

Original Research Article

Evaluation of Wheat Genotypes for Disease Reaction against Spot Blotch Pathogen (*Bipolaris sorokiniana*) and Yield Traits

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ABSTRACT

Eighty eight Wheat (*Triticum aestivum* L.) genotypes/lines were evaluated for disease resistant reaction against Spot blotch disease (*Bipolaris sorokiniana*) and twelve different yield attributing traits. Nineteen genotypes were fallen in to resistant category for the area under disease progress curve over check Chiriyia-3. Sonalika may be used as donor for early flowering. Only CRP-9 genotype could produce heads similar to the resistant check Chiriyia-3 which could stay green for maximum duration also. None of the genotype could produce significant higher number of tillers than the resistant check Chiriyia-3. Nineteen genotypes may be used as parent in the resistant breeding programme as had smaller lesion size than check Chiriyia-3. Five genotypes had taken significant minimum number of days for grain filling and none could reach significantly earlier at the physiological maturity. Forty eight genotypes were weighed for higher test weight and genotype TEPOKO could produce significantly higher biomass and forty two genotypes produced significant higher yield than check Chiriyia-3. Genotypic correlation among the traits under study were also estimated and revealed significant positive association of grain yield to the test weight and biomass which may be used as secondary yield predictor, while making the selection criteria to improve yield. Negative association was observed for Area Under Disease Producing Curve, Heading, Anthesis, Days to greenness, Canopy Temperature, Physiological maturity, Number of tiller per plant and Grain filling duration indicating that caution should be exercised to minimize the yield loss, when selection is targeted for these characters.

Keywords

Wheat, Spot blotch disease, Resistant, yield, Correlation

Introduction

Wheat (*Triticum aestivum* L.) is the second most important cereal crop after rice in India for the dietary food of the people. Spot blotch disease of wheat caused by *Bipolaris sorokiniana* is one of the most destructive biotic stresses limits the production and productivity of the crop. Rice-wheat cropping system of South Asia provides

favorable environment for survival and multiplication of pathogens because rice serves as a host for the spot blotch fungi and rice-stubble are working as substrate for the fungi after harvest (Saari, 1998). The area under North Eastern Plain of India is extremely affected by spot blotch disease (Villareal *et al.*, 1995; Chand *et al.*, 2003)

and reduces grain yield up to 25 per cent. The *Bipolaris sorokiniana* shows enormous morphological and physiological variability due to multinucleate condition of mycelium and conidia, with subsequent heterokaryosis (Mitra, 1931; Day, 1974). Earlier morphological, pathogenic and molecular variability has been studied by Aggarwal *et. al.* (2010) in Indian isolates prevalent in the Bihar state. Lot of variable genotypes of wheat are available in the gene pool having different yield attributing traits and resistant characters may be evaluated for utilization in the development of high yielding disease resistant genotypes.

Keeping in view the above facts and urgent need the present investigation was formulated to evaluate the wheat genotypes/lines for disease reaction against spot blotch pathogen and yield contributing traits.

Materials and Methods

The present investigation was carried out during 2014-15 at the experimental fields of Pusa farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar and BISA (Borloug Institute of South Asia). The experimental site is geographically situated at North latitude of 25.984, East longitude of 85.674 and altitude of 52.20 m above mean sea level. Total 88 exotic and indigenous genotypes/varieties including two checks (Sonalika and Chiriy-3) were obtained from the university and used for the evaluation under study.

All 88 genotypes were sown at 10 x 22.5 cm spacing in three meter length row following randomized block design (RBD) with three replications. All recommended cultural and agronomical practices were followed uniformly to have a good crop. The data were recorded on five randomly selected

plants in each plot excluding border plants for twelve yield attributing traits namely; Area under disease progress curve, heading, anthesis, days to greenness, canopy temperature, lesion size, days to physiological maturity, number of tiller per plant, grain filling duration, test weight (1000-seed weight), biomass per square meter and yield per plot.

Highly aggressive pure culture of local isolates of *B. Sorokiniana* (RAU-GTL-19) were identified for spot blotch inoculation, was multiplied on wheat grains and spores were harvested in water. To augment the disease in field condition, the inoculums were spread uniformly on spreader rows as well as all other plants during the evening hours with a spore-water suspension (10^4 spores ml^{-1}) thrice i. e. at tillering stage, flag leaf emergence stage and at anthesis (Chaurasia *et. al.*, 1999; Joshi *et. al.*, 2002). The field was frequently irrigated to maintain high humidity (congenial environment) and promote disease development.

Disease severity assessment (in per cent) of spot blotch was recorded using the double-digit scale (DD, 00- 99), which is a modification of Saari and Prescott's severity scale to assess foliar disease in wheat (Eyal *et. al.*, 1987 and Saari and Prescott, 1975) as per formula given below:

$$\text{Per cent disease severity} = \frac{(D1/9) \times (D2/9)}{100} \times 100$$

Where,

D1-disease progress in canopy height from ground level.

D2-severity measure based on diseased leaf area.

The data were subjected to statistical analyses for Analysis of variance, Genetic variability and correlation association among the traits and results of the investigation are presented

Results and Discussion

The success of any crop improvement programme is almost dependent on genetic variation present in the breeding pool. The magnitude and extent of genetic variability present among the genotypes is very important for crop improvement. Thus, more variability provides more chance to recombine the gene/ trait from one genotype to another for effective utilization and the improvement of crops.

Morphological traits

A total of 88 genotypes of wheat including two checks namely; Sonalika and Chiriy-3 were used for the purpose of evaluation and characterization. Data depicted in the table 1 revealed that all wheat genotypes showed significant differences for all the agromorphological traits under study while coefficient of variation was less than 20 per cent having considerable amount of mean differences.

The trait area under disease progress curve were measured and out of 88 genotypes, 19 genotype namely CRP-9, CRP-10, CRP-11, CRP-12, CRP-19, CRP-27, CRP-28, CRP-29, CRP-30, CRP-31, CRP-32, CRP-34, CRP-36, CRP-37, CRP-39, CRP-40, CRP-43, CRP-51, CRP-54 were fell under resistant category over resistant check Chiriy-3. These genotypes may be used in breeding programme aimed to spot blotch resistance Khan and Chowdhury (2011) and Ojha *et. al.* (2017). Sonalika may be used as donor for early flowering in wheat breeding programme. Days to heading ranged from

69.00 to 88 days with general mean of 82.91 \pm 0.46 days. Out of 88 genotypes, only CRP-9 (88.0) genotype could produce heads similar to the resistant check Chiriy-3 (82.33). Only Chiriy-3 could stay green for maximum duration i.e. 88.00 days (Joshi *et. al.* 2007) and maintained highest canopy temperature amongst all. Out of 88 genotypes, none of the genotypes could produce significant higher number of tillers than the resistant check Chiriy-3. Only Sonalika could flower significantly earliest i.e. 74.00 days amongst all genotypes under study.

Nineteen genotypes namely, CRP- 37,CRP-63,CRP- 65,CRP- 67,CRP- 71,CRP- 72, CRP- 73, CRP- 74, CRP- 77, CRP- 78, CRP- 79, CRP -81, CRP- 82, CRP- 83, CRP- 84, CRP- 85, CRP- 86, CRP- 87 and CRP-88 may be used as parent in the resistant breeding programme as had smaller lesion size than the Chiriy-3.

The genotypes CRP-9, CRP-18, CRP-19, CRP-22 and CRP-23 had taken significant minimum number of days (general mean 29.05) for grain filling than check Chiriy-3. Whereas rest genotypes showed *at par* value of days to grain filling. Physiological maturity of the genotypes under experiment was counted and none of the line/genotype could mature significantly earlier than the resistant check Chiriy-3. This helps to store the more energy/ weight in seeds. Therefore, long grain filling duration helps to improve the seed size, seed weight and finally grain yield.

Test weight (1000-seed weight) is an important yield attributing trait because yield can be enhance by increasing the test weight. Test weight ranged from 24.23 g. to 55.03 g. and out of 88 genotypes, 48 genotypes i.e. CRP-1,CRP- 3,CRP- 5,CRP-8,CRP- 9,CRP- 10, CRP-12, CRP-13,CRP-

15, CRP-18, CRP-21,CRP- 23, CRP-25,CRP- 26, CRP-27,CRP- 28,CRP-31,CRP- 33 to CRP-54,CRP- 58 to CRP- 64, CRP-70, CRP-71, CRP-72, CRP-73,CRP-75,CRP- 77 to CRP-84 and CRP-86 were having the higher test weight than Chiriya-3.

In most of the crops there is direct correlation between biomass and yield because it is only the key factor responsible for accumulation of photosynthates. Per square meter biomass was weighed and observed that only one genotype TEPOKO could produce significantly higher biomass than check Chiriya-3. So, this genotype can be used to improve the biomass of the recipient genotype(s).

Grain Yield is the ultimate goal of any grain crops and genotypes subjected for the study showed variable range from 210.00 to 401.33 g with the general mean of 314.80 ± 14.30 g. The genotypes viz.,CRP-1,CRP- 3 to CRP- 9, CRP- 11, CRP- 12, CRP-13,CRP- 15, CRP- 16, CRP- 17, CRP- 18, CRP- 21, CRP- 25, CRP- 28, CRP- 33, CRP- 36 to CRP- 45, CRP-47, CRP-49, CRP-51, BWL-0814, BWL-9022, DHARWAD DRY, RAJ-3765, WH-730 to TEPOKO,IC 532653, ARIANA-66, GIZA-153, IC-118737, PBW 343 were found significantly superior than check Chiriya-3. These genotypes may also be used as a parental line for breeding programme aimed to crop improvements.

Table.1 Analysis of variance for design of experiment for twelve quantitative characters in wheat

Sl. No.	Characters	Mean Sum of Squares			C.V.
		Replication d. f. = 2	Treatments d. f. = 87	Error d.f.= 174	
1.	Area under disease progress curve	2,629.00	23,351.56**	4,257.34	3.27
2.	Heading	13.15	17.18*	12.66	4.29
3.	No. of tiller per plant	78.00	4.90**	.73.00	12.29
4.	Anthesis	9.09	19.45**	12.20	3.91
5.	Days to greenness	2647.71	218.20**	114.20	15.58
6.	Canopy temperature	7063.09	196.82**	59.34	19.91
7.	Lesion size	10.21	77.13**	0.86	12.25
8.	Grain filling duration	105.64	43.73**	20.30	15.49
9.	Physiological maturity	76.87	51.20**	18.91	3.68
10.	1000 grain weight	46.13	162.95**	1.62	3.10
11.	Biomass per square meter	133337.35	69964.12**	5346.38	6.64
12.	Grain yield	101.66	7882.19**	78.64	2.84

** Singnificant at 1%level* of singnificance at 5%

(AUDPC = Area under disease progress curve, HAD = Heading, ANT = Anthesis, DG = Days to greenness, CT = Canopy temperature, LS = Lesion size, PM = Physiological maturity, NT = No. of tiller per plant, GFD = Grain filling duration, TGW = 1000 grain weight, BM = Biomass per squre meter, GY = Grain yield)

Table.2 Character association of twelve traits in wheat genotypes

	AUDPC	HAD	ANT	DG	CT	LS	PM	NT	GFD	TGW	BM	GY
AUDPC	1											
HAD	-0.324**											
ANT	-0.369**	0.812**										
DG	-0.054	-0.097	-0.160									
CT	-0.686**	0.194	0.372**	-0.023								
LS	0.397**	-0.109	-0.269*	0.033	-0.553**							
PM	-0.517**	0.292**	0.413**	-0.073	0.682**	-0.359**						
NT	0.620**	-0.358**	-0.495**	-0.036	-0.663**	0.449**	-0.477**					
GFD	-0.275**	-0.187	-0.189	-0.027	0.424**	-0.241*	0.755**	-0.115				
TGW	-0.147	0.037	0.078	-0.088	0.220*	0.089	0.105	-0.125	-0.010			
BM	0.434**	-0.234*	-0.288**	0.066	-0.618**	0.426**	-0.499**	0.467**	-0.315**	0.035		
GY	-0.027	-0.115	-0.078	-0.053	-0.076	0.109	-0.150	0.050	-0.088	0.476**	0.498**	1

Character association

Appearance of a phenotype is manifestation of given genotype, environment and its interaction. Seed yield, an extremely complex entity, is result of many growth and development processes in plant and each step is liable to environmental fluctuations. So much so Grafius, (1959) suggested that there may not be genes for yield but rather for various components, the multiplicative interaction of which results in artifact of yield. Since, selection for increased yield is usually concern with changing two or more characters simultaneously, an understanding of the nature and magnitude of their relationship in segregating and non-segregating populations would be of immense value in assigning rational weights to the different component characters during selection. Higher magnitude of genotypic correlation coefficient than the phenotypic correlation coefficient indicated that the traits were little influenced by environmental effects. The positive and significant association between Grain yield with, 1000 grain weight and biomass indicated that these traits (directly and/or indirectly) may be included for yield improvement of wheat (Table 2). The negative association of Grain yield with Area Under Disease Producing Curve, Heading, Anthesis, Days to greenness, Canopy Temperature, Physiological maturity, Number of tiller per plant and Grain filling duration, indicating that caution should be exercised to minimize the yield loss, when selection will be made for these characters. The negative relationship of Grain yield to the Heading & Anthesis has also earlier been reported by Sharma *et. al.* (2006) and Kumar *et. al.* (2009).

The positive association of Biomass per square meter with Grain yield indicated that reproductive growth was highly influenced

by vegetative growth and biomass is also depends on time taken by plants before starting the reproductive growth. This may be due to the fact that late flowering varieties are having more time duration for growth and thus have more biomass or biological yield. The strong positive association of Biomass with Grain yield indicated that biomass improve the number of tillers and ultimately improve the yield by translocation of photosynthates from source to sink. Our results are also corroborating the work of Kumar *et. al.* (2009) as positive association of wheat yield was observed for Biomass per square meter, 1000 grain weight and No. of tiller per plant.

On the basis of results and discussion it can be concluded that Nineteen genotypes were fallen in to resistant category for the area under disease progress curve over check Chiriya-3. Sonalika may be used as donor for early flowering. Only CRP-9 genotype can be used for increasing the heads and Chiriya-3 could stay green for maximum duration.. Nineteen genotypes may be used as parent in the resistant breeding programme having smaller lesion size. Five genotypes had taken significant minimum number of days for grain filling but none could reach significantly earlier at the physiological maturity. Forty eight genotypes were weighed for higher test weight and genotype TEPOKO could produce significantly higher biomass and forty two genotypes produced significant higher yield than check Chiriya-3.

Genotypic correlation among the traits under study were also estimated and revealed significant positive association of grain yield to the test weight and biomass which may be used as secondary yield predictor, while making the selection criteria to improve yield. Negative association was observed for Area Under Disease Producing Curve,

Heading, Anthesis, Days to greenness, Canopy Temperature, Physiological maturity, Number of tiller per plant and Grain filling duration indicating that caution should be exercised to minimize the yield loss, when selection is targeted for these characters.

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