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Genetic variability for yield parameters in F₂ population of wheat (*Triticum aestivum* L.) under rainfed condition

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Abstract

The aim of this study was to estimate the extent of genetic variability for grain yield, its component traits and physiological traits in F₂ population of the crosses GW 322 X UASBW 11949 and NI 5439 x UASBW 11949. High Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were observed for number of productive tillers per plant, grain yield per plant and leaf waxiness while, moderate GCV and high PCV were recorded for thousand grain weight, number of grains per plant and canopy temperature at anthesis stage. For the traits, relative water content and membrane stability index moderate GCV and PCV were noticed. High heritability coupled with high genetic advance over mean was recorded for grain yield per plant and yield related traits *ie.*, number of productive tiller per plant and number of grains per spike as well as for canopy temperature at booting stage while, high heritability coupled with moderate genetic advance over mean was observed for physiological traits *viz.*, relative water content, canopy temperature at anthesis stage and NDVI at anthesis stage indicating better scope for selecting superior transgressive segregants under rainfed condition. Present investigation suggests that selection in F₂ population of GW 322 X UASBW 11949 and NI 5439 x UASBW 11949 would be effective in isolating superior plants for yield parameters in evolving high yielding drought tolerant genotype in wheat.

Keywords: Wheat, F₂ population, Heritability, Genetic advance, relative water content, membrane stability index, rainfed condition

Introduction

Wheat (*Triticum aestivum* L.) is one of the major staple food crops in many countries of the world including India and is grown both under irrigated and rainfed conditions. Wheat grains are rich sources of carbohydrates (71%) followed by proteins (13%), minerals (2.7%), fat (1.7%), fibre (2%) and vitamins (0.04%). Hence, production of wheat in the world has reached about 749 million tons from 260 million hectares with the productivity of 2717 kg per hectare (Anon. 2020) [4]. India is the second largest wheat producer after China in world with the production of 107.18 million tonnes covering about 30.55 million hectares area with the productivity of 3508 kg per ha. Though it is a remarkable achievement, India continues to face formidable problem of ever increasing population and the demand for wheat crop is expected to increase by 60% by 2050, if the population growth reaches up to 9.7 billion (Esmail *et al.*, 2016) [10]. In Karnataka is one of the major *rabi* crops and covers about 1.66 lakh hectares area with annual production of 2.08 lakh tonnes and productivity of 1250 kg per ha (Anon. 2020) [4]. Wheat production of the state is very low compared to national average, mainly due to the fact that large area is grown under rainfed conditions and only a small part of the growing period experiences the cold condition.

Drought is the single largest abiotic stress factor leading to reduced crop yield hence, high yielding crops even in environmentally stressful conditions are essential. However, genetic increase in wheat yield in dry areas is not so high as in more favourable environments or irrigated condition due to unpredictable and highly variable seasonal rainfall and hence highly variable yields. Improvement of yield for rainfed condition is one of the most difficult tasks for wheat breeders as it is a complex physiological trait and polygenic in nature. Genetic manipulation is the best way to boost up wheat production. Therefore, it is necessary to assess and study the genetic variation and its mode of inheritance in yield and its related parameters and physiological characters to initiate productive wheat breeding programs.

Study of genetic parameters from segregating population is useful in understanding the genetic consequences of hybridization. Heritability, a measure of the phenotypic variance provides an

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estimate of genetic advance a breeder could expect from selection applied to a population under certain environment. High heritability associated with high genetic advance for yield and its components have a better scope for selecting high yielding genotypes (Mangi *et al.*, 2007) [16]. Genetic variability studies in bread wheat genotypes were attempted by Abinasa *et al.*, 2011 [1], Bharat *et al.*, 2013 [7], Binodkumar *et al.*, 2013 [8], Said, 2014 [21] and Deepak (2016) [9]. Genetic variability study in segregating population of wheat is also reported by several co-workers (Mangi *et al.*, 2007) [16], (Hokrani *et al.*, 2013) [12], (Veeresh, 2016) [25] and (Swathykrishna, 2018) [24]. But there is no much effort has been made to study the genetic variability for drought tolerance in segregating populations of bread wheat.

Hence, the present investigation was carried out to assess the extent of genetic variability, heritability and possible magnitude of genetic gain expected to occur during the selection for yield parameters under rainfed condition in F₂ population of crosses GW 322 X UASBW 11949 and crosses NI 5439 X UASBW 11949. Genetic studies of present research work will enable breeder to make predictions regarding possible progress that can be achieved by making the selection more effective.

Materials and Methods

The present experiment consisting of two F₂ segregating populations was carried out at Agricultural Research, Bailhongal, University of Agricultural Sciences, Dharwad during *rabi* 2018-19. The experimental material of the present investigation was derived using two high yielding wheat genotypes (GW 322 and NI 5439) as females and one drought tolerant genotype UASBW 11949 as male parent during *rabi*-2016-17 (Deepak, 2016) [9]. Seeds of F₂ populations were space planted along with their parents GW 322, NI 5439 and UASBW 11949 in a row length of five meter keeping plant to plant distance of 20cm and row to row distance of 23 cm.

Observations recorded: During the course of study observations were recorded on 18 morpho-physiological traits: Grain yield per plant and its attributing traits *viz.*, number of productive tillers per plant, plant height, spike length, number of spikelets per spike, grains per spike, 1000 grain weight and days to 50 percent flowering, days to maturity and physiological traits *viz.*, chlorophyll content, canopy temperature, normalized vegetation Index, relative water content, membrane stability index and leaf waxiness (Pask *et al.*, 2012) [17].

Statistical analysis

Statistical analysis was done on the observation recorded on each individual plant in F₂ populations. Genetic parameters and the statistical methods adopted are as follows.

General mean (\bar{X}) = Sum of observations of selected plants in each genotype/ Number of plants selected

Range = The minimum and maximum values for each trait within a genotype.

Estimation of genetic parameters

Phenotypic variance (σ^2_p) = Var F₂

Where, Var F₂ = variance of F₂ population

Environmental variance (σ^2_e) = (Var P₁ + Var P₂) / 2

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

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

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

Genotypic coefficient of variability (GCV)

$$\text{GCV (\%)} = \left(\frac{\sigma^2_g}{\bar{X}} \right) \times 100$$

Phenotypic co-efficient of variability (PCV)

$$\text{PCV (\%)} = \left(\frac{\sigma^2_p}{\bar{X}} \right) \times 100$$

Where

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

\bar{X} = Grand mean of the character.

GCV and PCV values were categorized as low, moderate and high as indicated by (Sivasubramanian and Menon, 1973) [22], 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 as suggested by (Hanson *et al.*, 1956) [11].

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The heritability was categorized as low, moderate and high as given by (Robinson *et al.*, 1951) [20] as 0-30% - Low, 30-60% - Moderate and 60% and above – High.

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) = $i h^2 b \sigma^2_p$

where, *i* = Intensity of selection, $h^2 b$ = Heritability in broad sense, σ^2_p = Phenotypic standard deviation. The value of *i* was taken as 2.06 assuming 5 percent selection intensity.

Genetic Advance over Mean (GAM)

Genetic advance over mean was estimated using the following formula.

$$\text{GAM} = \frac{\text{GA}}{\text{Mean}} \times 100$$

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) [13] as 0- 10% - Low, 10-20% - Moderate and 20% and above – High.

Results and Discussion

Range of variation

The genetic variability assessment studies in F₂ population indicated high mean and wider range for most of the traits studied under rainfed condition suggesting the existence of sufficient genetic variability in the populations (Table 1). However, difference between the two segregating populations for most of the characters under study suggests the influence of environmental factors like water stress on yield, yield parameters as well as on physiological characters.

Critical examination of range values exhibited some important and meaningful information. The range value of 12-88 and 23-88 recorded for the trait number of grains per spike is the highest among all the traits in both the F₂ populations viz., GW 322 X UASBW 11949 and NI 5439 X UASBW 11949 respectively. Similarly, thousand grain weight which contributes for yield recorded high mean value and wide range in both the populations. High range was also observed for grain yield per plant compared to parental genotypes in both the populations. With respect to plant height range values of 46-91 cm and 49-91 cm would give breeder to select the segregants with desired plant height. For physiological traits like relative water content and membrane stability index also higher range of variation and mean was recorded.

Genetic variability

Genotypic and phenotypic coefficients of variation are indicators of the variability that exists in a given population. Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability (h²b) and genetic advance as per cent of mean (GAM) of the characters studied are presented in Table 1. In general, the PCV values were greater than GCV values although the differences were small in most of the characters studied.

Higher GCV and PCV values were observed for the traits viz., number of productive tillers per plant and grain yield per plant while, high PCV and moderate GCV for thousand grain weight and number of grains per spike indicating that there is high phenotypic and genotypic variation for these traits in both the crosses. 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 Abinasa *et al.*, 2011 [1].

For the trait leaf waxiness, high PCV and GCV and moderate GCV and high PCV was recorded in F₂ populations of the cross GW 322 x UASBW 11949 and NI 5439 x UASBW 11949 respectively while, moderate PCV and GCV was noticed for the physiological traits viz., relative water content and membrane stability index and leaf waxiness in segregating populations of the cross NI 5439 x UASBW 11949 indicating that presence of high variability and ample scope for selecting superior segregants for drought tolerance in later segregating generations of the population.

Moderate to low GCV and PCV recorded for days to 50 per cent flowering, days to maturity, plant height, number of spikelets per plant, number of grains per spike, chlorophyll content at grain filling stage, NDVI at booting, anthesis and grain filling stage, relative water content and membrane stability index suggested that selection in early segregating population may not be effective. These various results of moderate PCV and GCV are in accordance with the findings

of Ajmal *et al.*, 2009 [3] and Subhashchandra *et al.*, 2009 [24] whereas of High PCV and GCV with Manal, 2009 [15], Kahrizi *et al.*, 2010 [14], Bharat *et al.*, 2013 [7] and Arpitha *et al.*, 2017 [5] and 2016 [26].

Heritability and Genetic Advance

Heritability is very significant parameter for the selection in any population improvement method. Single plant selection in the early segregating generations may be much effective for a trait that is highly heritable as compared to character which has low less heritability.

The high estimates of heritability were recorded for grain yield per plant (85.86%) and yield contributing traits like number of productive tiller per plant (77.30%), plant height (79.65%), number of grains per spike (67.34%) and thousand grain weight (62.77%) as well as for physiological traits viz., relative water content (60.66%), NDVI at anthesis stage (61.11%) and canopy temperature at booting stage (76.25%) and anthesis stage (64.61%) in the segregating population of the cross GW 322 x UASBW 11949 while, in the F₂ population of the cross NI 5439 x UASBW 11949 high heritability was recorded for grain yield per plant (94.35%), number of grains per spike (77.93%), number of productive tillers per plant (84.23%) and relative water content (61.60%). 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 as well as for physiological traits under rainfed condition.

Many authors reported high heritability along with high to moderate genetic advance for grain yield in wheat (Singh *et al.*, 2006) [23], Ahmed and Kaliq [2], 2007, Rahman, 2009 [19], Deepak, 2016 [9], Swathykrishna 2018 [25] and Veerasha, 2016 [26]. The heritability of the most important trait *i.e.* grain yield per plant was rather high (above 80%) clearly indicates higher influence of genetic factors than the environment on the expression of this trait. The finding of present study is in agreement with the findings of Rehaman *et al.*, 2016 [18]. Hence, selection for grain yield and yield related traits like number of productive tiller per plant, thousand grain weight along with physiological traits viz., relative water content, membrane stability index and leaf waxiness is suggested to improve the yield under rainfed condition.

Further heritability estimates coupled with genetic advance are normally more useful in predicting the genetic gain under selection than heritability estimates alone (Johnson *et al.* 1955) [13]. High heritability coupled with high genetic advance as percent of mean was recorded for number of productive tillers per plant, number of grains per spike and grain yield per plant. Similar results were also reported by Asif *et al.*, 2010 [6]. High heritability coupled with moderate genetic advance over mean was noticed for thousand grain weight in segregating population of the cross GW 322 x UASBW 11949.

Moderate heritability coupled with low genetic advance as percent of mean observed for number of spikelets per spike, plant height, days to maturity, membrane stability index, NDVI at anthesis and grain filling stage, chlorophyll content at anthesis and grain filling stage. The results of the study are in accordance with reports of Said (2014) [21] indicating presence of non-additive gene action.

Table 1: Estimates of Genetic variability parameters for morpho-physiological traits in F₂ populations of GW 322 x UASBW 11949 and NI 5439 x UASBW 11949 under rainfed condition.

Characters	GW 322 x UASBW 11949							NI 5439 x UASBW 11949						
	Range			PCV (%)	GCV (%)	h ² (BS)	GAM (%)	Range			PCV (%)	GCV (%)	h ² (BS)	GAM (%)
Mean	Min	Max	Mean					Min	Max					
Chlorophyll content at booting stage	49.18	38.60	59.60	7.98	4.38	30.17	4.96	51.25	40.60	58.60	8.84	4.09	21.44	3.90
Chlorophyll content at anthesis stage	51.47	36.30	58.60	8.26	4.96	36.03	6.13	51.10	42.00	59.40	7.86	4.40	31.35	5.08
Chlorophyll content at grain filling stage	36.82	30.20	49.40	10.98	6.43	34.34	7.77	36.02	30.20	45.10	10.70	5.99	31.36	6.91
Canopy temperature at booting stage	24.80	21.30	30.20	15.33	12.52	76.25	22.52	25.73	21.30	32.73	5.62	2.77	24.27	2.81
Canopy temperature at anthesis stage	26.14	22.80	29.50	11.08	8.90	64.61	14.74	26.80	23.30	37.10	22.00	17.29	41.76	27.99
Canopy temperature content at grain filling stage	28.80	25.40	32.10	7.40	5.48	54.88	8.37	30.68	27.30	35.70	8.28	5.19	39.31	6.70
NDVI at booting stage	0.56	0.48	0.59	10.59	8.06	57.86	12.62	0.53	0.38	0.63	10.45	6.90	34.27	7.38
NDVI at anthesis stage	0.54	0.51	0.57	13.23	9.58	61.11	10.52	0.54	0.49	0.62	10.39	6.78	42.57	9.11
NDVI at grain filling stage	0.36	0.29	0.40	13.11	8.99	46.95	12.68	0.39	0.31	0.48	12.09	6.02	24.82	6.18
Relative water content	65.01	42.50	74.70	12.45	9.70	60.66	15.56	66.28	43.80	71.60	16.98	10.27	61.60	12.80
Membrane stability index	54.34	38.10	65.31	15.82	6.20	41.32	4.30	63.81	40.20	78.50	18.76	14.66	56.07	13.59
Leaf waxyness	6.03	2.00	10.00	23.50	20.91	59.77	18.28	5.39	1.00	9.00	21.38	11.89	30.92	13.61
Days to 50% flowering	51.80	48.00	60.00	6.07	5.41	58.50	7.37	53.70	46.00	61.00	9.40	7.64	19.91	4.27
Days to maturity	90.19	82.00	99.00	5.41	2.72	33.53	3.24	93.10	81.00	107.00	4.34	2.49	32.96	6.95
Plant height	70.15	46.00	91.00	10.75	9.60	79.65	17.64	80.25	49.00	91.00	10.40	6.98	45.06	9.65
Number of productive tiller per plant	8.75	3.00	24.00	40.53	34.52	77.30	66.14	14.20	4.00	25.00	45.97	42.19	84.23	79.76
Spike length	9.33	6.00	13.50	13.74	5.55	16.34	4.62	9.64	7.00	13.00	13.58	6.52	23.01	6.44
Number of spikelets per spike	16.32	6.00	20.00	12.17	6.94	32.49	8.14	17.80	11.00	23.00	14.06	9.46	6.06	1.75
Number of grains per spike	49.19	12.00	88.00	21.93	17.99	67.34	30.41	54.50	23.00	88.00	22.60	19.95	77.93	36.21
Thousand grain weight	32.22	10.85	48.30	20.69	16.40	62.77	26.76	28.30	10.00	45.20	15.34	11.63	57.52	18.177
Grain yield	11.42	1.25	41.20	50.00	46.33	85.86	88.43	14.60	2.40	42.40	55.87	54.26	94.35	108.58

Conclusion

Both segregating populations of the cross GW 322 X UASBW 11949 and NI 5439 X UASBW 11949 may be regarded as potential source populations for some of important yield component traits like, number of productive tiller per plant, number of grains per spike, thousand grain weight and grain yield per plant as well as for physiological traits viz., relative water content, leaf waxyness, membrane stability index, NDVI at grain filling stage under rainfed condition as the study revealed presence of substantial genetic variability for yield, its component traits as well as physiological traits. Hence, these characters shall be taken into account while selecting superior and desirable plants for further improvement of yield parameters and drought tolerance in developing high yielding genotype for rainfed condition in wheat. Further, selective inter population mating involving these populations might increase variation for yield providing better scope for enhancing genetic gain under rainfed condition.

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