Indian Journal of Agricultural Sciences **91** (11): 1684–9, November 2021/Article
https://doi.org/10.56093/ijas.v91i11.118586

Genetic variability and diversity analysis in wheat (*Triticum* spp.) genotypes using multivariate techniques

SUSHMA SHARMA[1], VIKRAM SINGH[1], VIRENDER SINGH MOR[1], RAMESH CHANDER PUNIA[1], HEMENDER[1], SHIKHA YASHVEER[1], MUJAHID KHAN[2]* and SONALI SANGWAN[1]

Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana 125 004, India

Received: 26 March 2021; Accepted: 08 April 2021

ABSTRACT

Thirty-four Indian wheat (*Triticum* spp.) varieties released from 1933 to 2010 were evaluated at CCS Haryana Agricultural University, Hisar (India) for genetic variability and diversity based on their morphological and seed vigour parameters during 2015–16. Significant variations were exhibited by the genotypes for all 26 traits under study. Awn length and dehydrogenase activity had maximum values of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percentage of mean for morphological and seed vigour traits, respectively. In the principal-component analysis of morphological traits, first five principal components accounted for about 77.56% of the total variation. Whereas, first three principal components explained about 84.19% of the total variation for seed vigour parameters. Principal-component analysis score identified variety WH 1105 as most vigorous variety as well potential genotype for morphological traits.

Keywords: Genetic variability, Heritability, Principal-component analysis, Wheat genotype

Importance of wheat is best described by the huge feeding population of humans and their livestock. Wheat is a major crop of India as well as the whole world, on which rests the food security of around 2.5 billion ‘wheat consuming’ people (CIMMYT 2019). Wheat is grown over an area of 200.83 million ha and the grain production exceeds 769.31 million tonnes annually. In India alone, area under wheat cultivation is 31.36 million ha which produces 107.86 million tonnes annually (USDA 2021). The breeding programmes on wheat progress with the ultimate aim of determining the best criteria for selection. These programmes undertake the selection method having genetic bases for grain yield and produce cultivars which would yield more.

Intensive plant breeding has reduced genetic diversity in farmed crops (Tanksley and McCouch 1997). Thus, genetic variety in the germplasm is required for the creation of a successful breeding programme. This makes estimation of germplasm diversity and variability worth studying. In hybridization, the choice of parent should be based on genetic diversity. Characters like grain yield are polygenic and heavily influenced by environmental conditions, making selection challenging. The heritable part is the result of genotype which goes from generation to generation and is an important aspect of any crop improvement strategy (Wright 1921). Genetic advance and heritability estimation would prove helpful in the assessment of gene action. The estimates of heritability along with GCV and genetic advance suggest the amount of possible advancement the selection can provide, and depicts the information which would be needed by the breeder (Amin and Singla 2010). The principal-component analysis provides guidance to researchers to analyze significant relationships among traits (Beheshtizadeh *et al.* 2013). This technique has been previously employed for assessment of trait specific association among multiple genotypes in wheat (Wani *et al.* 2018, Ferreira *et al.* 2019). Therefore, the present study was carried out to estimate the genetic variability, heritability and genetic advance for different traits. Principal-component analysis was performed for identification of potential genotypes and most suitable traits of wheat germplasm for addition in breeding programmes.

MATERIALS AND METHODS

Thirty four Indian wheat (*Triticum* spp.) varieties of hexaploid wheat along with tetraploid wheat (Durum) (30 *Triticum aestivum* and 4 *Triticum durum*) originated from different states (Haryana, Delhi, Punjab, Uttar Pradesh, Uttarakhand and Rajasthan) and of a wide time zone (1933-2010) were evaluated for genetic variability and diversity

---

Present address: [1]CCS Haryana Agricultural University, Hisar; [2]Agricultural Research Station (SKN Agriculture University, Jobner), Fatehpur-Shekhawati, Sikar. *Corresponding author e-mail: mkhanstat@gmail.com.

based on morphological traits and parameters contributing to seed vigour. The field experiment was conducted during 2015–16 in randomized-block design layout with three replicated levels in the fields of Department of Seed Science and Technology, Chaudhary Charan Singh Haryana Agricultural University, Hisar (latitude 29° 09´ 6.70" N, longitude 75° 43´ 16.04" E and altitude 215 m). The site of the field comes under sub-tropical to semi-arid zone. The 34 wheat genotypes were evaluated for the genetic variability and genetic diversity which are as follows with their standard released notification name, C 518, C 306, Kharchia 65, Sonalika, WH 147, HUW 234, HD 2285, Kundan, WH 283, PBW 175, WH 157, WH 542, Kanchan, RAJ 3765, PBW 373, HD 2733, NW 1014, Sonak, UP 2425, KRL 19, MR 1, DBW 14, DBW 16, DBW 17, WH 1025, HD 2967, WH 1105, WH 1124, WH 1129, WH 1138, WH 896, WH 912, WHD 943 and WHD 948.

The data were collected on randomly selected five plants from each replication for the following morphological characters, viz. plant height (PH), no. of productive tillers/plant (TP), flag-leaf length (FLL), flag-leaf breadth (FLB), flag-leaf area (FLA), peduncle length (PL), spike length (SL), awn length (AL), spikelets/spike (SS), spike weight (SW), grains/spike (GS), grain yield/plant (GY. P), biological yield/plant (BY. P) and harvest index (HI). Among the seed vigour parameters, data were generated for test weight (TW), standard germination (SG) (ISTA 1999), seedling length (SL), seedling dry weight (SDW), vigour indices (VI_I and VI_II) as suggested by Abdul-Baki and Anderson (1973), accelerated ageing test (AAT) (AOSA, 1983), dehydrogenase activity (DHA) (Kittock and Law 1968), tetrazolium test (TzT) (Moore 1973), electrical conductivity test (ECT) (ISTA 1999), seedling establishment (SE) and field emergence index (FEI).

Statistical analysis: All the characters were analysed for GCV and PCV (Burton 1952), heritability in broad

Table 1 Mean, variability, heritability and genetic advance as percent of mean for morphological and seed vigour traits of different wheat genotypes

Trait	Mean	Mean square genotype	Mean square error	PCV	GCV	Heritability in broad sense (%)	Genetic advance as percent of mean (%)
Morphological traits							
Plant height	98.97	230.67	45.89	10.47	7.93	57.30	12.37
Tillers/plant	13.59	24.38	4.85	24.81	18.78	57.30	29.28
Flag leaf length	28.02	86.94	3.62	20.00	18.81	88.50	36.45
Flag leaf breadth	2.20	0.248	0.040	15.09	11.97	62.90	19.56
Flag leaf area	46.42	425.36	33.07	27.57	24.63	79.80	45.33
Peduncle length	37.21	91.60	11.18	16.56	13.92	70.60	24.08
Spike length	10.87	10.27	0.43	17.72	16.65	88.30	32.24
Awn length	8.09	17.68	0.378	30.65	29.69	93.80	59.25
Spikelets/spike	19.05	16.83	2.25	14.00	11.57	68.30	19.70
Spike weight	2.77	1.86	0.035	28.90	28.10	94.60	56.30
Grains/spike	48.12	274.56	18.60	21.19	19.20	82.10	35.83
Grain yield/plant	28.89	148.56	2.53	24.77	24.15	95.10	48.50
Biological yield/plant	70.02	472.91	10.40	24.77	24.15	93.70	35.36
Harvest index	41.07	60.12	10.06	12.59	9.94	62.40	16.18
Seed vigour traits							
Test weight	43.42	92.09	0.27	12.80	12.74	99.10	26.13
Standard germination	88.26	157.91	2.56	8.35	8.15	95.30	16.39
Seedling length	22.83	37.75	0.25	15.64	15.48	98.10	31.59
Seedling dry weight	0.14	0.002	0.00002	18.78	15.48	97.30	37.65
Vigour index I	2025	499945	3208	20.28	20.09	98.10	40.99
Vigour index II	12.84	26.13	0.19	23.16	22.90	97.80	46.66
Accelerated ageing test	45.12	65.96	3.92	10.99	10.08	84.10	19.04
Tetrazolium test	93.37	74.18	2.36	5.49	5.24	91.00	10.29
Electrical conductivity test	140	2232	13.5	19.60	19.42	98.20	39.64
Dehydrogenase activity	0.29	0.03	0.00008	33.64	33.50	99.20	68.71
Seedling establishment	75.22	210.95	7.011	11.51	10.96	90.70	21.50
Field emergence index	11.554	8.22	0.672	15.45	13.72	78.90	25.11

sense (Falconer 1981) and genetic advance as percent of mean (Johnson *et al.* 1955). The data were subjected to the principal-component analysis using XLSTAT (version 2014.5.03), for reducing the dimensionality and retaining the variability of the data at the same time. R (version 3.6.0) software was used to display the scatter plots.

RESULTS AND DISCUSSION

Assessment of genetic variations: The distribution of each variable on the diagonal, the bivariate scatters plots with a fitted line below the diagonal and correlation values above the diagonal are presented in Supplementary Figure. About all the traits of wheat genotypes were following normal distribution. Correlation analysis among various morphological traits has been also presented with the help of scatter plots. Grain and biological yields were positively correlated with number of tillers per plant. Flag leaf traits, viz. length, breadth and area showed a positive correlation with spike length and number of spikelets per spike. However, awn length showed minor negative association with all the traits except peduncle length and spike weight. For seed vigour traits, all the correlation values were positive within medium to high categories except electrical conductivity test which exhibited negative correlation with all other seed vigour traits.

The obtained results have shown variability of wider range for morphological and seed vigour traits (Table 1). For all the examined traits, PCV was over heading the GCV indicates the role of environment in the expression of traits, which is in line with the results obtained by Bahera *et al.* (2018), Sunil *et al.* (2017), Tuhina-Khatun *et al.* (2015) and Fathelrahman *et al.* (2015). The difference between GCV and PCV is very less, indicating the least role of environment and explaining the genetic makeup as the cause of major portion of variability in them (Amin and Singla 2010, Osman *et al.* 2012).

In morphological traits, the highest values of PCV and GCV were observed for awn length (30.65 and 29.69% respectively), followed by spike weight (28.90 and 28.10%). On the contrary, plant height (10.47 and 7.93%) showed lowest values. Lower estimates for these traits indicated that the wheat genotypes included in this study were close to mean for these characters and these characters have a scope of improvement through hybridization followed by pedigree selection in advance generation (Gangashetty *et al.* 2013, Bahera *et al.* 2018). The genetic relationship between parent and offspring is measured by narrow-sense heritability. Heritability determines the degree of transmission of a specific trait from one generation to the next and also assists in estimation of genetic gain from that selection. Heritability in broad sense was maximum for grain yield/plant (95.10%), and maximum value of genetic advance as percentage of mean was present for awn length (59.25%). For the seed vigour parameters, dehydrogenase activity has shown the highest values for PCV (33.64%), GCV (33.50%), heritability in broad sense (99.20%) and genetic advance (68.71%). The seed vigour parameters have shown a higher heritability (78.90–99.20%) than the morphological characters (57.30–95.10%). For most of the seed vigour parameters heritability was high (more than 80%) indicating the least effect of environment on them and hence, can be used in formulating selection criteria. Yield contributing traits in maize had also shown high heritability as reported by Ogunniyan *et al.* (2014) and Rafiq *et al.* (2010).

Heritability and genetic advance are better criteria for developing selection to develop superior crop varieties as high heritability does not always yield high genetic gain. The high estimates of heritability and high genetic advance as percentage of mean (identified for awn length, grain yield/plant, spike weight, dehydrogenase activity and vigour index II) are attributed to the simple inheritance and additive gene effects (Singh *et al.* 2014). Characters having high heritability coupled with moderate to low genetic advance as percentage of mean could be due to non-additive gene effects and improvement of these traits can be achieved through hybridization.

Assessment of genetic diversity: The Kaiser-Meyer-Olkin measure of the sampling adequacy tests that the observations given with the sample are adequate or not. Kaiser (1974) recommends a test value above 0.5 is proper for continuing the analysis. The Kaiser-Meyer-Olkin value of 0.338 and 0.742 for morphological and seed vigour traits respectively were acceptable. Bartlett's test of sphericity was another expression for the strength of the association among variables. The Bartlett's test value was significant for both morphological (χ^2 = 423.224) and seed vigour (χ^2 = 568.745) traits. Taken in sync, these tests produce a minimum basic which should be passed before conduction of factor analysis or a principal-components analysis.

Principal-component analysis: Principal-component analysis is an important statistical tool for analysis of multivariate data which transforms a large number of correlated variables into a smaller number of uncorrelated variables, called principal components with minimal information loss. In the present study, the first five principal components accounted for about 77.56% of the total variation for morphological traits and exhibited a very high correlation among them (Table 2). The first five principal components explained about 23.65%, 42.63%, 57.80%, 69.64% and 77.56% of the variation observed in the original variables. In the first principal component, grain yield/plant (0.508), biological yield/plant (0.425) and harvest index (0.406) were the most important contributing traits. Similarly, flag-leaf breadth (0.474) and flag-leaf area (0.468) were important parameters in second principal component.

In the principal component analysis of seed vigour parameters, first three principal components explained about 84.19% of the total variation and exhibited a very high correlation among them (Table 2). First, second and third principal components explained about 55.90%, 74.57% and 84.19% of variation. The most significant contributing characters of first principal component were vigour index I (0.347), standard germination (0.343), vigour index II

Table 2 PC loadings for morphological and seed vigour traits of wheat genotypes

Trait	Morphological					Trait	Seed vigour		
	PC1	PC2	PC3	PC4	PC5		PC1	PC2	PC3
Eigen value	3.31	2.66	2.12	1.66	1.11	Eigen value	6.71	2.24	1.15
% variation	23.65	18.98	15.17	11.84	7.92	% variation	55.90	18.67	9.62
% cumulative variation	23.65	42.63	57.80	69.64	77.56	% cumulative variation	55.90	74.57	84.19
Plant height	-0.262	-0.165	0.685	0.015	0.507	Test weight	0.374	0.345	0.735
Tillers/plant	0.691	-0.542	0.135	-0.220	0.035	Standard germination	0.888	-0.307	0.050
Flag leaf length	0.299	0.466	0.550	0.263	-0.482	Seedling length	0.710	0.626	-0.210
Flag leaf breadth	0.310	0.773	-0.018	-0.129	0.286	Seedling dry weight	0.704	0.649	-0.158
Flag leaf area	0.383	0.763	0.401	0.118	-0.224	Vigour index I	0.899	0.364	-0.152
Peduncle length	-0.123	-0.370	0.473	0.462	-0.192	Vigour index II	0.877	0.421	-0.126
Spike length	0.302	0.417	0.416	-0.144	0.329	Accelerated ageing test	0.772	-0.395	-0.195
Awn length	-0.404	-0.063	-0.304	0.439	-0.189	Tetrazolium test	0.864	-0.116	0.119
Spikelets/spike	0.045	0.475	-0.630	0.042	0.274	Electrical-conductivity test	-0.427	0.590	0.306
Spike weight	0.280	-0.150	-0.207	0.773	0.228	Dehydrogenase activity	0.752	-0.416	-0.262
Grains/spike	0.291	0.147	-0.033	0.692	0.317	Seedling establishment	0.807	-0.278	0.390
Grain yield/plant	0.925	-0.300	-0.107	-0.054	-0.013	Field emergence index	0.679	-0.383	0.367
Biological yield/plant	0.773	-0.497	0.149	-0.016	0.107				
Harvest index	0.738	0.142	-0.457	-0.011	-0.256				

(0.339) and tetrazolium test (0.334), whereas in second principal component, seedling dry weight (0.433), seedling length (0.417) and electrical conductivity (0.393) explained significant contribution. The accountability of first five and three principal components was very high for morphological traits and seed vigour parameters, respectively. The contributing variables in the first principal component of both types of traits could be selected for initiation of a good-breeding program. Many researchers, viz. Habibpour *et al.* (2012) and Beheshtizadeh *et al.* (2013), Tuhina-Khatun *et al.* (2015), Vandenberg *et al.* (2019) have also attempted principal component analysis for obtaining the percentage of variation explained by various characters studied.

Principal component analysis score-based identification of genotypes were attempted and loading plots were also constructed. For morphological traits, WH 1105 (5.322), Kharchia 65 (-4.462), HD 2967 (2.973) and HD 2285 (2.491) were identified to be the best scorers in first principal

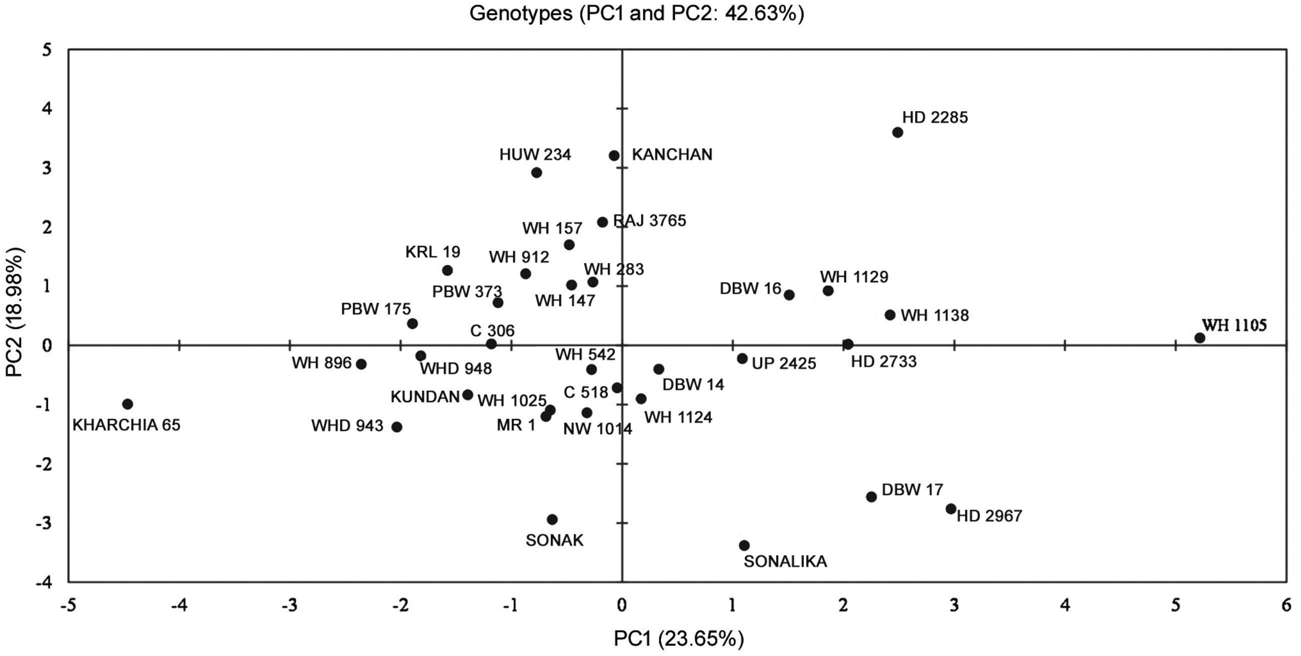

Fig 1 Loading plot of genotypes for morphological traits.

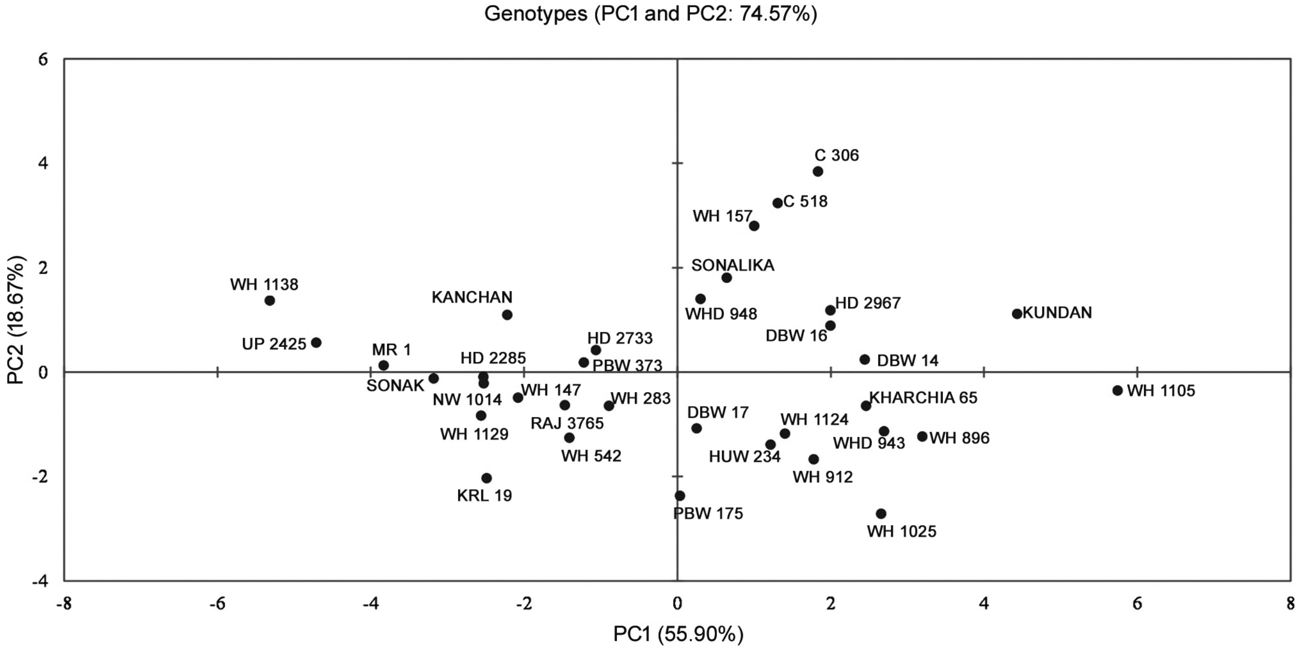

Fig 2 Loading plot of genotypes for seed vigour traits.

component while, HD 2285 (3.593), Sonalika (-3.388), Kanchan (3.200) and Sonak (-2.949) had highest score in second principal component (Fig 1). In first principal component of seed vigour parameters, the best varieties identified were WH 1105 (5.743), WH 1138 (-5.313), UP 2425 (-4.709) and Kundan (4.434), whereas in case of second principal component, C 306 (3.839), C 518 (3.229), WH 157 (2.794) and WH 1025 (-2.720) were found more vigorous (Fig 2). Varietal identification based on principal-component analysis is also reported by Riaz *et al.* (2018).

The present investigation has identified the considerable levels of diversity prevailing among the 34 genotypes of Indian wheat. Grain yield/plant, spike weight, awn length and dehydrogenase activity were identified to be the characters having high heritability demonstrating their successful transmission to offspring's if hybridization programmes rest their selection on them. Awn length, flag-leaf area, grain yield/plant, spike weight, DHA and vigour index I & II had high genetic advance as percentage of mean. Genotype, WH 1105 was identified as significant breeding material for morphological and seed vigour traits.

REFERENCES

Abdul-Baki A A and Anderson J D. 1973. Vigour determination in soybean seed by multiple criteria. *Crop Science* **13**: 630–33.

Amin A and Singla J. 2010. Genetic variability, heritability and genetic advance studies in carrot (*Daucus carota* var. sativa L.). *Electronic Journal of Plant Breeding* **1**: 1504–08.

Association of Official Seed Analysts. 1983. *Seed vigor testing handbook (Contribution to the handbook on seed testing no. 32)*. Ithaca, New York, p 93.

Beavers A S, Lounsbury J W, Richards J K, Huck S W, Skolits G J and Esquivel S L. 2013. Practical considerations for using exploratory factor analysis in educational research. *Practical Assessment, Research and Evaluation* **18**: 1–13.

Behera B, Sahu S, Kar R K and Pandey R K. 2018. Studies on genetic variability for some metric traits in slender grain rice genotypes. *Journal of Applied and Natural Science* **10**: 375–78.

Beheshtizadeh H, Rezaie A, Rezaie A and Ghandi A. 2013. Principal component analysis and determination of the selection criteria in bread wheat (*Triticum aestivum* L.) genotypes. *International Journal of Agriculture and Crop Science* **5**: 2024–27.

Burton G W. 1952. Quantitative inheritance in grasses. *(In) Proceeding of 6th International Grassland Congress,* Pennsylvania State College, United States, pp. 277-83.

CIMMYT. 2019. https://wheat.org

Falconer D S. 1981. *An Introduction to Quantitative Genetics*. Longman, New York, p 45.

Fathelrahman S A, Alsadig A I and Dagash Y I. 2015. Genetic variability in rice genotypes (*Oryza sativa* L.) in yield and yield component under semi-arid zone (Sudan). *Journal of Forest Products and Industries* **4**: 21–32.

Ferreira M H, Rocha B H, Silva G H and Macedo W R. 2019. Multivariate analysis for wheat genotypes cultivated in Brazilian Savanna (Cerrado). *Poljoprivreda i Sumarstvo* **65**(4): 183–92.

Gangashetty P I, Salimath P M and Hanamaratti N G. 2013. Genetic variability studies in genetically diverse non basmati local aromatic genotypes of rice (*Oryza sativa* L.). *Rice Genomics and Genetics* **4**: 4–8.

Habibpour M, Ahmadizadeh M and Shahbazi H. 2012. Assessment relationship between agro-morphological traits and grain yield in bread wheat genotypes under drought stress condition. *African Journal of Biotechnology* **11**: 8698–704.

ISTA. 1999. International rules for seed testing. *Seed Science and Technology* **23**: 1–334.

Johnson H W, Robinson H F and Comstock R E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal* **47**: 314–18.

Kaiser H. 1974. An index of factor simplicity. *Psychometrika* **39**: 31–36.

Kittock D L and Law AG. 1968. Relationship of seedling vigour to respiration and tetrazolium chloride reduction by germinating wheat seeds. *Agronomy Journal* **60**: 286–88.

Moore R P. 1973. Tetrazolium staining for assessing seed quality. *Seed Ecology*, pp. 347–66. Heydecher W (Ed). Butterworth, London.

Ogunniyan D J and Olakojo S A. 2014. Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Nigerian Journal of Genetics* **28**: 24–28.

Osman K A, Mustafa A M, Ali F, Yonglain Z and Fazhan Q. 2012. Genetic variability for yield and related attributes of upland rice genotypes in semi-arid zone (Sudan). *African Journal of Agricultural Research* **7**: 4613–19.

Rafiq CM, Rafique M, Hussain A and Altaf M. 2010. Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). *Agricultural Research* **48**: 35–38.

Riaz A, Bibi T, Raza Q, Sabar M and Akhter M. 2018. Evaluation of rice (*Oryza sativa* L.) advance uniform lines using multivariate analysis. *African Journal of Plant Science* **12**: 284–89.

Singh J, Prasad L C, Madakemohekar A H and Bornare S S. 2014. Genetic variability and character association in diverse genotypes of barley (*Hordeum vulgare* L.). *Bioscan* **9**: 759–61.

Sunil, Sehrawat K D and Khan M. 2017. Investigation of genetic variability for yield and yield related traits in barley (*Hordeum vulgare* L.) genotypes. *Indian Journal of Ecology* **44**: 869–72.

Tanksley S D and McCouch S R. 1997. Seed banks and molecular maps: unlocking genetic potential from the wild. *Science* **277** (5329): 1063–66.

Tuhina-Khatun M, Hanafi M M, Yusop M R, Wong M Y, Salleh F M and Ferdous J. 2015. Genetic variation, heritability and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *BioMed Research International* **2015**: 1–8.

USDA. 2021. United States Department of Agriculture. https://ipad.fas.usda.gov

Vandenberg A and Stoddard F L. 2019. Genetic analysis of photosynthesis-related traits in faba bean (*Vicia faba)* for crop improvement. *Plant Breeding* **00**: 1–9.

Wani S H, Sheikh F A, Najeeb S, Sofi M, Iqbal A M, Kordrostami M, Parray G A and Jeberson M S. 2018. Genetic variability study in bread wheat (*Triticum aestivum* L.) under temperate conditions. *Current Agriculture Research Journal* **6**(3): 268–77.