RESPONSE TO ABIOTIC FACTOR
RESULTS OF CLUSTER ANALYSIS OF NEW BARLEY AND SELECTED LINES

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ENTER. Cluster analysis allows the separation of complex blocks into separate groups (classes or clusters) and non-traditional classification of data.

As a result of cross-breeding of geographically distant forms, productive genes formed in different places in plant genetics create a basis for the emergence of hybrid organisms. It is known that the interaction between genes changes under the influence of the conditions in which the plant is grown.

Many research studies use cluster analysis to study genetic kinship, the advantage of this method is that varieties or samples are divided into separate groups by complex characters rather than by a single character.

According to the results of the dendrogram, the studied varieties and ridges were divided into 3 clusters (A, B, C.).

The highest yielding varieties were divided into cluster S, cluster A included 11 genotypes, cluster S included 6 genotypes, and cluster V included 3 genotypes.

Dendrogram
Ward's Method, Euclidean
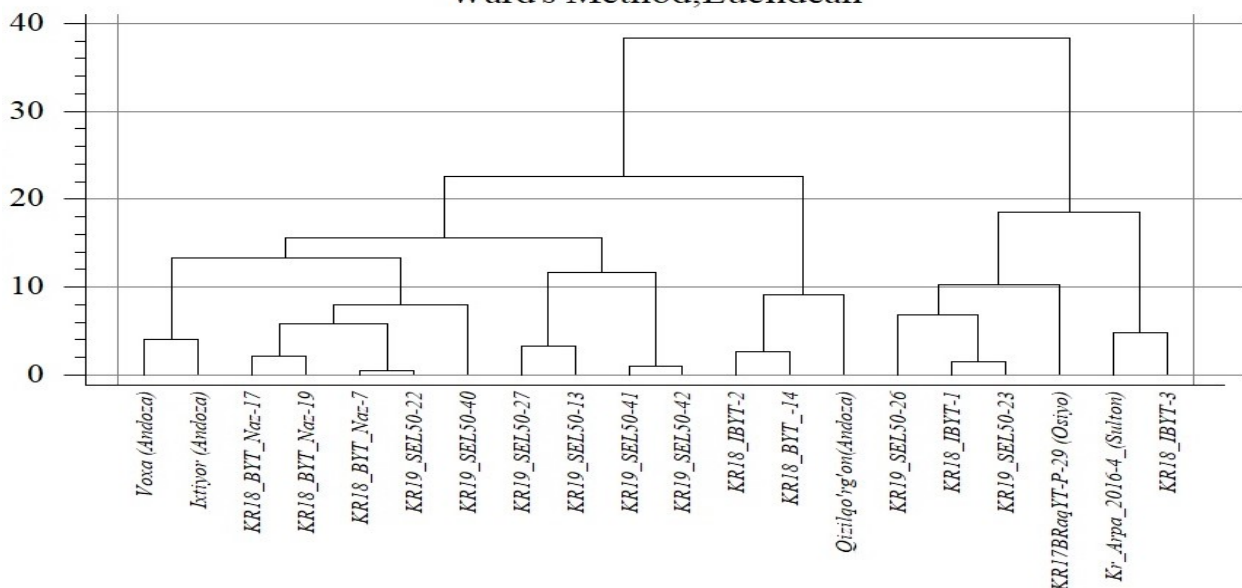
The KR18_IBYT-2, KR18_IBYT-14 winter barley lines, created on the basis of selection using quantitative characters from the SIMMIT gene pool as markers, were added to the 1st group in cluster B, and the closest to this group in terms of productivity were the varieties and lines belonging to the IKARDA selection. It was found that these two groups of varieties have different origins due to the closeness of the yield index, the number of grains per ear, and the number of productive stems per 1 m2.

High-yielding varieties selected from the IBON-W nursery are included in cluster A. Compared to other varieties, grain yield, number of spikes per 1 m2, number of grains per spike is high even in drought conditions, and the weight of 1000 grains is low, because it is not irrigated. under conditions, the genetic potential of the plant is important not with the

size of the grain, but with the large number of grains. Among these varieties, the SIMMIT No. Oasis variety sample had the highest grain yield (52 t/ha), number of grains per spike (26 pieces).

The variety Voha, created at the Southern Agricultural Research Institute, genotypically joined cluster A, and this variety had an average yield among all studied varieties.

Table 1
Clustering of winter barley cultivars and lines

№	Нав ва намуналар номи	Кластерлар					
		Кластер А		Кластер Б		Кластер С	
		Ўртача	Стандарт оғиш	Ўртача	Стандарт оғиш	Ўртача	Стандарт оғиш
1	Бошоқлашгача бўлган кун	158	2,33	158	2,65	153	1,05
2	Пишишгача бўлган кун	205	1,85	205	0,58	199	0,55
3	Ўсимлик бўйи, см	102	2,31	102	2,05	109	2,86
4	Охирги бўғин узунлиги, см	33,1	3,39	32,3	3,45	40,5	2,55
5	Бошоқ узунлиги, см	9,8	0,28	8,9	0,21	9,0	2,12
6	Бошоқчалар сони, дона	27	1,30	30	4,51	35	6,40
7	Ҳосилдорлик, ц/га	43,7	5,66	42,8	5,14	52,6	1,57
8	1000 та дон вазни, гр	37,2	2,57	36,9	0,46	42,5	0,56
9	Дон натураси, гр/л	661,1	17,81	658,2	1,08	691,6	5,34
10	Оқсил миқдори, %	12,6	0,79	12,3	0,17	13,9	1,19

Varieties in the first group of cluster A were assigned to one group due to the fact that the yield per 1 m2, total biomass, number of productive stems was low compared to other varieties, and the number of grains per ear was high. The KR19_SEL50-42 line selected from the SIMMIT collection with high grain quality in the second group of cluster A was found to be resistant to diseases and have high grain quality indicators.

The varieties of winter barley belonging to the C cluster are characterized by the height of the ridges, high grain quality and yield. To identify drought-resistant genes, selecting genes close to heat-tolerant genes and isolating non-tolerant genes, one of the alternative options is to identify common genes that are differentially expressed between drought-resistant genotypes and drought-sensitive genotypes of different genetic origins under drought conditions [1].

The obtained results show that the comparison of the obtained results on the fertility traits revealed common genetic patterns. Regardless of the geographical origin and growing season, clustering of varieties in cluster A and V into one group means that they are genetically similar.

In the cluster analysis, even though the cultivars and lines differ in terms of certain yield characteristics, it is possible to group the cultivars with similar genetic potential into one group [2].

In the dendrogram, it was found that the A group includes all imported varieties, the V cluster includes local varieties, and the C group contains selected samples from the nursery that are resistant to drought.

E. After obtaining DNA data on several indicators of plant stress resistance in Lisitsyn research, the next stage of genotype selection is statistical processing using multivariate analysis methods, such as cluster analysis [3].

In short, it is possible to apply the genotypes in cluster A and C together. Because high-yielding varieties are concentrated in cluster C, while cluster A showed varieties and lines that give high yield even in drought conditions.

LIST OF USED LITERATURE

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3. Linchevsky A.A., Honcharuk N.A. Problemy i resultaty yarovogo sixtiryadnogo yachmenya dlya usloviy intensivenogo zemledeliya. // Yachmen v usloviyakh intensivenogo zemledeliya. Sbornik nauchnykh trudov VSGI. Odessa, 2019. -S. 44-51. 108