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Evaluation of genetic divergence in bread wheat (*Triticum aestivum* L.) genotypes for yield parameters and heat tolerance traits

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Abstract

An experiment was conducted on 108 bread wheat genotypes to evaluate the genetic diversity for yield and yield contributing parameters under heat stress conditions. The genotypes congregated into eleven clusters, and distribution pattern designates that maximum number of genotypes were grouped into the cluster VI (25) followed by cluster I (16) and IX (12). The inter cluster distances were higher than the intra-cluster distance, indicating broader genetic diversity among the genotypes of different groups. The highest inter cluster distance was observed between cluster VIII and IV (613.84) followed by clusters XI and IV (586.42), suggesting presence of wide diversity among the groups. The maximum intra-cluster distance (D^2) were recorded for cluster XI (171.58), followed by cluster VIII (129.73), and minimum intra-cluster distance was recorded for cluster VI (66.33). This suggested that genotypes like SHIATS BW- 1606, SHIATS BW- 1630, and SHIATS BW- 1698 from cluster VIII and SHIATS BW- 1695 from cluster I could be used as potential donors for hybridization program to develop recombinant genotypes with high grain yield adapted to heat stress conditions.

Keywords: wheat, heat stress, genetic diversity, cluster distance

1. Introduction

Wheat (*Triticum aestivum* L.) is the main staple food crop for a large number of world populations. The area under wheat cultivation in the world 222 mha, while a production of 714.74 million tons and productivity 2.99 Mt/ha (CIMMYT, 2016) [1]. It is the second main winter cereal in India after rice. India had a remarkable success during Green revolution in wheat production and could increase productivity to the extent through it could bring itself out from insufficiency to a self-sufficient status. This is certainly a significant and comforting outcome. The area under wheat in India is 28.42 mha, with a production of 84.20 million tons and productivity of 2.6 Mt/ha. However at Uttar Pradesh level, it occupy an area of 10.42 mha, with production of 29.32 million tons and productivity of 2.8 Mt/ha (DWR, 2016) [4]. Wheat will continue to attract substantial research attentions in the face of the challenge of feeding a predictable population of 9 billion by 2050. Yield increases are essential to meet this demand, as expanding the wheat area is not possible (Rajaram and Braun, 2008) [12]. (Gill *et al.*, 2004) [5] stated that in order to meet growing human needs; wheat grain production must increase at an annual rate of 2%. Unfortunately, heat stress is a major environmental factor that substantially reduces wheat grain yield globally especially in arid, semi-arid, tropical, and sub-tropical regions that are associated with higher temperature. (Wahid *et al.*, 2007) [21] Defined heat stress as the rise in temperature beyond a threshold level for a period of time sufficient to cause irreversible damage to plant growth and development. Global warming as a result of climate change negatively affects wheat grain yield, which potentially increases food insecurity and poverty (Ortiz *et al.*, 2008) [10]. Each day delay in sowing of wheat after 20 November onward in decreases grain yield at the rate of 36 kg ha⁻¹day⁻¹ (Hussain *et al.*, 1998) [7]. Delayed sowing from normal to late and very late increased the canopy temperature depression significantly, whereas other parameters such as a thesis, maturity, spike length, and grain-filling period were reduced as sowing was delayed. (Tripathi *et al.*, 2005) [19]. the optimum temperature range for attaining maximum grain weight is 18-22°C. Wheat grain weight is decreased from 4 to 8% per degree rise in mean temperature over the range of 12- 26°C during grain filling period (Wiegand and Cuellar1981) [22]. Stress due to high-temperature has emerged as a major constraint for the successful wheat production worldwide (Hays *et al.*, 2007) [6]. Nearly 40 % of total irrigated area, where wheat is grown, is severely affected by heat stress (Reynolds *et al.*, 2001) [14]. Yield loss of 29 % is expected by 2080 due to global warming, in wheat. Annual yield loss in wheat due to global warming is expected to be 7.7 billion dollars,

and by 2025, this would be around 18 billion dollars. Stress due to high-temperature has emerged as a major constraint for the successful wheat production worldwide (Hays *et al.*, 2007) [6]. Nearly 40 % of total irrigated area, where wheat is grown, is severely affected by heat stress (Reynolds *et al.*, 2001) [14]. Therefore information on genetic diversity for grain yield in heat stress condition is important to meet diversified goal of plant breeding, such as breeding for increasing yield, wide adaptation and desirable quality (Kumar *et al.*, 2009) [9]. Information on genetic diversity in wheat under heat stress environment is less. Therefore the experiment was conducted to identify genetically divergent genotypes as donors with desirable traits for hybridization particularly for heat stress coupled with high yield and its contributing traits.

2. Materials and Methods

A study was conducted taking 108 diverse genotypes including three checks (Halna, K-8962, and HD-2733). The experiment was planted during *Rabi* 2014-15 and *Rabi* 2015-16 at the Experimentation Centre of Department of Genetics and Plant Breeding, NAI. School of Agriculture, SHUATS, Allahabad (U.P.), which is located at 25° 24' 42" N latitude, 81° 50' 56" E longitude and at altitude of 98 m above the mean sea level. The experimental material was grown in Randomized Block Design (RBD) replicated thrice. Each genotype was grown in one row plot of 5 meters with 25 centimeter distance between rows. The recommended cultural practices were adopted to rise a good crop. Data were recorded on five randomly selected competitive plants from each plot on sixteen quantitative characters namely, days to 50 % heading, days to 50 % flowering, plant height (cm), spike length (cm), spike weight (cm), number of productive tillers per plant, grain filling period, grain per spike, test weight (g), chlorophyll content (%), membrane thermo-stability (%), harvest index, canopy temperature depression, days to 50 % maturity, biological yield per plant (g), and grain yield per plant (g). The estimate genetic parameters, broad sense heritability (h^2), genetic advance (GA % of mean), genotypic coefficient of variance (GCV), and phenotypic coefficient of variance (PCV), work out. Also data were subjected to non-hierarchical Euclidian cluster statistic.

3. Result and Discussion

The analysis of variance indicated that there was a significant difference between all the traits under heat stress condition. The mean sum of square due to genotypes were significant for all the character studied, suggesting the existence of high genetic variability among the genotypes for all the traits. The presence large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes. The phenotypic coefficient variation was higher than genotypic coefficient variation for all the traits. Higher PCV and GCV indicated that there was variability existing among the genotypes. High value for genetic coefficient of variability (GCV) are shown for spike weight, number of grains per spike, grain yield per plant, biological yield per plant and canopy temperature depression under heat stress condition indicating better opportunity for improvement in these traits through selection. The heritability estimate range from 0.35- 0.95 for harvest index and biological yield per plant respectively in heat stress condition. High estimate of heritability acquired for all the traits with the exception of harvest index. This might be due to low effect of environment on these traits. High heritability combined with high genetic advance give the most actual criteria for

selection. (Johanson *et al.*, 1955) [8]. in the current study high heritability estimate coupled with high genetic advance were perceived for plant height, grain per spike, and membrane thermo- stability. (Panse and Sukhatme (1978) [11] expressed if a character is governed by additive gene action the heritability and genetic advance both would be high. High to moderate heritability along with low genetic advance were notice for days to heading, days to flowering, spike length, tiller per plant, grain filling period and days to maturity, indicating that these character might be controlled by non-additive gene action and improvement for these character through selection would be rather limited. High heritability along with high genetic advance for some metric trait was reported by (Singh *et al.*, 2010) [9]. Moreover in hybridization program selection of genetically diverse parent is important to create a wide range of recombinant, and this mean that the knowledge of genetic diversity among the genotypes is necessary. Based on the result of diversity 108 genotypes were grouped into eleven clusters by non-hierarchical Euclidian cluster statistics in such method that genotypes within a cluster had a small D^2 value than those of in between the clusters. The structure of clusters presented (Table 2) that cluster VI had largest number of genotypes (25) followed by cluster I (16) and cluster IX (12) where cluster IV has least number of genotypes (3). The inter-cluster distance was higher than intra-cluster distance, indicating wide genetic diversity among the genotypes (Table 3). The inter-cluster distance varied from 613.845 (cluster VIII and IV) to 124.873 (cluster VII and VI). The inter-cluster that indicated close relationship among genotypes of these clusters would not provide good level of segregation. It is well identify that greater the distance between the clusters wider the genetic diversity would be between the genotypes. Therefore highly divergent genotypes would produce a broad range of segregation in the successive generation facilitating further selection and improvement. The hybrid developed from the selected genotypes from these clusters may produce appropriate transgressive segregation of high magnitude of hetrosis. This would be useful in a wheat breeding program particularly for pointing aggressive condition of wheat under heat stress condition. (Redhu *et al.*, 1995) [13], (Sharma *et al.*, 1998) [15], (Singh *et al.*, 2012) [16], (Deshumukh *et al.*, 1999) [3], also found similar result of diversity in wheat. The maximum intra –cluster distance was detected for cluster XI (171.581), followed by VIII (129.736), and cluster VII (117.362). In contrast cluster VII had minimum intra – cluster distance (66.339) (Table 1). It was reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance. (Singh *et al.*, 2010) [17]. the eleven clusters showed considerable differences in mean value for different characteristic under study. Cluster II comprising (6) genotypes was responsible for highest cluster mean value for grain filling period (36.67), cluster VI comprising (25) genotypes exhibited by highest cluster mean for harvest index (32.07), cluster VIII consist of (6) genotypes presented highest cluster mean value for spike length with awn (17.94), cluster IX contain (12) genotypes displayed highest cluster mean for test weight (40.90), chlorophyll content (41.81) cluster IX contain (12) genotypes showed maximum cluster mean for number of tillers per plant (6.54).

Two entries of cluster VI, SHIATS BW-1695 and SHIATS BW-1702 were responsible for highest cluster mean for grain yield (8.55) and (8.37) respectively. The minimum plant height was found in genotype SHIATS BW- 1614 of cluster III, the maximum spike length with awn was depicted by

genotype SHIATS BW- 1630 of cluster VIII. The genotype SHIATS BW- 1647 in cluster IX showed highest harvest index. A study on genetic diversity by (Kumar *et al.*,2009) [9] has revealed that grain yield per plant, tiller per plant and plant height, spike length, grain per spike, and early maturity contributed maximum to genetic diversity. On the basis of divergence and cluster mean it may be concluded that maximum heterosis and good recombinant would be possible from crosses between genotypes of clusters.

On the basis of divergence and cluster means it may be concluded that maximum heterosis and good recombinants are likely to be produced when genotypes having high grain yield adapted to terminal heat stress are crossed across clusters VIII, IV, VII and VI in a varietal improvement program. For bringing traits specific improvement, genotypes like SHIATS BW-1695 from cluster VI for grain yield, SHIATS BW-1647 from cluster IX for harvest index, SHIATS BW-1630 from cluster VIII for spike length and SHIATS BW-1614 from cluster VII for plant height may be considered for assortative

pre-breeding. The transgressive segregates coming out from such a crossing program are likely to perform better under heat stress conditions provided proper breeding methodology and careful selection is resorted to for recombining and methodizing genotypes with specific traits suited to the condition required, i.e., terminal heat stress tolerance. The percent distribution of sixteen characters towards total genetic divergence is listed in (Tab 5). The selection and choice of parents mainly depends upon contribution of characters towards divergence (De *et al.*, 1992) [2]. In the present investigation the highest contribution in expression of genetic divergence was exhibited by chlorophyll content (34.09) followed by membrane stability (16.36), plant height (12.34), number of grain per spike (11.75), days to 50 % maturity (0.03) and harvest index showed the minimum percent contribution characters toward genetic divergence.

Table 1: Estimation of component of variance and genetic parameters for 16 quantitative characters in wheat genotypes under heat stress condition.

Characters	σ^2_g	σ^2_p	Coefficient of variation		Heritability (h^2 bs)	Genetic advance	Genetic advance as % of mean
			GCV	PCV			
Days to 50 % Heading	9.53	11.32	4.20	4.58	0.84	5.84	7.94
Days to 50 % Flowering	10.35	11.67	4.07	4.32	0.89	6.24	7.90
Plant Height (cm)	159.25	175.86	13.78	14.48	0.91	24.74	27.01
Spike Length	6.65	7.97	15.24	16.65	0.84	4.87	28.73
Spike Weight	0.31	0.45	23.28	28.08	0.69	0.95	39.75
Tillers/ Plant	1.02	1.86	16.75	22.59	0.55	1.54	25.57
Grain Filling Period	10.29	13.77	9.39	10.87	0.75	5.71	16.73
Grains /Spike	89.84	99.53	24.46	25.75	0.90	18.55	47.88
Grain Yield/ Plant	1.39	2.83	20.15	28.71	0.49	1.71	29.13
Test Weight	28.28	35.21	13.70	15.29	0.80	9.82	25.30
harvest Index	25.97	73.46	16.72	28.12	0.35	6.24	20.48
Biological Yield/ Plant	18.64	22.23	22.15	24.19	0.84	8.15	41.80
Days to 50% Maturity	11.04	16.42	2.93	3.58	0.67	5.61	4.96
Chlorophyll content	30.96	32.48	13.89	14.23	0.95	11.19	27.94
Canopy Temperature Depression	1.52	1.84	25.03	27.51	0.83	2.31	46.90
Membrane Thermo-stability	42.44	46.85	21.08	22.15	0.91	12.77	41.33

Where- V_g = Genotypic variance V_P = Phenotypic variance GCV = Genotypic coefficient of variance
PCV = Phenotypic coefficient of variance h^2 (bs) = Heritability (broad sense) GA = Genetic advance

Table 2: Distribution pattern of wheat genotypes into eleven clusters based on non-hierarchical Euclidean cluster analysis.

S. No	Members Within the Cluster (n)	Within Cluster SS	Cluster Members
1	16.00	4.42	SHIATS BW-1609, SHIATS BW -1615, SHIATS BW-1625, SHIATS BW-1640, SHIATS BW-1651, SHIATS BW-1652, SHIATS BW-1658, SHIATS BW-1664, SHIATS BW-1668, SHIATS BW-1673, SHIATS BW-1677, SHIATS BW-1681, SHIATS BW-1683, SHIATS BW-1694, SHIATS BW-1700
2	6.00	11.88	SHIATS BW-1619, SHIATS BW-1635, SHIATS BW-1659, SHIATS BW-1662, SHIATS BW-1706, SHIATS BW-1708
3	9.00	6.97	SHIATS BW-1614, SHIATS BW-1620, SHIATS BW-1621, SHIATS BW-1622, SHIATS BW-1627, SHIATS BW-1628, SHIATS BW-1638, SHIATS BW-1641, SHIATS BW-1643
4	3.00	0.74	SHIATS BW-1636, SHIATS BW-1691, SHIATS BW-1701
5	8.00	1.88	SHIATS BW-1645, SHIATS BW-1670, SHIATS BW-1680, SHIATS BW-1685, SHIATS BW-1686, SHIATS BW-1704, SHIATS BW-1705, SHIATS BW-1707
6	25.00	10.29	SHIATS BW-1602, SHIATS BW-1604, SHIATS BW-1610, SHIATS BW-1612, SHIATS BW-16, SHIATS BW-1613, SHIATS BW-1616, SHIATS BW-1618, SHIATS BW-1631, SHIATS BW-1633, SHIATS BW-1637, SHIATS BW-1642, SHIATS BW-1646, SHIATS BW-1649, SHIATS BW-1654, SHIATS BW-1661, SHIATS BW-1663, SHIATS BW-1672, SHIATS BW-1675, SHIATS BW-1678, SHIATS BW-1682, SHIATS BW-1693, SHIATS BW-1695, SHIATS BW-1698, SHIATS BW-1702 SHIATS BW-1703
7	9.00	6.60	SHIATS BW-1607, SHIATS BW-1608, SHIATS BW-1617, SHIATS BW-1632, SHIATS BW-1650, SHIATS BW-1666, SHIATS BW-1671, SHIATS BW-1679, SHIATS BW-1696
8	6.00	8.63	SHIATS BW-1601, SHIATS BW-1606, SHIATS BW-1629, SHIATS BW-1630, SHIATS BW-1648, SHIATS BW-1655,

9	12.00	6.36	SHIATS BW-1603, SHIATS BW-1605, SHIATS BW-1626, SHIATS BW-1634, SHIATS BW-1639, SHIATS BW-1647, SHIATS BW-1653, SHIATS BW-1656, SHIATS BW-1657, SHIATS BW-1660, SHIATS BW-1669, SHIATS BW-1676
10	7.00	2.55	SHIATS BW-1611, SHIATS BW-1624, SHIATS BW-1684, SHIATS BW-1687, SHIATS BW-1688, SHIATS BW-1690, SHIATS BW-1692
11	7.00	0.96	SHIATS BW-1644, SHIATS BW-1665, SHIATS BW-1667, SHIATS BW-1674, SHIATS BW-1689, SHIATS BW-1697, SHIATS BW-1699

Table 3: Average intra and inter cluster values among eleven clusters for wheat genotypes

	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster	VII Cluster	VIII Cluster	IX Cluster	X Cluster	XI Cluster
I Cluster	85.29	125.7	180.15	174.57	119.14	134.44	150.63	298.48	233.97	209.84	450.94
II Cluster		94.22	171.6	175.49	155.19	139.3	154.05	330.96	183.68	182.77	456.94
III Cluster			83.58	188.37	190.57	161.56	182.73	405.08	289.08	292.51	378.97
IV Cluster				93.03	293.55	204.05	277.39	613.85	450.85	394.26	586.43
V Cluster					91.96	173.08	154.15	191.96	163.94	164.29	401.04
VI Cluster						66.34	124.87	377.68	269.75	189.07	433.05
VII Cluster							117.36	303.39	196.56	212.88	489.14
VIII Cluster								129.74	178.05	211.89	456.74
IX Cluster									90.24	161.14	433.13
X Cluster										99.57	324.64
XI Cluster											171.58

Table 4: Mean performance of wheat genotypes included in eleven clusters for sixteen characters.

S. No.	Days to 50 % Heading	Days to 50 % Flowering	Plant Height	Spike Length	Spike Weight	Tillers/ Plant	Grain Filling Period	Grains /Spike	Grain Yield/ Plant	Test Weight	Chlorophyll Content	Membrane Thermo-stability	Harvest Index	Canopy Temperature Depression	Days to 50% Maturity	Biological Yield/ Plant
I Cluster	72.60	78.21	94.61	17.52	2.38	5.95	34.02	38.48	6.30	39.73	40.45	32.46	30.99	5.28	112.23	20.46
II Cluster	73.47	78.31	91.34	15.88	2.50	6.37	36.67	39.14	5.55	38.22	39.33	31.65	30.70	5.65	115.08	18.60
III Cluster	74.63	79.44	99.26	17.16	1.88	5.52	32.82	31.07	4.72	37.81	37.52	33.66	26.34	4.50	112.26	18.00
IV Cluster	73.39	79.11	90.58	15.77	2.57	5.01	31.44	41.62	7.04	40.12	41.38	27.27	27.72	4.96	110.56	24.46
V Cluster	73.00	78.73	87.60	16.49	2.65	6.24	35.10	41.67	5.83	37.82	41.63	31.48	31.37	5.33	114.85	18.87
VI Cluster	73.36	78.95	88.84	16.94	2.38	6.32	34.23	39.98	5.98	39.22	40.11	31.04	32.07	4.54	113.19	19.11
VII Cluster	73.65	79.24	86.35	17.33	2.47	5.67	33.15	42.99	5.79	38.81	39.16	28.21	30.15	4.94	112.39	20.18
VIII Cluster	74.69	80.53	89.68	17.94	2.43	6.16	35.31	36.74	5.90	38.43	40.73	28.72	28.03	4.18	115.83	20.88
IX Cluster	74.36	79.99	93.67	16.45	2.47	6.54	34.42	40.32	6.28	40.90	41.81	30.19	31.64	5.15	114.40	20.59
X Cluster	73.55	79.26	90.01	17.37	2.43	5.41	33.67	37.86	5.80	38.93	40.28	29.46	29.86	4.54	112.93	19.33
XI Cluster	72.45	77.74	96.44	16.64	2.34	6.01	34.14	34.38	5.02	34.24	37.84	31.59	30.02	5.61	111.88	16.06

Table 5: Percentage contribution of each character to divergence

S. No.	Source	Contribution %
1	Days to 50 % heading	2.08
2	Days to 50 % flowering	4.81
3	Plant height	12.34
4	Spike length	4.71
5	Spike weight	0.19
6	Tillers/ plant	0.62
7	Grain filling period	3.17
8	Grains /spike	11.75
9	Grain yield/ plant	0.01
10	Test weight	0.40
11	Chlorophyll content	34.09
12	Membrane stability	16.63
13	Harvest index	0.01
14	Canopy temperature Depression	5.73
15	Days to 50% maturity	0.03
16	Biological yield/ plant	3.44

Conclusion

The mean sum of square due to genotypes were significant for all the character studied, High value for genetic coefficient of variability (GCV) are shown for spike weight, number of

grains per spike, grain yield per plant, biological yield per plant and canopy temperature depression under heat stress condition. High estimate of heritability acquired for all the traits with the exception of harvest index. In the current study high heritability estimate coupled with high genetic advance were observed for plant height, grain per spike, and membrane stability. Based on the result of diversity 108 genotypes were grouped into eleven cluster. Cluster VI had largest number of genotypes (25) followed by cluster I (16), where cluster IV has least number of genotypes (3). The maximum intra –cluster distance was detected for cluster XI (171.581), followed by VIII (129.736), In contrast cluster VII had minimum intra – cluster distance (66.339). In the present investigation the highest contribution in expression of genetic divergence was exhibited by chlorophyll content (34.09) followed by membrane stability (16.36), whereas harvest index showed the minimum percent contribution character toward genetic divergence.

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6. References

1. CIMMYT. Wheat-Global Alliance for Improving Food Security and the Livelihoods of the Resources-Poor in the Developing World. 2016.
2. De RN, Reddy JN, Rao AVS, Mohanty KK. Genetic divergence in early rice under two situation. Indian Journal. Genetics. 1992; 52:225-229.
3. Deshmukh PB, Atale SB, Pandey MK, Vithare DG, Golhar SR. Genetic divergence in durum wheat. Crop Improvement, 1999; 26(1):95-98.
4. DWR. Proceedings, Recommendations & Plan of Work (2011-12). In: 49th All India Wheat and Barley Research Workers' Meet, 2016, 27-30.
5. Gill B, Appels RA, Botha-Oberholster C, Buell J, Bennetzen B, Chalhoub. Workshop report on wheat genome sequencing: International genome research on wheat consortium. Genetics. 2004; 168:1087-1096.
6. Hays DB, Mason RE, Morgan G, Finlayson SA. Heat stress induced ethylene production in developing wheat grains induces kernel abortion and increased maturation in a susceptible cultivar. Plant Science, 2007; 172:1113-1123.
7. Hussain AM, Maqsood A, Ahmad S, Aftab, Ahmad Z. Effect of irrigation during various development stages on yield, component of yield and harvest index of different wheat cultivars. Pakistan Journal of Agricultural Sciences. 1998; 34:104-106.
8. Johnson HW, Robinson AE, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955; 47:314-318.
9. Kumar B, Lal GM, Upadhyay A. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). Asian Journal of Agricultural Sciences. 2009; 1(1):4-6.
10. Ortiz R, Sayre KD, Govaerts B, Gupta R, Subbarao GV, Ban T *et al.* Climate change: can wheat beat the heat? Agriculture, Ecosystems & Environment. 2008; 126:46-58.
11. Panse VG, Sukhatme PV. Statistical methods for agricultural workers, ICAR Publication, New Delhi, (IInd edition), 1967, 381.
12. Rajaram S, Braun H. Wheat yield potential International Symposium on Wheat Yield Potential: Challenges to International Wheat Breeding. CIMMYT, Mexico, D, 2008, 103-107.
13. Redhu AS, Solanki YPS, Sethi SK, Singh I. Genetic diversity in some Indian exotic wheat varieties. Crop Improvement. 1995; 22(2):214-217.
14. Reynolds MP, Nagarajan S, Razzaque MA, Ageeb OAA. Application of physiology in wheat breeding. CIMMYT, Mexico, DF, 2001.
15. Sharma PK, Gupta PK, Balyan HS. Genetic diversity in a large collection of wheat (*Triticum spp.*). Indian Journal of Genetics and Plant Breeding. 1998; 58(3):271-278.
16. Singh AK, Singh SB, Singh AP, Sharma AK. Genetic variability, character association and path analysis for seed yield and its component characters in wheat (*Triticum aestivum* L.) under rain-fed environment. Indian Journal of Agriculture Research. 2012; 46(1):48-53.
17. Singh BN, Vishwakarma SR, Singh VK. Character association and path analysis in elite lines of wheat (*Triticum aestivum* L.). Plant Archives. 2010; 10(2):845-847.
18. Singh SP, Jha PB, Singh DN. Genetic variability for polygenic traits in late sown wheat genotypes. Annals of Agriculture Research. 2001; 22(1):124-129.
19. Tripathi D, Dessalegn T, Dessalegn Y, Share G. Genetic variability, correlation and path analysis in durum wheat germplasm (*Triticum durum*). Agriculture Research and Reveals, 2005, 107-112.
20. Verma PN, Singh BN, Singh G, Singh MK, Tim L, Setter TL. Genetic diversity analysis for yield and other agronomic traits in bread wheat under water logged sodic soil condition. Journal of Wheat Research. 2014; 6(1):51-58.
21. Wahid A, Gelani S, Ashraf M, Foolad MR. Heat tolerance in plants: an overview Environmental and Experimental Botany. 2007; 61(3):199-223.
22. Wiegand CL, Cuellar JA. Duration of grain filling and kernel weight of wheat as affected by temperature. Crop Science. 1981; 21:95-101.