

GENETIC DIVERSITY OF SUNFLOWER (*Helianthus annuus* L.) VARIETAL POPULATIONS ASSESSED BY CLUSTER ANALYSIS

R. Marinković, M. Mihaljcevic, J. Joksimović

Faculty of Agriculture, Institute of Field and Vegetable Crops,
M. Gorkog 30, 21000 Novi Sad, Yugoslavia

Summary

Genetic diversity for 1,000-seed mass, husk and kernel percentages, and oil concentration in seed was assessed in 78 varietal populations of sunflower (*Helianthus annuus* L.) by the hierarchical cluster analysis with the Euclidean distance treated as a metric distance. The populations were grouped in five clusters. Cluster 5 was considered interesting for further study regarding the mass of 1,000 seeds, cluster 1 for the other characteristics.

Introduction

Sunflower (*Helianthus annuus* L.) is among the four most important oil crops in the world. Its acreage has increased steadily but its further expansion will depend on the crop's genetic potentials for seed yield and oil concentration.

To realize these breeding targets, genetically diverse materials must be available and an appropriate breeding method should be employed. A knowledge of genetic diversity within and between population groups or genotypes is useful for reducing the number of parental pairs in initial phases of the breeding program.

When a large germplasm collection is available, it is sometimes a problem to classify and group the individuals in the collection according to their variability. The method of hierarchical cluster analysis is convenient for that purpose because it allows qualitative and quantitative data to be combined, a large number of attributes to be assigned to each member, each individual to have an equal function in the analysis, and the genetic similarities and differences to be evaluated.

The cluster analysis has been used for maize (CAMUSSI, 1979), rice (VAIRAVAN ET AL., 1973), castor bean (PATEL ET AL., 1985; ĆERANIĆ, 1990), wheat (JAIN ET AL., 1975; MURPHY ET AL., 1986; CARVER ET AL., 1987), etc. Despite its evident applicability, the analysis has not been used extensively in sunflower research. MIHALICEVIC (1991) and YADOVA (1985) used it to classify sunflower hybrids and populations.

The objective of this paper was to study the diversity of 78 sunflower populations.

Material and Method

Of the 78 sunflower populations analyzed, a portion was obtained from the North Central Regional Introduction Station, Ames, Iowa, USA, another portion from VIR, Petersburg, CIS.

In 1991, the materials were sown at the experiment field of the Institute of Field and Vegetable Crops at Rimski Šančevi. The sowing was done after the design of random blocks, in three replications. The sowing arrangement was 70 x 30 cm. Each population was sown in four rows per replication but the two inner rows were analyzed. In the course of the growing season, the experiment was chemically treated and hoed, to control weeds.

The mass of 1,000 seeds (g), husk and kernel percentages, and oil concentration in seed (%) were assessed in the laboratory.

The sample for the percentages of husk and kernel was 2 x 5 g per plant. The husks were separated manually.

Oil concentration was determined by the method of nuclear magnetic resonance.

The statistical calculations were done by the System for Statistics SYSTAT Ver. 5.0, software modules STATS and CLUSTER. The sample size was 60 plants per population. For clarity, we used the five-group K means analysis with the Euclidean distance treated as a metric distance.

Results and Discussion

The minimum values of 1,000-seed mass, husk percentage, kernel percentage, and oil concentration were 50.68 g (Trudovik), 17.62% (Harkovski), 52.05% (Select), and 21.64%

(Grey Stripe), respectively. The corresponding maximum values were 107.95 g (Grey Stripe), 47.95% (Chernyanka), 82.11% (Harkovski), and 50.79% (Voshod), respectively (Table 1).

Tab. 1 - Summary statistics for the four characters in the collection

Character	No. of	Mean	Se	Min	Max	S	Skewness	C.V.
1,000-seed mass	78	69.69	0.22	45.50	115.00	10.74	0.85	0.15
Husk %	78	30.30	0.18	14.00	55.60	8.49	0.37	0.28
Kernel %	78	69.72	0.18	44.40	86.00	8.49	-0.37	0.12
Oil conc.	78	39.38	0.16	17.81	52.37	7.66	-0.28	0.19

The positive values of skewness for 1,000-seed mass and kernel percentage indicate asymmetry in respect to the values higher than the mean value. The negative values, for husk percentage and oil concentration, indicate asymmetry in respect to the values lower than the mean value.

The coefficients of variation ranged from 0.12 for husk percentage to 0.28 for kernel percentage.

Tab. 2 - Summary statistics for the five clusters

Character	Between SS	DF	Within SS	DF	F ratio
1,000-seed mass	7842.22	4	755.06	73	189.55
Husk %	5247.70	4	191.50	73	500.11
Kernel %	5257.96	4	186.55	73	514.37
Oil conc.	4141.29	4	304.82	73	247.95

In addition to plant number per unit area and seed number per plant, 1,000-seeds mass is an important yield component. In our case, most populations (59) were in clusters 1 and 2. However, only the populations in clusters 3 and 4, which have highest values of 1,000-seed mass, should be included in future breeding programs (Table 3).

Unlike the other characters studied, high husk percentage is not desirable. Most populations were in cluster 1 (30), but only those with the husk percentage below the cluster's mean

value are of interest for breeding. The populations in clusters 3, 4, and 5 are absolutely inapplicable for breeding purposes.

Tab. 3 - Mean values, limits and number of populations belonging to the five clusters

Character	Cluster	Mean	Min	Max	S	No. of populations
1,000-seed mass (g)	5	53.48	50.68	56.08	2.04	6
	1	61.84	57.73	66.13	2.31	25
	2	71.56	66.73	77.63	3.35	34
	3	84.59	78.97	91.18	3.79	11
	4	102.58	97.22	107.95	5.35	2
Husk percentage	1	21.99	17.62	24.80	1.63	30
	2	28.03	25.36	31.07	1.75	17
	3	35.43	33.13	37.49	1.26	12
	4	41.42	38.73	43.65	1.52	16
	5	46.56	45.27	47.95	1.10	3
Kernel percentage	5	53.48	52.05	54.83	1.14	3
	4	58.58	56.35	61.27	1.53	16
	3	64.61	62.52	66.87	1.26	12
	2	71.97	68.93	74.57	1.75	17
	1	78.05	75.20	82.11	1.57	30
Oil concentration (%)	5	21.64	21.64	21.64	0.00	1
	4	27.12	25.51	28.10	0.89	6
	3	31.72	29.48	34.37	1.40	18
	2	37.53	34.72	41.32	1.85	16
	1	46.38	42.21	50.79	2.38	37

In accordance with the opinion that the selection for high oil yield is possible on the basis of kernel percentage (DIAKOV, 1966), the populations in cluster 1 are applicable for breeding on account of high values for this character. Most of the tested populations were in this cluster, but only those with the oil concentration above the cluster's mean value ($> 46.38\%$) will be included in future breeding programs.

The population Sputnik 70, with the oil concentration in seed of 21.64%, was the only member of cluster 5.

Tab. 4 - The populations and cluster number for the examined characters

Population	1	2	3	4	Population	1	2	3	4
Sunrise	1	4	4	3	Černjanka select	5	5	5	4
Klein	2	4	4	3	Černjanka 66	1	2	2	1
Novosadski 4	2	4	4	3	Orizont	2	1	1	1
Iregi Alscsony	3	4	4	3	Gigant 549	3	4	4	4
VNIIMK 1646	1	2	2	2	Arikara	3	4	4	4
VNIIMK 8931	3	3	3	2	Havasupai	5	4	4	4
Ždanovskij 8281	1	2	2	2	Seneca	3	4	4	3
Ždanovskij 8281 mont.res.	1	2	2	2	Jugoslavskij	1	2	2	1
Armavirskij 9342	2	2	2	2	Voshod	2	1	1	1
VNIIMK 8883 mont.res.	2	1	1	1	Vympel	1	1	1	1
Černjanka 66	2	2	2	2	Peredovik 301 59% oil	1	1	1	1
Cinza 42	2	4	4	3	Luch	1	1	1	1
Černjanka 11	2	3	3	2	Dark stripe	3	4	4	3
Saratov	5	4	4	3	Gray stripe	4	5	5	5
VNIIMK 4966	2	5	5	4	Cordobes inta	1	3	3	2
VNIIMK 6540	1	2	2	2	Guayacan inta	2	3	3	3
Iregi Koraj Csikos	1	4	4	3	Impira inta	2	4	4	2
Nain Noir	3	4	4	4	Pehuan	3	3	3	2
Saratovskij rani	3	3	3	3	P-20	2	1	1	1
Saratovskij 10	2	2	2	2	Wielkopolski	1	2	2	1
Zeljonka 10	2	3	3	3	Sputnik 70	1	1	1	1
Bamniszkij 1501	5	3	3	3	Majak	1	2	2	1
Smena 51% oil	5	1	1	1	Saratovskij karlik	2	3	3	1
Jenisej	3	2	2	2	Karlik	1	1	1	3
Comet	2	4	4	3	Armavirskij 1813	1	2	2	1
Jupiter	1	3	3	2	Volgar 74	3	1	1	1
Smena	2	1	1	1	Saljut	2	1	1	1
VNIIMK 8883	1	2	2	2	Harkovski	1	1	1	1
Saratovskij 49% oil	4	2	2	1	Tambovskij Skorospelij	2	1	1	1
Donskij	1	1	1	1	Novinka	2	1	1	1
Jugovastok	1	2	2	2	Čakinskij 269	2	1	1	1
Černjanka 11	2	3	3	3	Nadjožnij	2	1	1	1
Černjanka 35	1	3	3	3	Jubilejnij 60	2	1	1	1
H. x multiflorus	2	4	4	3	Progres	2	1	1	1
Armavirskij 3497	2	1	1	1	Trudovik	5	2	2	1
Majak	2	1	1	1	Skorospelij	2	1	1	1
Felenka	2	1	1	1	Avangard	1	1	1	1
Smena	2	1	1	1	Zarija	2	1	1	1
Krasnodarec	1	1	1	1	Voronežskij 436	2	1	1	1

1 - 1,000-seed mass, 2 - Husk %, 3 - Kernel %, 4 - Oil concentration

Conclusion

The results obtained indicate that the hierarchical cluster analysis is a useful tool for the study of variability in germplasm collections. The analysis allows for the most interesting genotypes to be selected and included in further work.

The populations in cluster 5 are recommended for breeding for high 1,000-seed mass. Regarding the other three characters, the populations in cluster 1 may be recommended.

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