Exploring the genetic variability for yield attributing traits among the Indigenous and Exotic collection of wheat in Cis-Himalayan region of West Bengal, India

Abstract

A field experiment was conducted at Instructional Farm, Uttar Banga Krishi Viswavidyalaya, during the 2018-19 rabi season to study the genetic components and genetic variability based on eleven number of quantitative traits in 254 bread wheat lines, which were collected from NBPGR, New Delhi. Analysis of variance for treatment showed high significance for all the traits except grain yield polt^{-1}. Estimated GCV and PCV were high for awn length, peduncle length, plant height and AUDPC. Plant height (97.83), awn length (95.49), peduncle length (94.88), test weight (90.98), days to 50% flowering (87.66), number of grains spike^{-1} (70.33) and spike length (62.3) showed high heritability along with a high degree of genetic advance. Finally, 254 wheat accessions were grouped into three clusters based on the dendrogram analysis using the ward method.

Key word: Wheat, Genetic components, Genetic variability and Ward method.

Introduction

Wheat is the most widely grown crop and staple food across the world. It plays an important role in human nutrition. It accounts for 20% of total calories consumed by millions of people who follow wheat-based diets (Goel et al., 2018).It provides 40% of their dietary intake of crucial micronutrients such as zinc, iron, manganese, magnesium, and vitamins B and E (Velu *et al.*, 2017). Wheat productivity must increase by more than 50% by 2050 to meet demand as the human population continues to grow (Tadesse *et al.*, 2019). Breeders face challenges in increasing current output levels of wheat production as the growing population of the world requires a higher amount of production than is currently available (Rahman *et al.*, 2021). It is not possible to expand the production area, hence, the only option is to boost the productivity by developing superior varieties and improving the agronomic production management in order to meet the rising food demands (Pradhan *et al.*, 2015).

Plant breeding with the help of the information from quantitative genetics is considered an active programme and selection is vastly effective when it depends on the presence of genetic variation within the accessions. Breeding for crop improvement is based on genetic richness and the selection of suitable genotypes. The study of genetic variability in plants is an important argument that provides a superior resolution for plant breeders to develop novel improved genotypes with desired traits (Govindaraj et al., 2015). Before selecting the most desirable genotypes, breeders want to assess genetic components such as phenotypic coefficient of variation, genotypic coefficient of variation, environmental coefficient of variation, heritability, genetic advance, etc., which are essential to estimate the genetic richness and superiority of any particular genotype (Atinafu *et al.*, 2020). It also helps in determining the effectiveness of selection for a particular trait in that genotype to get improved cultivars (Atinafu *et al.*, 2020).

The present study was conducted at Cis-Himalayan plains of West Bengal which is located in the terai region where rice is the predominant crop with the rice-wheat cropping system being prevalent in adjoining areas with rice prevailing during the monsoon season and wheat in the rabi season. The major problems for wheat cultivation in this region include short winter, early onset of monsoon, micro nutrient deficiency along with prevalence of foliar diseases such as spot blotch etc. To combat these issues the present study was undertaken with 254 wheat genotypes of both exotic and indigenous collection from NBPGR to study the genetic variability along with estimation of genetic components for selection of suitable genotypes in this region.

Materials and Methods

Field research was conducted in Instructional Farm, Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar, West Bengal, during rabi season of 2018-19, for morphological characterization and screening for spot blotch of 254 wheat accessions.The experimental field is situated at 26° 24′ 16.11″ N latitude, 89° 23′ 1.69″ E longitude and at an altitude of 43 m above the mean sea level. The wheat collections were consisted with two hundred indigenous accessions and fifty-four exotic accessions which were collected from ICAR-National Bureau of Plant Genetic Resources, New Delhi, India. All the genotypes were evaluated in Augmented Block Design (ABD) with four checks HD 2967, BHU 35, UBW 9 (highly resistant to moderately resistant to spot blotch) and Sonalika (susceptible to spot blotch disease). Each genotype was grown in three rows in 100 × 75 cm^2 plot size. The recommended cultural and agronomic practices were implemented to raise good crop (Mondal *et al.,* 2018). Field screening for spot blotch disease was done by creating disease pressure using Sonalika (susceptible check) in throughout the border. AUDPC and rAUDPC were calculated according to Chattopadhyay *et al.,* (2021). All the data were recorded for 11 morphological characters *viz.,* flag leaf length (FL) and width (FW), days to 50 % heading (DF), plant height (PH), spike length (SL), peduncle length (PL), number of grains spike^{-1} (NG), awn length (AL), 1000 grain weight (TW), grain yield (YL) along with rAUDPC (AU) for spot blotch disease. All the statistical analysis were done by using “augmented RCBD” package in R v. 3.6.0 software.

Result and discussion

Mean performances and ANOVA

The average days to 50% flowering was 77.65 days, which varied from 57.13 (IC574387) to 120.38 (IC542063) days. Among the 254 genotypes, EC534432, IC527929, IC28622, IC28872, IC28554, IC252742 and IC335683 showed early flowering. The plant height ranged from 65.3 cm (IC576640) to 172.55 cm (EC576578) with an average value of 102.88. Some short height genotypes (IC530005, EC575981, IC416043, IC415870 and IC530086) were observed within the 254 accessions, which are important for making dwarf populations in the breeding program. The average flag leaf length was 23.43 cm and it varied from 14.35 to 46.92 cm. The highest flag leaf length was observed in IC539313 and the genotype EC187159 had the lowest flag leaf length. The mean flag leaf width was 1.72 and it ranged from 0.98 to 2.99. Genotype IC539313 showed the highest width length, whereas EC575732 showed the lowest width length. Plants with increased leaf area produced more photosynthates, which increased grain yield per plant (Weraduwage et al., 2015). Variability in spike length ranged from 5.95 cm to 20.95 cm with a mean value of 10.68 cm. EC445374 had the lowest spike length and the highest spike length was observed in IC531862. Variability in peduncle length ranged from 4.76 cm in IC445528 to 42.9 cm in IC529196 with a mean value of 20.13 cm. The awn length ranged from 0 to 16.31 cm with an average value of 6.42. It was observed that, among the 254 genotypes, only nine accessions (IC529052, IC530086, IC584159, EC576591, EC577738, EC10970, IC144903, EC576578 and IC406521) were awn less and noted as 0. The number of grains spike^{-1} ranged from 41.65 to 109.57, with an average of 71.84. The genotype IC28755 showed the lowest number of grains and IC539313 showed the highest number of grains spike^{-1}, respectively. The test weight of grain ranged from 16.88 g in IC539314 to 49.54 g in IC542076 with the value mean vale of 29.72 g. Grain yield plot^{-1} varied from 48.49 g to 537.24 g with an average of 264.18 g. IC393877 and IC35715 possessed the minimum and maximum number of grain yield plot^{-1}, respectively. Yield was also high for IC530058 (503.49g), IC445425 (504.99g) and IC402042 (516.74g), which are the promising genotypes for future breeding programmes. The average rAUDPC for spot blotch disease was 13.61 and it varied from 4.12 to 28.32. . IC527448, EC339632, EC187159, IC539313, and EC463396 had the lowest rAUDPC, while IC252954 had the highest. This indicated higher degree of variability for disease resistance reactions against spot blotch. The mean performance of 254 genotypes for 11 characters were represented in the supplementary table 1.

The analysis of variance of 254 genotypes of wheat for 11 quantitative characters, *viz.*, awn length, days to 50% flowering, ear length, flag leaf length, flag leaf width, number of grains spike^{-1}, plant height, length of peduncle, test weight, and grain yield along with rAUDPC of spot blotch is presented in Table 1. Mean squares due to block for all the above characters except flag leaf length were highly significant, indicating the adequacy of the block for statistical analysis of the characters. Mean squares due to genotypes for all the above-mentioned characters except grain yield plot^{-1} were highly significant which indicated presence of genetic variability among the experimental materials. Mean squares due to checks for all the above characters were highly significant, which indicated the presence of genetic variability among the check materials too, whereas interaction between check and accession was significant for all the above characters except grain yield plot^{-1} which indicated differential performance of the genotypes under different crop growing conditions.

Table 1: Analysis of variance for eleven quantitative characters in wheat

Source	Df	DF	PH	FL	FW	EL	PL	AL	NG	TW	YL	AU
Block	24	374.76**	1303.74**	8.71^{ns}	0.11**	3.61**	80.88**	3.84**	626.19**	33.99**	23452.94**	27.02**
Total entries	253	131.53**	329.02**	17.45**	0.1**	4.99**	31.6**	6.46**	192.3**	39.35**	9943.17^{ns}	26.61**
Check	3	1001.4**	913.79**	163.18**	1.43**	82.53**	134.37**	10.87**	1632.25**	768.09**	36605.57**	773.78**
Check x Accessions	250	121.09**	322**	15.71**	0.09**	4.06**	30.37**	6.4**	175.02**	30.6**	9623.22^{ns}	17.64**
Residuals	72	19	9.48	6.08	0.03	1.43	1.91	0.3	48.48	2.66	7390.89	9.41

Estimation of Genetic components

According to Singh and Chaudhary (1979), estimated genotypic and phenotypic coefficients of variation (GCV and PCV) were analysed and classified into three categories: low (10%), moderate (10-20%), and high (> 20%).On the basis of the above grouping, days to 50% flowering, flag leaf length, flag leaf width, spike length, number of grains spike^{-1}, test weight had moderate GCV and PCV, whereas awn length, peduncle length, plant height, and rAUDPC showed high GCV and PCV. Moderate GCV and high PCV were observed for grain yield plot^{-1} (Supplementary table 2). Similar results were reported for moderate GCV and high PCV for spike length (Gerema, 2020), for number of grains spike^{-1} (Dhananjoy *et al*, 2012; Singh *et al*, 2013), for flag leaf area (Singh *et al.*, 2013), for days to 50% flowering (Kolakar *et al.*, 2012). High GCV and PCV were reported for plant height (Singh *et al.*, 2013), for peduncle length (Kumar *et al.*, 2016) and for AUDPC (De *et al.*, 2014). Elevated magnitude between GCV and PCV were observed for flag leaf length, flag leaf width, ear length, number of grains spike^{-1}, plot yield along with rAUDPC values for spot blotch indicating higher influence of environmental factors in expression of these characters (Figure 1). Very low difference was observed for awn length, days to flowering, plant height and test weight indicating low sensitivity to environment and consequently greater role of genetic factor influencing the expression of these characters. This also revealed the effectiveness of selection for genetic improvement of those characters which have lower impact of environmental factors.

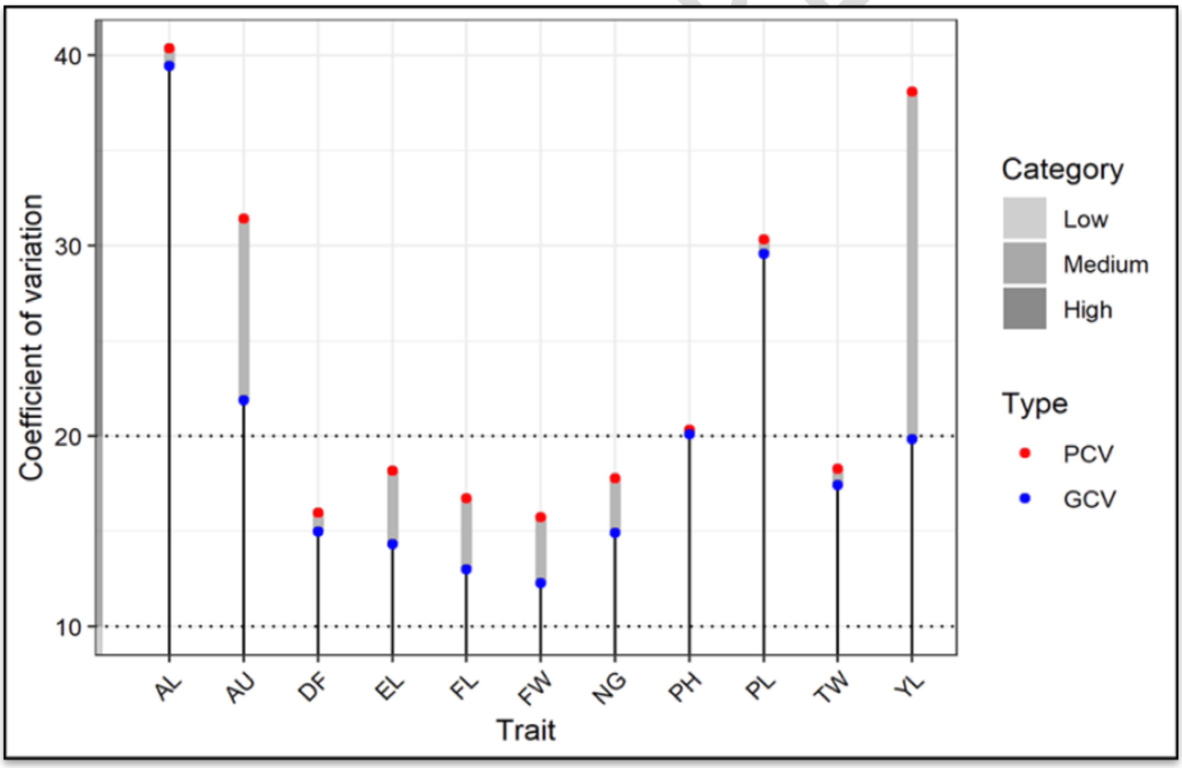

Fig 1. Estimated GCV and PCV of eleven quantitative traits for 254 wheat accessions

The high heritability in the broad sense (Figure 2) was found for characters such as plant height (97.83), awn length (95.49), peduncle length (94.88), test weight (90.98), days to 50% flowering (87.66), number of grains spike^{-1} (70.33), spike length (62.3), whereas moderate to low heritability (Figure 2) was found for rAUDPC (48.59) and grain yield plot^{-1}(27.06). Similar results have been reported for plant height and test weight (Singh and Upadhyay, 2013; Devesh *et al.*, 2018; Hossain *et al*, 2021); awn length (Teich, 1984); for peduncle length (Baranwal *et a.l*, 2012; Shehrawat and Kumar, 2021), days to 50% flowering (Fellahi *et al.*, 2013; Baranwal *et al.*, 2012), number of grains spike^{-1} (Ullah *et al*, 2012; Fellahi *et al.*, 2013, Roy *et al.*, 2021), spike length (Birhanu *et al.*, 2016).

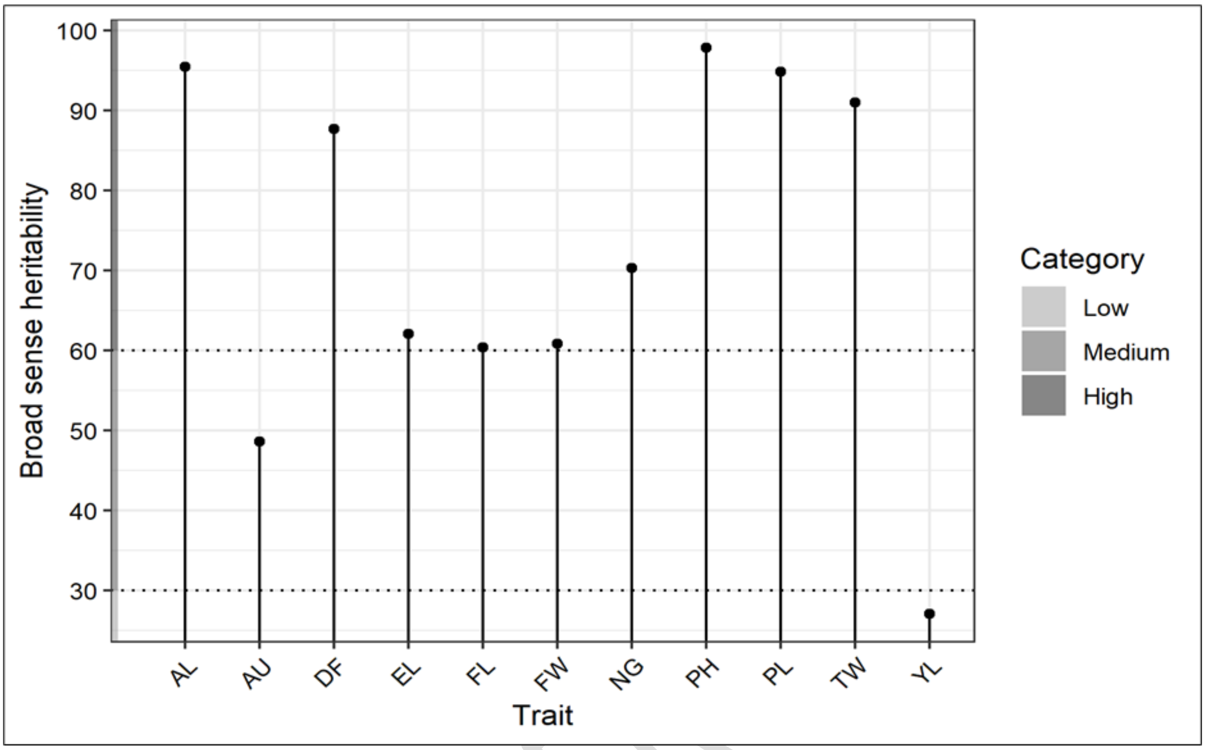

Fig 2. Estimated broad sense heritability of eleven quantitative traits for 254 wheat accessions

According to Falconer and Mackay (1996), genetic advance as a percentage of mean (GAM) was classified as low (15%), moderate (15-20%), and high (> 20%), as shown in Figure 3. Based on the results, GAM was high for awn length (79.51), peduncle length (59.4), plant height (41.01), test weight (34.31), rAUDPC (31.49), days 50% to flowering (28.9), number of grains spike^{-1} (25.81), spike length (23.29), grain yield plot^{-1} (21.27) and flag leaf length (20.84), whereas moderate for flag leaf width (19.78). Similar results were obtained earlier for peduncle length and number of grain spike^{-1} (Baranwal *et al.*, 2012), test weight and plant height (Fellahi *et al.*, 2013), grain yield plot^{-1} (Birhanu *et al.*, 2016), spike length and days to 50% flowering (Belay and Fisseha, 2021), and flag leaf width (Ahmad, 2017).

High genetic advance coupled with high heritability was observed in days to 50% flowering, number of grain spike^{-1}, test weight, awn length, peduncle length and flag leaf length, which are important characters for selection of genotypes in a breeding programme. These results helped in a good understanding of heritability and genetic advance present in different yield contributing characters, which are the first options for crop improvement (Larik *et al.*, 1999).

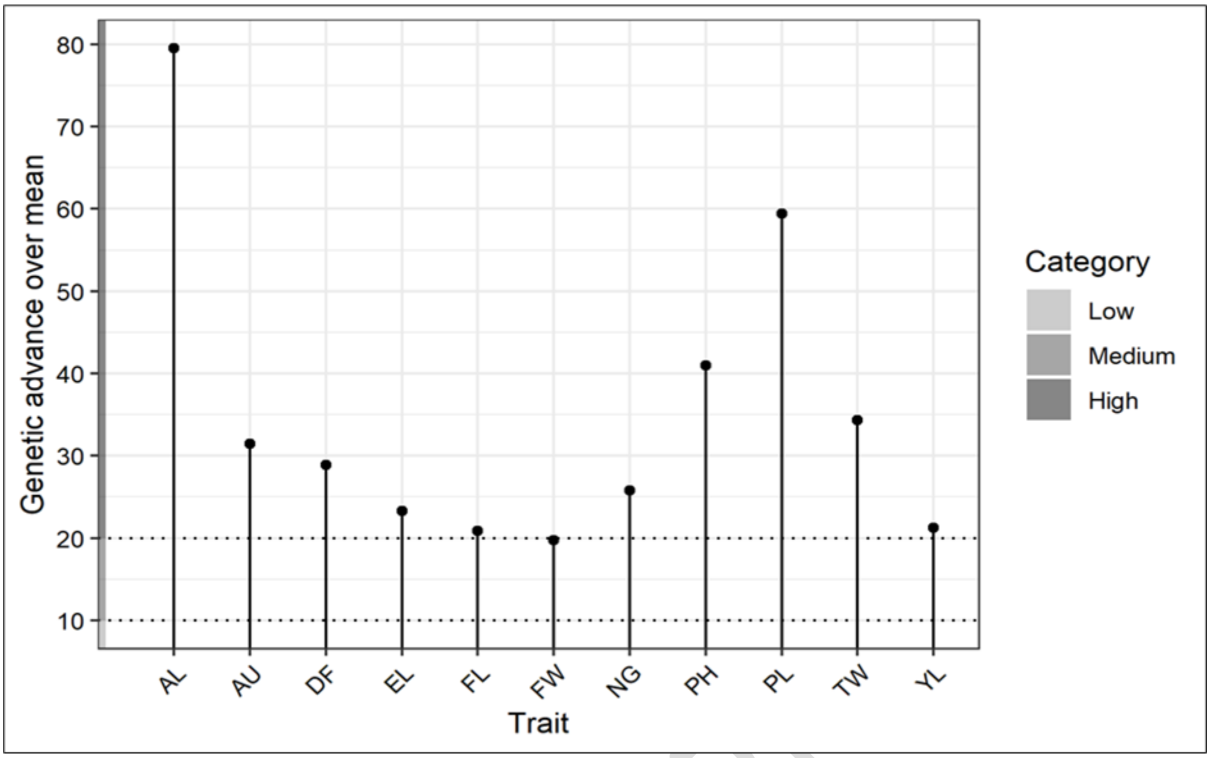

Fig 3. Estimated genetic advance in percent of mean of eleven quantitative traits for 254 wheat accessions

Genetic variability

Genetic variability was detected through dendrogram analysis for 254 genotypes utilizing 11 quantitative traits. In the present investigation, dendrogram analysis was performed with four different methods (“complete” “average” “single” and “ward”) and finally the “ward method” was considered based on the higher agglomerative coefficient value (Table 2).

Table 2: Different methods for dendrogram analysis with their agglomerative coefficient value

Method	**Agglomerative coefficient**
Complete	0.85
Average	0.75
Single	0.56
Ward	0.92

According to the dendrogram (Figure 4), all the wheat accessions were grouped into 3 distinct clusters. Cluster I (red) consisted of 132 genotypes, whereas cluster II (green) included 82 genotypes and cluster III (black) had 40 genotypes. This finding indicated that great genetic variability existed among the 254 wheat genotypes, which is an important key factor for future breading programmes. Similar results for dendrogram analysis were reported by Pujar *et al.*, 2020 and Sansaloni *et al.*, 2020.

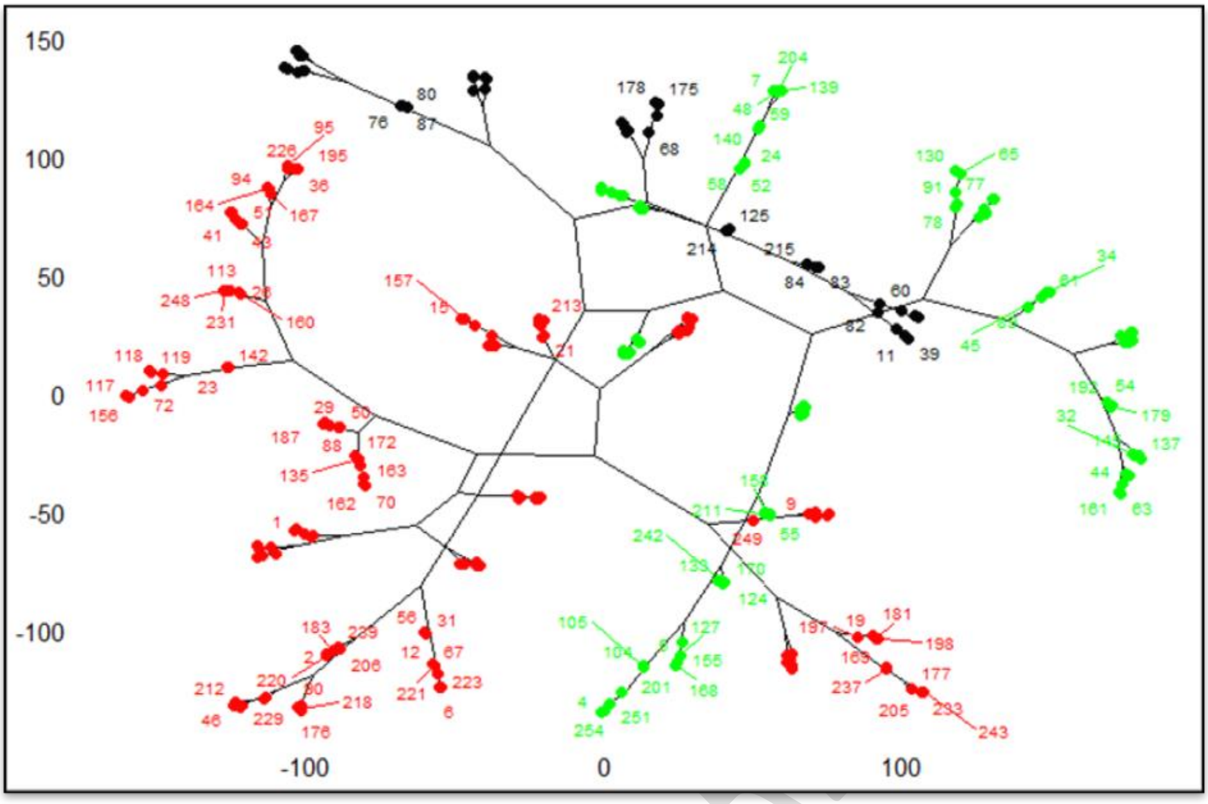

Fig.4. Dendrogram based on the ward method for 254 wheat genotypes utilizing eleven quantitative traits

Conclusion

Overall, the findings indicated that eleven quantitative traits explored a significant and extensive amount of genetic diversity among 254 wheat varieties. The dendrogram analysis will be helpful for selecting diverse parents in a breeding programme and for preserving the genetic diversity of the present wheat germplasm.

COMPETING INTERESTS DISCLAIMER:

The authors have declared that no competing interests exist. The products used for this research are commonly and predominantly used products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company; rather, it was funded by the personal efforts of the authors.

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