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COMBINING ABILITY ANALYSIS IN WHEAT

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A 4 x 4 diallel cross of wheat were evaluated for combining ability at Wheat Research Institute, Faisalabad during 2004-05. Data were recorded from F_1 generation for plant height, number of tillers plant^{-1}, biomass plant^{-1}, 1000-grain weight, harvest index, number of grains spike^{-1} and grain yield plant^{-1}. The additive gene effects were operating in plant height, biomass plant^{-1}, number of grains spike^{-1} and grain yield plant^{-1} while number of tillers plant^{-1} and 1000-grain weight were controlled by non-additive gene effects. The genotypes of "Uqab 2000" proved to be good general combiner for grain yield, 1000-grain weight, biomass plant^{-1}, number of tillers plant^{-1} and plant height. While V-00055 was found good general combiner for grain yield, biomass plant^{-1}, plant height and number of grains spike^{-1}. The cross "SH-02 × Uqab 2000" and its reciprocal and "V-00125 × V-00055" were the best specific combiners for grain yield plant^{-1} and yield components.

Keywords: Full diallel crosses, combining ability analysis, additive gene action, wheat grain yield improvement.

INTRODUCTION

Pakistan is one of the wheat producing countries of the world. It produced 21612.3 thousand tones wheat on an area of 8358 thousand hectares (2586 kg/ha) (Agriculture Statistics of Pakistan, 2004-5) but geometrical increase in Pakistan population has been a challenge for agricultural scientists. To feed the ever-increasing population of Pakistan, there is a dire need of improving genotypes for better wheat yield potential per unit area basis. This could be achieved by exploring the maximum genetic potential from the available germplasm of wheat. Breeders should concentrate on development of productive wheat varieties by crossing good general combining lines for grain yield and selecting transgressive segregants from the resulting hybrids. Information regarding general and specific combining ability of wheat genotypes is a prerequisite to launch a successful wheat-breeding program. Diallel mating design has been extensively used to analyze the combining ability effects of wheat genotypes and also to provide information regarding genetic mechanisms controlling grain yield and other traits. Ahmadi *et al.* (2003) reported that general combining ability (GCA) and specific combining ability (SCA) effects were highly significant in wheat for all the traits except spike length. The mean squares of GCA and SCA were significant for all the traits studied. It was observed that majority of genetic variances of grain yield as well as yield components were under control of additive nature of genes. Similarly Akbar *et al.* (1997) concluded from his research findings that number of tillers plant^{-1} and spikelets plant^{-1} were controlled by additive type of gene action while; 1000-grain weight was controlled by non-additive type of gene action.

Joshi *et al.* (2003) indicated significant differences between the parents for general combining ability (GCA) and between the crosses for specific combining ability (SCA) for all the characters studied. The GCA to SCA variance ratio indicated the predominance of additive gene effects for the traits studied. In another study Masood and Kronstad (2000) depicted that both general combining ability (GCA) and specific combining ability (SCA) estimates were significant for most of the traits examined. The magnitude of SCA was lower than GCA but remained significant in all generations.

High GCA to SCA variance ratio indicated preponderance of additive gene action. The estimates of GCA effects were quite consistent for all the traits evaluated in the study. Mavi *et al.* (2003) observed that the variances due to general (GCA) and specific combining ability (SCA) and reciprocal effects were significant for all the characters except the reciprocal effects for 1000-grain weight.

Singh *et al.* (2000) evaluated combining ability for number of grains spike^{-1}, grain weight of five spikes, 100-grain weight and grain yield plant^{-1} in bread wheat. The magnitude of the additive genetic variance was higher than non-additive variance for all the characters studied while Singh *et al.* (2002) reported preponderance of non additive genetic variance for number of tillers plant^{-1}, plant height, number of grains spike^{-1}, 1000-grain weight and grain yield plant^{-1}.

The present study was designed to find out the good general combining genotypes for sound breeding program and to select high yielding combiners for the development of productive wheat varieties and good specific combiners for hybrid seed production in wheat.

MATERIALS AND METHODS

Four genotypes of wheat viz. SH-2002, V-00125, V-00055 and Uqab 2000 were crossed in complete diallel fashion during the year 2003-2004. F_0 seed of all the crosses including reciprocals and parents were planted in a triplicate randomized complete block design. A single row of 5 meter was taken as an experimental treatment. The seed were dibbled by keeping plant-to-plant and row-to-row distances of 15 cm and 30 cm respectively. Two seeds per hole were sown, later thinned to single seedling site^{-1}. Ten guarded plants from each row were selected at random. At physiological maturity data were recorded for plant height, number of tillers plant^{-1}, number of grains spike^{-1}, 1000-grain weight, biomass plant^{-1}, grain yield plant^{-1} and harvest index. The data for the characters studied were subjected to analysis of variance according to Steel and Torrie (1984). Traits showing genotypic differences subjected to further genetic analysis for GCA and SCA effects according to Griffing approach (1956) using method 1 model 1.

Table 1. Parentage and pedigree of parental genotypes used in the diallel crosses

Variety/line	Parentage	Pedigree
SH-2002	Inqlab-91/Fink's'	PB25553-1A-0A-0A-1A-0A
Uqab 2000	CROW'S'/NAC//BOW'S'	PB22138-3a-0a-0a-234a-0a
V-00055	PB-81//F3.71/TRM/3/BULBUL//F3.71/TRM	PB26720-9A-0A-0A-4A-0A
V-00125	BULBUL//F3.71/TRM/3/CROW'S'	PB26508-9A-0A-0A-1A-0A

RESULTS AND DICUSSION

Analysis of variance revealed presence of significant variability among all the genotypes studied for all the traits except harvest index. The genetic variation attributable to GCA, SCA and reciprocals were highly significant for all the traits studied except for the genetic variation attributable to GCA for 1000-grain weight which was non significant. The GCA to SCA ratio exhibited that plant height, biomass plant^{-1}, number of grains spike^{-1} (Hasnain *et al.* 2006) and grain yield plant^{-1} were predominantly controlled by Additive type of gene action as earlier findings of Ahmadi *et al.* (2003), Joshi *et al.* (2003) and Masood and Kronstad (2000) while tillers plant^{-1} was pre-dominantly controlled by non additive type of gene action and 1000-grain weight purely controlled by dominant genes (Khaliq *et al.* 2006) Therefore, mass selection or pedigree selection might be fruitful in early segregating generations for the improvement of the traits controlled by additive type of genes.

Selection for harvest index would not bring about significant improvement because non-significant difference existed in genotypic mean square for this trait. Significant difference was found for 1000-grain weight. The GCA/SCA variance ratio for 1000-grain weight depicted that it was controlled by non-additive type of gene action as studied Singh *et al.* (2002) Therefore, selection must be delayed to late segregating generations (F_6) as in bulk method for this trait if necessary as discussed by Ahmadi *et al.* (2003) and Khaliq *et al.* (2006). The genotype "V-00055" could

Table 2. Mean squares due to genotypes, GCA, SCA and reciprocals for grain yield and its components in wheat.

SOV	DF	Mean squares						
		Plant Height	Tillers plant^{-1}	Biomass plant^{-1}	1000-grain weight	Harvest index	Grains Spike^{-1}	Grain yield plant^{-1}
Genotypes	2	25.95**	3.83**	554.32**	8.76*	234.77 $^{N.S}$	1.62**	22.50**
GCA	3	28.03**	2.27**	276.21**	2.96^{NS}	81.20**	1.62**	14.20**
SCA	6	6.12**	0.59**	27.81**	3.37**	17.49**	0.24*	2.41**
Reciprocal effects	6	1.47**	0.80**	287.00**	2.43**	137.55**	0.28**	9.22**
Error	30	2.76	0.18	0.92	1.43	2.65	0.12	0.55
GCA Variance	3	2.77	0.22	31.31	0.033	8.11	0.17	1.49
SCA Variance	6	2.07	0.25	16.55	1.195	9.13	0.08	1.15
Ratio of GCA/SCA variance	-	1.34	0.86	1.89	0.03	0.89	2.33	1.30

**=P<0.01, *= P<0.05 and N.S=Non significant

Table 3. Estimates of general combining ability (GCA) effects and mean values of the parents (in parenthesis) for grain yield and yield components involved in 4 x 4 diallel cross of wheat, 2004-05.

Parents	Plant Height (cm)	Tillers plant $^{-1}$	Biomass plant $^{-1}$ (g)	1000- grain weight (g)	Grains Spike $^{-1}$	Grain yield plant $^{-1}$ (g)
SH-02	-1.219	-0.690	-3.325	-0.252	**0.327**	-0.392
	(99.500)	(8.300)	(39.00)	(37.933)	**(60.95)**	(19.067)
V-00125	-1.719	**0.573**	-6.425	-2.666	-0.604	-1.630
	(102.50)	**(11.600)**	(37.00)	(38.460)	(38.89)	(17.130)
V-00055	2.406	0.090	**6.238**	0.156	**0.364**	**1.496**
	(112.50)	(10.300)	**(58.50)**	(39.820)	**(57.43)**	**(23.550)**
Uqab 2000	0.531	0.206	**3.513**	**0.762**	-0.087	**0.526**
	(105.500)	(10.333)	**(60.50)**	**(42.400)**	(52.35)	**(22.900)**
S.E.(Gi)	0.509	0.131	0.295	0.367	0.107	0.227

be declared good general combiner for plant height, biomass plant^{-1}, number of grains spike^{-1} and grain yield plant^{-1} While Uqab 2000 for plant height, number of tillers plant^{-1}, biomass plant^{-1}, 1000-grain weight and grain yield plant^{-1} but negative combiner number of grains spike^{-1}. SH-02 proved good general combiner for number of grains spike^{-1} and negative general combiner for plant height; tillers plant^{-1}, biomass plant^{-1}, 1000-grain weight and grain yield plant^{-1}. Similarly the genotype "V-00125" was good general combiner for tillers plant^{-1} and negative general combiner for plant height, tillers plant^{-1}, biomass plant^{-1}, 1000 grain weight, number of grains spike^{-1} and grain yield plant^{-1}. Keeping in view overall performance of the genotypes, V-00055 and Uqab 2000 were declared best general combiners and recommended for utilization in breeding program.

Specific combining ability and their reciprocal effects are explained in table-4. The cross "SH-02 × Uqab 2000" gave positive SCA with higher mean values for all the traits studied. The reciprocal of the cross "SH-02 × Uqab 2000" also gave positive SCA and better mean values for biomass plant^{-1}, 1000-grain weight as discussed by Masood and Kronstad (2000), for number of tillers plant^{-1} and plant height because it involved at least one good general combining parent "Uqab 2000". But it had negative SCA effects on number of grains spike^{-1}. The cross "V-00125 × V-00055" showed better SCA effects with optimum mean values for grain yield, 1000-grain weight, number of grains plant^{-1} and negative SCA effects for plant height, tillers plant^{-1}. It involved one good general combining parent "V-00055" but its reciprocal effect was found negative except plant height. Its mean extra nuclear inheritance of V-00125 played vital role in SCA effects of the cross "V-00125 × V-00055". The crosses SH-02 x Uqab 2000, Uqab 2000 × SH-02 and V-00125 × V-00055 may give transgressive segregants in their progenies so, must be critically evaluated. However, cross of both good general combining parents V-00055 and Uqab 2000 was expected to exhibit best performance but perhaps due to inhibitory epistatic effects this cross and its reciprocal did not yield good cross combination. Other cross having one good combining parent was "SH-02 × V-00055" which gave better SCA and optimum mean values for biomass weight and 1000-grain weight.

The cross "Uqab 2000 × V-00125" gave highest mean value and reciprocal effect only for tillers plant^{-1}. Similarly "Uqab 2000 × V-00055" gave better reciprocal effect for grains per spike with better mean value for this trait. This cross also involved one good general combiner.

The cross "V-00125 × SH-02" gave higher reciprocal effect for tillers plant^{-1}, biomass plant^{-1} and 1000-grain weight and involved both poor parents and performed better due to recessive x recessive gene interaction. It would not yield transgressive segregants so it had no worth.

CONCLUSION

Uqab 2000 proved to be the good general combiner for grain yield, 1000-grain weight, biomass plant^{-1}, number of tillers plant^{-1} and plant height. Another genotype "V-00055" was found good general combiner for grain yield plant^{-1}, biomass plant^{-1}, plant height and number of grains spike^{-1}. The crosses involving genotypes of V-00055 and Uqab 2000 are recommended for utilization in breeding program. The cross "SH-02 × Uqab2000", its reciprocal and "V-00125 × V-00055" were found the best specific combiners for grain yield plant^{-1} and yield components and may be utilized in hybrid seed production.

Table 4. Estimates of specific combining ability (SCA), reciprocal effects and mean values (in parenthesis) of hybrids a 4 x 4 diallel cross of wheat 2004-05

Cross	Plant Height (cm)	Tillers plant $^{-1}$	Biomass plant^{-1} (g)	1000- grain weight (g)	Grains Spike^{-1}	Grain yield plant $^{-1}$ (g)
SH-02 × V-00125	0.656	-0.185	-1.550	**1.185**	-0.073	0.058
	(103.50)	(10.00)	(42.50)	**(43.10)**	(44.7)	(19.07)
SH-02 × V-00055	0.531	0.277	1.188	0.758	-0.236	-0.002
	(106.50)	(8.70)	(41.50)	(42.35)	(58.3)	(21.29)
SH-02 × Uqab 2000	**1.906**	-0.169	**2.512**	**0.832**	**0.268**	**1.196**
	(107.00)	(9.40)	**(53.50)**	**(43.03)**	**(58.4)**	**(23.56)**
V-00125 × SH-02	0.750	0.700	6.000	1.620	-0.586	-0.072
	(102.00)	(8.60)	(30.50)	(39.86)	(56.4)	(19.21)
V-00125 × V-00055	-1.719	-0.835	4.137	0.838	0.639	1.571
	(104.00)	(8.60)	(29.00)	(39.54)	(53.2)	(18.07)
V-00125 × Uqab 2000	0.156	**0.169**	-4.638	-0.602	-0.260	-0.918
	(102.50)	**(10.0)**	(28.00)	(41.17)	(41.3)	(16.86)
V-00055 × SH-02	-0.250	-0.400	-10.400	0.475	-0.024	-0.915
	(107.00)	(9.50)	(62.30)	(41.40)	(58.8)	(23.12)
V-00055 × V-00125	0.001	-0.650	-22.750	-2.000	-0.480	-4.470
	(104.00)	(9.90)	(74.50)	(43.54)	(62.8)	(27.01)
V-00055 × Uqab 2000	1.469	-0.319	-3.550	0.109	-0.016	-1.024
	(107.50)	(8.50)	(47.50)	(42.08)	(60.6)	(21.30)
Uqab2000 × SH-02	0.750	0.450	3.000	0.475	-0.074	**1.132**
	(105.50)	(8.50)	(47.50)	(42.08)	(59.8)	**(21.30)**
Uqab 2000 × V-00125	-1.500	**0.550**	-12.250	0.647	-0.326	-2.220
	(105.50)	**(11.10)**	(52.50)	(40.24)	(47.8)	(21.30)
Uqab 2000 × V-00055	-1.000	-0.900	-6.500	-0.160	0.398	-0.800
	(105.50)	(10.30)	(60.50)	(42.40)	(52.7)	(22.90)
SE Sij-Sik Sij-Skl Rij-rkl	1.430 1.176 1.633	0.371 0.303 0.428	0.833 0.680 0.962	1.037 0.846 1.197	0.303 0.247 0.349	0.641 0.524 0.740

Bold values showed the interest of the breeder.

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