STUDY ON SELECTION PARAMETERS AND INTER-ASSOCIATIONS OF YIELD, AGRONOMIC TRAITS AND CANOPY TEMPERATURE IN RELATION TO DROUGHT TOLERANCE IN WHEAT

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ABSTRACT
Twenty genotypes of wheat revealed highly significant differences for all the characters studied, indicating the presence of substantial genetic variability in the material screened under drought condition. The phenotypic and genotypic coefficient of variation (PCV and GCV) was moderate for grain yield, spike length, thousand grain weight, grain weight per spike, number of spikelets per spike and number of tillers per meter. High heritability along with high genetic advance as percent of mean was observed for grain yield, spike length, number of spikelets per spike and thousand grain weight might ultimately be considered as a tool for effective selection of drought tolerant genotypes. Results also revealed strong positive genotypic associations for grain yield with number of tillers per meter (0.951), whereas moderate to low association with grain weight per spike (0.220) and plant height (0.196) was observed. Under drought stress condition canopy temperature (-0.271) correlated negatively with grain yield also suggested the importance of cooler genotypes for drought stress condition. The interrelationship among these traits studied revealed that grain yield could be efficiently improved by obtaining maximum expression of tillers per meter followed by plant height, grain weight per spike and lower canopy temperature under drought conditions.

INTRODUCTION

Wheat (*T. aestivum*) is the second most important staple food crop of the world after rice and is one of the leading cereals of many countries of the world including India. Drought (water deficits) stress is the prime abiotic limitation, under the current and climate change scenario in future. Drought stress is one of the consequences of climate change that has a negative impact on crop growth and yield especially when occurred at reproductive stage causing considerable yield losses. As countries across the world work to contain and combat the novel corona virus (COVID-19) outbreak, U.S. Wheat Associates (USW) closely monitoring the effects of the outbreak on global wheat trade dynamics. Over the past several weeks, several major wheat exporters have implemented measures to curb 2019/20 wheat exports to stabilize domestic prices amidst greater demand uncertain spurring upward price movement across the world. (US wheat associates wheat letter April 2020). Monsoon rains provide 80% annual precipitation in India, and when this is reduced, water deficit becomes a significant problem. Moreover, it is well known that the ground water table in India is declining day by day. According to the IPCC (2014) report, the decline in food productivity and quality, primarily due to extreme temperatures and water deficit conditions, poses a serious threat to agriculture (IPCC, 2014; Zandalinas et al., 2018). Water shortage is reported to cause 17% to 70% yield losses. Wheat yield reduced to 50% to 90% of its irrigated potential in developing countries due to

water deficit (Ali *et al*. 2013). Tillering is a very important stage at which the plant develops tillers, primodia of spike, spikelets, and florets in the wheat plant. Canopy temperature measurements have been widely used in recent years to study genotypic response to drought. The canopy temperature of wheat is directly related to its water status (Cohen *et al*., 2015). Result from several recent studies show that canopy temperature under well-watered conditions also provides an indication of potential yield performance during drought and could effectively is used as a technique to assess genotypic response to drought.

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. The knowledge of heritability helps the plant breeder in predicting the behavior of the succeeding generation and making desirable selections. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program.

The present investigation with twenty wheat genotypes was conducted with a objective to estimate the level of genetic coefficient of variation, heritability and genetic advance, and to get information on the correlation of yield components with grain yield for the purpose to ascertain and develop appropriate selection indices for the increased grain production under drought conditions.

MATERIALS AND METHODS

Twenty bread wheat genotypes, from diverse origins were chosen based on their broad range of response to drought stress and yield performance and were planted in Randomized Complete Block design (RCBD) with two replications during Rabi season 2018-19 at Wheat Research Station, Vijapur under drought stress condition in which only pre sowing irrigation was applied and crop was left until maturity. Each genotype was sown in six rows of 2.50 meter length and 20 cm apart, with seed rate of 120 kg/ha. Grain yield was recorded excluding two border rows to avoid the shading effects of taller genotypes on dwarf genotypes. Weeds were controlled manually. Planting was done by hand drilling in November-2018. Standard agronomic package of practices recommended for rainfed wheat was followed to raise the good crop. During the crop season no rainfall was received so experiment was conducted in truly drought condition. Agro-metereological data was recorded at the Wheat Research Station., Vijapur during the crop period. (Fig 1). Five plants were selected randomly from each genotype per replication for recording agronomic data and observation on days to maturity and canopy temperature was recorded on plot basis. Averages of the data from each replication in respect of different characters were used for various statistical analyses.

Statistical analysis

Analysis of variance (ANOVA) estimated according to Panse and Sukhatme (1967). Genotypic and phenotypic coefficients of variation were estimated by the formula suggested by Burton and De Vane (1953) for each character.

Genotypic coefficient of variation (GCV):

$$GCV(\%) = \frac{\sqrt{\sigma^2 g}}{\overline{X}} X100$$

Phenotypic coefficient of variation (PCV)

$$PCV(\%) = \frac{\sqrt{\sigma^2 p}}{\overline{x}} x100$$

Where,

$\sigma^2 P, \sigma^2 G$ = Phenotypic and genotypic variance, respectively and

$\overline{x}$ = Mean value of character.

Phenotypic Coefficient of Variation (PCV) and genotypic coefficient of variation (GCV) were classified as suggested by Sivasubramanian and Madhavamenon (1973) as follows:

< 10 %   =   Low
10 - 20 %   =   Moderate
> 20 %   =   High

Heritability (Broad sense)

It is the proportion of phenotypic variability that is due to

genetic reasons. It was computed in per cent using the formula given by Allard (1960).

$$h^2{}_{(b)}(\%) = \frac{\sigma^2 g}{\sigma^2 p} X100$$

Where,

$h^2{}_{(b)}$ = Heritability (broad sense),

$\sigma^2 g$ = Genotypic variance, and

$\sigma^2 p$ = Phenotypic variance.

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949).

< 30 %   =   Low
30 - 60 %   =   Moderate
> 60 %   =   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) = I h² σp

Where,

i   = Intensity of selection
h²   = Heritability in broadsense
σp   = Phenotypic standard deviation

The value of i was taken as 2.06 assuming 5 per cent selection intensity.

Genetic Advance over Mean (GAM)

The genetic advance expressed as per cent of mean was estimated as under.

$$GA(\%\text{of mean})\frac{GA}{\overline{X}} X100$$

Where,

GA = Expected genetic advance, and

$\overline{X}$ = Mean value of the character

The genetic advance as per cent was categorized as demonstrated by Johnson et al. (1955).

< 10 %   =   Low
10 - 20 %   =   Moderate
> 20 %   =   High

Genotypic coefficient of correlation (rg) and phenotypic coefficient of correlation (rp) were computed as per Robinson *et al.* (1951) and tested for statistical significance against the correlation table values at 5 and 1% levels of significance (Fischer and Yates, 1963).

Measurement of Canopy Temperature: Canopy temperature was measured with an infrared thermometer (Model THI-500, TASCO, Japan) in cleared sunshine hours. The thermometer was held so that the sensor viewed only the canopy at an oblique angle above the horizontal; this position gave an elliptical canopy target as per suggested by O'Toole and Real (1984) and prevented the thermometer from sensing the soil surface when the leaves were rolled. All canopy temperature measurements were made five places in a plot and in a south

facing direction to minimize sun angle effects as suggested by Turner et al. (1986).

RESULTS AND DISCUSSION

The analysis of variance for different characters is presented in Table 1. The results showed highly significant difference for most of the traits under investigation among twenty genotypes. This suggested that there is an inherent genetic difference among the genotypes studied.

Phenotypic and Genotypic Coefficient of Variation

The estimates of genetic variability parameters for all the traits were worked out and are presented in Table-2. It was evident from the result that the phenotypic variance was greater than genotypic variance indicating the influence of environment on the expression of the trait. Among the yield attributes maximum PCV and GCV was depicted by grain yield (19.38 and 17.30) followed by Spike length (16.57 and 15.40), thousand grain weight (16.15 and 14.29), grain weight per spike (18.82 and 13.78), number of spikelets per spike (16.57 and 13.13) and number of tillers per meter (21.21 and 13.29), respectively. The high values of PCV and GCV indicating direct selection may be rewarding on improvement of these traits. The lowest and close affinity between values for PCV and GCV was depicted by days to maturity (4.33 and 4.23), canopy

Table 1: Analysis of variance for yield and its contributing traits of 20 genotypes of bread wheat under drought condition.

Source of Variance	df	G Y	DM	TIl/M	SL	PH	SPKL/SPK	GW/SPK	TGW	CT
Replication	1	3660250	16.9	846.4	0.992	497.025	0.9	0.006	35.532	1.806
Genotype	19	621312.5**	39.978**	495.626*	4.559*	145.457**	9.236*	0.225**	87.456**	7.850**
Error	19	70381.58	0.9	215.93	0.33	35.46	0.69	0.07	10.65	2.56

*, ** significant at 5 and 1 per cent respectively;GY = Grain yield , DM = Days to maturity, TIL/M = Number of tillers per meter, SL = Spike length, PH = Plant height, SPKL/SPK = Number of spikelets per spike, GW/SPK = Grain weight per spike, TGW = Thousand grain weight, CT = Canopy temperature

Table 2: Estimates of genetic parameters for various traits of 20 bread wheat genotypes under drought condition

Characters	Range	Mean	GCV (%)	PCV (%)	$H^2_{(b)}$	GA	GAM (%)
GY (Kg/ha)	1625-4050	3036.25	17.3	19.38	79.68	964.98	31.81
DM (days)	99.5-116.0	104.4	4.23	4.33	95.6	8.9	8.52
Til/M	57.0-115.5	88.95	13.29	21.21	39.31	15.28	17.17
SL (cm)	6.90-11.55	9.44	15.4	16.57	86.35	2.78	29.47
PH (cm)	58.5-89.2	73.9	10.03	12.86	60.8	11.92	16.11
SPKL/SPK	12.0-20.0	15.7	13.13	14.14	86.11	3.95	25.08
GW/SPK (g.)	1.60-3.00	2.03	13.78	18.82	53.66	0.42	20.8
TGW (g.)	32.5-56.6	43.4	14.29	16.15	78.29	11.29	26.05
CT- (ºC)	22.7-29.8	26.3	6.19	8.68	50.8	2.39	9.08

$H^2_{(b)}$ = Broad sense heritability; GCV = Coefficient of genotypic variance;PCV = coefficient of phenotypic variance; GA = genetic advance.GAM = Genetic advance as per cent of mean

Table 3: Genotypic correlation for yield and its attributes among 20 genotypes of bread wheat under drought condition

Characters	G Y	DM	Til/M	SL	PH	SPKL/SPK	GW/SPK	TGW	CT
G Y	1								
DM	-0.365	1							
TIl/M	0.951**	-0.445*	1						
SL	-0.045	0.486*	-0.247	1					
PH	0.196	0.122	-0.028	0.406	1				
SPKL/SPK	-0.454*	0.581**	-0.914**	0.678**	0.144	1			
GW/SPK	0.22	0.233	0.449*	0.518*	0.536*	0.11	1		
TGW	0.092	-0.646**	0.239	-0.525*	0.175	-0.592**	0.212	1	
CT	-0.271	0.846**	-0.566**	0.711**	-0.059	0.714**	0.224	-0.763**	1

*, ** significant at 5 and 1 per cent respectively.

Table 4: Phenotypic correlation for yield and its attributes traits among 20 genotypes of bread wheat under drought condition

Characters	G Y	DM	Til/M	SL	PH	SPKL/SPK	GW/SPK	TGW	CT
G Y	1								
DM	-0.33	1							
Til/M	0.308	-0.26	1						
SL	-0.063	0.445*	-0.091	1					
PH	0.128	0.094	0.129	0.436	1				
SPKL/SPK	-0.428	0.559*	-0.443	0.613**	0.174	1			
GW/SPK	0.136	0.172	0.261	0.466*	0.486*	0.068	1		
TGW	-0.014	-0.544*	0.189	-0.385	0.179	-0.480*	0.315	1	
CT	-0.253	0.549*	-0.199	0.482*	-0.086	0.474*	0.076	-0.521*	1

*, ** significant at 5 and 1 per cent respectively.
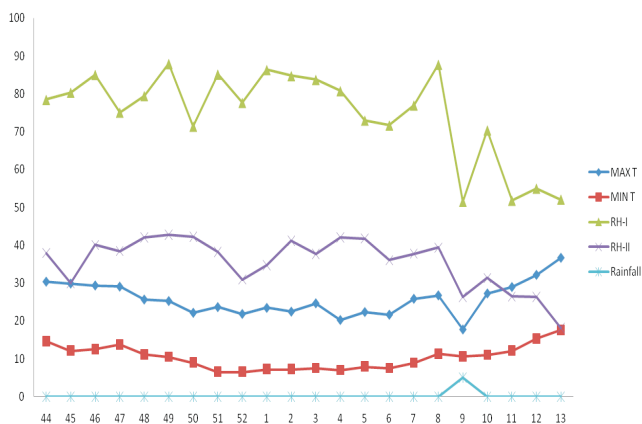
Figure 1: Weather Data recorded during Rabi 2018-19

temperature (8.68 and 6.19) and plant height (12.86 and 10.03) indicating less scope of selection as they are under less influence of environment. Wide difference between PCV and GCV was observed for number of tillers per meters and grain weight per spike which may indicate the high contribution of environmental variance to the phenotypic variance. Results of the present study concur with that of Yadawad *et al.*, (2015), Nishant *et al.* (2018), Tambe *et al.* (2013) and Tripathi *et al.* (2015).

Heritability (broad sense) and Genetic Advance

The present study of heritability reflects that the characters are highly heritable ranged from days to maturity (95.60 %) to number of tillers per meter (39.31%) and are presented in Table-2. The high estimate for heritability indicates that most of the variation is caused by genotype and very small due to environment, therefore, a simple selection procedure would be helpful in improvement of these traits.

Estimates of heritability are more advantageous when expressed in terms of genetic advance for improvement of the traits. It might be assigned to additive gene effect governing their inheritance. In the present study grain yield (79.68 % and 31.81%), spike length (86.35% and 29.47%), number of spikelets per spike (86.11% and 25.08%) and thousand grain weight (78.29% and 26.05%) showed high heritability coupled with high genetic advance as percent of mean indicating that these traits are controlled by additive gene action and direct selection of superior genotype may be effective for these traits. Similar findings of high heritability for yield related traits like spike length, thousand grain weight and grain yield have been reported by Binod Kumar *et al.* (2013), Mishra *et al.* (2019) and Salman S. (2014). Similarly, other traits with high or low heritability had low genetic advance as percent mean, like days to maturity and canopy temperature, portrayed a high or low heritability value but a very low genetic gain and was controlled by non-additive gene action suggesting expression of this trait might be influenced by non-genetic factors. These findings were in agreement with findings of Binod Kumar *et al.* (2013) and Yadawad *et al.* (2015) for different traits.

Correlation

In present study, the phenotypic and genotypic correlation coefficients among nine characters have been worked out and are presented in Table-3 and 4. The results on genotypic

and phenotypic correlation coefficients revealed that the genotypic correlations were higher than phenotypic ones for most of the characters due to their strong association among characters genetically and less phenotypic value is due to the influence of significant interaction of environment and only significant correlations are discussed here.

Grain yield showed strong and positive correlation with number of tillers per meter (0.951), whereas, moderate and positive correlation with grain weight per spike (0.220) and plant height (0.196) however, grain yield showed negative association with days to maturity, spike length, number of spikelets per spike and canopy temperature. A day to maturity was positively associated with spike length (0.486), number of spiklets per spike (0.581) and canopy temperature (0.846). Number of tillers per meter showed significantly positive correlation with grain weight per spike (0.449). Spike length showed significantly positive correlation with number of spikelets per spike (0.678), grain weight per spike (0.518) and canopy temperature (0.711). Number of spikelets per spike showed positive and significant correlation with canopy temperature (0.714). Grain weight per spike showed positive significant correlation with plant height (0.536). Under drought stress condition canopy temperature (CT) was correlated negatively with grain yield (r = -0.271) indicating importance of cooler genotypes. Significant genotypic correlation between grain yield and number of tillers per meter has also been reported by Khan *et al.* (2015) and Usman *et al.* (2006). The grain yield had non-significantly negative association with days to maturity (Nishant *et al.*, 2018). This indicates that the early genotypes in semi arid condition are capable of escaping the drought stress which is the major yield reduction factor.

In addition, Fischer *et al.* (1998) reported that stomatal conductance, photosynthesis and canopy temperature were closely related with yield in spring wheat. Under drought stress canopy temperature was positively correlated with spike length and spikelets per spike but fails to convert in the increment to the final product indicating seeking care while selection for these traits. The evaluations and line selection of drought tolerance based on the canopy temperature could also be effective in wheat to develop highly tolerant varieties to drought. Significantly negative correlation was observed for days to maturity and number of spikelets per spike with thousand grain weight indicating significance of early maturing genotypes under drought stress. On the other hand, significant negative correlation of spike length was noticed with thousand grain weight (-0.525) indicating that with increase in spike length, there would be decrease in the grain weight ultimately reduction in grain yield. These results are in partial agreement with the results obtained by Degewione *et al.* (2013) and Jasmine and Kumar (2017).

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