|---|---|---|---|
| | Source of variation<br>Degree of freedom | Lines(L)<br>11 | Testers (T)<br>3 | L x T<br>33 | Error<br>141 |
| 1. | Plant height | 227.35** | 2138.07** | 36.62** | 4.61 |
| 2. | No. of tillers/plant | 19.32** | 87.23** | 46.82** | 4.94 |
| 3. | Days to flower | 18.19** | 34.64** | 3.94 | 3.01 |
| 4. | No. of days to maturity | 1.61 | 29.16** | 2.76 | 2.49 |
| 5. | No. of spikelets/spike | 14.91** | 3.66** | 5.79** | 0.49 |
| 6. | Lenth of the spike | 5.25** | 10.69** | 0.78** | 0.10 |
| 7. | No. of grains/spike | 222.34** | 20.19 | 79.77** | 22.71 |
| 8. | Weight of grains/spike | 0.31** | 1.42** | 0.21** | 0.086 |
| 9. | 1000-grains weight | 96.20** | 450.54** | 23.63** | 2.96 |
| 10. | Single plant yield | 42.61** | 37.61* | 97.45** | 11.05 |
| 11. | Protein percentage | 4.58** | 11.46** | 1.31** | 0.31 |
| 12. | Pelshenke value | 860.03** | 8231.04** | 446.34** | 66.07 |
| 13. | Tryptophan content | 0.00024** | 0.00023** | 0.00034** | 0.000028 |
| 14. | DBC value | 0.00057** | 0.0029** | 0.00066** | 0.000057 |

*, ** : Significant at 5% and 1% level respectively.

## RESULTS AND DISCUSSION

The analysis of variance for combining ability in respect of 14 characters (Table 1) revealed that estimates of treatment mean sum of squares were highly significant for all the characters except for number of days to maturity in lines, grain number/spike in testers and for days to flower and days to maturity in line x tester interaction. Thus, it is very clear from the results that a large amount of variability exists for almost all the characters among lines, testers and their hybrids. The total variance was partitioned into variance due to the GCA of the parents and variance due to SCA of the hybrids (Table 2). It is clear from the table that for days to flower and days to maturity only variance due to SCA was not significant indicating the importance of additive gene effects for these charactrs which can be exploited by simple selection procedures. Similar results were reported earlier for days to flowering (Raghavaiah and Joshi,1986 and Iqbal Singh and Paroda,1987) and days to maturity (Sharma, Singh and Sethe, 1986).

For plant height, spike length, 1000 grain weight and pelshenke value, eventhough both additive and nonadditive gene effects were involved in their expression, the additive gene actions were found to be more predominant as the GCA variaces were higher compared to SCA variances (Maloo,1992).

The SCA variance were of much higher order in comparison with GCA variances or the characters, tiller/plant (Mann and Sharma,1995), Spikelets/spike, number and weight of grains per spike and DBC value indicating the predominant role of nonadditives gene actions in their expression. GCA and SCA variances are equally important for protein content. For the improvement of these characters where both additive and nonadditive gene actions are important. breeding methods like biparental mating and selection of superior segregants in advanced generations are suggested to exploit both the gene effects.

For single plant yield and tryptophan content, only SCA variance was found to be important

Table 2: Estimates of variance components from line x tester experiment

| S.No. | Characters | Estimates of variance components | | | | |
|---|---|---|---|---|---|---|
| | | $6^2$ lines | $6^2$ testers | $6^2$ gca | $6^2$ sca | $6^2$ gca/$6^2$ sca |
| 1. | Plant height | 11.92** | 43.78** | 35.82** | 8.00** | 4.48 |
| 2. | No. of tillers/plant | - | 0.84** | 0.20** | 10.47** | 0.019 |
| 3. | Days to flower | 0.89** | 0.64** | 0.70** | 0.23 | 3.01 |
| 4. | No. of days to maturity | - | 0.55** | 0.39** | 0.07 | 5.78 |
| 5. | No. of spikelets/spike | 0.57** | - | o.11** | 1.33** | 0.083 |
| 6. | Length of spike | 0.28** | 0.21** | 0.22** | 0.17** | 1.29 |
| 7. | No. of grains/spike | 8.91** | - | 1.30** | 14.27** | 0.091 |
| 8. | Weight of grains/spike | 0.01** | 0.03** | 0.020** | 0.031** | 0.65 |
| 9. | 1000-grain weight | 4.54** | 8.89** | 7.80** | 5.17** | 1.51 |
| 10. | Single plant yield | - | - | - | 21.6** | |
| 11. | Protein percentage | 0.20** | 0.21** | 0.21** | 0.25** | 0.84 |
| 12. | Pelshenke value | 25.86** | 162.18** | 128.19** | 95.07** | 1.35 |
| 13. | Tryptophan content | - | - | - | $7.8 \times 10^{-6}$** | |
| 14. | DBC value | - | $4.7 \times 10^{-5}$** | $3.4 \times 10^{-6}$** | $1.5 \times 10^{-5}$** | 0.23 |

*, ** : Significant at 5% and 1% level respectively.

showing the nonadditive nature of gene action as was also reported by Iqbal Singh and Pzroda(1987) and Mann and Sharma(1995). Direct selection for these traits may not be effective, suggesting recurrent selection in these cases to exploit nonadditive gene action. P932 among lines was proved to be the best general combiner with high gca effects for six characters i.e. plant height, spikelets per spike, spike length, number and weight of grains per spike and protein percentage(Table3).

P118-2 appeared to be specially good combiner for dwarfness and earliness along with good combining ability for tiller number, spike length, 1000 grain weight and protein percentage. For plant yield. only two lines, Pusa5-3 and WLR154 showed high gca, while for pelshenke value, P104, P608 and Pusa5-3 exhibited good gca. The fact that some of the lines and testers have shown high gca effects for these componets indicated their usefulness in building up of yield components. High gca effects are related to additive gene effects and/or additive x additive interaction effects (Griffing,1956) which represented the fixable genetic component of variation. Hence, the parents

having high gca are highly useful in any breeding programme with much scope of selecting high yielding lines.

Taking all the characters together, the cross HD2329 x P1035 was found to have desirable sca effects for seven characters, viz. tiller number per plant, spikelets/spike, spike length, grains/spike, 1000 grain weight, yield/plant and protein percentage (Table4). The cross combinations with high sca effects for grain yield per plant were HD2285 with P38-15, KLM26 and WLR154. HD2428 with Pusa5-3, HD2329 with P1035 and P932 and DL153-2 with P608, P769 and P768. Incidentally. except for WLR154 and Pusa5-3, none of the parents involved in these crisses were good general combiners for yield. Nevertheless, it would be useful to takeup selective hybridisation among the segregating generations of these crosses so as to increase the gene frequency for yield by adopting recurrent selection procedures.

It was observed in many cases that only one of the parents is having good combining ability and not the other parent, viz. HD2428 x WLR154 for tiller number/plant, HD2329 x P118-2 for plant

Table 3. Estimates of general combining ability effects of lines and testers for different characters

| S.No. | Parents | Plant height (cm) (1) | No. of tillers/ plant (2) | Days to flower (3) | No. of days to maturity (4) | No. of spikelets/ spike (5) | Length of spike (6) | No. of grains/ spike (7) | Wt. of grains/ spike (8) | 1000- grain/ spike (9) | Single plant yield (10) | Protein percentage (11) | Pelshenka value (12) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | LINES | | | | | | |
| 1. | P38-15 | -1.27** | -0.51 | -0.06 | -1.23** | -0.48** | -0.16** | -1.18 | 0.15 | -1.44 | | | |
| 2. | P118-2 | -1.16** | 1.16* | -1.83** | 0.57 | -0.85** | 0.22** | -3.09** | -0.12* | 1.94** | -0.17 | 0.89** | -7.25** |
| 3. | KLM-26 | 3.92** | 0.91* | -0.83* | 0.01 | -1.40** | 0.52** | -4.64** | 0.06 | -4.67** | 0.90 | 0.59** | 1.31 |
| 4. | P104 | 0.50 | -0.35 | 0.73* | 0.07 | 0.49** | 0.52** | 3.40** | 0.03 | -2.15** | -2.15** | -0.47** | 7.06** |
| 5. | P608 | -2.14** | -1.63** | -0.14 | 0.01 | -0.26 | -0.71** | -0.67 | -0.15** | -1.27** | 0.91 | -0.59** | 3.94* |
| 6. | P769 | -2.89** | -1.04* | -1.02** | -0.15 | -0.39** | 0.02 | 0.02 | -1.40** | -2.22** | -0.29 | -11.21** | |
| 7. | P925 | -3.15** | -0.14 | 0.17 | -0.56 | 0.37** | -0.03** | -0.57 | -0.06 | -3.40** | -1.46** | -0.25* | 1.81 |
| 8. | Pusa5-3 | 3.83** | 2.35** | 0.61 | 0.32 | -0.83** | 0.09** | -4.27** | -0.12** | 1.01** | 2.84** | -0.28* | 16.25** |
| 9. | P768 | -6.23** | 0.36 | 0.61 | -0.43 | 0.75** | -1.13** | 2.04* | -0.08 | -2.25** | 1.30 | 0.42** | 2.00 |
| 10. | P1035 | 4.10** | -0.75 | 1.05** | -0.12 | 1.72** | 0.17** | 6.42** | 0.15** | -0.98** | -1.26 | -0.82** | -5.19** |
| 11. | P932 | -1.91** | -0.78 | 0.92* | -0.06 | 1.14** | 0.22** | -1.51** | 1.09 | 0.59*** | -0.50 | | |
| 12. | WLR 154 | 6.40** | 0.43 | 1.30** | 0.38 | 0.23 | 0.91** | 1.33 | 0.22** | 3.36** | 1.42** | 0.06 | -6.88** |
| | S.E.(gi) | 0.44 | 0.46 | 0.36 | 0.33 | 0.14 | 0.07 | 0.99 | 0.06 | 0.36 | 0.69 | 0.12 | 1.68 |
| | | | | | | | TESTERS | | | | | | |
| 1. | HD 2285 | 4.57** | -1.06** | -0.95** | -0.06 | 0.06 | 0.21** | 0.08 | 0.01 | 0.14 | 0.70 | -0.19** | -8.79** |
| 2. | HD 2428 | -9.39** | 1.37** | -0.16 | 0.28 | -0.17* | 0.56** | -0.32 | -0.09** | -2.13* | -1.28** | -0.58** | -13.60** |
| 3. | HD 2329 | -0.14 | 0.94** | 0.01 | -1.04** | 0.36** | -0.34** | 0.87 | -0.15** | -2.29* | 0.11 | 0.24** | 12.00** |
| 4. | DL 153-2 | 4.96** | -1.25** | 1.11** | 0.82** | -0.25** | -0.44** | -0.63 | 0.24** | 4.28* | 0.46 | 0.53** | 10.40** |
| | S.E.(gi) | 0.23 | 0.24 | 0.19 | 0.17 | 0.07 | 0.03 | 0.52 | 0.03 | 0.19 | 0.36 | 0.06 | 0.88 |

* : Significant at 5% level of significance
** : Significant at 1% level of significance

Table 4   Crosses showing desirable sca effects for different characters

| Plant height (1) | No. of tillers/plant (2) | Days to flower (3) | Days to maturity (4) | No. of spikelets/spike (5) | Spike length (6) | Grain number/spike (7) | Grain weight/spike (8) | 1000-grain weight (9) | Single plant yield (10) | Protein (%) (11) | Pelshenke value (12) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| $L_1 \times T_1^*$ | $L_1 \times T_1^{**}$ | $L_{12} \times T_3^{**}$ | $L_9 \times T_1^*$ | $L_1 \times T_1^{**}$ | $L_3 \times T_1^{**}$ | $L_1 \times T_1^{**}$ | $L_5 \times T_1^{**}$ | $L_9 \times T_1^*$ | $L_1 \times T_1^{**}$ | $L_3 \times T_1^{**}$ | $L_2 \times T_1^{**}$ |
| $L_2 \times T_1^{**}$ | $L_2 \times T_1^{**}$ | $L_1 \times T_4^*$ | | $L_3 \times T_1^{**}$ | $L_8 \times T_1^{**}$ | $L_2 \times T_2^*$ | $L_2 \times T_2^*$ | $L_{10} \times T_1^{**}$ | $L_3 \times T_1^{**}$ | $L_8 \times T_1^{**}$ | $L_6 \times T_1^{**}$ |
| $L_{10} \times T_1^{***}$ | $L_7 \times T_1^*$ | | | $L_3 \times T_1^{**}$ | $L_5 \times T_2^{**}$ | $L_3 \times T_2^{**}$ | $L_4 \times T_2^*$ | $L_4 \times T_2^{**}$ | $L_8 \times T_1^*$ | $L_1 \times T_2^{**}$ | $L_{10} \times T_1^{***}$ |
| $L_{12} \times T_1^{***}$ | $L_8 \times T_1^{**}$ | | | $L_3 \times T_2^{**}$ | $L_{11} \times T_2^{**}$ | $L_8 \times T_2^{**}$ | $L_8 \times T_2^{**}$ | $L_3 \times T_3^*$ | $L_{12} \times T_1^{**}$ | $L_4 \times T_2^*$ | $L_6 \times T_2^{**}$ |
| $L_5 \times T_2^{**}$ | $L_1 \times T_2^*$ | | | $L_4 \times T_2^{**}$ | $L_{12} \times T_2^{**}$ | $L_3 \times T_4^{**}$ | $L_{10} \times T_3^{**}$ | $L_{11} \times T_3^{**}$ | $L_8 \times T_2^*$ | $L_{11} \times T_2^*$ | $L_{10} \times T_2^{**}$ |
| $L_6 \times T_2^*$ | $L_{12} \times T_2^{**}$ | | | $L_4 \times T_2^{**}$ | $L_2 \times T_3^*$ | $L_7 \times T_4^*$ | $L_5 \times T_4^{**}$ | $L_1 \times T_3^{**}$ | $L_7 \times T_3^*$ | $L_4 \times T_2^{**}$ | $L_5 \times T_3^*$ |
| $L_8 \times T_2^{**}$ | $L_{12} \times T_2^*$ | | | $L_8 \times T_2^{**}$ | $L_2 \times T_3^*$ | $L_2 \times T_4^*$ | $L_5 \times T_4^{**}$ | $L_1 \times T_3^{**}$ | $L_7 \times T_3^*$ | $L_9 \times T_3^{**}$ | $L_3 \times T_3^{**}$ |
| $L_6 \times T_2^*$ | $L_{12} \times T_3^{**}$ | | | $L_8 \times T_2^{**}$ | $L_2 \times T_3^*$ | $L_7 \times T_4^*$ | $L_5 \times T_4^{**}$ | $L_1 \times T_3^{**}$ | $L_7 \times T_3^*$ | $L_9 \times T_3^{**}$ | $L_2 \times T_3^{**}$ |
| $L_8 \times T_2^{**}$ | $L_5 \times T_3^*$ | | | $L_{12} \times T_2^{**}$ | $L_5 \times T_3^*$ | $L_9 \times T_4^{**}$ | $L_7 \times T_4^*$ | $L_5 \times T_3^{**}$ | $L_{10} \times T_3^*$ | $L_{10} \times T_3^{**}$ | $L_2 \times T_3^{**}$ |
| $L_7 \times T_3^{**}$ | $L_{10} \times T_3^{**}$ | | | $L_5 \times T_3^{**}$ | $L_{10} \times T_3^{**}$ | $L_{10} \times T_4^*$ | $L_8 \times T_3^*$ | $L_{11} \times T_3^{**}$ | $L_{12} \times T_3^*$ | $L_7 \times T_4^*$ | |
| $L_{11} \times T_2^{**}$ | $L_3 \times T_4^*$ | | | $L_{10} \times T_3^{**}$ | $L_7 \times T_4^{**}$ | $L_{10} \times T_3^{**}$ | $L_5 \times T_4^{**}$ | $L_3 \times T_4^{**}$ | $L_2 \times T_4^{**}$ | $L_3 \times T_4^{**}$ | |
| $L_1 \times T_4^{**}$ | | | | $L_9 \times T_4^{**}$ | $L_{11} \times T_3^{**}$ | $L_9 \times T_4^{**}$ | | $L_2 \times T_4^{**}$ | $L_6 \times T_4^{**}$ | $L_2 \times T_4^{**}$ | |
| | | | | $L_7 \times T_4^{**}$ | $L_{11} \times T_4^{**}$ | | | $L_3 \times T_4^{**}$ | $L_9 \times T_4^{**}$ | | |
| | | | | $L_{10} \times T_4^*$ | $L_6 \times T_4^*$ | | | $L_6 \times T_4^*$ | | | |
| | | | | $L_9 \times T_4^*$ | | | | | | | |
| | | | | $L_{10} \times T_4^{**}$ | | | | | | | |
| | | | | $L_{11} \times T_4^*$ | | | | | | | |

*, ** : Significance at 5% and 1% levels respectively. $L_1$ : P38-15 ; $L_2$ : P118-2 ; $L_3$ : KLM-26 ; $L_4$ : P-104 ; $L_5$ : P-608 $L_6$ : P-769 ; $L_7$ : P-925 ; $L_8$ : Pusa 5-3 ; $L_9$ : P-932 ; $L_{12}$ : WLR-154 ; $T_1$ : HD-2285 ; $T_2$ : HD-2428 ; $T_3$ : HD-2329 ; $T_4$ : DL153-2 ; $L_{10}$ : P-1035 ; $L_{11}$ : P-768.

height, HD2329 x P1035 for spike length, DL153-2 x P768 for grains/spike, HD2329 x P1035 for grain weight/spike, HD2329 x P38-15 for 1000 grain weight, DL153-2 x P104 for protein and DL153-2 x P925 for pelshenke value. These may throw up desirable transgressive segregants in the following generations if the additive genetic system present in the good combiner and complementary epistatic effects, if present in the cross, act in the same direction so as to maximise the desirable plant attribute.

Most interesting hybrids will be those which involve both the parents with high gca and possess high specific combining ability. The major part of such variance would be fixable in later generations. Such crosses are HD2428 x WLR154 for spike length, DL153-2 x P118-2 for 1000 grain weight, HD2329 x P768 for protein and HD2329 x P608 for pelshenke value. Recombinant breeding through multiple crosses involving these hybrids would be desiable to breed geneotypes showing these characters.

If the objective of the breeding is to improve content of a cultivar, the high protein lines, P118-2, KLM26, P768 and P932 with high gca values for this trait were found to be highly useful. Likewise, P104,P608 and Pusa5-3 among lines and HD2329 and DL153-2 among testers with high pelshenke value were found to be suitable for improvement of gluten quality. For the improvement of both yield components and protein, it is suggested to use promising lines, KLM26, P118-2 and P932 and testers HD2329 and DL153-2. For inducing earliness, dawrfenss along with improvement in protein content, the line P118-2 was found to be the best strain. For the improvement of both yield and yield components Pusa5-3 and WLR154 were found to be most suitable.

The testers, HD2329 and DL153-2 with high gca for protein and pelshenke value can be efficiently utilised in combination with the above mentioned high protein lines in a breeding programme where the objective is to improve both yield and quality parameters, mainly for bread making purposes.

Among the lins, P38-15, P118-2, KLM26, Pusa 5-3, P932 and WLR154 with hard gluten quality (with high pelshenke value) along with high protein content will be suitable for bread making purpose. P608, P769, P925 among lines and HD2285 and HD2428 among testers possess medium gluten quality which are suitable for chapati making purposes. The strain P104 with very hard gluten can be used for blending purposes and also for the preparation of suji and macaroni.

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