Research Article

Studies on Intra-Species Genetic Divergence in *Triticum* Spp. In Western Rajasthan

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Abstract

Genetic divergence among 24 genotypes of *Triticum spp*. (12 *T. durum* and 12 *T. aestivum*) was assessed in randomized block design (RBD) with three replications for yield and yield attributes. contributing traits duringSignificant genetic variance was observed for days to heading, days to maturity, number of effective tillers per row, spike length, number of grains per spike, thousand grain weight (g), hundred grain weight (g), biological yield per plant (g), grain yield per plant (g) and harvest index (%) amongst the morphological characters chosen for study. The genetic divergence analysis was done for all the ten characters and the hierarchical cluster analysis of 24 genotypes yielded five clusters at 100 Mahalnobis Euclidean^2 Distance as per Ward's minimum variance dendrogram with variable number of genotypes which indicates the presence of considerable degree of genetic diversity in the material. The perusal of mean values revealed that intra-cluster distances were greater than inter-cluster distances, showing a considerable degree of genetic diversity among the genotype studied. The highest inter-cluster distance was noted between clusters I and II (11.87) followed by cluster I and V (9.91), II and V (9.77), III and IV (8.63) and so on. The genotypes grouped in these clusters are found to be of diverse.

Keywords: Genetic Divergence, ANOVA, Cluster analysis, Harvest Index, Test Weight

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Introduction

Wheat is a member of Poaceae family and believed to have originated from the Middle East region of Asia. The wild species are diploid (2n=14) or tetraploids (2n=28). The most common cultivated hexaploid wheat now a days is *T. aestivum* L. (2n= 42), [1]. Its wide adaptability, unique visco-elasticity properties of its grain-derived dough, milling and baking qualities make it a staple food of over one third of the world's population**.** Wheat provides nearly 55% of carbohydrate and 20% of the food calories. Endosperm contains considerable proportions of minerals (zinc, iron) and vitamins (thiamine, vitamin-B, riboflavin and niacin) with 78.10% carbohydrate, 14.70% protein, 2.10% fat and 2.10% minerals. Wheat is also a good source of traces minerals like selenium and magnesium, nutrients essential to good health [2-8].

Being second most important food crop after rice wheat attains distinctive important position in agriculture and economic point of view of our country. India has achieved drastic increase in production, productivity and area of wheat in past 3 decades. Development of dwarf and semi-dwarf widely adopted high yielding cultivars and release of fertilizer responsive, lodging resistant varieties of wheat are imperative factor liable for satisfying picture in wheat production. It is a general prerequisite for crop improvement provides broad scope for selection in genetic variability for wheat breeders concentrating to improve the yield potential of wheat by developing new varieties with enviable genetic framework in order to overcome the consumption pressure of ever increasing population [9]. This can be achieve by development of improved cultivars by using genetic potential and genetic diversity present for traits in a breeding population [10]. The assessment of the genetic diversity relationship among and between individuals, population, plant varieties and species is important for any crop improvement programme. Evaluation of genetic diversity in wheat offer to select the genotypes in early segregating generations by using high heritability associated with high genetic advance for quantitative traits. For planning the breeding strategy heritability plays an important role [11]. The improvement of cultivated plants considerably depends on the extent of genetic variability available within the species. The genetic variation that exists among plant populations is a basic requirement for efficient development and improvement of such populations. The genetic variation that exists among plant populations is a

basic requirement for efficient development and improvement of such populations. Various types of markers such as morphological, biochemical and molecular markers are used for this purpose [12]. Different genotypes within population can be used to assess genetic diversity among individuals which reflects the presence of different alleles in the gene pool. The assessment of the genetic relationships among the cultivated plants at morphological, biochemical and molecular levels is a fundamental component of crop improvement programmes. This will provide information about genetic variability, classification of assorted parental combinations to develop segregating progenies with highest genetic variability for advance selection, duplication in germplasm, and introgression of desirable genes or chromosome segments from different sources into elite germplasm [13, 14].

Material Method

Experimental site

The field studies were undertaken at Instructional Farm and Laboratory studies were taken at Department of Molecular Biology and Biotechnology, Rajasthan College of Agriculture, Udaipur. Udaipur situated in South Eastern part of Rajasthan state, and located at an elevation of 579.50 meter above mean sea level on latitude of $24^0$35' North and longitude of $70^0$42' East. The climate of the region is sub-humid type with an average rainfall of about 637 mm with sandy-loam soil.

Experimental material

In the present investigation seed of 24 diverse genotypes/varieties of *Triticum* spp. were procured from Indian Institute of Wheat and Barley Research, Karnal (Haryana) and Department of Agronomy, RCA, Udaipur. The source and pedigree of material used are given in **Table 1**.

Table 1 Pedigree and source of 24 genotypes of *Triticum spp.* used for study

Genotype	Pedigree/Parentage	Source
1. Duram Wheat		
Raj-6560	TOPDY 6	Durgapura, Rajasthan
GDW-1255	WH 922// NI 8757/ GW 1053	Vijapur, Gujarat
PDW-314	AJAIA 12/F3 LOCAL (SEL. ETHIO.135.85)//PLATA 13/3/SOMAT 3/4/SOOTY9/RASCON 37	Ludhiana, Punjab
MPO-1215	GW 1113/ GW 1114//HI 8381	JNKVV, Powarkheda
DWR-1006	LULA / CREX // AAZ	UAS, Dharwad
HI-8713	HD 4672 / PDW 233	IARI, RS, Indore
WHD-943	GLARE/PLATA-16//AJAIA -3/SILVER16	CCSHAU, Hisar
UAS-415	GW 9506/PRL//PRL	UAS, Dharwad
MACS-2846	CPAN 6079 /MACS 2340.	ARI, Pune
HI-8381	JO69'S'//AA'S'/ FGO'S'	IARI, RS, Indore
HD-4530	TPT/MOGHK//4/PI/TML//2*TC60/3/ZENATI/BTL//WLS	IARI, New Delhi
NIDW-295	BOOMER 33 / PLATA 8	MPKV, Niphad
2. Bread Wheat		
VL-907	DYBR 1982-83/842 ABVD 50/VW 9365//PBW 343	VPKAS, Almora
DBW-88	KAUZ//ALTAR84/AOS/3MILAN/KAUZ/4/HUITES	DWR, Karnal
DBW-90	HUW468/WH730	DWR, Karnal
PBW-550	WH 594/RAJ 3858//W 485	Ludhiana, Punjab
HD-3043	PJN/BOW//OPATA*2/3/CROC_1/Ae.squarrosa (224)//OPA	IARI, New Delhi
DBW-39	ATTILA/HUI	DWR, Karnal
HI-1500	HW 2002*2//STREMPALLI/PNC 5	IARI, RS, Indore
GW-11	LOK 1/HW 1042//LOK 1	Vijapur, Gujarat
Raj- 4079	UP 2363/WH 595	Durgapura, Rajasthan
NW-5054	THELIN//2*ATTILA*2/PASTOR)	NDUA&T, Faizabad
NIAW-1415	GW 9506/PRL//PRL	MPKV, Niphad
HW-2044	HD226*5/SUNSTAR*6/C-80-1	IARI, RS, Wellington

Field studies

Experimental design

The field experiment was laid out in randomized block design with three replications. Sowing was done by dibbling the seeds at a distance of 10 cm in the rows of 2 m length with row to row spacing of 30 cm. To eliminate border effects non experimental rows were planted around the layout. Fertilizers were applied @ 120 kg N: 60 kg P_2O_5 and 40 kg K_2O/ha at the time of sowing while 60 kg N/ha was top-dressed in 2 split doses at 20 and 30 days after sowing (DAS) coinciding with crown root initiation. Immediately after sowing a irrigation was given. Five irrigations were given during the entire cropping period with recommended agronomical practices and plant protection measures.

Morphological/agronomical characters

Five competitive plants were randomly selected from each replication of a genotype for recording observations for following characters viz., Days to heading, Days to maturity, Number of effective tillers per row, Spike length (cm), Number of grains per spike, Thousand grain weight (g), Hundred grain weight (g), Biological yield per plant (g), Grain yield per plant (g), Harvest index (%). The selected plants were tagged and data on individual plant were recorded for the following characters except for days to 50 per cent heading and days to maturity. The recorded data was subjected to analysis of variance [15].

Result and Discussion

Morphological markers are those distinguishable traits that are evident to human naked eyes. These markers are selected based on the experience of the breeder to correlate a phenotypic trait with a trait of interest [16]. However, these traits are largely affected by environmental variations until and unless these are studied minutely over locations and variable environmental conditions. In the present investigation, 10 important morphological and quality characters have been studied to evaluate the pattern and extent of genetic variability and relatedness among 24 genotypes of *Triticum spp.* The results obtained are discussed under the following headings:

ANOVA

The average mean squares from the ANOVA for different characters (**Table 2**) revealed that the mean squares due to genotypes were highly significant for all the characters. [17] studied 60 local and exotic wheat genotypes for diversity analysis, correlations and path coefficients for 8 metric traits i.e., number of grains per spike number of productive tillers per plant, spike length, number of spikelets per spike, plant height, test weight and yield per plant and observed momentous genotypic differences for all the traits studied indicating considerable amount of variation among genotypes for each character. [18] assessed genetic diversity of twenty-three wheat genotypes along with two checked for nine agro-morphological and physiological traits. The data was further subjected to PCA (principal component analysis) and genotype by trait biplot analysis. The first five principal components accounted for 90.5% of total variation.

Table 2 ANOVA for the 10 chosen characters in 24 genotypes of *Triticum spp*.

S. No.	Characters	Source of variation		
		df Replications (2)	Treatments (23)	Error (46)
1.	Days to heading	7.0250	686.870**	15.5455
2.	Days to maturity	21.3906	1822.435**	43.7142
3.	Number of effective tillers per row	1804.0486	53435.457**	2113.8032
4.	Spike length (cm)	0.1699	16.753**	0.3539
5.	Number of grains per spike	3.2667	359.413**	7.7572
6.	Thousand grain weight (g)	5.1549	203.770**	6.8858
7.	Hundred grain weight (g)	0.0515	2.038**	0.0689
8.	Biological yield per plant (g)	0.4639	34.324**	1.2457
9.	Grain yield per plant (g)	0.1591	6.582**	0.2021
10.	Harvest index (%)	12.6968	256.482**	10.1743

* Significant at 5 per cent and
**Significant at 1 per cent probability level

Genetic divergence analysis

For developing improved varieties, exploitation of available genetic diversity is one of the most important criteria for evolution. This knowledge is valuable for germplasm conservation, individual, population, variety or breed identification and genetic improvement via effective breeding programmes [19].

The genetic divergence analysis was done for all the ten characters and the hierarchical cluster analysis of 24 genotypes yielded five clusters at 100 Mahalnobis Euclidean^2 Distance as per Ward's minimum variance dendrogram with variable number of genotypes is presented in **Table 3** which indicates the presence of considerable degree of genetic diversity in the material.

Table 3 Cluster profile of 24 genotypes of *Triticum spp.*

Cluster	No. of genotypes	Genotypes
I	1	Raj-6550
II	10	HI-8713, WHD-943, NIDW-295, VL-907, DBW-88, DBW-90, PBW-550, HD-3043, HI-1500, GW-11,
III	7	GDW-1255, PDW-314, UAS-415, DBW-39, NW-5054, NIAW-1415, HW-2044
IV	3	MPO-1215, DWR-1006, Raj- 4079
V	3	MACS-2846, HI-8381, HD-4530

It can be inferred from the Table 3 that cluster II was the largest consisting of 10 genotypes (or 41.66 per cent of genotypes) belonged to this cluster followed by cluster III (7) and cluster IV and V that consisted of 3 genotypes each. The cluster I consisted only 1 genotypes.

Intra and Inter Cluster Distances

The intra- and inter cluster distance values between 5 clusters are presented in **Table 4** and also Euclidean^2 Distance in **Figure 1**. The perusal of mean values in Table 4 revealed that intra-cluster distances were larger than inter-cluster distances, presenting a significant degree of genetic variability between the genotype studied. Hybridization between genotypes in divergent clusters is likely to produce wide variability with desirable segregant and genotypes belongs to clusters with maximum intra-cluster distance are genetically more diverse [20]. The average intra-cluster distance between the genotypes was maximum (42.48) for the cluster II followed in descending order by cluster III (24.29), IV (11.84), V (9.71) and I (0.00), respectively.

Table 4 Estimates of Intra (diagonal) and Inter-Cluster Distances in 24 genotypes of *Triticum spp.*

Cluster	I	II	III	IV	V
I	0.00	11.87	8.18	7.81	9.91
II		42.48	6.50	8.40	9.77
III			24.29	7.93	8.63
IV				11.84	8.11
V					9.71

The highest inter-cluster distance was noted between clusters I and II (11.87) followed by cluster I and V (9.91), II and V (9.77), III and IV (8.63) and so on. The genotypes grouped in these clusters are found to be of diverse. The least (6.50) inter-cluster distance was observed for cluster II and III indicating their genetic relatedness.

Classification of the genotypes using Ward's cluster analysis

Ward's hierarchical cluster analysis was carried out on the basis of ten morphological characters, used to measure genetic distance between the 24 *Triticum* spp. Genotypes. Cluster analysis revealed that the genotypes could be grouped into two clusters, cluster I and II that were apart at 25 rescaled values (**Figure 2**).

Cluster I included 11 genotypes *viz.,* PDW-314, NIAW-1415, HW-2044, NW-5054, GDW-1255, WHD-943, DBW-90, NIDW-295, VL-907, DBW-88 and PBW-550. It could further be divided into 2 subclusters at 16 rescaled distances. Subcluster I included 5 genotypes *viz.,* PDW-314, NIAW-1415, HW-2044, NW-5054 and GDW-1255. Subcluster II consisted of 6 genotypes *viz.,* WHD-943, DBW-90, NIDW-295, VL-907, DBW-88 and PBW-550 which were 1 rescaled distance apart from each other.

Cluster II included 13 genotypes *viz.,* UAS-415, MACS-2846, DWR-1006, HD-4530, HI-8381, HI-8713, HD-3043, HI-1500, GW-11, DBW-39, Raj-4079, Raj6560 and MPO-1215. Cluster II could be divided into 2 subclusters

at 11 rescaled distances. Subcluster I included 5 genotypes *viz.*, UAS-415, MACS-2846, DWR-1006, HD-4530 and HI-8381. Subcluster II consisted of 8 genotypes *viz.*, HI-8713, HD-3043, HI-1500, GW-11, DBW-39, Raj-4079, Raj-6560 and MPO-1215. Subcluster II further consist a subgroup that included 2 genotypes *viz.*, Raj-6560 and MPO-1215 which were 1 rescaled distance apart from each other.

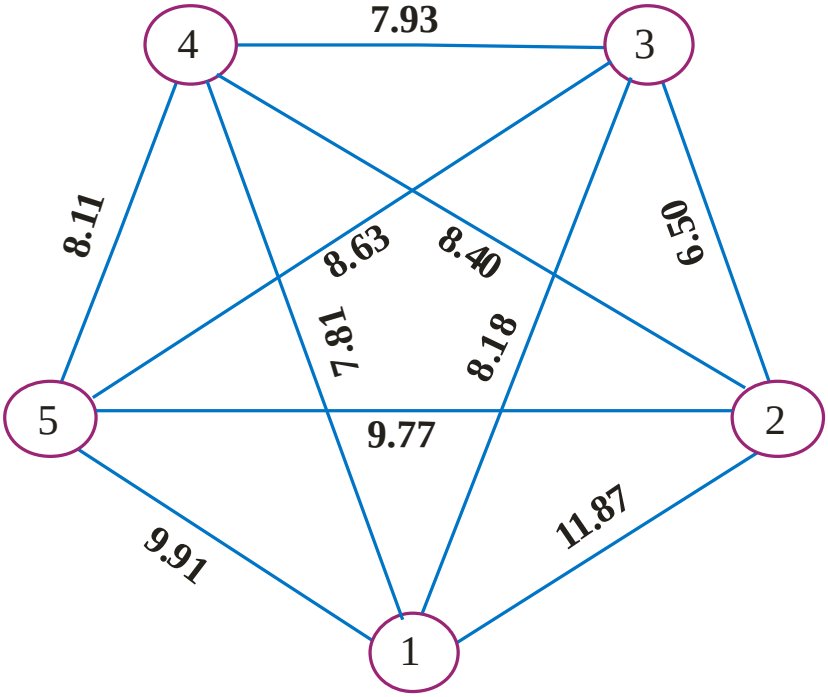

Figure 1 Intra and inter cluster distance for 24 genotypes of *Triticum* spp.

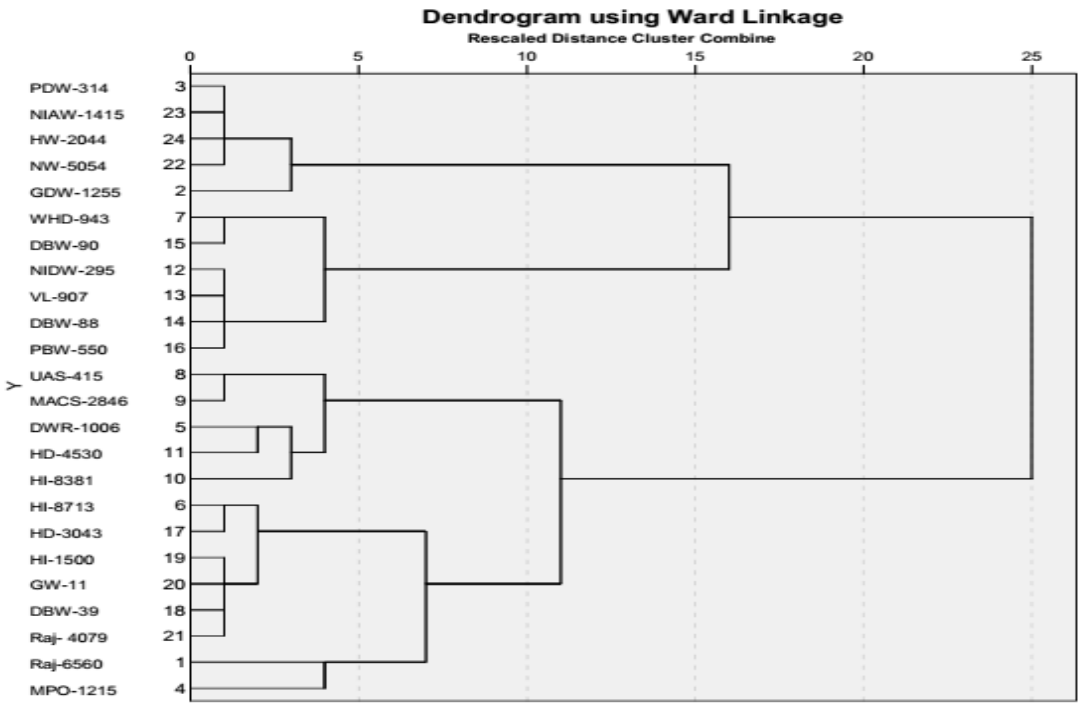

Figure 2 Ward's Minimum Variance Dandrogram for 24 genotype of *Triticum* spp.

Conclusion

Genetic variability studies can categorize alleles that might influence the ability of the organism to survive in its existing habitat, or might enable it to survive in new diverse habitats [19]. The current finding will be helpful to plant breeders for selection and diversity analysis of genotypes and developing new varieties showing significant variation

in different traits of *Triticum* spp. for future crop improvement programme. Our results describe significant variability among agro-morphological traits and yield attributes between diverse Bread and Durum wheat genotypes. According to our results we can conclude that wheat genotypes represent a significant variation in spike length, grain yield, test weight and grain yield could be successively used to increase production in different environment.

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