



Diversity analysis for quality traits in exotic and Syrian genetic resources of wheat

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Received: November 16th 2020; Accepted: January 19th 2021

Abstract

Eleven genetic resources of primitive wheat originated from (Italy, Ethiopia and Syria) belongs to three species (*Triticum. dicoccum*, *Triticum. polonicum* and *Triticum. carthlicum*) were planted in RCBD design with three replicates at Homs research centre, General Commission for Scientific Agriculture Research GCSAR, Syria, during the two growing seasons 2018/2019 and 2019/2020. The objectives of this study were to estimate the potential diversity between studied wheat genotypes in quality by using multivariate (GGE, PCA and Cluster) analysis, and to define the best genotypes to be used in wheat breeding for quality. Studied grain quality traits were: Dry matter%, protein%, wet gluten%, Starch% and hectoliter. Results showed that only PC1 and PC2 were indicators of 77.7% of diversity (mainly 54.7% due to protein, wet gluten and Starch related to PC1). Cluster results revealed that the Syrian and Ethiopian genotypes were clustered together with almost 79% of similarity. GGE results indicated that three Italian genetic resources (1939, 1947 and 1952) were the best in protein% and wet gluten%, While the Italian genotype 1989 followed by the Syrian genotype 1709 were the best in starch%. Hence, the mentioned genotypes will be a proper genetic resources for improving wheat quality.

Keywords: Wheat, PCA, Cluster, GGE Biplot, Grain Quality.

Introduction

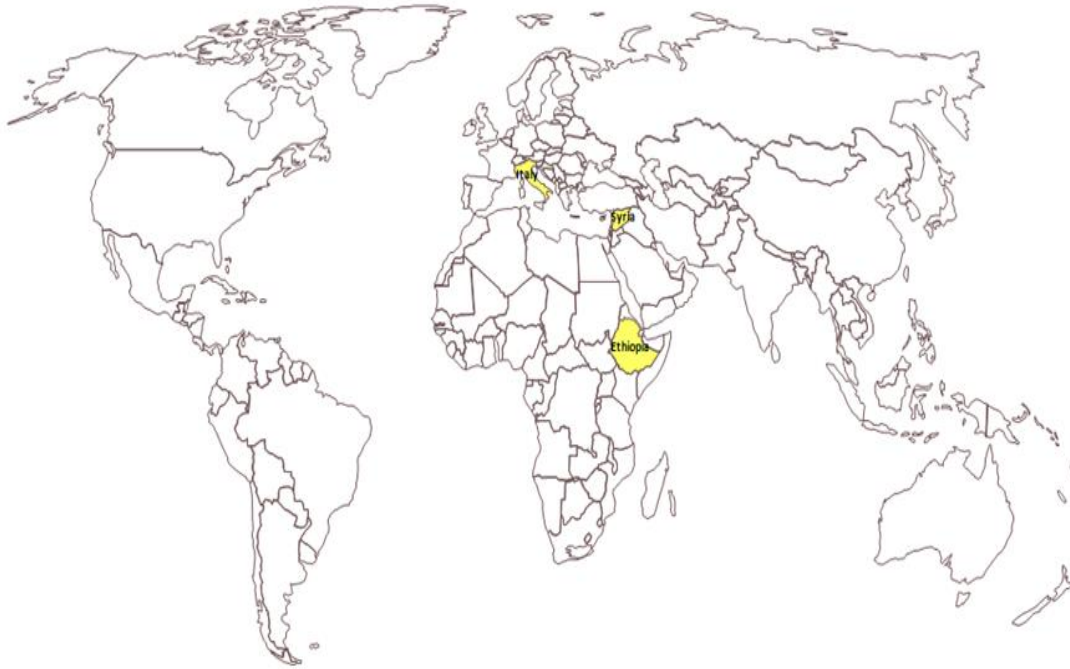
Wheat is the most food consumed from grain crops in the world, hence, improving grain quality is an important goal for breeders (Abdipour *et al.*, 2016). Concerning wheat quality, the basic indices to determine nutrition value is protein content, and differs according to the genotype and surrounding ecosystem (Malik *et al.*, 2013), and play a main role in assuring good quality of flour (Dupont *et al.*, 2003). In dry areas, the hard genotypes of cultivated wheat are distinguished for their strong gluten (Saleem *et al.*, 2015). Superiority of any genotype is accredited on its adaptation to many environments (Ahmad *et al.*, 2014), which can be analyzed by many methods like multi environments analysis. Singh *et al.*, (2020) referred to the importance of multivariate

analysis in estimating the diversity, and they focused especially on the efficiency of principle component and cluster analysis as specific indicators in sorting genotypes and in defining the most vital characteristics that contribute in the entire variation between genotypes. GGE Biplot method was suggested by Yan *et al.* (2000) as a tool for illustration data, in which we can determine the best yielded genotype across different locations (Kaya *et al.*, 2006). This research aimed to: (i) estimate the potential diversity in quality traits between foreign and Syrian wheat genetic resources by using multivariate (GGE, PCA and Cluster) analysis, (ii) to assist illustration evaluation among studied genetic resources and years, (iii) detect the superior genetic resources regarding quality for breeding programs.

Material and Methods

Plant materials: Eleven genetic resources of primitive wheat originated from different origins (Italy, Ethiopia and Syria) (Figure 1). The plant material were awarded from the International Centre for Agricultural Research in the Dry Areas

(ICARDA) and the genetic resources department in the General Commission for Scientific Agricultural Research (GCSAR), Syria, belongs to three species (*Triticum. dicoccum*, *Triticum. polonicum* and *Triticum. carthlicum*) were all used in this research (Table 1).



World map by www.freeworldmaps.net

Figure 1. Origin of the studied Genetic resources .

Table (1): List of the used wheat genetic resources

No	Species	Code	Origin
1	<i>Triticum polonicum</i>	1939	Italy
2	<i>Triticum polonicum</i>	1945	Italy
3	<i>Triticum polonicum</i>	1946	Italy
4	<i>Triticum polonicum</i>	1947	Italy
5	<i>Triticum polonicum</i>	1949	Italy
6	<i>Triticum polonicum</i>	1950	Italy
7	<i>Triticum polonicum</i>	1952	Italy
8	<i>Triticum carthlicum</i>	1980	Italy
9	<i>Triticum carthlicum</i>	1989	Italy
10	<i>Triticum dicoccum</i>	1604	Ethiopia
11	<i>Triticum dicoccum</i>	1709	Syria

Field experiments: The genetic resources of this research were all planted at Homs research centre in the General Commission for Scientific Agricultural Research (GCSAR), Syria during two growing seasons 2018/2019 and 2019/2020 under rainfed conditions, in a randomized complete block design (RCBD), with

three replications. Each replicate was divided into eleven plots represented by the eleven genotypes, and each plot contained four rows, each row of 1 meter long, with 20 cm between rows and 5cm between plants, depth of planting was 3-5 cm. Recommended cultural practices were applied

according to Agricultural ministry guides. After harvest, five grain quality traits (Dry matter%, Starch content%, Protein content%, Wet gluten content% and hectoliter) were measured by using Inframatic IM 9500 electronic device.

Statistical analysis: Minitap.12 software was used to conduct both the principle component analysis PCA to evaluate the variation in quality traits between the targeted genetic resources, and cluster analysis depending on the method of Euclidean distance measure to categorize them according to their similarity concerning quality traits. Genstat.12 software was used to assist illustration evaluation among genetic resources and years using GGE analysis.

Results and Discussion

Principle Component Analysis: Our results revealed that out of five principal components achieved for the studied traits, just the first two principal components PC1 and PC2 significantly indicated the

variability among wheat genotypes concerning quality traits since their Eigen value were bigger than 1.0 (2.7370 for PC1 and 1.1499 for PC2) respectively, whereas other components were discarded because their Eigen value were less than 1.0 (0.9401 for PC3, 0.165 for PC4, 0.0077 for PC5) (Figure .1). The highest cumulative variation was 77.7%, in which the PC1 proportion of variation was 54.7% and the PC2 Proportion of variation was 23% (Table 2). Results showed that each of protein, wet gluten and starch content were correlated with the first principal component PC1 (0.592, 0.595, -0.386) respectively, while both dry matter content and hectoliter were correlated to the second principle component PC2 (0.616, -0.681) respectively (Table 3). Loading plot of quality traits in the first two principle components is reflects the negative correlation between starch content and both PC1and PC2 in contrary of protein and wet gluten content which were both positively correlated to both PC1 and PC2 (Figure .2).

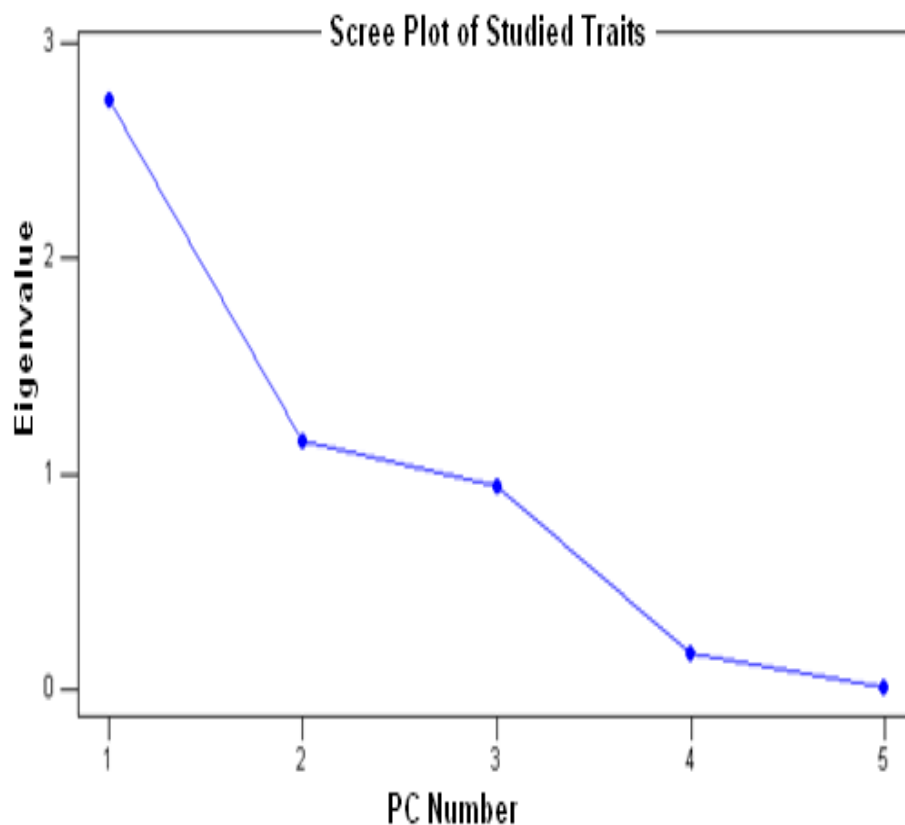


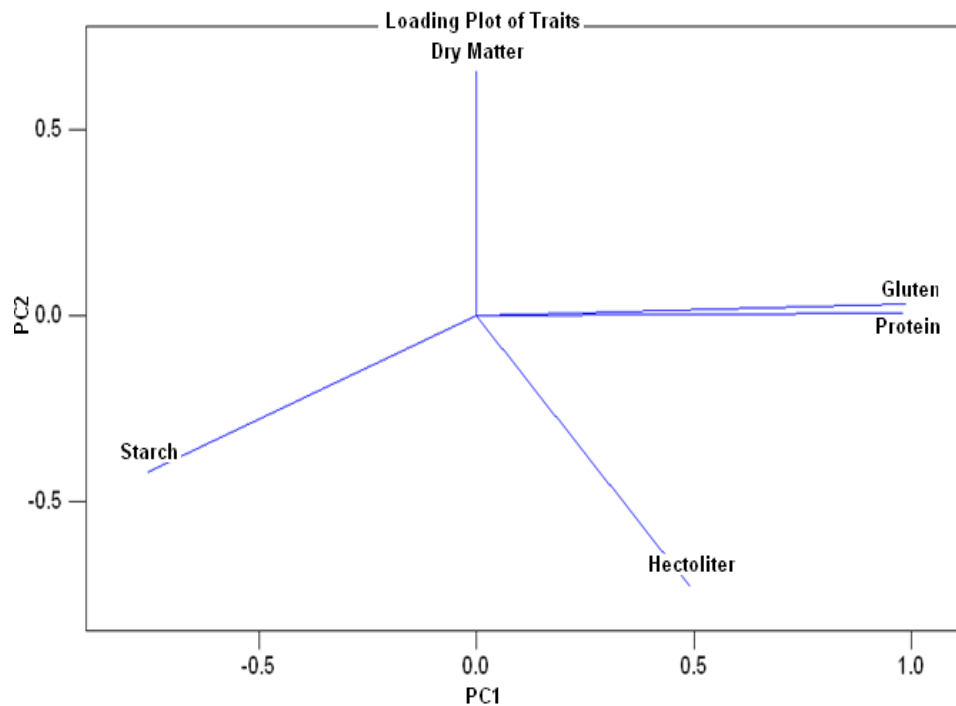
Figure 1. Scree plot showing Eigenvalue variation.

Table (2). Eigen value, proportion and cumulative variation of analyzed components

Principal Components	Eigen Value	Proportion of Variation%	Cumulative Variation%
PC1	2.7370	0.547	0.547
PC2	1.1499	0.230	0.777
PC3	0.9401	0.188	0.965
PC4	0.1653	0.033	0.998
PC5	0.0077	0.002	1.000

Table (3). The first two principle components for the studied traits

Trait	PC1	PC2
Dry Matter	-0.000	0.616
Protein	0.592	0.007
Wet gluten	0.595	0.030
Starch	-0.455	-0.394
Hectoliter	0.296	-0.681

**Figure 2. Loading plot of studied traits in the first two Components**

Cluster Analysis: Depending on the measured quality traits, cluster analysis results indicated that the similarity coefficient ranged from 32.55 % to 100%. and that the eleven genetic resources were clustered in two clusters, the first cluster contained

only the Syrian and Ethiopian wheat genotypes (1604 and 1709) with almost 79% of similarity, while the other nine Italian wheat genotypes were gathered in the second cluster with about 89% of similarity (Figure. 3).

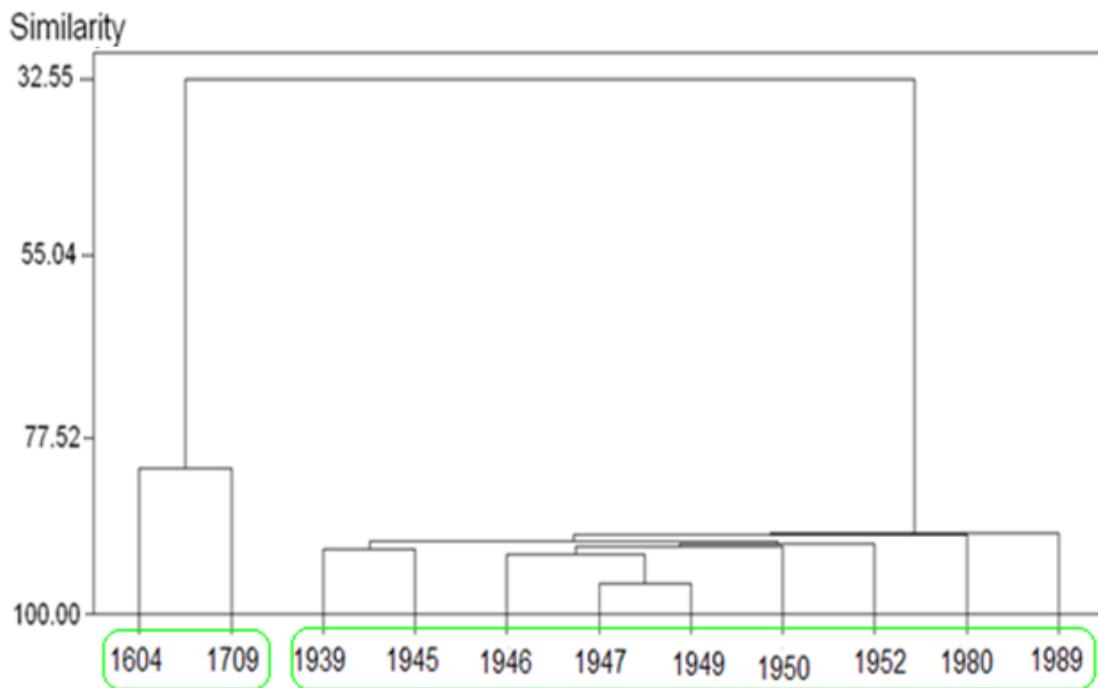


Figure 3. Dendrogram of wheat genotypes during two seasons for quality traits.

GGE Biplot: The GGE Biplot was applied to evaluate the performance of tested genetic resources during two seasons (two environments) concerning only three quality traits which are protein, wet gluten and starch content. Results of GGE Biplot for protein content revealed that all genotypes were distributed within the PC1 which represented 94.83% of variation and the PC2 which represented 5.17% of variation, Results indicated that the genotype 1939 was the best in protein content, followed by the genotype 1974 then the genotype 1952, and the grand mean of protein content for all genotypes in season 2019 was better than it in season 2020 (Figure 4). For wet gluten content, PC1 explained

93.23% of variation and PC2 explained 6.77% of variation, and also the best genotypes in wet gluten content were 1939 then 1947 followed by 1952, as well as the grand mean of wet gluten content during season 2019 was better than it during season 2020 (Figure 5).

Variation in starch content was explained by the PC1 (89.75%) and PC2 (10.25%) in which the genotype 1989 was the highest in starch content followed by the genotype 1709 then 1980. The grand mean of starch content for all genotypes during season 2019 was the highest comparing to season 2020 (Figure 6).

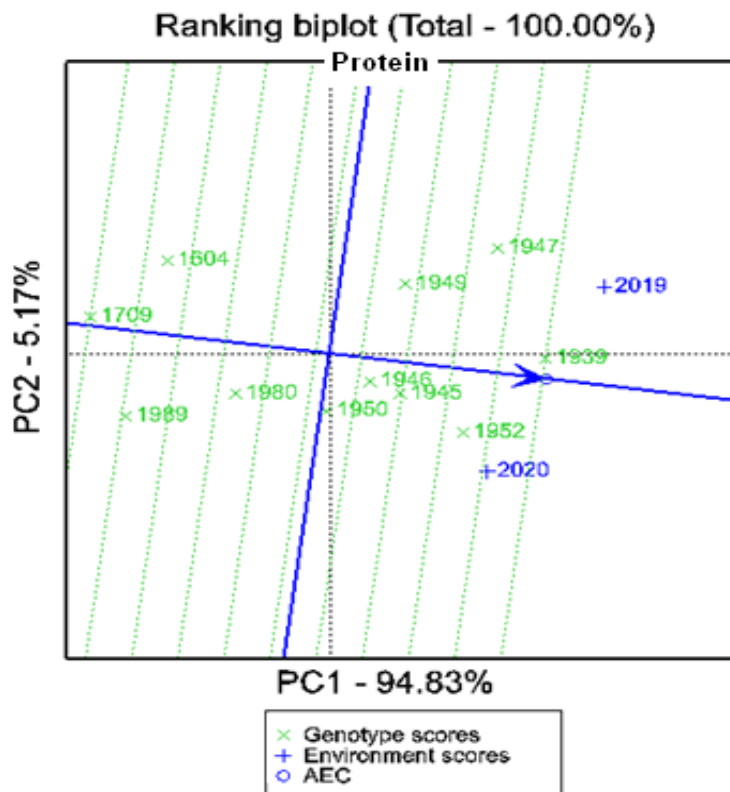


Figure 4. Ranking GGE Biplot for protein% among genotypes and years

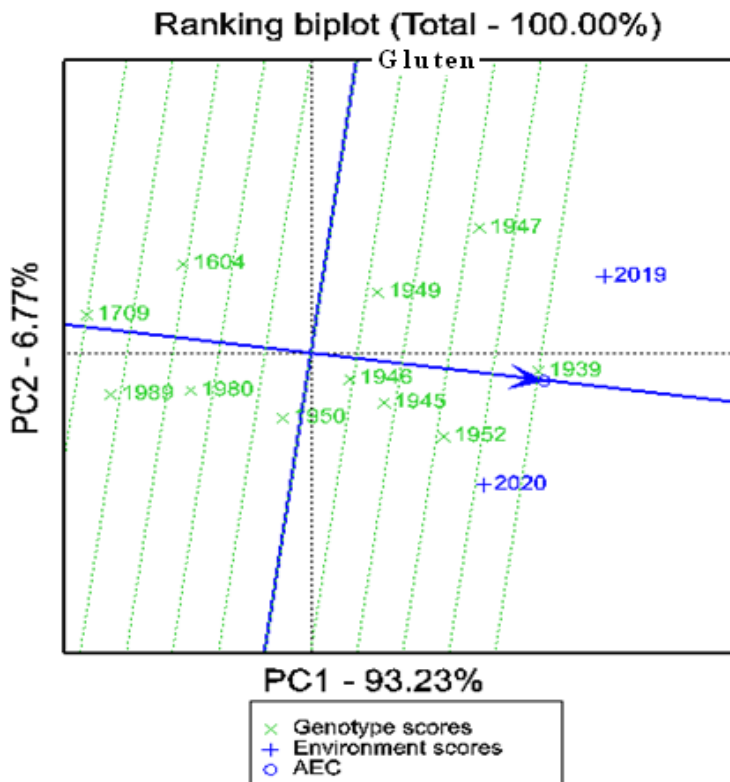


Figure 5. Ranking GGE Biplot for wet gluten% among genotypes and years

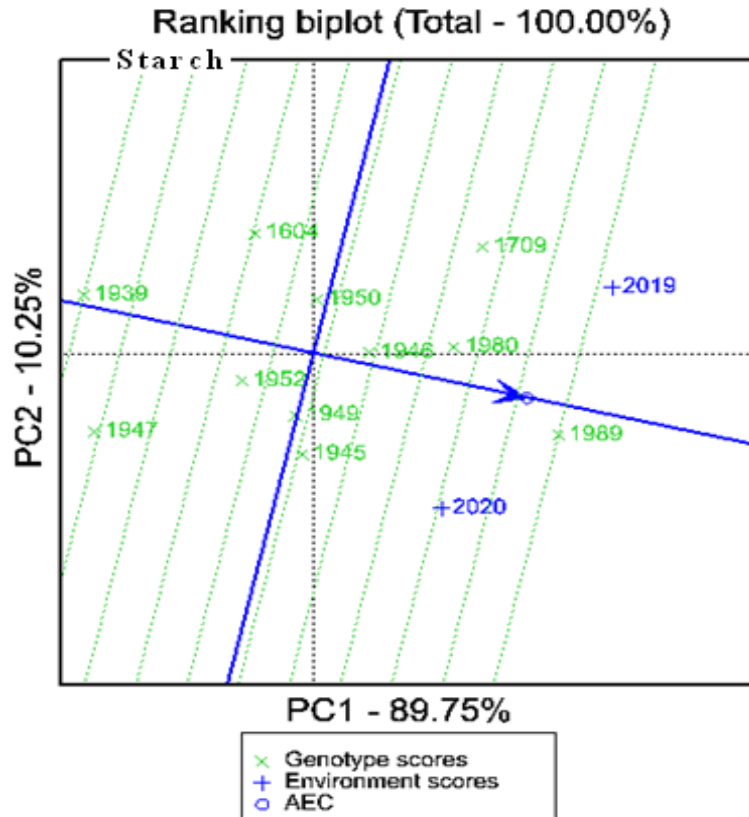


Figure 6. GGE Biplot for starch% among genotypes and years

Applying different analytical methods of diversity analysis sounds to be an effective way to explore the percentage of variation that could be highly useful for breeders (Jaiswal et al., 2010). The measured quality traits explained high percentage of variation via the first two principle components, this result reflects the importance of traits, this agrees with Annusisodia et al., (2017) who mentioned that major of variability is explained by the first PC. Results also indicated that all Italian genetic resources were grouped in the same cluster, while the Syrian and Ethiopian genetic resources were grouped together in the first cluster since they belongs to the same species (*Triticum dicoccum*), which means that the origin or the classification plays a main role in clustering wheat germplasm, and this agrees with many researches who confirmed our results (Mutwali et al., 2016; Jaiswal et al., 2010; Awan et al., 2015). Each cluster contained the closest genotypes, for that, it was clear that the variation within the same cluster is less than the variation between both clusters. This means that best crosses will be between genotypes belongs to many clusters, this agrees with Eivazi et al., (2007) whose results

referred to existence of two clusters of wheat germplasm regarding quality traits. Our results of GGE Biplot analysis clarified the best genotype in each quality trait in both seasons, which are supported by the findings of Kaya et al., (2018) and Saint Pierre et al., (2008) who explained that the performance of genetic resources is accompanied with their characters when grouping in GGE Biplot.

Conclusions

Precious divergence was assured among Syrian, Italian and Ethiopian genetic resources of wheat in quality traits which enable them to be a proper parents for improving wheat quality. The analytical tools used in this research were effective in describing the diversity among tested genotypes. The genotypes (1939, 1947 and 1952) originated from Italy were the best in both protein% and wet gluten%, While the genotype 1989 from Italy and the genotype 1709 originated from Syria were the best in starch%.

Conflict of Interest

The authors declared that there is no conflict of interest.

Author Contributions

All authors contributed equally in this research.

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