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Genetic Variability, Trait Association and Multivariate Analysis of Elite CIMMYT Wheat (*Triticum aestivum* L.) Germplasm for Yield and Sodicity Tolerance

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Abstract

Salinity of land and water is one of the major constraints in agricultural crop production especially for wheat in India. Genetically variable base population along with reliable screening technique is prerequisite for developing high yielding and salt tolerant wheat cultivar. The present study was undertaken in partially reclaimed sodic field as well as micro-plots to estimate genetic variability, trait association and identification of key traits for salt tolerance coupled with high yield in wheat. Fifty elite wheat germplasm lines obtained from CIMMYT's 19th SAWYT trial were used in the study. Highly significant variation for various traits signifies that genotypes can be improved through breeding and selection. Eight superior genotypes were identified having yield advantage of 5 to 13 per cent compared with check KRL 210 coupled with good amount of salt tolerance. Biomass had significant relationship with yield while test weight was associated with salinity tolerance. Cluster analysis could able to classify genotypes in three clusters based on observed traits. Principal component analysis could able to resolve four PCs explaining 85.87% of total variance in the data. Days to 50% heading, biomass and tolerance score were identified as key traits causing variation among genotypes.

Key words: Bread wheat, Cluster analysis, Correlation, Genetic variability, Principal component analysis, Salinity.

Introduction

Wheat is second most important cereal crop of the world next to rice. Due to its adaptability and versatile nature in a wide range of agro-climatic conditions, it is grown in more than 44 countries worldwide. In India, it is grown over 30 million hectares area with total production of 95 million tonnes (2013-14) and average yield of 3.0 tonnes ha^{-1} (Anonymous, 2014). Salinity of land and water is a major constraint in our ability to ensure food security of the nation. Worldwide, over 800 million hectares of land (6% of the total area) are salt-affected either by salinity or sodicity (FAO, 2005). Increasing the yield of crop plants in normal soils and in less productive lands, including salinized lands, is an absolute requirement for feeding the world (Yamaguchi and Blumwald, 2005). Among abiotic factors, salinity stress is the major yield limiting factors influencing wheat production in India (Anonymous, 2011). Stress can be defined as any environmental factor capable of reducing the yield below the potential level, i.e., the highest possible yield for a given set of conditions (Blum, 1980). Salt tolerance of crops may vary with its growth stage (Maas *et al.*, 1994). In general, cereal plants are the most sensitive to salinity during the vegetative stage (Maas and Poss, 1989). Wheat is a classified as moderately salt-tolerant crop (Maas and Hoffman, 1977). Salt tolerance is a polygenic trait and selection based on one or few traits has been found ineffective during past (Flower, 2004).

Improving salt tolerance of wheat genotypes has been inhibited by a number of factors, such as the lack of effective evaluation methods for salt tolerance to screen the genotypes in breeding programs, low selection efficiency using overall agronomic parameters, and a complex phenomenon involving morphological, physiological and biochemical parameters among genotypes (Singh *et al.,* 2014). There is difference among the salt tolerance level of different wheat genotypes. Therefore, the salt tolerance of different wheat genotypes must be

evaluated. Such evaluations may facilitate improvement of salt tolerance of tested genotypes in breeding programs or it may prove feasible to irrigate with saline water to the highly tolerant genotypes. Screening of genotypes for salinity tolerance is necessary to understand the different mechanisms of salt tolerance between genotypes (Munns *et al.*, 2006).

The success of any breeding programme will depend upon the extent of genetic diversity present in germplasm, heritability and harnessing genetic advance present in different yield associated parameters. Correlation coefficients provide a better understanding of the association of different trait(s) with grain yield. Cluster analysis is group of multivariate techniques which helps in grouping genotypes based on the characteristics they possess. Principal component analysis is multivariate technique of data reduction which helps in identifying factors/ traits/ genotypes contributing maximum variability in population. Keeping all this in view, elite CIMMYT genotypes of wheat were evaluated to generate information on genetic variability, relationships of various traits with yield and its components coupled with salinity tolerance; and their implication in selection of better high yielding and salt tolerant genotypes of wheat for saline/sodic soils in India.

Material and Methods

The experiment was conducted in the field having partially reclaimed sodic soil (pH 8.5) at Central Soil Salinity Research Institute, Karnal which is geographically located at 29^0 42' N and 77^0 02' E. The study was conducted during *Rabi* season of 2012-13 in randomized complete block design with two replications. Forty nine elite wheat germplasm of 19th Semi Arid Wheat Yield Trial (19th SAWYT) (Table 1) received from CIMMYT, Mexico along with one salt tolerant check (KRL-210) were grown in three rows/entry with 2.5 m row length and 22.5 cm row spacing. Trial was conducted in 4th week of November, 2011 and standard agronomic practices were followed to raise a good crop. Observations were recorded for Days to 50% heading (HEAD), plant height (PHT), biomass (BIO), harvest index (HI), 1000 grain weight (TWT), leaf injury rating due to salinity (TOL) and plot yield (YLD). Five competitive plants were selected for recording observations except for Days to 50% heading, yield and biomass which were recorded on plot basis. Visual salt injury to leaf at seedling stage was also recorded for evaluating response of genotypes to salt stress. Same set of elite wheat germplasm was also planted in single row of 1 m length in microplot having soil pH of 8.8 to observe the material carefully for leaf injury due to salinity stress and validate the results of field experiment. Data were analyzed using latest softwares (SPSS & SAS version 9.2). Sqaure root transformed value of TOL was used for statistical analysis.

Analysis of variance was done following the standard procedures (Singh and Chaudhary, 1985). Phenotypic and genotypic coefficients of variability (PCV & GCV) were calculated according to the method suggested by Burton (1952), heritability (broad sense) and genetic advance were estimated as per Johnson *et al*. (1955). The estimates of variability for traits were ranked high, moderate and low as per following: PCV and GCV >20% (high), 10–20% (moderate), <10% (low); heritability >70% (high), 50–70% (moderate), <50% (low) and genetic

Table 1. Elite CIMMYT wheat germplasm of 19th SAWYT trial used in the present study

Entry No.	Pedigree	Accession Code
1	KRL210(LOCAL CHECK)	CHECK
2	DHARWAR DRY	19SAWYT-1
3	VOROBEY	19SAWYT-2
4	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	19SAWYT-3
5	POTCH93/4/MILAN/KAUZ//PRINIA/3/BAV92/5/MILAN/KAUZ//PRINIA/3/BAV92	19SAWYT-4
6	ACHTAR*3//KANZ/KS85-8-5/4/MILAN/KAUZ//PRINIA/3/BAV92/5/MILAN/KAUZ//PRINIA/3/BAV92	19SAWYT-5
7	QG4.37A/4/MILAN/KAUZ//PRINIA/3/BAV92/5/MILAN/KAUZ//PRINIA/3/BAV92	19SAWYT-6
8	NSM*4/14-2//FRTL/2*PIFED/3/VORB	19SAWYT-7

contd...

Entry No.	Pedigree	Accession Code
9	BABAX/LR42//BABAX/3/BABAX/LR42//BABAX/4/T.DICOCCON PI94625/AE. SQUARROSA (372)//3*PASTOR/5/T.DICOCCON PI94625/AE.SQUARROSA (372)//3* PASTOR	19SAWYT-8
10	BABAX/LR42//BABAX/3/BABAX/LR42//BABAX/4/T.DICOCCON PI94625/AE. SQUARROSA (372)//3*PASTOR/5/T.DICOCCON PI94625/AE.SQUARROSA (372)//3* PASTOR	19SAWYT-9
11	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/ONIX	19SAWYT-10
12	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/ONIX	19SAWYT-11
13	ONIX/ROLF07	19SAWYT-12
14	ONIX/ROLF07	19SAWYT-13
15	ONIX/4/MILAN/KAUZ//PRINIA/3/BAV92	19SAWYT-14
16	ACHTAR/4/MILAN/KAUZ//PRINIA/3/BAV92	19SAWYT-15
17	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/ KAUZ//PRINIA/3/BAV92	19SAWYT-16
18	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/ KAUZ//PRINIA/3/BAV92	19SAWYT-17
19	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/ KAUZ//PRINIA/3/BAV92	19SAWYT-18
20	CNO79//PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/ KAUZ//PRINIA/3/BAV92	19SAWYT-19
21	MILAN/KAUZ//PRINIA/3/BAV92/4/ATTILA/BAV92//PASTOR/5/CNO79//PF70354/ MUS/3/PASTOR/4/BAV92	19SAWYT-20
22	SOKOLL*2/TROST	19SAWYT-21
23	SOKOLL*2/TROST	19SAWYT-22
24	SOKOLL//PBW343*2/KUKUNA/3/ATTILA/PASTOR	19SAWYT-23
25	SOKOLL*2/ROLF07	19SAWYT-24
26	GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92	19SAWYT-25
27	GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92	19SAWYT-26
28	GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92	19SAWYT-27
29	SW89-5124*2/FASAN/3/ALTAR 84/AE.SQ//2*OPATA	19SAWYT-28
30	SOKOLL/ROLF07	19SAWYT-29
31	SOKOLL//FRTL/2*PIFED	19SAWYT-30
32	SOKOLL//FRTL/2*PIFED	19SAWYT-31
33	BAV92/SERI	19SAWYT-32
34	ROLF07/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTOR	19SAWYT-33
35	ROLF07/3/T.DICOCCON PI94625/AE.SQUARROSA (372)//3*PASTOR	19SAWYT-34
36	MILAN/KAUZ//PRINIA/3/BAV92/4/WBLL1*2/KUKUNA	19SAWYT-35
37	ATTILA/BAV92//PASTOR/3/ATTILA*2/PBW65	19SAWYT-36
38	CUNNINGHAM/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ	19SAWYT-37
39	ESDA/KKTS	19SAWYT-38
40	GOUBARA-1/2*SOKOLL	19SAWYT-39
41	SOKOLL*2/3/PASTOR//MUNIA/ALTAR 84	19SAWYT-40
42	SOKOLL*2/3/PASTOR//MUNIA/ALTAR 84	19SAWYT-41
43	SOKOLL*2/4/CHEN/AEGILOPS SQUARROSA (TAUS)//FCT/3/STAR	19SAWYT-42
44	SOKOLL*2/4/CHEN/AEGILOPS SQUARROSA (TAUS)//FCT/3/STAR	19SAWYT-43
45	BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE. SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	19SAWYT-44
46	BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE. SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	19SAWYT-45
47	BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE. SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	19SAWYT-46
48	GONDO//WBLL1*2/TUKURU/4/GONDO//SHA5/WEAVER/3/PASTOR	19SAWYT-47
49	PASTOR*2/BAV92/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ	19SAWYT-48
50	PASTOR*2/BAV92/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ	19SAWYT-49

Table 2. Mean square effect of genotypes, phenotypic variance (V_P), genotypic variance (V_g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance (GA) for various traits

	HEAD (Days)	PHT (cm)	BIO (g)	HI (%)	TWT (g)	TOL (Value#)	YLD (g/plot)
Analysis of variance							
Replication	237.16**	12.25	311.52	0.35	5.29	0.36**	50.41
Genotype	37.78**	39.64	2665.30**	25.26**	33.07**	0.21**	260.61**
Error	10.61	27.66	245.30	8.14	2.15	0.02	77.94
Statistical parameters							
Mean	96.66	96.46	224.52	37.69	41.49	1.87	83.87
Std Dev	3.26	5.26	15.66	2.85	1.47	0.14	8.33
C.V.	3.37	5.45	6.98	7.57	3.53	7.55	10.53
$SE_m\pm$	2.30	3.72	11.07	2.02	1.04	0.10	6.24
$SE_d\pm$	3.26	5.26	15.66	2.85	1.47	0.14	8.83
C.D. (0.05)	6.55	10.57	31.47	5.73	2.94	0.28	17.74
C.D. (0.01)	8.73	14.10	41.97	7.65	3.93	0.38	23.66
V_g	13.59	5.99	1210.00	8.56	15.46	0.09	91.33
V_p	24.20	33.65	1455.30	16.70	17.61	0.11	169.27
V_e	10.61	27.66	245.30	8.14	2.15	0.02	77.94
GCV	3.81	2.54	15.49	7.76	9.48	16.37	11.39
PCV	5.09	6.01	16.99	10.84	10.11	18.03	15.51
ECV	3.37	5.45	6.98	7.57	3.53	7.55	10.53
$h^2_{(bs)}$	56.16	17.80	83.14	51.27	87.81	82.47	53.96
G.A.	5.69	2.13	65.34	4.32	7.59	0.57	14.46
G.A. % of Mean	5.89	2.20	29.10	11.45	18.29	30.63	17.24

** = p<0.01; * = P<0.05, K = 2.06 for estimating Genetic Advance; # Square root transformed value

advance (% mean) >30% (high), 20–30% (moderate), <20% (low).The phenotypic and genotypic correlations were calculated as per methods of Al-Jibouri *et al.* (1958). Path coefficient analysis was carried out with genotypic correlations with help of method suggested by Dewey and Lu (1959). Correlated response to selection was estimated as per method suggested by Falconer (1981). Hierarchical clustering techniques involving Euclidean distance was used in present investigation to classify genotypes and dendogram was constructed. Covariance matrix was utilised for principal component analysis.

Result and Discussion

Analysis of variation (ANOVA)

Analysis of variance for analyzed traits (Table 2) revealed that mean square was significant for all traits except for PHT. Highly significant variation signifies that genotypes have significant variation for these traits which can be utilised for further improvement. Significant amount of variation in CIMMYT wheat lines for yield and salnity tolerance was also reported by Ashraf and Shahbaz (2003). High diversity for salt tolerance and yield related attributes in 300 wheat genotpes was also reported by Singh *et al.* (2009). High GCV was recorded for TOL which indicating improvement potential of the trait through direct selection. PCV was higher than GCV for all the traits indicating that these traits are under influence of environment rather than strcit genetic control. Esimates of heritability ranged from 17.80 to 87.81. High broad sense heritability was observed for BIO, TWT and TOL while moderate heritability was estimated for YLD. Less effect of environment on traits gives high estimates of heritability which can be useful for plat breeders while performing selection.Similar views were expressed by Singh *et al.*(2006), Singh *et al.*(2014) while studying salnity and waterlogging tolerance of bread wheat genoypes. High heritabilty coupled with high genetic advance was reported for BIO and HI which signifies additive nature of genes controlling these traits. Similar view were expressed by Ahmad (2011) while evaluating wheat genotypes in salt stress condition. High heritability coupled with high genetic advance was suggested to be most effective criteria for selection

Table 3. High yielding and salt tolerant wheat genotypes identified

Genotype	YLD (g/plot)	TOL (score)	Salinity score in Microplot
19SAWYT-29	105	4.5	2
19SAWYT-7	104	3.5	3
19SAWYT-3	102	6.5	4
19SAWYT-12	101.5	2.5	2
19SAWYT-43	101	3	2
19SAWYT-38	99.5	3	1
19SAWYT-21	98	4.5	2
19SAWYT-26	97.5	2.5	2

TOL/Salinity score 1-9; 1=Best, 9=Poor.

(Johnson *et al.*, 1955). Panse and Sukhatme (1978) also reported that traits governed by additive genes gave high estimates of heritability and gentic advance.

Eight genotypes were found to be singnificantly superior than check KRL 210 in terms of YLD (Table 3). 19SAWYT-29 was highest yielding genotypes (105 g/plot) followed by 19SAWYT-7 and 19SAWYT-3. These superior genotypes were having yield advantage of 5-13 per cent when compared with check (Figure 1).These eight genotypes were also having better TOL score; both in field and microplot (Table 3) compared to check except for 19SAWYT-3. So these entries can be utilised as parents for high yield and salt tolerance.

Correlation and path analysis

Estimates of correlation coefficients between traits (Table 4) revealed that genotypic correlation coefficients are in general higher than phenotypic correlation coefficients which suggest strong association between traits with lesser influence of environment. Therefore, phenotypic selection of these traits will be fruitful. Positive and significant genotypic correlation was found for BIO with YLD; while PHT and HI were significantly and negatively associated with YLD. Positive and significant association was also reported between TOL and TWT suggesting that genotype having bolder grains may be more salt tolerant. Singh *et al*. (2006) also reported that plant height, biomass and days to heading have significant association with yield under stress condition.

Knowledge of association between different traits is very important for indirect selection of traits which are having low heritability and difficult to measure. Under complex situations, correlation coefficients may be misleading due to mutual cancellation of component traits. Under such situations, path analysis is very useful which simultaneously takes account of causal relationship in addition to degree of relationship. The path coefficient analysis of wheat genotypes for YLD is presented in table 5. BIO was having maximum positive direct effect (1.56) on YLD followed by HI (0.84). Highest negative and direct effect was exerted

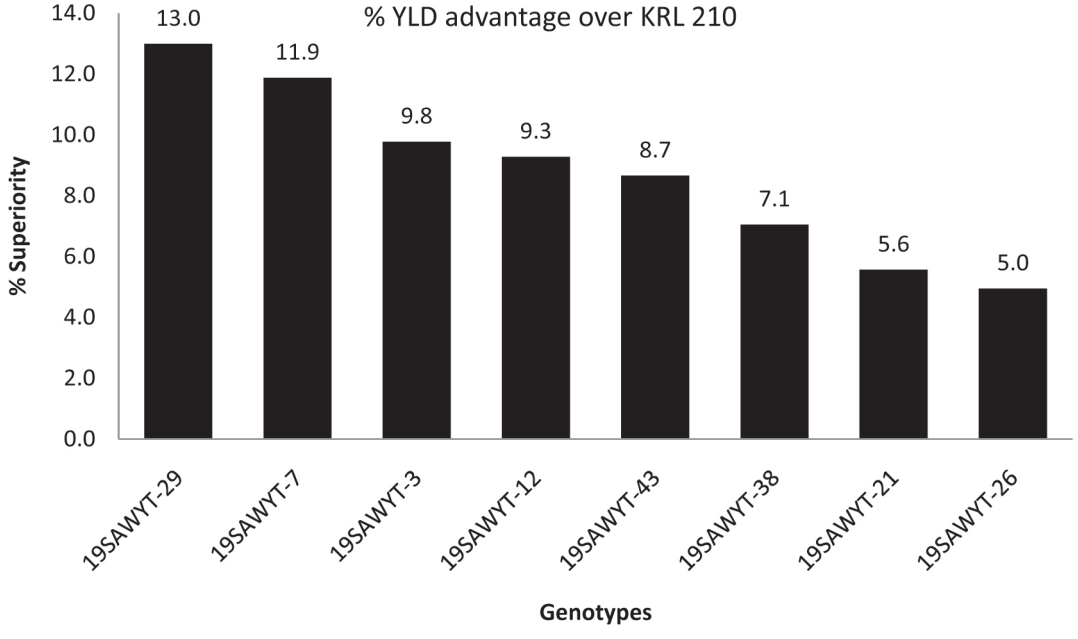

Fig. 1. Yield superiority of wheat genotypes over check KRL 210

Table 4. Phenotypic (P) and Genotypic (G) correlation coefficients among studied traits in wheat germplasm

		HEAD (Days)	PHT (cm)	BIO (g)	HI (%)	TWT (g)	TOL (Value#)	YLD (g/plot)
HEAD	P	1						
	G	1						
PHT	P	0.031NS	1					
	G	0.364**	1					
BIO	P	-0.036NS	-0.024NS	1				
	G	-0.018NS	-0.230*	1				
HI	P	-0.212*	0.097NS	-0.490**	1			
	G	-0.065NS	0.048NS	-0.717**	1			
TWT	P	-0.392**	0.150NS	0.014NS	-0.002NS	1		
	G	-0.543**	0.416**	0.032NS	0.041NS	1		
TOL	P	-0.610**	-0.063NS	-0.041NS	0.160NS	0.211*	1	
	G	-0.778**	-0.169NS	-0.006NS	0.180NS	0.200*	1	
YLD	P	-0.206*	0.063NS	0.764**	0.168NS	0.035NS	0.081NS	1
	G	-0.083NS	-0.303**	0.879**	-0.300**	0.090NS	0.124NS	1

by HEAD (-0.63). Maximum positive and indirect effect on YLD was shown by TOL via HEAD (0.49).Correlated response for YLD as a result of combined selection with different were also calculated (Table 5). Maximum correlated response was observed for BIO (46.26) with YLD. It signifies that YLD can be improved by simultaneous selection of genotypes having high biomass in partially reclaimed sodic soil.

Cluster analysis

Cluster analysis classifies objects (e.g., genotypes, products, or other entities) so that each object is very similar to others in the cluster with respect to some predetermined selection criterion. The resulting clusters of objects should then exhibit high internal (within-cluster) homogeneity and high external (between-cluster) heterogeneity. Thus, if the classification is successful, the objects within clusters will be close together when plotted geometrically, and different clusters will be far apart. Hierarchical clustering techniques proceed by either a series of successive mergers or a series of successive divisions. Agglomerative hierarchical methods start with the individual objects. Thus, there are initially as many clusters as objects. The most similar objects are first grouped, and these initial groups are merged according to their similarities. Eventually, as the similarity decreases, all subgroups are fused into a single cluster.

Based on cluster analysis, fifty genotypes of wheat were classified in three clusters. The three clusters namely Cluster I, Cluster II and Cluster III formed by hierarchical cluster analysis have been illustrated in Fig 2. Cluster I consisted of 11 genotypes. Cluster II was having maximum number of genotypes (24) followed by cluster III having 15 genotypes (Table 6). In breeding programmes,

Table 5. Genotypic path coefficients showing direct (bold) and indirect effects; and correlated response of various traits with YLD

	HEAD (Days)	PHT (cm)	BIO (g)	HI (%)	TWT (g)	TOL (Value#)	rg with YLD	Correlated response with YLD
HEAD	**-0.64**	0.13	-0.02	-0.05	0.23	0.27	-0.083NS	-0.464
PHT	-0.23	**0.36**	-0.36	0.04	-0.17	0.06	-0.303**	-1.123
BIO	0.01	-0.08	**1.56**	-0.60	-0.01	0.00	0.879**	**46.263**
HI	0.04	0.02	-1.12	**0.84**	-0.01	-0.05	-0.299**	-1.329
TWT	0.34	0.15	0.04	0.03	**-0.42**	-0.07	0.090NS	0.533
TOL	**0.49**	-0.06	-0.01	0.14	-0.08	**-0.36**	0.124NS	0.058

Residual are 0.0165; NS = Non- significant, ** = $p < 0.01$; * = $P < 0.05$; # Square root transformed value

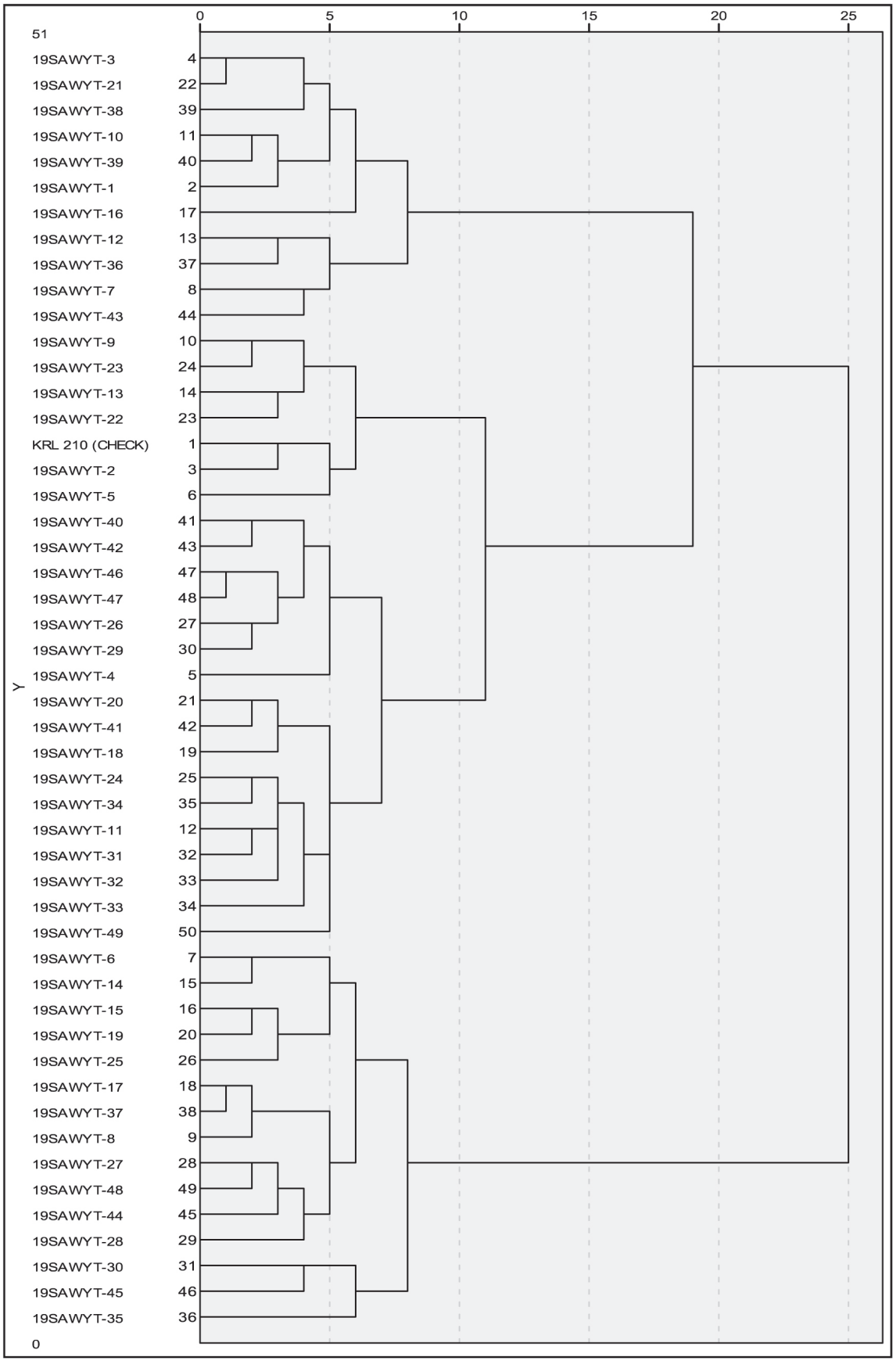

Fig. 2. Dendogram of fifty wheat genotypes based on seven traits

Table 6. Number of genotypes in each cluster

Cluster Number	No of genotypes in each cluster	Entry No.
I	11	2,4,8,11,13,17,22,37,39,40,44
II	24	1,3,5,6,10,12,14,19,21,23,24, 25,27,30,32,33,34,35,41,42, 43,47,48,50
III	15	7,9,15,16,18,20,26,28,29,31, 36,38,45,46,49

crosses should be made using genotypes from different clusters to generate diverse material. Singh *et al*. (2014) clustered 108 wheat genotypes in four groups for salinity and water logging tolerance. Singh *et al*. (2009) also classified 300 wheat genotypes in seven clusters based on agronomic features and salt tolerance using non-hierarchical Euclidean cluster analysis. With the help of sophisticated multivariate techniques, genotypes can be classified based on their agronomic traits which reduce time and money in crop improvement. Eight genotypes having significant yield advantage over check were grouped in cluster II and cluster III. It signifies that genotypes in these clusters are high yielder and can be used as parents for high yield in breeding programmes. Genotypes having good salt tolerance were classified in cluster III followed by cluster II. Thus Cluster I, II and III may be represented by genotypes having low, medium and high salt tolerance, respectively.

Principal component analysis

Principal component analysis (PCA), a multivariate data analysis technique; has been extensively used in plant sciences for data reduction and grouping of genotypes (Khavari *et al.,* 2011). In the present study, covariance matrix was used for PCA. According to principal component analysis, four PCA had Eigen value >1 and accounted for 85.87% of total variance in the data (Table 7). The proportions of total variance attributable to the first four PCs were 28, 26, 16 and 15%. The results showed that HEAD had the highest loadings in PC1 which indicates significant importance of days to 50% heading for this component.BIO and TOL were important traits for PC2; HI and PHT for PC3 and HI and YLD for PC4, respectively. PC1 was mainly associated with phenological trait HEAD which was contributing towards maximum variance. Second and third principal components were associated with yield and salt stress related traits such as BIO, HI and TOL which were contributing maximum variance.

Table 7. Coefficients and Eigen vectors associated with four principal components

Statistics	PC1	PC2	PC3	PC4
Standard deviation	1.41	1.36	1.06	1.03
Proportion of Variance	0.28	0.26	0.16	0.15
Cumulative Proportion	0.28	0.55	0.71	0.86
Eigen Values	1.98	1.84	1.13	1.07
Eigen Vectors				
HEAD	0.63	-0.04	0.16	-0.06
PHT	-0.07	0.02	0.54	-0.70
BIO	-0.06	-0.73	-0.06	-0.02
HI	-0.25	0.34	0.65	0.35
TWT	-0.40	0.02	-0.18	-0.56
TOL	-0.56	0.12	-0.23	0.17
YLD	-0.26	-0.58	0.41	0.22

For abbreviations see text.

Similarly, Zakova and Benkova (2006) identified traits that were the main sources of variation of genetic diversity among 106 Slovakian barley accessions. Cartea *et al.* (2002) and Salihu *et al.* (2006) used PCA and cluster analysis to group kale populations and winter wheat genotypes, respectively.

Conclusion

Genetic variability is prerequisite for improving yield potential and tolerance to abiotic stresses in wheat. Significant variation was noticed among genotypes for key traits having high heritability which can be improved via direct selection. Association study was able to establish relationship of different traits with yield and salinity tolerance. Multivariate data analysis successfully clustered genotypes in groups based on agronomical features. However, further investigation based multi-location/multi-year trial is required to study stability of different traits and mechanism of tolerance operating in these genotypes.

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