Characterization of bread wheat (T. aestivum L.) germplasm stored in Albanian genebank by agronomical and biochemical markers

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Introduction:

- Development of wheat cultivars with high production capacity and excellent quality, which meets market requirements, is the goal of each breeding program.

- The genetic improvement of wheat intends to obtain the best characters of the new cultivar, and this objective has determined the choice of the parental forms.

- The genetic variance, genetic gain and heritability estimations are of great importance in plant breeding programmer.

- Plant breeders estimate genetic variances in their populations so that they can predict the response to selection, determine the best selection and breeding procedure for the populations.
Methodology: materials and methods

- **Plant materials:** Winter wheat (*T. aestivum* L.), 100 accessions /genotypes (stored in base collection of Albanian Gene Bank).
- **Experimental site:** Experimental field of Agriculture Institute of Kosovo (Peja - Republic of Kosovo): Altitude of 513 m; Latitude 42°41'21.10"N; Longitude 20°19'31.14"E.
- **Climate** in this region is continental, mean annual temperature 16-17 °C and mean annual precipitation 700 mm. The **soil type** is yellow colour on sandy sediment.
- **Method:** All assessments were carried out on the plots (one replication) during the autumn season of 2015/2016.
- **Row and plant distances:** Row 2.5 m long x 0.25 m between rows x 0.10 m between plants.
- **Fertilizer** used on the plots were at the rate of 400 kg ha⁻¹, N.P.K. 8:16:20.
Methodology: materials and methods

Agro-bio-morphologic characters/markers as:

• Sowing-germination (SG), growth class (seasonality), spikelet time (ST), days to flower (DF), falling of plants tillering capacity (Fall) (TC), plant height (PH) (cm), 1000-seed weight (AW) (g), hectolitre weight (HW) (kg), were observed and measured, and

Biochemical markers as:

• seed humidity (HC) (%), protein content (PrCo) (%), gluten (Glut) (%) and sediment (Sed) (%) were analyzed.

• At physiological maturity, seeds were harvested and after they were cleaned for analysis.
Methodology: Data analysis

- Descriptive statistics,
- Analysis of variance,
- the mean values comparison,
- standard deviations,
- cluster and principal component analysis

**were performed**

to take maximum information for each bread wheat accession/genotypes and to identify the most important morphological traits.
Results and Discussions

• **ANOVA analysis and comparison of means** showed the presence of variability among the bread wheat (*T. aestivum* L.) accessions and between quantitative agronomical traits analysed.

• Highly significant variation was found in all quantitative traits, except for SG and TC not significant at the probability $P_{0.05}$.

• Highly significant variances among agronomical traits as **Sed, DF, ST** and **HW** were found.

(see table data)
## Results and Discussions – table data

<table>
<thead>
<tr>
<th>Traits</th>
<th>Descriptive Statistics</th>
<th>Cluster</th>
<th>Error</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Deviation</td>
<td>Mean Square</td>
</tr>
<tr>
<td>SG</td>
<td>17.6500</td>
<td>2.68319</td>
<td>14.583</td>
</tr>
<tr>
<td>ST</td>
<td>163.3200**</td>
<td>7.67507</td>
<td>4412.350</td>
</tr>
<tr>
<td>DF</td>
<td>167.7400**</td>
<td>7.93104</td>
<td>4839.688</td>
</tr>
<tr>
<td>PH</td>
<td>1.0913**</td>
<td>.24326</td>
<td>2.950</td>
</tr>
<tr>
<td>AW</td>
<td>47.7446*</td>
<td>5.41937</td>
<td>234.655</td>
</tr>
<tr>
<td>HW</td>
<td>76.7874*</td>
<td>2.53849</td>
<td>87.933</td>
</tr>
<tr>
<td>PrCo</td>
<td>16.1749**</td>
<td>1.37740</td>
<td>46.215</td>
</tr>
<tr>
<td>Glut</td>
<td>36.4790**</td>
<td>3.63727</td>
<td>281.820</td>
</tr>
<tr>
<td>Sed</td>
<td>62.8059**</td>
<td>8.87530</td>
<td>1484.668</td>
</tr>
<tr>
<td>TC</td>
<td>10.7490</td>
<td>.40887</td>
<td>.013</td>
</tr>
</tbody>
</table>

_F_ - F-ratio; _Sig._ - significance level (*) equal to the 0.05 and (**) equal to the 0.01 of probability.
df - degree of freedom
Results and Discussions

• **Principal component** and **cluster analysis on correlations** divide the whole wheat genotypes into **five cluster groups** in respect of genetic diversity and similarity.

• PCA results showed the first **three PCs** account for a substantial proportion of total variation, 72.66%.

• The percentages of total variation accounted for by each of the first three PCs were 40.9%, 20.2% and 11.58%, respectively.

• Cluster analysis allowed the identification of wheat accessions with large variability.
### Results and Discussions

#### Principal Components/factor analysis

<table>
<thead>
<tr>
<th>PC No.</th>
<th>Eigenvalue</th>
<th>Percent variance</th>
<th>Cumulative Percent</th>
<th>$\chi^2$</th>
<th>DF</th>
<th>Prob. &gt; $\chi^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4.0857</td>
<td>40.857</td>
<td>40.857</td>
<td>1226.89</td>
<td>44.221</td>
<td>&lt;.0001**</td>
</tr>
<tr>
<td>2</td>
<td>2.0220</td>
<td>20.220</td>
<td>61.077</td>
<td>992.699</td>
<td>41.422</td>
<td>&lt;.0001**</td>
</tr>
<tr>
<td>3</td>
<td>1.1581</td>
<td>11.581</td>
<td>72.659</td>
<td>864.707</td>
<td>35.701</td>
<td>&lt;.0001**</td>
</tr>
<tr>
<td>4</td>
<td>0.9767</td>
<td>9.767</td>
<td>82.426</td>
<td>795.713</td>
<td>28.440</td>
<td>&lt;.0001**</td>
</tr>
<tr>
<td>5</td>
<td>0.8265</td>
<td>8.265</td>
<td>90.691</td>
<td>714.559</td>
<td>21.623</td>
<td>&lt;.0001**</td>
</tr>
</tbody>
</table>

$\chi^2$ – Chi Square, DF – degree of freedom; Prob. – probability; **significance level 0.01 of probability
Results and Discussions

- PCA and factorial analysis ranged wheat genotypes into three groups:
  - first group includes 45 genotypes of cluster 1;
  - the 2<sup>nd</sup> includes 26 genotypes of cluster 2 and 5, and
  - the 3<sup>rd</sup> group includes 26 genotypes of cluster 4.

- Relationships analysis between the quantitative traits and wheat genotypes using principal component analysis show that there were 6 most important quantitative traits (ST, DF, PH, PrCo, Glut and Sed) in PC1 that account for 40.9% of total variance and that differentiated cluster groups. (see next fig.).
Results and Discussions

Fig. 1. Relationships among the 100 bread wheat accessions based on quantitative agronomical traits revealed by principal component analyses
### Results and Discussions

Eigenvalue vectors for three principal components of 10 quantitative traits in bread wheat.

<table>
<thead>
<tr>
<th>Morphological Quantitative Characters</th>
<th>PC1</th>
<th>PC2</th>
<th>PC3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sowing - germination</td>
<td>SG</td>
<td>-0.15659</td>
<td>0.21349</td>
</tr>
<tr>
<td>Spikelet Time</td>
<td>ST</td>
<td>0.37406</td>
<td>-0.40235</td>
</tr>
<tr>
<td>Days to flower</td>
<td>DF</td>
<td>0.37484</td>
<td>-0.39748</td>
</tr>
<tr>
<td>Plant height</td>
<td>PH</td>
<td>0.35283</td>
<td>-0.31357</td>
</tr>
<tr>
<td>Absolute Weight</td>
<td>AW</td>
<td>-0.19845</td>
<td>0.06827</td>
</tr>
<tr>
<td>Hectolitre Weight</td>
<td>HW</td>
<td>-0.23793</td>
<td>0.13286</td>
</tr>
<tr>
<td>Protein content</td>
<td>PrCo</td>
<td>0.40508</td>
<td>0.38614</td>
</tr>
<tr>
<td>Gluten (%)</td>
<td>Glut</td>
<td>0.39299</td>
<td>0.40526</td>
</tr>
<tr>
<td>Sediment</td>
<td>Sed</td>
<td>0.38342</td>
<td>0.40281</td>
</tr>
<tr>
<td>Humidity Content</td>
<td>HC</td>
<td>-0.09503</td>
<td>-0.19572</td>
</tr>
<tr>
<td>Falling of plants</td>
<td>Fall</td>
<td>0.28006</td>
<td>-0.70877</td>
</tr>
<tr>
<td>Tillering capacity</td>
<td>TC</td>
<td>0.70711</td>
<td>0.30734</td>
</tr>
</tbody>
</table>
Results and Discussions

• Highly significant positive correlations were found between *days to flower*, *plant height*, *spikelet time*, and *protein content* and *gluten traits* (coefficient of correlation range from 0.308 to 0.958).

• The high amount of genetic variability found in the present study suggests the Albanian bread wheat (*T. aestivum* L.) germplasm maintain considerable level of variance, potentially **available to the breeders**.

• Albanian bread wheat (*T. aestivum* L.) germplasm seems to be a sufficient base for the creation of new favourable gene combinations.
Results and Discussions

• The study identifies traits with agronomic interest that account for genetic diversity and which will facilitate the maintenance and agronomic evaluation of the wheat collections.

• Similarity among some of wheat genotypes found in each cluster group could be explained by common parent origin in their pedigree.

• Study results suggest possible parental lines among the bread wheat accessions analysed can be selected and utilised for sustainable field bread wheat breeding programs.
Results and Discussions

• Identification of the most important quantitative agronomical traits in wheat can facilitate selection of any individual accession and of desirable traits (genes), increasing the information of the wheat germplasm in gene bank.

• The traits with more significant weighting on respective PC variance can be utilised successfully as quantitative markers for evaluation, characterization of the wheat germplasm stored in gene bank, and in plant breeding programs.
Conclusions

• The field trials permitted the assessment of the most important agronomical traits and determined the patterns of variation of Albanian bread wheat germplasm with potential for sustainable their future breeding programs.

• PCA results showed the first three PCs account for a substantial proportion of total variation, 72.66%.

• Cluster analysis clearly ranged bread wheat accessions with similarity between them into the five different cluster groups, and allowed the identification of wheat accessions with large variability.
Conclusions

• The study identified the agronomical traits with more significant weighting on PC1 variance (ST, DF, PH, PrCo, Glut and Sed) significant at the probability F < P_{0.01}.

• The significant differences show the existence of a high genetic variability among the wheat genotypes (available to the breeders) sufficient for selection of desirable traits, and creation of new favourable gene combinations.

• Possible parental lines among these bread wheat genotypes could be selected and utilised for sustainable field wheat breeding programs.
REFERENCES

Thank you