



ANALYSIS OF GENETIC VARIABILITY PARAMETERS FOR MORPHO-PHYSIOLOGICAL, YIELD AND QUALITY TRAITS UNDER HEAT STRESS CONDITION IN BREAD WHEAT

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Abstract- A field experiment was conducted to study the genetic variability parameters, heritability and expected genetic advance for morpho-physiological, yield and quality traits in bread wheat under late sown irrigated condition in hundred bread wheat genotypes. The analysis of variance for all the morpho-physiological, yield and yield contributing and quality characters revealed highly significant differences except for chlorophyll content reading at anthesis indicate the presence of substantial genetic variation among the genotypes for all the traits. The variability among different genotypes varied highly for all the characters under study. The magnitude of range for Chlorophyll content reading at anthesis was ranged from 45.10 to 55.93 with the mean value of 50.34, canopy temperature at anthesis from 22.48 to 28.75 with the mean value 26.18, days to heading from 47.50 to 74.50 with the mean value of 58.75, thousand grain weight from 11.80 to 47.80 with the mean value of 33.74, protein content ranged from 13.90 to 20.25 with the mean value of 17.25 and sedimentation value varied from 42.50 to 83.00 with the mean value of 60.53. The high PCV and GCV values were recorded for traits like flag leaf width, relative water content, leaf waxiness, number of productive tillers per meter and grain yield, which indicates that, these characters have high variability that in turn offers good scope for selection. The high heritability estimates along with high genetic advance was obtained for flag leaf length, flag leaf width, flag leaf area, relative water content, leaf waxiness, days to fifty percent flowering, plant height, spike length, number of productive tillers per meter, number grains per spike, thousand grain weight, grain yield and sedimentation value. These traits are the most important to be taken into consideration for effective selection in wheat.

Keywords- Genetic variability, Heritability, Genetic advance, Morpho-physiological and quality traits and Grain yield.

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Introduction

Wheat (*Triticum aestivum* L.) is an important cereal food crop for people all over the world, with commanding position in Indian Agriculture. It occupies 28 percent area under cereals and contributing 33 percent of the total food grain production in India [1]. Use of varieties with better yield potential and wide range of adaptability is of prime importance for increasing wheat production. High temperature during floral initiation and spikelets development reduced the potential number of grains. Heat and drought are the most important abiotic stresses, which affect the crop physiological traits. Thus, the yield of wheat is limited under heat stress conditions [2]. Heat stress during the post-anthesis, grain filling stage affects availability and translocation of photosynthates to the developing kernel, starch synthesis and deposition within the kernel, thus resulting in lower grain weight and altered grain quality [3]. The traits like thousand grain weight and grain yield itself are also highly responsive to heat tolerance and acceptable spike fertility, higher spike number, grains per spike, early ground cover etc. to be associated with yield under heat stress and tolerance. In recent years, researchers shown that some physiological criteria such as canopy temperature depression [4] and chlorophyll content [5] used as effective screening criteria in wheat. However, yield and yield components are still been used as most effective screening criteria in wheat under heat stressed conditions [6]. Wheat quality becomes a major target in wheat breeding program. Hence, wheat breeder is not only needed to increase grain yield but also to improve the grain quality for end products to meet the consumer requirement. The development of high yielding wheat cultivars with better and acceptable quality has always been a major focus in wheat breeding [7]. Generating information about the genetic variability, relationships and mechanisms of inheritance of the genetic traits involved is the key task in genetic

improvement of any crop plant. Variability is essential for wide adaptability and resistance to biotic and abiotic factors and hence, an insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. The knowledge of heritability helps the plant breeder in predicting the behaviour of the succeeding generation and making desirable selections. Genetic advance indicates the magnitude of the expected genetic gain from one cycle of selection and it is an important selection parameter that aids breeder in a selection program [8]. The level of genetic coefficient of variation, heritability and genetic advance were estimated to develop appropriate selection indices for the increased grain production with better quality. Thus, the objective of the present study was to identify suitable wheat genotypes for growing in late sown irrigated condition in bread wheat. To identify such genotypes, study on genetic variability of yield contributing characters and their transmissibility into the progeny is essential [9]. Keeping this in view, a field experiment was conducted to assess the genetic variation present in the genotypes for morpho-physiological, yield and yield contributing and quality characters under late sown irrigated condition.

Materials and Methods

The present experiment was conducted to assess the genetic variability parameters bread wheat genotypes late sown irrigated condition. One hundred bread wheat genotypes were sown in 10 x10 Simple Lattice Design with two replications during *rabi* 2014-2015 at All India Coordinated Wheat Improvement Project, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad. The plot/block dimension was four rows of 2.0m length with 0.20m row

spacing. The crop was raised with all the recommended package of practices Data were recorded on five randomly selected plants for morpho-physiological traits, viz., chlorophyll content before anthesis (SPAD-1), chlorophyll content at anthesis (SPAD-2), chlorophyll content after anthesis (SPAD-3), leaf vegetation before anthesis (NDVI-1), leaf vegetation at anthesis (NDVI-2), leaf vegetation after anthesis (NDVI-3), canopy temperature before anthesis (CT-1), canopy temperature at anthesis (CT-2), canopy temperature after anthesis (CT-3), flag leaf length (cm), flag leaf width (cm), flag leaf area (cm²), relative water content (%), leaf waxyness, days to fifty percent flowering, plant height (cm), spike length (cm), number of productive tillers per meter, number spikelets per spike, number grains per spike, thousand grain weight (g), grain yield (kg/ha) and quality traits viz., protein content (%) and sedimentation value (cm). The yield was recorded by harvesting four rows of one meter length. The data obtained were subjected to the biometrical analysis that included analysis of variance and genetic variability parameters. Genotypic

coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), broad sense heritability (h² (bs) %) and genetic advance as percent mean (GAM) were estimated by the formula suggested by [10]. The estimate of GCV and PCV were classified as low, medium and high [11]. The heritability was categorized as suggested by [12] and genetic advance was classified by adopting the method of [13].

Results and Discussion

The analysis of variance for all the morpho-physiological, yield and yield contributing and quality characters revealed highly significant differences except for Chlorophyll content reading at anthesis [Table-1]. This indicates presence of substantial genetic variation among the genotypes for all the traits. These result implied that this population of wheat genotypes would respond positively to selection. The present findings are in accordance with the earlier reports of [14,15].

Table-1 Analysis of variance for simple lattice design under heat stress (late sown irrigated) condition in bread wheat genotypes

Source of Variance	DF	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
Replications	1	52.224	35.617	0.050	0.010	0.000	0.000	7.334	19.189	0.041	0.078	0.005	0.226	26.209	0.080
Treatments (unadj)	99	12.080**	9.804	34.380**	0.004**	0.004**	0.005**	3.839**	4.199**	1.649**	9.560**	0.077**	27.958**	347.260**	5.639**
Block in rep (adj)	18	3.934	9.815	3.097	0.002	0.002	0.001	4.003	1.877	1.126	0.114	0.003	0.404	0.362	0.012
Error (Intra block)	81	3.518	7.516	3.159	0.002	0.003	0.003	1.849	1.624	1.436	0.115	0.002	0.399	0.461	0.070

contd...

Source of Variance	DF	X15	X16	X17	X18	X19	X20	X21	X22	X23	X24	X25
Replications	1	36.125	100.820	37.810	0.719	1.445	23.018	1.696	0.008	18769.531	0.423	18.000
Treatments (unadj)	99	117.631**	109.490**	104.930**	3.179**	527.622**	9.495**	94.982**	91.989**	1273780.769**	3.513**	192.574**
Block in rep (adj)	18	0.057	0.210	0.605	0.026	20.714	0.219	1.050	0.534	18449.002	0.056	0.150
Error (Intra block)	81	0.214	0.462	0.900	0.034	14.280	2.991	6.540	2.964	26630.112	0.131	0.251

X1 = Chlorophyll content before anthesis (SPAD-1), X2 = Chlorophyll content at anthesis (SPAD-2), X3 = Chlorophyll content after anthesis (SPAD-3), X4 = Leaf vegetation before anthesis (NDVI-1), X5 = Leaf vegetation at anthesis (NDVI-2), X6 = Leaf vegetation after anthesis (NDVI-3), X7 = Canopy temperature before anthesis (°C), X8 = Canopy temperature at anthesis (°C), X9 = Canopy temperature after anthesis (°C), X10 = Flag leaf length (cm), X11 = Flag leaf width (cm), X12 = Flag leaf area (cm²), X13 = Relative water content (%), X14 = Leaf Waxyness, X15 = Days to fifty percent flowering, X16 = Days to maturity, X17 = Plant height (cm), X18 = Spike length (cm), X19 = Number of productive tillers per meter, X20 = Number spikelets per spike, X21 = Number grains per spike, X22 = Thousand grain weight (g), X23 = Grain yield (kg/ha), X24 = Protein content (%), X25 = Sedimentation value (cm)

Variability measured in terms of range, mean, PCV and GCV, heritability in broad sense and genetic advance as per cent of mean have been presented in [Table-2]. The values for range among different genotypes varied highly for all the characters under study. The magnitude of range for chlorophyll content at anthesis was ranged from 45.10 to 55.93 with the mean value of 50.34, leaf vegetation before anthesis from 0.41 to 0.71 with the mean value 0.61, canopy temperature at anthesis from 22.48 to 28.75 with the mean value 26.18, days to heading from 47.50 to 74.50 with the mean value of 58.75, number of grains per spike from 23.65 to 56.80 with the mean value of 42.22, thousand grain weight from 11.80 to 47.80 with the mean value of 33.74. Variability of protein content ranged from 13.90 to 20.25 with the mean value of 17.25 and sedimentation value varied from 42.50 to 83.00 with the mean value of 60.53. Thus, these results indicate the presence of wide range of genetic variability in the material. Similar observations were made by [16]. Generally, the magnitude of phenotypic coefficient variation was higher than the corresponding genotypic coefficient variation as noted by [17] and [14]. The highest values for GCV and PCV were recorded for the character leaf waxyness and grain yield. A less difference between GCV and PCV values for almost all the characters revealed less influence of the environment on expression of the characters [14] and [18]. The high PCV and GCV values were recorded for traits like flag leaf width, relative water content, leaf waxyness, number of productive tillers per meter and grain yield which indicates that, these characters have high variability that in turn offers good scope for selection, whereas thousand grain weight has shown high PCV with medium GCV value. The traits like leaf vegetation before anthesis, leaf vegetation after anthesis, flag leaf length, days to fifty percent flowering, plant height, spike length, number spikelets per spike, number grains per spike and sedimentation value had medium PCV and GCV values. The low GCV and PCV were recorded for rest of the traits

along with protein content, indicating difficulty in the improvement of these traits through selection. The results are in accordance with [19] and [20]. Estimates of heritability and genetic advance are critical for predicting genetic improvement for any quantitative trait [21]. Heritability estimates indicate effectiveness of selection for phenotypic performance of particular character. The high heritability estimates along with high genetic advance is more useful for the selection [13]. In the present study high heritability along with high genetic advance was obtained for flag leaf length, flag leaf width, flag leaf area, relative water content, leaf waxyness, days to fifty percent flowering, plant height, spike length, number of productive tillers per meter, number grains per spike, thousand grain weight, grain yield and sedimentation value. The selection pressure can be applied in the desired direction on the basis of phenotype to improve these characters. These traits are the most important quantitative traits to be taken into consideration for effective selection in wheat. Similar results have been reported by [14,19,20,22-24].

Conclusion

From the present study, it is evident that material under study could be good source for further breeding program. The information on the genetic parameters can help the breeder to evolve cultivars suitable to particular growing condition. The knowledge on heritability is helpful to decide the selection procedure to be followed to improve the trait. Hence, it is concluded that traits like flag leaf length, flag leaf width, flag leaf area, relative water content, leaf waxyness, plant height, spike length, number of productive tillers per meter, number grains per spike, thousand kernel weight, sedimentation value and grain yield can be considered as suitable selection criteria for the development of high yielding bread wheat varieties with better quality that suited to late sown irrigated condition.

Table-2 Estimation of genetic variability parameters under heat stress (late sown irrigated) condition in bread wheat genotypes

Sl. No.	Genetic Parameters	Mean	Range		PCV %	GCV %	h ² (bs)	GAM
			Min	Max				
1	Chlorophyll content before anthesis (SPAD-1)	45.42	40.35	50.48	6.16	4.54	0.54	6.88
2	Chlorophyll content at anthesis (SPAD-2)	50.34	45.10	55.93	5.92	1.92	0.11	1.29
3	Chlorophyll content after anthesis (SPAD-3)	44.87	31.20	56.63	9.65	8.81	0.83	16.55
4	Leaf vegetation before anthesis (NDVI-1)	0.52	0.41	0.62	10.29	5.88	0.33	6.93
5	Leaf vegetation at anthesis (NDVI-2)	0.61	0.47	0.71	9.51	4.91	0.27	5.21
6	Leaf vegetation after anthesis (NDVI-3)	0.45	0.30	0.60	13.46	8.10	0.36	10.04
7	Canopy temperature before anthesis (°C)	23.98	20.65	26.60	7.27	3.73	0.26	3.94
8	Canopy temperature at anthesis (°C)	26.18	22.48	28.75	6.54	4.30	0.43	5.81
9	Canopy temperature after anthesis (°C)	29.09	26.88	31.25	4.23	1.26	0.09	0.78
10	Flag leaf length (cm)	18.28	13.26	23.64	12.03	11.89	0.98	24.19
11	Flag leaf width (cm)	0.81	0.43	1.32	24.47	23.90	0.95	48.10
12	Flag leaf area (cm ²)	11.16	5.48	21.49	33.74	33.26	0.97	67.54
13	Relative water content (%)	62.08	33.43	98.06	21.24	21.21	0.99	43.64
14	Leaf Waxyness	3.17	0.00	7.00	53.25	52.69	0.98	107.39
15	Days to fifty percent flowering	58.75	47.50	74.50	13.07	13.05	0.99	26.83
16	Days to maturity	100.05	89.00	115.00	7.41	7.38	0.99	15.15
17	Plant height (cm)	65.54	49.84	84.97	11.10	11.01	0.98	22.49
18	Spike length (cm)	9.21	6.41	12.37	13.77	13.63	0.98	27.78
19	Number of productive tillers per meter	75.80	42.00	109.00	21.74	21.11	0.94	42.24
20	Number spikelets per spike	16.75	12.23	20.75	14.61	11.18	0.59	17.61
21	Number grains per spike	42.22	23.65	56.80	16.79	15.84	0.89	30.78
22	Thousand grain weight (g)	33.74	11.80	47.80	20.37	19.82	0.95	39.73
23	Grain yield (kg/ha)	1931.31	575.00	3987.50	41.73	40.91	0.96	82.63
24	Protein content (%)	17.25	13.90	20.25	7.81	7.55	0.94	15.05
25	Sedimentation value (cm)	60.53	42.50	83.00	16.22	16.20	0.99	33.34

PCV: phenotypic coefficient of variation; GCV: Genotypic coefficient of variation; h² (bs): heritability in broad sense; GA: genetic advance; GAM: genetic advance as percent of mean

Conflict of Interest: None declared

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