



INHERITANCE STUDY OF YIELD TRAITS AND SPOT BLOTCH DISEASE RESISTANCE IN WHEAT UNDER EPIPHYTOTIC ENVIRONMENT

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Abstract

The resultant 24 crosses along with 10 parents were evaluated in artificial epiphytotic stress environment to study inheritance of characters governed by either additive or nonadditive gene action. The results revealed that magnitude of SCA variance was higher than GCA variance for majority of the traits showed that predominance of non-additive gene action in inheritance of these traits, which suggested that exploitation of these traits for improvement of yield through heterosis breeding. Area under disease progress curve (AUDPC) exhibited high GCA variance which is specified that additive gene actions is primarily responsible for inheritance of resistance to spot blotch. Among the parents 3 resistant testers *viz.*, Chiriy 3, Yangmai#6 and PBW 343 showed good GCA effect. 3 cross combinations *viz.*, (Sonalika × MONS, HUW 234 × NING 8201 and HD 2329 × Yangmai#6) were found good cross combiners for yield. The cross, HUW 234 × Chiriy 3 manifested good cross combiner for spot blotch disease resistance.

Key words: general combining ability (GCA), specific combining ability (SCA), area under disease progress curve (AUDPC).

Introduction

Wheat is an important staple food crops of the world, occupied 17% of crop acreage over worldwide, feeding about 40% of the world population and providing 20% of total food calories and protein in human nutrition (Gupta *et al.*, 2008). Due to drastic changes in climatic conditions such as biotic and abiotic stresses directly effect on yield. One of the major biotic stress that effect on wheat production is spot blotch disease caused by *Bipolaris sorokiniana* (Sacc.) Shoemaker. Particularly in the Eastern Gangetic Plains (EGP) of South Asia, which include India, Nepal and Bangladesh (Joshi *et al.*, 2007a). Manipulation of heterosis is an important strategy for increasing the yield potential of wheat (Rauf *et al.*, 2012). It is necessary to identify superior parents with disease tolerance in terms of reduced yield production. Combining ability analysis is a potent tool to identify the parents and sorting out promising crosses as per desired characters. It also elucidates the nature of gene action involved in the inheritance of the characters.

According to Jain and Sastry, (2012) heterosis and combining studies in wheat gives idea about different types of gene action which can be utilized further for improvement in production of Hybrid wheat is an alternative approach to increase the productivity and most important step in the hybrid breeding program is the detection of suitable parents with high general (GCA) and specific combining ability (SCA) for grain yield and then the exploitation of heterosis. Understanding the gene action of the spot blotch disease is of prime importance. Accordingly, a good knowledge of gene action involved in the inheritance of quantitative characters of economic importance is required in order to frame an efficient breeding plan leading to rapid improvement. Thus, the present study aims to assess the relative magnitude of GCA and SCA for the yield and yield contributing traits and disease resistance to select the best combiner for successful wheat hybridization.

Materials and Methods

The experiment material consist of 4 susceptible lines and 6 resistant testers were crossed in line tester mating

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Table 1: Analysis of variance for combining ability for different characters in wheat.

	DF	DF	DM	GFD	PH	TILL	PED	SL	AL	BYPP	SYPP	HI	1000 SW	AUDPC
Crosses	23	13.87**	14.62**	6.20**	52.98**	6.390**	8.71**	2.39**	1.10**	12.37**	6.97**	36.50**	19.82**	26131.64**
Line effect	3	13.47*	4.97	5.83	107.03**	3.560	17.44**	2.71	2.82**	7.76	4.10	29.88	13.09	81362.87**
Tester effect	5	45.73**	39.15**	7.93	113.70**	13.735*	20.92**	5.02	1.04**	40.10**	18.81**	52.06	46.59*	36877.91*
Line vs tester effect	15	3.32*	8.37**	5.70	21.93**	4.507**	2.90**	1.45	0.78**	4.05	3.60*	32.64*	12.24	11503.30**
error	47	1.52	0.89	1.94	4.83	0.81	0.67	0.54	0.27	2.70	1.37	13.93	6.30	3739.63
Total	67	7.78	7.60	4.33	29.28	3.52	4.60	1.44	0.67	7.69	4.09	25.06	15.53	14780.07
Components of Variance														
σ^2 Females		0.97	0.31	0.25	8.16	0.23	1.39	0.19	0.21	0.38	0.25	1.43	0.69	6445.22
σ^2 Males		5.49	4.74	0.63	13.07	1.62	2.52	0.57	0.10	4.61	2.22	4.92	5.22	4107.21
σ^2_{gca}		2.478	2.08	0.40	10.12	0.79	1.84	0.34	0.17	2.07	1.04	2.82	2.50	5510.02
σ^2_{sca}		0.76	3.56	1.41	6.39	1.86	10.6	0.51	0.26	0.40	1.26	9.95	3.71	3741.55
$\sigma^2_{gca} / \sigma^2_{sca}$		3.25	0.58	0.28	1.58	0.42	0.17	0.66	0.65	5.17	0.82	0.28	0.67	1.47

design to produce 24 F1 hybrid crosses during rabi 2018-2019. Artificial epiphytotic conditions were created to evaluate F1s along with their parents identify superior parents and heterotic F1s during rabi 2019-2020 at agricultural farm, Banaras Hindu University, Varanasi. All package of practices was followed and data was collected on yield and its associated traits and as well as disease scoring of spot blotch. The data was recorded on plot basis for days to 50% heading (DF) and days to maturity (DM) and Five randomly selected competitive plants for 11 traits grain filling duration (GFD), plant height (PH), number of tillers per plant (NTPP), peduncle length (PED L.), spike length (SP) awn length (AL), biological yield per plant (BYPP), seed yield per plant (SYPP), harvest index (HI), 1000 seed weight (1000 SW), area under disease progress curve (AUDPC). Collected data on above 13 traits was subjected to combining ability analysis using INDOSTAT version 9.2.

Creation of epiphytotic environment and disease assessment

The most aggressive isolate of *Bipolaris sorokiniana* (strain HD_3069) was multiplied on sorghum grains and spore suspension of 10^4 spores/ml of water was adjusted and sprayed on crop at different growth stages during evening hours and plot was irrigated immediately to provide humidity which is favorable environment for reckless sporulation. Disease scoring was recorded at three different growth stages viz., GS63 (beginning of anthesis to half completion), GS69 (anthesis complete) and GS77 (late milking) of Zadok's scale (Zadoks *et al.*, 1974) using double digit scoring method of Saari and Prescott, (1975). The area under disease progress curve (AUDPC), was calculated based on disease severity suggested by (Roelfs *et al.*, 1992). The formula for estimation of AUDPC was mentioned below:

$$AUDPC = \sum_{i=1}^n [(Y_i + Y_{(i+1)}) / 2] \times (t_{(i+1)} - t_i)$$

Where

Y_i = disease level at time t_i

$t_{(i+1)} - t_i$ = Time (days) between two disease scores

n = Number of dates on which spot blotch was recorded

Results and Discussion

The obtained 24 F1 crosses along with parents were evaluated under artificial epiphytotic environment and recorded data were subjected to line tester analysis can be used for identification of superior parents and cross combinations. The findings of ANOVA of combining ability and components of variance presented in (Table 1). Mean squares of line effect showed significant differences for days to 50% heading, plant height, peduncle length, awn length and AUDPC. Variation due to tester effect for majority of traits showed significant differences except for grain filling duration, spike length and harvest index. Line tester interaction effect revealed that significant differences were found for all the traits except grain filling duration, spike length, biological yield per plant and 1000 seed weight.

Sprague and Tatum, (1942) proposed the concept of general combining ability (GCA) and specific combining ability (SCA) to measure gene effects. The presence of non-additive genetic variance is the primary justification for initiating the hybrid-breeding programme Cockerham, (1961). Magnitude of components of variance showed that SCA variance for majority of the traits showed highly significant differences except for days to 50% flowering, plant height, biological yield per plant and area under disease progress curve. SCA variance was higher for

Table 2: Estimates of general combining ability (GCA) effects of the parents for various characters in Wheat.

Parents Lines	DF	DM	GFD	PH	TILL	PED	SL	AL	BYPP	SYPP	HI	1000SW	AUDPC
sonalika	1.21**	0.29	-0.92	0.59	0.75**	-1.18**	-0.11	-0.43**	-0.27	0.26	1.11	-0.52	833.72**
HUW 234	-1.38**	-0.88*	0.50	1.35	0.01	0.53*	-0.09	-0.37*	0.36	0.60	1.60	1.45*	-35.828
HD 2329	0.04	0.63	0.58	2.40*	-0.21	-0.78**	0.67**	0.23	0.89	-0.08	-1.41	-0.95	109.28**
HUW 510	0.13	-0.04	-0.17	-4.34**	-0.54*	1.44**	-0.46*	0.57**	-0.98	-0.77*	-1.30	0.02	10.26
Testers													
Chiriyā 3	-4.08**	-3.38**	0.71	-5.37**	-1.74**	1.01**	-0.57*	0.25	-0.25	-0.34	-0.78	-1.39	-26.65*
A. N.8226	0.17	1.00*	0.83	-2.22*	-1.32**	-2.56**	-0.66**	0.07	-3.59**	-2.79**	-4.33**	-3.68**	-10.442
Yangmai#6	-0.21	0.75	0.96	1.54	1.20**	2.08**	-0.73**	0.07	-1.38*	0.20	2.86*	-0.24	-88.22**
NING 8201	-0.46	-2.00**	-1.54*	5.09	0.60	0.10	1.18**	-0.51*	1.61*	1.58	-0.39	0.21	31.15
PBW343	1.54**	1.13**	-0.42	-1.60	-0.16	-1.01**	0.67**	-0.34	2.53**	1.76**	2.14	2.06*	-44.325**
MONS	3.04**	2.50**	-0.54	2.55*	1.42**	0.38	0.11	0.46*	1.58**	1.59	0.49	3.04**	-20.165
*, ** Significant at 5 percent and 1 per cent levels, respectively													

most of traits than *GCA* variance. These findings showed similarity with results of Kamaluddin *et al.*, 2007; Murugan and Kannan, 2017; Patel *et al.*, 2018. Therefore, this indicates importance of non-additive gene action in inheritance of these traits, which suggested that exploitation of these traits for improvement of yield through heterosis breeding. The ratio of $\sigma^2_{GCA} / \sigma^2_{sca}$ being less than unity was found for days to maturity, grain filling duration, number tillers per plant, peduncle length, spike length, awn length, seed yield per plant, harvest index, 1000 seed weight, suggested that all these traits are predominantly under dominance gene action and their superior performance cannot be fixed by using simple selection. These results were in similar manner for most of the traits governed by non-additive gene action were reported by Kumar *et al.*, 2011; Patel *et al.*, 2018. The ratio of more than unity were observed for days to 50% flowering. Plant height, biological yield per plant and area under disease progressive curve. The results were similar with findings of Patel *et al.*, 2018; Kumar, 2012, for days to 50% flowering. *GCA* variance is higher than *SCA* variance for AUDPC which indicated that the additive gene actions were primarily responsible for inheritance of resistance to spot blotch in these crosses. The results were similar to the findings of Sharma *et al.*, 2004; Khan *et al.*, 2010; Tembo *et al.*, 2017.

The estimates of general combining ability (*GCA*) effects of lines and testers and specific combining ability (*SCA*) effects of crosses for all the characters are presented in table 2 and 3. The *GCA* and *SCA* effect of the parents and hybrids in negative direction were considered desirable, as the earliness is preferred over the late varieties. Among the lines, HUW 234 (-1.38) and testers *i.e.*, Chiriyā 3(-4.08) and NING 8201 (-2) exhibited significant and negative *GCA* effect in desirable direction for days 50% flowering and as well as days to

maturity were considered to be good general combiners. For plant height, female parent such as, HUW 510 (-4.34) and testers were, Chiriyā 3(-4.08) and A.N. 8226 (-2.22) showed reduced height in significant and desirable direction. Good general combiner for number of tillers per plant among female lines, Sonalika (0.75) and of testers were, Yangmai#6 (1.20), MONS (1.42) exhibited significant and positive direction. *GCA* effects for peduncle length with positive and significant values among lines are, HUW 234 AND (0.53) HUW 510 (1.44) and testers of Chiriyā3 (1.01), Y#6 (2.08). For spike length, HD 2329 (0.67) female line and NING 8201 (1.18), PBW 343 (0.67) testers were showed *GCA* effects in significant and desirable direction. For biological yield for plant, seed yield per plant and for harvest index, none of the female lines showed significant results due epiphytotic stress condition of spot blotch disease.

Among testers, NING 8201 (1.61% 1.58), PBW 343 (2.53 & 1.76), MONS (1.58% 1.59) exhibited positive and significant results for biological yield per plant & seed yield per plant, respectively. For 1000 seed weight, HUW 234 female line (1.45) and testers, PBW 343 (2.06), MONS (3.04) were showed significant and positive *GCA* effect in desirable direction acts as good general combiners. The lines such as Sonalika and HD2329 were showed positive and significant *GCA* effect for AUDPC and among testers, Chiriyā 3 (-26.65), Yangmai#6 (-88.22) and PBW 343 (-44.35) exhibited negative and significant *GCA* effect in desirable direction.

None of the parents showed good *GCA* effect for all the traits in desirable direction. But among susceptible lines, HUW 234 manifested results of *GCA* effects in desirable direction for majority of the traits but not in significant direction compare other female lines, which indicates that this parent can be considered to some extent for source of genes for improvement of yield and other

Table 3: Estimates of specific combining ability (SCA) effects of crosses for various characters in wheat.

	DF	DM	GFD	PH	NTPP	PEDL	SL	AL	BYPP	SYPP	HI	1000SW	AUDPC
Sonalika×Chiriya 3	-1.833	-3.042***	-1.208	-6.727**	-0.745	0.18	0.471	-0.089	1.047	0.803	1.289	-1.131	103.702*
Sonalika ×AN8226	0.917	0.583	-0.333	5.007*	-1.164	1.914**	-0.718	-0.337	-0.931	-1.083	-2.904	-2.693	57.255
Sonalika ×Y#6	0.292	1.333	1.042	-2.439	-0.032	-0.141	0.571	0.872*	-0.842	-0.953	-1.751	-0.769	29.167
Sonalika ×NING 8201	0.542	-0.417	-0.958	3.338	1.702*	-0.17	0.662	-0.262	0.409	0.089	-0.104	1.369	-59.954
Sonalika ×PBW343	-0.458	0.958	1.417	-0.347	-0.16	-1.564*	-0.617	0.109	-0.231	-0.415	-0.881	2.142	-52.393
Sonalika ×MONS	0.542	0.583	0.042	1.167	0.4	-0.218	-0.369	-0.293	0.548	1.559*	4.35	1.082	-77.778
HUW 234×chiriya 3	-1.75	-2.875**	-1.125	1.647	-0.005	1.082	-0.743	0.111	-0.053	0.343	1.218	-0.048	-145.114**
HUW 234×AN8226	0	0.75	0.75	-0.355	2.077**	-0.049	-0.822	-0.086	-0.861	0.652	4.351	-0.811	84.979
HUW 234×Y#6	0.375	-0.5	-0.875	1.099	-0.486	-0.104	0.252	-0.382	0.378	-1.018	-4.327	3.748*	-23.044
HUW 234×NING 8201	-0.375	1.75*	2.125	-0.543	0.163	-1.133	0.448	0.474	1.259	1.774*	3.586	-0.748	73.635
HUW 234×PBW343	0.125	0.625	0.5	0.542	-1.585*	-0.181	0.254	0.34	-0.436	-1.87*	-5.392*	-4.756**	20.706
HUW 234×MONS	1.625	0.25	-1.375	-2.39	-0.165	0.385	0.612	-0.457	-0.287	0.119	0.564	2.614	-11.164
HD2329×chiriya 3	2.333*	4.125***	1.792	0.145	0.212	-0.856	-0.269	-0.533	-1.178	-1.739*	-4.398	1.502	46.81
HD2329×AN8226	-1.417	-0.75	0.667	-1.836	-0.037	-0.722	2.117***	0.615	2.815*	0.53	-2.055	0.839	-90.383
HD2329×Y#6	0.458	-1.5	-1.958	2.218	1.596*	-0.342	-0.689	-0.446	-0.601	1.83*	7.097**	-2.152	2.52
HD2329×NING 8201	-0.292	1.25	1.542	-0.975	-3.12***	1.859**	-1.018*	0.325	-2.24	-1.383	-1.395	0.802	-26.106
HD2329×PBW343	-0.292	-1.875*	-1.583	2.04	2.127**	1.485*	-0.057	0.446	-0.385	1.469	5.012	1.744	57.075
HD2329×MONS	-0.792	-1.25	-0.458	-1.591	-0.778	-1.424*	-0.084	-0.406	1.589	-0.707	-4.261	-2.736	10.085
HUW510×chiriya 3	1.25	1.792*	0.542	4.935*	0.538	-0.406	0.542	0.511	0.184	0.593	1.891	-0.323	-5.399
HUW510×AN8226	0.5	-0.583	-1.083	-2.816	-0.876	-1.142	-0.577	-0.192	-1.023	-0.098	0.608	2.664	-51.851
HUW510×Y#6	-1.125	0.667	1.792	-0.878	-1.078	0.588	-0.133	-0.043	1.065	0.142	-1.019	-0.827	-8.644
HUW510×NING 8201	0.125	-2.583**	-2.708*	-1.82	1.255	-0.556	-0.092	-0.537	0.572	-0.481	-2.087	-1.423	12.425
HUW510×PBW343	0.625	0.292	-0.333	-2.235	-0.382	0.26	0.419	-0.896*	1.052	0.815	1.261	0.869	-25.389
HUW510×MONS	-1.375	0.417	1.792	2.814	0.543	1.256	-0.158	1.157**	-1.85	-0.971	-0.653	-0.961	78.856

traits except for AUDPC. Among the testers, Yangmai#6, NING 8201, PBW 343, MONS showed good GCA effects for most of traits. This indicates those resistant testers with broad genetic base can be further used to test agronomically superior but susceptible parents for their combining ability. The susceptible female lines showed high GCA effect of AUDPC in positive direction and low GCA effect of yield per plant in negative direction shows that their yield was affected.

Good SCA effects are the index for selection of superior hybrid crosses in form of exploitation of heterosis. The results of SCA effects were presented in table 3. The findings revealed that none of the crosses manifested negative and significant results of SCA effects for days to 50% heading. However, 10 crosses showed negative SCA effect for days to 50% heading. Four crosses, (Sonalika × Chiriya 3, HUW 234 × Chiriya 3, HD2329 × PBW 343 and HUW 510 × NING 8201) were exhibited significant SCA effects in negative direction which was considered to be good specific combiner for early maturity. Grain filling duration is an important trait when wheat is grown under stress conditions like spot blotch and terminal heat stress, both were coinciding because of late sowing. For grain filling duration and for plant height cross, HUW 510 × NING 8201 and Sonalika × Chiriya 3, respectively were showed significant SCA effects in negative direction which was considered to be good specific combiner. SCA effects of four crosses such as, (Sonalika × NING 8201, HUW 234 × A.N. 8226, HD2329 × Yangmai#6 and HD 2329 × PBW 343) exploited good specific combiners in significantly positive direction. Three crosses, (Sonalika × A.N. 8226, HD 2329 × NING 8201 and HD 2329 ×

PBW 343), were showed significant and positive SCA effects for peduncle length. For spike length only one hybrid showed significant and positive SCA effects *i.e.*, HD 2329 × A.N. 8226. None of crosses showed good SCA effects for biological yield per plant, except one cross HD 2329 × A.N. 8226 showed results in desirable direction. For seed yield per plant, three crosses *i.e.*, (Sonalika × MONS, HUW 234 × NING 8201 and HD 2329 × Yangmai#6) were exhibited significant SCA effects in positive direction which was considered to be good specific combiner. One hybrid showed positive and significant SCA effect for harvest index *i.e.*, (HD 2329 × Yangmai#6) and only single cross showed significant SCA effect for 1000 seed weight (HUW 234 × Yangmai#6) in desirable direction. The SCA effect of (HUW 234 × Chiriya 3) manifested significant result for AUDPC in negative direction considered to good cross for less disease progress.

Among the 24 crosses none of the hybrids showed good SCA effect for all traits. Three cross combinations exhibited significant and positive SCA effects *i.e.*, (Sonalika × MONS, HUW 234 × NING 8201 and HD 2329 × Yangmai#6) were the best specific cross combinations for number of seed yield per plant. Those three one cross, HD 2329 × Yangmai#6 also showed high SCA effects for its contributing traits *viz.* number of tillers per plant and harvest index. biological yield and harvest index. For AUDPC none of the crosses exhibited significant and desirable results. However, one cross, HUW 234 × Chiriya 3 manifested significant SCA effect for AUDPC and days to maturity in desirable direction can be considered as good specific combiner can be

exploited through heterosis breeding.

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