

GENETIC VARIABILITY FOR YIELD PARAMETERS AND RUST RESISTANCE IN F₂ POPULATION OF WHEAT (*TRITICUM AESTIVUM* L.)

ARATI YADAWAD*, R. R. HANCHINAL, H. L. NADAF, S. A. DESAI, SUMA BIRADAR AND V. RUDRA NAIK

Department of Genetics and Plant Breeding,
University of Agriculture Sciences Dharwad - 580 005, Karnataka, INDIA
e-mail: aratiyadawad@gmail.com

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*Corresponding
author

ABSTRACT

The aim of this study was to estimate the extent of genetic variability for grain yield, its component traits and leaf rust resistance in F₂ population of the cross DWR162 X PBW343. 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, spike length and number of spikelet's per spike. This suggested better scope for selecting superior transgressive segregants in this population. For leaf rust 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 leaf rust resistance. Present investigation suggests that selection in F₂ population of DWR162 X PBW343 will be effective in selecting superior plants for yield parameters and leaf rust resistance in evolving high yielding leaf rust resistant genotype in wheat.

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. It belongs to family Poaceae or Graminae. Wheat has always been subjected to extensive and ceaseless research so as to maximize grain production and also to improve grain yield per unit area. However, there is still considerable room for improvement, especially to amplify efforts for continued genetic improvement of wheat to meet the growing requirements of an ever increasing population. Genetic manipulation is the best way to boost up wheat production.

Yield is a quantitative trait controlled by many genes and is greatly influenced by the environment. Variation in yield from year to year due to unpredictable weather and biotic stresses can have major economic impact. The extent of genetic variability has been considered as an important factor which is an essential pre-requisite for a successful hybridization aimed at producing high yielding progenies. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters (Santosh *et al.*, 2013). Therefore, it is necessary to estimate and study the genetic variation and mode of inheritance in different yield parameters and biotic stress resistance to initiate productive wheat breeding programs.

Study of genetic parameters from segregating population is useful in understanding the genetic consequences of

hybridization. The heritability of a character describes the extent to which it is transmitted from one generation to the next. The genetic advance is the further estimation of expected gain resulting from selection pressure in breeding material. High heritability associated with high genetic advance for different yield components have a better scope for selecting high yielding genotypes (Shoukat Ali *et al.*, 2007). Genetic information like heritability and genetic advance for different yield contributing traits would be of great value enabling the breeder to use best genetic stock for improvement in breeding programme.

Genetic variability in bread wheat genotypes has been studied by Abinasa *et al.* (2011), Bhushan *et al.* (2013), Binod Kumar *et al.* (2013) and Said Salman (2014). Genetic variability study in segregating population of wheat is also reported by several co-workers (Vijayakumar *et al.*, 2013, and Shoukat Ali *et al.*, 2007). But there is no much effort has been made to study the genetic variability for leaf rust resistance in segregating populations of bread 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 leaf rust resistance in the F₂ population of cross DWR162 X PBW343. Genetic studies presented in this research work will enable breeder to make predictions about the possible progress that can be achieved by making the selection more effective.

MATERIALS AND METHODS

The present study was conducted in the experimental area of Dr. Sanjay Rajaram Wheat Laboratory, All India Coordinated Wheat Improvement Project (AICWIP), Main Agricultural Research Station (MARS), University of Agricultural Sciences, Dharwad. The experimental material comprised of the F_2 population of cross DWR162 X PBW343. F_2 seeds were space planted along with parents DWR162, PBW343 and five checks, HI977, GW322, UAS304, MACS6222 and HS240 in a row length of three meter with the help of a dibble, keeping plant to plant distance of 20cm and row to row distance of 23 cm during rabi 2012-13. 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) and protein.

Statistical analysis

Statistical analysis was done on the observation recorded on each individual plant in F_2 genetic parameters and the statistical methods adopted were as follows.

Phenotypic variance (σ^2_p) = Var F_2

Where, Var F_2 = variance of F_2 population

Environmental variance (σ^2_e) = (Var P_1 + Var P_2) / 2

Where, Var P_1 = Variance of P_1 parent and Var P_2 = Variance of P_2 parent

Genotypic variance (σ^2_g) = σ^2_p - σ^2_e

Where, σ^2_p = Phenotypic variance and σ^2_e = Environmental variance

Genotypic coefficient of variability (GCV)

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

Where, σ_g = Genotypic standard deviation and \bar{X} = General mean of the characters

Phenotypic coefficient of variability (PCV)

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

Where, σ_p = Phenotypic standard deviation

\bar{X} = General mean of the characters

GCV and PCV values were categorized as low, moderate and high as indicated by Sivasubramanian and Menon (1973) 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.

$$\text{Heritability (h}^2\text{) (\%)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The heritability was categorized as low, moderate and high as given by Robinson *et al.* (1951) 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

Genetic advance (GA) = $ih^2\sigma_p$ where, i = Intensity of selection, h^2 = Heritability in broadsense, 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

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where, GA = Genetic advance, \bar{X} = general mean of the character

Genetic advance as per cent mean was categorized as low, moderate and high as given by Johnson *et al.* (1955) as 0-10% - Low, 10-20% - Moderate and 20% and above - High.

Leaf rust resistance

For leaf rust resistance, each individual plant of F_2 was scored in percentage at both vegetative and reproductive stages. Response of the plants to disease was assessed using a modified Cobb's scale (Peterson *et al.*, 1948). The final disease severity data for the leaf rust was converted into a coefficient of infection (CI) by multiplying severity with a constant value for field response given in Table 1.

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 2.

Genetic variability

The genetic variability studies in F_2 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 (Vijayakumar *et al.*, 2013, Abinasa *et al.*, 2011 and Subhashchandra *et al.*, 2009).

Higher GCV and PCV values observed for all the traits except for three *viz.*, days to 50 per cent flowering, spike length and spikelets per spike suggested that there is high phenotypic and genotypic variation for all the traits except these three traits. This indicates that there is an ample scope for selection of promising plants from the present population for yield and its components. Abinasa *et al.* (2011) also reported high genetic variability for grain yield and its component characters in early segregating generations of wheat.

Moderate to low GCV and PCV recorded for days to 50 per

Table 2: Estimates of components of variability, heritability (broad sense), genetic advance and genetic advance as percent of mean for different quantitative traits in F₂ population of DWR 162 X PBW 343.

Character	Mean	Minimum	Maximum	PCV (%)	GCV (%)	Heritability	Genetic Advance	Genetic Advance as percent of Mean
Days to 50 per cent flowering	71.58	60.00	89.00	29.01	16.15	55.67	29.01	23.81
Plant height (cm)	74.49	32.00	100.00	152.26	122.63	80.54	152.26	188.18
Number of tillers	11.73	1.00	33.00	176.36	107.87	61.17	176.36	26.06
Spike length (cm)	9.53	4.00	12.00	15.78	7.73	48.99	15.78	1.52
Number of spikelets per spike	18.75	8.00	23.00	27.88	11.34	40.70	27.88	4.38
Grain yield per plant (g)	17.60	0.70	63.40	470.95	384.48	81.64	470.95	139.36
Thousand grain weight (g)	35.97	21.00	55.50	139.74	110.43	79.03	139.74	81.83
Leaf Rust Incidence	2.56	0.00	60.00	375.54	229.47	61.11	375.54	120.83

Table 1: Leaf rust reaction, code for field response and response value

Reaction	code	Field response	Responsevalue
No disease	0	No visible infection	0.0
Resistant	R	Necrotic areas with or without minute uredia	0.2
Moderately resistant	MR	Small uredia present surrounded by necrotic area	0.4
Moderately resistant	MRMS	Small uredia present surrounded by necrotic areas as well as medium uredia with no necrosis but possible some distinct chlorosis.	0.6
Moderately susceptible	MS	Medium uredia with no necrosis but possible some distinct chlorosis	0.8
Moderately susceptible	MSS	Medium uredia with no necrosis but possible some distinct chlorosis as well as large uredia with little or chlorosis present	0.9
Susceptible	S	Large uredia and little or no chlorosis present	1.0

Cobb's scale (Peterson *et al.*, 1948) was used only to record the rust severity data

cent flowering, spike length and spikelets per spike 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 Bhushan *et al.* (2013). For leaf rust incidence, high PCV and GCV was recorded, indicating that there is high variability and ample scope for selecting leaf rust resistant segregants in this population.

Heritability and genetic advance

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 high 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 Kumar *et al.* (2013), Dwivedi *et al.* (2002) and Yousaf *et al.* (2008) also reported 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 support the present findings. 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 (Johnson *et al.*, 1955). High heritability accompanied with high genetic advance as percent of mean was recorded for number of productive tiller per plant, plant height, yield per plant and thousand grain weight. Asif *et al.* (2010) also recorded high heritability estimates for grain yield per plant and number of tillers per plant which supports these findings. Moderate heritability coupled with high genetic advance over mean was recorded for days fifty percent flowering and number of spikelets per spike. Moderate heritability coupled with low genetic advance as percent of mean observed for spike length indicates non additive gene effects suggesting that there is a limited scope for selection for spike length in yield improvement in wheat. Said Salman (2014) also reported higher heritability with low expected genetic advance for number of tillers per plant, spike length and number of spikelets per spike indicating non additive gene effects and very limited scope for improvement of these traits. For leaf rust incidence, high heritability coupled with high genetic advance as percent of mean was recorded. This suggested the effectiveness of selection for leaf rust resistance plants in this 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 DWR 162 X PBW 343. 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 leaf rust resistance. Therefore, these traits should be taken into account while selecting superior and desirable plants for further improvement of yield parameters and leaf rust resistance in evolving high yielding and leaf rust resistant genotype in wheat.

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