Indian J. Plant Genet. Resour. 34(1): 86–89 (2021)
DOI 10.5958/0976-1926.2021.00014.0

SHORT COMMUNICATION

Genetic Diversity Analysis of Bread Wheat Varieties and Pre-release Lines Evaluated Under Timely Sown Irrigated Conditions

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(Received: 28 May, 2020; Revised: 25 November, 2020; Accepted: 22 January, 2021)

The involvement of genetically diverse parental lines in crossing programme of spring wheat is of prime importance to create desirable variability. To assess the magnitude of genetic divergence for grain yield and its component characters, a set of 36 spring wheat genotypes were grown consecutively for two crop seasons i.e., 2016-17 and 2017-18 at ICAR-IARI, New Delhi in a randomized complete block design with three replications in timely sown irrigated conditions Significant genotypic differences were observed for all 13 morpho-physiological characters in both the crop seasons suggesting the presence of substantial genetic variability among the genotypes studied. Cluster formation through Euclidean analysis based on the morpho-physiological characters, grouped the 36 genotypes into four clusters and ten clusters during the crop season 2016-17 and 2017-18, respectively. Considerable differences in the cluster means for different traits led to identification of diverse genetic parental lines for different traits, which could be used in recombination breeding to generate desirable genetic variability.

Key Words: Bread Wheat, Cluster Analysis, Genetic diversity, Morpho-physiological

Introduction

Wheat (*Triticum aestivum* L. em. Thell.) is an important staple food which fulfills the major portion of total calories and protein requirement. In India, wheat was grown in 29.55 m ha under diverse environments with a record production of 101.20 mt and productivity of 3424 kg ha^{-1}during 2018-19. However, to sustain the food security for ever increasing population, there is a necessity to further improve the productivity level of wheat. Selection of genetically diverse parental lines for planned hybridization programme is essential to create broad spectrum of variability in segregating generation. Evaluation of genetic diversity among the newly developed and released genotypes or adapted germplasm lines can provide predictive estimates of genetic variation among the segregating progeny (Manjarrez- Sandoral *et al.*, 1997). The Mahalanobis D^2 statistic gives information about the genetic divergence and provides the basis for selection of parental lines form breeding programme. Here we report the magnitude of genetic diversity among a set of released and newly developed advanced lines evaluated under timely sown irrigated conditions.

Materials and Methods

The experimental material consisted of 36 genotypes (Table 1) that included released wheat varieties recommended for various production situations of different zones of the country and pre-release advance lines of bread wheat developed at Indian Agricultural Research Institute, New Delhi. The experiment was laid out in Randomized Block Design (RBD) replicated thrice under timely sown irrigated conditions and was conducted consecutively for two crop seasons *i.e.*, 2016-17 and 2017-18. Each genotype was sown in a six-row plot having a gross area of 5 m × 1.20 m with a row spacing of 20 cm using self-propelled Norwegian Seed Drill in a well prepared field. Recommended package of practices was followed to raise the healthy wheat crop. Observations in field were recorded from each experimental plot either on five randomly selected plants or on plot basis for 13 morpho-physiological characters *viz*., plant height (PH), days to 50 % heading (HDNG), number of spike per square meter (SPMS), number of grains per spike (GNPS), grain weight per spike in grams (GWPS), spike length in cm (SL), days

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Table 1. Details of experimental materials used in the study and developed at IARI, New Delhi

S.No.	Genotype	Pedigree/Parentage	Prod Cond.	Material
1	HD3171	PBW343/HD2879	Rainfed, Timley sown	Released Variety
2	DW1616	HW5028/HD2643//UP2565	Irrigated, Timely sown	Pre-released Line
3	HD2864	DL509-2/DL377-8	Irrigated, Late sown	Released Variety
4	HD3086	DBW14HD2733/HUW468	Irrigated, Timely Sown	Released Variety
5	HD3249	PBW343*2/KUKUNA//SRTU/3/PBW343*2/KHVKAI	Irrigated, Timely Sown	Released Variety
6	DW1627	DW1422/WR1441//HRLSN-7	Irrigated, Timely Sown	Pre-released Line
7	DW1628	DW1411/HP1744//DW1440	Irrigated, Timely sown	Pre-released Line
8	DW1629	HD2967/LBE2003-1//LBRL-11	Irrigated, Late sown	Pre-released Line
9	HD3284	HD2844/F81513//MILAN-2/3/WH730	Irrigated, Timely sown	Pre-released Line
10	HD3252	BABX/LR43//BABAX/6/MOR/VEE#5DUCULA/3/DUCULA/4/MILAN/5/BAU/NILAN/7/SKAUZ/BAV92	Irrigated, Timely sown	Released Variety
11	DW1630	CL2762/HP1744//CHIRYA3	Irrigated, Late sown	Pre-released Line
12	HD2932	KAUZ/STAR//HD2643		Released Variety
13	DW1631	HD2967/ CHIRYA3//DW1451	Irrigated, Late sown	Pre-released Line
14	DW1632	HD2998/HD2733//DW1432	Irrigated, Late sown	Pre-released Line
15	WR544	NW 2078/CL1739//HD2960	Irrigated, V Late sown	Released Variety
16	HD3255	SOKOLL//PBW343*R/KUKUNA/3/ATTAILA/PASTOR	Irrigated, Timely sown	Released Variety
17	DW1633	VL796/HD2009//HD3003	Irrigated, Late sown	Pre-released Line
18	DW1634	HD2682/CL3156//WH542	Irrigated, Late sown	Pre-released Line
19	DW1635	UP2338/WR1909//NING8319//HD2967	Irrigated, Late sown	Pre-released Line
20	HD3090	SFW/VAISHALI//UP2405	Irrigated, Late sown	Released Variety
21	HD 3262	VL796/HD2009//HD3003	Irrigated, Timely sown	Released Variety
22	DW1636	HD2998/HD3160//PDW621-50	Irrigated, Late sown	Pre-released Line
23	DW1637	HD2967/HD3027	Irrigated, Late sown	Pre-released Line
24	DW1638	HD2967/HP1744//LBRL1	Irrigated, Late sown	Pre-released Line
25	DW1639	HD2998/HD2894//PS940	Irrigated, Late Sown	Pre-released Line
26	DW1640	HD2967/LBR1724//VHW4668	Irrigated, Late sown	Pre-released Line
27	HD3118		Irrigated, Late Sown	Released Variety
28	HD3265	DW1311/HD2894/HW5028	Irrigated, Timely sown	Pre-released Line
29	DW1642	HD2967/HD2844/F81-513//MAILAN2/3/WH730	Irrigated, V. Late sown	Pre-released Line
30	DW1643	HD 2967/E-4870	Irrigated, V. Late sown	Pre-released Line
31	DW1644	HD2998/DW1403	Irrigated, V. Late sown	Pre-released Line
32	DW1645	HD2921/HPW277//PBW 621-50	Irrigated, V. Late sown	Pre-released Line
33	HD3059	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	Irrigated, Late sown	Released Variety
34	HD3266	TRCH/5/REH/HARE//2*BCN/CROC-1AE.SQUARROSA(213)//PGO/4/HUITES	Irrigated, Late sown	Pre-released Line
35	DW1615	NW 2078/CL1739//HD2960	Irrigated, Timely sown	Pre-released Line
36	HDCSW18	PBW343/CL1538	CA Early sown	Released Variety

Table 2. Analysis of variance (ANOVA) for 13 traits recored for 36 wheat genotypes during Rabi 2016-17 and 2017-18

2016-2017														
Sv	D.F.	HDNG	DTM	GFD	PH	SL	GWPS	GNPS	SPMS	YPMS	BYPMS	HI	TGW	CTD
Replication	2	0.8405	6.25	2.507	4.037	0.07	0.001	4.8425	100.75	0.1205	1144.732	8.6945	7.1545	0.261
Genotype	35	117.659**	68.233**	54.435**	140.835**	2.100**	0.316**	58.558**	17952.590**	96195.006**	153277.783**	1207.752**	167.702**	2.743**
Error	70	0.383	0.836	0.493	0.237	0.029	0.001	0.7	37.464	211.749	389.789	5.171	1.508	0.01
Se(D)		0.505	0.746	0.573	0.398	0.139	0.03	0.683	4.998	11.881	16.12	1.857	1.003	0.082
C.D. (1%)		1.01	1.492	1.145	0.795	0.279	0.06	1.365	9.989	23.748	32.22	3.711	2.004	0.163
C.V.(%)		0.891	0.963	2.76	0.71	1.944	3.285	2.269	1.749	3.637	2.123	5.078	4.108	3.379
2017-2018														
Replication	2	3.528	3.028	2.287	2.4815	0.01	0.002	1.9535	40.2595	75.3425	1973.03	0.2055	5.003	0.0135
Genotype	35	336.312**	320.105**	56.047**	171.745**	2.910**	0.197**	202.662**	15829.666**	81075.507**	280902.598**	144.025**	262.160**	2.755**
Error	70	0.299	0.428	0.258	1.053	0.043	0.009	1.078	93.954	2,150.53	617.142	7.749	6.493	0.01
Se(D)		0.447	0.534	0.415	0.838	0.169	0.078	0.848	7.914	37.864	20.284	2.273	2.081	0.08
C.D. (1%)		0.893	1.067	0.83	1.675	0.338	0.155	1.694	15.819	75.68	40.542	4.543	4.158	0.161
C.V. (%)		1.058	0.82	1.806	1.43	2.077	5.518	2.292	1.998	5.555	1.383	5.957	6.476	2.752

Expansion of trait acronyms is given in material and method section

Table 3. Clustering of 36 genotypes based on D^2 Statistic during rabi 2016-17 and 2017-18

Cluster #	Genotypes #	Genotypes in cluster
Crop season 2016-17		
I	12	DW1639, DW1640, HD3318, HD3265, DW1642, DW1643, DW1644, DW1645, HD3059, HD3266, DW1615, HDCSW18
II	11	DW1631, DW1632, DW1630, DW1633, DW1634, DW1635, HD3090, HD3262, DW1636, DW1637, DW1638
III	12	HD3171, DW1616, HD2864, HD3086, HD3249, DW1627, DW1628, DW1629, HD3184, HD3252, HD3255, HD2932
IV	1	WR544
Crop season 2017-18		
I	22	HD3171, DW1616, HD3249, DW1628, DW1629, HD3184, HD3252, DW1630, DW1631, DW1632, HD3255, DW1634, DW1635, HD3090, HD3262, DW1636, DW1637, DW1639, HD3318, DW1642, DW1645, HD3266
II	1	HD2864
III	6	DW1633, DW1640, DW1643, DW1644, HD3059, HDCSW18
IV	1	DW1638
V	1	WR544
VI	1	HD3265
VII	1	DW1627
VIII	1	HD2932
IX	1	HD3086
X	1	DW1615

to maturity (DTM), grain filling period (GFD), grain yield per square meter in grams (GYPMS), biological yield per square meter in grams (BYPMS), harvest index (HI) and 1000-grain weight (TGW). The canopy temperature depression (CTD) was measured at anthesis stage using portable infra-red thermometer, Model AG-42, with a view of 2.5°. The data collected from field trials were subjected to statistical analyses. Analysis of variance was carried out following Panse and Sukhatame (1975). The genetic divergence among the genotypes was assessed by *inter se* genetic distances using D^2 statistic of Mahalanobis (generalized distance as recommended by Rao, 1952). The genotypes were grouped using Euclidean cluster analysis.

Result and Discussion

Significant genotypic differences were observed for all the traits under study in both the crop seasons suggesting the presence of substantial genetic variability among the genotypes chosen for the study (Table 2). Cluster formation based on Euclidean analysis of the morpho-physiological characters during the crop season 2016-17 grouped 36 genotypes into four clusters, but into 10 clusters based on 2017-18 data (Table 3). Out of 36 genotypes, some genotypes were grouped together in both the years. For example, a group of six genotypes *viz*., DW1639, HD3262, HD3318, DW1632, DW1645 and HD3266 occupied cluster I during both the crop seasons. Similarly, a group of nine genotypes *viz*., DW1630, DW1631, DW1632, DW1634, DW1635 DW1636, DW1637, HD 3262 and HD 3090 came together in cluster II and cluster I during 2016-17 and 2017-18, respectively. Likewise, eight genotypes *viz*., HD3171, DW1616, HD3255, HD 3249, DW 1628, DW 1629, HD 3184 and HD 3252 appeared together in cluster III in 2016-17 and cluster I in 2017-18. Interestingly, one genotype WR 544 appeared in different clusters in two cropping seasons. Seven genotypes DW1633, DW1638, HD3265 DW1615 DW1627 and HD2932 appeared in cluster I, II and III during 2016-17 but formed different clusters in 2017-18. This might be due to the differential expression of these genotypes to the varied environmental conditions of these two seasons.

Comparative evaluation of cluster means indicated that, for improving a specific character, choose the genotypes from the cluster exhibiting desirable mean values for that character. This indicated that cluster I and II during 2016-17 and cluster II and III during 2017-18 had desirable cluster means for more number of characters, therefore these clusters might be considered for selecting genotypes for breeding programmes. The diversity analysis in conjunction with the mean performance during both the crop seasons, genotypes DW1631 (grain and biological yield), HD 3318 and HD 3252 (higher grain weight/spike), HD 3318 and DW 1631 (more grain number /spike) HD 2932 (longer grain filling duration) and WR 544 (earliness), DW1630 and HD 3255 (longer spike) were apparently the best suited genotypes for improving the respective traits and can be included in crossing programme to create genetic variability and to select for transgressive segregants.

Acknowledgement

The first author is grateful to Indian Council of Agricultural Research (ICAR), New Delhi, for providing Junior Research Fellowship for Master's Degree programme.

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