# Enumeration of genetic parameters and genetic diversity of morpho-physiological traits in CIMMYT bread wheataccessions [*Triticum aestivum* (L.) em. Thell]

## Abstract

Fifty genotypes of CIMMYT bread wheat were evaluated at Agricultural Research Farm, BHU, Varanasi during 2019-2020.The analysis of variance revealed significant differences among genotypes for all traits. High Phenotypic coefficient of variation was recorded compared to the genotypic coefficient of variation. However. high genotypic coefficients of variationwere found particularly for: grain yield per plot (8.71), harvest index (9.22), test weight (8.9), normalized difference vegetative index (9.59) and chlorophyll content (9.79), suggesting that these traits are having ample genetic potential for selection amongst genotypes, in breeding programs. The highest broad sense heritability manifested for harvest index (91.61%); remaining traits showed moderate estimates of heritability. Low to moderate genetic advance as percent mean was estimated for all the traits studied. This suggests the existence of variability for agronomic traits in the studied wheat genotypes which, should be exploited during future breeding programmes. Fifty genotypes were divided into six non-overlapping distinct clusters using tocher's method based on Euclideandistances. Thirty-one genotypes were classified in the first cluster accounting 62% of total genotypes followed by 15 genotypes categorized in the second cluster. The remaining four clusters have one genotype each. Divergence and cluster mean show that, crossings between genotypes of clusters (II, III), and VI could lead to recovery of good transgressive segregants for maximum heterosis inwheat varietal improvement.

**Keywords**: PCV, GCV, Heritability, Genetic advance as percent mean, Genetic diversity, Genetic variability

## 1. Introduction

Wheat (*Triticum aestivum* (L.) em. Thell; $2n = 6x = 42$) is one of the most important cereals of the world, belonging to thePoaceae family. It, accounts for one-sixth of all agricultural land (Kumar, 2014). Wheat is cultivated on about 220.83 mha with an annual yield of about 769.31 million tonnes (Giraldoet al.,2019). It is anticipated that by 2050, demand for wheat will have expanded by 50%, from current levels. There is no way to expand the area under production (CIMMYT, 2022).The only remaining option therefore, is to boost productivity by developing better high yielding wheat varieties and better,management of crop production.

The Global Wheat Program of the International Maize and Wheat Improvement Centre (CIMMYT), is one of the most important public sources of nutritious, high-yielding, disease- and climate-resilient wheat varieties for Africa, Asia, and Latin America. CIMMYT is therefore, a central pillar for more resilient agri-food systems in the above said continents countries (Dreisigackeret al., 2021). CIMMYT breeding lines can be traced in the pedigree of varieties sown on over 60 mha, around the world (CIMMYT, 2022).

Grain yield is a highly complex polygenic trait that is influenced by many component traits and the environment (Kumari et al.,2017). Increasing yield through direct selection is difficult thus, component traits should be considered while selecting to increase yield. Understanding the genetic makeup of various of yield traits, is crucial for this purpose (Kumari et al.,2017). Variabilitycan be additionally partitioned into phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) which, further aids in the selection of potential genotypes from amongst the available germplasm. The coefficient of variation simply reveals the level of variability existing for traits, but it provided no information on the heritable portion of that existing variability (Nzuveet al.,2014). In order to analyse the relative contributions of genetic and non-genetic components to the overall phenotypic variance in a population, it is important to consider both, heritability, and genetic variability. Genetic advance is the estimation of expected gain resulting from selection pressure on the breeding material. High heritability associated with high genetic advance for different yield components has a better scope for selecting high-yielding genotypes (Yadawadet al.,2015). Hence heritability and genetic advance are critical selection parameters.

Crop genetic diversity provides an opportunity to develop varieties that are widely adapted to a specific environment (Govindarajet al.,2015). In order to address changing end-user demands, increase productivity and adaptability to unpredictable climate change are desirable in a crop. Crop genetic diversity is regarded as a source of novel alleles for crop development (Tester and Langridge,2010). The greater the genetic separation between parents, the more is the possibility to produce heterosis in progeny (Joshi and Dhawan, 1966). Therefore, the present investigation was carried out to achieve information on various genetic parameters and genetic diversity existing in importantmorpho-physiological traits in CIMMYT bread wheat accessions.

## 2. Material and methods

### 2.1. Plant materials and phenotypic evaluations

Material used for the experiment was sown during *Rabi* season 2019-20 at the Agriculture Research Farm, Banaras Hindu University, Varanasi, consisting of 49diverse genotypes of bread wheat collected from CIMMYT, Mexico along with local check variety DBW 187 (Supplementary Table 1).Thematerial was sown in randomized block design (RBD) with 2 replications by maintaining inter-plot gap of 50 cm and within each replication, genotypes were sown in 6 rows of 5 m length with an inter-row spacing of 20 cm and plant to plant spacing of 5 cm. Recommended agronomic practices and plant protection measures were followed to raise a healthy crop. Weather conditions during the crop season are given in Supplementary Figure 1.

The observations were recorded on thirteen traits like germination percentage (GNP), days to 50 %flowering (DTFF), days to maturity (DTM), chlorophyll content (CFC), normalized difference vegetative index (NDVI), canopy temperature (CNTP) in°C, plant height (PTH) in cm, spike length (SKL) in cm,tillers per square metre (TPSM), test weight (TWT)in grams, biological yield per plot (BYPP) in kg, grain yield per plot (GYPP) in kg, harvest index (HI) in %.With a Minolta SPAD-502 Chlorophyll metre, CFC was measured at the heading and anthesis phases, while CNTP was measured from the vegetative stage to dough stages using, a hand-held infrared thermometer.

### 2.2 Statistical analysis

Descriptive statistics and analysis of variance (Panse and Sukhatme (1969) model) were carried out using INDOSTAT software.GCV and PCV were calculated as per the standard formula suggested bySearle (1961). The formula provided by Allard (1960) was used to calculate genetic advance as percentage of mean (GAM) and broad sense heritability ($h^2_b$). Mahalanobis (1936) $D^2$ statistic was used to measure the genetic divergence among 50 genotypes.

## 3. Results and discussion

### 3.1 Phenotypic evaluation

ANOVA showed significant differences among the genotypes indicating presence of sufficient variability in the germplasm for the studied traits suggesting, ample scope for further improvement (Table 1). Similar results were also reported by Arya et al. (2017), and Upadhyayet al. (2020).

**Table 1: Analysis of variance for 13 morpho-physiological traits in 50 bread wheat accessions**

| Sl.No. | Source | MeanSumofSquares(MSS) | | |
|---|---|---|---|---|
| | | Replication | Treatment | Error |
| | Degreesoffreedom | 1 | 49 | 49 |

|  |  |  |  |  |
|---|---|---|---|---|
| 1 | GNP | 4.0760 | 48.499** | 20.953 |
| 2 | DTFF | 11.4580 | 39.868** | 20.3 |
| 3 | CNTP | 6.6820 | 9.11* | 4.656 |
| 4 | NDVI | 0.8850 | 103.58** | 31.696 |
| 5 | DTM | 128.6180 | 188.278** | 85.935 |
| 6 | CFC | 22.5630 | 47.931** | 12.449 |
| 7 | TPSM | 0.3270 | 155.782** | 62.202 |
| 8 | PTH | 13.3740 | 100.39* | 51.31 |
| 9 | SKL | 0.6270 | 2.526** | 1.286 |
| 10 | BYPP | 0.0180 | 1.817** | 0.923 |
| 11 | TWT | 14.3110 | 63.024** | 32.037 |
| 12 | HI | 1.610 | 18.455** | 0.807 |
| 13 | GYPP | 0.0010 | 0.231** | 0.118 |

* Significant at P = 0.05, ** Significant at P = 0.01

Where, GNP- Germination Percentage; DTFF- Days to 50 % Flowering; DTM- Days to Maturity; CFC- Chlorophyll Content; NDVI- Normalized Difference Vegetative Index; CNTP- Canopy Temperature; PTH- Plant Height (cm); SKL- Spike Length(cm); TPSM- Tillers Per Square Metre; TWT- Test Weight (g); BYPP- Biological Yield Per Plot (Kg); GYPP- Grain Yield Per Plot (Kg); HI- Harvest Index (%).

The range and mean value of all the traits have been provided in Supplementary table 2. TPSM showed a wider variation of 61(ACC-12) to 103 (ACC-30) with a mean value of 85. The lowest and highest value of GNP was observed in ACC-29 (78%) and ACC-47 (110%) respectively with a mean value of 92%. The lowest and highest values for DTFF were observed in ACC-47 (70 days) and ACC-46 (88 days) respectively with an average value of 78 days. The lowest and highest values of CNTPwere observed inACC-42(22.13°C) andACC-27 (32.74°C) respectively, with a population mean of 25.36°c. The lowest and highest values of NDVI recorded in ACC-22 (46.09) and ACC-37(82.14) respectively with an average value of 62.49. DTM exhibited a range from 103 (ACC-10) to 138 days (ACC-32,33) with a mean value of 117 days. CFC ranged from 34.67(ACC-23) to 56.25(ACC-17) with a mean of 42.99. For PTH lowest and highest values were recorded in ACC-18 (82.7 cm) and ACC-38 (117.1 cm)respectively with an average of 98.8 cm. SKL ranged from 9.4(ACC-9,11,31) to 14.9cm (ACC-14.9) with a mean of 11.34 cm.BYPP ranged from 6.85(ACC-18) to 11.66kg (ACC-32, ACC-33) with a population mean of 8.58 kg. GYPP ranged from 1.71(ACC-41) to 3.57kg (ACC-36) with a population mean of 2.72 kg. TWT ranged from 28.65 (ACC-41) to 55.03 g (ACC-6) with a population mean of 44.22 g. HI ranged from 24.41(AC-41) to 39.11%(ACC-36) with a population mean of 32.19%. GYPP ranged from 1.71(ACC-41) to 3.57kg (ACC-36) with a population mean of 2.74.

### 3.2 Genotypic and phenotypic variability

The study revealed that, PCV were higher than their corresponding GCV for all the traits among the genotypes (Figure1). This indicates that, characters were influenced by the environment. Selection based on phenotype alone, can be effective for the traits where variation between PCV and GCV were less, means such traits are less influenced by the environment. These findings are in agreement with a previous study in wheat (Upadhyayet al.,2020).

Higher values of GCV were recorded for CFC (9.79) followed by NDVI (9.59), HI (9.22), TWT (8.9), and GYPP (8.71) suggesting that, these traits possess ample genetic potential for selection among genotypes in breeding programs.Lower values however, were recorded for CNTP (5.88), DTM (5.79), GNP (4.04), DTFF (4.026).

Higher PCV values were observed for TWT (15.58), GYPP (15.27), BYPP (13.64), NDVI (13.16) while, lower values were recorded for GNP (6.42), DTFF (7.05) among the traits. A wide difference between GCV and PCV was observed for TWT (6.689), GYPP (6.566), SKL (5.234), and BYPP (5.847) respectively, indicating the influence of environment on these traits. However, the least difference was observed in HI (0.413), GNP(2.38), and CFC(2.98) indicating that, these traits have a high heritable genetic variation and are less influenced by the environment. The current results are in agreement with those of Arya et al.(2017), Kumar et al. (2019), and Upadhyayet al. (2020).

### 3.3 Heritability and genetic advance

Estimates of heritability and GAM are presented in Supplementary Table2. The highest value of heritability was revealed by HI (91.61), while all remainingtraits showed moderate estimates of heritability. Heritability estimations aid plant breeders in choosing superior genotypes from a variety of genetic groups. Similar results were also observed by Mohsin et al. (2019), Bayisaet al. (2020), and Bhanu et al. (2018).The highest GAM was recorded for HI (18.19) and lowest for GNP (5.25). Similar findings have also been reported by Mohsin et al. (2019), Upadhyayet al. (2020), Roy et al. (2021), and Yadav et al. (2021).

A character with high heritability does not necessarily also have high genetic advance, according to Johnson et al. (1955). A character may be assessed more precisely when heritability and genetic advance are investigated together, (Dudley and Moll, 1969). Consequently, Heritability estimates and GAM are typically more useful in finding gene action thatis involved in the expression of different polygenic traits along with, estimating the gain. High heritability coupled with moderate GAM was observed for HI (91.61 and 18.19) while moderate heritability with moderate GAM was recorded for NDVI (53.13 and 14.40), TPSM (42.93 and 10.89), CFC (58.76 and 15.47), TWT (32.59 and 10.46), and GYPP (32.51

and 10.23). Remaining traits exhibited moderate heritability coupled with, low GAM. Estimates of heritability, genetic advance, PCV, GCV for all the traits are displayed in Figure 1.

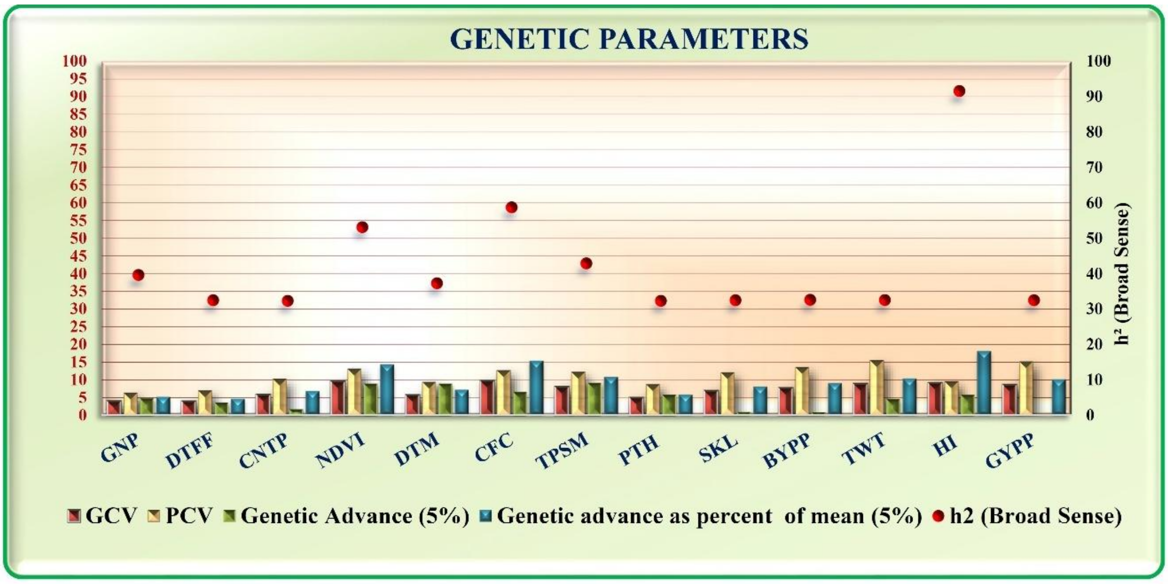

**Figure 1:** Graphical representation of genetic parameters of variation (GCV, PCV, Genetic Advance (5%), Genetic advance as percent of mean (5%), $h^2_b$ for 13 traits among 50 bread wheat accessions

*Abbreviations: GCV-Genotypic coefficient of variation, PCV-phenotypic coefficient of variation, $h^2_b$-Broad Sense heritability

### 3.4 Genetic divergence ($D^2$) Analysis

One effective method of determining genetic divergence is $D^2$ analysis (Mahalanobis,1936). To calculate the relative contribution of each component trait to the overall divergence and to measure the degree of differentiation at the intra- and inter-cluster levels, $D^2$ statistics is useful. Fifty genotypes were divided into six non-overlapping distinct clusters using Tocher's method based on, Euclidean distances so that, the genotypes within each cluster had lower $D^2$ values than the genotypes between the clusters (Figure 2). Similar findings have been reported by Kumar et al. (2013), Tsegayeet al., (2014), Arya et al., (2017), Singh et al., (2017) Santosh etal., (2019), and Devesh et al, (2019)Tocher's method for genotypes clustering.Table 2 shows the percent contribution of each trait towards total genetic divergence. The more a trait contributes to diversity, the more times it ranked first. The traits like GYPP ranked a greater number of times (196) in first position and showed the highest percent contribution (15.65%) towards total genetic divergence followed by, TWT (13.55), and PTH (13.34). Lowest percent contribution was reported by the trait CNTP (0.24) followed by, DTFF (1.71).

**Table 2: Percent contribution of each trait towards total genetic divergence**

| Sl.No. | Source | Contribution(%) | Timesranked1st |
|---|---|---|---|
| 1 | **GNP** | 4.24 | 53 |
| 2 | **DTFF** | 1.71 | 21 |
| 3 | **CNTP** | 0.24 | 3 |
| 4 | **NDVI** | 8.5 | 106 |
| 5 | **DTM** | 6.54 | 82 |
| 6 | **CFC** | 4.98 | 62 |
| 7 | **TPSM** | 2.38 | 30 |
| 8 | **PTH** | 13.34 | 167 |
| 9 | **SKL** | 9.62 | 120 |
| 10 | **BYPP** | 6.9 | 86 |
| 11 | **TWT** | 13.55 | 169 |
| 12 | **HI** | 12.35 | 154 |
| 13 | **GYPP** | 15.65 | 196 |

Cluster I had the most genotypes (31), followed by cluster II (15), while clusters III, IV, V, VI had just one genotype each (Table 3). Even though a particular cluster was produced, the genotypes within it were obtained from various locations. The genotype clustering pattern showed that, the genotypes acquired from the same location did not make up a single cluster. This shows that genetic and geographic diversity are not always related. Similar results were also reported by Upadhyayet al. (2020).

**Table 3: Clustering of 50 bread wheat accessions by tocher's optimization method**

| ClusterGroup | No. OfGenotypes | ListofGenotypes |
|---|---|---|
| **1Cluster** | 31 | ACC-32, ACC-33, ACC-50, ACC-26, ACC-40, ACC-44, ACC-49, ACC-35, ACC-34, ACC-4,ACC-9, ACC-8, ACC-15, ACC-31, ACC-13, ACC-36, ACC-23, ACC-39, ACC-27, ACC-45,ACC-14, ACC-42, ACC-43, ACC-46, ACC-48, ACC-24, ACC-1, ACC-30, ACC-19, ACC-28&ACC-3 |
| **2Cluster** | 15 | ACC-2, ACC-5, ACC-16, ACC-21, ACC-7, ACC-25, ACC-20, ACC-18, ACC-12, ACC-6,ACC-17,ACC-11, ACC-22, ACC-10 & ACC-29 |
| **3Cluster** | 1 | ACC-38 |
| **4Cluster** | 1 | ACC-41 |
| **5Cluster** | 1 | ACC-37 |

| | | |
|---|---|---|
| **6Cluster** | 1 | ACC-47 |

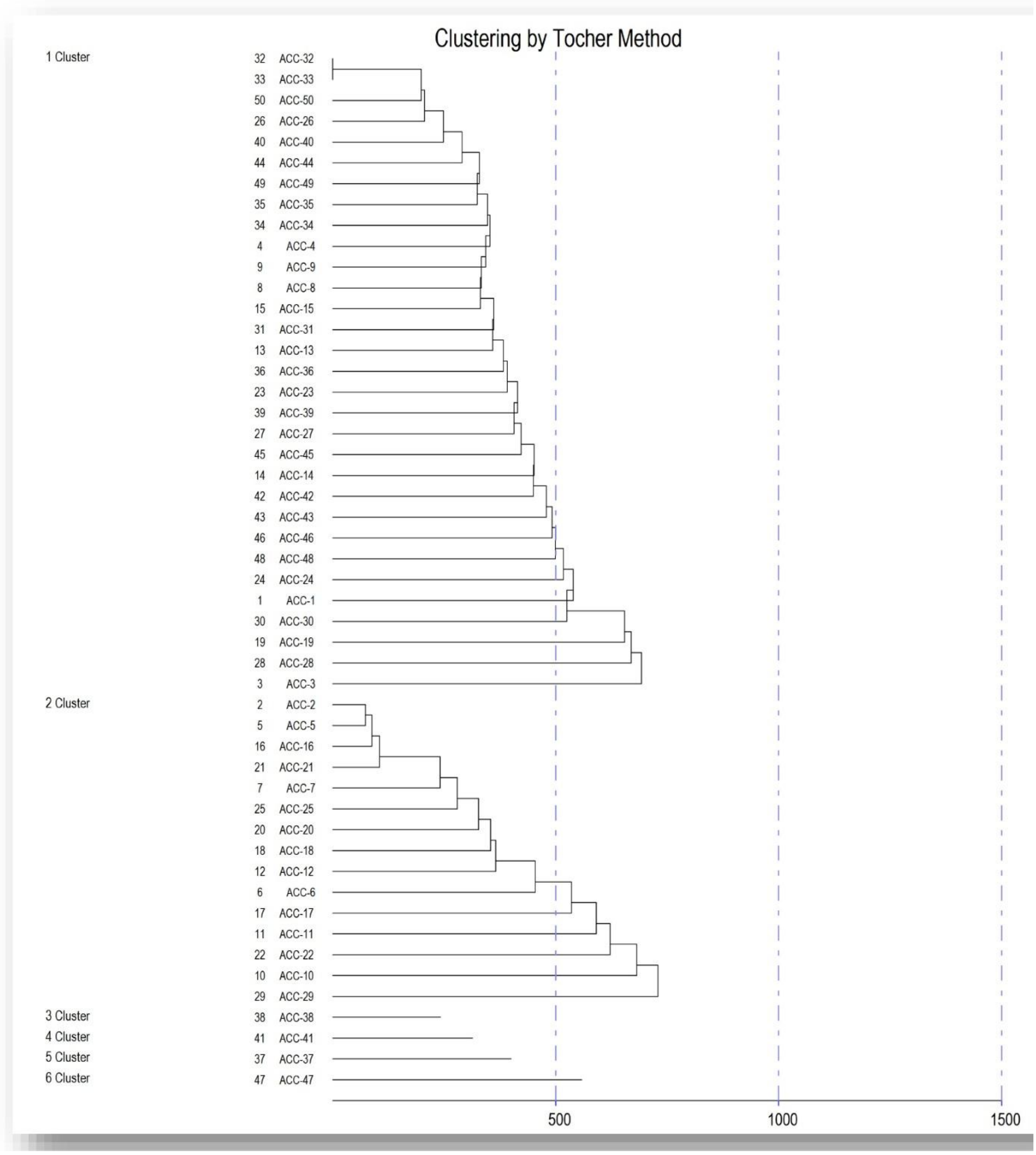

**Figure 2: Dendrogram of 50 bread wheat accessions for 13 traits**

In the current study, intra-cluster distances were lower than inter-cluster distances indicating the presence of a high degree of genetic diversity (Figure 3). Cluster II recorded the largest intra-cluster distance (553.67), followed by cluster I (500.53). While clusters III, IV, V and VI had only one genotype, no intra-cluster distance was thus, found (Table 4). It may therefore be concluded that, genotypes inside a cluster with a high degree of divergence would offer more suitable breeding materials for crop improvement (Dobariya et al., 2006).

The inter-cluster distance values ranged from 553.13 to 1908.08(Table 4). Cluster II and VI had the largest inter-cluster distance (1908.08), followed by cluster II and III (1774.78). The genotypes found in these clusters had a wide range of genetic diversity and might be employed in a wheat hybridization programme to recover better transgressive segregants,aiding the production of highyielding varieties. The smallest inter-cluster distances were found between clusters III and V (553.13), demonstrating a close association between these clusters and indicating that, they would not lead to satisfying outcomes.

**Table 4: Average intra cluster (diagonal) – inter cluster distances**

| | Cluster1 | Cluster2 | Cluster3 | Cluster4 | Cluster5 | Cluster6 |
|---|---|---|---|---|---|---|
| **Cluster1** | **500.53** | 970.94 | 796.76 | 814.50 | 862.76 | 1100.85 |
| **Cluster2** | 970.94 | **553.67** | 1774.78 | 1463.05 | 1180.62 | 1908.08 |
| **Cluster3** | 796.76 | 1774.78 | **0.00** | 1557.04 | 553.13 | 895.55 |
| **Cluster4** | 814.50 | 1463.05 | 1557.04 | **0.00** | 1228.44 | 1474.54 |
| **Cluster5** | 862.76 | 1180.62 | 553.13 | 1228.44 | **0.00** | 1083.11 |
| **Cluster6** | 1100.85 | 1908.08 | 895.55 | 1474.54 | 1083.11 | **0.00** |

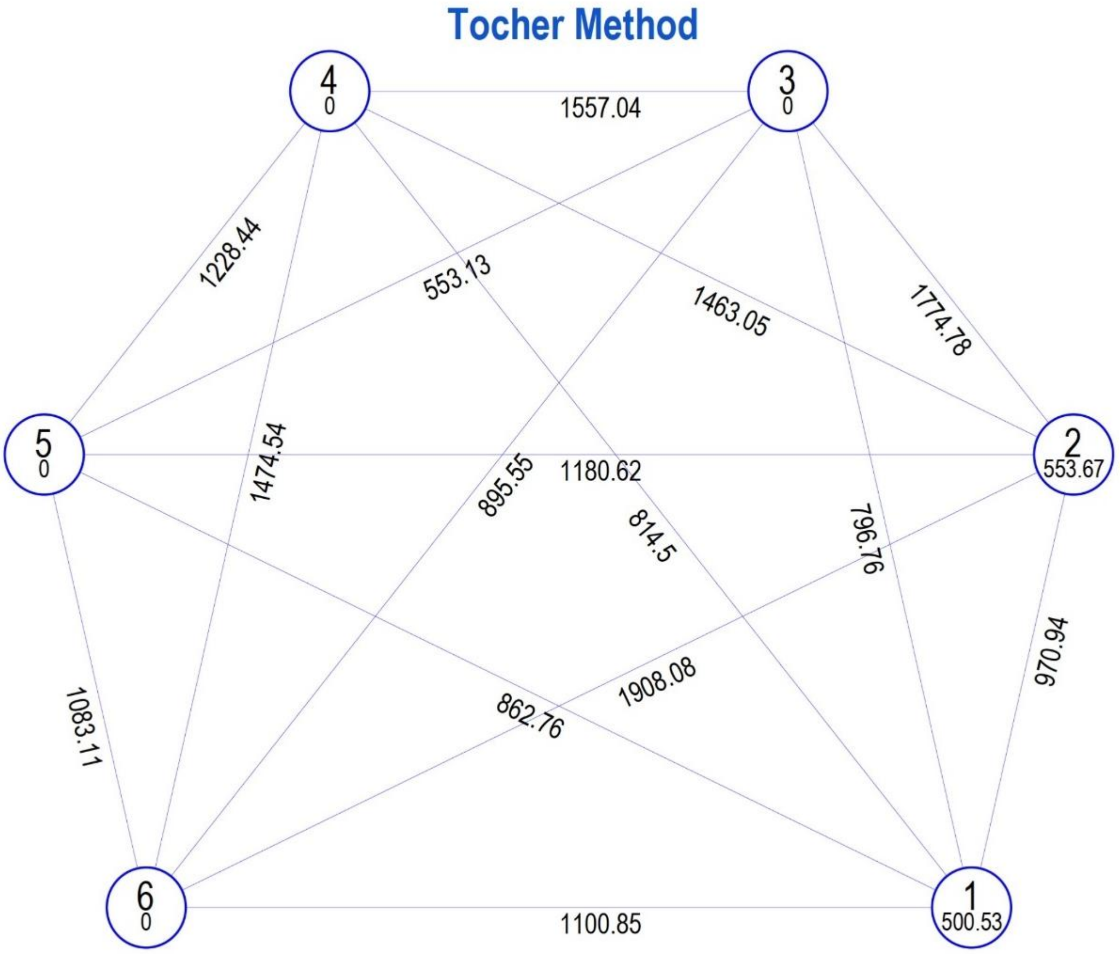

**Figure 3: Cluster diagram of 50 bread wheat accessions using tocher method**

The cluster means of all studied traits are presented in Table 5. The differences between the clusters for each trait were revealed by the values of the cluster meansfor those traits. GNP cluster mean values ranged from 88.13 (cluster IV) to 110.75 (cluster VI). Cluster means of DTFFvaried from 70.65 (cluster II) to 84.22 cm (cluster V). For CNTP cluster means ranged from 24.53(cluster VI) to 27.57(cluster IV). For NDVI cluster means ranged from 59.50(cluster II) to 82.14(cluster V). DTM cluster mean values ranged from 111.76 (cluster II) to 133.02 (cluster III and IV). CFC cluster mean values ranged from 38.44 (cluster III) to 48.47 (cluster VI). TPSM cluster mean values ranged from 77.71 (cluster II) to 96.92 (cluster VI). For PTH cluster means ranged from 84.53(cluster IV) to 117.12(clusterIII). For SKL cluster means ranged from 10.42(cluster IV and VI) to 12.55(cluster III). For BYPP cluster means ranged from 7.16(cluster IV) to 9.72(cluster V). Cluster means of TWT varied from 28.65 (cluster IV) to 48.42 (cluster II). Cluster means of HI varied from 24.41 (cluster IV) to 33.79 (cluster II). GYPP Cluster means varied from 1.71 (cluster IV) to 3.20 (cluster I). The highest mean value for DTM and the lowest for GYPP were observed among all clusters. Results on divergence and cluster mean reveal that, crossings between genotypes of clustersII, III, and VI could lead to achievement of maximum heterosis and recovery of better transgressive segregants; for wheat improvement (Arya et al.2017).

**Table 5: Cluster Means for 13 morpho -physiological traits in 50 bread wheat accessions**

| | GNP | DTFF | CNTP | NDVI | DTM | CFC | TPSM | PTH | SKL | BYPP | TWT | HI | GYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Cluster1** | 91.48 | 78.97 | 25.28 | 62.20 | 128.48 | 42.61 | 87.39 | 100.39 | 11.59 | 8.89 | 42.69 | 31.69 | 2.79 |
| **Cluster2** | 91.15 | 74.64 | 25.44 | 59.50 | 111.76 | 43.32 | 77.71 | 94.78 | 10.88 | 7.90 | 48.42 | 33.79 | 2.65 |
| **Cluster3** | 93.09 | 83.09 | 24.54 | 76.45 | 133.02 | 38.44 | 89.91 | 117.12 | 12.55 | 9.10 | 44.79 | 30.29 | 2.70 |
| **Cluster4** | 88.13 | 79.13 | 27.57 | 66.96 | 133.02 | 44.71 | 86.41 | 84.53 | 10.42 | 7.16 | 28.65 | 24.41 | 1.71 |
| **Cluster5** | 88.14 | 84.22 | 26.05 | 82.14 | 116.83 | 46.97 | 88.41 | 105.35 | 10.96 | 9.72 | 42.19 | 32.95 | 3.20 |
| **Cluster6** | 110.75 | 70.65 | 24.53 | 78.35 | 133.01 | 48.47 | 96.92 | 100.83 | 10.42 | 8.90 | 45.76 | 32.48 | 2.89 |

## Conclusion

Wide range of variability for most of the traits were observed among the germplasm accessions evaluated, indicating a considerable scope for the selection of desired genotypes that contribute directly or indirectly towards crop improvement. High heritability with high genetic advance was recorded for grain yield per plot, representing the contribution of on additive gene effect and the probability of improving the traits, by selection.It is possible to determine the type of gene action involved in the manifestation of various polygenic traits as well as, estimate the genetic advance, under selection, by using the derived heritability estimates and genetic advance. Divergence and cluster mean show that genotype crosses among clusters II, III, and VI may lead to higher heterosis and,recovery of best transgressive segregants for the development of better wheat varieties/hybrids.

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**Supplementary Table 1:** List of accessions procured from CIMMYT and their codes

| S.no | Accession | Name |
|---|---|---|
| 1 | ACC-1 | **DBW 187** |
| 2 | ACC-2 | **NADI #2** |
| 3 | ACC-3 | **QUAIU #1/SUP152** |
| 4 | ACC-4 | **WBLL1*2/BRAMBLING/4/BABAX/LR42//BABAX*2/3/SHAMA*2/5/PBW343*2/KUKUNA*2//FRTL/PIFED** |
| 5 | ACC-5 | **KACHU #1/KIRITATI//KACHU/3/BECARD/FRNCLN** |
| 6 | ACC-6 | **BABAX/LR42//BABAX*2/3/KUKUNA/4/BACEU #1/5/BECARD/6/KACHU/KINDE** |
| 7 | ACC-7 | **BABAX/LR42//BABAX/3/ER2000/4/KACHU #1/KIRITATI//KACHU** |
| 8 | ACC-8 | **KACHU*2/SUP152** |
| 9 | ACC-9 | **SAUAL/YANAC//SAUAL/3/2*KFA/2*KACHU** |
| 10 | ACC-10 | **KANCHAN*2/JUCHI//2*BORL14** |
| 11 | ACC-11 | **WBLL1*2/BRAMBLING//WBLL1*2/BRAMBLING/3/2*BORL14** |
| 12 | ACC-12 | **FRANCOLIN #1*2/HAWFINCH #1//2*MUCUY** |
| 13 | ACC-13 | **PBW65/2*PASTOR//TACUPETO F2001*2/BRAMBLING/3/TACUPETO F2001*2/BRAMBLING/6/2*SHORTENED SR26 TRANSLOCATION/4/ATTILA/3*BCN//BAV92/3/PASTOR/5/MUNAL** |
| 14 | ACC-14 | **MUU/KBIRD//2*KACHU/KIRITATI** |
| 15 | ACC-15 | **MUU/KBIRD//2*KACHU/KIRITATI** |
| 16 | ACC-16 | **WBLL1*2/BRAMBLING//VORB/FISCAL/3/BECARD/4/MUCUY/5/MUCUY** |

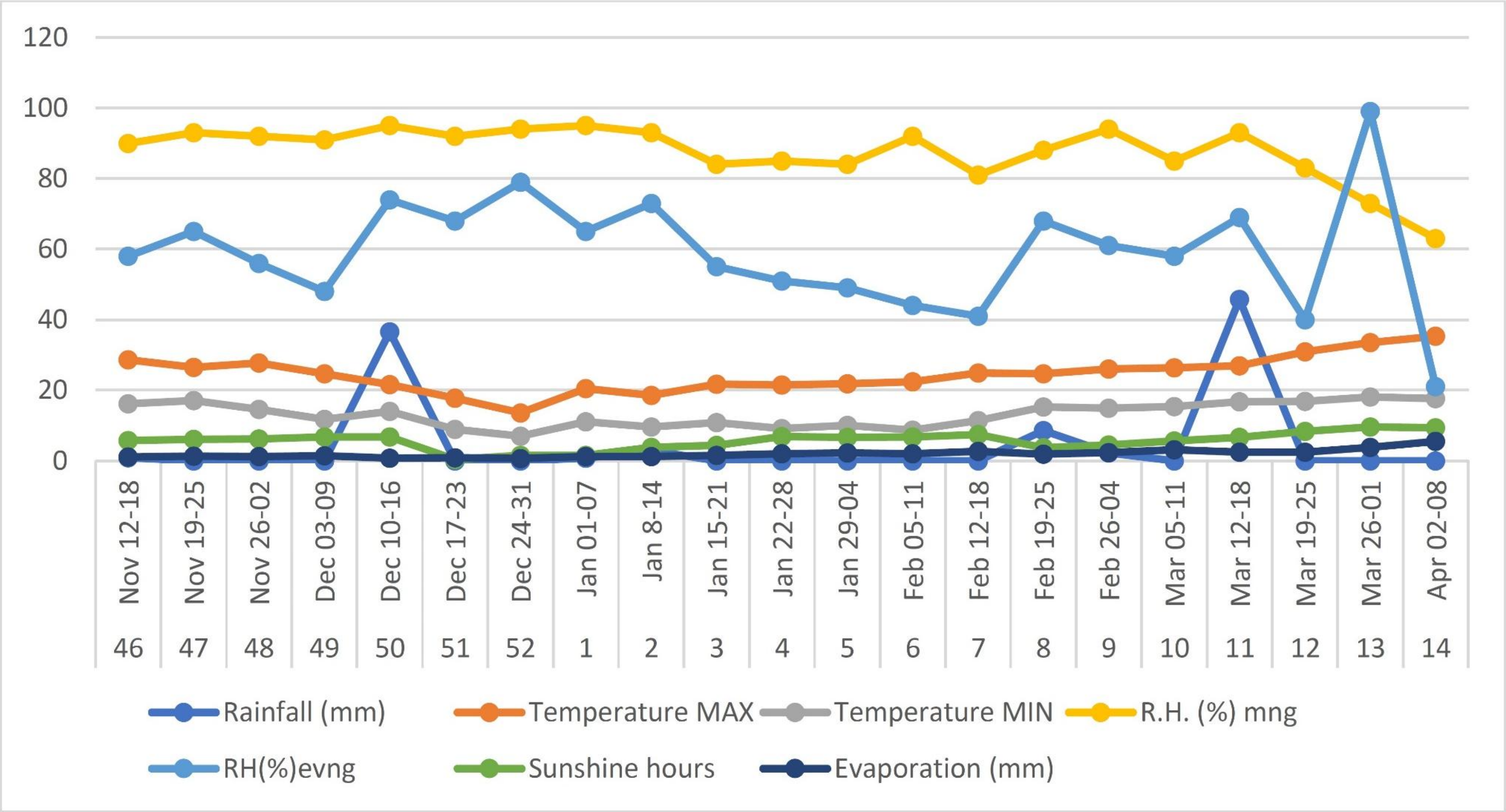
| | | |
|---|---|---|
| 17 | ACC-17 | **SUP152/BLOUK #1//BECARD/FRNCLN** |
| 18 | ACC-18 | **ALTAR 84/AE.SQUARROSA (221)//3*BORL95/3/URES/JUN//KAUZ/4/WBLL1/5/MUTUS/6/SUP152/BAJ #1** |
| 19 | ACC-19 | **BECARD/FRNCLN//BORL14** |
| 20 | ACC-20 | **SNTL/3/KACHU//WBLL1*2/BRAMBLING** |
| 21 | ACC-21 | **BORL14*2//BECARD/QUAIU #1** |
| 22 | ACC-22 | **BORL14*2//BECARD/QUAIU #1** |
| 23 | ACC-23 | **BORL14*2//BECARD/QUAIU #1** |
| 24 | ACC-24 | **WBLL1*2/BRAMBLING/4/BABAX/LR42//BABAX*2/3/SHAMA*2/5/BECARD/QUAIU #1** |
| 25 | ACC-25 | **NADI#1*2/3/MUTUS/AKURI #1//MUTUS** |
| 26 | ACC-26 | **SHAKTI/6/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/T.DICOCCON PI94625/AE.SQUARROSA (372)//SHA4/CHIL/5/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1** |
| 27 | ACC-27 | **CHIPAK/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU** |
| 28 | ACC-28 | **BORL14*2/MISR 1** |
| 29 | ACC-29 | **SAUAL/3/ACHTAR*3//KANZ/KS85-8-4/4/SAUAL/5/2*BAJ #1/3/KIRITATI//ATTILA*2/PASTOR** |
| 30 | ACC-30 | **SUP152/BLOUK #1//2*BECARD/FRNCLN** |
| 31 | ACC-31 | **MUTUS*2/MUU//2*MUCUY** |
| 32 | ACC-32 | **BECARD/FRNCLN*2//BORL14** |
| 33 | ACC-33 | **KACHU/BECARD//WBLL1*2/BRAMBLING*2/3/ONIX/KBIRD** |
| 34 | ACC-34 | **KACHU/BECARD//WBLL1*2/BRAMBLING*2/3/FRNCLN*2/TECUE #1** |
| 35 | ACC-35 | **KACHU/BECARD//WBLL1*2/BRAMBLING*2/3/KACHU/KINDE** |
| 36 | ACC-36 | **KACHU/BECARD//WBLL1*2/BRAMBLING*2/8/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA** |

| | | |
|---|---|---|
| | | **(213)//PGO/4/HUITES/5/T.DICOCCON PI94624/AE.SQUARROSA (409)//BCN/6/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES/7/MUTUS** |
| 37 | ACC-37 | **KACHU #1/3/T.DICOCCON PI94624/AE.SQUARROSA (409)//BCN/4/2*KACHU*2/5/KACHU/KINDE** |
| 38 | ACC-38 | **NADI#2*2/6/BECARD #1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ** |
| 39 | ACC-39 | **MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/2*SUP152*2/TECUE #1** |
| 40 | ACC-40 | **MACE/5/TILILA/JUCHI/4/SERI.1B//KAUZ/HEVO/3/AMAD/6/KACHU/BECARD//WBLL1*2/BRAMBLING** |
| 41 | ACC-41 | **KACHU//KIRITATI/2*TRCH/3/KFA/2*KACHU** |
| 42 | ACC-42 | **KACHU//KIRITATI/2*TRCH/3/KFA/2*KACHU** |
| 43 | ACC-43 | **MUU/FRNCLN//FRANCOLIN #1/3/BORL14** |
| 44 | ACC-44 | **WBLL1*2/BRAMBLING*2//BAVIS/3/KACHU #1/KIRITATI//KACHU** |
| 45 | ACC-45 | **WBLL1*2/BRAMBLING*2//BAVIS/3/KFA/2*KACHU** |
| 46 | ACC-46 | **KENYA SUNBIRD/2*KACHU/3/WBLL1*2/BRAMBLING*2//BAVIS** |
| 47 | ACC-47 | **SUNCO.6/FRAME//PASTOR/3/NAVJ07/4/1447/PASTOR//KRICHAUFF/5/BORL14** |
| 48 | ACC-48 | **BABAX/LR42//BABAX*2/3/SHAMA/4/TACUPETO F2001*2/BRAMBLING/5/BORL14** |
| 49 | ACC-49 | **KACHU*2/3/ND643//2*PRL/2*PASTOR/4/KIDEA** |
| 50 | ACC-50 | **BORL14*2/FITIS** |

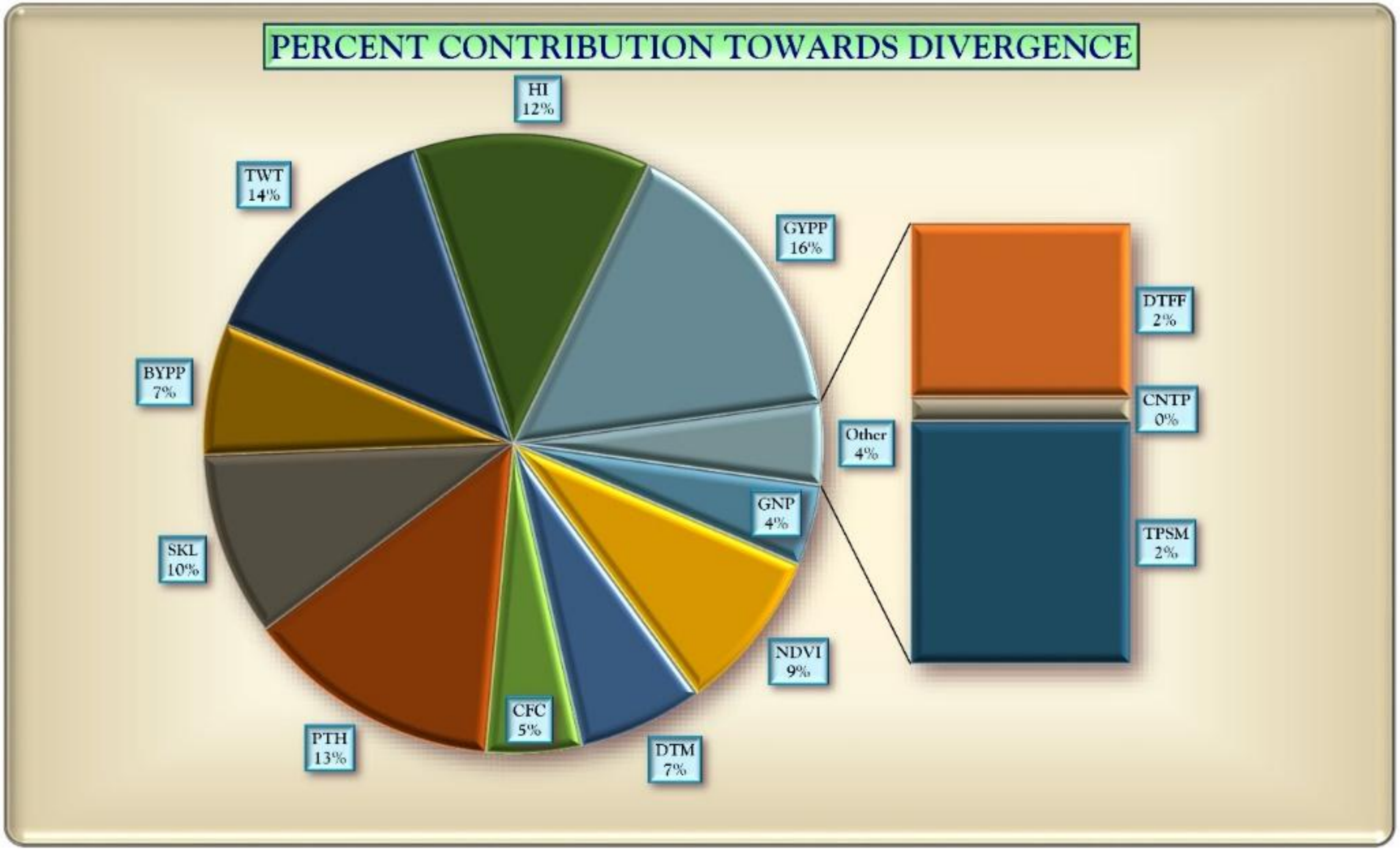
**Supplementary Table 2: Genetic variability parameters for 13 morpho -physiological traits in 50 bread wheat accessions**

| Sl. No. | Traits | Minimum | Maximum | mean | $V_g$ | GCV | $V_p$ | PCV | $h^2_b$ | GA(5 %) | GAM(5 %) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | **GNP** | 78 | 110 | 92 | 13.773 | 4.049 | 34.726 | 6.429 | 39.662 | 4.815 | 5.252 |
| **2** | **DTFF** | 70 | 88 | 78 | 9.784 | 4.026 | 30.084 | 7.059 | 32.522 | 3.675 | 4.729 |
| **3** | **CNTP** | 22.13 | 32.74 | 25.36 | 2.227 | 5.885 | 6.883 | 10.345 | 32.359 | 1.749 | 6.896 |
| **4** | **NDVI** | 46.09 | 82.14 | 62.49 | 35.942 | 9.594 | 67.638 | 13.161 | 53.139 | 9.003 | 14.407 |
| **5** | **DTM** | 103 | 138 | 117 | 51.171 | 5.792 | 137.106 | 9.481 | 37.322 | 9.003 | 7.289 |
| **6** | **CFC** | 34.67 | 56.25 | 42.99 | 17.741 | 9.798 | 30.19 | 12.782 | 58.764 | 6.651 | 15.473 |
| **7** | **TPSM** | 61 | 103 | 85 | 46.79 | 8.073 | 108.992 | 12.322 | 42.93 | 9.233 | 10.897 |
| **8** | **PTH** | 82.7 | 117.1 | 98.8 | 24.54 | 5.012 | 75.85 | 8.812 | 32.353 | 5.804 | 5.873 |
| **9** | **SKL** | 9.4 | 14.9 | 11.34 | 0.62 | 6.945 | 1.906 | 12.179 | 32.524 | 0.925 | 8.16 |
| **10** | **BYPP** | 6.85 | 11.66 | 8.58 | 0.447 | 7.795 | 1.37 | 13.642 | 32.653 | 0.787 | 9.176 |
| **11** | **TWT** | 28.65 | 55.03 | 44.22 | 15.493 | 8.9 | 47.531 | 15.589 | 32.596 | 4.629 | 10.468 |
| **12** | **HI** | 24.41 | 39.11 | 32.19 | 8.824 | 9.229 | 9.631 | 9.642 | 91.618 | 5.857 | 18.197 |
| **13** | **GYPP** | 1.71 | 3.57 | 2.74 | 0.057 | 8.711 | 0.175 | 15.277 | 32.518 | 0.28 | 10.233 |

Where, GNP- Germination Percentage; DTFF- Days to 50 % Flowering; DTM- Days to Maturity; CFC- Chlorophyll Content; NDVI- Normalized Difference Vegetative Index; CNTP- Canopy Temperature; PTH- Plant Height (cm); SKL- Spike Length (cm); TPSM- Tillers Per Square Metre; TWT- Test Weight (g); BYPP- Biological Yield Per Plot (Kg); GYPP- Grain Yield Per Plot (Kg); HI- Harvest Index (%), Vg-Genotypic variance, GCV- Genotypic coefficient of variation, Vp- Phenotypic variance, PCV-Phenotypic coefficient of variation,$h^2_b$ -Broad sense heritability, GA-Genetic advance, GAM-Genetic advance as percent mean



**Supplementary Figure 1:** Mean weakly meteorological data (rainfall in mm, temperature maximum in∘C , temperature minimum∘C, RH% morning, RH% evening, sunshine hours, evaporation in mm) during 2019-20 *Abbreviations- RH-Relative humidity



**Supplementary Figure 2:** Pie chart showing thePercent contribution of each trait towards total genetic divergence among 50 bread wheataccessions