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Study on genetic variability and divergence under sodic soil in indigenous lines of wheat (*Triticum aestivum* L. em. Thell)

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Abstract
Present investigation was carried out to evaluate 90 indigenous lines of wheat with 4 check varieties for genetic variability and divergence. The characters studied were days to 50% flowering, days to maturity, plant height, tillers per plant, spike length, flag leaf area, peduncle length, 1000-grain weight, biological yield per plant, harvest index and grain yield per plant. The assessment of existing genetic variability and divergence in the indigenous collections was done by computing mean value of various characters. Analysis of variance (ANOVA) revealed significant differences among all the genotypes for majority of the traits except tillers per plant, test weight and harvest index. The genotypes showed moderate to high level of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV). The magnitudes of phenotypic coefficient of variance (PCV) for all the characters were slightly higher than their corresponding genotypic coefficient of variance (GCV), indicated very less environmental influence on the expression of the characters. The maximum GCV was reported for flag leaf area (18.892), grain yield per plant (18.338), biology yield per plant (17.002) and peduncle length (15.789). This indicated that these characters can be utilized as selection criteria to achieve maximum yield. The 90 indigenous lines and 4 check varieties of wheat were grouped into 10 distinct clusters by using nonhierarchical Euclidean cluster analysis. It indicated the existence of high degree of genetic diversity present in the varieties/lines. Therefore, these varieties/lines may serve as valuable source for selection of diverse parents. Maximum intra-cluster distance was found for cluster-IX followed by cluster-IV, the minimum intra-cluster distance was recorded for cluster-VI followed by cluster-X. The highest inter-cluster distance was observed between cluster-V and cluster-VIII followed by cluster-VIII and cluster-IX. The lowest inter-cluster distance was observed between cluster-II and cluster-III followed by cluster-I and cluster-III. Hence, crosses should be made between these widely related genotypes located in intra and inter cluster distances, to get desirable extinct of heterotic potential.

Keywords: genetic variability, genetic divergence, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV) and wheat (*Triticum aestivum* l. em. Thell)

Introduction
Wheat (*Triticum aestivum* L. em. Thell) a crop of Poaceae family is a major staple food crop of the world after rice. It is primarily grown in temperate region, higher altitude and also at medium altitude of tropical climate. However, it is cultivated widely around the world due to wide adaption and greater role in human nutrition as well as in agricultural economy. The majority of the cultivated wheat varieties belong to three main species of the genus Triticum. These are the hexaploid, *T. aestivum* L. (bread wheat), the tetrapod, *T. durum* and the diploid, *T. dicoccum*. and *T. monococcum*. Globally, aestivum wheat is most important species which covers 90 per cent of the area.

India stands second rank in production and consumption of wheat next to china in the world. India's share in world wheat production is about 12.98% of world's wheat production. Wheat is the only crop where production increase approx. fifteen fold during last sixty six years (6.5 million tonnes in 1950 to 97.44 million tonnes in 2017 (Anonymous, 2017) [1]. The world acreage under wheat crop during 2016-17 was 222.51 million ha with production of 755.00 million metric tonnes with an average yield of 33.90q/ha. (USDA Report, 2017).

In India, the total area sown for raising the wheat crop during 2016-17 was 30.72 million hectares with the production of 97.44 million tones and average productivity was 31.72 q/ha.

(Project Directorate Report, IIWBR 2016-17).
During the year 2016-17 in Uttar Pradesh, the total wheat production was 30.40 million tones and average productivity was 30.75 q/ha. Uttar Pradesh ranked first with an area of 9.885 Mha

with the production of 30.40 million tones with average productivity of 30.75 q/ha. The productivity of wheat in other state is comparatively lower than that of Punjab and Haryana. Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of paramount importance in breeding programme. So, the knowledge of genetic diversity and relatedness in the germplasm is a pre-requisite for crop improvement programmes. Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes. So information on the nature and degree of genetic diversity present in wheat collections is essential to select divergent parents. For the genetic amelioration of this crop, diverse genotypes from the existing germplasm should be selected and used in further breeding programme. In the present study, 94 geographically diverse indigenous genotypes were used for assessing the genetic diversity considering yield as one of the important selection criterion.

Keeping in view the above facts, the present investigation entitled was done.

Materials and Methods

The present investigation entitled "Analysis of genetic variability and divergence in indigenous lines of wheat (*Triticum aestivum* L. em. Thell) under sodic soil." was conducted at Main Experiment Station (MES) of N.D. University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during *Rabi* 2016-17 taking 90 indigenous lines of bread wheat with four check varieties. The experiment was laid out in Augmented Block Design. The entire experimental field was divided into 6 blocks of equal size and each block had 15 plots of test entries with 4 check varieties in each block. The characters studied were days to 50% flowering, days to maturity, plant height, tillers per plant, spike length, flag leaf area, peduncle length, 1000-grain weight, biological yield per plant, harvest index and grain yield per plant. Observations were recorded on randomly selected five competitive plants from each genotypes for nine characters, viz., plant height, tillers per plant, spike length, flag leaf area, peduncle length, 1000-grain weight, biological yield per plant, harvest index and grain yield per plant, while two characters viz., days to 50 per cent flowering and days to maturity were recorded on the plot basis. In order to study genetic divergence these data were subjected to D^2 analysis and their estimates are presented in Table 3, 4 and 5. Analysis employed TOCHER's and WARD's methods so as to group the genotypes into different clusters. The analysis of variance for augmented block design was done as per Federer 1956 and GCV and PCV were estimated as per Burton and de Vane 1953. Non-hierarchical Euclidean cluster analysis was done by method, described by Beale, 1969 [3]. and Spark, 1973 [17].

Result and discussion

Analysis of variance was done for different traits and it is given in Table 1. Mean, range, SD and coefficient of variance are given in Table 2.

Analysis of variance (ANOVA) revealed significant differences among all the genotypes for majority of the traits except tillers per plant, test weight and harvest index. Kumar *et al.* (2017) [9]. Lone *et al.* (2017) [11]. Desheva and Cholakov (2015) [7]. And Meena *et al.* (2014) [12]. Also found significant differences among all the genotypes for almost all the characters studied. The genotypes showed moderate to high level of genotypic coefficient of variance (GCV) and

phenotypic coefficient of variance (PCV). The magnitudes of phenotypic coefficient of variance (PCV) for all the characters were slightly higher than their corresponding genotypic coefficient of variance (GCV), indicated very less environmental influence on the expression of the characters. The maximum GCV was reported for flag leaf area (18.892), grain yield per plant (18.338), biological yield per plant (17.002) and peduncle length (15.789). Similar results were also reported by Kumar *et al.* (2017) [9]. Kumar *et al.* (2010) [10]. and Siddharthan and Malik (2007)[15].

The selection of suitable diverse parents for hybridization is an important step for any crop improvement programme to get desired recombinants. The importance of genetic divergence in plant breeding has also been emphasized by several researchers. Therefore, this study was carried out by using Non-hierarchical Euclidean cluster analysis by method which was described by Beale, 1969 [3] and Spark, 1973 [17]. to assess the genetic divergence in bread wheat genotypes for seed yield and its contributing traits. Through WARD's method all the genotypes were grouped into ten different non-overlapping clusters in which clusters V and VIII were found to be smallest including three genotypes namely, HI-1608, DWAP-1531, NIAW-2030 and DWAP-1532, UP-2970, UP-3000, respectively while, cluster III was found to be largest including twenty genotypes. Analysis of inter and intra cluster distance was showed higher intra cluster distance within cluster IX (15.449), cluster IV (13.938) and cluster VIII (13.501). The maximum inter cluster distance was found between cluster V and cluster VIII (75.217), cluster VIII and cluster IX (66.331), cluster IV and cluster VIII (52.598) and between cluster II and cluster VIII (51.894). The study of cluster mean showed that the genotypes belonging to cluster V were early for days to 50% flowering as well as maturity and showed highest mean value for peduncle length (39.013). The highest mean value for flag leaf area and spike length was reported for genotypes of cluster IV (37.618) and (19.741) respectively. The highest mean value of plant height was reported for genotypes of cluster V (96.885), while the lowest mean value was reported for the genotypes of cluster VI (78.679). The genotypes belonging to cluster X showed average mean value for plant height and highest mean value for biological yield per plant (39.798) as well as maximum mean value for grain yield per plant (14.514). The genotypes of cluster VII were showed highest mean value for tillers per plant (7.439) and for harvest index (40.04).The highest mean value for grain yield per plant was reported for the genotypes of cluster IX (14.782). The boldest seeds were reported for the genotypes of cluster V which showed highest mean value for test weight (51.208). The results reported in this study are also in agreement with the results reported by the researchers such as Pandey *et al.* (2017) [14]. Mishra *et al.* (2015) [13]. Bhushan *et al.* (2014) [5]. Singh and Upadhayay (2013) [16]. And Verma *et al.* (2013) [18].

The analysis of character contributions towards genetic divergence among ninety genotypes and four check varieties of wheat are given in Table 6. The maximum contributions in manifestation of total genetic divergence were made by plant height (32.24), flag leaf area (22.79), biological yield per plant (15.99) and test weight (11.16). The minimum contributions in manifestation of total genetic divergence were made by grain yield per plant (0.01). Bergale *et al.* (2001) [4]. Also reported that the plant height had the greatest contribution to genetic divergence.

Table 1: Analysis of variance of augmented design for 11 characters in wheat genotypes

	df	Days to 50% flowering	Flag leaf area (cm²)	Plant height (cm)	Day to maturity	Tillers Per plant	Spike Length (cm)	Peduncle length (cm)	Biological yield per plant (g)	Grain yield per plant (g)	Test weight (g)	Harvest Index (%)
Block (Ignoring Treatments)	5	7.361 **	26.943 *	240.892 **	4.135 **	3.749	1.700	10.662 **	97.167 **	11.608 **	8.173	4.909
Treatment (eliminating blocks)	93	8.438 **	41.961 **	74.832 **	4.167 **	1.281	3.830 *	28.824 **	28.055 **	4.889 **	28.869	9.591
Checks	3	17.500 **	127.391 **	270.215 **	14.375 **	1.612	6.658 *	233.480 **	58.000 **	13.260 **	171.469 **	11.596
Checks + Var vs. Var.	90	8.136 **	39.113 **	68.319 **	3.827 **	1.270	3.736 *	22.002 **	27.057 **	4.610 **	24.116	9.524
Error	15	0.300	8.397	0.542	0.275	1.549	1.520	0.897	3.400	0.695	20.285	7.762
Block (Eliminating Check + Var.)	5	0.300	0.930	5.417 **	0.075	0.023	2.318	0.370	1.267	0.437	0.063	14.518
Entries (ignoring blocks)	93	8.818 **	43.360 **	87.492 **	4.386 **	1.481	3.797 *	29.377 **	33.211 **	5.490 **	29.305	9.074
Checks	3	17.500 **	127.391 **	270.215 **	14.375 **	1.612	6.658 *	233.480 **	58.000 **	13.260 **	171.469 **	11.596
Varieties	89	8.462 **	39.085 **	80.389 **	3.985 **	1.493	3.478 *	21.634 **	32.338 **	5.236 **	21.147	9.091
Checks vs. Varieties	1	14.415 **	171.675 **	171.428 **	10.112 **	0.068	23.558 **	106.166 **	36.550 **	4.760 *	328.860 **	0.017
Error	15	0.300	8.397	0.542	0.275	1.549	1.520	0.897	3.400	0.695	20.285	7.762
Ci – Cj	1	0.674	3.566	0.906	0.645	1.531	1.517	1.165	2.269	1.026	5.542	3.428
BiVi – BiVj	1	1.651	8.735	2.219	1.581	3.751	3.717	2.855	5.558	2.512	13.576	8.398
BiVi – BjVj	1	1.846	9.766	2.481	1.767	4.194	4.155	3.191	6.214	2.809	15.179	9.389
Ci – VI	1	1.410	7.459	1.895	1.350	3.203	3.174	3.174	4.746	2.145	11.593	7.171

Table 2: Mean, Range and Coefficient of Variation (CV) for 11 characters in wheat

Characters	Range (min-max)	Mean value	GCV (%)	PCV (%)	CV (%)
Days to 50% Flowering	75.250-92.250	79.585	3.257	3.329	3.661
Flag Leaf Area (cm²)	14.923-47.638	36.485	18.896	21.809	23.792
Plant Height (cm)	65.710-110.410	83.365	9.715	9.755	10.537
Days to Maturity	117.125-128.125	21.324	1.44	1.504	1.641
Tillers per Plant	3.675-9.750	6.143	-3.499	19.963	19.341
Spike Length (cm)	12.563-22.212	16.780	7.549	10.520	11.859
Peduncle Length (cm2)	15.075-43.000	26.284	15.789	16.198	18.031
Biological Yield per Plant (g)	19.833-48.583	28.663	17.002	18.174	19.744
Test Weight (g)	33.692-54.692	42.980	1.953	10.617	10.880
Harvest Index (%)	26.661-43.751	36.688	2.853	8.110	9.864
Grain yield (g)	5.823-16.255	10.528	18.338	19.967	22.230

Table 3: Clustering pattern of 94 wheat genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 11 characters

Cluster Number	No. Of Genotypes	Genotypes
I	11	AKAW-4849, WH-147, DBW-224, HI-1614, HD-2009, HI-1613, GW-2014-563, LBPY-2014-9, DWAP-1538, PBY-2016-01, PBY-2016-02
II	11	LBPY-2014-01, DWAP-1541, WS-1503, RAJ-4507, WS-1501-1, HI-1616, DWAP-1540, GW-2014-545, GW-2014-560, GW-2014-562, UP-2969
III	20	GW-2013-471, GW-2014, LBPY-2016-05, GW-2013-489, GW-2014-582, LBPY-2014-12, LOK-1, LBPY-2015-07, RAJ-4480, LBPY-2014-4, RAJ-4508, HI-1610, RAJ-4479, LBPY-2015-03, GW-2014-571, GW-2014-580, HI-16007, KV-2015-01(M2-415), NIAW-3033, RAJ-4510
IV	9	AKAW-4900, AKAW-4800, LBPY-2014-3, DWAP-1536, GW-2013-478, GW-2013-491, GW-2014-574, DWAP-1533, GW-2014-544
V	3	HI-1608, DWAP-1531, NIAW-2030
VI	10	LBPY-2014-5, DWAP-1534, LBPY-201, RAJ-4472, AKAW-4923, DWAP-1535, DWAP-1530, LBPY-2015-8,DBW-17, RAJ-4444
VII	14	LBPY-2014-7, AKAW-4901, RAJ-4441, UP-2968, UP-2971, DBPY-2016-02, KV-2015-02(KV), DBPY-2016-02, KV-2015-02(KV), DBPY-2016-01, HI-1609, RAJ-4478, RAJ-4509, NIAW-3033, LBPY-2015-01, LBPY-2015-04
VIII	3	DWAP-1532, UP-2970, UP-3000
IX	6	NIAW-2844, RAJ-4511, LBPY-2014-10, DWAP-1537, NIAW-3033, GW-2014-547
X	7	LBVP-2015-05, LBPY-2016-02, LBPY-2016-01, DBW-140, LBPY-2016-03, LBPY-2016-04, LBPY-2014-8

Table 4: Estimates of average intra- and inter-cluster distances for 11 characters

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
Cluster 1	11.983	16.892	16.354	23.655	25.254	18.078	18.647	44.882	27.405	19.433
Cluster 2		10.139	16.337	18.493	27.73	18.380	21.580	51.894	32.468	29.961
Cluster 3			11.158	22.295	27.948	15.512	15.843	51.885	24.971	24.571
Cluster 4				13.938	27.118	26.235	27.154	52.598	26.889	32.718
Cluster 5					10.637	46.312	36.743	75.217	29.535	35.100
Cluster 6						6.752	15.539	29.688	34.257	23.023
Cluster 7							11.085	44.292	22.990	17.178
Cluster 8								13.501	66.331	43.445
Cluster 9									15.449	19.101
Cluster 10										9.500

Bold figure indicates Intra-cluster distance.

**Table 5**: Clusters means for 11 characters in wheat

	Days to 50% flowering	Flag leaf area (cm²)	Plant height (cm)	Days to maturity	Tillers Per plant	Spike length (cm)	Peduncle Length (cm)	Biological yield per plant (g)	Grain yield per plant (g)	Test weight (g)	Harvest index (%)
Cluster 1	78.977	23.058	89.714	120.852	6.757	17.605	29.417	28.765	10.073	38.724*	35.346
Cluster 2	78.159	28.493	79.685	120.443	6.225	17.533	26.011	24.379*	7.781*	44.142	31.641*
Cluster 3	78.238	24.610	79.811	120.281	5.568	15.944	27.582	25.621	9.844	43.274	38.994
Cluster 4	79.639	37.618**	83.663	121.486	4.692*	19.741**	26.756	27.972	9.776	44.461	34.875
Cluster 5	76.583*	27.266	96.885**	118.958*	5.475	19.481	39.013**	31.000	10.776	51.208**	34.625
Cluster 6	81.475	21.597*	78.679*	123.463	5.763	15.316	21.307*	25.533	9.359	39.132	36.629
Cluster 7	80.071	25.521	79.789	121.857	7.439**	16.098	23.589	29.030	11.670	44.752	40.040**
Cluster 8	92.083**	22.352	95.544	127.375**	5.908	15.304*	24.067	28.417	9.593	40.425	33.780
Cluster 9	77.917	34.364	88.252	119.542	5.767	16.625	25.788	37.833	14.782**	46.100	39.105
Cluster 10	80.250	23.353	87.591	122.054	7.211	15.945	25.889	39.798**	14.514	41.952	35.906

Minimum value-*
Maximum value-**

Table 6: Contribution of characters towards genetic divergence

Source	Contribution %	Times Ranked 1st
1 Days to 50% Flowering	2.17	95.000
2 Flag Leaf Area (cm²)	22.79	996.000
3 Plant Height (cm)	32.24	1409.000
4 Days to Maturity	0.05	2.000
5 Tillers/ Plant	0.07	3.000
6 Spike Length (cm)	0.25	11.000
7 Peduncle Length (cm)	9.59	419.000
8 Biological Yield/ Plant	15.99	699.000
9 Grain Yield/ Plant (g)	0.01	0.000
10 Test Weight (g)	11.16	488.000
11 Harvest Index (%)	5.70	249.000
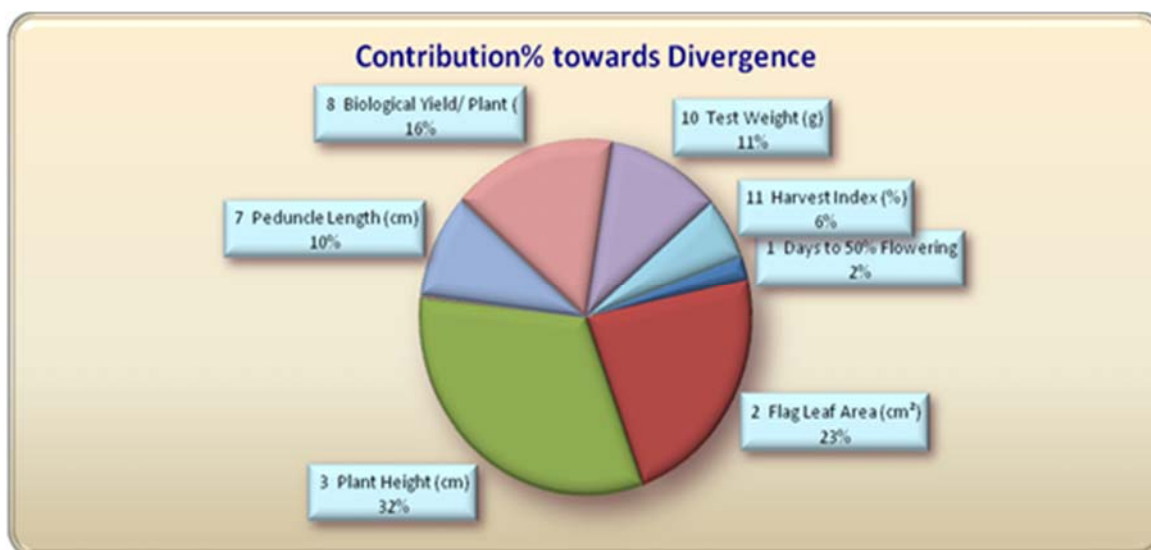
Fig 1

Conclusion
From all over the analysis, it can be concluded that high amount of variability was present in the genotypes under study which provided a better opportunity for selection of desirable genotypes. All the genotypes were grouped into ten different non-overlapping clusters based on D^2 values. The genotypes of Cluster V namely, HI-1608, DWAP-1531 and NIAW-2030 showed maximum mean value for test weight and above average mean value for yield contributing traits as well as they also showed a wide spectrum of diversity with the genotypes of cluster VIII. Therefore, it can be emphasized that the genotypes belonging from cluster V, VIII and cluster IX may be selected for production of transgressive segregants in relation of grain yield and its contributing traits.

References
1. Anonymous. Statistical data base. www.fao.org, 2017.
2. Anonymous. Wheat 101: Nutrition facts and health effects, Authority nutrition an evidence based approach, 2015.
3. Beale EML. Euclidean cluster analysis. A paper contribution to 37th Session of the International Statistical Institute, 1969.
4. Bergale S, Billore M, Holkar AS, Ruwali KN, Prasad SVS. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). Madras Agril. J. 2001; (7/0): 457-461.
5. Bhushan B, Gaurav SS, Verma PN, Ali M, Meena MR. Character association and genetic divergence for

quantitative traits in bread wheat (*Triticum aestivum* L.). Annals of Biol. 2014; 30(1): 62-67.

6. Burton GW, de Vane EW. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron. J. 1953; 45:178-181.

7. Desheva G, Cholakov T. Variability, heritability and genetic progress for some yield components in common winter wheat genotypes (*Triticum aestivum* L.). Genetics and Plant Physiology. 2015; 4(3–4):191–200.

8. Federer WI. Augmented design. Hawain Planters Record. 1956; 40:191-207.

9. Kumar A, Biradar SS, Kumar KJY, Desai SA, Patel BN, Deepak DA. *et al.* Studies on Genetic Variability and Heritability for Yield and Yield Attributing Traits in Advanced Backcross Segregating Populations in Bread Wheat (*Triticum aestivum* L.). Int. J Curr. Microbiol. App. Sci. 2017; 6(10):3664-3670.

10. Kumar H, Khosla G, Sharma PK. Utilization of genetic variability, correlation and path analysis for seed yield improvement in bread wheat (*Triticum aestivum* L.*)* genotypes. Environment and Ecology. 2010; 28(1):91-94.

11. Lone RA, Tuhina Dey, Bhagwati Charan Sharma, Gyanendra Kumar Rai, Shabir Hussain Wani Javeed Ahmad Lone. Genetic Variability and Correlation Studies in Winter Wheat (*Triticum aestivum* L.) Germplasm for Morphological and Biochemical Characters. Int. J. Pure App. Biosci. 2017; 5(1):82-91

12. Meena HS, Kumar D, Prasad SR. Genetic variability and character association in bread wheat (*Triticum aestivum* L.). Indian J. Agril. Sci. 2014; 84(4):487-491.

13. Mishra CN, Tiwari V, Kumar S, Gupta V, Kumar A. Sharma I. Genetic diversity and genotype by trait analysis for agro morphological and physiological traits of wheat (*Triticum aestivum* L.*)* SABRAO J. Breed. and Genet. 2015; 47(1):40-48.

14. Pandey MK, Bind HN, Kumar S, Singh BN. Genetic Divergence in Wheat (*Triticum aestivum* L. Thell.) Under Saline Sodic Condition. Int. J. Curr. Microbiol. App. Sci. 2017; 6(5):181-189.

15. Siddharthan SP, Malik VK. Character association and path analysis in wheat (*Triticum aestivum* L.). Agril Sci. Digest. 2007; 22(4); 255-257.

16. Singh B, Upadhyay PK. Genetic divergence analysis in wheat (*T. aestivum* L.). Int. J. Plant Sci. 2013; 8(2):297-299.

17. Spark DN. Euclidean cluster analysis. *Algorithm,* A. 58. Appl. Statistics. 1973; 22:126-130.

18. Verma PN, Singh BN, Yadav RK. Genetic variability and divergence analysis of yield and its contributing traits under sodic soil condition in wheat (*Triticum aestivum* L.). Int. J Ag. Sci. 2013; 3(2):395-399.