



Research Article

GENETIC VARIABILITY FOR YIELD PARAMETERS AND SPOT BLOTCH RESISTANCE IN F₂ POPULATION OF DURUM WHEAT (*Triticum turgidum var durum*)

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Abstract- The experiment was conducted to study the extent of genetic variability for grain yield, its component traits and spot blotch in F₂ population of the cross Bijaga yellowx NIDW-295. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for all the characters except for days to fifty percent flowering, spike length and number of spikelet's per spike. High heritability and genetic advance were recorded for all the characters except days to fifty percent flowering, awn length, spike length, number of spikelet's per spike, thousand grain weight and seed yield per plant. These results suggested that better scope for selecting superior transgressive segregants in this population. For spot blotch incidence, high genetic coefficients of variation along with high heritability and genetic advance were recorded indicating the greater effectiveness of selection and improvement can be expected for spot blotch resistance. Present investigation suggests that selection in F₂ population of Bijaga yellowx NIDW-295 will be effective in selecting superior plants for yield parameters and spot blotch resistance in evolving high yielding disease resistant genotype in wheat.

Keywords- Area Under Disease Progress Curve (AUDPC), Genetic variability, Wheat, Spot blotch.

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Introduction

Wheat (*Triticum aestivum* L.) is one of the world's major cereal crops and staple food of many regions grown under both irrigated and rain-fed conditions. India is the world's second largest wheat producer, behind China and ahead of USA. It is a remarkable achievement but India continues to face formidable problem of ever increasing population and future wheat demand will be 110 mt to feed 1.5 billion people of India by 2020 [1]. The wheat production and productivity is affected by various fungal, bacterial, viral diseases etc. Among these, Spot blotch caused by fungi *Bipolaris sorokiniana*, also known as leaf blight is a devastating disease of wheat particularly in warm and humid regions such as NEPZ of India, South East Asia, Latin America, the tarai of Nepal, China and Africa [2]. Due to continuous rise in temperature during the wheat growing season and high humidity coupled with winter rains, spot blotch is getting favourable conditions to develop aggressively and causes damage to wheat crop at larger scale by causing significant yield loss up to 18-50 per cent loss in favourable conditions [3]. The spot blotch disease is gaining much importance in Karnataka state of India because of the occurrence of severe outbreak every year [4] where majority of area under tetraploid wheat cultivation characterized by dry and irrigated weather conditions favours spot blotch disease incidence in our area. Generally, tetraploid wheat is endowed with natural resistance rusts but is highly susceptible to spot blotch. The genetic understanding of spot blotch resistance is limited and not well documented so far.

Information on genetic variability, heritability and other genetic parameters of spot blotch resistance with other agro-morphological attributes is pre-requisite for genetic improvement through systemic breeding programmes targeted at improving spot blotch disease resistance. It is generally believed that the level of resistance to spot blotch in high-yielding wheat genotypes is still unsatisfactory

and needs to be improved significantly in warmer and humid regions of South Asia. The genetic variability study in segregating population of wheat is also reported by several researchers on yield and its attributing traits. Although, studies on genetics of spot blotch resistance are limited and there is little effort has been made to study the genetic variability for spot blotch resistance in segregating populations of durum wheat. Hence, the present investigation was conducted to study the extent of variability, heritability and possible amount of genetic gain expected to occur during the selection for yield parameters and spot blotch resistance in the F₂ population of cross Bijaga yellow x NIDW 295. Genetic studies presented in this study will enable breeder to make predictions about the possible progress that can be achieved by making the selection more effective for genetic improvement of spot blotch disease resistance.

Materials and Methods

The experimental material for the present study comprised of the F₂ population of cross involving spot blotch susceptible (Bijaga yellow) and resistant (NIDW-295) genotypes. The present study was conducted in the experimental area of Agricultural Research Station (ARS), Arabhavi, University of Agriculture Sciences, Dharwad considered as hotspot for spot blotch screening located between 15° 26' N latitude and 75° 07' E longitude. The F₂ seeds of cross Bijaga yellow x NIDW 295 were space planted along with parents Bijaga yellow and NIDW-295. The susceptible checks viz., Kiran, Bijaga Yellow and Amruth were also sown as an infector row to increase and uniform spread of disease in an experimental field. The F₂ seeds and checks were sown in a row length of one meter length with the help of a dibble, keeping plant to plant distance of 20cm and row to row distance of 23 cm during Rabi 2014-15. The recommended agronomic practices were followed during the crop growth period. Each individual F₂ plants were tagged to

record the observation on spot blotch disease, yield and yield attributing traits.

Creation of epiphytotic conditions and Disease assessment

The spore suspension was prepared from 15 days old culture of *Bipolaris sorokiniana* multiplied on sorghum seeds and was inoculated at tillering stage, flag leaf stage and anthesis stages during evening hours following the method described [5]. Plots were irrigated immediately after inoculation to maintain a high relative humidity for facilitating disease establishment and development in field. The five individual disease score was taken at weekly intervals using the double digit scale (00-99) developed as a modifications of Saari and Prescott's (1975) at three different growth stages (GS), viz., GS 63 (beginning of anthesis to half complete), GS 69 (anthesis complete) and GS 77 (late milking). Percentage disease severity is estimated based on the following formula [6].

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

The area under disease progress curve (AUDPC) based on disease severity over time was estimated using the following formula given by [7].

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

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 disease scoring was recorded.

Data was recorded on grain yield (YPP) and its attributing traits viz., days to fifty percent flowering, number of productive tillers per plant, plant height, spike length, number of spikelets per spike and 1000-grain weight (TGW).

Statistical analysis

Statistical analysis was done on the observation recorded on each individual plant in F₂. Genetic parameters and the statistical methods adopted in the present study were given as follows.

Phenotypic variance (σ_p) = Var F₂

Where, Var F₂ = variance of F₂ population

Environmental variance (σ_e) = (Var P₁ + Var P₂) / 2

Where, Var P₁ = Variance of P₁ parent and Var P₂ = Variance of P₂ parent

Genotypic variance (σ_g) = $\sigma_p - \sigma_e$

Where, σ_p = Phenotypic variance and σ_e = Environmental variance.

Genotypic coefficient of variability (GCV)

$$GCV (\%) = \frac{\sigma_g}{X} \times 100$$

Where, σ_g = Genotypic standard deviation and X = General mean of the characters.

Phenotypic coefficient of variability (PCV)

$$PCV (\%) = \frac{\sigma_p}{X} \times 100$$

Where, σ_p = Phenotypic standard deviation

X = General mean of the characters.

GCV and PCV values were categorized as low, moderate and high as indicated in [8] as 0-10% – Low; 10%-20%- Moderate; > 20%-High.

Heritability (Broad Sense)

Heritability in broad sense was estimated as the ratio of genotypic to the phenotypic variance and was expressed in percentage.

$$h^2_{bs} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The heritability was categorized as low, moderate and high as 0-30%- Low; 30-60%-Moderate and 60% and above – High.

Genetic Advance (GA)

The extent of genetic advance to be expected from selecting five per cent of the superior progeny was calculated by using the following formula

$$\text{Genetic advance (GA)} = ih^2 \sigma_p$$

Whereas, i = Intensity of selection, h^2 = Heritability in broad sense, σ_p = Phenotypic standard deviation. The value of i was taken as 2.06 assuming 5 per cent selection intensity.

Genetic Advance over Mean (GAM)

Genetic advance over mean was estimated using the following formula

$$GAM (\%) = \frac{\text{Genetic advance}}{\text{Grand mean of the character}} \times 100$$

Where, GA = Genetic advance, X = general mean of the Character.

Genetic advance as per cent mean was categorized as low, moderate and high as given by [9] as 0-10% - Low, 10-20% - Moderate and 20% and above – High.

Results and Discussion

The amount of genotypic and phenotypic variability that exist in a species is of utmost importance in breeding better varieties and in initiating a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population. Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability (h^2) and genetic advance as percent of mean (GA) of the traits studied are presented in [Table-1].

The genetic variability studies in F₂ indicated high mean and wider range for all the traits under evaluation. This suggested the existence of sufficient genetic variability in this population.

In general, the PCV values were greater than GCV values although the differences were small. Narrower difference between the values of GCV and PCV indicated that the environmental effect was small for the expression of these characters and these traits are governed by additive gene action. The results obtained were in agreement with the results for yield and its contributing characters [10].

Table-1 Estimates of Genetic variability parameters for different quantitative traits in F₂ population of Bijaga yellow x NIDW-295.

Genetic parameters	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄
Phenotypic Variance	2.79	5.16	50.01	241.64	166.16	21.34	1.63	5.16	4.13	69.96	35.90	65.22	284.75	355.61
Genotypic variance	1.24	3.27	46.85	238.62	171.24	27.31	1.53	4.17	4.52	68.39	36.23	59.68	226.86	942.88
PCV	150.17	125.64	103.32	100.79	103.67	107.26	103.11	115.25	106.66	102.02	103.34	104.54	112.28	102.74
GCV	1.76	1.60	49.21	112.88	12.32	25.23	15.35	14.65	12.29	69.80	18.67	16.57	44.59	63.61
Heritability (%) broad sense	44.34	63.35	93.68	98.75	103.06	127.93	94.06	80.71	109.41	97.75	100.91	91.50	79.67	85.29
Expected Genetic advance @5%	1.53	2.96	13.65	31.67	28.80	14.77	2.47	3.91	5.11	16.99	12.93	15.22	27.76	172.30
Genetic Advance % of mean	2.42	2.62	98.11	231.44	27.11	71.32	30.67	28.08	29.53	143.40	40.11	32.65	82.16	356.96

X₁ – Days to 50% flowering

X₂ – Days to maturity

X₃ – Number of tillers/plant

X₄ – Number of productive tillers/plant

X₅ – Plant height (cm)

X₆ – Peduncle length (cm)

X₇ – Spike lengths (cm)

X₈ – Awn length (cm)

X₉ – Number of spikelet's per spike

X₁₀ – Seed yield per plant (g)

X₁₁ – 1000 grain weight (g)

X₁₂ – Number of seeds per spike

X₁₃ – AUDPC

X₁₄ – Disease severity (%)

Higher GCV and PCV values observed for all the traits except for few traits viz., days to 50 per cent flowering, days to maturity, plant height, awn length, number of spikelet's per plant, number of grains/spike and AUDPC suggested that there is high phenotypic and genotypic variation for all the traits except these traits. This indicates that there is an ample scope for selection of promising plants from the present population for yield and its components. high genetic variability for grain yield and its component characters in early segregating generations of wheat also reported by [11].

Moderate to low GCV and PCV recorded for days to maturity, plant height, awn length, number of spikelet's per plant, number of grains/spike and AUDPC suggested the difficulty of manipulating these traits through plant breeding. Similar results of moderate PCV and GCV has been reported for spikelets per spike in wheat by [12]. For spot blotch resistance, high PCV and GCV was recorded for disease severity (%) and AUDPC values, indicating that there is high variability and ample scope for selecting superior resistant segregants in this population.

Heritability is a significant parameter for the selection of an efficient population improvement method. Single plant selection and that in the earlier generations may be much effective for a character that is highly heritable as compared to character which is less heritable. The higher estimates of heritability were observed in the present study for grain yield and yield related traits like number of productive tiller per plant, plant height, yield per plant and thousand grain weight. This suggested that heritability is due to the additive genetic effects and selection could be effective in early segregating generations for these traits and the possibility of improving wheat grain yield through direct selection for grain yield related traits. Binod The high heritability estimates for grain yield per plant, number of seeds per spike, plant height, 1000 seed weight and number of tillers per plant, which were in agreement with the present findings reported by [13] and [14]. Hence selection for grain yield and yield related traits like number of productive tiller per plant, plant height, yield per plant and thousand grain weight is suggested to improve the yield.

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. High heritability accompanied with high genetic advance as *percent* of mean was recorded for number of number tiller per plant, productive tillers/plant, plant height, spike length, awn length, number of spikelet's/spike, Number of grains/spike, yield per plant and thousand grain weight. The high heritability estimates for grain yield per plant and number of tillers per plant which supports findings in the present study was reported [15].

For spot blotch resistance, high heritability coupled with high genetic advance as *percent* of mean was observed for Area under disease progress curve (AUDPC) and *per cent* disease severity. This suggested the effectiveness of selection for spot blotch superior resistance plants in the F₂ population. Thus, it is evident from the present finding that substantial genetic variability was envisaged for yield and its component traits in the F₂ population of cross Bijaga yellowx NIDW-295 population. It also exhibited high heritability coupled with high genetic advance as *percent* of mean for grain yield per plant, plant height, number of tillers per plant, thousand grain weights and spot blotch resistance characters like AUDPC and *per cent* disease severity.

Conclusion:

The high genetic variability exists in the F₂ population of cross Bijaga yellow x NIDW 295 for spot blotch resistance, yield and yield attributing traits in tetraploid wheat. Therefore, these traits should be taken into account while selecting superior and desirable plants for further improvement of yield parameters and spot blotch resistance in development of high yielding and leaf rust resistant genotype in wheat.

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Conflict of Interest: None declared

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