

Genetic Diversity in Durum Wheat [*Triticum durum* Desf.]

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MAYUR DAVE

Thesis

Master of Science in Agriculture

(Genetics and Plant Breeding)



2021

DEPARTMENT OF GENETICS AND PLANT BREEDING
RAJASTHAN COLLEGE OF AGRICULTURE
MAHARANA PRATAP UNIVERSITY OF AGRICULTURE AND TECHNOLOGY
UDAIPUR – 313001 (RAJASTHAN)

Genetic Diversity in Durum Wheat **[*Triticum durum* Desf.]**

दक्षिण भारत में *Triticum durum* Desf. की आनुवंशिक विविधता का अध्ययन

Thesis

Submitted to the
Maharana Pratap University of Agriculture and Technology, Udaipur
In partial fulfillment of the requirements for the Degree of

Master of Science in Agriculture
(Genetics and Plant Breeding)



BY
MAYUR DAVE
2021

CERTIFICATE–I

CERTIFICATE OF ORIGINALITY

The research work embodied in the thesis titled “**Genetic Diversity in Durum Wheat (*Triticum durum* Desf.)**” submitted for the award of degree of M.Sc. (Ag.) Genetics and Plant Breeding to Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan), is original and bonafide record of research work carried out by me under the supervision of **Dr. Abhay Dashora**, Assistant Professor, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, Udaipur. The contents of the thesis, either partially or fully, have not been submitted or will not be submitted to any other institute or university for the award of any degree or diploma.

The work embodied in the thesis represents my ideas in my own words and where others ideas or words have been included. I have adequately cited and referenced the original sources. I also declare that I have adhered to all principles of academic honesty and integrity and have not misrepresented or fabricated or falsified any idea/data/fact/source in my submission. I understand that any violation of the above will be cause for disciplinary action by the university and can also evoke panel action from the sources which have thus not been properly cited or from whom proper permission has not been taken when needed.

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Place: Udaipur

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Dated: / /2021

This is to certify that the thesis entitled “**Genetic Diversity in Durum Wheat (*Triticum durum* Desf.)**” submitted for the degree of **Master of Science in Agriculture** in the subject of **Genetics and Plant Breeding**, embodies bonafide research work carried out by **Mr. Mayur Dave** under my guidance and supervision and that no part of this thesis has been submitted for any other degree. The assistance and help received during the course of investigation have been fully acknowledged. The draft of this thesis was also approved by the advisory committee on / /2021.

The manuscript has been subjected to plagiarism checked by software Urkund. It is certified that as per the check, the similarity index of the content is 09% and is within permissible limit as per the MPUAT guidelines on checking Plagiarism.

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This is to certify that **Mr. Mayur Dave** student of Master of Science in Agriculture, **Department of Genetics and Plant Breeding**, Rajasthan College of Agriculture; Udaipur has made all the corrections/modifications in the thesis **“Genetic Diversity in Durum Wheat (*Triticum durum* Desf.)”** which were suggested by the external examiner and the advisory committee in the oral examination held on 12/08/2021. The final copies of the thesis duly bound and corrected were submitted on / /2021, are enclosed here with for approval.

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1. INTRODUCTION

Wheat belongs to the genus *Triticum* of the Poaceae family and is one of the world's most common staple foods. It covers 17 percent (one-sixth) of global cropland, feeds about 40% of the world's population, and accounts for 20% of overall food calories and protein in human nutrition.

Wheat is a self-pollinated, monocotyledonous plant that had originated from South West Asia. There are different species of wheat, out of which only three *Triticum* species are mostly cultivated throughout the world. These are *Triticum aestivum* (bread wheat), *Triticum durum* (macaroni wheat) and *Triticum dicoccum* (emmer wheat).

Globally, wheat (*Triticum spp.*) is grown in about 224.09 million hectares holding the position of highest acreage among all crops with annual production hovering around 794.44 million metric tons (USDA, 2021). In India, it is grown in an area of 31.76 million hectares (14.17% of the global area) with a production of 108.75 million metric tons (13.68% of world production) and productivity of 3424 kg/ha. In Rajasthan, it is grown in an area of 3.02 m ha with a production and productivity of 10.57 mt and 3501 kg/ha respectively (Anonymous, 2020). Wheat is mostly grown in the districts of Shri Ganganagar, Hanumangarh, Bharatpur, Churu, Jaipur, Kota, Baran, Alwar, Bundi, and other parts of Rajasthan.

Durum wheat (*Triticum durum* Desf.) is the second most cultivated species of wheat both globally and nationally, after bread wheat. Durum wheat is a tetraploid species (AABB; $2n=4X=28$) of wheat. The typical durum wheat grain is very hard, vitreous and amber-colored with a rich in protein content.

The world's durum wheat acreage and production is concentrated in West Asia, North Africa, Canada, Mexico, India and Mediterranean Europe. Durum is predominantly spring wheat, although winter durum is also grown to a limited extent. Worldwide, durum wheat is grown approximately over 13 million hectares with an approximate annual production of 30 million tones (Kadkol and Sissons, 2016) which contributes less than 5% of the world's wheat production.

The composition of durum wheat is comparable to that of ordinary wheat. In durum wheat kernel starch and lipids have about equal amounts but protein content is a little more than bread wheat. The mineral distribution in the kernel is one of the most noticeable differences. This difference may have a role in the higher cooking quality of durum wheat pasta (Matsuo, 1994). This crop has many common ways of eating including spaghetti, couscous, burghul, *gofio* and semolina, to name a few.

A crop improvement programme requires information of genetic variability in the genetic system of a specific crop. The plant breeder's key goal is to develop the genotype in order to increase yield. Grain yield in wheat is a complex character and is dependent on its component traits. Therefore, to enhance grain yield, selection must exploit the variability existing within each component trait. Correlation and path coefficient analysis together provide a clear-cut picture of the inter-relationships and relative contributions of independent characters to the dependent variable, allowing a plant breeder to apply appropriate selection procedures for crop improvement. The use of Mahalanobis D^2 statistics to determine the extent of divergence and the relative contribution of various components to overall divergence aids in the identification of divergence parameters for hybridization and yield improvement in wheat.

Keeping these in view, the present examination entitled “**Genetic Diversity in Durum Wheat (*Triticum durum* Desf.)**” had conducted during *Rabi*, 2019-20 to obtain the information on the following aspects:

- i. To estimate genetic parameters of variability for yield and its attributing traits in wheat.
- ii. To work out the path coefficient analysis for yield and yield contributing traits.
- iii. To assess the extent of genetic diversity (D^2) among the genotypes.

2. REVIEW OF LITERATURE

The present research was undertaken to study the immensity of genetic divergence for a number of qualitative and quantitative traits in 57 genotypes of durum wheat. The available pertinent literature on the present research in durum wheat (*Triticum durum* Desf.) has been reviewed under the following heads.

- 2.1 Genetic variability parameters
- 2.2 Correlation coefficient and path analysis
- 2.3 Genetic divergence

2.1 GENETIC VARIABILITY PARAMETERS

Dhakar *et al.*, (2012) conducted variability studies in 25 genotypes of *Triticum aestivum* and *Triticum durum* under timely sown irrigated conditions. They reported a wide range of variability for number of grains per spike, plant height and grain yield per plant. The highest GCV and PCV were noted for yield per plot, grain yield per plant, numbers of effective tillers per plant, weight of 1000-grain, length of spike and plant height.

Tsegaye *et al.*, (2012) carried out an experiment to examine the genetic variability parameter in 23 durum wheat genotypes. The results revealed that the analysis of variance exhibited significant differences among the genotypes for all the traits studied. The PCV values for most of the characters were similar to GCV values indicating that the environment had little influence on the expression of these characters. Broad-sense heritability was determined to be between 11% for biological yield to 90% for days to heading.

Tambe *et al.*, (2013) studied genetic variability analysis, correlation coefficient and path coefficient analysis for grain yield and its components traits using 28 genotypes of durum wheat. The high GCV and PCV were observed for grain yield, number of effective tillers per plant, length of main spike and 1000-grain weight indicating that these traits had a lot of genetic variation.

Wolde *et al.*, (2016) conducted an experiment to study the genetic variability, heritability and genetic advance for yield and yield attributing traits using 68 genotypes of durum wheat. The analysis of variance exhibited a highly significant

difference among genotypes for all the traits under study. High GCV and PCV values were observed for effective tillers per plant, number of grains per spike, 1000-grain weight, grain yield per plant and harvest index. The heritability (broad sense) values were high for all the traits of under study.

Adhikari *et al.*, (2018) studied variability in 20 advanced lines of durum genotypes. Mean sum of squares manifested highly significant differences among genotypes for all traits investigated. High heritability associated with high genetic gain came through on some traits namely; flag leaf area, 1000-grain weight and days to heading indicated the involvement of additive gene action in controlling these traits.

Rathwa *et al.*, (2018) studied genetic variability with respect to grain yield and its components traits in durum wheat. The values of PCV in both sowing conditions were slightly higher than that of GCV for all the traits studied. The genetic advance was found high under D₀ condition for number of grains per spike, harvest index and biological yield per plant. Under D₀ condition moderate genetic advance was found out for days to 50% flowering, plant height, grain filling period, days to maturity, chlorophyll content at anthesis (CHLa) and grain yield per plant, while under D₁ condition for number of grains per spike and harvest index.

Zemedu *et al.*, (2019) studied genetic variability analysis in 64 durum wheat genotypes. Analysis of variance revealed that there were significant variations among durum wheat genotypes for 08 out of 15 traits under study suggesting the possibility of improving durum wheat for these traits. The broad sense heritability was lowest for harvest index and highest for days to heading and grain filling period.

Malbhage *et al.*, (2020) conducted an experiment to assess genetic variability using 40 genotypes of durum wheat. For all of the characters examined, the analysis of variance revealed extremely substantial variations for all the traits due to genotypes. The value of PCV was slightly higher than that of GCV for all the traits under study. The values of GCV and PCV were found to be higher for the characters *viz.*, grain yield per plant, grain weight per spike, 1000-grain weight, number of grains per main spike number of effective tillers per plant and biological yield per plant.

Alemu *et al.*, (2020) conducted an experiment to examine the nature, magnitude and patterns of genotypic and phenotypic variation in durum wheat germplasm for yield, yield component traits and quality character using 64 durum wheat genotypes. Analysis of variance showed the existence of highly significant variation for all the traits. For plant height, high values for heritability and genetic advance as *per cent* mean exhibit a greater possibility and accessibility of improving the trait by selection.

2.2 CORRELATION AND PATH COEFFICIENT ANALYSIS

Deshmukh *et al.*, (2009) studied path coefficient analysis for grain yield and yield components traits in 30 durum wheat (*Triticum durum*) genotypes. The correlation between number of ears/m and grain yield was positive and significant. The positive direct effect of number of ears/m was attributed to the indirect positive effects of 1000-grain weight and number of days to maturity. The number of grains per spike exhibited the greatest negative direct effect on grain yield *via* 1000-grain weight and grain weight per ear.

Sakhare *et al.*, (2011) conducted an experiment with a view to determine affiliation between yield and yield components and thereby to assess the direct and indirect effects of yield attributing traits on yield. The genotypic correlations between yield plot⁻¹ and grain weight ear⁻¹, number of ears meter⁻¹, seed index, number of grains ear⁻¹, and plant height at maturity and days to 50% flowering indicated the direct contribution of the characters for improvement of yield.

Tsegaye *et al.*, (2012) conducted an experiment to assess the correlation and path analysis using 23 durum wheat genotypes. He reported that the grain yield was highly correlated with biological yield, number of tillers per plant and 1000-grain weight. The outcome of path coefficient analysis revealed that the biological yield and harvest index have a direct impact on grain yield.

Tambe *et al.*, (2013) studied correlation coefficient and path analysis for grain yield and its components using 28 genotypes of durum wheat. The experimental outcome revealed that the grain yield per plant exhibited significant and positive correlation with grain filling period, 1000-grain weight and number of productive tillers per plant at both genotypic and phenotypic levels pointing out that these three traits were the key yield contributing traits. The path coefficient analysis declared that the number of effective tillers per plant had maximum direct effect on grain yield followed by grain filling period and 1000-grain weight.

Singh (2016) evaluated 50 durum wheat genotypes as timely and late sowing for two years. The grain yield per plant showed significant and positive association with number of tillers per plant, biological yield per plant and harvest index in all the environments; with plant height in E III and E IV; with days to maturity and 1000-grain weight in E IV only.

2.3 GENETIC DIVERSITY (D²) ANALYSIS

Tsegaye *et al.*, (2012) conducted an experiment to examine the extent of genetic divergence among 23 durum wheat genotypes. Mahalanobis D² statistics were used to calculate genetic divergence. The result revealed that the Euclidean genetic distance values ranged from 2.69 (between D-1 and D-11) to 9.68 (between D-13 and D-21), and 82.2 percent of the pair comparisons had values between 3.76 and 7.50, according to genetic distance review. Genotypes were clustered into 06 genetically distinct groups using cluster analysis. He reported that the largest inter-cluster distance was 8.30 (between clusters III and VI), followed by 7.99 (between clusters V and VI), showing that these clusters had a lot of genetic variation. Cluster I (4.91) had the greatest intra-cluster distance, while Cluster III had the smallest (2.36).

Kumar *et al.*, (2014) evaluated 150 durum wheat (*Triticum durum* Desf.) genotypes from diverse sources to estimate the genetic diversity. Genotypes were clustered into 16 genetically distinct groups using cluster analysis. According to D² statistics, it was finalized that grain yield per plant, plant height, days to maturity, days to flowering and 1000-grain weight contributed to the genetic diversity. The clustering pattern suggests that there is no parallelism between the geographical distribution and genetic diversity.

Singh (2015) evaluated 50 durum wheat genotypes in four environments to estimate the genetic divergence and clustering pattern of genotypes. The maximum contribution to genetic divergence was made by number of spikelets per spike followed by number of grains per spike and 100-grain weight.

Malviya *et al.*, (2018) conducted an experiment on genetic divergence for 16 parameters in 102 varieties of durum wheat (*Triticum turgidum* var. *durum* Desf.). Analysis of variance revealed significant differences among varieties for all the traits

studied. The varieties were grouped into 16 clusters based on the magnitude of the divergence value. Cluster IV had the greatest intra-cluster gap followed by Cluster XIII. The maximum inter-cluster gap between clusters VII and XIII reflects high genetic divergence between these two groups' varieties.

Ambati *et al.*, (2020) evaluated 604 durum wheat germplasm originated from different geographical areas to estimate the genetic diversity. Data were recorded for eight quantitative characters including agronomic and grain quality traits. Descriptive statistics revealed large variation for all investigated traits. Box plot analysis for 9 different sets of germplasm exhibited that there was large variation for agronomic and quality traits. Principle component analysis for the first four-principle component explained 71% of the cumulative variation and grouped germplasm in the main two group.

3. MATERIALS AND METHODS

The present investigation entitled “Genetic Diversity in Durum Wheat (*Triticum durum* Desf.)” was conducted during *Rabi*, 2019-20. The following are descriptions of the methods employed and the materials used during the investigation.

3.1 SITE OF EXPERIMENT

The experiment was conducted at Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur. It is situated at an elevation of 579.5 M above mean sea level in southeast Rajasthan at latitude of 24° 35' N and longitude of 70° 42' E. The meteorological data recorded during the crop period are presented in Appendix I and Fig. 3.1.

3.2 MATERIALS USED FOR EXPERIMENT

Fifty two durum wheat genotypes along with 5 checks evaluated in this experiment were obtained from the AICRP on Wheat and Barley, Department of Genetics and Plant Breeding, RCA, MPUAT, Udaipur. The name of genotypes/varieties and their pedigrees are given in Table 3.1.

3.3 EXPERIMENTAL DESIGN

All the 52 genotypes along with 5 checks were grown in Augmented Randomized Block Design using four blocks, in which only checks were replicated. Genotypes were sown in 2 rows of 2.5 m row length with row to row and plant to plant spacing of 23 cm and 5 cm respectively. The experiment was sown on November 16, 2019. All the required agronomic practices and plant protection measures were adopted to raise a good crop

3.4 OBSERVATIONS RECORDED

Five competitive plants from each genotype were chosen at random for recording observation for all the traits under study from each plot. However, observation for days to 50% heading and days to maturity were recorded on the basis of plant population of each genotype. The protocols for recording observations for the traits under investigation are as follows.

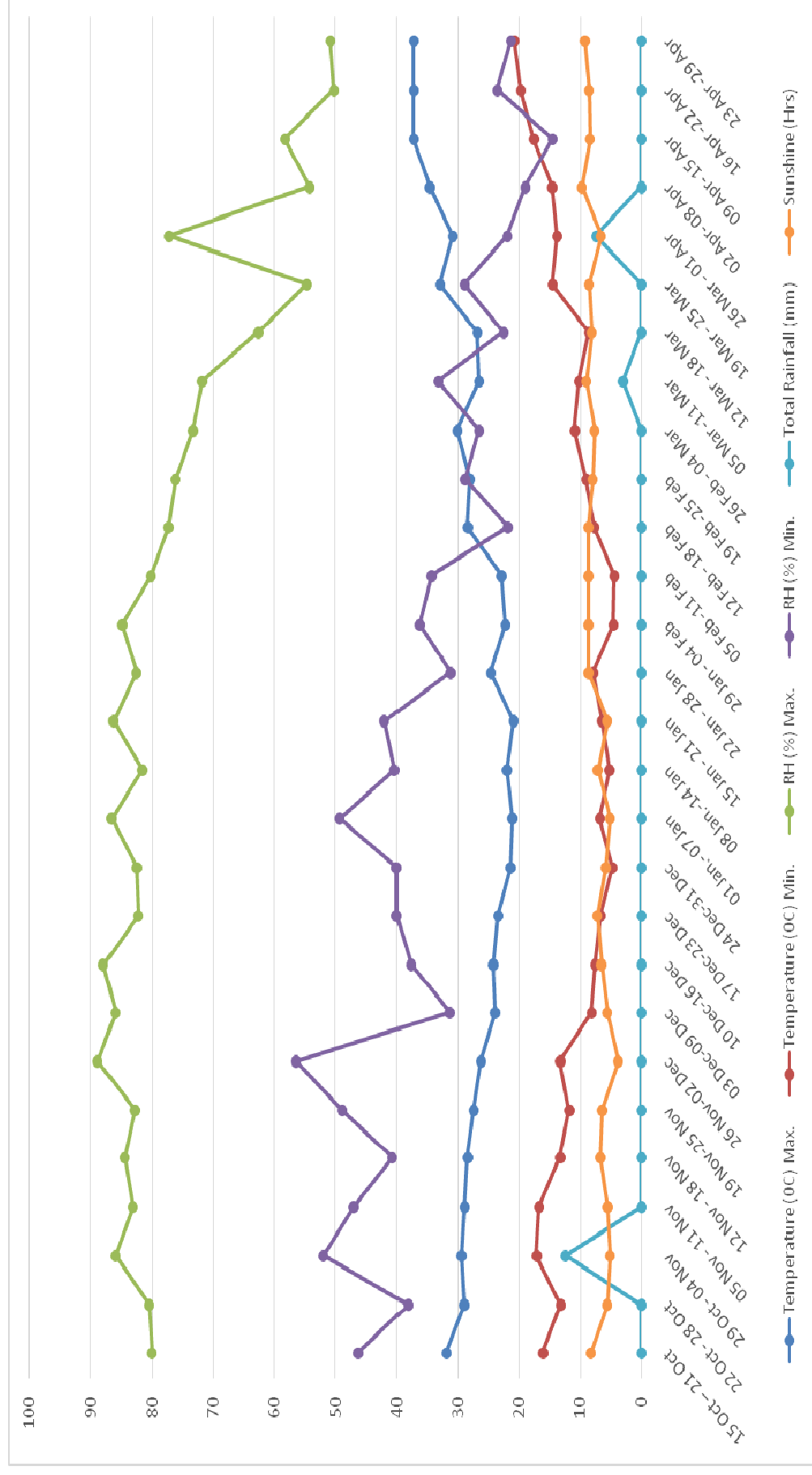


Fig. 3.1: Mean weekly data on meteorological parameters during the crop growth period

Table 3.1: Name and pedigrees of durum wheat genotypes/varieties

S. No.	Name of Genotypes	Pedigrees of Genotypes
1.	PDW 291	Check
2.	HI 8498	Check
3.	HI 8737	Check
4.	HI 8759	Check
5.	HI 8777	Check
6.	50 th IDYN 706	BYBLOS/6/TOPDY_18/FOCHA_1//ALTAR84/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/4/SOMAT_3/GREEN_22/5/VRKS_3/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA13/7/GUAYACANINIA/GUANAY/PORRON_4/B EIAH-7/3/VANRRIKSE 12/SNITAI
7.	50 th IDYN 709	GUAYACANINUA/2*SNITAN/10/TAD1Z/9/USDA595/3/D6 7.3/RABI/CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/Y AV79/8/POD_9
8.	50 th IDYN 712	ALTAR84/STINT/SILVER_45/3/GUANAY/4/GREEN_14//Y AV_10/AUK/5/SOMAT_4/INTI6/CMH85.797//CADO/BOO MER_33/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1
9.	50 th IDYN 718	ADAMAR_15//ALBIA_1/ALTAR84/3/SNITAN/4/SOMAT_4 /INTER_8/5/SOOTY_9/RASC06/BICHENA/AKAKI_7/4/LIS _8/FILLO_6/3/FUUT//HORA/JOR/5/YAZL_1/AKAKL_4//SO MA3/AUK/GUIL//GREEN/7/TOPDY_18/FOCHA1//ALTAR8 4/3/AJAIA_12/F3LOCAL I (SEL.ETHIO.135.85)/PLATA_13/4/SO
10.	50 th IDYN 719	GUAYACANINIA/GUANAY/8/GEDIZ/FGO//GTA/3/SRN_1/ 4/TOTUS/5/ENTE/MEXE_2//HUI/YAV_1/3/LD357E/2*TC60 //069/6/SOMBRA_20/7/JUPREC2001/9/BICHENA/AKAKI_S OMAT_3/PHAX_1/TILO_1/LOTUS_4/7/CHEN_11/POC//TA NTLO/5/ENTE/MEXI_2//HUI/YAV_1/3/LD357E/2*TC60//JO
11.	50 th IDYN 721	MOHAWK/6/LOTUS_5/F3LOCAL(SEL.ETHIO.135.85)/5/C HEN/ALTAR84/3/HU/POC//BURUFO/4/FNFOOT/7/SORA/2 *PLATA_12/3/SORA/2*PLATA_12//SOMAT_3/4/AJAIA_13 / YAZI//DIPPER_2/BUSHEN_3
12.	50 th IDYN 722	MOHAWK/6/LOTUS_5/F3LOCAL(SEL.ETHIO.135.85)/5/C HEN/ALTAR84/3/HU/PCC/BURUFO/4/FNFOOT/7/SORA/2* PLATA_12/3/SORA/2*PLATA_12//SOMAT_3/4/AJAIA 13/ YAZI//DIPPER_2/BUSHEN_3

S. No.	Name of Genotypes	Pedigrees of Genotypes
13.	50 th IDYN 729	CBC509CHLE/6/ECO/CMH76A.722/BIT/3/ALTAR4/4/AJAI A_2/5/KJOVE_1/7/AJAIA_1F3LOCAL(SEL.ETHIO0.135.85) //PLATA_13/8/SOOTY_9/RASCON37//WODUCK/CHAM_3 SOOTY_9/RASCON_37//JUPAREC2001/3/SOOTY_9/RASC ON_37//GUAYACANINI
14.	50 th IDYN 735	SIIVER_14/MOEWE/BISU_1/PATKA_3/3/PORRON_4/YUA N_1/9/USDA595/3/D67.3/RACRA/4/ALO/5/HUI/YAV_1/6/A RDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUANII_ AIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_ 9.1/11/CBC 514 CHILE/3/AUK/GUIL//GREEN
15.	50 th IDYN 737	SOMAT_3/GREEN_22//2*RASCON_37/2*TARRO_2/5/CM H85.797/CADO/BOOMER_33/ARMENT/SRN_3/NIGRI_4/3/ CANELO_9.1/6/ALTAR84/STINT//SILVER_45/3/GUANAY/ GREEN_14//YAV_10/AUK/5/SOMAT_4/INTER_8
16.	50 th IDYN 740	GUAYACANINIA/GUANAY/PORRON_4/BEJAH_7/6/TOP DY_18/FOCHA_1//ALTAR84/3/AJAIA_12/F3LOCAL(SEL. ETHIO.135.85)//PLATA_13/4/SOMAT_3/GREEN_22/5/VRK S3/3AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/7 /SOMAT_3/GREEN22//2*RASCON37/2*TARRO_2
17.	50 th IDYN 741	ALTAR84/5STINT/SIVER_45/3/GUANAV/4/GREN_14//YA V_10/AUK/S/SOMAT_4/INTER_8/6/CMH85.797//CADO/BO OMER_33/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/7/ GUAYACANINIA/POMA_2//SNITAN/4/D86135/ACO89//P ORRON_4/3/SNTTAN
18.	50 th IDYN 744	ALTAR84/5STINT/SIVER_45/3/GUANAV/4/GREN_14//YA V_10/AUK/S/SOMAT_4/INTER_8/6/CMH85.797//CADO/BO OMER_33/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/7/ GUAYACANINIA/POMA_2//SNITAN/4/D86135/ACO89//P ORRON_4/3/SNTTAN
19.	50 th IDSN 7013	SWAHEN_2/KIRKI_8/PROZANA_1/4/ADAMAR_15//ALBI A_1/ALTAR84/3/SNITAN/9/GUAYACANINIA/GUANAY/8/ GEDIZ/FGO/GTA/3/SRN_1/4/TOTUS/5/ENTE/MEXI_2//HUI /YAV_1/3/LD357E/2"TC60//069/6/SOMBRA_20/7/UPAREC 2001/10/CHEN_1/TEZ/3/GUIL /CIT71/CII/4/SORA/PLATA_12/5/
20.	50 th IDSN 7034	SILVER_14/MOEWEI/BISU_1/PATKA_3/3/PORRON_4/YU AN1/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HU/YAV_1/ 6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUA N_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CA NELO_9.1/11/ALTAR84/STINT// SILVER_45/3/ GUANAY/4/GREEN_14//Y

S. No.	Name of Genotypes	Pedigrees of Genotypes
21.	50 th IDSN 7037	SOMAT_3/GREEN_22//2*RASCON_37/2*TARRO_2/5/CMH85.797/CADO/BOOMER_33/ARMENT/SRN_3/NIGRIS_4/3/CANELO_9.1/6/ALTAR84/STINT//SILVER_45/3/GUANAY/ GREEN_14//YAV_10/AUK/5/SOMAT_4/INTER_8
22.	50 th IDSN 7040	GUAYACANINIA/GUANAY/PORRON_4/BEJAH_7/6/TOPDY_18/FOCHA_1//ALTAR84/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/4/SOMAT_3/GREEN_22/5/VRK S3/3AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/7 /SOMAT_3/GREEN22//2*RASCON37/2*TARRO_2
23.	50 th IDSN 7049	SILVER_14/MOEWEI/BISU_1/PATKA_3/3/PORRON_4/YUAN1/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HU/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_3SOOTY_9/RASCON_37//JUPARE C 2001/3/SOOTY_9/RASCON
24.	50 th IDSN 7067	WBDTBO/11/MALU/10/ALTAR84/CMH82A1062//ALTAR84/3/YAZI_10/4/5SNITAN/9/USDAS95/3/D67.3/RABI/CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/12 SELIM/9/ALTAR84/860137//YAZI_1/4/LIS_8/FILLO_6/3/FUUT//HORA/JOR/8/GEDIZ/FGO//GTA/3/SRN_1/4/TOTUS/5/EN
25.	50 th IDSN 7072	WID22256/5/ALTAR84/STINT//SILVER_45/3/GUANAY/4/GREEN_14//YAV_10/AUK/6/SNITURKM18384503/LOTUS_4//MUSK_4/3/CANELO_9/4/YAZI_1/AKAKI_4//SOMAT_3 /3/AUK/GUIL//GREEN/7/SOOTY_9/RASCON_37//GUAYACANINIA/3/SOOTY_9/RASCON_37// STORLOM
26.	50 th IDSN 7076	CBC 509CHILE/6/ECO/CMH76A.72//BIT/7/ALTAR84/4/AJAIA_2 /5/KJOVE_1/7/AJAIA_1212/F3LOCAL(SEL.ETHIO.135.85)/PLATA_13/8/SOOTY_9/RASCON_37/WODUCK/CHAM_3/9/SOMAT_3/GREEN_22//2*RASCON_37/2*TARRO_2
27.	50 th IDSN 7077	SILVER_14/MOEWE/BISU_1/PATKA_3/3/PORRON_4/YUAN_1/9/USDA595/3/D67.3/RABI/CRA/4/ALO/5/HUI/YAV_1 /6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/WID22256/5/ALTAR I 84/STINT//SILVER_45/3/GUANAY/4/
28.	50 th IDSN 7078	SILVER_14/MOEWE//BISUL_/PATKA3/3/PORRON_4A/YUAN_1/9/USDA595/3/D67.3/RABV/CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TARRO_1/2*YUAN_1//AJAIA_13/YAZI/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/AJAIA_12/F3LOCAL (SEL.ETHIO.135.85)//PLATA_13/3/S

S. No.	Name of Genotypes	Pedigrees of Genotypes
29.	50 th IDSN 7100	MOHAWK/10/PLATA10/6/MOUE/A/USDAS73/OFN/AA7/3/ALBAD/5/AVO/HU/7/PLATA13/8/THKNEE_11/9/CHEN/ALTAR84/3/HU/POC//BUB/RUFO/4/FNFOOT/11/PLATA_6/GREEN 17//SNITAN/4/YAZI 1/AKAKI 4//SOMAT-3/3/AUK/GUIL//GREEN/12/GUAYACAN I INIA/GUANAY//PORRON 4/BEJAH 7/3/V
30.	50 th IDSN 7113	TRIDENT/3*KUCUK/7/CMH83.2578/4/D88059//WARD/YA V79/3/ACO89/5/2*SOOTY_67 RASCON_37/6/1A.1D 5+1- 06/3*MOJ0/3/AJAIA_ 12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13
31.	50 th IDSN 7135	ALTAR84/STINT//SILVER_45/3/GUANAY/4/GREEN_14//Y AV_10/AUK/5/SOMAT_4/INTER_8/6/CMH85.797/CADO/B OOMER_33/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1
32.	50 th IDSN 7177	ALTAR84/STINT/SIVER_45/3/GUANAY/4/GREEN_14//YA V_10/AUK/10/CMH79.959/CHEN/SOOTY_9/RASCON_37/9 /USDA595/3/D67.3/RABI/CRA/4/ALO/5/HUI/YAV1/6/ARDE NTEI7/HUI/YAV79/8/POD_9/11/RCOL/SHAG_23/LAPDY_2 5/4/ARMENT/SRN_3/NIGRIS_4/3/CANELO_9.1/12/KOFA/9 /USDA5
33.	GW (D) 2019-969	CPAN 1783// 86/H1 8671/3/ IMMER/ GRI// RAJ 1555
34.	GW (D) 2019-970	V-88-162-9-1W-1-1W/GW 1057// GDW 1255
35.	GW (D) 2019-971	RD 1029/ GDW 1255
36.	GW (D) 2019-972	RD 1029/ GDW 1255
37.	GW (D) 2019-973	RAJ 6543/ MEXI 75//GW 1104/ DW 20
38.	GW (D) 2019-974	GW 1088/IWP 5061//GDW 1255
39.	GW (D) 2019-975	WR 1617/ PBNB 1625// GW 1104/DW 20
40.	GW (D) 2019-976	HI 8012/GW 1160// V-88-162-9-1W-1-1W/GW 1057 / 3/ H1 8012/ GW 1160
41.	GW (D) 2019-977	IWP 5061/ GW 1021//GW 1115/3/GW 1151/ MEXI 75/4/ 1WP 5061/ GW 1021//GW 1115
42.	GW (D) 2019-978	RD 1271/ HI 8704 / 3/ HI 8012// V 86/ H1 8371
43.	GW (D) 2019-979	RAJ 6292// GW 1029//JU 180/3/ IWP 5061/ GW 1021/ GW 1115/5/ ALTAR 84/ STINT// SILVER-45/4/SKEST//HUI
44.	GW (D) 2019-980	KUCUK / H1 8678
45.	GW (D) 2019-981	HYDRANA SSA-30/ SIG-511-13// WR 1617/3/GW 1139
46.	GW (D) 2019-982	GW 1087 / IWP 5067// RAJ 6566

S. No.	Name of Genotypes	Pedigrees of Genotypes
47.	49 th IDYN 713	GEROMTEL-3/10/CHEN_1/TEZ/3/GUIL/CT71/C/4/SORA/PLATA_12/5/STOT//ALTAR 84/ALD/9/USDA595/3/D67.3/RABI//CRA/4/ ALO5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9
48.	49 th IDYN 718	GUAYACANINIA/2*SNITAN/10/TADIZ/9/USDA595/3/D67.3/RABI/CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/IHUI/YAV79/S/POD_9
49.	49 th IDYN 733	ADAMAR_15//ALBIA1/ALTAR84/3/SNITAN/4/SOMAT_4/INTER_8/5/SOOTY_9/RASCON37/6/BICHENAANKAKI_7/4/LISB/FILLO_6/3/FUUT/HORA/JOR/5/YAZI1/AKAKL_4/SOMAT_3/3/AUK/GUIL//GREEN/10/TADIZ/9USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAVT 8/P
50.	49 th IDYN 747	CMH83.2578/4/D88059//WARD/YAV79/3/ACO89/5/2*SOOTY_9/RASCON37/6/1A.1D5+106/3*MO10/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85) PLATA_13/7/KOFA/4/DUKEM1//PATKA_7/YAZI_-1/3/PATKA_7/YAZL_1/8/U PARE C 2001*2/KHAPLL
51.	49 th IDSN 7107	E90040/MFOWL_13/LOTAIL6/3/PROZANA/ARLIN/MUSK_6/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD_9/10/TOSKA_26/RASCON-37//SNITAN/4/ARMENT//SRN_3/NIGRIS_4/3/CANELI 001
52.	41 st IDYT 4	lcasyr1/3/Bcr/Sbl5/Turartu/4/13376/Bcrch 1/Ossl1/Stj5
53.	41 st IDYT 10	Azeghar1//Blrn/Mrf2/3/Bicredera1/Azeghar2
54.	41 st IDYT 15	ICAMORTA0469/4/ICAMORTA0463/3/CandocrosSH-25/Msbl 1/Ouarmai04182/5/lcasyr2/6/Geromtel1/lcasyr1
55.	41 st IDYT 18	KoriflalAegSpeltoidesSyr//Amedakul
56.	GW 2017 859	HI 8691/GW 1189
57.	GW 2017-865	CINTA 1 /MACS 3446

3.4.1 Days to 50% Heading

It is counted in days from sowing to when 50% of the plants show ear emergence.

3.4.2 Days to Maturity

The number of days required from date of sowing to date when 75% plants achieve physiological maturity.

3.4.3 Plant Height (cm)

The plant's height was estimated in centimeters from the base to the tip of the tallest spike as it reached maturity (excluding awns).

3.4.4 Number of Effective Tillers per Plant

It was estimated from sampled plants by counting the number of spiked tillers at maturity.

3.4.5 Length of Main Spike (cm)

It was measured in centimeters from the tip of apical spikelets (excluding awns) to the base or collar of the spike.

3.4.6 Number of Spikelets per Spike

At maturity, the total number of spikelets in each spike of the sampled plant was counted.

3.4.7 Number of Grains per Spike

It was estimated by counting the total number of grains from the main spike of sampled plant after harvesting.

3.4.8 Grain Weight per Spike (g)

The grain weight per spike was recorded in grams by weighing grain of main spike of sampled plant after threshing.

3.4.9 1000-grain Weight (g)

It was estimated by counting and weighing 1000-grains randomly selected from the harvested bulk of each genotypes and weighed in grams.

3.4.10 Biological Yield per Plant (g)

It was determined by weighing a single plant sample including ears after complete sun drying and recorded the weight in grams.

3.4.11 Grain Yield per Plant (g)

The total grain per plant weighed in grams after manual threshing of sampled plants.

3.4.12 Harvest Index (%)

Harvest index was expressed in percentage and recorded as per the formula given below:

$$\text{Harvest index (\%)} = \frac{\text{Grain yield per plant(g)}}{\text{Biological yield per plant(g)}} \times 100$$

3.4.13 Sedimentation Value (SDS value in ml.)

It measures the quality of protein and is based on the fact that when gluten protein is treated with lactic acid in the presence of Sodium Dodecyl Sulphate (SDS), it absorbs water and expands significantly. The sedimentation value measured as per the method described in Appendix II.

3.4.14 Protein Content (%)

Protein content in the grains was determined for each genotype as per the method suggested by Lindner (1944). (Appendix III)

3.5 STATISTICAL METHODOLOGY

The observed values of each character from each genotype were subjected to the following standard statistical procedures.

3.5.1 Analysis of Variance

The analysis of variance for different characters was worked out in Augmented Randomized Block Design as per the method suggested by Federer (1956). The ANOVA skeleton was as follows:

Table 3.3: ANOVA for Augmented Randomized Block Design

S. No.	Source	D.F.	SS	MS	EMS
1.	Block	r-1	$\sum_{j=1}^r (\sum_{i=1}^c X_{ij})^2 / c - (\sum_{i=1}^c \sum_{j=1}^r X_{ij})^2 / rc$	MSR	
2.	Check	c-1	$\sum_{i=1}^c (\sum_{j=1}^r X_{ij})^2 / r - (\sum_{i=1}^c \sum_{j=1}^r X_{ij})^2 / rc$	MSC	$\sigma_e^2 + r\sigma^2_c$
3.	Germplasm	g-1	$\sum_{j=1}^g X_i^2 / g - (\sum_{i=1}^g X_i)^2 / g$	MSG	$\sigma_e^2 + r\sigma^2_g$
5.	Error	(r-1) (c-1)	Total SS–RSS–CSS	MSE	σ_e^2
6.	Total	cr-1	$\sum_{i=1}^c \sum_{j=1}^r X_{ij}^2 - (\sum_{i=1}^c \sum_{j=1}^r X_{ij})^2 / cr$		

Where	X_{ij}	=	Value of i^{th} check in j^{th} block
	X_i	=	Value of i^{th} germplasm
	r	=	Number of blocks
	c	=	Number of checks
	g	=	Number of germplasm
	df	=	Degrees of freedom
	SS	=	Sum of squares
	MS	=	Mean sum of squares
	SSR	=	Sum of squares due to replications
	SSC	=	Sum of squares due to checks
	SSE	=	Sum of squares due error
	MSR	=	Mean sum of squares due to blocks
	MSG	=	Mean sum of squares due to genotypes
	MSC	=	Mean sum of squares due to checks
	MSE	=	Mean sum of squares due to error

Standard Error of Mean (S.E.M.): It was calculated as follows:-

$$S.E.M. \pm = \sqrt{\frac{MSE}{r}}$$

MSE = Error variance

r = Number of replications

Standard Error of Difference (S.E.D.)

Standard error of difference between treatment means was formulated by using the given formula:-

$$S.E.D \pm = \sqrt{\frac{2MSE}{r}}$$

Where,

MSE = Error mean sum of square

r = Number of replications in the experiment

Critical Difference (C.D.)

For every character, the critical difference as the difference of any two mean values in order to compare the treatment means was calculated using the following formula and tabulated 't' value at error degree of freedom and at 5 or 1% level of significance.

Critical difference was estimated by the formula:

$$CD = \sqrt{\frac{2MSE}{r}} \times t \text{ value}$$

Where,

t value = Tabulated value at error degree of freedom at 5 percent or 1 percent probability of significance

Coefficient of variation (C.V.)

CV is the ratio of the standard deviation to the arithmetic mean. It is expressed as percentage.

$$CV = \frac{SD}{\bar{X}} \times 100$$

Where,

SD = Standard deviation

$\bar{X}$ = Mean

Analysis of variance components

The genotypic, phenotypic and error variance were calculated as follow:-

3.5.1.1 Genotypic variance

The genotypic variance is due to the differences among genotypes included in the study. It was measured as per the formula suggested by Burton and Devane (1953).

$$\sigma^2 g = \frac{(MS_g - MS_e)}{r}$$

Where,

$\sigma^2 g$ = Genotypic variance

MS_g = Mean sum of squares due to germplasm

MS_e = Error mean sum of squares

r = Number of replications

3.5.1.2 Phenotypic variance

It is the sum of variance contributed by genetic causes and environmental factors. The following formula was used to quantify it, as proposed by Burton and Devane (1953)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where,

$$\sigma^2 p = \text{Phenotypic variance}$$

$$\sigma^2 g = \text{Genotypic variance}$$

$$\sigma^2 e = \text{Error variance i.e. MSE}$$

3.5.1.3 Error variance

The mean sum of squares of error represented by the variation attributed to environmental causes.

$$\text{Error variance } (\sigma^2 e) = \text{MSE}$$

3.5.2 Variability Parameters

The following parameters were calculated for the characters having significant mean squares due to the genotypes.

3.5.2.1 Range

The difference between highest and lowest values of each character was recorded.

$$\text{Range} = \text{Highest value} - \text{Lowest value}$$

3.5.2.2 Mean ($\bar{X}$)

The mean value of each character was worked out by dividing the sum of all observations in a sample by the corresponding number of observations.

$$\bar{X} = \frac{\sum X_i}{N}$$

Where,

$$\bar{X} = \text{General mean}$$

$$\sum X_i = \text{Summation of all the observations}$$

$$N = \text{Number of observations}$$

3.5.2.3 Standard Error of Mean (S.E.M.): It was calculated as follows:-

$$S.E.M. \pm = \sqrt{\frac{MSE}{r}}$$

Where,

MSE = Error variance

r = Number of replications

3.5.2.4 Coefficient of variation (C.V)

The coefficient of genotypic and phenotypic variation was calculated by using the formula suggested by Burton (1952)

(a) Genotypic coefficient of variation (GCV)

$$GCV (\%) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{X}$ = General mean

(b) Phenotypic coefficient of variation (PCV)

$$PCV (\%) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\bar{X}$ = General mean

The genotypic and phenotypic coefficient of variation was categorized as per the classification given by Sivasubramanian and Madhavamenon (1973).

0-10% = Low

10-20% = Moderate

>20% = High

3.5.2.5 Heritability in broad sense (h^2_{BS})

Heritability refers to the portion of variability, which is heritable in nature out of the total variability. It is due to genetic causes. Heritability in broad sense (h^2_{BS}) was calculated as per the formula given by Burton and Devane (1953).

$$h^2_{bs} (\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

$$\begin{aligned}\sigma^2_g &= \text{Genotypic variance} \\ \sigma^2_p &= \text{Phenotypic variance} \\ h^2_{(bs)} &= \text{Heritability in broad sense}\end{aligned}$$

The calculated heritability was classified into three groups as suggested by Johnson *et al.* (1955).

$$\begin{aligned}0-30\% &= \text{Low} \\ 30-60\% &= \text{Moderate} \\ >60\% &= \text{High}\end{aligned}$$

3.5.2.6 Genetic advance

It depicts the shift in a population mean towards the superior side under selection pressure after a single generation of selection. It was estimated as per the formula suggested by Johnson *et al.* (1955).

$$GA = H_{(bs)} \times k \times \sigma_p$$

Where,

$$\begin{aligned}GA &= \text{Genetic advance} \\ \sigma_p &= \text{Phenotypic standard deviation} \\ k &= \text{Selection intensity (k = 2.06 at 5\% selection intensity)}\end{aligned}$$

3.5.2.7 Genetic gain

It is *per cent* expected genetic advance over the population mean. It was computed as per the formula suggested by Johnson *et al.* (1955)

$$GG = \frac{GA}{\bar{X}} \times 100$$

Where,

GG = Genetic Gain

GA = Genetic advance

$\bar{X}$ = Population mean

Classification of genetic advance as percent mean was categorized as follows:-

0-10% = Low

10-20% = Moderate

>20% = High

3.5.3 Correlation Coefficient Analysis

The correlation coefficient was calculated to determine the degree of association of the characters with yield and its attributes. Genotypic and phenotypic correlation coefficient between different characters was calculated using the genotypic and phenotypic variance and covariances as per the method suggested by Al-Jibouri *et al.* (1958).

Genotypic correlation coefficient (r_g)

$$r_{xy}(g) = \frac{Cov_{xy}(g)}{\sqrt{V_x(g) \cdot V_y(g)}}$$

Phenotypic correlation coefficient (r_p)

$$r_{xy}(p) = \frac{Cov_{xy}(p)}{\sqrt{V_x(p) \cdot V_y(p)}}$$

Where,

$r_{xy}(g)$ = Genotypic correlation coefficient between x and y traits

$r_{xy}(p)$ = Phenotypic correlation coefficient between x and y traits

$V_x(g)$ = Genotypic variance for x trait

$V_y(g)$ = Genotypic variance for y trait

$V_x(p)$ = Phenotypic variance for x trait

$V_y(p)$ = Phenotypic variance for y trait

$Cov_{xy}(g)$ = Genotypic covariance of x and y traits

$Cov_{xy}(p)$ = Phenotypic covariance of x and y traits

Test of significance

The significance of the correlation coefficient with (n-2) degree of freedom was tested by the 't' test given by W.S. Gosset (1908).

$$t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$

Where,

r = Correlation coefficient

n = Total number of observations

This t value is tested against the table value of 't' for n-2 degree of freedom.

3.5.4 Path Coefficient Analysis

The proportion of the standard deviation of the effect due to a given cause to the total standard deviation of the effect is known as the path coefficient. Path coefficient analysis, as proposed by Wright (1921) and elaborated by Dewey and Lu (1959) was used to quantify the direct and indirect results. The step-by-step protocol is as follows:

Direct effects

$$r_{(x_1,y)} = P_{ly} + r_{(x_1,x_2)}P_{2y} + r_{(x_1,x_3)}P_{3y} + \dots \dots r_{(x_1, x_{l3})}P_{l3y}$$

$r_{(x_1,y)}$ = Correlation coefficient between x_1 and y

P_{ly} = Direct effect of x_1 on y

$r_{(x_1,x_2)}P_{2y}$ = Indirect effect of x_1 on y via x_2

$r_{(x_1, x_{l3})}P_{l3y}$ = Indirect effect of x_1 on y via x_{l3}

Similar method is used for $r(x_2, y)$ to $r(x_{l3}, y)$.

Residual effect

$$R = \sqrt{1 - (\sum P_{iy} - r_{iy})}$$

Where,

R = Residual effect

P_{iy} = Direct effect of x_i on y

r_{iy} = Correlation coefficient between x_i on y

The direct and indirect effects are rated as follows by Lenka and Misra (1973).

0.00-0.09	=	Negligible
0.10-0.19	=	Low
0.20-0.29	=	Moderate
0.30-1.00	=	High
>1.00	=	Very high

3.5.5 Genetic Divergence Analysis

The Genetic divergence amongst different genotypes is determined based on the estimated *inter-se* genetic distances amongst the genotypes. The D^2 statistics proposed by Mahalanobis in 1936, is one of the most efficient tool for determining genetic divergence. The D^2 statistics technique measures the differentiation forces at two levels, namely intra-cluster and inter-cluster, and thus facilitates in the identification of genetically divergent parents for exploitation in hybridization programmes.

3.5.5.1 Clustering of genotypes using the D^2 values

The genotypes were clustered into different groups using Tocher's method (Rao, 1952). The idea behind this type of clustering was that any two varieties belonging to the same cluster would have lower D^2 values than those belonging to two distinct clusters. This approach began with two closely related populations in order to identify a third population with the smallest average D^2 value. Similarly, the fourth one was selected because it had the lowest average of D^2 values from the first three, and so on. Except for those genotypes that were used in the previous cluster, this step was repeated until D^2 values of all the genotypes were exhausted.

3.5.5.2 Testing differences in the population

A dispersion table was created from the variance analysis when the null hypothesis of no differences failed for individual characters. A simultaneous examination of differences between mean values of different or associated variables

was performed using the v statistic, which in turn used Wilk's criteria (Δ) (Rao, 1952).

$$\text{Wilk's criterion}(\Delta) = \frac{\text{Determinants of error variance and covariance matrix}(E)}{\text{Determinants of genotypic + error variance and covariance matrix}}$$

$$V \text{ statistic} = -m \log_e \Lambda = -\left(n - \frac{p + q + 1}{2}\right) \log \Lambda$$

Where,

$$m = \left(n - \frac{p + q + 1}{2}\right)$$

p = Number of variables or characters

q = Degree of freedom for population (*i.e.*, number of genotypes -1)

n = Degrees of freedom for error + genotypes

$$\log_e \Lambda = 2.3026 \log_{10} \Lambda$$

'V' statistic is distributed as χ^2 with pq degrees of freedom. The test of significance of 'V' statistic showed that the differences between the mean value in terms of the pooled effect of p characters between different populations were significant. Hence, further analyses were made to estimate D^2 values.

3.5.5.3 Mahalanobis D^2 statistics

The genetic divergence in this study was estimated using Mahalanobis generalized distance as defined by Rao (1952). The pivotal condensation method of inversion matrix transformation was used to convert original variable means to uncorrelated variables. The D^2 values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. For each pair of combinations the mean deviation *i.e.* $d_i = Y_i^1 - Y_i^2$, where Y_i denotes the transformed variables ($i = 1, 2, 3, 4, 5, \dots, p$) were calculated and the D^2 was then calculated as sum of the squares of those deviations, *i.e.*

$$D^2 = \sum (Y_i^1 - Y_i^2)^2$$

Where, p = Number of characters

The significance of D^2 values was tested by treating them as chi-square (χ^2) at p degrees of freedom where p is the number of characters considered.

3.5.5.4 Grouping of genotypes by Tocher's method

After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952). The criterion used in this method was that any two varieties belonging to the same cluster, at least on an average, show a smaller D^2 value than those belonging to two different clusters. Then inter and intra-cluster distances were calculated and their relationships were diagrammatically represented.

4. EXPERIMENTAL RESULTS

The aim of this study was to determine the nature and magnitude of variability parameters, character associations and genetic divergence for 14 characters among 57 genotypes of durum wheat. The experiment was set up in an Augmented Randomized Block Design during *Rabi*, 2019-20. The experiment data obtained was statistically analyzed. The following sub-heads are well appointed to the experimental results.

- 4.1 Analysis of variance
- 4.2 Mean performance of the genotypes and range
- 4.3 Genetic variability parameters
- 4.4 Correlation coefficient analysis
- 4.5 Path analysis
- 4.6 Genetic divergence

4.1 ANALYSIS OF VARIANCE (ANOVA)

The analysis of variance (ANOVA) indicated that the mean sum of squares due to genotypes were significant for the characters *viz.*, days to 50% heading, days to maturity, number of grains per spike, Grain weight per spike (g), 1000-grain weight (g), Biological yield per plant (g), Sedimentation value (ml) and Protein content (%). The mean sum of squares due to blocks showed non-significant difference for most of the traits except protein content indicating there is no difference in block mean. Therefore, the original mean used for such traits. Mean sum squares from analysis of variance for various characters are given in Table 4.1.

4.2 MEAN PERFORMANCE OF THE GENOTYPES AND RANGE

Mean performance of genotypes and range for all the 14 characters are presented in Appendix IV and V.

4.2.1 Days to 50% Heading

The days to 50% heading ranged from 70 to 93 with a mean value of 83.33. The genotype GW (D) 2019-982 was the first to head (70 days), while the genotypes 50th IDYN 744, 50th IDSN 7049, 49th IDYN 733 and 49th IDSN 7107 were the last to head (93 days). Among the checks, HI-8759 was early in heading (80 days).

Table 4.1: Analysis of variance for yield and its contributing traits in durum wheat

S. No.	Character	Block	Treatment	Check	Germplasm	C v/s G	Error
		[3]	[56]	[4]	[51]	[1]	[12]
1.	Days to 50% heading	1.12	34.37**	51.18**	33.56**	8.72	2.07
2.	Days to maturity	0.85	37.89**	11.68**	40.63**	2.93	1.98
3.	Plant height (cm)	15.93	44.71	9.80	47.53	40.53	22.17
4.	Number of effective tillers per plant	1.08	1.68	0.99	1.76	0.39	0.84
5.	Length of main spike (cm)	0.23	0.93	1.33	0.91	0.03	0.63
6.	Number of spikelets per spike	1.11	3.27	3.00	3.24	6.29	1.40
7.	Number of grains per spike	29.89	155.46**	58.96	128.36**	1923.59**	23.38
8.	Grain weight per spike (g)	0.30	0.34*	0.64*	0.29	1.60**	0.13
9.	1000-grain weight (g)	0.68	26.75**	32.66**	23.68**	159.78**	1.22
10.	Biological yield per plant (g)	1.88	30.58*	58.43*	28.99	0.30	12.41
11.	Grain yield per plant (g)	1.41	5.43	7.16	5.40	0.15	2.90
12.	Harvest Index (%)	4.19	7.20	2.39	7.68	1.90	4.37
13.	Sedimentation Value(ml)	0.05	18.11**	11.20**	18.45**	28.62**	0.80
14.	Protein (%)	0.64*	0.72**	2.80**	0.54*	1.56*	0.18

* Significant at P = 0.05

** Significant at P = 0.01

4.2.2 Days to Maturity

Days to maturity ranged from 112 days (GW (D) 2019-982) to 138 days (50th IDSN 7067 and 50th IDSN 7113) with a mean value of 124 days. HI-8759 was the early maturing check (121.50 days) amongst all checks under study.

4.2.3 Plant Height (cm)

The plant height ranged from 74.00 cm to 100.70 cm with a general mean of 88.42 cm. Among Genotypes, minimum plant height was recorded for 50th IDSN 7037, while among the checks, HI 8759 (85.45 cm) had minimum plant height.

4.2.4 Number of Effective Tillers per Plant

The effective tillers per plant ranged from 5.20 to 9.40 with mean value of 7.23. Among the genotypes, 50th IDSN 7076, GW (D) 2019-970 and GW (D) 2019-976 highest effective tillers per plant. Among the checks, highest number of effective tillers per plant was observed for HI 8498 (8.05).

4.2.5 Length of Main Spike (cm)

The average length of the main spike was noted as 7.47 cm. It ranged from 5.80 cm to 9.80 cm. Among genotypes, 41st IDYT 18 had a long spike *i.e.* 9.80 cm. The longest spike amongst checks was observed for HI 8737 (7.92 cm).

4.2.6 Number of Spikelets per Spike

The number of spikelets per spike ranged from 15.80 to 23.00 with a mean value of 19.35. The highest number of spikelets per spike was observed for 40st IDYT 18 (23.00) while check HI 8737 had highest number of spikelets per spike (19.45).

4.2.7 Number of Grains per Spike

The number of grains per spike ranged from 43.80 to 88.30 with a mean value of 64.83. The genotypes 50th IDSN 7100 had highest grains per spike while among checks, highest grains per spike were observed for HI 8737 (56.53).

4.2.8 Grain Weight per Spike (g)

The grain weight per spike ranged from 2.31 g to 5.16 g with mean value of 3.70 g. The highest grain weight per spike was observed for the genotype GW (D) 2017-859 whereas check HI 8498 had highest grain weight per spike *i.e.* 3.66 g. The best check for the grain weight per spike was HI 8498 (3.66 g).

4.2.9 1000-grain Weight (g)

The mean value of 1000-grain weight was 41.95 g and it ranged from 33.60 g to 53.40 g. The genotype GW (D) 2019-972 had highest 1000-grain weight *i.e.* 53.40 g while the best check variety for 1000-grain weight was HI 8737 (47.25 g).

4.2.10 Biological Yield per Plant (g)

The biological yield per plant ranged from 32.40 g to 55.20 g with mean value of 42.47 g. The highest biological yield per plant was observed for the genotypes GW 2017-865 while the best check for biological yield per plant was HI 8777 (48.75 g).

4.2.11 Grain Yield per Plant (g)

The grain yield per plant ranged from 11.25 g to 20.20 g with mean value of 15.88 g. The genotypes GW 2017-865 (20.20 g) had highest grain yield per plant while among checks, HI 8777 (18.07 g) had highest grain yield per plant.

4.2.12 Harvest Index (%)

The mean value of harvest index was 37.38% and it ranged from 30.24% to 41.82%. The highest harvest index was observed for the genotype 50th IDSN 7049 (41.82%) while check variety HI 8737 had highest harvest index *i.e.* 38.61%.

4.2.13 Sedimentation Value (ml)

The sedimentation value ranged from 18 ml to 38 ml with an average value of 28.06 ml. The genotypes 50th IDSN 7067 had highest sedimentation value *i.e.* 38 ml while check variety HI 8737 (28.06 ml) had highest sedimentation value.

4.2.14 Protein Content (%)

Protein content ranged from 11.70% to 15.00% with a mean value of 13.16%. The genotype 50th IDYN 729 had highest protein content *i.e.* 15.00% while it was recorded highest for check PDW 291.

4.3 GENETIC VARIABILITY PARAMETERS

The parameter of genetic variability *viz.*, mean, range, phenotypic and genotypic coefficient of variation (%), heritability (%) in broad sense, genetic advance and genetic advance as per cent of mean (genetic gain) for each trait has been referenced in Table 4.2.

4.3.1 Genotypic Coefficient of Variation (GCV)

The magnitude of GCV varied from 4.53% in protein content to 15.81% in number of grains per spike. It was found that GCV was found low (<10%) for the characters, protein content (4.53%), harvest index (4.87 %), days to maturity (5.01%), plant height (5.70%), days to 50% heading (6.73%), number of spikelets per spike (6.99%), length of main spike (7.17%), biological yield per plant (9.59%) and grain yield per plant (9.95%) while, it was moderate (10-20%) in grain weight per spike (10.87%), 1000-grain weight (11.30%), number of effective tillers per plant (13.28%), sedimentation value (14.97%) and 15.81% for the number of grains per spike.

4.3.2 Phenotypic Coefficient of variation (PCV)

For all of the characters studied, the magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation. The highest PCV was recorded for number of effective tillers per plant (18.34%) followed by number of grains per spike (17.48%), sedimentation value (15.31%) and grain yield per plant (14.63%). The characters *viz.*, days to maturity (5.14%), protein content (5.57%) and days to 50% heading (6.95%) showed low phenotypic coefficient of variation.

4.3.3 Heritability (h^2)

Broad sense heritability was estimated for all of the characters under investigation. The majority of the characters had high heritability and it was recorded highest for the sedimentation value (95.66%) followed by days to maturity (95.14%), 1000-grain weight (94.85%) and days to 50% heading (93.82%). However, length of main spike (31.39%) and harvest index (43.17%) showed low estimates of heritability.

Table 4.2: Genetic variability parameters for yield and its contributing traits in durum wheat

S.No.	Character	Mean	Range		GCV (%)	PCV (%)	H ² (%)	GA	GG
			Min.	Max.					
1.	Days to 50% heading	83.33	70.00	93.00	6.73	6.95	93.82	11.20	13.44
2.	Days to Maturity	124.00	112.00	138.00	5.01	5.14	95.14	12.49	10.07
3.	Plant height (cm)	88.42	74.00	100.70	5.70	7.80	53.36	7.58	8.57
4.	Number of effective tillers per plant	7.23	5.20	9.40	13.28	18.34	52.43	1.43	19.81
5.	Length of main spike (cm)	7.47	5.80	9.80	7.17	12.79	31.39	0.62	8.27
6.	Number of spikelets per spike	19.35	15.80	23.00	6.99	9.30	56.59	2.10	10.84
7.	Number of grains per spike	64.83	43.80	88.30	15.81	17.48	81.78	19.09	29.44
8.	Grains weight per spike (g)	3.70	2.31	5.16	10.87	14.59	55.56	0.62	16.70
9.	1000 grain weight (g)	41.95	33.60	53.40	11.30	11.60	94.85	9.51	22.67
10.	Biological yield per plant (g)	42.47	32.40	55.20	9.59	12.68	57.20	6.34	14.94
11.	Grain yield per plant (g)	15.88	11.25	20.20	9.95	14.63	46.27	2.21	13.95
12.	Harvest Index (%)	37.38	30.24	41.82	4.87	7.42	43.17	2.47	6.60
13.	Sedimentation Value(ml)	28.06	18.00	38.00	14.97	15.31	95.66	8.46	30.17
14.	Protein content (%)	13.06	11.70	15.00	4.53	5.57	66.03	1.00	7.58

4.3.4 Genetic Advance (GA)

The high genetic advance was recorded for number of grains per spike (19.09%) followed by days to maturity (12.49%) and days to 50% heading (11.20%) while the characters *viz.*, length of main spike (0.62%), protein content (1.00%) and number of effective tillers per plant (1.43%) showed low genetic advance..

4.3.5 Genetic Gain (GG)

The highest genetic advance as *per cent* of mean (genetic gain) was recorded for sedimentation value (30.17%) followed by number of grains per spike (29.44%), 1000-grain weight (22.67%) and number of effective tillers per plant (19.81%) while it was found lower for harvest index (6.60%) followed by protein content (7.58%) and plant height (8.57%).

4.4 CORRELATION COEFFICIENT ANALYSIS

When a breeder is faced with the problem of combining high yield potential with desirable agronomical and quality parameters, knowledge of genetic correlation for yield, its components, and various quality characteristics becomes very important. The type, extent, and direction of selection may all be determined using association studies. The degree of mutual relationship between yields and their component traits was worked out by estimating the correlation coefficient at the phenotypic and genotypic levels using 57 genotypes of durum wheat and are presented in Table 4.3. In general, genotypic correlation coefficients were higher in magnitude than their respective phenotypic correlation coefficients for most of the character pairs. The correlation between different characters is being presented as under:

Days to 50% heading expressed positive and significant correlation with days to maturity ($r_g = 0.95^{**}$ and $r_p = 0.95^{**}$) and sedimentation value ($r_g = 0.46^{**}$ and $r_p = 0.43^{**}$) at both genotypic and phenotypic levels while, it exhibited positive and significant correlation with plant height ($r_g = 0.32^*$) at genotypic level only. It showed negative and significant correlation with length of main spike ($r_g = -0.46^{**}$) at genotypic level.

Days to maturity displayed positive and significant correlation with plant height ($r_g = 0.38^{**}$ and $r_p = 0.32^*$) and sedimentation value ($r_g = 0.42^{**}$ and $r_p = 0.41^{**}$) at both genotypic and phenotypic level but it showed negative and significant

correlation with number of effective tillers per plant ($r_g = -0.37^{**}$), length of main spike ($r_g = -0.48^{**}$), biological yield per plant ($r_g = -0.34^*$) and grain yield per plant ($r_g = -0.28^*$) at genotypic level only.

Plant height expressed positive and significant correlation with grain weight per spike ($r_g = 0.38^{**}$ and $r_p = 0.31^*$) at both genotypic and phenotypic level while it was positive and significantly correlated with number of grains per spike ($r_p = 0.30^*$) at genotypic level only. Plant height exhibited negative and significant correlation with number of effective tillers per plant ($r_g = -0.50^{**}$), length of main spike ($r_g = -0.36^{**}$), harvest index ($r_g = -0.51^{**}$) and grain yield per plant ($r_g = -0.45^{**}$) at genotypic level only.

Number of effective tillers per plant indicated positive and significant correlation with biological yield per plant ($r_g = 0.67^{**}$ and $r_p = 0.42^{**}$), grain yield per plant ($r_g = 0.55^{**}$ and $r_p = 0.40^{**}$) at both genotypic and phenotypic levels and number of spikelets per spike ($r_g = 0.30^*$) at genotypic level only. It showed negative and significant correlation with length of main spike ($r_g = -0.33^*$) and sedimentation value ($r_g = -0.40^{**}$) at genotypic level only.

Length of main spike showed positive and significant correlation with number of spikelets per spike ($r_g = 0.83^{**}$ and $r_p = 0.51^{**}$) at both genotypic and phenotypic level and protein content ($r_g = 0.48^{**}$) and grain yield per plant ($r_g = 0.66^{**}$) at genotypic level only. It showed positive and significant correlation with grain weight per spike ($r_p = 0.48^{**}$) at phenotypic level only while it showed negative and significant correlation with harvest index ($r_g = -0.65^{**}$) and sedimentation value ($r_g = -0.52^{**}$) at genotypic level.

Number of spikelets per spike exhibited positive and significant correlation with number of grains per spike ($r_g = 0.49^{**}$ and $r_p = 0.39^{**}$), grain weight per spike ($r_g = 0.43^{**}$ and $r_p = 0.35^*$) and grain yield per plant ($r_g = 0.34^{**}$ and $r_p = 0.29^{**}$) at both genotypic and phenotypic levels.

Number of grains per spike had positive and significant correlation with grain weight per spike ($r_g = 0.40^{**}$ and $r_p = 0.49^{**}$) at both genotypic and phenotypic level and positive and significant correlation at genotypic level with harvest index ($r_g = 0.34^*$). It showed negative and significant correlation at both genotypic and phenotypic level with 1000-grain weight ($r_g = -0.66^{**}$ and $r_p = -0.58^{**}$) and protein content ($r_g = -0.33$) at genotypic level only.

Table 4.3: Estimation of genotypic (rg) and phenotypic (rp) correlation coefficient for different characters in durum wheat

S. No.	Character	r	Days to 50% heading	Plant height	Number of effective tillers per plant	Length of main spike	Number of spikelets per spike	Number of grains per spike	Grain weight per spike	1000-grain weight	Biological yield per plant	Harvest index	Sedimentation Value	Protein content	Grain Yield per plant
1.	Days to 50% heading	rg	0.95**	0.32*	-0.17	-0.46**	-0.12	0.25	-0.19	-0.20	-0.27	0.23	0.46**	-0.14	-0.13
		rp	0.95**	0.27	-0.12	-0.25	-0.01	0.20	-0.17	-0.21	-0.17	0.14	0.43**	-0.17	-0.07
2.	Days to maturity	rg		0.38**	-0.37**	-0.48**	-0.19	0.23	-0.22	-0.27	-0.34*	0.07	0.42**	-0.12	-0.28*
		rp		0.32*	-0.23	-0.22	-0.08	0.19	-0.20	-0.26	-0.21	0.08	0.41**	-0.15	-0.14
3.	Plant height	rg			-0.50**	-0.36**	0.04	0.30*	0.38**	-0.13	-0.19	-0.51**	-0.25	0.17	-0.45**
		rp			-0.04	0.14	0.13	0.22	0.31*	-0.12	-0.10	-0.05	-0.18	-0.05	-0.12
4.	Number of effective tillers per plant	rg				-0.33*	0.30*	-0.01	-0.08	0.03	0.67**	-0.22	-0.40**	0.07	0.55**
		rp				-0.04	0.12	-0.00	-0.02	0.04	0.42**	0.07	-0.21	0.10	0.40**
5.	Length of main spike	rg					0.83**	0.26	1.02	-0.19	1.03	-0.65**	-0.52**	0.48**	0.66**
		rp					0.51**	0.24	0.48**	-0.03	0.18	0.01	-0.23	0.01	0.15
6.	Number of spikelets per spike	rg						0.49**	0.43**	-0.11	0.27	0.15	-0.25	-0.04	0.34*
		rp						0.39**	0.35*	-0.11	0.23	0.19	-0.19	-0.03	0.29*
7.	Number of grains per spike	rg							0.40**	-0.66**	0.03	0.34*	0.07	-0.33*	0.20
		rp							0.49**	-0.58**	-0.01	0.10	0.05	-0.23	0.04
8.	Grain weight per spike	rg								-0.23	0.22	0.21	-0.50**	-0.70**	0.31*
		rp								-0.16	0.13	-0.01	-0.39**	-0.33*	0.11
9.	1000 grain weight	rg									0.12	-0.24	-0.12	0.09	-0.00
		rp									0.07	-0.12	-0.08	0.05	-0.00
10.	Biological yield per plant	rg										-0.14	-0.16	-0.34*	0.87**
		rp										0.01	-0.14	-0.09	0.86**
12.	Harvest index	rg											0.21	0.25	0.51**
		rp											0.16	0.11	0.36**
13.	Sedimentation Value	rg												-0.11	-0.03
		rp												-0.10	-0.05
14.	Protein content	rg													-0.04
		rp													-0.23

*, **, *** Significant at 5% and 1% respectively, Here 0.00 values indicates negligible correlation

Grain weight per spike manifested positive and significant correlation with grain yield per plant ($r_g = 0.31^*$) at genotypic level only while it had negative and significant correlation with sedimentation value ($r_g = -0.50^{**}$ and $r_p = -0.39^{**}$) and protein content ($r_g = -0.70^{**}$ and $r_p = -0.33^{**}$) at both genotypic and phenotypic level.

Biological yield per plant expressed positive and significant correlation at both genotypic and phenotypic level with grain yield per plant ($r_g = 0.87^{**}$ and $r_p = 0.86^{**}$) while it showed negative and significant correlation with protein content ($r_g = -0.34$) at genotypic level only.

Harvest index exhibited positive and significant correlation with grain yield per plant ($r_g = 0.51^{**}$ and $r_p = 0.36^{**}$) at both genotypic and phenotypic level.

4.5 PATH COEFFICIENT ANALYSIS

Simple correlation experiments are insufficient to obtain a clear-cut understanding of the cause and effect relationship between yield and attributes, accompanied by the degree of their association. Wright (1921) and later Dewey and Lu (1959) proposed path coefficient analysis to determine direct and indirect effects of traits by splitting the correlation into direct and indirect effects.

As the grain yield per plant was found non-significant, so path coefficient analysis cannot be worked out for the present investigation.

4.6 GENETIC DIVERGENCE

To estimate the genetic divergence between two genotypes/lines or a group of genotypes/lines, Tocher's method (Rao, 1952) was used to group genotypes into different clusters using Mahalanobis' D^2 statistics (1936), as described by Rao (1952).

4.6.1 Genotypes Grouping into Clusters

Fifty-seven durum wheat genotypes were classified into nineteen clusters based on their relative magnitude of D^2 values. The result of the genotypes grouping into clusters is displayed in Table 4.4. Cluster I was the largest one with 23 genotypes followed by cluster III having 5 genotypes, cluster IV with 4 genotype, clusters II and VI with 3 genotypes, clusters V, VII, VIII, IX and X with 2 genotypes and remaining clusters *viz.*, XI, XII, XIII, XIV, XV, XVI, XVII, XVIII and XIX with a single genotype.

Table 4.4: Grouping of 57 durum wheat genotypes into nineteen clusters (by Tocher's method)

Cluster No.	Name of genotype	Number of genotype
I	50 th IDYN 712, 50 th IDYN 719, 50 th IDYN 722, 50 th IDYN 741, 50 th IDYN 744, 50 th IDSN 7040, 50 th IDSN 7077, 50 th IDSN 7100, 50 th IDSN 7078, 50 th IDSN 7177, GW (D) 2019 969, GW (D) 2019-971, GW (D) 2019-973, GW (D) 2019-974, GW (D) 2019-977, 49 th IDYN 713, 49 th IDSN 7107, 41 st IDYT 10, 41 st IDYT 15, HI 8498, HI 8737, HI 8759, HI 8777	23
II	GW (D) 2019-970, GW (D) 2019-972, GW (D) 2019-976	3
III	50 th IDYN 706, 50 th IDYN 721, 50 th IDSN 7013, 49 th IDYN 718, 49 th IDYN 747	5
IV	50 th IDYN 735, 50 th IDSN 7049, 50 th IDSN 7076, 50 th IDSN 7113	4
V	PDW 291, 50 th IDYN 709	2
VI	50 th IDYN 737, 50 th IDSN 7072, 50 th IDYN 718	3
VII	50 th IDSN 7135, GW (D) 2019-979	2
VIII	50 th IDYN 729, 50 th IDSN 7037	2
IX	GW (D) 2019-978, GW (D) 2017-859	2
X	GW (D) 2019-981, 49 th IDYN 733	2
XI	41 st IDYT 18	1
XII	GW (D) 2019-975	1
XIII	GW (D) 2019-982	1
XIV	50 th IDYN 740	1
XV	41 st IDYT 4	1
XVI	GW (D) 2019-980	1
XVII	GW 2017-865	1
XVIII	50 th IDSN 7067	1
XIX	50 th IDSN 7034	1

4.6.2 Average Intra and Inter Cluster Distance

Average inters and intra-cluster distance among nineteen clusters was displayed in Table 4.5. The mean intra-cluster distance ranged from 0.00 (cluster XI to Cluster XIX) to 0.39 (cluster X). The cluster X had maximum intra-cluster distance (0.39) followed by cluster IX and VI (0.37), cluster IV, VII and VIII (0.35), cluster III (0.32), cluster I and V (0.31) and 0.29 for cluster II.

Maximum inter-cluster distance was exhibited by cluster XII and XIV (1.19) followed by cluster XVI and XVIII (1.18), cluster XVI and XVII (1.12), cluster XII and XVIII (1.10), cluster XV and XIX (1.05), cluster X and XVII (1.00), cluster VII and XVII, XVI and XIX and XV and XVII (0.98), cluster XIV and XVII (0.97), cluster XIII and XV (0.96) and 0.94 for cluster XVII and XIX. Minimum inter-cluster distance was observed between cluster I and III (0.42) followed by cluster I and IV, VII and VIII (0.44), cluster IV and XIX (0.44), cluster I and IX (0.45) and cluster I and V, VI and XIII (0.46).

4.6.3 Cluster Mean

The cluster means of various characters are shown in Table 4.6. The extent of difference among cluster means for different characters was found to be prominent. The variation for days to 50% heading was ranged from 70 days (cluster XIII) to 92 days (cluster XVIII), days to maturity from 112 days (cluster XIII) to 138 days (cluster XVIII), plant height from 77.6 cm (cluster VIII) to 100.7 cm (cluster XIV), number of effective tillers per plant from 5.2 (cluster XVII) to 9.2 (cluster XV), length of main spike from 6.13 cm (cluster V) to 9.8 cm (cluster XI), number of spikelets per spike from 16.2 (cluster XVIII) to 23 (cluster XI), number of grain per spike from 43.8 (cluster XIII) to 79.3 (cluster XIX), grain weight per spike from 2.5 g (cluster V) to 4.9 g (cluster IX), 1000-grain weight from 34.96 g (cluster IV) to 50.73 g (cluster II), biological yield per plant from 32.4 g (cluster XIV) to 55.2 g (cluster XVII), grain yield per plant from 11.89 g (cluster XIX) to 20.2 g (cluster XVII), harvest index from 31.53 g (cluster X) to 41.18 g (cluster VIII), sedimentation value from 18 ml (cluster XVI) to 38 ml (cluster XVIII) and for protein content it ranged from 11.7% (cluster XIV) to 14.8% (cluster XII).

Table 4.6: Mean values of different characters for 57 durum wheat genotypes grouped into nineteen clusters

Cluster	Days to 50% heading	Days to maturity	Plant height (cm)	Number of effective tiller per plant	Length of main spike (cm)	Number of spikelets per spike	Number of grains per spike	Grain weight per spike (g)	1000-grain weight (g)	Biological yield per plant (g)	Grain Yield per plant	Harvest index (%)	Sedimentation Value (ml)	Protein content (%)
I	83.13	123.74	86.41	7.11	7.81	19.96	65.92	3.76	42.55	41.99	15.88	37.83	27.47	13.05
II	83.00	121.67	95.77	9.07	7.37	20.33	49.53	3.76	50.73	47.87	19.11	40.07	27.33	13.43
III	83.20	123.40	86.62	8.08	6.54	17.80	61.44	3.41	43.10	44.16	14.87	33.68	30.20	12.80
IV	88.00	130.50	92.17	7.75	6.80	17.90	68.28	3.58	34.96	41.25	15.90	38.29	31.00	12.73
V	90.38	128.88	89.81	6.28	6.13	16.90	46.45	2.50	44.68	37.40	14.34	38.31	30.75	14.13
VI	80.67	121.67	92.93	5.87	6.50	18.87	71.27	4.02	39.29	41.47	16.52	39.65	24.33	13.03
VII	80.50	122.00	94.90	8.30	8.60	19.00	70.05	3.52	45.16	42.70	16.18	37.85	27.00	13.40
VIII	79.00	119.00	77.60	7.50	6.70	17.80	64.30	3.48	41.27	41.10	16.91	41.18	31.50	14.45
IX	85.50	126.00	98.50	6.60	8.80	19.60	69.90	4.90	37.64	39.35	14.88	37.82	24.00	13.10
X	85.50	127.00	82.65	6.40	6.75	19.00	54.75	3.50	46.24	38.35	12.11	31.53	24.00	12.90
XI	79.00	122.00	92.80	7.60	9.80	23.00	71.00	3.72	38.40	49.50	16.85	34.04	30.00	14.10
XII	75.00	115.00	82.60	8.60	7.50	19.80	49.30	3.75	37.50	51.20	18.75	36.62	19.00	14.80
XIII	70.00	112.00	78.80	5.60	7.60	18.60	43.80	2.70	46.46	36.50	14.50	39.73	28.00	13.70
XIV	91.00	131.00	100.70	5.40	7.20	21.40	75.00	3.57	42.08	32.40	12.08	37.28	32.00	11.70
XV	87.00	121.00	80.10	9.20	7.90	19.40	64.00	4.08	46.92	51.60	19.00	36.82	26.00	12.30
XVI	83.00	125.00	98.60	8.40	7.50	21.00	71.30	3.35	41.06	54.20	18.96	34.99	18.00	13.90
XVII	78.00	121.00	86.00	5.20	8.60	19.40	53.30	4.10	38.00	55.20	20.20	36.59	34.00	12.00
XVIII	92.00	138.00	84.70	5.40	7.70	16.20	60.50	3.55	48.12	37.20	14.20	38.17	38.00	12.50
XIX	78.00	120.00	85.20	7.60	6.70	19.00	79.30	3.48	35.06	35.20	11.89	33.78	31.00	13.20

4.6.4 Relative Contribution of different Character towards Total Divergence

The percent contribution of independent characters in the direction of total divergence has been presented in Table 4.7. The number of grains per spike was found to be the most important character in contributing to overall divergence, accounting for 43.86% followed by plant height (17.40%), days to 50% heading (14.03%), biological yield per plant (9.21%), 1000-grain weight (6.27%), and sedimentation value (4.61%), days to maturity (2.00%), number of spikelets per spike (0.88%), number of effective tillers per plant (0.64%), grain yield per plant (0.51%) length of main spike (0.33%), protein content (0.17%), grain weight per spike (0.06%) and harvest index (0.03%).

Table 4.7: Percent contribution of different characters in durum wheat

Character Name	Per cent Contribution
Days to 50% heading	14.03
Days to maturity	2.00
Plant height (cm)	17.40
Number of effective tillers per plant	0.64
Length of main spike (cm)	0.33
Number of spikelets per spike	0.88
Number of grains per spike	43.86
Grain weight per spike (g)	0.06
1000 grain weight (g)	6.27
Biological yield per plant (g)	9.21
Grain yield per plant (g)	0.51
Harvest index (%)	0.03
Sedimentation value (ml)	4.61
Protein content (%)	0.17

5. DISCUSSION

The importance of the breeding programme of durum wheat is to develop a variety combining high yielding and better quality attributes. An effective breeding programme can be formulated only if information regarding magnitude and nature of variability for different characters and their association with each other and with grain yield is available.

Keeping that in view, the present investigation entitled "**Genetic diversity in durum wheat [*Triticum durum* Desf.]**" was, therefore, undertaken at the Instructional Farm, RCA, Udaipur during *Rabi*, 2019-20 to determine the magnitude of genetic diversity among 57 genotypes of durum wheat. Results of the present investigation including study of fourteen characters are discussed under following heads:

- 5.1 Analysis of variance
- 5.2 Genetic variability parameters
- 5.3 Correlation coefficient analysis
- 5.4 Path analysis
- 5.5 Genetic divergence

5.1 ANALYSIS OF VARIANCE

The analysis of variance indicated significant difference among the genotypes for the characters under investigation indicating existence of ample variability among the genotypes for the traits *viz.*, days to 50% heading, days to maturity, number of grains per spike, grain weight per spike (g), 1000-grain weight (g), biological yield per plant (g), sedimentation value (ml) and protein content (%). Presence of significant variability in durum wheat was earlier reported by Dhakar *et al.*, (2012) for number of grains per spike, plant height and grain yield per plant. Tambe *et al.*, (2013) also observed a wide range of variability for all the traits under study.

5.2 GENETIC VARIABILITY PARAMETER

The existence of sufficient genetic variability is necessary and its association with heritability (broad sense), will help to determine the relative contributions of

genetic and environmental factors to overall phenotypic variance in a population. In this study, the phenotypic coefficient of variation (PCV) is slightly higher than the genotypic coefficient of variation (GCV) for all of the traits indicating little effect of environmental variations on the characters. Highest coefficient of variation in terms of both genotypic and phenotypic value was exhibited by number of grains per spike followed by sedimentation value, number of effective tillers per plant and 1000-grain weight while lowest coefficient of variation was observed for protein content and days to maturity. The high values of GCV and PCV were earlier reported by Dhakar *et al.*, (2012) for number of effective tillers per plant and weight of 1000-grain. Tambe *et al.*, (2013) also reported high values of GCV and PCV for number of effective tillers per plant and 1000-grain weight.

The coefficient of variation only showed the degree of heterogeneity for different traits, but it had no information on the heritable component of the variability. Selection can be effective where there is a high or moderate amount of heritability followed by a high or moderate genetic advance. This indicates that additive gene action is involved in the inheritance of the traits in question. The heritability estimates (broad sense) for most of the characters were very substantial, suggesting a strong genetic nature for all of the traits studied. Because of the higher heritability, selection for the majority of the traits could be effective in this group of genotypes. Estimates of high heritability coupled with the high genetic gain for the traits like sedimentation value (ml), days to 50 % heading, number of grains per spike and 1000-grain weight indicated that all these characters are regulated by additive gene action and the direct selection be expected to show improvement in such traits. These results are in agreement with earlier reports of Tsegaye *et al.*, (2012) for days to heading. These results are similar to Adhikari *et al.*, (2018) *i.e.* higher estimates of heritability associated with genetic gain for 1000-grain weight and days to heading.

5.3 CORRELATION COEFFICIENT ANALYSIS

Correlation studies indicated the nature and magnitude of the relationship between two pairs of characters. It will then be possible to achieve genetic advancement in one character by selecting the other pair. Evidently, understanding the relationships between characters may aid in identifying the characters to pick for higher grain yield, as well as determining the degree and nature of the relationships that exist within grain yield contributing traits. It optimizes the selection of an appropriate breeding method and the contribution of parents to crop improvement.

During present investigation, genotypic and phenotypic correlation coefficient was worked out for different characters including grain yield. The genotypic correlation coefficient was generally higher than the respective phenotypic correlation coefficient. Lower phenotypic correlation may result from the modifying effect of environment on the association of characters at the genetic level. Genotypic correlation coefficient indicates a measure of genetic association between characters and therefore, helps in identifying the traits which are important and need to be considered for improvement of yield. The grain yield per plant had positive and significant correlation with number of effective tillers per plant, number of spikelets per spike, biological yield per plant, harvest index at both genotypic and phenotypic level while it showed positive and significant correlation with length of main spike at genotypic level only. Genotypic and phenotypic correlation among various characters is given in Table 5.1. The similar results were recorded by Tsegaye *et al.*, (2012) *i.e.* grain yield per plant highly correlated with biological yield per plant and number of effective tillers per plant. Singh (2016) also recorded the similar results *i.e.* grain yield per plant significant and positively correlated with number of effective tillers per plant, biological yield per plant and harvest index.

5.4 PATH COEFFICIENT ANALYSIS

Correlation coefficients showed the existence of a relationship between pair characters, but a dependent character is an interaction of several mutually correlated component characters and change in any one-component character would disrupt the whole network of cause and effect mechanism. Wright (1921) and later Dewey and Lu (1959) proposed path coefficient analysis to determine direct and indirect effects of traits by splitting the correlation coefficient into direct and indirect effects *via* dependent character. The relative importance of the causal factors involved is often measured using the path coefficient analysis. The path coefficient analysis was determined for grain yield per plant at the genotypic level, considering grain yield per plant as a dependent variable.

As the grain yield per plant was found non-significant, so path coefficient analysis cannot be worked out for the present investigation.

Table 5.1: List of genotypic and phenotypic correlation among various characters

S. No.	Character	Positive and Significantly correlated	Negative and Significantly correlated
1.	Days to 50% heading	DM, SDS, PH	LMS
2.	Days to maturity	PH, SDS	ETP, LMS, BY, GY
3.	Plant height (cm)	GWS, GPS	ETP, LMS, HI, GY
4.	Number of effective tillers per plant	BY, GYP, SS	LMS, SDS
5.	Length of main spike (cm)	SS, PC, GY, GWS	HI, SDS
6.	Number of spikelets per spike	GS, GWS, GY	-----
7.	Number of grains per spike	GWS, HI	1000-GW, PC
8.	Grain weight per spike (g)	GY	SDS, PC
9.	Biological yield per plant (g)	GY	PC
10.	Harvest Index (%)	GY	-----

DF	= Days to 50% heading	SS	= Number of Spikelets per spike
PH	= Plant height	GWS	= Grain weight per spike (g)
LMS	= Length of main Spike (cm)	GPS	= Number of grain per spike
1000-GW	= 1000-grain weight (g)	BY	= Biological yield per plant (g)
GY	= Grain yield per plant (g)	HI	= Harvest index (%)
PC	= Protein content (%)	SDS	= Sedimentation value (ml)
ETP	= Number of effective tillers per plant		

5.5 GENETIC DIVERGENCE

In plant breeding, genetic diversity plays an indispensable role because, hybrids between diverse origins, ordinarily exhibit a greater hybrid vigor and confer more recombinant than those between closely related parents. Hence, for a successful breeding programme, the genetic diversity of the parents is of uttermost importance. For that reason, it is recommendable to select more divergent from the available germplasm, based on the information regarding to genetic diversity existing in the available germplasm, one of the ergastic technique for estimating the genetic diversity

is the D^2 statistic introduced by Mahalanobis in 1936. The D^2 statistic determines the relative contribution of each character to overall divergence by measuring the degree of diversification.

Fifty-seven durum wheat genotypes were grouped into 19 clusters, based on the multivariate hierarchical cluster analysis as per Mahalanobis D^2 statistics. The maximum number of genotypes was grouped into cluster I which had 23 genotypes followed by cluster III having 5 genotypes, cluster IV with 4 genotype, cluster II and VI with 3 genotypes, cluster V, VII, VIII, IX and X with 2 genotypes and remaining all the clusters having a single genotype in each cluster. The present findings are in accordance with those reported by Tsegaye *et al.*, (2012) *i.e.* genotypes were clustered into 06 genetically distinct groups. Kumar *et al.*, (2014) also reported similar clustering patterns *i.e.* genotypes were grouped into 16 clusters.

Inter-cluster distance is expressed in terms of the genetic distance between two clusters, while intra-cluster distance is measured in terms of the genetic diversity between genotypes in the same cluster. The estimates of inter-cluster distance were higher than that of intra-cluster distance, reflecting that the experimental genotypes had a lot of genetic diversity. The inter-cluster distance was varied from 0.42 (cluster III and I) to 1.19 for cluster XII and XIV. Some other notable inter-cluster distance were observed between cluster XVI and XVIII, cluster XVI and XVII, cluster XII and XVIII, cluster XV and XIX and cluster X and XVII revealed that the genotypes engaged with such clusters have a lot of genetic diversity, so that these genotypes could be used in durum wheat hybridization programmes to improve grain yield. Similar findings were also reported by Tsegaye *et al.*, (2012) and Malviya *et al.*, (2018).

The highest intra-cluster distance was shown by cluster X followed by cluster IX, cluster VI, cluster IV, cluster VII and cluster VIII. The genotypes of these clusters had the largest intra-cluster gap due to the genotypes' wide genetic diversity. The findings of this study were consistent with those of Tsegaye *et al.*, (2012) and Malviya *et al.*, (2018).

The characteristics that contributed the most to the divergence will give more attention in deciding the cluster for the intention of further selection and the selection of parents for the hybridization programme to develop high yield durum wheat

varieties. The outcome of this study manifested that the character plant height contributed most to total divergence and some other noteworthy character contributed more to total divergence such as days to 50% heading, biological yield per plant, 1000-grain weight, and sedimentation value among fifty-seven genotypes of durum wheat. As shown by the number of times these traits occurred or placed first during contribution to diversity, direct selection for this character would be beneficial. Kumar *et al.*, (2014), Singh (2015), and Ambati *et al.*, (2020) also reported similar results.

Cluster XVII had genotypes having higher mean value for grain yield per plant and biological yield per plant, cluster XI had highest mean value for length of main spike and number of spikelets per spike, cluster VIII having highest mean value for harvest index and lowest mean value for plant height, cluster II had greater mean value for 1000-grain weight, cluster IX had highest mean value for grain weight per spike, cluster XII had highest mean value for protein content, cluster XV had highest mean value for number of effective tillers per plant and cluster XIX for number of grain per spike. Therefore, hybridization between selected genotypes from divergent clusters is desired to sparingly combine all of the targeted traits.

6. SUMMARY AND CONCLUSION

The present investigation entitled “**Genetic Diversity in Durum Wheat [*Triticum durum* Desf.]**” was conducted during *Rabi*, 2019-20 at Instructional Farm, RCA, Udaipur. The experimental material consisted of 57 durum wheat genotypes were tested using Augmented Randomized Block Design with four replication (only checks replicated).

The observations were recorded on five randomly selected competitive plants for characters, *viz.*, plant height (cm), number of effective tillers per plant, length of main spike (cm), number of spikelets per spike, number of grains spike, grain weight per spike (g), 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), sedimentation value (ml) and protein content (%) while for the days to 50% heading and days to maturity, the observation were noted on the basis of plant population of each genotype. The data obtained were subjected to statistical analysis. The significant results based on field and lab studies are briefly summarized as under:

1. The mean sum of squares due to genotypes was found significant for most of the characters under this investigation showing that there is enough variability among genotypes for different traits.
2. The estimated values of Phenotypic Coefficient of Variation (PCV) were a little higher than their corresponding Genotypic Coefficient of Variation (GCV) pointing out that the environment had a minor effect on the expression of the different traits. GCV was found to be higher for the character *viz.*, number of grains per spike, sedimentation value, number of effective tillers per plant and 1000-grain weight while it was lower for the character *viz.*, harvest index, days to maturity, plant height and days to 50% heading.
3. The values of PCV were found to be high for the character *viz.*, number of effective tillers per plant, number of grains per spike, sedimentation value and grain yield per plant while lowest phenotypic coefficient of variation were found for days to maturity followed by protein content.

4. Heritability estimates were high for the character *viz.*, sedimentation value, followed by days to maturity, 1000-grain weight and days to 50% heading while, it was lower for the characters *viz.*, length of main spike and harvest index.
5. Genetic gains were high for the characters *viz.*, sedimentation value, number of grain per spike and number of effective tillers per plant while it was low for harvest index, protein content and plant height.
6. The genotypic correlation coefficients had higher values than phenotypic correlation coefficient for all the traits under investigation. The grain yield per plant had positive and significant correlation with number of effective tillers per plant, number of spikelets per spike, biological yield per plant, harvest index at both genotypic and phenotypic level while it showed positive and significant correlation with length of main spike at genotypic level only.
7. Based on the multivariate hierarchical cluster analysis as per Mahalanobis D^2 statistics 57 genotypes were grouped into 19 clusters. The maximum number of genotypes was grouped into cluster I with 23 genotypes while clusters XI to XIX were solitary. The maximum intra-cluster distance was shown by cluster X followed by cluster IX and cluster VI. Maximum inter-cluster distance was observed between cluster XII and XIV followed by cluster XVI and XVIII. The greater the distance between two clusters, wider is the expected genetic diversity.
8. The characters *viz.*, plant height, days to 50% heading, biological yield per plant, 1000-grain weight and sedimentation value contributed most to genetic divergence in fifty-seven genotypes of durum wheat.
9. Cluster XVII had genotypes having higher mean values for the biological yield per plant and grain yield per plant. Cluster XI had highest mean value for the length of main spike and number of spikelets per spike. Cluster VIII having highest mean value for harvest index. Cluster II was found to have the highest mean value for 1000-grain weight. Cluster XV had highest mean value for the number of effective tillers per plant. Cluster XIX had greater mean value for the trait number of grains per spike.

10. In the present investigation, genotypes *viz.*, 50th IDSN 7037, 50th IDSN 7049, GW 2017-865, 50th IDSN 7072, 50th IDSN 7077, GW (D) 2019-970, GW (D) 2019-972, GW (D) 2019-975, GW (D) 2019-980 and 41st IDYT 4 were superior not only in term of grain yield per plant but also in terms of traits like protein content, 1000-grain weight, grain weight per spike, plant height, number of effective tillers per plant, number of spikelets per spike and biological yield per plant. These diverse genotypes could be used in the future for the genetic improvement of durum wheat.

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Genetic Diversity in Durum Wheat (*Triticum durum* Desf.)

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ABSTRACT

The present study, entitled “Genetic Diversity in durum wheat [*Triticum durum* Desf.]” was conducted using 57 durum wheat genotypes including 05 checks at Instructional Farm, Rajasthan College of Agriculture, Udaipur during *Rabi*, 2019-2020. The genotypes were evaluated in Augmented Randomized Block Design.

The observations were made on the five randomly selected competitive plants for characters *viz.*, plant height (cm), number of effective tillers per plant, length of main spike (cm), number of spikelets per spike, number of grains per spike, grain weight per spike (g), 1000-grain weight, biological yield per plant (g), grain yield per plant, harvest index (%), sedimentation value (ml) and protein content (%) while for the days to 50% heading and days to maturity the observation were noted on the basis of plant population of each genotype.

Analysis of variance demonstrated a significant difference among genotypes for most of the traits indicating that the experimental material under investigation has an ample amount of variability.

High estimates of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were observed for number of grains per spike, sedimentation value, number of effective tillers per plant and 1000-grain weight pointed out the existence of wide genetic variability for these traits. Estimates of high heritability coupled with the high genetic gain for the traits like sedimentation value, days to 50% heading, number of grains per spike and 1000-grain weight indicated that all these characters are regulated by additive gene action and the direct selection be expected to show improvement in such traits.

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Association study exhibited that the grain yield per plant had positive and significant correlation with number of effective tillers per plant, number of spikelets per spike, biological yield per plant, harvest index at both genotypic and phenotypic level while it showed positive and significant correlation with length of main spike at genotypic level only.

Based on the multivariate hierarchical cluster analysis the maximum number of genotypes was grouped into cluster I which had 23 genotypes while the clusters XI, XII, XIII, XIV, XV, XVI, XVII, XVIII and XIX had a single genotype. The maximum intra-cluster gap was noted in cluster X followed by cluster IX and VI. Maximum inter-cluster distance exhibited by cluster XII and XIV indicated that the genotypes associated with these clusters has wide genetic diversity and these genotypes could be used in future for durum wheat crossing programme for the upliftment in grain yield.

In the present investigation, genotypes viz., 50th IDSN 7037, 50th IDSN 7049, GW 2017-865, 50th IDSN 7072, 50th IDSN 7077, GW (D) 2019-970, GW (D) 2019-972, GW (D) 2019-975, GW (D) 2019-980 and 41st IDYT 4 were superior not only in term of grain yield per plant but also in terms of traits like protein content, 1000-grain weight, grain weight per spike, plant height, number of effective tillers per plant, number of spikelets per spike and biological yield per plant. These elite genotypes could be used in the future for the genetic improvement of durum wheat.

अनुक्षेपण

वर्तमान अन्वेषण dkfB ;k xg ¼fVfVde Mîje MLQ½ e vkuof'kd foHkn शीर्षक के अंतर्गत काठिया गेहूँ के 57 समपैत्रकों का पांच नियंत्रणों सहित उपयोग करते हुए राजस्थान कृषि महाविद्यालय, उदयपुर के निर्देशात्मक प्रक्षेत्र में रबी, 2019–20 में संपन्न किया गया। समपैत्रकों का मूल्यांकन संवर्धित यादृच्छिक खंडक अभिकल्पना में संपन्न किया गया था।

पौधे की ऊंचाई (सेमी), प्रति पौधा प्रभावी टिलर की संख्या, मुख्य बाली की लंबाई (सेमी), प्रति बाली स्पाइकलेट की संख्या, प्रति बाली दानों की संख्या, प्रति बाली दानों का वजन (ग्राम), 1000–दानों का वजन (ग्राम), प्रति पौधा जैविक उपज (ग्राम), दानों की उपज प्रति पौधा (ग्राम), फसल सूचकांक (प्रतिशत), अवसादन मूल्य (एमएल) और प्रोटीन सामग्री (प्रतिशत) लक्षणों के लिए 5 यादृच्छिक रूप से चुने गए प्रतिस्पर्धी पौधों पर अवलोकन किया गया। जबकि 50 प्रतिशत पुष्पावस्था एवं परिपक्वता में लगे दिन लक्षणों का अवलोकन प्रति समपैत्रक पौधों की आबादी के आधार पर किया गया।

विचरण विश्लेषण से ज्ञात हुआ कि समपैत्रकों में प्रायः सभी लक्षणों के लिए अर्थपूर्ण अंतर है जो कि उनमें पर्याप्त विविधता की उपस्थिति को दर्शाता है।

प्रति बाली दानों की संख्या, अवसादन मूल्य, प्रति पौधा प्रभावी टिलर की संख्या और 1000–दानों के वजन के लिए उच्चजीन प्ररूपी गुणांक का भिन्नता का प्रतिशत (जीसीवी) और लक्षण प्ररूपी गुणांक का भिन्नता प्रतिशत (पीसीवी) के उच्च अनुमानों ने इन लक्षणों के लिए व्यापक आनुवंशिक विविधता के अस्तित्व को इंगित किया।

उच्च आनुवंशिक लाभ के साथ उच्च आनुवंशिकता के अनुमानों को अवसादन मूल्य, 50 प्रतिशत पुष्पावस्था में लगे दिन, प्रति बाली दानों की संख्या और 1000–दानों के भार जैसे लक्षणों के लिए अधिक पाया गया जो कि यह दर्शाता है कि ये सभी लक्षण योज्य जीन क्रिया द्वारा नियंत्रित होते हैं और प्रत्यक्ष चयन की उम्मीद ऐसे लक्षणों में सुधार के लिए की जाती है।

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सहसंबंध विश्लेषण के अध्ययन से ज्ञात हुआ कि प्रति पौधे दानों की उपज का प्रति पौधे प्रभावी टिलर की संख्या, प्रति बाली स्पाइकलेट की संख्या, प्रति पौधे जैविक उपज एवं फसल सूचकांक का जीन प्ररूपी और लक्षण प्ररूपी दोनों स्तरों पर सकारात्मक और सार्थक सहसंबंध था जबकि मुख्य बाली की लंबाई के साथ सकारात्मक और सार्थक सहसंबंध केवल जीन प्ररूपी स्तर पर था।

बहुभिन्नरूपी पदानुक्रमित समूह विश्लेषण के आधार पर समपैत्रकों की अधिकतम संख्या को समूह I में समूहीकृत किया गया था जिसमें 23 समपैत्रक थे जबकि समूह XI, XII, XIII, XIV, XV, XVI, XVII, XVIII एवं XIX में एक-एक ही समपैत्रक था। समूह X के बाद में समूह IX एवं XI में अधिकतम अंतरा-समूह दूरी को पाया गया। समूह XII और XIV द्वारा प्रदर्शित अधिकतम अंतरा-समूह दूरी ने संकेत दिया कि इन समूहों से जुड़े समपैत्रकों में व्यापक आनुवंशिक विविधता है और भविष्य में इन समपैत्रकों का उपयोग दानों की उपज में सुधार के लिए काठिया गेहूँ के संकरण कार्यक्रम के लिए किया जा सकता है।

वर्तमान शोध में, समपैत्रकों अर्थात् 50वां आईडीएसएन 7037, 50वां आईडीएसएन 7049, 50वां आईडीएसएन 7072, 50वां आईडीएसएन 7113, जीडब्ल्यू 2017–865, 50वां आईडीएसएन 7077, जीडब्ल्यू (डी) 2019–970, जीडब्ल्यू (डी) 2019–972, जीडब्ल्यू (डी) 2019–975, जीडब्ल्यू (डी) 2019–980 और 41वीं आईडीवायटी 4 न केवल प्रति पौधे दानों की उपज के मामले में बल्कि प्रोटीन सामग्री, 1000-दानों का वजन, प्रति बाली दानों वजन, पौधे की ऊंचाई, प्रति पौधे प्रभावी टिलर की संख्या, प्रति बाली स्पाइकलेट्स की संख्या और प्रति पौधा जैविक उपज जैसे लक्षणों के मामले में भी बेहतर थे। इन विशिष्ट समपैत्रकों का उपयोग भविष्य में आनुवंशिक सुधार हेतु काठिया गेहूँ के लिए किया जा सकता है।

APPENDIX - I

Mean weekly meteorological parameters during the crop growth period for *Rabi* 2019-20

Standard Week	Time Period	Temperature (%)		Relative Humidity (%)		Total rainfall (mm)	Sunshine (Hrs)
		Max.	Min.	Max.	Min.		
42	15 Oct - 21 Oct	31.96	16.14	80.14	46.29	0.0	8.2
43	22 Oct - 28 Oct	29.06	13.24	80.57	38.14	00	5.6
44	29 Oct - 04 Nov	29.51	17.16	86.14	52.00	12.40	5.1
45	05 Nov – 11Nov	29.0	16.8	83.3	47.0	0.0	5.5
46	12 Nov – 18 Nov	28.5	13.3	84.6	40.7	0.0	6.7
47	19 Nov-25 Nov	27.5	11.8	82.9	48.9	0.0	6.1
48	26 Nov-02 Dec	26.3	13.3	88.9	56.4	0.0	3.8
49	03 Dec-09 Dec	24.0	8.1	86.1	31.4	0.0	5.6
50	10 Dec-16 Dec	24.3	7.5	88.0	37.7	0.0	6.5
51	17 Dec-23 Dec	23.5	6.6	82.4	40.1	0.0	7.2
52	24 Dec-31 Dec	21.5	4.7	82.6	40.1	0.0	5.8
01	01 Jan.- 07 Jan	21.2	6.8	86.7	49.3	0.0	5.1
02	08 Jan.-14 Jan	22.1	5.2	81.7	40.4	0.0	7.1
03	15 Jan - 21 Jan	21.0	6.4	86.4	42.0	0.0	5.6
04	22 Jan - 28 Jan	24.7	7.9	82.7	31.3	0.0	8.6
05	29 Jan - 04 Feb	22.3	4.5	85.0	36.3	0.0	8.6
06	05 Feb -11 Feb	23.0	4.4	80.3	34.4	0.0	8.6
07	12 Feb - 18 Feb	28.5	7.7	77.4	21.9	0.0	8.6
08	19 Feb -25 Feb	28.1	9.0	76.3	28.9	0.0	7.9
09	26 Feb - 04 Mar	30.2	10.9	73.4	26.6	0.0	7.6
10	05 Mar -11 Mar	26.6	10.2	71.9	33.3	3.0	9
11	12 Mar - 18 Mar	26.9	8.6	62.7	22.6	0.0	8.1
12	19 Mar - 25 Mar	33.0	14.5	54.7	29.0	0.0	8.5
13	26 Mar - 01 Apr	30.9	13.8	77.3	22.0	7.4	6.6
14	02 Apr- 08 Apr	34.7	14.6	54.3	19.0	0.0	9.7
15	09 Apr- 15 Apr	37.3	17.6	58.3	14.6	0.0	8.4
16	16 Apr -22 Apr	37.3	19.8	50.3	23.6	0.0	8.5
17	23 Apr -29 Apr	37.3	20.8	50.9	21.4	0.0	9.2

APPENDIX – II

Estimation of Sedimentation Value (SDS value in ml)

It measures the quality of proteins and is based on the fact that gluten protein absorbs water and swells considerably when treated with lactic acid in the presence of Sodium Dodecyl Sulphate (SDS). The volume of sediment depends on the extent of swelling of gluten protein and correlates significantly (+0.7) with loaf volume.

Apparatus: Stop clock, water bath, 100 ml stopper measuring cylinder (these should have identical internal Diameter and the distance between the 0 and 23. 100 ml graduations should be 160 mm approximately) and 50 ml measuring cylinders.

Reagents

1. Lactic acid solution: 3 ml of 88% lactic acid is diluted (1: 8 v/v) to 27 ml with distilled water.
2. SDS solution (2%): Dissolve 20g SDS (Sodium Dodecyl Sulphate “Especially pure”) in distilled water to make 1 liter.
3. Lactic acid-SDS stock solution: Add 20 ml of Reagent (1) to (2).

The desired SDS/lactic acid reagent may be prepared by dissolving 20 g SDS in one liter of distilled water, to this 20 ml of stock dilute lactic acid prepared by diluting one part by volume of lactic acid 88% with 8 parts by volume of distilled water. The reagent is shaken or otherwise agitated until homogeneous.

Method

The following method permits four determinations to be carried out at the same time, an additional four tests may be started during the period in which first four sediments are setting. 50 ml of distilled water should be poured in each of the required number of 100 ml cylinders prior to starting the test, similarly the required number of 50 ml measuring cylinders should each be pre-filled with 50 ml SDS/lactic acid reagent.

Add 6 g whole meal to 50 ml water (cylinder 1) and start the stop clock. Shake rapidly for 15 seconds; keep the clock running continuously throughout the rest of the experiment. The time for commencement of the other preparations is given, in minutes, in the following table.

Shake and rest interval for SDS value determination

Cylinder No.	15 sec. shake in water	15 sec. shake in water	15 sec shake in water, add 50 ml SDS, invert 4 times	Invert 4 times	Invert 4 times	Invert 4 times	Read sedimentation value
1.	0.0	2.0	4.0	6.0	8.0	10.0	30.0
2.	0.5	2.5	4.5	6.5	8.5	10.5	30.5
3.	1.0	3.0	5.0	7.0	9.0	11.0	31.0
4.	1.5	3.5	5.5	7.5	9.5	11.5	31.5

APPENDIX – III

Estimation of Protein Content by Micro Kjeldahl's Method, Lindner (1944)

Principle

Samples are digested with H_2SO_4 and then with H_2O_2 till it becomes colorless. The intensity of the color developed by Nessler's reagent in the presence of sodium hydroxide (NaOH) and sodium silicate (Na_2SiO_3) is measured on a spectrophotometer at 420-650 nm. (For more sensitivity, shorter wavelengths should be taken).

Procedure

- Put 0.1 g (100 mg) well-ground and dried seed sample into a 100 ml dry Kjeldahl's flask.
- Add 2 ml of concentrated H_2SO_4 to the Kjeldahl's flask, mix the contents of the flask and place it on the digestion assembly (hot plate) and heat it till the sample is digested (for 1:30 hour).
- Cool the flask and add 0.5 ml (8-10 drops) of 30% H_2O_2 and again heat the contents till it becomes clear and colorless.
- Transfer the digested contents of Kjeldahl's flask into 100 ml of volumetric flask by washing it 2-3 times with distilled water and make the volume.
- Take 5 ml of digested solution into a 50 ml volumetric flask and add a few ml distilled water. Then add 2 ml of 10% sodium hydroxide and 1 ml of 10% sodium silicate solutions respectively and then add some distilled water.
- Mix the contents and add 1.6 ml of Nessler's reagent to the flask while shaking. After this, make its volume and allow 10 minutes for color development.
- Run a control with distilled water by the same procedure.
- Take the reading of standard working solutions by adjusting the spectrophotometer at wavelength of 420-650 nm. (In this experiment readings were taken at 420 nm)
- Plot the concentration of N on X- axis and the spectrophotometer reading on Y- axis and prepare a standard curve.
- Now take the reading of the plant sample and calculate the ppm N with the help of standard curve.

Standard Curve

Dissolve 0.118 g of AR grade in water and make the volume one litre in volumetric flask. This solution contains 25 ppm N. For working standards, take 1, 2, 3, 4, 5, 6, 7, 8 ml of 25 ppm N solution in 50 ml volumetric flasks. Add 2 ml 10% NaOH and 1 ml 10% sodium silicate solution in 50 ml volumetric flasks. Add some water and shake the contents. Now add 1.6 ml Nessler's reagent slowly drops while shaking and makes the volume. The flasks will contain 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5 and 4.0 ppm N, respectively.

Estimation of Protein

Determine the nitrogen content using the standard curve. Then calculate the crude protein contents by multiplying the N contents with 6.25.

APPENDIX – IV

Mean values for Days to 50% heading, Days to maturity, Plant height (cm), Number of effective tillers per plant and Length of main spike (cm), Number of spikelets per spike, Number of grains per spike, Grain weight per spike (g)

S. No.	Genotype	Days to 50 % heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Length of main spike (cm)	Number of spikelets per spike	Number of grains per spike	Grain weight per spike (g)
		Mean	Mean	Mean	Mean	Mean	Mean	Mean	Mean
1	50 th IDYN 706	77.00	118.00	85.70	7.20	6.10	16.60	50.30	3.15
2	50 th IDYN 709	92.00	133.00	92.20	5.60	5.80	16.60	45.80	2.31
3	50 th IDYN 712	77.00	116.00	85.70	6.40	7.50	17.00	70.50	4.07
4	50 th IDYN 718	79.00	121.00	98.70	5.60	6.40	17.00	65.00	3.84
5	50 th IDYN 719	80.00	120.00	80.60	5.80	8.80	20.20	71.30	4.12
6	50 th IDYN 721	82.00	124.00	99.40	9.20	7.70	19.00	76.00	4.12
7	50 th IDYN 722	82.00	122.00	81.70	8.60	7.40	20.20	72.80	4.11
8	50 th IDYN 729	80.00	122.00	81.20	6.80	7.30	17.00	63.30	3.22
9	50 th IDYN 735	85.00	126.00	96.80	7.40	7.10	16.60	68.30	3.98
10	50 th IDYN 737	83.00	124.00	95.50	5.40	6.70	21.00	81.80	4.39
11	50 th IDYN 740	91.00	131.00	100.70	5.40	7.20	21.40	75.00	3.57
12	50 th IDYN 741	89.00	129.00	84.00	6.40	7.80	21.00	60.00	3.41
13	50 th IDYN 744	93.00	134.00	93.90	5.40	8.00	20.60	73.80	3.82
14	50 th IDSN 7013	81.00	121.00	82.90	8.40	6.40	17.80	71.30	4.18
15	50 th IDSN 7034	78.00	120.00	85.20	7.60	6.70	19.00	79.30	3.48
16	50 th IDSN 7037	78.00	116.00	74.00	8.20	6.10	18.60	65.30	3.74
17	50 th IDSN 7040	82.00	122.00	91.80	6.80	7.30	21.80	80.00	4.32
18	50 th IDSN 7049	93.00	135.00	88.20	8.40	6.90	19.40	72.30	3.47
19	50 th IDSN 7067	92.00	138.00	84.70	5.40	7.70	16.20	60.50	3.55
20	50 th IDSN 7072	80.00	120.00	84.60	6.60	6.40	18.60	67.00	3.82
21	50 th IDSN 7076	82.00	123.00	89.70	9.40	7.30	19.80	74.00	4.00
22	50 th IDSN 7077	90.00	131.00	85.40	7.80	7.10	20.20	68.80	3.14
23	50 th IDSN 7078	87.00	128.00	81.00	9.20	7.10	22.60	82.50	3.48
24	50 th IDSN 7100	89.00	129.00	94.40	8.20	8.70	21.40	88.30	4.25
25	50 th IDSN 7113	92.00	138.00	94.00	5.80	5.90	15.80	58.50	2.87
26	50 th IDSN 7135	80.00	120.00	91.20	9.20	7.50	16.60	63.80	3.07
27	50 th IDSN 7177	92.00	136.00	84.70	6.40	7.10	18.20	62.00	3.46
28	GW (D) 2019-969	79.00	118.00	85.20	7.60	8.30	22.20	62.30	3.92
29	GW (D) 2019-970	83.00	121.00	92.80	9.40	6.70	20.60	46.00	3.28
30	GW (D) 2019-971	76.00	117.00	83.60	6.60	8.10	19.80	46.50	3.82
31	GW (D) 2019-972	79.00	121.00	100.00	8.40	8.10	19.40	48.30	4.44
32	GW (D) 2019-973	84.00	124.00	83.20	5.40	9.00	21.40	75.50	3.67
33	GW (D) 2019-974	82.00	123.00	93.60	7.40	7.10	18.20	49.50	3.91
34	GW (D) 2019-975	75.00	115.00	82.60	8.60	7.50	19.80	49.30	3.75
35	GW (D) 2019-976	87.00	123.00	94.50	9.40	7.30	21.00	54.30	3.57
36	GW (D) 2019-977	77.00	118.00	89.00	7.60	8.60	19.00	74.30	4.29
37	GW (D) 2019-978	89.00	130.00	100.00	7.80	8.60	19.40	59.80	4.64
38	GW (D) 2019-979	81.00	124.00	98.60	7.40	9.70	21.40	76.30	3.97
39	GW (D) 2019-980	83.00	125.00	98.60	8.40	7.50	21.00	71.30	3.35
40	GW (D) 2019-981	78.00	119.00	75.70	6.40	7.60	19.40	52.50	3.73
41	GW (D) 2019-982	70.00	112.00	78.80	5.60	7.60	18.60	43.80	2.70

S. No.	Genotype	Days to 50 % heading	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Length of main spike (cm)	Number of spikelets per spike	Number of grains per spike	Grain weight per spike (g)
		Mean	Mean	Mean	Mean	Mean	Mean	Mean	Mean
42	49 th IDYN 713	77.00	115.00	84.70	7.80	7.50	20.60	64.00	3.88
43	49 th IDYN 718	88.00	126.00	80.50	8.40	6.20	15.80	56.80	2.75
44	49 th IDYN 733	93.00	135.00	89.60	6.40	5.90	18.60	57.00	3.28
45	49 th IDYN 747	88.00	128.00	84.60	7.20	6.30	19.80	52.80	2.86
46	49 th IDSN 7107	93.00	133.00	89.60	5.60	7.10	20.20	80.50	4.05
47	41 st IDYT 4	87.00	121.00	80.10	9.20	7.90	19.40	64.00	4.08
48	41 st IDYT 10	81.00	119.00	89.40	6.20	8.00	19.80	61.50	3.74
49	41 st IDYT 15	78.00	119.00	79.70	8.40	8.40	18.40	52.80	2.84
50	41 st IDYT 18	79.00	122.00	92.80	7.60	9.80	23.00	71.00	3.72
51	GW 2017 859	82.00	122.00	97.00	5.40	9.00	19.80	80.00	5.16
52	GW 2017-865	78.00	121.00	86.00	5.20	8.60	19.40	53.30	4.10
	GP Mean	83.33	124.00	88.42	7.23	7.47	19.35	64.83	3.70
	Min	70.00	112.00	74.00	5.20	5.80	15.80	43.80	2.31
	Max	93.00	138.00	100.70	9.40	9.80	23.00	88.30	5.16
	Checks								
1	PDW 291	88.75	124.75	87.42	6.97	6.45	17.20	47.10	2.68
2	HI 8498	82.00	125.75	85.58	8.05	7.78	18.80	56.15	3.66
3	HI 8737	80.25	123.25	89.18	7.30	7.92	19.45	56.53	3.57
4	HI 8759	80.00	121.50	85.45	6.90	7.47	19.00	54.33	3.37
5	HI 8777	81.75	122.50	86.13	7.75	7.50	19.00	52.33	3.56
	Check Mean	82.55	123.55	86.75	7.39	7.43	18.69	53.28	3.37
	Min	80.00	121.50	85.45	6.90	6.45	17.20	47.10	2.68
	Max	88.75	125.75	89.18	8.05	7.92	19.45	56.53	3.66
	GM	83.11	123.88	87.96	7.28	7.46	19.17	61.62	3.61
	SEd Check	1.02	0.99	3.33	0.65	0.56	0.84	3.42	0.25
	CD (5%)	2.22	2.16	-	-	-	-	7.44	0.55
	CD (1%)	3.11	3.04	-	-	-	-	10.45	0.78
	SEd AdM WB	2.04	1.99	6.66	1.29	1.12	1.68	6.84	0.51
	CD (5%)	4.43	4.33	-	-	-	-	14.88	-
	CD (1%)	6.23	6.07	-	-	-	-	20.90	-
	SEd AdM DB	2.23	2.18	7.29	1.42	1.23	1.84	7.49	0.56
	CD (5%)	4.86	4.74	-	-	-	-	16.30	-
	CD (1%)	6.82	6.65	-	-	-	-	22.89	-
	SEd C &AdM	1.76	1.72	5.77	1.12	0.97	1.45	5.92	0.44
	CD (5%)	3.84	3.75	-	-	-	-	12.89	-
	CD (1%)	5.39	5.26	-	-	-	-	18.10	-
	SEd Avg.	2.14	2.08	6.98	1.36	1.17	1.76	7.17	0.53
	CD (5%)	4.65	4.54	-	-	-	-	15.61	-
	CD (1%)	6.53	6.37	-	-	-	-	21.92	-
	CV (%)	1.74	1.14	5.43	12.37	10.66	6.34	9.07	10.68

APPENDIX – V

Mean values for 1000-grain weight (g), Biological yield per plant (g), Grain yield per plant (g), Harvest index (%), Sedimentation Value (ml), Protein content (%)

S. No.	Genotype	1000-grain weight (g)	Biological yield per plant (g)	Grain yield per plant (g)	Harvest index (%)	Sedimentation Value (ml)	Protein content (%)
		Mean	Mean	Mean	Mean	Mean	AdM
1	50 th IDYN 706	48.05	46.20	15.51	33.58	28.00	12.07
2	50 th IDYN 709	49.10	35.40	13.58	38.37	34.00	13.57
3	50 th IDYN 712	41.24	43.20	14.94	34.58	26.00	12.88
4	50 th IDYN 718	36.00	33.80	12.89	38.14	21.00	13.48
5	50 th IDYN 719	41.08	42.20	16.61	39.36	26.00	11.77
6	50 th IDYN 721	40.80	43.60	13.94	31.97	27.00	12.38
7	50 th IDYN 722	42.84	43.20	16.60	38.43	26.00	12.38
8	50 th IDYN 729	40.00	37.60	15.61	41.52	29.00	14.57
9	50 th IDYN 735	34.40	37.20	12.74	34.25	30.00	12.07
10	50 th IDYN 737	41.06	42.20	16.58	39.29	28.00	12.27
11	50 th IDYN 740	42.08	32.40	12.08	37.28	32.00	11.27
12	50 th IDYN 741	41.80	44.20	17.89	40.48	32.00	12.48
13	50 th IDYN 744	37.26	34.60	13.89	40.14	30.00	12.67
14	50 th IDSN 7013	44.98	45.60	15.73	34.50	28.00	12.89
15	50 th IDSN 7034	35.06	35.20	11.89	33.78	31.00	13.49
16	50 th IDSN 7037	42.54	44.60	18.22	40.85	34.00	14.19
17	50 th IDSN 7040	35.46	40.20	15.80	39.30	29.00	12.29
18	50 th IDSN 7049	33.80	46.80	19.57	41.82	34.00	12.59
19	50 th IDSN 7067	48.12	37.20	14.20	38.17	38.00	12.79
20	50 th IDSN 7072	40.80	48.40	20.10	41.53	24.00	12.79
21	50 th IDSN 7076	34.20	42.50	17.20	40.47	26.00	12.39
22	50 th IDSN 7077	41.22	49.20	19.10	38.82	29.00	13.19
23	50 th IDSN 7078	36.90	45.60	18.46	40.48	27.00	13.29
24	50 th IDSN 7100	33.60	41.50	16.50	39.76	27.00	13.89
25	50 th IDSN 7113	37.44	38.50	14.10	36.62	34.00	14.29
26	50 th IDSN 7135	44.10	44.20	17.39	39.34	30.00	13.59
27	50 th IDSN 7177	38.50	39.60	14.22	35.91	26.00	13.30
28	GW (D) 2019-969	43.66	38.50	14.39	37.38	26.00	14.49
29	GW (D) 2019-970	51.60	45.20	18.86	41.73	28.00	14.10
30	GW (D) 2019-971	49.80	36.50	14.15	38.77	23.00	13.90
31	GW (D) 2019-972	53.40	53.60	20.20	37.69	22.00	12.80
32	GW (D) 2019-973	40.10	45.80	17.10	37.34	30.00	13.30
33	GW (D) 2019-974	47.26	36.50	12.88	35.29	22.00	13.10
34	GW (D) 2019-975	37.50	51.20	18.75	36.62	19.00	15.10
35	GW (D) 2019-976	47.20	44.80	18.27	40.78	32.00	14.30
36	GW (D) 2019-977	46.05	47.20	17.18	36.40	27.00	13.40
37	GW (D) 2019-978	37.40	38.50	14.85	38.57	22.00	13.20
38	GW (D) 2019-979	46.22	41.20	14.98	36.36	24.00	13.80
39	GW (D) 2019-980	41.06	54.20	18.96	34.99	18.00	14.20
40	GW (D) 2019-981	48.54	37.20	11.25	30.24	22.00	12.14

S. No.	Genotype	1000-grain weight (g)	Biological yield per plant (g)	Grain yield per plant (g)	Harvest index (%)	Sedimentation Value (ml)	Protein content (%)
		Mean	Mean	Mean	Mean	Mean	AdM
41	GW (D) 2019-982	46.46	36.50	14.50	39.73	28.00	13.53
42	49 th IDYN 713	46.10	39.20	14.28	36.43	28.00	13.33
43	49 th IDYN 718	40.95	42.20	14.65	34.72	34.00	12.73
44	49 th IDYN 733	43.94	39.50	12.96	32.81	26.00	13.33
45	49 th IDYN 747	40.72	43.20	14.52	33.62	34.00	13.03
46	49 th IDSN 7107	42.00	41.20	15.96	38.74	34.00	13.53
47	41 st IDYT 4	46.92	51.60	19.00	36.82	26.00	12.14
48	41 st IDYT 10	46.16	44.60	14.89	33.39	29.00	13.14
49	41 st IDYT 15	41.50	40.50	15.68	38.72	29.00	14.14
50	41 st IDYT 18	38.40	49.50	16.85	34.04	30.00	13.93
51	GW 2017 859	37.88	40.20	14.90	37.06	26.00	13.14
52	GW 2017-865	38.00	55.20	20.20	36.59	34.00	11.83
	GP Mean	41.95	42.47	15.88	37.38	28.06	13.16
	Min	33.60	32.40	11.25	30.24	18.00	11.27
	Max	53.40	55.20	20.20	41.82	38.00	15.10
	Checks						
1	PDW 291	40.26	39.40	15.09	38.26	27.50	14.25
2	HI 8498	46.85	39.50	14.57	36.82	26.00	12.38
3	HI 8737	47.25	41.55	16.03	38.61	28.00	12.95
4	HI 8759	46.19	42.45	16.12	37.96	24.00	12.32
5	HI 8777	45.82	48.75	18.07	37.05	27.75	12.27
	Check Mean	45.27	42.33	15.98	37.74	26.65	12.83
	Min	40.26	39.40	14.57	36.82	24.00	12.27
	Max	47.25	48.75	18.07	38.61	28.00	14.25
	GM	42.87	42.43	15.90	37.48	27.67	13.07
	SEd Check	0.78	2.49	1.20	1.48	0.63	0.30
	CD (5%)	1.70	5.42	-	-	1.38	0.66
	CD (1%)	2.39	7.61	-	-	1.93	0.92
	SEd AdM WB	1.56	4.98	2.41	2.95	1.26	0.60
	CD (5%)	3.40	-	-	-	2.75	1.32
	CD (1%)	4.77	-	-	-	3.87	1.85
	SEd AdM DB	1.71	5.46	2.64	3.24	1.39	0.66
	CD (5%)	3.72	-	-	-	3.02	1.44
	CD (1%)	5.23	-	-	-	4.23	2.02
	SEd C & AdM	1.35	4.31	2.09	2.56	1.10	0.52
	CD (5%)	2.94	-	-	-	2.38	1.14
	CD (1%)	4.13	-	-	-	3.35	1.60
	SEd Avg.	1.64	5.22	2.53	3.10	1.33	0.63
	CD (5%)	3.56	-	-	-	2.89	1.38
	CD (1%)	5.00	-	-	-	4.05	1.94
	CV (%)	2.44	8.32	10.66	5.54	3.36	3.33

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