Inheritance study of quantifiable characters in intraspecific hybrids of promising *Triticum aestivum* (bread wheat) lines under normal field conditions.

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Abstract: Regions of the world with temperate climate are more conducive to wheat production and play chief role in the agricultural planning of any wheat producing nations. Food supply is inadequate to meet the requirement of the expanding population of world. To encounter the demand of contemporary and forthcoming, there is need to develop value-added cultivar with broad genetic base and high yielding potential. Existence of genetic diversity is preconditioned to develop a promising variety with yield stability and disease resistance. The proposed research was conducted in the research area of Department of Plant Breeding and Genetics under normal field conditions on Triticum aestivum. Five wheat (Triticum aestivum L.) genotypes: i.e. 9459-1, 9492, 9489, 9488 and Punjab-11 were crossed in all possible combinations by following the complete diallel scheme. Twenty five crosses and their parents were sown under Randomized Complete Block Design with three replications. Data of morphological and physiological traits were recorded like: flag leaf area, plant height, spike length, spike density, number of grains/spike, grain weight/spike and 1000-grain weight. The recorded data were subjected to analysis of variance (ANOVA) and general and combining abilities were estimates to identify potential parents and crosses. The results withdrawn from the research experiment are dynamic for creation of promising genetic combinations and outperforming genotypes can be utilized for further evaluation or could be incorporated in breeding programs to development high yielding cultivars.

Index terms: Combining ability, Conventional breeding, Diallel, Genotypic, Intraspecific hybridization, Triticum aestivum, Normal conditions.

Introduction:

Bread wheat (Triticum aestivum L.) is the cultivated in temperate climates of world from ages, as it is the most imperative and strategic cereal crop, for the bulk of world's inhabitants. Wheat serves as main staple food of about two billion individuals worldwide, approximately 35 % of the world population (Debasis and Khurana, 2001), as edible grain. Overall, globally it delivers almost 55% of the carbohydrates and 20% of food calories (Breiman and Graur, 1995). It over dominates at other cereal grain crops (including rice, maize etc) in case of cultivated area and also its high production. Hence, it is the most valuable cereal crop worldwide and is cultivated over wide range of climates. It plays chief role in gathering nutritive essentials and is used for production of chapatti, leavened bread, cookies/biscuits, pastries, cakes and other important bakery products in Pakistan. The protein found in bread wheat (Triticum aestivum L.) has major proportion of gluten which renders it as a versatile crop and is considered as main protein cradle for natives' worldwide (Hogg et al., 2004). Area under its production increased from 24.30 M tonnes in 2012-13 to 25.28 M tonnes in 2013-14, showing a rise of 4.4 percent (Pakistan Economic survey, 2012-13/2013-14). The foremost objective of breeders is to develop wheat cultivars/varieties with disease resistance and superior yielding ability (Ehdaie and Waines, 1989).

It is required to have correct information about genetic architecture of yield related attributes and kind of gene action to run a fruitful breeding program. That is why; understanding of its genetic makeup and genome wise organization via advance breeding strategies is gaining importance in plant breeding programs. Exploration of gene pool to find out the variability and its genetic foundation, combining ability analysis (GCA, SCA effects) provides valuable information. Thence, foremost step in any breeding program is to identify the good general combiners to develop the high yielding cultivars. Potential parents are selected on the basis of general combining ability and good cross combinations on the basis of their specific combining ability and heterosis. Then cross these good general combiners to select transgressive segregants from subsequent hybrids genotypes. Selection of genotypes based upon these assessments aids to improve multifaceted characters, associated to yield genetically (Sokoto et al., 2012; Mohammadi et al., 2012; Anwar et al. 2014; Ali et al. 2013; Khan et al. 2014; Tariq et al. 2014; Muhammad et al. 2013). It is thence, recommended as an important means in selecting parental genotypes to develop high yielding hybrids.

Increased population has exerted pressure upon wheat consumption thence to fulfill requirements of ever increasing population we usually import wheat from neighboring countries, to meet our domestic demand of wheat (*Triticum aestivum* L.). Because yield is a polygenic trait and is significantly influenced by the variable environment, the objective of the this proposed study was to create variability, uncover good general combiners and highlight crosses having better specific combining ability (SCA) for yield related characters by employing diallel crossing system. The information gained from present study would be exploited in wheat breeding programs for the evolution of new cultivars with wider malleability and higher yield potential.

Materials & methods:

The present study was conducted in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad by using the diverse genotypes of Triticum aestivum for yield and its related traits. Genotypes were sown in randomized complete block deesign with three replications per genotype under normal field conditions. Five genotypes of bread wheat (Triticum aestivum L.) viz., Punjab-2011, 9489, 9488, 9459-1 and 9492, were utilized in this experiment. These were maintained by the Wheat research group of the Department of Plant Breeding and Genetics. The genotypes were grown during first year (2012) and were crossed in diallel fashion. Twenty five crosses and their parents were grown during (2013). Each replication comprised of five lines (Parents) and 25 F1 hybrid genotypes (5×5 diallel) with 3m stretched single row for treatment. Plant to plant and row to row distance were maintained 15 and 30 cm, respectively. Two to three seeds per hole were planted using dibbler and thinned to one seedling per hole after the germination of seeds. The experimental populations were kept under normal condition from sowing to maturity. Appropriate production technology was implemented throughout the experimental evaluation.

Data of ten randomly selected lines were recorded from each line per replication on the following parameters viz., Plant height, flag leaf area, spike length, spike density, 1000-grain weight, grain yield/spike and grain weight/plant.

Statistical analysis

Recorded data were subjected to analysis of variance (ANOVA) to determine level of significant differences among parental genotypes and F₁ hybrid crosses defined by Steel *et al.* (1997). Genotypes exhibited significant difference based upon their characters were then subjected to Griffing's (1956) combining ability analysis to find out general and specific combining ability effects as follow:

Performance of a genotype in a single cross can be determined by:

 $Sij = \frac{1}{2} (Xij + Xji) - \frac{1}{2}p (Xi + X.i + X.j + Xj.) + \frac{1}{2}X.$

Here,

 S_{ij} = Specific combining ability effects of the cross between i_{th} and j_{th} parent.

 X_{ij} = Mean values of F_1 resulting from crossing the i_{th} and j_{th} parent.

 X_{ji} = Mean value of F_1 resulting from crossing j_{th} and i_{th} parent.

 $X_{i.} = Total \ of \ mean \ values \ of \ F_1's \ resulting \ from \ crossing \ j_{th} \ with \ i_{th} \ parent.$

 X_{ij} = Reciprocal values of X_{i} .

 $X_{j.}$ = Total mean values of F_1 resulting from crossing the i_{th} with j_{th} parent.

X_{.j} = Reciprocal values of X_j.

Performance of a genotype in series of crosses can be determined by:

$$gi = 1/2p (Xi + X.i) - 1/p2X..$$

Here,

gi = General combining ability of Ith Parents.

P = Number of parental genotypes

 $X_{i.}$ = Total of mean values of F1 hybrids resulting from crossing jth parent with ith parent

 X_j = total of mean values of F1 hybrids resulting from crossing ith parent with jth parent

X.. = Grand total of all the mean values in diallel table **Reciprocal effects**

Reciprocal effects were estimated using following expression:

Here,

re = Reciprocal effects of cross between ith and jth parents.

 X_i = Mean values of F_1 resulting from crossing i_{th} and j_{th} parents.

Xr = Reciprocal values of F1 resulting from Xi

Results and discussion

In order to start an efficacious breeding program to achieve desired objective, the selection of appropriate parental genotypes is the most vivacious aspects. The information about the genetic control of yield and yield contributing attributes help plant breeders in the choice of the promising parents and determining the suitable breeding strategies in order to have far sited benefits. Therefore, an assortment of five wheat genotypes was evaluated by using the diallel analysis.

Analysis of variance revealed that mean square values were highly significant for flag leaf area (cm²), spike length (cm), number of grains/spike and were significant for plant height (cm), spike density, grain weight/spike (g), and 1000grain weight (g) given in table.

SOV	df	Plant	Flag leaf	Spike	Number of	Grain	1000-grain	Number of
		height	area	length	grains/spike	weight/spike	weight	grains/spike
Rep.	2	47.61	235.3	0.22	14.89	0.27	365.6	14.89
Genotype	24	25.46*	59.79**	1.62**	175.78**	0.55*	101.2**	175.78**
Error	48	14.47	29.35	0.13	133.49	0.33	39.17	133.49

Table 1- Analysis of variance for some polygenic traits of spring wheat in a 5 × 5 diallel cross

Table 2- Mean values for some polygenic traits of spring wheat in 5×5 diallel cross

Varieties	Plant height	Flag leaf	Spike	Spike density	Grain	1000-grain	Number of
		area	length		weight/spike	weight	grains/spike
9459-1	82.23	34.1	13.06	11.01	2.65	37.37	48.83
9492	87.57	36.13	13.14	11.02	2.49	41.43	50.33
9489	85.8	30.84	11.94	12.04	2.37	35.6	45
9488	87.63	41.58	12.75	12.14	2.95	40.93	53.25
Punjab-11	9.8	43.9	14.06	11.81	3.2	43.73	57.92

Table 3- Mean value for some polygenic traits of all possible direct and reciprocal crosses in 5 × 5 diallel.

Crosses	Plant	Flag	Spike length	Spike	Grain	1000-grain	Number of
	height	leaf		density	weight/spike	weight	grains/spike
		area					
9459 × 9492	91.66	36.88	13.36	10.61	2.85	46.8	54
9459-1 × 9489	86.3	36.06	13.95	11.67	2.75	48.4	49.98
9459-1 × 9488	87.47	37.93	13.37	11.72	2.55	39.93	43.83
9459-1 × Punjab-11	89.73	39.93	14.19	11.72	2.38	44.26	47.07
9492 × 9459-1	90.16	35.43	13.56	11.1	2.33	40.14	42.83
9492 × 9489	89.76	36.67	13.3	11.72	3.28	47.73	58.91
9492 × 9488	92.6	39.89	12.95	12.27	3.03	45.5	56.75
9492 × Punjab-11	93.03	43.42	14.71	11.9	1.75	46	33.06
9489 × 9459-1	85.53	28.49	12.99	11.92	2.99	41.66	48.25
9489 × 9492	91.2	33.58	13.22	12.16	2.94	39.4	55
9489 × 9488	90.03	36.06	12.8	12.82	3.24	40.33	62.67
9489 × Punjab-11	86.03	29.11	13.68	11.75	2.9	42.4	54.16
9488 × 9459-1	90.13	41.49	13.53	11.81	2.81	48.6	50.91
9488 × 9492	91.06	44.83	14.39	12.72	2.94	39.86	54.08
9488 × 9489	90.53	36.46	13	12.39	3.27	42.06	59.18
9488 × Punjab-11	93.56	37.9	14.03	12.26	3.05	40.46	55.5
Punjab-11 × 9459-1	93.63	37.68	15.34	11.63	3.45	39.86	65.33
Punjab-11 × 9492	92.56	35.11	15.59	11.21	2.73	42.06	50.08
Punjab-11 × 9489	88	33.25	13.96	12.1	3.32	46.2	61.03
Punjab2011 × 9488	92.4	44.47	14.35	12.03	3.13	39.86	56.16

Combining ability studies

Success of hybridization of desirable genotype depends upon selection of suitable parental genotypes having potential to combine and produce anticipated genetic combination. Study of combining ability is extremely vital in determining the best donor parents for particular traits. The results of combining ability analysis are discussed as under. Total genetic variability for all characters can be divided into its components i.e. GCA, SCA and reciprocal effects. The GCA, SCA and reciprocal effects for studied character are presented in respective tables. These estimates are computed in numerical terms for parents, direct and their reciprocal crosses conferring to their field performance.

Plant Height

Splitting of variance for plant height signified that genotypic difference was prominent. Mean squares for plant height range from 82.23 to 93.63 cm. combining ability mean square indicated that GCA and SCA effects were prominent. While, reciprocal effects were non-significant in this case. GCA variance was more than SCA variance and calculation of variance components disclosed that SCA effects were larger than GCA effect which showed the predominance of non-additive type of gene action for the plant height. Expression of this character was governed additively and non-additive. Short statured plants are preferred because they do not lodge and more responsive to fertilizers, therefore, negative combining ability effects are preferred for plant height in wheat. Undesirable high positive GCA effects were recorded for the parents Punjab-2011 followed by genotype 9492. Two parents viz., 9459-1 and 9489 exhibited desirable negative GCA effects of -1.679 and -1.663 respectively. The highest positive SCA was obtained in the cross combination of 9459-1 × Punjab-2011, 9459-1 × 9492, 9492 × 9488, 9488 × Punjab-2011, 9492-1 × 9488 and 9459-1 × 9488 with values 2.279, 1.876, 1.426, 1.639, 1.183, 0.586, 0.396 and 0.173, resp.. While the desirable negative SCA effects were revealed by combination of 9489 × punjab-11 (-2.271) and 9459-1 × 9489 (-0.331) in present study. The highest positive reciprocal effects were exhibited by hybrid Punjab × 9459-1 (1.950), 9488 × 9489, 9489 × 9492 and Punjab-11 × 9489 with values 1.333, 0.250, 0.717 and 0.850 respectively. Whereas, the hybrid 9492 × 9459-1 (-0.750), 9489 × 9458-1 (-0.383), 9488 × 9492 (-0.767). Punjab-11 × 9459-1 (-0.233) and Punjab-11 × 9488 (-0.583) showed negative reciprocal effects.

Flag leaf area

Observed range of flag leaf area for parents was 30.84 to 43.90cm². Flag leaf area play significant role in filling and development of grain. 9488 was showing the max. Positive GCA effects (2.979), followed by Punjab-11 and 9492 which were 1.597 and 0.567 respectively. While genotype 9459-1(-1.041) and 9489 (-4.104) demonstrated negative GCA

effects. Maximum positive SCA effects were illustrated for cross 9492 × 9489 (1.418), 9459-1 × 9488 (0.533), 9459-1 × 9489 (0.183), 9459-1 × Punjab-11 (0.860) and 9489 × 9488(0.146). Whereas, negative SCA effects were shown by crosses 9492 × Punjab-11, 9459-1 × 9492, 9488 × Punjab-11 and 9489 × Punjab-11 with values -0.139, -0.611, -0.635 and -3.552 resp.. Five reciprocal crosses have exhibited positive effects 9488 × 9459-1 (1.702), Punjab-11 × 9489 (2.072) 9488 × 9492 (2.470) and Punjab × 9488 (3.882). Whereas, negative reciprocal effects, for flag leaf area ranged from -4.158 to -0.722.

Spike length

The observed mean square for this trait for parents ranged from 11.94 to 14.06cm. Combining ability analysis has showed that effects of SCA and reciprocal were highly significant compared to GCA effects. The high SCA effects for the spike length showed that non-additive type of gene action contribution towards the genetic variability. Best general combiner for spike length were Punjab (0.666) followed by 9492 (0,053) and 9459-1 (0.027) whereas, 9489(0.542) was poorest general combiner. The hybrid 9459-1 (0.428) showed the highest positive SCA effects. The crosses 9489 × Punjab-11 and 9459-1 × 9492 displayed the negative effects i.e. -0.030 and -0.213, respectively. The maximum reciprocal effects were demonstrated by cross combinations 9488 × 9492 (0.720). While, negative reciprocal effects were exhibited by cross combinations Punjab-11 × 9492, 9489 × 9459-1, with values -0.062 and -0.427, respectively.

Number of grains per spike

This is one of the prominent yield attributing traits in wheat. It was obvious from the analysis of variance for this trait showed that highly significant differences exist among genotypes. It was cleared that GCA effects were highly prominent. General combiner was 9488, followed by 9489 and Punjab-11 with values 0.672, 0.345 and 0.025 res.. Whereas, 9459-1 has shown the negative GCA effects. The cross combination 9492 × 9488 seems to be the best specific combiner with values 0.435. Four hybrids showed negative SCA effects i.e. 9459-1 × 9492, 9459-1 × 9488, 9489 × Punjab-11 and 9492 × Punjab. Punjab-11 × 9489 has showed the highest positive reciprocal effects. The negative reciprocal effects ranged -0.533 to -0.067, exhibited by four hybrids Punjab × 9492, 9488 × 9489, Punjab-11 × 9488 and 9488 × 9459-1.

Spike density

After portioning of variance, it is revealed that genotypic differences were significant (Table 1). The analysis of

combining ability elucidated that general combining ability mean squares were highly significant, the SCA and reciprocal mean square were significant (Table 4). The presence of additive genetic effects from table 10, that line 9489 (0.086) proved to be good general combiner, followed by 9488 (0.0710). While, the genotypes 9459-1, 9492 and Punjab-2011 indicated the negative general combining ability effects. The positive specific performance (Table 10) were shown by the cross combinations between 9489 × 9488, 9492 × 9488 and 9459-1 × 9492 with effects 0.018, 0.010 and 0.005, respectively

The highest positive reciprocal effects (Table10) were demonstrated by the hybrid 9489×9459 -1 with value 0.058, followed by Punjab-11 × 9489 (0.045), 9489 × 9492 (0.027) and 9492 × 9459-1 (0.010), while all other showed negative effects.

Grain weight per spike

The GCA, SCA and reciprocal estimates for seed weight/spike were -0.003, -0.159 and -0.094. Out of five parents the best general combiner was 9489 with value 0.129 followed by Punjab-11 (0.097) and 9488 (0.063) while 9459-1 and 9492 were poor general combiner having negative effects. The best specific combiner was suggested by the hybrid 9492 × 9489 (0.339) followed by hybrid 9492 × 9488, 9489 × 9488, 9459-1 × Punjab-11 and 9459-1 × 9489, with effects 0.2478, 0.249, 0.119, 0.114, 0.044. Whereas hybrid 9459-1 × 9488, 9459-1 × 9492 and 9492 × Punjab-11 have negative SCA effects. Hybrid Punjab 2011 × 9459-1 had highest reciprocal effects ranged 0.013 to 0.537, while negative reciprocal effects ranged from -0.463 to -0.047.

The expression of trait ranged from 42.07 to 61.28 g. 9488 had highest combining ability followed by 9459-1 with value 1.458 and 0.126 respectively. The rest of the three genotypes were poor combiner. The hybrid 9492 × 9489 had the highest SCA effects (6.599). The cross combination 9459-1 × 9488, 9488 × Punjab-11 , 9459-1 × 9489, and 9489 × Punjab-11 also showed good specific combining ability. While the hybrid 9492 × Punjab-11 exhibited poor specific combining ability. It was evident that 75% of hybrids were presenting positive reciprocal effects but the cross combination between 9489 × 9459-1 manifested the highest positive reciprocal effects (5.603). Three crosses were showing negative effects i.e. 9488 × 9489 (-2.743), 9488 × 9459-1 (-1.123) and 9492 × 9459-1 (-0.292).

Conclusion

In Toto, it is suggested that promising parental genotypes would go under further evaluation to incorporate them into hybrid development programs. Whereas, best specific cross combinations will also to be evaluated to develop future breeding strategy, which will have higher chances of success as compared to other cross combinations.

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