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Identification of physiological and quality traits in bread wheat genotypes under terminal heat stress environment

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Abstract
Central zone usually faces terminal heat stress at the time of grain filling under late planting conditions hence, the present experimentation were conducted on 30 genotypes in randomized block design with three replications under terminal heat stressed condition. The analysis variance showed significant difference for all the studied traits. The high value of PCV and GCV were observed for harvest index and yield plant^{-1}. The high heritability coupled with high genetic advance were observed for most of the studied traits *viz*; harvest index (%), yield plant^{-1} (g), number of leafs plant^{-1}, biological yield plant^{-1} (g), peduncle length (cm), wet gluten (%), SDS (mm) and 1000 grain weight (g). Correlation coefficient revealed that the grain yield per plant exhibited highest significant positive association both at genotypic and phenotypic level with harvest index (%), biological yield plant^{-1} (g), number of leaves plant-^{1}and significant negative association with moisture (%), protein (%) and starch (%) and 1000 grain weight (g).Path analysis showed that highest positive direct effect on grain yield were exerted by harvest index, biological yield plant^{-1} and number of leafs per plant whereas highest negative direct effect were exhibited by 1000 grain weight, protein % and canopy temperature. Under stressed conditions these traits were important for any selection programme and quality analysis will help to find out those traits which will improve at the cost of yield.

Keywords: Wheat, heritability, genetic advance, correlation, path analysis, heat, abiotic stress

Introduction
In wheat bread the main goal is to complement genetic improvement in the harvested grain. As it has low gains and complex legacy, so is the exciting goal of selection (Crossa *et al*. 2017) [4] and its dependent advantages in the breeding program (Rife *et al*. 2018) [18]. Examination of physiological features and their quality characteristics in the genotypes of bread is an important aspect of the current situation. Where we need identify varieties for all crops, wheat is the staple food in India. The Indians use wheat in the form of *chapatis* or bread. Therefore, improvements in healthy food quality to known genotypes of bread will help us in building biofortified wheat (Singh *et al*. 2018) [24]. Since quality is one of the most important factors to learn, physical factors are equally important as they affect the source of the grain. Identifying the characteristics will help to determine the local effect on wheat crops, and can provide accurate results and indicate which genotypes are suitable for adverse conditions. However, many genotypes were released that tolerated various types of stresses to increase wheat yield. Improving or maintaining quality is the second goal in a number of wheat breeding programs, and the selection of indirect baking quality features is done by using protein content. Quality features covered under the current investigation *viz*., Sedimentation rate (mm), Hectolitre weight, Protein, Wet gluten, Starch and physiological properties such as RWC leaf flag, Chlorophyll content and Canopy temperature.

Now a day's wheat with high protein is needed for nutritional development and improved processing. Production of high protein is difficult due to a large proportion of variability due to non-genetic factors. The number of genotypes was analysed in the present study. Gliadins and glutenins make up to 63-90% of the total grain protein defining the ability of wheat flour to be processed into different foods. This unique visco-elastic structure of gliadins and glutenin is responsible for the quality of making whole wheat bread. Physical factors such as photosynthetic development, the content of chlorophyll in each leaf area and the effects of N deficiency such as green leaves, identified with the help of SPAD 502 in plants (Chunjiang *et al*. 2007; Murdock *et al*. 2004) [3, 10]. Such selection of photosynthetic ability in various genotypes depends on the number of photosynthetic cells present in a single leaf area.

Therefore, the total amount of chlorophyll content / leaf area can be a good photosynthetic tissue (Nageswara *et al*. 2001; Fotovat *et al*. 2007; Singh *et al*. 2015; Singh *et al*. 2016) [11, 7, 21, 22]. High chlorophyll content is required with a low degree of inhibition of photosynthetic machinery. The water content associated with the flag leaf is another important factor affected by the drought as it leads to stomata closure and decreased water content, loss of turgor and can sometimes lead to plant death due to allergies (Jaleel *et al*. 2008) [9]. Canopy temperatures have been widely used in recent years to obtain genotypic responses to wheat genotypes under drought pressure to test different wetlands (Blum *et al*. 1989) [2]. Canopy temperatures and yields under conditions of moisture stress have shown significant correlation (Rashid *et al*. 1999) [13]. Decreased water content (RWC), chlorophyll and bed temperature are also evident under water stress conditions. Therefore, current experiments were performed to assess genetic mutations in wheat genotypes under conditions of thermal stress. The purpose of this experiment was to analyse the relationship between the various physiological factors namely, chlorophyll in the leaf area of the unit, the moderate water content, bed temperature and quality characteristics and also to meet the grain yield in the wheat genotypes.

Materials and Methods

Planting material of the present investigation includes thirty different genotypes received from different wheat improvement research stations and from CIMMYT, Mexico. These genotypes were planted in randomized complete block design with three replications, keeping row to row distance 25 cm apart during 2013-14. All the prescribed package of practices was followed during experimentation. Both physiological and quality traits were evaluated for variance and association analysis carried out by statistical procedure given by ANOVA technique (Panse and Sukhatme, 1954) [14], Burton and Devane (1953) [1] and Path analysis was done as described by Dewey and Lu (1959) [5] and Ramanujam and Rai (1963) [16].

Physiological and quality traits were evaluated by following methods:

1. **Relative Leaf water content:** It is the water content of the flag leaves is determined by Schonfeld *et al*. 1988 [19]. RLWC (%) = {(Fresh weight - Dry weight) / (Turgid weight - Dry weight)} × 100
2. **Chlorophyll content:** It was measured with a Portable chlorophyll meter SPAD-502 of the Japanese company Konica-Minolta (Soil Plant Analysis Development) used to measure chlorophyll content (also known as green leaf parameter). The SPAD value was taken from three different parts (leaf base, middle and upper) of the flag leaf and the estimated value was used to study the chlorophyll content.
3. **Canopy Temperature Depression (CTD):** Handy portable Infra Red Thermometer (Model LT 300 Sixth Sense) used to measure CTD at the grain filling stage during the day in bright sun and slow air.
4. **"Infratec™ 1241 analyzer":** Quality features namely; protein, wet gluten, starch and moisture (%) are measured using a non-corrosive method with the FIRS NIR-instrument "Infratec™ 1241 analyzer".
5. **Sedimentation value:** was analysed by hand shake: Reagents: Sodium dodecyl sulphate (sodium lauryl sulphate 88% lactic acid). The desired SDS / lactic acid reagent can be prepared by dissolving 20 g SDS in one litre of distilled water, in this 20 ml stock is diluted with lactic acid prepared by mixing one part with 88% lactic acid volume with 8 parts per volume of distilled water. The reagent is stirred or shaken until uniform.

Results and Discussion

Analysis of variance, PCV and GCV: In the present study, the variance analysis confirmed that the square number was found to be as large as the result showing, the availability of a sufficient number of genetic variants between all genotypes and the hypotheses considered (table 1). The Phenotypic coefficient of variance was found to be better than the genotypic coefficient of variance in all study variables meaning the environmental impact on the expression of these characters. The high cost of PCV and GCV have been found for harvest index (PCV=26.14; GCV 22.04) and yield plant-1(PCV=25.29; GCV=21.48).

Heritability and Genetic advance: Heritability estimates together with genetic advance is more unique in guessing the genetic gain below. Genetic advance indicates the distinction among the imply genotypic values of selected population and the authentic population from which these have been selected. High heritability was observed for relative water content (97.6%), wet gluten (97.3%), protein (%) (96.8%), biological yield plant^{-1}(g) (92.6%), SDS (mm) (92.0%), 1000 grain weight (g) (90.9%), starch (%) (88.2%), number of leafs plant^{-1} (84.1%), yield plant^{-1} (g) (72.2%), harvest index (%) (71.1%), peduncle length (70.4%) and chlorophyll content (65.5%). These traits were totally under the influence of the highest genetic advance as a percentage of mean were observed for harvest index (%) (38.28), yield plant^{-1} (g) (37.60), number of leafs plant^{-1} (34.11), biological yield plant^{-1} (g) (27.46), peduncle length (cm) (25.11), wet gluten (%) (24.38), SDS (mm) (23.42) and 1000 grain weight (g) (22.66). (Table 2).

Correlation analysis: Correlation analysis is a measure of the degree of relationship and relationship between the two variables. It is important for plant breeding as it can be used for indirect selection. The study of the interplay of different characters can help a plant grower to know that improving one character will bring about simultaneous changes to other characters. The grain yield per plant exhibited highest significant positive association with harvest index (%) (rg=0.762**;rp=0.816**), both at genotypic and phenotypic level followed by, biological yield plant^{-1}(g) (rg=0.270*; rp=0.240*), 1000 grain weight (g) (rg=0.224*) and number of leaves plant-^{1} (rg=0.256.) is also positively associated with yield. Whereas, it had significant negative association with moisture (%) (rg= -0.585**), and quality traits like protein (%) (rg=-0.315**; rp=-0.249*), starch (%) (rg=0.433**, rp=0.319**), both at genotypic and phenotypic level.

At phenotypic level correlation of different traits were described as follow: Peduncle length (cm) has positive significant correlation with harvest index (%) (rp=0.254*) and negative with biological yield plant^{-1} (g) (rp=-0.337**). Number of leaves plant^{-1}had significant positive correlation with biological yield plant^{-1} (0.447**) (g) and significant negative correlation with sedimentation value (mm) (rp=-0.275**). 1000 grain weight (g) showed significant positive correlation with protein (%) (rp=0.377**), (rp=0.225*), wet gluten (%), (rp=0.295**), biological yield plant^{-1} (g) and it reported significant negative correlation with harvest index (%) (rp=-0.281**), canopy temperature (rp=-0.235*) and starch (%) (rp=-0.235*). Biological yield plant^{-1} reported significant negative correlation with (g) harvest index (%) (rp=-0.353**) and wet gluten (%) (-0.299**). Harvest index (%) had positive correlation with starch (%) (rp=0.202*). RWC of flag leaf had significant negative correlation with chlorophyll content (rp=-0.331**). However, Chlorophyll content exhibited positive correlation with protein (%) (rp=0.222*). Canopy temperature had significant negative correlation with starch (%) (rp=-0.229*). Sedimentation value reported highly significant positive correlation with wet gluten (%) (rp=0.642**), starch (%) and protein (%) (rp=0.523**) and significant negative correlation with starch (%) (rp=-0.286**). Protein (%) showed high positive significant correlation with wet gluten (%) (rp=0.726**) and starch (%)(rp=-0.299**). Wet gluten (%) exhibited significant negative correlation with starch (%) (rp=-0.219*). (Table3 and Figure 1).

In genotypic correlation matrix significant inter-correlations of the traits are as follows: Peduncle length (cm) reported significant positive correlation with harvest index (%) (rg=0.377**), canopy temperature (rg=0.252*) and highest significant negative correlation with moisture (%)(rg=-1.093**), biological yield plant^{-1} (g) (rg=-0.434**), chlorophyll content (rg=-0.268*), hectolitre weight (g / litre) (rg=-0.235*) and number of leaves plant^{-1}(rg=-0.236*). Number of leaves plant^{-1} showed significant positive correlations with biological yield plant^{-1} (g) (rg=0.475**), moisture (%) (rg=0.357**), 1000 grain weight (g) and moisture (%) (rg=0.357**).1000 grain weight greported significant genotypic positive correlation with protein (%) (rg=0.409**), biological yield plant^{-1} (g) (rg=0.311**), wet gluten (%) (rg=0.238*), chlorophyll content(rg=0.219*) and significant negative association with harvest index (%) (rg=-0.403**),canopy temperature (rg=-0.407**),starch (%) (rg=-0.277**) and moisture (%) (rg=-0.277**). The Biological yield plant^{-1}(g) reported significant negative genetic correlations with harvest index (%) (rg=-0.411**), wet gluten (%)(rg=-0.321**) and sedimentation value (mm) (rg= -0.210*). Harvest index (%) also reported significant negative genetic correlation with starch (%) (rg= 0.289**) and moisture (%) (rg=-0.510**). Whereas, RWC of flag leaf had significant negative correlation with chlorophyll content (rg=-0.419**). Although, Chlorophyll content had significant positive correlation with protein (%) (rg=0.295**) and significant negative correlation with canopy temperature (rg=-0.217*) The canopy temperature had significant positive association with moisture (%) (rg=0.317**) and significant negative correlation with starch (%) (rg=-0.482**), hectolitre weight (g / litre) (rg=-0.477**) and protein (%) (rg=-0.352**). Whereas, sedimentation value (mm) reported significant positive association with wet gluten (%) (rg=0.679**), protein (%) (rg=0.562**) and significant negative association with starch (%) (rg=-0.311**). Hectolitre weight (g / litre) had positive significant association with wet gluten (%) (rg=0.358**), starch (%) (rg= 0.267*) and negative significant association with moisture (%) (rg=-0.519**). Protein (%) exhibited significant negative association with wet gluten (%) (rg=0.751**), moisture (%) (rg=0.338**) and negative significant association with starch (%) (rg=-0.314**). Wet gluten (%) reported significant negative association with moisture (%)(rg=-0.374**) and starch (%)(rg=-0.228*). (Table 3 and Figure2).

Path coefficient analysis: Path analysis may reported that the highest positive direct effect on grain yield were exerted by harvest index (0.987) followed by, biological yield plant^{-1}(0.671), number of leafs per plant (0.104), whereas highest negative direct effect were exhibited by grain weight (-0.086) followed by protein % (-0.073) and canopy temperature (-0.073).

Harvest index exhibited positive indirect effect via peduncle length (0.372) and starch % (0.285) and highest negative indirect effect on yield *via* other traits *viz;* biological yield plant^{-1} (-0.406), thousand grain weight (-0.398). Biological yield plant^{-1} exhibited highest positive effect *via*., number of leafs plant-1 (0.319), thousand grain weight (0.209) and negative indirect effect via peduncle length (-0.291), harvest index (-0.276), wet gluten (-0.215), SDS (-0.141), relative water content of flag leaf (-0.124) and protein % (-0.115). The residual effect is (0.0736).

Discussion

In the present experimentation, the variance analysis reported high mean sum of square representing the sufficient amount of genetic variation between all genotypes. The Phenotypic coefficient of variance was found to be higher than the genotypic coefficient of variance in all the variables showing higher environmental impact on the expression of these characters. Whereas high PCV and GCV were reported by harvest index and yield plant^{-1}. Generally, a high coefficient of the variance reflects the range of options in favor of the characteristics of interest and the low coefficient of diversity reflects the need for the construction of diversity and selection. Heritability estimates together with genetic advance showed genetic gain selection. Which indicates the distinction among genotypic values of selected population and the authentic population from which these have been selected. Whereas, High heritability were reported by for relative water content, wet gluten, protein (%), biological yield plant^{-1}(g), SDS (mm), 1000 grain weight (g), starch (%), number of leafs plant^{-1}, yield plant^{-1} (g), harvest index (%), peduncle length and chlorophyll content. Above findings showed the presence of additive genes in the trait and suggested reliable for improvement of wheat grain yield. These traits were totally under the influence of the highest genetic advance as a percentage of mean were observed for harvest index (%), yield plant^{-1} (g), number of leafs plant^{-1}, biological yield plant^{-1} (g), peduncle length (cm), wet gluten (%), SDS (mm) and 1000 grain weight (g). Similar findings were supported by (Payal *et al*. 2007; Gupta *et al*. 2000; Rashidi *et al*. 2011; Singh *et al*. 2016 and Tamer *et al*. 2010) [8, 17, 23, 26]. Features with high intensity and high genetic development have a great potential for developing these traits with easy selection as it shows the magnitude of the additional genetic activity in producing these traits**.** Correlation analysis is a measure of the degree of relationship and relationship between the two variables. It is important for plant breeding as it can be used for indirect selection. The study of the interplay of different characters can help a plant grower to know that improving one character will bring about simultaneous changes to other characters. Here in this investigation grain yield per plant exhibited highest significant positive association with harvest index (%) both at genotypic and phenotypic level followed by, biological yield plant^{-1} (g) and 1000 grain weight (g) is also positively associated with yield suggesting that these quantitative traits may have pleiotropic effect on yield and increasing the frequency of such traits in selection programme may lead to increase in yield and positive correlation with number of leaves plant-^{1} reveals that increasing the source that is leaf for site of photosynthesis may leads to increase in the ultimate sink that is grain in wheat plant. Whereas, it had significant negative association with moisture (%) and quality traits like protein (%) and starch (%), both at genotypic and phenotypic level, showed that selection for these traits should be done at the cost of yield per se performance. Similar results were obtained by (Dencic *et al*. 2000; Singh *et al*. 2003; Rashidi 2011 and Shubhash chandra *et al*. 2009) [6, 20, 17, 25]. In this investigation most of the quality traits were negatively correlated with yield and positively associated with those traits which will indirectly associate positively with yield. It means careful indirect selection should be done in order to get highly nutritious varieties with optimum yield. Path analysis may reveal that traits having high impact on yield. Generally, the characters that exerting positive direct effect and positive and significant correlation coefficient with grain yield were known to affect grain yield in the favorable direction and need much attention during the process of selection cases. The highest positive direct effect on grain yield were exerted by harvest index, biological yield plant^{-1} and number of leafs per plant, and highest negative direct effect were exhibited by grain weight, protein % and canopy temperature. Similar results were depicted by Singh *et al.*, 2015 [21]; Singh *et al.*, 2016 [23]. For selecting high yielding genotypes, selection should be done by taking heritability and correlation of various characters with grain yield per plant into consideration. As grain yield per plant exhibited high heritability, indirect selection through the traits having close correlation with yield and high to moderate heritability can aid in selection. For the selection of quality parameters, number of leafs plant^{-1} and 1000 grain weight can be used as a selection parameter to improve the protein content, gluten content, which indirectly will improve the grain yield of the genotypes. Also, chlorophyll content and sedimentation value had highly significant positive correlation with wet gluten (%), starch (%) and protein (%). Genotypes with high chlorophyll content can be selected for better quality under terminal heat stressed environment. Therefore, these traits can be used as a compromising traits to evolve high yielding and good quality genotypes of bread wheat.

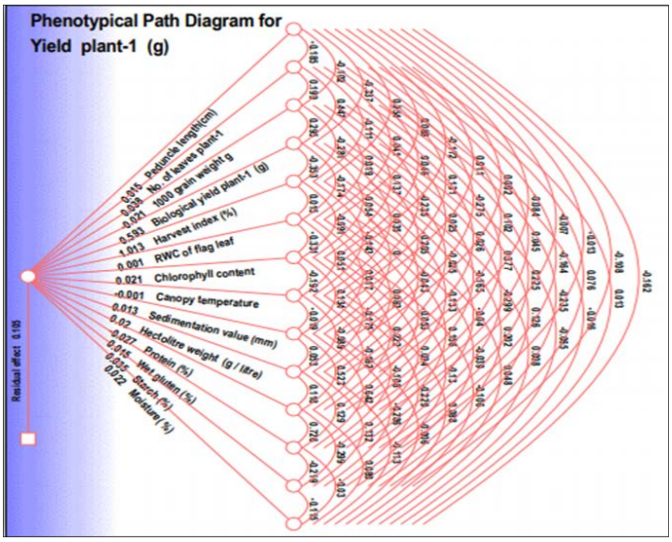

Fig 1: Phenotypic path diagram

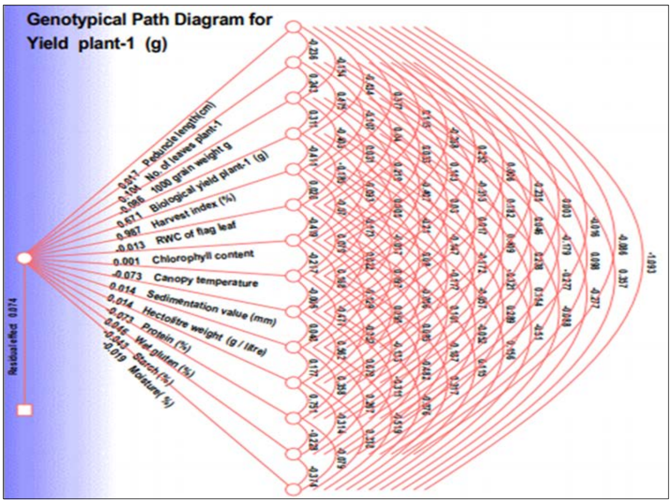

Fig 2: Genotypic path diagram

Table 1: Analysis of variance

SV	DF	PL	NLP^{-1}	1000 GW (g)	BYP^{-1} (g)	HI (%)		RWC (FL)	CC
R	2	10.54	11.66	8.70	6.99	79.94		6.82	15.40
T	29	22.50**	57.86**	68.54**	71.86**	181.98**		88.91**	29.73*
E	58	2.76	3.42	2.22	1.86	21.72		0.72	4.44
SV	**DF**	**CT**	**SDS (mm)**	**HW (g / litre)**	**Pro. (%)**	**WG (%)**	**St. (%)**	**Mois. (%)**	**YP^{-1} (g)**
R	2	3.99	19.92	63.54	0.07	0.73	4.46	0.78	11.09
T	29	1.71*	35.49**	16.59**	1.35*	26.47*	8.58**	0.54*	20.36*
E	58	0.70	1.00	9.52	0.01	0.25	0.36	0.47	2.32

* and **: significant at 5%, 1% probability levels, respectively

Table 2: Parameters of genetic variability

Traits	Mean	Range Lowest	Range Highest	PCV	GCV	ECV	h² (Broad Sense)	Gen. Adv as % of Mean 5%
PL(cm)	17.66	12.83	25.93	17.30	14.52	9.41	70.4	25.11
NLP^{-1}	23.60	16.23	36.83	19.68	18.05	7.84	84.1	34.11
1000 GW (g)	40.75	29.24	52.87	12.10	11.53	3.65	90.9	22.66
BYP^{-1} (g)	34.87	21.62	45.49	14.39	13.85	3.91	92.6	27.46
HI (%)	33.16	19.82	51.73	26.14	22.04	14.05	71.1	38.28
RWC (FL)	80.76	69.88	90.60	6.79	6.71	1.04	97.6	13.66

CC	45.44	36.23	51.27	7.89	6.39	4.63	65.5	10.65
CT	22.97	21.17	24.60	4.43	2.53	3.63	32.7	2.98
SDS (mm)	28.61	23.03	36.07	12.35	11.85	3.48	92.0	23.42
HW (g / litre)	76.52	73.00	81.00	4.50	2.01	4.03	19.8	1.84
P (%)	10.68	9.67	12.37	6.35	6.25	1.14	96.8	12.67
WG (%)	24.63	19.57	30.40	12.17	12.01	2.01	97.3	24.38
St. (%)	66.26	63.20	68.80	2.65	2.49	0.91	88.2	4.83
Mois. (%)	7.01	6.17	7.77	10.04	2.10	9.81	04.4	0.91
YP^{-1} (g)	11.41	7.34	17.86	25.29	21.48	13.33	72.2	37.60

#PL: Peduncle length(cm), NLP^{-1}:No. of leaves $plant^{-1}$, GW:1000 grain weight (g), BYP^{-1}:Biological yield plant-1 (g), HI: Harvest index (%),RWC (FL): RWC of flag leaf, CC: Chlorophyll content, CT: Canopy temperature, SDS: Sedimentation value (mm), HW: Hectolitre weight (g / litre), Pro.: Protein (%),WG: Wet gluten (%), St.; Starch (%) and Mois.:Moisture (%)
* &** Significant at 5% & 1% respectively

Table 3: Presentation of genotypic and phenotypic correlation coefficients of different physiological and quality traits with yield

Traits	PL(cm)	NLP^{-1}	GW(g)	BYP^{-1} (g)	HI (%)	RWC (FL)	CC	CT	SDS (mm)	HW(g / litre)	Pro. (%)	WG (%)	St. (%)	Mois. (%)	YP^{-1} (g)
PL(cm)	rg	-0.236*	-0.154	-0.434**	0.377**	0.115	-0.268*	0.252*	0.006	-0.235*	0.003	-0.016	-0.086	-1.093**	0.088
	rp	-0.185	-0.102	-0.337**	0.254*	0.088	-0.172	0.011	0.002	-0.084	-0.007	-0.013	-0.108	-0.162	0.054
NLP^{-1}	rg	1.000	0.243*	0.475**	-0.107	0.040	0.033	0.143	-0.313**	0.182	0.046	-0.179	0.098	0.357**	0.256*
	rp		0.199	0.447**	-0.111	0.041	0.046	0.131	-0.275**	0.102	0.045	-0.164	0.076	0.013	0.183
GW(g)	rg		1.000	0.311**	-0.403**	0.031	0.219*	-0.407**	0.030	0.017	0.409**	0.238*	-0.277**	-0.277**	0.224*
	rp			0.295**	-0.281**	0.019	0.137	-0.235*	0.025	0.026	0.377**	0.225*	-0.235*	-0.016	0.135
BYP^{-1} (g)	rg			1.000	-0.411**	-0.185	-0.093	0.005	-0.210*	-0.147	-0.172	-0.321**	0.154	-0.088	0.270*
	rp				-0.353**	-0.174	-0.054	0.035	-0.205	-0.025	-0.165	-0.299**	0.126	-0.065	0.240*
HI (%)	rg				1.000	0.026	-0.070	-0.173	-0.017	0.080	-0.177	-0.057	0.289**	-0.510**	0.762**
	rp					0.015	-0.091	-0.143	0.000	-0.043	-0.133	-0.040	0.202	0.008	0.816**
RWC (FL)	rg					1.000	-0.419**	0.079	0.022	0.197	-0.056	0.161	-0.052	0.156	-0.101
	rp						-0.331**	0.051	0.017	0.082	-0.053	0.156	-0.039	0.048	-0.087
CC	rg						1.000	-0.217*	0.168	-0.129	0.295**	0.085	-0.187	0.115	-0.140
	rp							-0.192	0.134	-0.175	0.222*	0.094	-0.130	-0.106	-0.120
CT	rg							1.000	-0.006	-0.477**	-0.352**	-0.133	-0.482**	0.317**	-0.160
	rp								-0.019	-0.089	-0.182	-0.108	-0.229*	0.088	-0.125
SDS (mm)	rg								1.000	0.048	0.562**	0.679**	-0.311**	-0.076	-0.173
	rp									0.053	0.523**	0.642**	-0.286**	-0.006	-0.129
HW (g / litre)	rg									1.000	0.177	0.358**	0.267*	-0.519**	0.043
	rp										0.118	0.129	0.132	-0.113	-0.038
P (%)	rg										1.000	0.751**	-0.314**	0.338**	-0.315**
	rp											0.726**	-0.299**	0.089	-0.249*
WG (%)	rg											1.000	-0.228*	-0.079	-0.286**
	rp												-0.219*	-0.030	-0.228*
St. (%)	rg												1.000	-0.374**	0.433**
	rp													-0.115	0.319**
Mois. (%)	rg													1.000	-0.585**
	rp														-0.022

#Abbreviation description were given in Table 2;* &** Significant at 5% & 1% respectively

Table 4: Path coefficient analysis of different physiological and quality traits of 30 wheat genotypes at during 2013-14

Traits	PL (cm)	NLP-1	GW (g)	BYP-1 (g)	HI (%)	RWC (FL)	CC	CT	SDS (mm)	HW (g / litre)	Pro. (%)	WG (%)	St. (%)	Mois. (%)
PL(cm)	0.017	-0.025	0.013	-0.291	0.372	-0.002	0.000	-0.018	0.000	-0.003	0.000	-0.001	0.004	0.021
NLP^{-1}	-0.004	0.104	-0.021	0.319	-0.106	-0.001	0.000	-0.010	-0.004	0.003	-0.003	-0.008	-0.004	-0.007
GW (g)	-0.003	0.025	-0.086	0.209	-0.398	0.000	0.000	0.030	0.000	0.000	-0.030	0.011	0.012	0.005
BYP^{-1} (g)	-0.007	0.049	-0.027	0.671	-0.406	0.002	0.000	0.000	-0.003	-0.002	0.013	-0.015	-0.007	0.002
HI (%)	0.006	-0.011	0.035	-0.276	0.987	0.000	0.000	0.013	0.000	0.001	0.013	-0.003	-0.012	0.010
RWC (FL)	0.002	0.004	-0.003	-0.124	0.026	-0.013	-0.001	-0.006	0.000	0.003	0.004	0.007	0.002	-0.003
CC	-0.005	0.004	-0.019	-0.063	-0.069	0.005	0.001	0.016	0.002	-0.002	-0.022	0.004	0.008	-0.002
CT	0.004	0.015	0.035	0.003	-0.171	-0.001	0.000	-0.073	0.000	-0.007	0.026	-0.006	0.021	-0.006
SDS (mm)	0.000	-0.033	-0.003	-0.141	-0.017	0.000	0.000	0.000	0.014	0.001	-0.041	0.031	0.013	0.002
HW (g / litre)	-0.004	0.019	-0.002	-0.098	0.079	-0.003	0.000	0.035	0.001	0.014	-0.013	0.017	-0.012	0.010
P (%)	0.000	0.005	-0.035	-0.115	-0.175	0.001	0.000	0.026	0.008	0.003	-0.073	0.035	0.014	-0.007
WG (%)	0.000	-0.019	-0.020	-0.215	-0.056	-0.002	0.000	0.010	0.009	0.005	-0.055	0.046	0.010	0.002
St. (%)	-0.002	0.010	0.024	0.104	0.285	0.001	0.000	0.035	-0.004	0.004	0.023	-0.011	-0.043	0.007
Mois. (%)	-0.019	0.037	0.024	-0.059	-0.503	-0.002	0.000	-0.023	-0.001	-0.007	-0.025	-0.004	0.016	-0.019

#Abbreviation description were given in Table 2*;* R SQUARE = 0.9946 Residual Effect = 0.0736
Bold values shows direct and normal values shows indirect effects

Conclusion
In this investigation, heat stress, is a common constraint during grain filling stages for production of wheat in most of the regions of central India. Heat stress abolished two of the most important mechanisms, growth and photosynthesis, up to some extent or completely, and leads to major decreased crop yield. The present investigation showed that the lower canopy temperature is associated with higher grain yield under different availability water conditions. Also, compromised has to be done for quality traits, if select in the

direction of higher yield as these traits like protein, starch, gluten showed negative association with yield. Although, inter-correlation among the different traits may be useful in indirect selection of yield attributing characters. The best option for yield improvement and yield stability under stressed conditions is to develop heat stress tolerant crop varieties. A physiological along with quality association approach would be the most striking way to develop novel bio-fortified varieties. Therefore, chlorophyll content, relative water content and canopy temperature can be used as a selected criterion for tolerance in terminal heat stress. Looking complete results, it is clear that these parameters could clarify some of the process in plant, which indicate heat tolerance, whereas, these are relevant in predicting the significant varietals variability for yield and quality traits.

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