



ӘЛ-ФАРАБИ АТЫНДАҒЫ ҚАЗАҚ ҰЛТТЫҚ УНИВЕРСИТЕТІ  
КАЗАХСКИЙ НАЦИОНАЛЬНЫЙ УНИВЕРСИТЕТ ИМЕНИ АЛЬ-ФАРАБИ  
AL-FARABI KAZAKH NATIONAL UNIVERSITY

БИОЛОГИЯ ЖӘНЕ БИОТЕХНОЛОГИЯ ФАКУЛЬТЕТІ  
ФАКУЛЬТЕТ БИОЛОГИИ И БИОТЕХНОЛОГИИ  
FACULTY OF BIOLOGY AND BIOTECHNOLOGY

## «ФАРАБИ ӘЛЕМІ»

атты студенттер мен жас ғалымдардың  
халықаралық ғылыми конференция  
МАТЕРИАЛДАРЫ

Алматы, Қазақстан, 6-8 сәуір 2022 жыл

## МАТЕРИАЛЫ

международной научной конференции  
студентов и молодых ученых

## «ФАРАБИ ӘЛЕМІ»

Алматы, Казахстан, 6-8 апреля 2022 года

## MATERIALS

International Scientific Conference  
of Students and Young Scientists

## «FARABI ALEMI»

Almaty, Kazakhstan, April 6-8, 2022

Алматы, 2022

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## GENETIC STRUCTURE OF THE WORLD BARLEY COLLECTION INCLUDING ACCESSIONS FROM KAZAKHSTAN

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The barley collection including 407 accessions from different regions of the World was formed for GWAS (genome-wide association studies). The collection comprises 264 accessions from the USA, 95 accessions from Kazakhstan, 37 accessions from Europe, and 11 accessions from Africa. The germplasm collection was genotyped with 1649 polymorphic SNP (single nucleotide polymorphism) markers. Based on the genotyping results, the World barley collection was studied for the genetic structure. For the accurate determination of genetic relationships among studied barley accessions, three methods were used: PCA (principal component analysis), UPGMA (unweighted pair group method with arithmetic mean) tree construction, and clusterization via STRUCTURE software.

Results of PCA and UPGMA analyses showed high genetic similarities between barley accessions from Kazakhstan and Europe. On the PCA plot, accessions from USA and accessions from Africa were grouped into two separate clusters. At the same time, accessions from Kazakhstan and Europe were plotted together in one cluster slightly overlapping with USA's and African clusters. UPGMA phylogenetic tree contained six clades. Two of them represented the USA's accessions, other two were accessions from Kazakhstan with one clade of European barley between them, and the last one was the mix of African accessions and several accessions from Europe and Kazakhstan. STRUCTURE software using Bayesian iterative algorithm had showed presence of three clusters in the studied barley collection. The first cluster included 138 accessions (88.4 % of Kazakhstan's accessions, 100 % European accessions, 100 % African accessions, and 2.3 % USA's accessions). The second cluster included 38.3 % of the USA's accessions and 1.0 % of all accessions from Kazakhstan (in total, 102 accessions). Finally, the third cluster included 59.5 % of all USA's accessions and 10.5 % of accessions from Kazakhstan (167 accessions).

Summarizing the above, in the World barley collection, accessions from Kazakhstan and Europe were clustered together in all three methods demonstrating high similarity between germplasms of two regions. Accessions from the USA were placed separately from others in all three methods demonstrating high genetic distance from Europe and Kazakhstan, and especially from Africa. Accessions from Africa were separate from others on the PCA plot, but close to Europe and Kazakhstan on the UPGMA tree and STRUCTURE bar plot. It indicate genetic closeness of African accessions to Europe and Kazakhstan. Thus, results of this study had demonstrated high genetic difference between barley from the USA and Africa with similar germplasm from Kazakhstan and Europe in-between.

This research has been funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan (Grant No. AP08052804).

*Scientific supervisor: Prof., Doctor of Biological Sci. Abugalieva S.I.*