

## Studies on some morphological characters of wild *Helianthus annuus* L. accessions with different origin

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### ABSTRACT

This study presents the evaluation of populations of wild annual *Helianthus annuus* L., the closest relative of cultivated sunflower, the variability and similarities in their morphological characters as well as the possible effect of cultivation in different environments on the traits of this species. The investigation included 73 accessions of wild *H. annuus* with a different origin from the wild species sunflower collection of Dobroudja Agricultural Institute, General Toshevo, Bulgaria. The phenotypic correlations between characters signified the importance of the studied cases and variables. The genotypes were distributed into eight clusters. The simultaneous testing of the significance of the differences in mean values between genotypes revealed significant differences among the studied genotypes of wild *H. annuus* with a different origin.

**Key words:** cluster analysis – correlation coefficient – wild *Helianthus annuus* L.

### INTRODUCTION

The *Compositae* (*Asteraceae*) is the largest and most diverse family of flowering plants. Collection and exploration of wild annual sunflower species have represented difficult and challenging activities in the process of conserving genetic diversity. Over the past several decades genes for resistance to some economically important diseases, parasites and pests have been successfully transferred into cultivated sunflower together with new valuable morphological characters.

Many investigations of scientific researchers in the field of interspecific hybridization in sunflower *Helianthus annuus* L. have confirmed that the wild species constitute an abundant source of genes determining important agricultural characters in sunflower (Pustovoit, 1975; Laferriere, 1986; Škorić, 1988, 1992; Seiler, 1988, 1992; Christov, 1996a, b; Christov et al., 1996).

*Helianthus annuus*, the wild ancestor from which the domesticated sunflower originated, is a diverse species in its center of origin and is also more variable in places where it was introduced. Wild *Helianthus* species possess not only a considerable variability for most of the traits, but also excellent environmental survival mechanisms (Thompson et al., 1981). They were widely used in sunflower breeding programs (Christov, 1999, 2004; Seiler and Brothers, 1999; Škorić et al., 1999).

This study evaluated populations of wild annual *H. annuus*, the closest relative of cultivated sunflower, the variability and similarities in their morphological characters as well as the possible effect of cultivation in different environments on the traits of this species.

### MATERIALS AND METHODS

In this investigation were included 73 accessions of wild *Helianthus annuus* from the wild species sunflower collection of Dobroudja Agricultural Institute, General Toshevo, Bulgaria. They originated from USA, France, Russia, Germany, England, Romania, China, Czech Republic, Serbia, Canada and Holland (Table 1). Their morphological traits were evaluated according to IBPGR Descriptor (IBPGR, 1985). These were: leaf length, leaf width, ratio length to width of leaves, length of leaf petiole, number of ray florets, length of ray florets, width of ray florets, number of bract leaves, length of bract leaves, width of bract leaves, ratio length to width of bract leaves, head diameter, length of the longest branch, plant height, 1000 seeds weight and seed oil content.

The morphological characterization of the wild *H. annuus* accessions has been performed for the last three years and the data presented were averaged over years. The observations were made on 10 plants, grown under field conditions. Oil content was determined by nuclear magnetic resonance (NMR).

The statistical estimations were performed by STATISTICA for WINDOWS 95 and included correlation coefficient, grouping into clusters and determining the Euclidean distances. In the method for grouping we used group analysis and the Euclidean units for estimating the differences between the groups. Groups of accessions were separated using single linkage method.

**Table 1.** Origin of studied *H. annuus* L. accessions.

Country	Accession number:
USA	GT-E-002, GT-E-003, GT-E-004, GT-E-088, GT-E-092, GT-E-093, GT-E-109, GT-E-110, GT-E-111, GT-E-112, GT-E-113, GT-E-114, GT-E-115, GT-E-116, GT-E-117, GT-E-118, GT-E-119, GT-E-120, GT-E-121, GT-E-122, GT-E-123, GT-E-124, GT-E-125, GT-E-126, GT-E-127, GT-E-128, GT-E-129, GT-E-153, GT-E-154, GT-E-155, GT-E-171, GT-E-172, GT-E-173, GT-E-174, GT-E-175, GT-E-176, GT-E-177, GT-E-178, GT-E-179, GT-E-180
France	GT-E-035, GT-E-042, GT-E-043, GT-E-044, GT-E-045, GT-E-055, GT-E-056, GT-E-057, GT-E-058, GT-E-059, GT-E-060, GT-E-061, GT-E-062, GT-E-063, GT-E-064
Russia	GT-E-040, GT-E-049, GT-E-103, GT-E-104, GT-E-105, GT-E-106
Germany	GT-E-066, GT-E-079, GT-E-184
England	GT-E-182, GT-E-183
Romania	GT-E-077, GT-E-081
China	GT-E-170
Czech Republic	GT-E-078
Serbia	GT-E-046
Canada	GT-E-053
Holland	GT-E-005

## RESULTS AND DISCUSSION

Groups of variables could be usually determined in these investigations. They were correlated due to complex interactions that were uncontrolled and obscured. The degree of association of such variables can be determined through correlation analysis. Correlations between characters illustrated the importance of the studied cases as pleiotropic action of genes, linkages, improvements brought about by selection through related characters and natural selection (Table 2).

**Table 2.** Correlation coefficients of studied morphological traits.

	Leaf length	Leaf width	Length of leaf petiole	No. of ray florets	Length of ray florets	Width of ray florets	No. of bract leaves	Length of bract leaves	Width of bract leaves	Head diameter	Length of longest branch	Plant height	1000 seed weight	Seed oil content	Ratio length/width leaves
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	1														
2	<b>0.86</b>	1													
3	<b>0.52</b>	<b>0.49</b>	1												
4	0.21	0.30	0.18	1											
5	<b>0.30</b>	<b>0.30</b>	<b>0.35</b>	0.06	1										
6	0.01	0.06	0.07	0.17	-0.16	1									
7	0.26	0.27	0.24	<b>0.53</b>	0.22	-0.03	1								
8	<b>0.46</b>	<b>0.59</b>	0.19	0.26	<b>0.34</b>	0.06	0.11	1							
9	<b>0.36</b>	<b>0.54</b>	0.19	0.28	0.16	0.03	0.20	<b>0.57</b>	1						
10	<b>0.37</b>	<b>0.49</b>	0.17	<b>0.35</b>	0.25	0.02	0.31	<b>0.59</b>	<b>0.49</b>	1					
11	0.29	0.24	0.02	-0.11	0.16	-0.05	0.01	0.05	0.14	0.07	1				
12	0.17	0.16	0.00	0.03	-0.28	0.34	-0.10	0.07	0.18	0.16	0.12	1			
13	0.02	0.01	-0.07	0.05	-0.02	0.10	-0.01	0.02	-0.06	-0.11	-0.19	-0.05	1		
14	0.09	0.08	0.10	<b>0.27</b>	-0.11	-0.13	0.09	-0.12	0.05	-0.05	-0.10	-0.06	<b>0.34</b>	1	
15	-0.27	<b>-0.64</b>	-0.37	-0.35	-0.11	-0.10	-0.26	-0.27	-0.35	-0.29	-0.08	-0.07	0.04	-0.12	1
16 <sup>1</sup>	0.13	0.03	-0.03	-0.03	0.29	0.01	-0.08	0.44	-0.43	0.09	0.01	-0.16	0.05	-0.16	0.15

<sup>1</sup>Ratio length/width bract leaves

There were several high and positive correlations, which are presented in Table 2. The phenotypic correlation between leaf length and leaf width was positive ( $r=0.86^*$ ) and higher than those with length of leaf petiole ( $r=0.52^*$ ) and length of bract leaves ( $r=0.46^*$ ).

The phenotypic correlation between leaf width and length of bract leaves was significantly high and positive ( $r=0.59^*$ ) as well the correlations with width of bract leaves ( $r=0.54^*$ ), with length of leaf petiole ( $r=0.49^*$ ) and head diameter ( $r=0.49^*$ ). The phenotypic correlation between number of ray florets and number of bract leaves was positive ( $r=0.53^*$ ). Length of bract leaves correlated positively with their width ( $r=0.57^*$ ) as well as with head diameter ( $r=0.59^*$ ). The width of the bract leaves only correlated positively with head diameter ( $r=0.49^*$ ). The analysis of variance showed significant differences among most of the genotypes.

Seed oil content correlated positively with 1000-seed weight ( $r=0.34^*$ ) and to a smaller degree with the number of ray florets ( $r=0.27^*$ ), which may be due to the reported positive correlation with the number of disk florets and seed set and yield (Doddamani et al., 1997). In general, in this study the association of oil content with most of the characters was either non-significant or the few significant correlations were of a lower magnitude, suggesting that indirect selection for oil content would be rather a difficult proposition.

The simultaneous testing of significance of difference in mean values between genotypes revealed significant differences between the studied genotypes. The 73 genotypes were grouped into eight clusters using Tree Diagram for 73 cases, unweighted pair-group average with Euclidean distances but the dendrogram obtained was too large, which was why the distribution of genotypes was presented in Table 3.

**Table 3.** Distribution of 73 genotypes of *H. annuus* L. into different clusters.

Cluster	Genotype	Number of genotypes
I	GT-E-003; GT-E-044; GT-E-002; GT-E-035; GT-E-105; GT-E-116; GT-E-056; GT-E-093; GT-E-112; GT-E-123; GT-E-106; GT-E-043; GT-E-154; GT-E-182; GT-E-046; GT-E-175; GT-E-184; GT-E-113; GT-E-178; GT-E-005; GT-E-045; GT-E-111; GT-E-004; GT-E-173; GT-E-118; GT-E-153	26
II	GT-E-040; GT-E-092; GT-E-110; GT-E-121; GT-E-124; GT-E-120; GT-E-042; GT-E-119; GT-E-078; GT-E-170; GT-E-053;	11
III	GT-E-079; GT-E-171; GT-E-114; GT-E-055; GT-E-117; GT-E-058; GT-E-109;	7
IV	GT-E-049; GT-E-061; GT-E-063; GT-E-066;	4
V	GT-E-125; GT-E-173; GT-E-172; GT-E-177; GT-E-077; GT-E-127; GT-E-060; GT-E-104; GT-E-062;	9
VI	GT-E-057; GT-E-059; GT-E-179; GT-E-174; GT-E-155; GT-E-183;	6
VII	GT-E-103; GT-E-129; GT-E-064; GT-E-081; GT-E-088; GT-E-126; GT-E-128; GT-E-122;	8
VIII	GT-E-115; GT-E-180;	2

The maximum number of genotypes was included in cluster I. Most of them were of USA origin and part of them from France, Russia, Germany, Serbia and England, which indicated that there was a slight association between clustering pattern and the influence of agro-climate conditions and the cultivation of the genotypes. Insignificant linkage distances according to the dendrogram obtained were found between GT-E-112 and GT-E-123 (origin USA), GT-E-043 and GT-E-044 (origin France) and GT-E-045 and GT-E-105 (origin France and Russia). The significant distances for all accessions included in this cluster as well in cluster 2, cluster 3 and cluster 4 were not high as a whole. The lack of significant inter-cluster linkage distance could be due to the closely related genotypes and similar climate conditions and introduction. There were significant linkage distances for the accessions in clusters 5, 6, 7 and 8. They differentiated on many of the studied characters. The accessions in cluster 8 distinguished themselves in most of the studied morphological traits. GT-E-115 and GT-E-180 of USA origin, could not be integrated to any of the other clusters because of the great linkage distance between them. These results showed that the purposive genetic drifts and an extended and prolonged introduction into different environments could cause a greater diversity among genotypes than their origin.



The wild *Helianthus annuus* L. collection of DAI-General Toshevo possesses great diversity for the studied morphological characters



**CONCLUSIONS**

The similarities of some morphological traits of the studied populations of different origins with the populations from the USA as well as a clear separation of some groups from the rest of the accessions supported the hypothesis that there was some different and repeated introduction of the wild *H. annuus* from its native places of origin.

Using the correlation analysis, which presented the nature and degree of association among various characters, further investigations could be made on the independent character with the aim of improving the dependent one. These results, together with the research carried out by Christov et al. (2004) and Encheva et al. (2006) on the resistance of these accessions to *Sclerotinia sclerotiorum*, *Phomopsis helianthi* and other diseases and pests gave a brief view of the possibilities for inclusion of the studied accessions into future breeding programs.

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