

*Full Length Research Paper*

# Assessment relationship between agro-morphological traits and grain yield in bread wheat genotypes under drought stress condition

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To evaluate the genetic diversity in bread wheat landraces along with six controls (Azar2, Fankang, Trakia, Siosson, Gaspard and Gascogne), an experiment based on randomized complete block design with three replications was carried out under drought stress condition in the Agricultural Research Station of Islamic Azad University, Ardabil, Iran. Analysis of variance indicated that there were highly significant differences among the genotypes in all of the traits. There were significant correlations between yield and all of the studied traits. Principal components (PC) analysis showed that five components explained 69.3% of the total variation among traits. The first PC assigned 29% and the second PC assigned 15% and of total variation between traits. The first PC was more related to tiller numbers, fertile tillers, biological yield, grain yield and volume of seed plants. Therefore, selection based on first component is helpful for a good hybridization breeding program. A principal component biplot showed low distance between grain yield and biological yield, volume of seed, plant height and hectoliter. From this study, it was concluded that a good hybridization breeding program can be initiated by the selection of genotypes from the PC1.

**Key words:** Bread wheat, biplot, landrace, drought stress, agronomic traits.

## INTRODUCTION

Wheat landraces are valuable sources to broaden the genetic base of cultivated wheat. The genetic structure of wheat landraces is an evolutionary approach to survival and performance, especially under arid and semi-arid growing conditions (Zou and Yang, 1995). In many parts of the region wheat production is replaced by modern cultivars, landraces are only cultivated by farmers in very limited areas. This landrace replacement by homogeneous cultivars has resulted in a significant loss of genetic variation in resistance to abiotic stresses. Landraces are usually tolerant to stress (Davood et al., 2004). Therefore, it is necessary to investigate genetic diversity in the currently used wheat germplasm in order to maintain a desirable level of genetic variation in future

wheat breeding. The development of high yielding wheat cultivars is a major objective in breeding programs (Ahmadizadeh et al., 2011a). Drought stress is an important limiting factor which can cause major loss in wheat productivity in arid and semi areas (Ahmadi et al., 2009). It has been estimated that up to 45% of the world agricultural lands are subjected to drought (Bot et al., 2000). Improving drought tolerance and productivity is the most difficult task for cereal breeders because of the diverse strategies adopted by plants at various stages of development among the species and cultivars to cope with water stress (Rajiv et al., 2010; Ahmadizadeh et al., 2011b).

Almost 32% of wheat culture confronts various types of drought stress during the growth season in developing countries (Shamsi, 2010). The development of high yielding wheat cultivars is a major objective in breeding programs (Leilah and AL-khateed, 2005). It is obvious that besides the yield, it is necessary to include some

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other (adapted) traits related to good resistance to drought into wheat breeding for drought conditions.

The enhancement in yield in most situations is more effectively fulfilled on the basis of performance of yield components, which are closely associated with grain yield (Ashfaq et al., 2003; Ahmadi et al., 2009). Moreover, the response of plants to drought stress depends on several factors such as developmental stage, severity and duration of stress and cultivar genetics (Beltrano and Marta, 2008).

The various yield components including plant height, number of tillers per plant, flag leaf width, flag leaf length, peduncle length, biological yield, spike length, awn length, number of grains per spikelet, number of grains per spike, 1000 grain weight and grain yield per plant were studied to evaluate the relationship of yield and its components under drought condition in wheat (Attarbashi, et al., 2002; Ashfaq et al., 2003; Blum, 2005; Khan et al., 2010). Guinata et al. (1993) showed that drought stress reduced all yield components so that number of fertile spikes as well as number of grains per spike was decreased by 60 and 48%, respectively. Drought stress can reduce grain yield, and an average yield loss of 17 to 70% in grain yield has been estimated due to drought stress (Nouri-Ganbalani et al., 2009).

Principal component analysis (PCA) identifies plant traits which characterize the distinctness among selected genotypes. They are often extended to the classification of a population into groups of distinct orders based on similarities in one or more characters, and thus guide in the choice of parents for hybridization (Nair et al., 1998; Afuape et al., 2011). The PCA has been used to partition observed agronomic variations in genotypes of many crops such as rubber (Omokhafa and Alike, 2000), sweet potato landraces (Afuape et al., 2011), rice (Nassir, 2002), sesame (Mponda et al., 1997) and durum wheat (Ahmadizadeh et al., 2011c). The purpose of this research was to investigate the genetic diversity in bread wheat landraces, determining effective traits on yield under drought stress condition.

## MATERIALS AND METHODS

In order to study the genetic diversity of bread wheat, 140 wheat (*Triticum Aestivum* L.) landraces selected from the collection of "Research Institute on Breeding and producing Seed and Seedling, Iran" along with six controls (Azar2, Fankang, Trakia, Siosson, Gaspard and Gascogne) was evaluated under drought stress condition based on randomized complete block design with three replications, the experiment was carried out in the agricultural research station of Islamic Azad University, Ardabil Branch, Northwest of Iran, during the 2009 and 2010 cropping year. Plot size was 6 × 1.5 m. The studied characters were number of tillers, number of fertile tillers, biological yield, plant height, peduncle length, spike length, awn length, number of grains per spikelet, number of grain per spike, flag leaf width, flag leaf length, 1000 grain weight, volume of seed plants, hectoliter and grain yield. Pearson's correlation was used to evaluate the relation between traits used. The data were statistically analyzed by SPSS-16 and Minitab-15 softwares.

## RESULTS AND DISCUSSION

Results from analysis of variance indicated that there was significant difference between the genotypes in terms of studied traits (Table 1). This represents a high variation among the genotypes to be used for selection of lines tolerant against drought stress and in various breeding programs. Garsia Del- Moral et al. (2003) reported meaningful differences between their studied genotypes for grain yield, number of grain per spike and grain weight. Ahmadizadeh et al. (2011a) while studying the genetic variation of durum wheat landraces from Iran and Azerbaijan indicated that there were highly significant differences among the genotypes in all of the morphological traits.

Result of correlation between the traits indicated that grain yield had the positively highest significant correlation with biological yield (Table 2). Sinebo (2002) and Kirigwi et al. (2004) have also reported similar results. Significant relationships between yield and biological yield have been reported in barley (Ramos et al., 1985) and durum wheat (Villegas et al., 2001; Ahmadizadeh et al., 2011b). Plant breeding for increasing biological yield is a method for improving grain yield rate in the small grain cereals (Boukerrou and Rasmusson, 1990). There was a positively significant correlation observed between grain number per spike, spike length and grain yield (Table 2). This means that increased yield of genotypes under stressed conditions was not a result of increased weight of 1000 grains, rather a result of increased spike length and grain number per spike. Positive correlation between awn length and grain yield was indicative of the importance of this trait in improving yield under drought stress condition. Such a relation is due to the ability of plants carry out photosynthesis through awns and lower transpiration rate on the surfaces of these organs (Leilah and AL-khateed, 2005; Naghavi et al., 2002). Evans and Wardlaw (1996) argued that peduncle of wheat due to its higher green area, highly intensive photosynthesis and proximity to spike plays an important role in grain filling. Some other authors attributed the positive correlation between peduncle length and grain yield of wheat to the accumulation of photosynthetic materials in this organ and their remobilization into the grains being filled (Ehdaie et al., 2006). It seems that the stored materials found in stem and particularly in peduncle, contribute more in grain filling under stressed condition through decrease of current photosynthesis (decrease of source power) and demand of grains for photosynthetic materials than under normal condition. In this experiment, as in others, there was a positive significant correlation between peduncle length and grain yield of plant. Plant height had a positive correlation with biological and grain yields of plant (Table 2). Ehdaie and Waines (1996) indicated that although wheat landraces are of lower yielding capability than dwarf ones, they have higher yield stability under terminal drought stress conditions.

**Table 1.** Mean squares of yield and yield components of 146 bread wheat genotypes under drought stress condition.

S.O.V	df	Mean square														
		Number of tillers	Number fertile tillers	Biological yield	Plant height	Peduncle length	Spike length	Awn length	Number grains per spikelet	Number grain per spike	Grain yield	Flag leaf width	Flag leaf length	1000 grain weight	Volume of seed plants	Hectoliter
Replication	2	500.11**	441.86**	1145980.66**	1334.94 <sup>ns</sup>	129.40 <sup>ns</sup>	107.67 <sup>ns</sup>	60.42 <sup>ns</sup>	0.15 <sup>ns</sup>	12.52 <sup>ns</sup>	62673.76**	2.70 <sup>ns</sup>	863.75 <sup>ns</sup>	27768.46 <sup>ns</sup>	1174.53**	117477.53**
Genotype	145	91.48**	78.50**	454376.56**	147445.36**	11957.15**	1551.19**	4459.29**	1.99**	2392.23**	17303.58**	19.84**	4142.71**	83380.15**	265.26**	26408.78**
Error	290	7.880	7.640	104173.14	8338.081	1280.76	132.19	50.09	0.141	20.25	1828.73	1.34	414.17	27847.17	32.40	3245.99

\*\*,\* and ns, significant at 1%, 5% level of probability and non-significant, respectively.

**Table 2.** Correlation between yield and yield components under drought condition.

Yield component	Number Tillers	of Fertile Tillers	Biological yield	Plant Height	Peduncle Length	Spike length	Awn Length	Number of grains per spikelet	Number of grain per Spike	Grain yield	Flag leaf width	Flag leaf length	leaf 1000 weight	grain Volume of seed plants
Number of fertile tillers	0.886**													
Biological yield	0.515**	0.501**												
Plant Height	0.223**	0.225**	0.307**											
Peduncle length	0.202**	0.204**	0.099*	0.249**										
Spike length	0.201**	0.185**	0.199**	0.464**	0.140**									
Awn length	0.113*	0.117*	0.203**	0.093	-0.067	0.272**								
No. of grains per spikelet	-0.131**	-0.165**	0.251	0.246**	-0.326**	0.162**	0.209**							
No. of grain per spike	-0.264	-0.350	0.229	-0.181**	-0.244**	0.177**	0.276**	0.273**						
Grain yield	0.636**	0.653**	0.781**	0.476**	0.490**	0.516**	0.413**	0.443**	0.536**					
Flag leaf width	-0.053	-0.045	0.076	-0.019	-0.176**	-0.018	0.078	0.333**	0.144**	0.153**				
Flag leaf length	0.155**	0.161**	0.148**	0.134**	-0.225**	0.169**	0.175**	0.048	0.086	0.175**	0.315**			
1000 grain weight	0.126*	0.128*	-0.123*	0.135	0.111*	0.131	-0.123**	-0.116*	-0.126*	-0.12*	-0.108	0.007		
Volume of seed plants	0.694**	0.722**	0.579**	0.300**	0.122*	0.246**	0.225**	0.079	0.048	0.875**	0.250**	0.259**	-0.017	
Hectoliter	-0.062	-0.029	-0.020	0.029	0.085	0.036	0.017	-0.080	0.038	0.347**	-0.169**	-0.119*	0.011	-0.112*

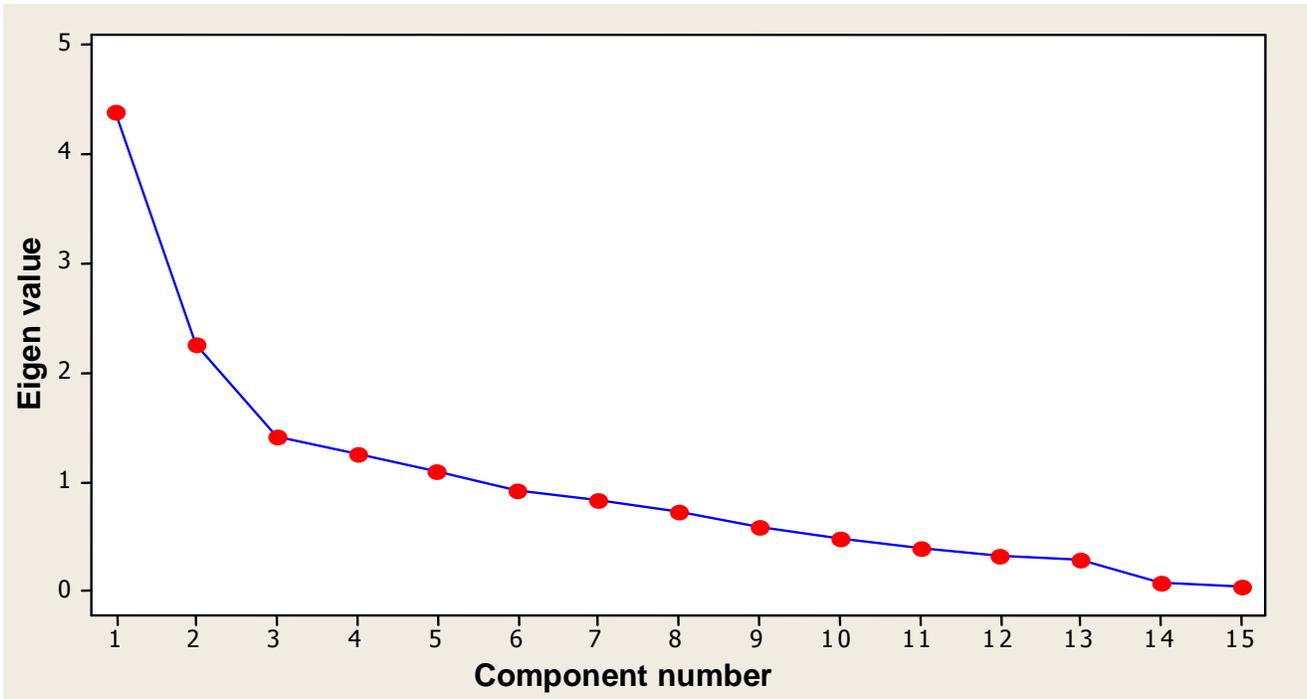
\*\* and \* significant at the 0.01 and 0.05 levels, respectively.

### Principal component analysis

In the principal component analysis, out of fifteen,

five principal components (Figure 1) exhibited more than one Eigen-value and showed 69.3% of variability. Hence, these five were given due

importance for further explanation (Table 3). The first PC was more related to tiller numbers, fertile tillers, biological yield, grain yield and volume of



**Figure 1.** Scree plot of principal component analysis between Eigen value and number of PC.

**Table 3.** Principal components (PCs) for seventeen characters in genotypes of wheat.

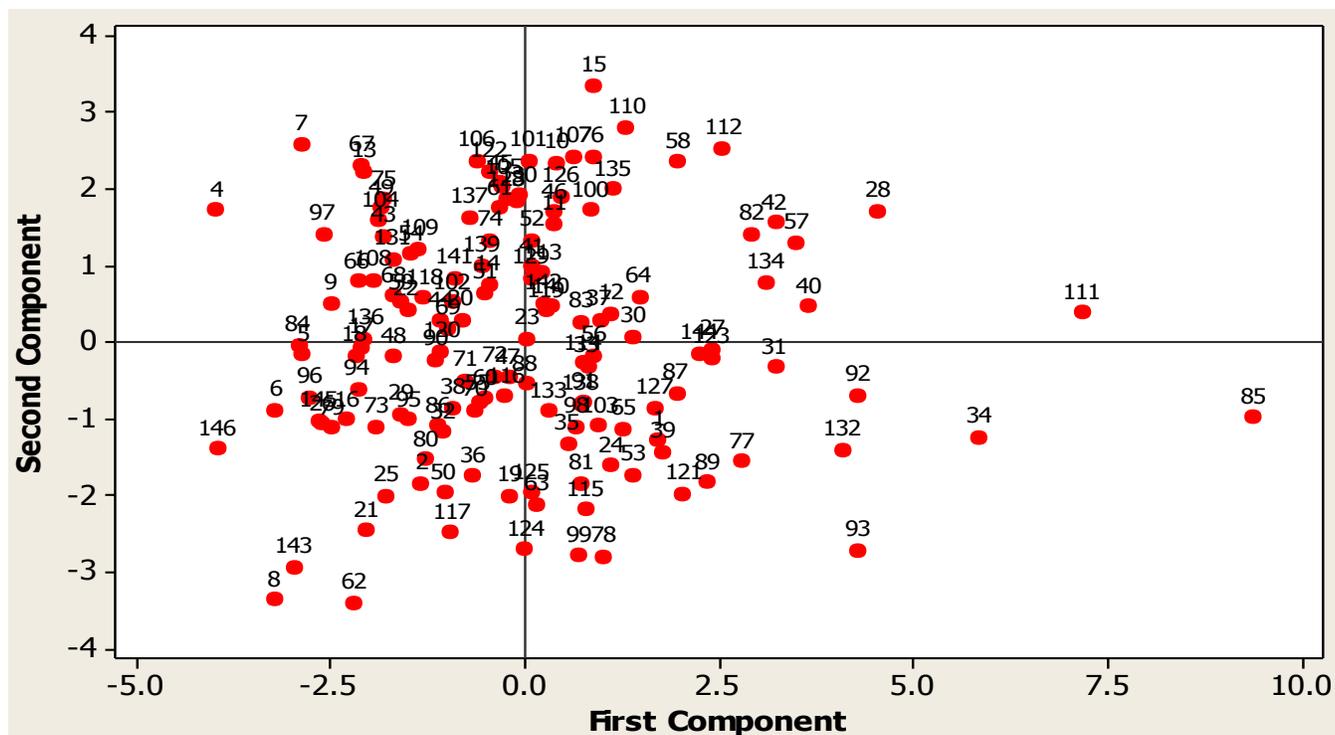
Variable	Eigen vector				
	PC1	PC2	PC3	PC4	PC5
No. of Tillers	0.407	0.140	0.177	0.207	0.151
Fertile Tillers	0.408	0.147	0.193	0.197	0.130
Biological yield	0.353	-0.050	0.124	0.030	-0.005
Plant Height	0.244	0.015	-0.504	-0.334	0.140
Peduncle Length	0.151	0.401	-0.250	-0.133	0.041
Spike length	0.223	-0.142	-0.530	-0.139	-0.010
Awn Length	0.153	-0.306	-0.202	0.327	0.028
No of grains per spikelet	-0.002	-0.510	-0.102	-0.131	-0.014
No. of grain per Spike	-0.005	-0.369	0.032	0.228	-0.460
Grain yield	0.410	-0.031	0.123	-0.040	-0.246
Flag leaf width	0.044	-0.374	0.313	-0.447	-0.024
Flag leaf length	0.137	-0.242	0.032	-0.256	0.381
1000 grain weight	0.018	0.285	0.049	-0.449	-0.607
Volume of seed plants	0.429	-0.063	0.200	-0.123	-0.120
Hectoliter	0.122	-0.034	-0.330	0.330	-0.371

seed plants as it was cleared from the values of Table 4 for PC1. The second principal component exhibited positive effects for peduncle length, but exhibited negative effects for number of grains per spikelet, number of grain per spike and flag leaf width. The third principal component was more related to flag leaf width. The fourth principal component exhibited positive effects for awn length, while the fifth principal component was

more related to flag leaf length (Table 4). From the five PCs it was clear that among all the 15 variables, tiller numbers, fertile tillers, biological yield, grain yield, volume of seed plants, peduncle length, flag leaf width and flag leaf length had high value. Mostly, yield contributing traits were poor in these PCs except for the first PC. From this study, it was concluded that a good hybridization breeding program can be initiated by the selection of

**Table 4.** Eigenvalues and cumulative % for 5 PCs.

Principal component	Eigen value	Proportion	Cumulative%
PC1	4.37	0.292	29.2
PC2	2.26	0.151	44.2
PC3	1.40	0.094	53.6
PC4	1.24	0.083	61.9
PC5	1.09	0.073	69.3

**Figure 2.** Biplot of wheat genotypes based on first and second components.

genotypes from the PC1. Furthermore, principal component analysis was drawn to review relationships between variables based on biplot first and second components (Figures 2 and 3), so that the horizontal axis was related to first component and the vertical axis was related to the second component.

### Scree plot

Scree plot explains the percentage of variance associated with each principal component obtained by drawing a graph between Eigen values and principal component number. PC1 showed 29% variability with Eigen value 4.4 in germplasm, which then reduced gradually (Figure 1). From the graph obtained, it was concluded that maximum variation was present in first PC. So selection of genotypes from this PC will be useful.

### Biplot

A principal component biplot showed that variables are super imposed on the plot as vectors. The distance of each variable with respect to PC1 showed the contribution of this variable in the variation of germplasm (Figure 3). Based on component values, the location of genotypes and their grouping were determined on top of biplot. Biplot had been used by many researchers in comparing different genotypes. For example, Kaya et al. (2002), Dadbakhsh et al. (2011) and Abdolshahi et al. (2010) were able to reveal that bread wheat genotypes with larger PCA1 and lower PCA2 scores gave high yields (stable genotypes) and genotypes with lower PCA1 and larger PCA2 scores had low yields (unstable genotypes). Evaluation of germplasm on the basis of morphological characters was also done by many researchers. Ranjbar et al. (2007), Escobar-hernandez et

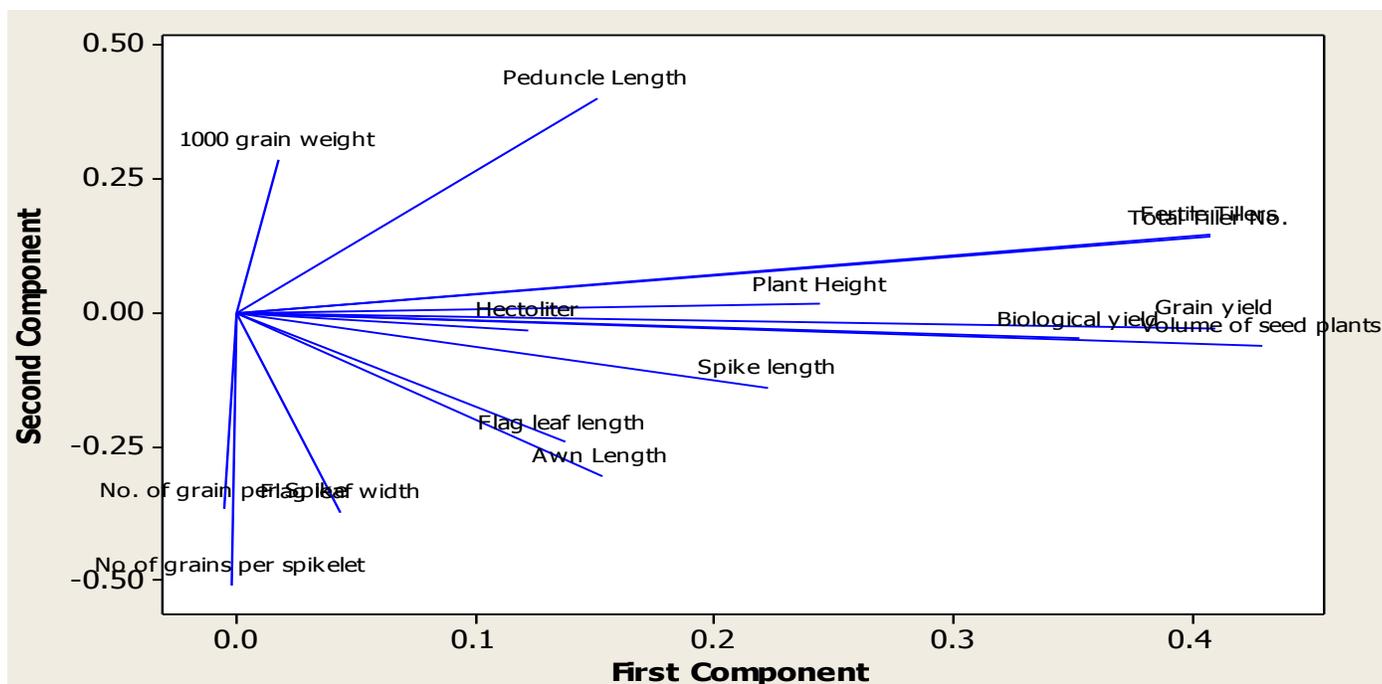


Figure 3. Biplot of studied traits based on first and second components.

al. (2005), Sapra and Lal (2003), Maqbool et al. (2010) and Ahmadzadeh et al. (2011c) used principal component method for grouping of germplasm. From these scores given to genotypes on the basis of first and second PC, breeders can select genotypes with highest score having desirable characters for further breeding programmes.

## Conclusion

Landraces are important genetic resources for improvement of crops in dry areas, since they have accumulated adaptation to harsh environment over long time. Collection and characterization of various agronomic and physiological traits of genotypes are primary steps in plant breeding programs. Principal component analysis and correlation coefficients analysis in wheat genotypes facilitate the identification of desirable traits and their relationship with yield and reliable classification of genotypes. According to the results of this study, it can be concluded that a good hybridization breeding program can be initiated by the selection of genotypes from the PC1 and PC2, as well as the identification of subset of core genotypes and correlated morphological characters with possible utility for specific breeding purposes.

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