

PHENOTYPE VARIABILITY AND INHERITANCE OF LEAF SHAPE IN F₁ GENERATION OF SUNFLOWER

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Populations of wild sunflower species were crossed with cms cultivated lines because of their high variability. Variability was determined by measuring inflorescence diameter, ray flower number and the leaf length and width. The data was used for hierarchical cluster analysis in the SYSTAT 10 program and the obtained dendrogram was used to interpret divergence of used populations. Comparing 25 hybrid populations with parents tested the modes of inheritance. Cluster analysis divided plants in to three groups. The first ones were inbred lines of cultivated sunflower. In the middle of the cluster tree were annual wild species and the third group were perennial wild species. The mean value differences in observed traits between parents were significant. All modes of inheritance were present in F₁ generation. Intermediate was the most frequent followed by equal number of partially dominant and dominant ones and in two hybrid combinations, negative heterotic effect was scored.

Key words: sunflower, wild species, interspecies hybridisation, variability, leaf shape, inheritance

INTRODUCTION

There are seven annual and 21 perennial species of wild sunflowers in the collection of oil crops department. They are being used because of high variability

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that has been confirmed by cluster analysis of morphological characters (SCHILING and HEISER, 1981) which also showed phylogenetic relationships inside the *Helianthus* genus. By sunflower descriptors (IBPGR 1985), there are five types of leaf shape: elongated, копљаста, троугаона, срцаста и rounded. For easier statistical processing and quantitative nature of data an index of leaf shape was used (VISCHI *et al.* 2002). The mode of inheritance for leaf shape is important because of the use of wild species in sunflower breeding and large variability of that trait. The goal of this work is to define the variability of the tested traits and the mode of inheritance for leaf shape. That will be done through hybridisation of cultivated inbred lines with the populations of wild sunflower.

MATERIALS AND METHODS

Seven perennial populations and eighteen annual populations have been used for hybridisation. Pollen from wild species has been applied to the inflorescence of cultivated cytoplasmatic sterile sunflower. Wild species that could not be crossed directly with cultivated lines were crossed with other wild species.

Leaf width and leaf length without petiole was measured on all F1 and parent populations. Those values were divided to obtain the index of leaf shape. The leaf width was measured in the broadest part and the length from the base to the top. Genetic distance was analysed by cluster method and shown through cluster tree. Three traits were used for the cluster analysis: index of leaf shape, inflorescence diameter and the number of ray flowers. All values were transformed by z transformation. The leaf length and width measures were used also for calculating mean values, standard deviation and the coefficient of variation. The mode of inheritance was determined by testing significance of mean values of F1 generation in compare to the mean value of parent populations (BOROJEVIĆ, 1965).

RESULTS

A cluster analysis was done to check the genetic distance of the used populations. Three groups of populations were formed with minor variations (Fig. 1). First, are the cultivated lines, annual wild species are second and the third are perennial wild species.

Population *H. argophyllus* 1805 forms the first cluster with cultivated inbred lines. In the middle cluster are annual wild species with the exception of three inbred lines PHBC1-202, 212 and 213, which are positioned next to the first cluster and two populations of perennial species *H. tuberosus* 1700 and *H. mollis* X that are next to the third cluster.

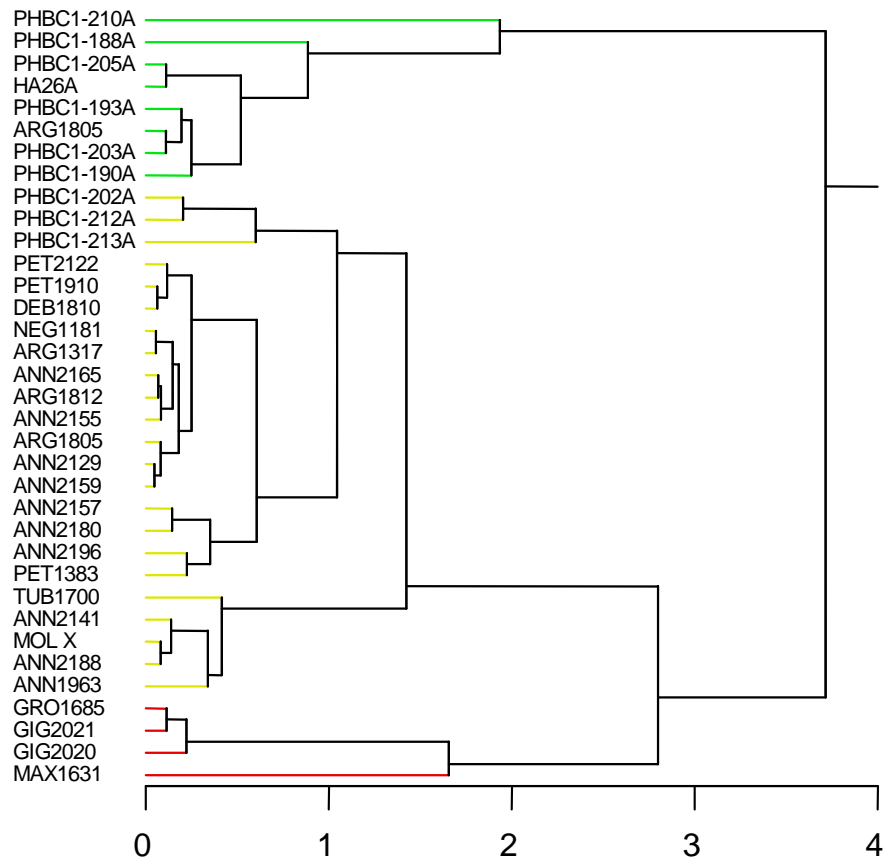


Fig. 1. Dendrogram of parent populations

All modes of inheritance were registered, from intermediate (48%) to heterosis (8%). Partial domination was noted at 24% of hybrid combinations and dominance at 20% (Table 1.).

Mean values of parent populations were significantly different in all hybrid combinations except at the cross PHBC1-203A X ARG1812 and PHBC1-202A X ARG1812 where the difference was significant only by 0.05. Of the used populations, the highest mean value was scored at MAX1631 (8.317) and the lowest HA26A (0.914). Negative heterotic effect was scored at two hybrid combinations: TUB1700 X MAX1631 and PHBC1-213A X ANN2165. The variability of leaf shape was always greater in the wild sunflower populations than the cultivated except at the cross PHBC1-188A X ANN1963.

Table 1. Hybrid combinations, basic statistics and modes of inheritance.

Hybrid combinations		$\bar{X} \pm s_x$	S	V	Inheritance*
PHBC1-190A	P	1.069 ± 0.018	0.058	5.4	
PHBC1-190A x ANN2159	F ₁	1.234 ± 0.032	0.101	8.2	i
ANN2159	P	1.376 ± 0.041	0.130	9.5	
ARG1805	P	1.520 ± 0.04	0.128	8.4	
ARG1805 x MAX1631	F ₁	1.402 ± 0.02	0.064	4.6	d
MAX1631	P	8.317 ± 0.296	0.935	11.2	
PHBC1-210A	P	1.233 ± 0.009	0.027	2.2	
PHBC1-210A x ANN2165	F ₁	1.261 ± 0.053	0.167	11.1	i
ANN2165	P	1.339 ± 0.032	0.101	7.6	
PHBC1-203A	P	1.189 ± 0.026	0.083	7	
PHBC1-203A x ARG1812	F ₁	1.148 ± 0.031	0.098	7.8	d ^k
ARG1812	P	1.278 ± 0.025	0.080	6.3	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x ANN2159	F ₁	1.235 ± 0.011	0.033	2.8	pd ^d
ANN2159	P	1.376 ± 0.041	0.130	9.5	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x ANN2188	F ₁	1.321 ± 0.022	0.069	5.6	i
ANN2188	P	1.700 ± 0.015	0.047	2.8	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x ANN2157	F ₁	1.246 ± 0.050	0.159	12.1	d ^d
ANN2157	P	1.350 ± 0.042	0.131	9.7	
PHBC1-205A	P	1.078 ± 0.018	0.058	5.4	
PHBC1-205A x ANN2196	F ₁	1.200 ± 0.035	0.112	9	i
ANN2196	P	1.261 ± 0.029	0.092	7.3	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x ANN2155	F ₁	1.183 ± 0.025	0.079	6.6	i
ANN2155	P	1.432 ± 0.022	0.071	4.9	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x ANN2129	F ₁	1.375 ± 0.038	0.120	10.1	pd ^d
ANN2129	P	1.504 ± 0.016	0.051	3.4	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x NEG1181	F ₁	1.235 ± 0.029	0.093	6.8	i
NEG1181	P	1.629 ± 0.058	0.184	11.3	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x ANN2141	F ₁	1.351 ± 0.029	0.092	7.5	pd ^k
ANN2141	P	2.005 ± 0.058	0.185	9.2	
PHBC1-188A	P	1.244 ± 0.022	0.069	5.5	
PHBC1-188A x ANN1963	F ₁	1.348 ± 0.024	0.076	5.7	pd ^k
ANN1963	P	1.633 ± 0.022	0.071	4.3	
PHBC1-202A	P	1.190 ± 0.018	0.058	4.9	
PHBC1-202A x ARG1812	F ₁	1.263 ± 0.034	0.107	8.5	d ^d
ARG1812	P	1.278 ± 0.025	0.080	6.3	

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Hybrid combinations		X ± sx	S	V	Inheritance*
PHBC1-213A	P	1.214 ± 0.027	0.086	7.1	
PHBC1-213A x ANN2165	F ₁	1.152 ± 0.008	0.026	2.2	h
ANN2165	P	1.339 ± 0.032	0.101	7.6	
PHBC1-212A	P	1.157 ± 0.009	0.029	2.5	
PHBC1-212A x DEB1810	F ₁	1.174 ± 0.003	0.008	0.7	d ^k
DEB1810	P	1.669 ± 0.038	0.119	7.1	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x ANN2180	F ₁	1.145 ± 0.02	0.064	5.6	i
ANN2180	P	1.280 ± 0.038	0.120	9.4	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x PET1383	F ₁	1.196 ± 0.005	0.016	1.4	i
PET1383	P	1.651 ± 0.077	0.242	14.7	
HA26A	P	0.914 ± 0.014	0.043	4.8	
HA26A x PET2122	F ₁	1.284 ± 0.001	0.005	0.4	pd ^k
PET2122	P	1.898 ± 0.058	0.182	9.6	
GIG2020	P	5.705 ± 0.265	0.837	14.7	
GIG2020 x ANN2159	F ₁	3.424 ± 0.087	0.274	8	i
ANN2159	P	1.376 ± 0.041	0.130	9.5	
GIG2021	P	5.376 ± 0.197	0.624	11.6	
GIG2021 x ARG1317	F ₁	3.798 ± 0.215	0.680	17.9	i
ARG1317	P	1.578 ± 0.046	0.147	9.3	
GRO1685	P	5.112 ± 0.227	0.719	14.1	
GRO1685 x MOLX	F ₁	3.513 ± 0.037	0.116	8.6	i
MOLX	P	1.777 ± 0.041	0.129	7.3	
TUB1700	P	2.653 ± 0.138	0.437	16.5	
TUB1700 x MAX1631	F ₁	1.811 ± 0.021	0.066	3.7	h
MAX1631	P	8.317 ± 0.296	0.935	11.2	
PHBC1-214A	P	1.126 ± 0.024	0.076	6.7	
PHBC1-214A x ARG1805	F ₁	1.246 ± 0.032	0.102	8.2	i
ARG1805	P	1.520 ± 0.04	0.128	8.4	
PHBC1-193A	P	1.200 ± 0.008	0.025	2.1	
PHBC1-193A x PET1910	F ₁	1.285 ± 0.004	0.013	1	pd ^k
PET1910	P	1.695 ± 0.037	0.116	6.8	

* i-intermediate, h-heterosis, pd^k-partial domination of cultivated sunflower, d^d-domination of wild sunflower, d^k-domination of cultivated sunflower.

DISCUSSION

The distance between the populations of the cluster tree matches their cross compatibility and the variations in compare to the three mentioned groups are the result of intraspecific variability (ATLAGIĆ *et al.*, 1999). Appearance of heterosis shows us that there are epistatic interactions between mentioned genotypes.

The leaf shape index shows continuous variability according to normal distribution of frequencies. Such variability is due to larger number of genes that

control the inheritance of leaf shape (MARINKOVIĆ *et al.*, 1993). Because of additive gene effect, the tested trait at F1 plants can be intermediate or partially dominant (VISCHI *et al.*, 2002). Dominant and superdominant modes of inheritance have been reported for leaf length and width and for the leaf area (MARINKOVIĆ, 1980; MARINKOVIĆ *et al.*, 1993). MACURA (1986) performed crosses between wild species and cultivated sunflower and found all modes of inheritance for leaf length and width and the most frequent one was partial domination.

More than one mode of inheritance occurred because of large variability in wild species and poligenic determination of leaf shape. The mean value differences between parents in majority of hybrid combinations were significant. Because of that determination of the mode of inheritance was influenced by genetic differences between parents as well as the interaction with environment.

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**VARIJABILNOST OSOBINA CVASTI I LISTA I NASLEĐIVANJE
OBLIKA LISKE SUNCOKRETA U F₁ GENERACIJI**

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Izvod

Zbog izražene varijabilnosti divlje vrste su korišćene za ukrštanja sa *cms* linijama gajenog suncokreta. Varijabilnost je utvrđena merenjem prečnika cvasti, broja jezičastih cvetova, dužine i širine liske. Podaci su obrađeni putem hijerarhijske klaster analize u programu SYSTAT 10 i dobijen je dendrogram na osnovu koga je tumačena divergentnost ispitivanih populacija. Način nasleđivanja je utvrđivan poređenjem 25 hibridnih kombinacija sa roditeljima. Klaster analizom su razdvojene tri grupe biljaka. Prvu čine inbred linije samooplodnog suncokreta. U srednjem delu dendrograma su jednogodišnje divlje vrste i treća grupa su višegodišnje divlje vrste. Razlike u srednjim vrednostima ispitivanih svojstava između roditelja su bile značajne. Zastupljeni su bili svi tipovi nasleđivanja. Najviše je bilo intermedijarnog, zatim parcijalno dominantnog i dominantnog, a u dve hibridne kombinacije manifestovao se negativni heterozis.

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