

Original Research Article

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Combining Ability Analysis for Yield and Spot Blotch Disease Resistance in Tetraploid Wheat

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ABSTRACT

Keywords

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The combining ability for yield and spot blotch disease resistance was studied in 21 cross combinations generated by crossing the selected spot blotch resistant and susceptible parents in 7 x 7 half half diallel design. Analysis of variance for combining ability indicated that SCA variance was higher than GCA variance for all the traits under study. The GCA component was significant for all the traits studied except for the trait thousand grain weight. The SCA component was significant for all the traits except for number of productive tillers per plant and thousand grain weight. The magnitude of sca variance was greater than gca variance for all the traits. The magnitude and direction of gca effects indicated HI 8663 and UAS 428 as good general combiners for yield and disease resistance. The cross combinations UAS 428 x A-9-30-1 and HI 8663 x DDK 1001 were identified as superior specific combiners for yield while, UAS 428 x DDK 1001, UAS 428 x A-9-30-1 and HI 8663 x NP 200 were found to be superior for disease resistance.

Introduction

Wheat is a crop of paramount importance in the present agricultural scenario and being the staple diet for more than one third of the world population it is regarded as the 'King of Cereals'. The ultimate aim of any plant breeding program is to develop cultivars with high yielding potential and consistent performance over diverse environments but realizing higher yields under diseased conditions is the major challenge faced. The

fungal diseases have cosmic influence in reducing the productivity potential of otherwise high yielding wheat varieties. Spot blotch disease of wheat caused by *Bipolaris sorokiniana* (Sacc.) Shoemaker has become a major bottleneck in the wheat production affecting the potential major wheat growing areas. Resistance breeding is the most reliable and feasible approach for the management of this destructive disease. At present, spot blotch resistance potential in high yielding wheat varieties is poor and needs rigorous

investigation, especially for warmer humid regions of South Asia (Sharma *et al.*, 2004; Joshi *et al.*, 2007).

The success of any breeding programme relies on the choice of parents. The combining ability of the parents which are too involved in hybridization play a prime role in deciding the performance of the progenies. Combining ability analysis is a biometrical method which identifies the parental varieties possessing best combining ability and genetic effects involved in inheritance of various plant traits (Griffing, 1956). Diallel analysis presents a greater opportunity to assess the performance of parental lines in all possible cross combinations. The present study was an initiated to identify the superior combiners and cross combinations for yield and resistance to spot blotch.

Materials and Methods

Two spot blotch disease resistant parents viz., HI 8663 NIDW 295 and five susceptible parents viz., Bijaga Yellow, A-9-30-1, DDK1001, DDK1025 and NP200 were crossed to obtain single crosses (excluding reciprocals) during *kharif* 2014-2015 in 7x7 half diallel fashion and the resulting 21 hybrids (six durum based crosses, three dicoccum based crosses and 12 crosses involving both durum and dicoccum parents) along with parents and checks were evaluated in two replications in randomized block design under spot blotch epiphytotic condition at All India Coordinated Wheat Improvement Project, Main Agricultural Research Station (MARS), University of Agricultural Sciences, Dharwad during *rabi* 2015-16. The list of crosses and checks used in the experiment are furnished in Table 1. The observations such as days to 50 per cent flowering, days to maturity, plant height (cm), number of productive tillers per plant, Spike length (cm), number of spikelets per spike, number of

grains per spike, thousand grain weight (g), grain yield per plant (g) were recorded on five randomly selected competitive plants per replication per entry except days to 50 per cent flowering, maturity and grain yield. Disease severity of spot blotch was recorded at three stages from anthesis to soft dough stage by following the Saari and Prescott (1975) scale. The following format was used for scoring the severity.

The first digit (D_1) gives the relative height of the plant and the second digit (D_2) shows the disease severity as a percentage of leaf area affected. Percent disease severity was calculated using the following formula (Sharma and Duveiller, 2007).

$$\text{Percent disease severity} = (D_1/9) \times (D_2/9) \times 100$$

Using the percent disease severity values for different intervals, "Area Under Disease Progress Curve" (AUDPC) was calculated by using the formula suggested by Wilcoxson *et al.*, (1975).

$$\text{AUDPC value} = \sum_{i=1}^k \frac{1}{2} (S_i + S_{i-1}) \times d$$

Where,

S_i = Disease severity at the end of time I ,
 K = Number of evaluations of disease and,
 d = Interval between two evaluations.

Results and Discussion

The obtained data was analyzed for combining ability. ANOVA for combining ability of 7x7 half diallel for all the traits studied was computed and the results are presented in the Table 2. The analysis of variance revealed that significant differences existed among the treatments for all the ten traits under study. The mean sum of squares due to parents

versus crosses was highly significant for all traits with the exception of plant height, spike length, number of productive tillers per plant, number of spikelets per spike and thousand grain weight, revealing the presence of heterosis due to the significant difference in the mean performance of hybrids and parents. For the trait thousand grain weight, the resistant durum parent HI 8663 recorded significant positive gca effects whereas, the susceptible durum parent A-9-30-1 recorded significant negative gca effect (Table 4). The maximum gca effect was observed in the resistant durum parent UAS 428 (1.06) and the minimum gca effect was recorded by the susceptible dicoccum parent NP 200 (-0.24) for yield per plant. Among the susceptible durum parents, Bijaga Yellow and A-9-30-1 exhibited highly significant positive gca effects and among the susceptible dicoccum parents NP 200 recorded significant positive gca effect whereas, the resistant durum parents HI 8663 and UAS 428 manifested highly

significant negative gca effects for disease incidence in terms of AUDPC. The GCA component was significant for all the traits studied except for the trait thousand grain weight and the SCA component was significant for all the traits except for number of productive tillers per plant and thousand grain weight. The magnitude of sca variance was greater than gca variance for all the traits (Table 3). The obtained results are in accordance with the findings of Kashif and Khaliq (2003), Kamaluddin *et al.*, (2007) but are in contrary with the findings of Akram *et al.*, (2011) and Khan *et al.*, (2007) who have reported the predominance of gca variance for the trait yield per plant. Further, the ratio of GCA to SCA variance was less than unity which indicated the preponderance of non-additive gene action in controlling these traits. There was predominance of non-additive variance for all the traits studied suggesting that the superiority for these traits cannot be fixed by employing simple selection.

Table.1 List of cross combinations and the checks used for combining ability

Sl. No.	Hybrids	Sl. No.	Hybrids
1	Bijaga Yellow x A-9-30-1	12	A-9-30-1 x DDK 1025
2	Bijaga yellow x DDK 1025	13	A-9-30-1 x DDK 1001
3	Bijaga yellow x DDK 1001	14	A-9-30-1 x NP 200
4	Bijaga yellow x NP 200	15	A-9-30-1 x UAS 428
5	Bijaga Yellow x UAS 428	16	DDK 1025 x DDK 1001
6	HI 8663 x Bijaga Yellow	17	DDK 1025 x NP 200
7	HI 8663 x A-9-30-1	18	DDK 1025 x UAS 428
8	HI 8663 x DDK 1025	19	DDK 1001 x NP 200
9	HI 8663 x DDK 1001	20	DDK 1001 x UAS 428
10	HI 8663 x NP 20	21	NP 200 x UAS 428
11	HI 8663 x UAS 428		Checks
		1	UAS 448
		2	UAS 415

Table.2 Analysis of variance for combining ability for yield, yield attributes and Spot blotch resistance

Source of Variations	Df	DFP	DM	PH	SL	NPTPP	NSPS	NGPS	TGW	YPP	AUDPC
Replicates	1	7.88	2.57	17.84	0.01	0.80	8.65	3.83	1.76	0.47	9337.03
Treatments	27	45.79**	35.61**	109.22**	1.08**	2.95**	6.74	55.04**	71.38**	5.07**	86471.99**
Parents	6	84.81	50.95	163.86	0.66	2.03	13.27	91.40	109.48	4.11	148407.21
Hybrids	20	34.22	29.57	98.15	1.25	3.35	4.83	46.23	63.41	4.06	70211.21
Parent Vs.Hybrids	1	43.01**	64.38**	2.63	0.17	0.27	5.85	12.96*	2.21	31.02**	40076.07**
Error	27	0.76	0.87	30.63	0.37	1.08	4.03	2.43	40.53	1.20	2674.73
Total	55	23.00	17.95	68.98	0.71	1.99	5.45	28.28	54.97	3.09	43932.70

*Significance at 0.05 probability ** Significance at 0.01 probability
 PH-Plant height (cm) NPTPP- Number of productive tillers per plant NGPS-Number of grains per spike
 SL- Spike length (cm) NSPS- Number of spikelets per spike TGW- Thousand grain weight (g)
 YPP- Yield per plant (g) DFP- Days to 50 per cent flowering DM-Days to maturity
 AUDPC- Area under disease progress curve

Table.3 General and specific combining ability variances for different quantitative traits in single cross hybrids of tetraploid wheat

Source of Variations	Df	DFP	DM	PH	SL	NPTPP	NSPS	NGPS	TGW	YPP	AUDPC
GCA	6	37.96**	13.88**	130.45**	0.87**	2.98**	6.17**	27.27**	37.13	26.07**	41932.83**
SCA	21	18.59**	18.93**	32.94**	0.45**	1.04	2.57**	27.59**	35.28	5.22**	43608.33**
Error	27	0.38	0.43	15.31	0.18	0.54	2.02	1.21	20.27	11.04	1337.37
s ² g	6	4.18	1.49	12.79	0.08	0.27	0.46	2.89	1.87	1.67	4510.61
s ² s	21	18.21	18.49	17.63	0.26	0.51	0.55	26.38	15.02	5.81	42270.96
GCA/SCA Ratio	-	0.23	0.08	0.73	0.29	0.54	0.83	0.11	0.12	0.29	0.11

*Significance at 0.05 probability ** Significance at 0.01 probability
 PH-Plant height (cm) NPTPP- Number of productive tillers per plant NGPS-Number of grains per spike
 SL- Spike length (cm) NSPS- Number of spikelets per spike TGW- Thousand grain weight (g)
 YPP- Yield per plant (g) DFP- Days to 50 per cent flowering DM-Days to maturity
 AUDPC- Area under disease progress curve

Table.4 Estimation of general combining ability effects of different susceptible and resistant genotypes for spot blotch disease resistance, yield and yield attributing traits in tetraploid wheat

Characters	DFP	DM	PH	SL	NPTPP	NSPS	NGPS	TGW	YPP	AUDPC
Resistant durum parents										
HI 8663	0.79**	0.31	-3.93**	-0.59**	0.40	0.64	0.22	2.05**	0.52*	-49.90**
UAS 428	-1.21**	-1.14**	5.97**	0.28**	-0.63**	0.60	1.31**	-2.38	1.06**	-109.02**
Susceptible durum parents										
A-9-30-1	-0.38	-0.69**	-3.67**	-0.06	0.35	-0.66	-0.32	-2.87*	0.06	104.73**
Bijaga Yellow	-2.66**	-1.30**	-0.89	0.36*	0.71**	0.12	-0.43	2.12	0.31	32.11**
Susceptible dicoccum parents										
DDK 1001	0.12	0.25	1.74	-0.06	-0.43	1.08*	2.37**	0.34	0.09	20.35
NP 200	-0.60**	0.20	-2.63*	-0.07	-0.72**	-1.18*	-3.24**	1.32	-0.24**	23.28*
DDK 1025	3.95	2.37**	3.15**	0.14	0.32	-0.59	0.09	-0.58	0.32	25.01

*Significance at 0.05 probability ** Significance at 0.01 probability
 PH-Plant height (cm) NPTPP- Number of productive tillers per plant NGPS-Number of grains per spike
 SL- Spike length (cm) NSPS- Number of spikelets per spike TGW- Thousand grain weight (g)
 YPP- Yield per plant (g) DFP- Days to 50 per cent flowering DM-Days to maturity
 AUDPC- Area under disease progress curve

Experiment Details

Percent leaf area coverage	Scale	Percent leaf area coverage	Scale
0	0	50	5
10	1	60	6
20	2	70	7
30	3	80	8
40	4	90	9

It can be summarized from the findings of the experiment that the durum parent HI 8663 was found to be good general combiner for thousand grain weight, yield and disease resistance while, the durum parent UAS 428 was identified as superior general combiner for number of grains per spike, yield and disease resistance.

The superior specific combiners like UAS 428 x A-9-30-1, HI 8663 x DDK 1001 for high yield and superior cross combinations HI 8663 x NP 200, UAS 428 x DDK 1001, UAS 428 x A-9-30-1 for disease resistance can be tested further under epiphytotic conditions to confirm their resistance to spot blotch with better yield and could be utilized as resistant source to develop spot blotch resistant cultivars. The identified resistant parents can be employed in further hybridization involved in resistance breeding. Out of three identified superior cross combinations for disease resistance, two were durum x dicoccum based crosses.

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