

# SOME CHARACTERISTICS OF THE HELIANTHUS SPECIES IN THE DOBROUDJA COLLECTION

## I. PROTEIN CONTENT AND AMINO ACID COMPOSITION IN PROTEINS

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### SUMMARY

Protein content in seed and amino acid composition of proteins were studied in 30 genotypes of 16 *Helianthus* species. The results indicate that some entries of wild *Helianthus* can be used as a source of genes for improving the protein nutrient value in modern cultivars and hybrids. The entries *H. hirsutus*-M 007, *H. rigidus*-M 002 and M 028, *H. mollis*-M 033, and *H. eggertii*-M 001 were distinguished for a much higher protein content as compared with cv. Peredovik. Compared with the standard, the entries *H. annuus*-E 004, *H. petiolaris*-E 021 and E 037, *H. praecox*-E 027, *H. laevigatus*-M 016, *H. eggertii*-M 001, and *H. rigidus*-M 002 had increased contents of some amino acids. These entries are maintained at the Dobroudja IWS and can be used for wide hybridization of sunflower.

**Key words:** *Helianthus*, species, protein, amino acids.

### INTRODUCTION

The collecting, maintenance, and study of *Helianthus* species are important activities of all sunflower breeding teams. A collection of 34 species has been established and studied at the Dobroudja IWS. Twenty-seven of these are perennials and seven are annuals. Each species is represented by a different number of variants, whose total number is 233. Most of these samples have been received from Bushland (Texas) and Ames (Iowa) USA. There are also materials obtained from the former USSR, France, as well as some other countries. All accessions have been registered according to the FAO requirements.

Data on the morphological, biological and phytopathological characteristics of plants and the chemical composition of seed of various *Helianthus* species have already been published (Heiser et al., 1969; Pustovoit, 1975; Georgieva-Todorova, 1976; Tompson et al., 1981; Rogers et al., 1982). These papers present their results without identifying the accessions studied. It is known that within each *Helianthus* species there is a great diversity in form and the value of individual traits (Heiser et al., 1969; Rogers et al., 1982; Škorić, 1982; Christov, 1990). In wide hybridization programs, species have been used without a clear idea about their actual genotypic characteristics. This is why it is better to associate all data with a particular genotype specified by its accession number.

The present investigation of the *Helianthus* species from the Dobroudja IWS collection was undertaken in order to study chemical characteristics of 30 genotypes of 16 *Helianthus* species, each labelled with its sown number. The first part of the study deals

Table 1. Amino acid composition (mol %) of wild *Helianthus* species with diploid chromosome number (n=34)

Genotype and amino acid	1	2	3	4	5	6	7
Protein in defatted seeds %	25.2	25.1	-	37.4c	33.6c	38.5c	34.3c
Lysine	3.4	3.2a	3.3	3.2a	3.4	3.5	3.4
Histidine	2.2	2.3a	2.3a	2.5b	2.3a	2.3a	2.3a
Arginine	6.8	7.4	7.1	7.6b	7.6b	7.5a	7.4
Aspartic acid	10.0	9.2c	9.5a	9.5a	9.6a	9.4b	9.6a
Threonine + Serine	10.5	9.7a	9.4b	8.9c	9.8a	9.0c	9.8a
Glutamic acid	20.8	22.4b	21.7a	22.4b	23.4c	22.2b	22.9b
Proline	5.4	5.2	5.6	5.0a	5.4	5.6	5.3
Glycine	11.0	10.2a	10.0b	9.6c	9.5c	9.5c	9.6c
Alanine	6.7	6.0c	6.5	6.1c	5.1c	6.1c	5.2c
Cystine	0.9	0.9	0.6	0.8	0.4a	0.7	0.9
Valine	5.6	5.3	5.8	6.1b	5.4	6.0a	5.5
Methionine	1.3	1.9b	1.5	1.5	1.6a	1.4	1.6a
Isoleucine	3.7	4.0a	4.4b	4.6c	4.1b	4.6c	4.2b
Leucine	6.4	6.4	6.6	6.3	6.5	6.5	6.5
Tyrosine	1.9	2.0	1.9	1.9	2.0	1.8	2.0
Phenylalanine	3.7	3.8	3.9	4.0a	4.0a	3.9	3.9

1 - *H. annuus* cv. Peredovik (St); 2 - *H. annuus* (E 004); 3 - *H. annuus* (E 040); 4 - *H. annuus* (E 045);  
5 - *H. argophyllus* (E 006); 6 - *H. argophyllus* (E 008); 7 - *H. debilis* ssp. *vestitus* (E 010)

Table 1. Amino acid composition (mol %) of wild *Helianthus* species with diploid chromosome number (n=34) (continued)

Genotype and amino acid	8	9	10	11	12	13	14
Protein in defatted seeds %	-	34.6c	36.0c	33.5c	-	34.5	-
Lysine	3.2a	3.5	3.4	3.5	3.4	3.3	3.5
Histidine	2.2	2.3a	2.5b	2.3a	2.4b	2.2	2.2
Arginine	7.3	7.4	7.6b	7.2	7.7b	7.4	7.4
Aspartic acid	9.5a	9.3c	9.4b	9.5a	9.4b	9.4b	9.5a
Threonine + Serine	9.1c	8.7c	8.6c	-	8.7c	9.6a	9.9
Glutamic acid	22.8c	22.4b	22.7c	22.2b	22.2b	22.5b	22.9c
Proline	5.2	5.8a	5.2	5.8a	5.1a	5.2	5.3
Glycine	9.4c	10.0b	9.1c	9.1c	9.8c	9.6c	9.6c
Alanine	6.3b	6.2b	6.3b	6.3b	6.3b	6.1c	5.2c
Cystine	0.9	0.7	0.7	0.9	0.5	1.4a	1.1
Valine	5.4	5.8	6.0a	5.6	5.9	5.5	5.8
Methionine	1.6a	1.4	1.6a	1.6a	1.5	1.9b	1.7a
Isoleucine	4.2b	4.4	4.5c	4.1b	4.5	4.0a	4.1b
Leucine	6.5	6.4	6.5	6.4	6.4	6.3	6.5
Tyrosine	1.9	1.8	1.9	2.0	2.0	2.0	1.9
Phenylalanine	3.9	4.0a	4.0a	3.9	4.2b	3.7	3.8

8 - *H. debilis* ssp. *debilis* (E 011); 9 - *H. debilis* ssp. *cucumerifolius* (E 012);  
10 - *H. debilis* ssp. *silvestris* (E 013); 11 - *H. debilis* ssp. *tardiflorus* (E 014); 12 - *H. debilis* (E 082);  
13 - *H. petiolaris* ssp. *petiolaris* (E 021); 14 - *H. petiolaris* ssp. *petiolaris* (E 022)

Table 1. Amino acid composition (mol %) of wild *Helianthus* species with diploid chromosome number (n=34) (continued)

Genotype and amino acid	15	16	17	18	19	20	21	Average
Protein in defatted seeds %	36.0c	23.9a	26.8a	29.3c	41.1c	43.6c	-	
Lysine	3.9b	3.8b	3.3	3.4	2.8c	3.2a	3.2a	3.4
Histidine	2.2	2.4b	2.3a	2.3a	2.1	2.4b	2.3a	2.3a
Arginine	7.3	6.9	7.3	7.4	7.8	8.4c	7.9c	7.5a
Aspartic acid	9.5a	9.5a	9.5a	9.6a	9.3c	9.2c	9.0c	9.4b
Threonine + Serine	9.4b	9.8a	9.8a	8.7c	9.0c	8.9c	9.3b	
Glutamic acid	21.9a	21.3a	23.3c	22.9c	24.4c	24.2c	24.5c	22.8c
Proline	5.6	5.2	4.8b	5.0a	5.2	5.0a	5.2	5.3
Glycine	9.5c	9.7c	10.0b	9.6c	9.4c	9.4c	9.3c	9.6c
Alanine	5.8c	6.2b	5.1c	5.1c	6.0c	6.1c	5.7c	5.8c
Cystine	0.9	0.8	1.1	0.9	0.9	1.4a	0.3a	0.8
Valine	5.6	6.3b	5.4	5.5	5.7	5.6	5.4	5.7
Methionine	1.6a	1.5	1.7a	1.7a	1.9b	1.4	1.5	1.6a
Isoleucine	4.1b	4.6c	4.1b	4.3c	4.7	4.6c	4.5c	4.3b
Leucine	6.6	6.7a	6.5	6.6	6.4	6.3	6.4	6.5
Tyrosine	1.9	1.7a	2.0	2.0	1.7a	1.8	2.0	1.9
Phenylalanine	3.8	3.9	3.9	3.9	3.8	4.0a	3.9	3.9

15 - *H. petiolaris* ssp. *petiolaris* (E 037); 16 - *H. praecox* ssp. *hirtus* (E 027);17 - *H. praecox* ssp. *praecox* (E 028); 18 - *H. praecox* ssp. *runyonii* (E 029); 19 - *H. mollis* (E 020);20 - *H. mollis* (E 033); 21 - *H. salicifolius* (E 045)Table 2. Amino acid composition (mol %) of wild *Helianthus* species with tetraploid chromosome number (n=68)

Genotype and amino acid	1	2	3	4	Average
Protein in defatted seeds %	25.2	-	50.7c	-	
Lysine	3.4	2.8c	2.9	3.2a	3.0b
Histidine	2.2	2.4b	2.2	2.3a	2.3a
Arginine	6.8	8.6c	7.9c	7.6b	8.0c
Aspartic acid	10.0	9.3	9.4	9.9	9.5
Threonine + Serine	10.5	8.7c	8.8c	8.7c	8.7c
Glutamic acid	20.8	24.0c	24.0c	23.6	23.9c
Proline	5.4	5.0	5.1	5.1	5.1
Glycine	11.0	8.9c	9.2c	9.0c	9.0c
Alanine	6.7	5.8c	5.9c	6.3	6.0b
Cystine	0.9	1.0	0.9	0.6	0.8
Valine	5.6	5.6	5.6	5.8	5.7
Methionine	1.3	1.4	1.4	1.6c	1.5a
Isoleucine	3.7	4.6c	4.6c	4.5c	4.6c
Leucine	6.4	6.3	6.2	6.3	6.3
Tyrosine	1.9	1.8	1.8	1.8	1.8
Phenylalanine	3.7	3.9	3.9	3.7	3.8

1 - *H. annuus* cv. Peredovik (St); 2 - *H. decapetalus* (M 043); 3 - *H. hirsutus* (M 007);4 - *H. laevigatus* (M 016)

Table 3. Amino acid composition (mol %) of wild *Helianthus* species with hexaploid chromosome number (n=102)

Genotype and amino acid	1	2	3	4	5	6	7	8	Average
Protein in defatted seeds %	25.2	43.1c	-	43.6c	46.1c	36.7c	-	-	-
Lysine	3.4	3.0c	3.0c	3.4	3.0c	3.0c	3.1b	3.1b	3.1b
Histidine	2.2	2.2	2.2	2.3a	2.2	2.3a	2.3a	2.3a	2.3a
Arginine	6.8	8.0	7.8c	8.4c	8.0c	8.1c	8.1c	8.6c	8.1c
Aspartic acid	10.0	9.2c	9.3b	9.8	9.1c	9.4	9.4	9.5	9.4
Threonine + Serine	10.5	8.5c	8.7c	9.2c	8.9c	8.9c	8.0c	8.8c	8.7c
Glutamic acid	20.8	24.2c	23.3c	22.5b	23.9c	24.5c	23.9c	23.4c	23.7c
Proline	5.4	5.0a	5.2	5.0a	5.0a	5.2	5.1a	5.1a	5.1a
Glycine	11.0	9.3c	9.4c	9.4c	9.2c	9.3c	9.2c	8.9c	9.2c
Alanine	6.7	5.9c	6.2b	6.1b	5.9c	5.8c	5.6c	6.2b	6.0b
Cystine	0.9	0.8	1.0	0.4	0.9	0.4	1.3	0.4	0.7
Valine	5.6	5.9	5.5	5.6	5.8	5.6	5.7	5.7	5.7
Methionine	1.3	1.4	1.5	1.3	1.6a	0.6c	1.5	1.2	1.3
Isoleucine	3.7	4.6c	4.4c	4.6c	4.6c	4.7c	4.5c	4.7c	4.6c
Leucine	6.4	6.3	6.5	6.3	6.3	6.4	6.4	6.4	6.4
Tyrosine	1.9	1.8	1.9	1.8	1.9	1.8	1.9	1.9	1.9
Phenylalanine	3.7	3.8	4.0a	3.8	3.8	4.0a	4.0a	3.9	3.9

1 - *H. annuus* cv Peredovik (St); 2 - *H. eggertii* (M 001); 3 - *H. resinosus* (M 046); 4 - *H. rigidus* (M 002); 5 - *H. rigidus* (M 028); 6 - *H. strumosus* (M 056); 7 - *H. strumosus* (M 059); 8 - *H. tuberosus* (M 037)

with the content and qualitative composition of proteins. Sunflower is a traditional source of proteins. If sunflower breeding is conducted in this direction, it needs a wide diversity of initial materials (Christov, 1990). Some forms of the genus *Helianthus* can be used as initial genetic source.

## MATERIAL AND METHODS

The Dobroudja IWS collection is maintained in a specially arranged nursery. The perennial species are maintained in tufts of different size and number of plants which are grown in the same place for 3-4 years. The annual species are maintained by a group pollination under isolator covering whole plants.

The seeds studied represented an average sample taken from all plants. The protein analysis was conducted according to the Kjeldahl method, in ground and defatted seeds. Protein hydrolysis was made by 6N HCl in ampules sealed under vacuum. The amino acid composition of proteins was determined by a highly efficient Hitachi Amino Acid Analyzer L 8500. The statistical calculations were done according to Snedecor and Cochran (1957).

## RESULTS AND DISCUSSION

The genotypes studied were identified according to the specifications of the institutes which had sent the accessions and some specification made at the IWS in accordance with the descriptions of Heiser et al. (1969) and Rogers et al. (1982).

The maintenance of genotypic specificity of the perennial species was done by vegetative propagation, of the annual ones by sib-pollination. As the *Helianthus* species are highly heterogeneous, vegetative propagation of the perennial species allows the stabilization of forms which differ considerably among themselves. In the annual species, differentiation of a genotype is possible as a result of self-pollination of a single plant in natural or artificial conditions. In this way, each species is represented by a different number of stabilized genotypes which, in total, express the diversity of the given species.

With the above in mind, we concentrated our investigation on the stabilized genotypes and separate data are given for each accession number. This approach was followed whenever a wild *Helianthus* species were involved in hybridization.

Thus, comparative specifications are given for the studied genotypes using the results of different authors.

The data in this study are arranged in accordance with ploidy level and are presented in Tables 1, 2, and 3. The characteristics of cv. Peredovik are given too.

The group of diploid species (Table 1) was largest and it contained the highest diversity of forms regarding the protein content in seeds. The variation ranged from 23.9% to 43.6%. The values for the other two groups are higher and they reach 50.7% (Tables 2 and 3). The accessions *H. hirsutus*-M 007, *H. rigidus*-M 002 and M 008, *H.*

Table 4. Essential amino acid score of the mean values of some wild *Helianthus* species from the collection of IWS "Dobroudja"

<i>Helianthus</i> ploidy group	Amino acid					
	Lysine	Cystine + Methionine	Valine	Isoleucine	Leucine	Tyrosine + Phenylalanine
cv. Peredovik						
Amino acids, %	3.7	2.8	4.2	3.7	6.4	7.3
Amino acids score, %	67.3	80.0	84.0	92.5	91.4	121.7
Diploid (2n=34)						
Amino acids, %	3.7	3.1	4.9	4.2	6.3	7.5
Amino acids score, %	67.3	88.6	98.0	105.0	90.0	125.0
Tetraploid (2n=68)						
Amino acids, %	3.3	3.3	5.0	4.3	6.1	7.0
Amino acids score, %	60.0	94.3	100.0	107.5	87.1	116.7
Hexaploid (2n=102)						
Amino acids, %	3.3	2.6	4.9	4.4	6.2	7.3
Amino acids score, %	60.0	74.3	98.0	110.0	88.6	121.7

*mollis*-M 033, and *H. eggertii*-M 001 are valuable for increasing protein content in cultivated sunflower.

Regarding protein quality, two entries from the group of diploid species, *H. petiolaris*-E 037 and *H. praxox*-E 027, are of interest. These were found to possess a high lysine content - 3.9% and 3.8%, respectively (Table 1). Concerning the contents of aspartic acid and glycine, all species of that group were below the standard, while they were above the standard in the contents of histidine, glutamic acid, and isoleucine. The level of the sulphur-containing amino acids (methionine and cysteine) was also increased. *H. petiolaris*-E 021, *H. annuus*-E 004, and *H. mollis*-M 020 are of some interest in this respect.

Table 2 presents the data for the group of tetraploid species. Their lysine, threonine + serine, glycine, and alanine contents were comparable with those of the standard, while the contents of arginine, glutamic acid, and isoleucine were higher.

Seven entries from five hexaploid species comprised the third group (Table 3). Lysine, the limiting amino acid in sunflower, was smaller in all representatives of this group except *H. rigidus*-M 002 whose lysine content was on the level of that found in cv. Peredovik. The contents of arginine, glutamic acid, and isoleucine were higher than those of the standard, the contents of threonine + serine, proline, glycine, and alanine were below those of the standard.

When summarizing the results, it was established that some wild species were distinguished for the higher contents of certain amino acids - lysine, arginine, and glutamic acid - as compared with the standard variety Peredovik.

In addition to *H. annuus*-E 004, *H. petiolaris*-E 021 and E 037, and *H. praxox*-E 027, the entries *H. laevigatus*-M 016, *H. eggertii*-M 001, and *H. rigidus*-M 002 were also found to be of interest for breeding.

The results of this investigation differ to a certain degree from those published before by Ivanov et al. (1984). The explanation for the differences is that other entries have been involved in the previous study. Consequently, it appears reasonable to assume that the entries in the Dobroudja IWS collection which did not take part in the two studies are of interest for further investigation.

The average values of the essential amino acids are given separately for each ploidy group in Table 4. The table contains also the amino acid score calculated as a ratio of the quantity of a single amino acid to its quantity expressed in a standard protein (FAO/WHA, 1973; Ribarova et al., 1987). The amino acid score for lysine in cv. Peredovik was 67% and was equal to that of the group of diploid species (67.3%). The indices for the other two ploidy groups were lower (60%).

The amino acid scores for the sulphur-containing amino acids, cysteine and methionine, in the standard, the diploid, tetraploid, and hexaploid group were 80%, 88.6%, 94.3%, and 74.3%, respectively.

The amino acid score for valine, an essential amino acid, was 84% in cv. Peredovik while in the groups of wild species it ranged between 98% and 100%. A similar relationship was obtained for isoleucine, e.g., 92.5% in cv. Peredovik and 110% in the hexaploid species.

A reverse tendency was observed for leucine: 91.4% in cv. Peredovik and 87.1% in the group of tetraploid species.

The amino acid score for alanine was 121.7% in the standard and it was more or less the same in the three groups of wild species.

It is well-known that each amino acid is important for biochemical processes in the living organism. Plant foodstuff is the main source of proteins in human food and animal feed alike. This demonstrates the importance of the knowledge of amino acid composition in the proteins of different wild *Helianthus* species for successful breeding work.

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#### ALGONAS CARACTERISTICAS DE LAS ESPECIES DEL GENERO *Helianthus* PRESENTADAS EN LA COLECCION "DOBROUDJA" ZWS. 1. CONTENIDO EN PROTEINA Y SU COMPOSICION DE AMINOACIDOS

#### RESUMEN

El contenido en proteína en las semillas y su composición de aminoácidos de 30 genotipos de 16 especies de *Helianthus* fueron estudiadas. Los resultados indicaron que algunas entradas de las especies de *Helianthus* podrían ser utilizadas como fuente de genes para mejorar el valor nutritivo de la proteína obtenida a partir de modernos cultivares e híbridos. Las entradas *H. hirsautus*: M007, *H. rigidus*, M002 y M028, *H. mollis*, M033, y *H. eggertii*, M001 mostraron mucho mas alto contenido en proteína en comparación con Peredovic. Comparadas con las entradas estandar *H. annuus* E004, *H. petiolaris*, E021 y E027, *H. praecox*, 027, *H. laevigatus*, M016, *H. eggertii*, M001 y *H. rigidus*, M002 tuvieron un contenido mas alto de algunos aminoácidos. Estas entradas son mantenidas en Dobroudja Iws y podrían ser utilizadas en hibridación interespecifica en girasol.

**CHARACTÉRISTIQUES D'ESPÈCES DU GENRE HELIANTHUS PRÉSENTÉES DANS LE COLLECTION IWS DE "DOBROUDJA"****RÉSUMÉ**

La teneur en protéines dans les graines et leur composition en acides aminés sont étudiées pour 30 génotypes de 16 espèces du genre *Helianthus*. Les résultats indiquent que certaines introductions des espèces sauvages d'*Helianthus* pourraient être utilisées comme sources de gènes pour améliorer la valeur protéique nutritionnelle obtenues par les cultivars modernes et hybrides. Les introductions *H. hirsutus* (M007), *H. rigidus* (M002 et M028), *H. mollis* (M033) and *H. eggertii* (M001) se distinguent par leur haute teneur en protéines en comparaison avec Peredovic. Comparées au témoin, les introductions *H. annuus* (E004), *H. petioleri* (E021 et E037), *H. praecox* (E027), *H. laevigatus* (M016), *H. eggertii* (M011) et *H. rigidus* (M002) ont de hautes teneurs en certains acides aminés. Ces introductions sont maintenues à l'IWS de "Dobroudja" et pourraient être utilisées dans un programme d'hybridation à base large chez le tournesol.