ÚSTAV ZEMĚDĚLSKÝCH A POTRAVINÁŘSKÝCH
INFORMACÍ

GENETIKA A ŠLECHTĚNÍ

GENETICS AND PLANT BREEDING

4

ROČNÍK 32 (LXIX)
PRAHA 1996
CS ISSN 0862-8629

ČESKÁ AKADEMIE ZEMĚDĚLSKÝCH VĚD

GENETIKA A ŠLECHTĚNÍ
GENETICS AND PLANT BREEDING

An international journal published by the Czech Academy of Agricultural Sciences and with the promotion of Ministry of Agriculture of the Czech Republic

Abstracts from the journal are comprised in the databases: Agrindex, Biol. Abstr., Bibl. Agri., Chem. Abstr., Field Crop Abstr., Helminthol. Abstr., Herb. Abstr., Landwirt. Zentralbl., Plant Breed. Abstr.

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Subscription information: Subscription orders can be entered only by calendar year and should be sent to the contact address.
Subscription price for 1996 is 178 Kč, 44 USD (Europe) and 46 USD (overseas)

Periodicity: The journal is published four times a year.

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Genet. a Šlecht., *32*, 1996 (4): 241-248

SEGREGATION OF SPECIFIC TRAITS IN DOUBLED HAPLOID REGENERANTS OF WINTER OILSEED RAPE*

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Abstract: Erucic acid (EA), glucosinolate (GSL) content and self-incompatibility (SI) degree segregation were investigated in doubled haploid regenerants of oilseed rape. No statistically significant difference was proved between the donor plant of a high 00 quality and its DH progeny on 95% confidence level in EA content that ranged from 0.15 to 0.74%. Seven of DH regenerants proved statistically significant lower content of GSL in comparison with the initial plant. GSL content in μmol/g seeds ranged from 7.33 to 20.00, the value of the initial plant was 27.33. DH regenerants derived from four F_1 combinations of SI and self-compatible (SC) 00 breeding material segregated in completely SI plants from 10.0 to 26.8 % whereas the expected rate SI to SC plants was 1:1. It could be caused by the effect of gametic selection in microspore cultures. No differences have been observed when inbred or DH lines were used as SI parental components. There is little chance to gain desired combinations of SI and 00 quality. That is why it is necessary to produce a large amount of DH regenerants per initial F_1 hybrids.

winter oilseed rape; doubled haploid; segregation of traits; erucic acid; glucosinolates; self-incompatibility

One of the possibilities to increase the rapeseed yield is the hybrid breeding. Application of doubled haploid (DH) system facilitates production of completely homozygous lines within one generation in comparison with traditional methods. The main demands for parental lines of hybrids are the high seed quality and stable and reliable degree of self sterility. We have recently obtained some genetic resources of doubled zero (00) quality and several homozygous self-incompatible lines. Self-incompatibility (SI) in our

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* Supported by Grant Agency of the Czech Republic (grant No. 506/94/1081).

lines proved to be determined by multiple recessive S alleles in one locus (Kučera et al., 1996; Havel, 1996). Low erucic acid (EA) and glucosinolate (GSL) content is controlled by several recessive genes. Therefore the stabilization and combination of these traits using conventional breeding methods is not efficient enough. The aim of our experiments is to obtain homozygous DH lines with a high degree of SI and 00 oil quality. This procedure could be complicated by the occurrence of gametic selection that may cause lower frequency of desired genotypes (Foisset et al., 1993). Our experimental work should enable obtaining necessary information about the doubled haploid utilization for creation the homozygous lines with combination of some characters determined mainly by recessive genes.

MATERIAL AND METHODS

One plant selected from a new bred material originated in Research Institute of Oilseed Crops (RIOC) Opava was chosen as a donor of 00 quality for variability of this trait in DH regenerants determination. Four F_1 hybrid combinations of homozygous SI lines and self-compatible (SC) 00 quality resources from RIOC Opava and Research Institute of Crop Production Prague-Ruzyně were prepared for DH lines production with combination of these characters. For obtaining DH line methods of pollen embryogenesis in microspore cultures and diploidization of haploids by the colchicine treatment *in vitro* were used (Vyvadilová, Zelenková, 1992; Vyvadilová et al., 1993). Regenerants from *in vitro* cultures were transferred to soil in 8 cm pots and after 7–8 weeks of vernalization were transplanted to 19 x 19 cm plast containers and grown in an insect protected glasshouse. Haploids and aneuploids detected by means of karyological analyses of young plants were excluded.

Determination of erucic acid and glucosinolate content were made with methods described by Kolovrat (1985) and Zukalová (1992), modified for a low number of seeds. Self-incompatibility degree and stability were tested by repeated self pollination in flowers of individual plants during the period December–March and the evaluation of seed set in 10 developed pods. As SI were considered plants with the mean number of seeds per pod approximately from 0.0 to 3.0 and partially SI from 3.1 to 5.0. Plants that proved the seed set above 5.0 were counted as completely self-compatible. Selected SI plants were additionally self pollinated in buds for their reproduction and quality analyses of seeds. One-way analysis of variance using confidence level 95% was used for statistical evaluation of obtained data. Seed quality data were evaluated by Scheffes and SI data by Tukey's test.

RESULTS AND DISCUSSION

Erucic acid and glucosinolate content segregation

Results of evaluation of 23 DH regenerants derived from the donor plant 309/ 94 are given in Table I. For EA content that was determined from two analyses of individual samples no statistically significant difference was proved between the initial plant and its DH progeny on 95% confidence level although *F*-ratio (2.399) was on the level of significance. EA content of individual regenerants ranged from 0.15 to 0.74%. Evaluation of GSLcontent was 3 to 4 times repeated for every sample. Seven of the evaluated regenerants proved statistically significant lower content of GSL in comparison with the initial plant (Fig. 1). GSL content in μmol per g of seeds ranged from 7.33 to 22.00 whereas the value of plant 309/94 was 27.33. Obtained results corresponding with our previous experiments with DH regenerants (Kučera et al., 1993) suggest the possibility to gain homozygous oilseed rape lines with improved and stabilized 00 seed quality by means of this method. However it is necessary to use donors of a high 00 quality for deriving DH lines.

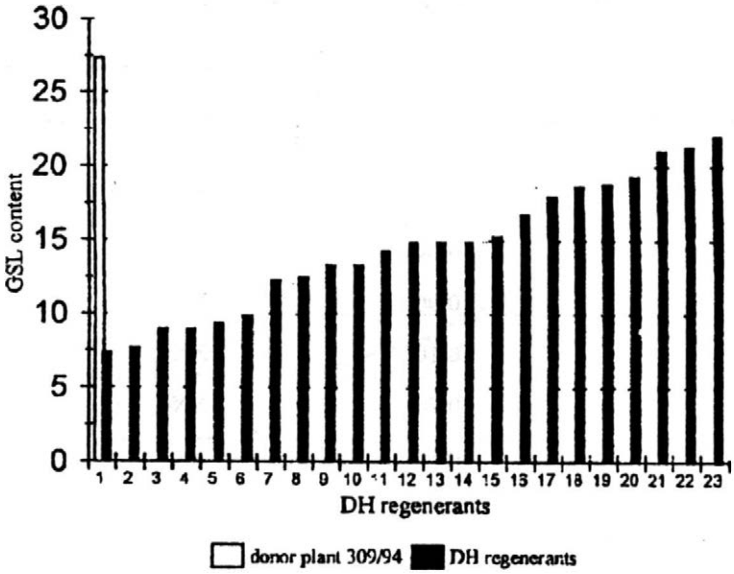
Self-incompatibility to self-compatibility segregation

Comprehensive results of testing DH regenerants originated from four F_1 combinations of SI lines and SC breeding materials are given in Table II. Number of SI plants in individual groups of regenerants ranged from 10.0 to 26.8%, partially SI plants from 0.0 to 8.0% and completely SC from 69.6 to 90.0%. Fig. 2 shows a broad range from completely and partially SI to highly SC plants that was observed in all of regenerants groups. Only the plants possessing the mean seed set per pod from 0.0 to 10.0 were chosen in every group of regenerants for statistical evaluation. Table III demonstrates segregation of SI to SC in DH regenerants derived from OP 600 F_1 genotype as an

I. Erucic acid and glucosinolate content segregation in DH regenerants from the donor plant 309/94

Plant No.	EA [%]	GSL [μmol/g seed]	Homogeneous groups for GSL content
309/24	0.40	7.33	X
309/67	0.24	7.67	X
309/16	0.53	9.00	X
309/18	0.32	9.00	X
309/12	0.21	9.33	X
309/11/1	0.74	10.00	X
309/102	0.15	12.33	X X
309/108	0.26	12.50	XXX
309/13	0.19	13.33	XXXX
309/87	0.46	13.33	XXXX
309/53	0.30	14.33	XXXX
309/32	0.30	15.00	XXXX
309/83	0.31	15.00	XXXX
309/120	0.19	15.00	XXXX
309/8	0.66	15.33	XXXX
309/128	0.17	16.75	XXXX
309/61	0.28	18.00	XXXX
309/11/2	0.60	18.67	XXXX
309/52	0.29	18.75	XXXX
309/9	0.50	19.33	XXXX
309/66	0.19	21.00	XXXX
309/80	0.32	21.33	XXXX
309/158	0.55	22.00	XXXX
309/94	0.52	27.33	X X

F-ratio EA content 2.399 *F*-ratio GSL content 8.104



1. Glucosinolate content in DH regenerants derived from the donor plant 309/94

example. Considering that there are no significant differences between partially SI and SC individuals in all cases it is recommended to select only plants with a high SI level for DH lines deriving. To make sure of SI degree and stability it should be verified in R_2 generation again. Although expected ratio of SI to SC regenerants is approximatelly 1 : 1, considerable shift to self-compatibility has been observed in our experimental material. It could

II. Evaluation of self-incompatible – self-compatible degree in DH regenerants of four F_1 origins

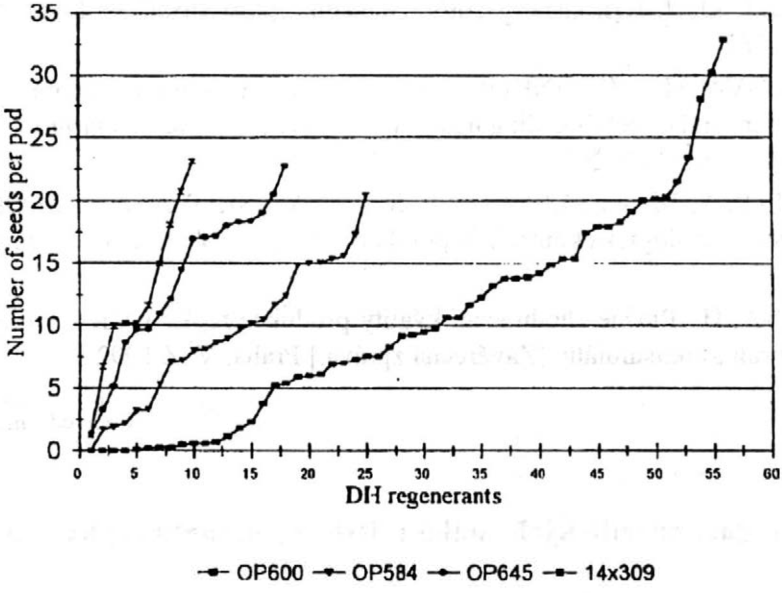
F_1combination	No of evaluated regenerants	Plants counted as					
		SI		partially SI		SC	
		No	[%]	No	[%]	No	[%]
OP 600	56	15	26.8	2	3.6	39	69.6
OP 584	25	4	16.0	2	8.0	19	76.0
OP 645	18	2	11.1	1	5.6	15	83.3
14 x 309	10	1	10	0	0	9	90.0

III. Self-incompatibile – self-compatible segregation in DH regenerants derived from OP 600 genotype

Plant No.	Average No. of seeds per pod	Homogeneous groups
41	0.00	X
9	0.00	X
36	0.00	X
25	0.00	X
48	0.10	XX
40	0.20	XX
12	0.30	XX
54	0.30	XX
49	0.50	XX
31	0.60	XX
32	0.60	XX
56	0.70	XX
38	1.20	XX
46	1.80	XXX
17	2.30	XX
19	3.80	XX
15	5.20	XX
59	6.00	XX
29	6.90	X

F-ratio 25.466

be caused by gametic selection in a microspore culture against SI genotypes. No substantial differences have been observed when inbred lines (OP materials) or DH line (No 14) were used as SI parental lines. That gives little chance to gain desired combinations of SI and 00 quality in a limited number of SI regenerants.



2. Range from self-incompatibility to self-compatibility in DH regenerants derived from individual F1 hybrid combinations

It may be concluded that there is necessary to produce a larger amount of regenerants per initial F_1 hybrid combination to get highly SI regenerants on a large scale. It is recommended to use DH lines as parents of F_1 hybrids to be sure of their homozygosity in desired traits.

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Recived June 26, 1996

Segregace specifických znaků u DH regenerantů řepky ozimé

U DH regenerantů řepky ozimé byla sledována segregace v obsahu kyseliny erukové (KE), glukosinolátů (GSL) a ve stupni autoinkompatibility (AI). V obsahu KE, který se pohyboval od 0,15 do 0,74 %, nebyl zjištěn statisticky významný rozdíl mezi výchozí rostlinou s vysokými parametry 00 kvality a jejím DH potomstvem na 95% hladině významnosti. Sedm z DH regenerantů vykázalo statisticky významně nižší obsah GSL ve srovnání s výchozí rostlinou. Hodnoty jednotlivých rostlin v µmol/g semen se pohybovaly od 7,33 do 20,00, zatímco u výchozí rostliny bylo zjištěno 27,33 µmol. Z DH regenerantů odvozených od čtyř F_1 kombinací AI a autokompatibilních (AK) 00 šlechtitelských materiálů vyštěpovalo od 10,0 do 26,8 % AI rostlin, zatímco očekávaný poměr AI : AK rostlin byl 1 : 1. Tato odchylka je zřejmě způsobena vlivem gametické selekce v mikrosporových kulturách. Nebyl shledán podstatný rozdíl při použití inzuchtních linií nebo dihaploidní linie jako AI rodičovských komponent. Z výsledků vyplývá malá pravděpodobnost získat požadované kombinace AI a parametrů 00 kvality. Proto bude nutné vytvářet větší počet DH regenerantů z výchozích F_1 hybridů.

řepka ozimá; dihaploidy; segregace znaků; eruková kyselina; glukosinoláty; autoinkompatibilita

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Genet. a Šlecht., *32*, 1996 (3) : 249-256

CONSTRUCTION OF A GENETIC LINKAGE MAP FOR *Brassica campestris* L. (SYN. *Brassica rapa* L.) *

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Abstract: The genetic linkage map of *Brassica campestris* has been derived from a progeny of recombinant inbred lines. Eighty-three loci were detected in 10 linkage groups of the total length 1138.1 cM. For the identification of the same loci the map was compared with a genomic map of *B. napus* constructed with the same DNA probes. The genetic map of recombinant inbred lines is slightly different from maps derived from other crosses and its use can be seen in comparative mapping and marker assisted selection.

Brassica campestris; RFLPs; genetic map; recombinant inbred lines

Restriction fragment length polymorphisms (RFLPs) are genetic markers detected by hybridizing cloned DNA sequences to DNA fragments from restriction enzyme digests. Advantages of RFLP markers are abundance, phenotypic neutrality and co-dominance when compared with other types of genetic markers (Beckman and Soller, 1983).

Detailed genetic linkage maps in plants are very useful tools for studying genome structure and evolution, identifying introgression between different genomes and localizing genes of interest (Song et al., 1991). RFLPs have been used to construct genetic linkage map in a wide variety of species including *Brassica campestris* L. (Song et al., 1991; Chyi et al., 1992; Salava, 1995).

Recombinant inbred lines offer an attractive alternative F_2 and backcross generations since they reprezent fixed, homozygous individuals that can be used indefinitely for gene mapping studies (Powell, 1987).

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* This project was funded by grants of EC TEMPUS JEP 1426 and BBSRC UK.

Recombinant inbred lines are used :

a) in map-based gene cloning based on the linkage map of *Arabidopsis thaliana* L.,

b) in marker aided selection (including gene tagging, QTLs, rapid introgression) (Tanksley, 1993).

The main aim of the research was to construct an RFLP linkage map of *Brassica campestris* and compare it with other maps of *B. campestris* and *B. napus* L. constructed with the same sets of DNA clones.

In this paper we report on the map of RILs, the map of B_1 progeny will be discussed in a following paper.

MATERIAL AND METHODS

Plant material and crosses

Description of used lines is referred in Table I.

I. Characterics of *Brassica campestris* lines used in this project

Designation	Subspecies	Origin	Genetic characteristics
RM29	*oleifera*	JIC Norwich	inbred line
R-c-50	*chinensis*	SCRI Dundee	inbred line

Obtaining RIL progeny for genetic mapping is shown in Fig. 1.

RIL

P: RM29 x R-c-50

F_1: (RM29 x R-c-50)

4 times selfpollinated

F_5: inbred progeny

1. Scheme of the used cross

To overcome problems with self-incompatibility the plants were sprayed with 1.5% NaCl solution. In a few cases we had to carry out the pollination in buds.

Conditions for plant growth

The plants were grown in a glasshouse, where the temperature was kept about 20 °C during the day and from 10 to 12 °C at night; day length was regulated to 8 hours. We used plastic pots with a substrate of soil, peat, gravel, chalk and the fertiliser Osmocote.

Plant tissue and DNA

Sixty-five RILs were used for construction of the linkage map. Harvest of plant material, freeze drying, isolation of plant DNA, restriction enzyme digestion (*Eco*RI), capillary blotting, hybridization and radioactive work with DNA probes were carried out as described by Sharpe et al. (1995) and Parkin et al. (1995).

RFLP probes

RFLP probes were derived from *Pst*I fragments (of length from 0,6 to 2,0 kb) taken from genomic libraries of *B. napus* ("pN" probes), *B. campestris* ("pR" probes) and *B. oleracea* L. ("pO" probes), which had been prepared at the *Brassica* and Oilseeds Research Department of John Innes Centre, Norwich, United Kingdom. We decided to complete them with "industrial probes" ("pW" probes) supplied by Thomas Osborn from the University of Wisconsin, Madison, USA. The three cDNA probes CERI, DESAT, SLG29 also originated from the Department at the John Innes Centre.

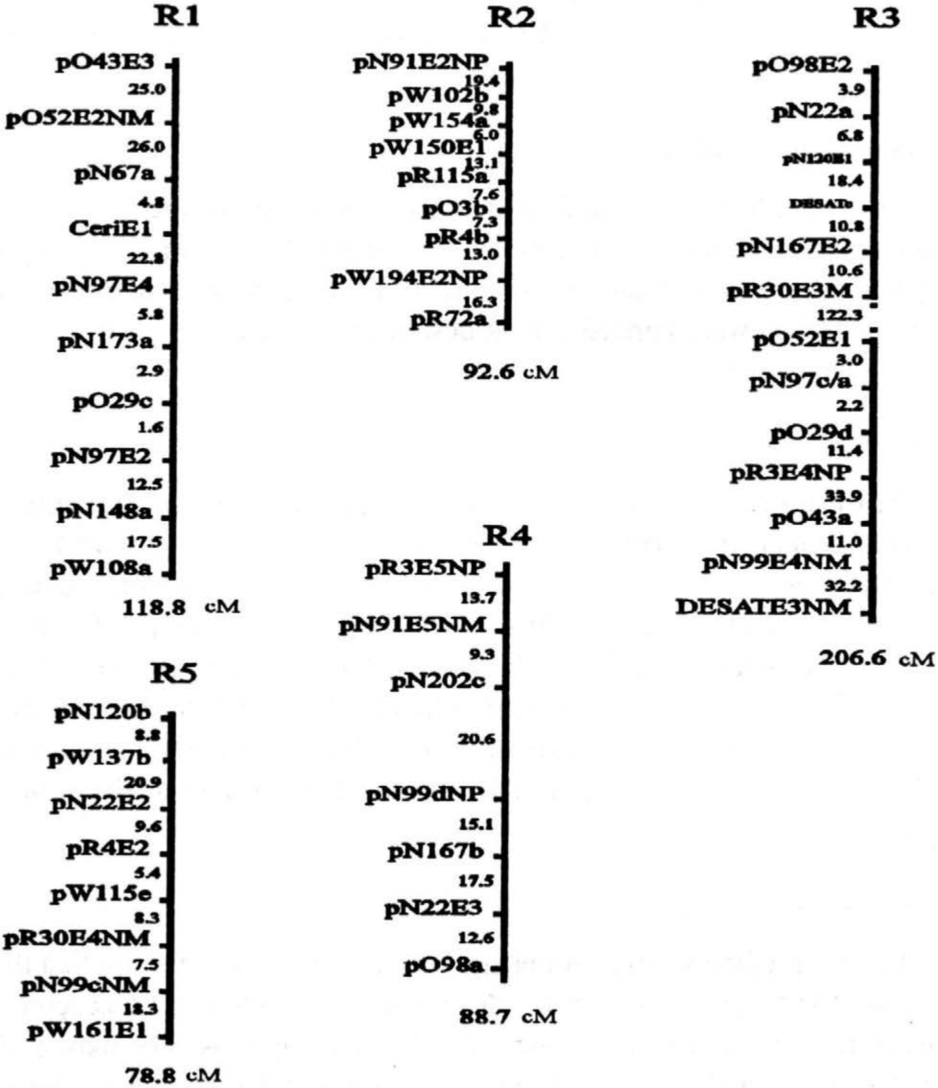
RFLP data

For the prediction of each linkage between single loci we applied the program MAPMAKER version 1.9 (Lander et al., 1987). A LOD score 5 was used to associate RFLP loci into initial linkage groups. The most probable order of detected loci in each linkage group was determined by three-point analysis. Frequency of recombinations was converted to map distances using Kosambi's mapping function (Kosambi in Sharpe et al., 1995).

RESULTS

Genomic map of *Brassica campestris*

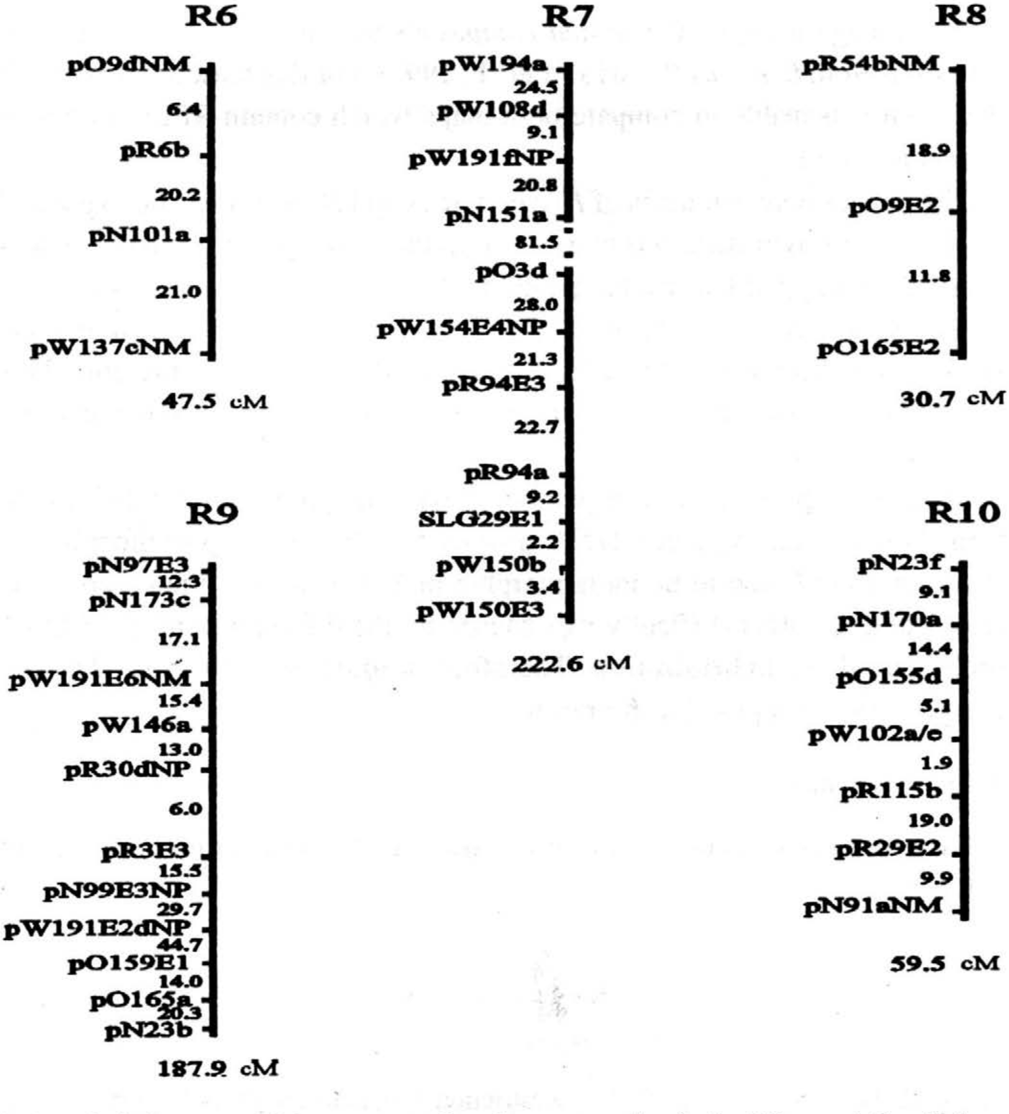
Fifty-five informative DNA probes detected in the RIL progeny 83 loci in 10 linkage groups, which means 1.5 detected loci per DNA probe. The size of single groups ranges from 30.7 to 222.6 cM, and the total length of the



2. Genetic linkage map of *B. campestris* based on segregation in the RIL population (linkage groups R1-R5)

map is 1 138.1 cM. The average distance between two markers is 15.02 cM, if we consider huge gaps in R3 and R7 linkage groups. The maximum distance is 44.7 cM in R9, and the minimum distance is 1.6 cM in R1.

Thirty-one markers were not linked, but it is planned to establish these linkages after carrying out some more hybridizations.The whole genomic map is shown in Fig. 2 and 3.



3. Genetic linkage map of *B. campestris* based on segregation in the RIL population (linkage groups R6–R10)

DISCUSSION

We obtained the map of RIL progeny which contains 10 linkage groups, corresponding with 10 chromosomes in this species, of a size ranging from 30.7 to 222.6 cM. The total length is 1 138.1 cM, and the number of loci mapped is 83. These results agree with the data published by Song et al. (1991) and Chyi et al. (1992).

Ten linkage groups of *Brassica campestris* belong to 19 linkage groups investigated in *B. napus* (Lydiate et al., 1993). For this reason it is possible and even reasonable to compare both maps which contain RFLP probes of the same origin.

Differences between maps of *B. campestris* and *B. napus* can be explained by the lack of hybridizations carried out in the *B. campestris* progeny. However, of 83 mapped loci we have found 52 in the same linkage groups as in *B. napus* loci, thus at a rate of 62.7%. Deviation ($p < 0.05$) from Mendelian segregation ratios was observed in 8.5% of marker loci in RIL progeny. This number is significantly lower than the 23% published by Teutonico and Osborn (1994).

The biggest problem, in comparison, is with the probes used in hybridization. Unfortunately, some DNA probes that had been polymorphic in *B. napus* were found to be monomorphic in *B. campestris*; the reverse was also found. Another difficulty was caused by the different number of DNA probes used for hybridization. Therefore, a more objective and detailed comparison is not possible at present.

Acknowledgement

We would like to thank Andrew Sharpe from JIC Norwich for his great support of the work.

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Received July 26, 1996

Genetická vazbová mapa *Brassica campestris* L. (syn. *Brassica rapa* L.)

Genetická mapa *Brassica campestris* byla odvozena z populace rekombinantních inbredních linií. Podařilo se identifikovat 10 vazbových skupin v celkové délce 1 138,1 cM, což je srovnatelné s dříve publikovanými mapami tohoto druhu (Song et al., 1991, Chyi et al., 1992). K identifikaci shodných lokusů na mapě byla použita genomová mapa *Brassica napus* L. (Sharpe et al., 1995), k jejíž konstrukci byly použity stejné DNA sondy. Získaná mapa rekombinantních inbredních linií se částečně liší od map pocházejících z jiných křížení (Salava, 1995) a její využití lze spatřovat hlavně pro komparativní mapování v rodu *Brassica* a u selekce využívající RFLP markerů.

Brassica campestris; RFLP genetická mapa; rekombinantní inbrední linie

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Genet. a Šlecht., *32*, 1996 (4) : 257-264

INHERITANCE OF SELF-FERTILITY IN SUNFLOWER

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Abstract: Studies in 1991–1993 used 45 commercial sunflower hybrids, 17 B and Rf inbred lines (LC) and 200 experimental hybrids representing the F_1, F_2, BC_1 and BC_2 populations obtained from crossing the 17 LC-s. The degree of self-fertility was investigated in lines and their crosses, and correlations between hybrid self-fertility and their yields, and between the degree of self-fertility in the lines and F_1 hybrids, were calculated. The total variance and its components were also calculated, together with the types of gene action and the number of gene pairs involved in the genetic control of sunflower self-fertility. This study showed that there is a positive and significant correlation between the degree of self-fertility and hybrid yield, and between self-fertility of the lines and their hybrids. In the F_1, dominance of self-fertility was demonstrated. Additivity and nonallelic gene effects were also proven. Heritability of this character is moderate (h^2_w = 0.31–0.82) and the estimated number of gene pairs involved in genetic control of self-fertility was 5–12.

sunflower; self-fertility; heritability

The self-fertility of sunflower lines as well as hybrids is one of the most important traits in breeding programmes. It is a decisive factor for yield, especially under less favourable weather conditions during flowering and in areas where the number of pollinators is low.

Several papers identified the importance of the subject. According to Vranceanu et al. (1978) the genetic influence on self-fertility is complex and environmental factors play a large role in its expression. Fick (1978) reported a high level of variability among sunflower lines, from complete to zero self-fertility. Segala et al. (1980) using the regression between parental forms and hybrids, found a low heritability for this trait (0.26). Burlov and Krutko (1986) found basic differences in inheritance of the expression of self-fertility by autogamy and geitonogamy. Škaloud and

Kováčik (1994) showed that a hybrid obtained from the cross of self-fertile lines is generally more self-fertile than the parental forms. The objective of this study was to establish the relationship between self-fertility of lines and their crosses, and to clarify some aspects of the genetic control of this trait.

MATERIALS AND METHODS

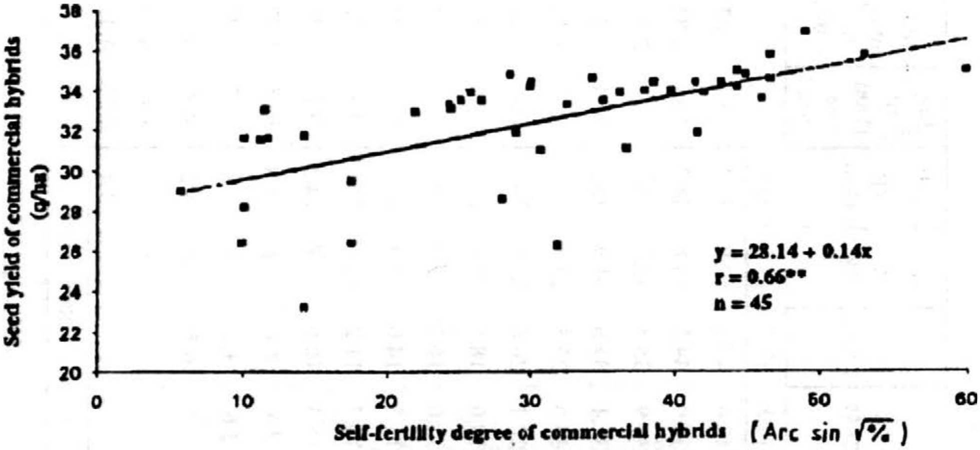
For this study, 45 commercial hybrid and 17 inbred lines possessing different degrees of self-fertility were used. From the crosses of 17 inbred lines, 200 hybrid populations F_1, F_2, BC_1 and BC_2 resulted. These hybrid populations were studied together with the parents under field conditions for two years (1992, 1993).

The design of the experiment utilised the randomised block with three replications. The degree of self-fertility was determined on 15 sunflower heads/variant. The type of gene action was calculated by the method proposed by Gamble (1962). Total, genotypic and environmental variances have been calculated using the formula proposed by Brewbacker (1964). The heredity coefficients in the wide sense were calculated using the formula proposed by Mahmud and Kramer (1951). The number of gene pairs involved in the genetic control of self-fertility was estimated using the formula proposed by Weber (1950).

RESULTS AND DISCUSSION

The analysis of the correlation between the self-fertility of commercial hybrids and their seed yield indicated a positive and significant relation, $r = 0.54$ (Fig. 1). In practice, the level of hybrid self-fertility is highly dependant on the self-fertility of the inbred lines. The results, with its positive and significant correlation, $r = 0.66$ (Fig. 2), emphasise that to obtain a hybrid with a high degree of self-fertility, it is necessary to increase the selection pressure on the inbred lines for this character.

The inbred lines used for genetic study of self-fertility in sunflower were significantly different in this respect (Tab. I). Based on mean differences, according to the Duncan test, the lines were classified into three groups: self-fertile (SF) – RHA-270, V-1304, T-66-8712, SVM-8791; medium self-ferti-



1. Relationship betwen self-fertilityand seed yield of 45 sunflower commercial hybrids

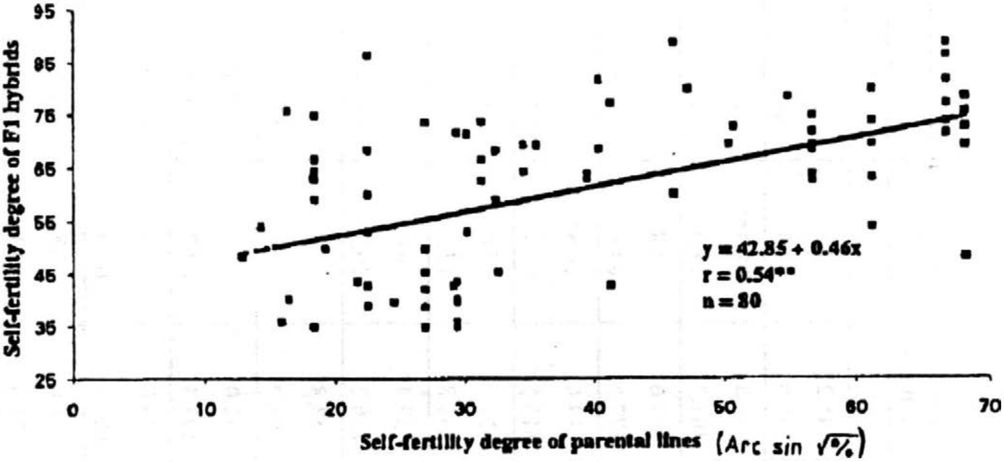
le (MSF) – ISS-14699, MD-4634, ND-1416; and self-sterile – O-7657, V-3281, SP-4559 (Table II). The hybrids from diallel crosses showed the presence of dominance for self-fertility. While overall variance was large, the genetic variance was clearly the most important one (Table III). In the genetic control of self-fertility, the effects for additivity were significant (Table IV). Effects for dominance and nonallelic interactions were also present (V-1304 x O-7493, OS-13338 x S-1358, RHA-270 x T-66-8712). With reference to the relationship between genetic variance (V_g) and the total variance (V_p), and

I. Self-fertility degree of B and Rf sunflower lines used in genetic study of self-fertility (Fundulea – 1992–1993)

Source of variation	Degrees of freedom	Sum of square	Mean square	Observed F	Tabular *F*	
					%	1%
Lines (A)	16	14.916	932.30	316.2***	1.97	2.62
Error (A)	32	94	2.94			
Years (B)	1	43	43.23	6.64*	4.13	7.44
Lines x Years (A x B)	16	9.643	602.71	92.66***	1.95	2.58
Error (B)	34	221	6.50			

II. Self-fertility degree of B and Rf sunflower lines (signification according to Duncan test) 1992–1993

RH 1270	V 1304	T-66-8712	SVM 8771	O 7493	ISS-14699	MD 4634	A 1566	ND-1416	V 1633	OS-13338	H 73-6874	S-1358	O-7657	O-78696	V 3281	SP 4554	Std. int (Duncan) 5%	Std. int S_x (S_x = 0.98)
64.8	61.8	52.7	48.9	42.8	37.9	35.8	33.4	31.3	28.5	28.1	25.4	20.4	17.8	17.3	17.0	13.6		
	3.0	12.1	15.9	22.0	26.9	29.0	31.4	33.5	36.3	36.7	39.4	44.4	47.0	47.5	47.8	51.2	2.89	2.83
		9.1	12.9	19.0	23.9	26.0	28.4	30.5	33.3	33.7	36.4	41.4	44.0	44.5	44.8	48.2	2.89	2.83
			3.8	9.9	14.8	16.9	19.3	21.4	24.2	24.6	27.3	32.3	34.9	35.4	35.7	39.1	2.97	2.91
				6.1	11.0	13.1	15.5	17.6	20.4	20.8	23.5	28.5	31.1	31.6	31.9	35.3	3.03	2.96
					4.9	7.0	9.4	11.5	14.3	14.7	17.4	22.4	25.0	25.5	25.8	29.2	3.2	3.14
						2.1	4.5	6.6	9.4	9.8	12.5	17.5	20.1	20.6	20.9	24.3	3.35	3.28
							2.4	4.5	7.3	7.7	10.4	15.4	18.0	18.5	18.8	22.2	3.56	3.49
								2.1	4.9	5.3	8.0	13.0	15.6	16.1	16.4	19.8	3.6	3.53
									2.8	3.2	5.9	10.9	13.5	14.0	14.3	17.7	3.79	3.71
										0.4	3.1	8.1	10.7	11.2	11.5	14.9	3.8	3.72
											2.7	7.7	10.3	10.8	11.1	14.5	3.8	3.72
												5.0	7.6	8.1	8.4	11.8	3.95	3.87
													2.6	3.1	3.4	6.8	4.15	4.07
														0.5	0.8	4.2	4.3	4.21
															0.3	3.7	4.45	4.36
																3.4	4.55	4.46
		SF						MSF						SS				



2. Relationship between self-fertility of sunflower and self-fertility of their crosses

with the genetic variance for additivity to the genetic variance, the heritability of self-fertility was moderate ($h^2_w = 0.11–0.67$) (Table V).

The results demonstrated that self-fertility of sunflower has to be considered as a complex phenomenon, and polygenically inherited. The number of

III. Phenotypic (V_p), genotypic (V_g) and environmental variance (V_e) for self-fertility in sunflower

Cross	1992					1993				
	V_p	V_g	% from V_p	V_e	% from V_p	V_p	V_g	% from V_p	V_e	% from V_p
V-1304 x O-7493	17.5	8.7	50	8.8	50	16.3	8.3	51	8.0	49
V-1304 x V-3281	59.3	47.8	81	11.5	19	28.9	17.9	62	11.0	38
OS-13338 x S-1358	10.5	5.9	56	4.6	44	9.9	2.8	28	7.1	72
RHA-270 x T-66-8712	21.7	7.4	34	14.2	66	16.7	2.4	14	14.3	86
RHA-270 x O-7869	56.8	46.8	82	10.0	18	39.9	28.6	72	11.3	28

IV. Gene action type involved in genetic control of sunflower self-fertility (1992–1993)

Cross	Year	Statistic parameter	M	Genes action type				
				A	D	AA	AD	DD
V-1304 x O-7493	1992	$\bar{x}$	55.7***	15.2*	77.1**	45.2*	4.8	–23.1
		V_p	17.5	28.7	410.5	395.0	32.3	801.5
	1993	$\bar{x}$	50.2***	37.0***	31.8	16.4	28.3***	–10.1
		V_p	16.3	25.1	376.4	361.2	28.0	723.2
V-1304 x V-3281	1992	$\bar{x}$	42.8***	22.1*	54.8	39.0	2.8	47.2
		V_p	59.3	82.3	1304.7	1277.5	84.6	2374.1
	1993	$\bar{x}$	68.4***	3.7	50.4	14.6	–16.8*	–86*
		V_p	36.8	56.7	837.9	815.5	60.2	1509.7
OS-13338 x S-1358	1992	$\bar{x}$	34.5***	9.8*	–7.6	–21.7	7.6	32.7
		V_p	10.5	16.1	242.9	231.8	17.2	469.8
	1993	$\bar{x}$	31.5***	14.1**	44.3*	33.4*	8.6	–75.4**
		V_p	9.9	17.4	237.5	226.2	20.7	482.2
RHA-270 x T-66-8712	1992	$\bar{x}$	60.8***	–1.3	67.2*	53.8*	–6.75	–100.5**
		V_p	16.7	31.5	414.7	393.0	38.6	858.1
	1993	$\bar{x}$	65.4***	13.2*	52.6	42.0	6.6	–65.9
		V_p	21.7	36.6	517.8	493.4	42.7	1030.5
RHA-270 x O-7569	1992	$\bar{x}$	60.2***	11.1	42.0	19.0	–10.4	186.5***
		V_p	39.9	56.3	884.4	864.4	61.0	1559.2
	1993	$\bar{x}$	61.2***	28.8**	37.6	11.6	2.8	–32.6
		V_p	56.8	76.2	1230.9	1214.6	80.1	2202.0

t 5% = 2.13; *t* 1% = 2.94; *t* 0.1% = 4.07

V. Wide h_w^2 and narrow sense h_n^2 heritability coefficients for self-fertility of sunflower (1992–1993)

Cross	h_w^2		h_n^2	
	1992	1993	1992	1993
V-1304 x O-7493	0.50	0.51	0.36	0.46
V-1304 x V-3281	0.80	0.49	0.67	0.46
OS-13338 x S-1358	0.54	0.28	0.46	0.25
RHA-270 x T-66-8712	0.34	0.14	0.31	0.11
RHA.270 x O-7869	0.82	0.71	0.66	0.59

gene pairs was 5.42–11.7 (Table VI). Clearly, to obtain hybrids possessing a good level of self-fertility requires the presence of a higher level of self-fertility in the inbred lines crossed.

VI. Estimated number of pair genes involved in genetic control of sunflower self-fertility

Cross	Number of pair genes	
	1992	1993
V-1304 x O-7493	9.44	9.15
V-1304 x V-3281	8.59	11.70
OS-13338 x S-1358	5.42	7.64
RHA-270 x T-66-8712	6.54	7.12
RHA-270 x O-7869	7.94	9.31

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Received June 26, 1996

Dědičnost autogamie u slunečnice

V letech 1991–1993 jsme uskutečnili pozorování týkající se 45 komerčních hybridů slunečnice, inbredních linií 17B a Rf (LC) a 200 pokusných hybridů, které představovaly populace F_1, F_2, BC_1 a BC_2 pocházející z křížení 17 LC. U linií a jejich kříženců jsme sledovali stupeň autogamie a vypočítali jsme korelace mezi autogamií hybridů a jejich výnosy, a dále mezi stupněm autogamie u linií a hybridů F_1. Rovněž jsme stanovili celkovou varianci a její složky, spolu s typem působení genů a počtem genových párů, které se podílejí na genetické kontrole autogemie u slunečnice. Výsledek této studie prokázal, že mezi stupněm autogamie a výnosem hybridů, jakož i mezi autogamií linií a jejich hybridů existuje pozitivní a významná korelace. V F_1 generaci jsme prokázali efekt dominance pro autogamii. Prokázali jsem též účinky aditivity a nealelických interakcí genů. Dědivost tohoto znaku je poměrně malá (h^2_w = 0,31–0,82) a počet genových párů podílejících se na genetické kontrole autogemie činil 5–12.

slunečnice; autogamie; dědivost

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Genet. a Šlecht., *32*, 1996 (4) : 265-274

EVALUATION OF SELF-FERTILITY IN SUNFLOWER LINES

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Abstract: Autogamy, geitonogamy and free pollination were used in mutual crosses of lines with various levels of self-fertility. After autogamy and geitonogamy it was shown that the inheritance of self-fertility is governed by a larger number of genes. Two basic principles, dominance and additivity, prevail in their interaction. The degree of trait expression largely depends on the way of pollination or on the form of self-fertilization. After geitonogamy, interactions between genes determining the inheritance of self-fertility are expressed in varying degrees of incomplete dominance of self-fertility, absence of dominance – intermediarity being the extreme case. In contrast, after autogamy the final effect shows a trend to incomplete dominance of self-sterility (eventually low degree of self-fertility) or again a trend to a state close to intermediarity. The use of lines with different levels of self-fertility for the development of hybrids is of importance for breeding, for different requirements of the maintenance of parental lines and for the ability of the hybrid to offer high yield even under adverse conditions for pollination.

line crosses; self-fertility; inheritance of trait; sunflower

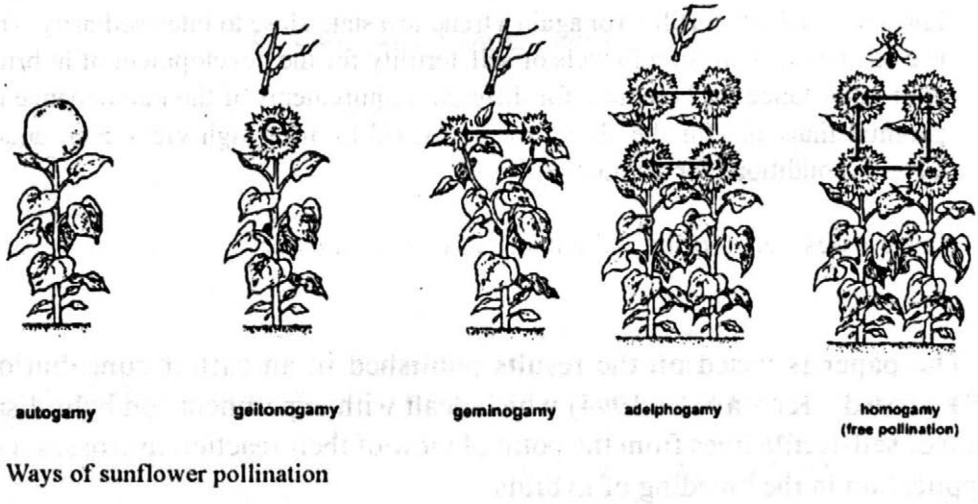
The paper is based on the results published in an earlier contribution (Škaloud, Kováčik, 1994) which dealt with experiments on hybridisation of self-fertile lines from the point of view of their reaction in crosses, i.e. application in the breeding of hybrids.

The present paper is a continuation of that contribution. It evaluates the inheritance of self-fertility of the same lines. The original trial was completed by an analysis of crosses of lines with an extreme expression of self-fertility; these lines were not yet available at the first stage of the experiment.

Several foreign papers characterize the subject as topical. According to Vranceanu et al. (1978) the genetic influence on self-fertility is very complex, and environmental factors contribute greatly to its expression. In the F_1, partial dominance prevails. George et al. (1980) point to a very broad variability among sunflower lines, from complete to almost zero self-fertility. Segala et al. (1980) express the heritability of self-fertility by means of regression between parents and hybrids by coefficient 0.26, which can be considered as a lower degree of heritability. Burlov and Krutko (1987) found a basic difference in inheritance of self-fertility after autogamy (self-pollination of one flower) and geitonogamy (pollination among flowers in one head). In geitonogamy, intermediarity or partial dominance are manifested in the F_1 generation. In autogamy, self-fertility is mostly of recessive character.

MATERIAL AND METHODS

The most important methodical part is application of various ways of pollination; these are shown in Fig. 1. Of the presented ways of pollination autogamy, geitonogamy and free pollination were used.



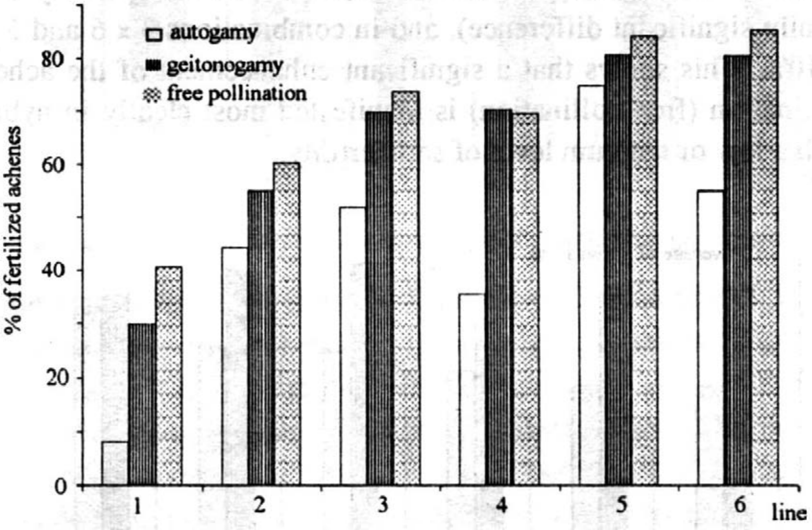
1. Ways of sunflower pollination

As material, lines differing in the achene set after application of autogamy and geitonogamy (further A and G) were used. Characteristics of the self-fertility level of lines are presented in Fig. 2. A classification of lines can be derived from it:

1. lines with a high level of self-fertility after A and G – line 5;
2. lines with a medium level of self-fertility after A and a high level after G – lines 3 and 6;

3. lines with a medium level of self-fertility after A and G – line 2;
4. lines with a low level of self-fertility after A and a medium level after G – line 4;
5. lines with a low level of self-fertility after A and G – line 1.

After free pollination three categories can be formed: achene set up to 60% (lines 1 and 2), achene set 60–80% (lines 3 and 4), achene set over 80% (lines 5 and 6).



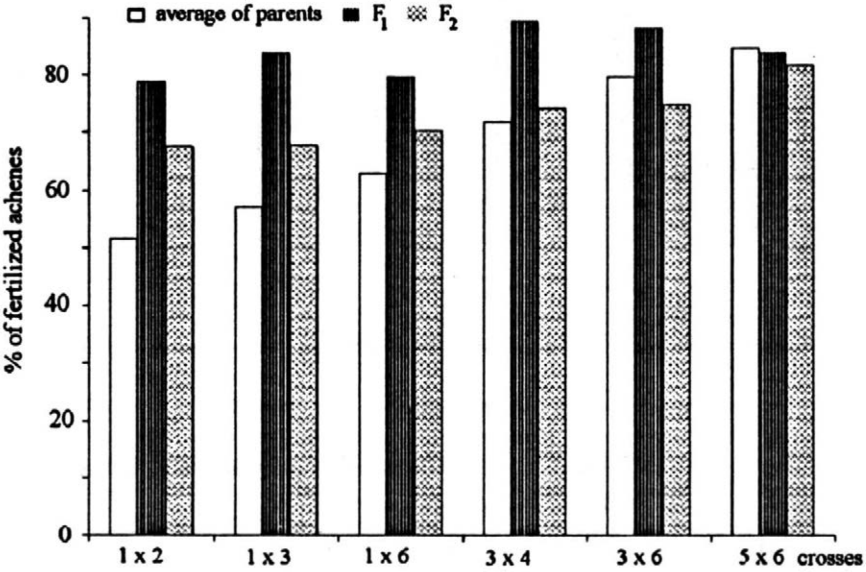
2. Comparison of lines as for fertilized achenes after autogamy, geitonogamy and free pollination

Used lines: Line 1 = SUNDAK (from the USA varietal population, of confection type)
Line 2 = HT 23 c (from Rumania)
Line 3 = D-34-2-10 (from France)
Line 4 = NS H 33 RM (from Yugoslavia)
Line 5 = AC 84 1015 B (from Rumania)
Line 6 = HA 89 (from USA)

The trial was carried out in three replications (three hybrid combinations of the same hybrid and three sister lines from one parental line). Each variant was represented by six heads in one replication. Given values of the achene set in % represent the average of all replications, i.e. of 18 heads (three replications of six heads each). Comparison of variants was carried out by means of *T*-test at 95% probability.

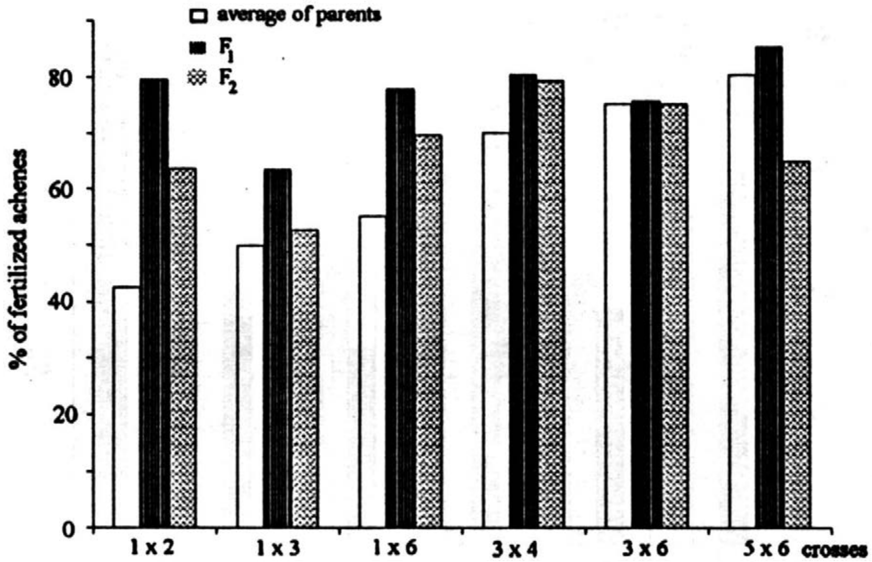
RESULTS

Fig. 3 indicates that the average of parental lines was exceeded in hybrids after free pollination in the combinations 1 x 2 and 1 x 3 by 25–30% (statistically significant difference), in the combinations 1 x 6 and 3 x 4 by 15–20% (statistically significant difference), and in combinations 3 x 6 and 5 x 6 by only 0–10%. This shows that a significant enhancement of the achene set after pollination (free pollination) is manifested most clearly in hybrids of lines with a low or medium level of self-fertility.



3. Comparison of hybrid generations with the average of parents after free pollination

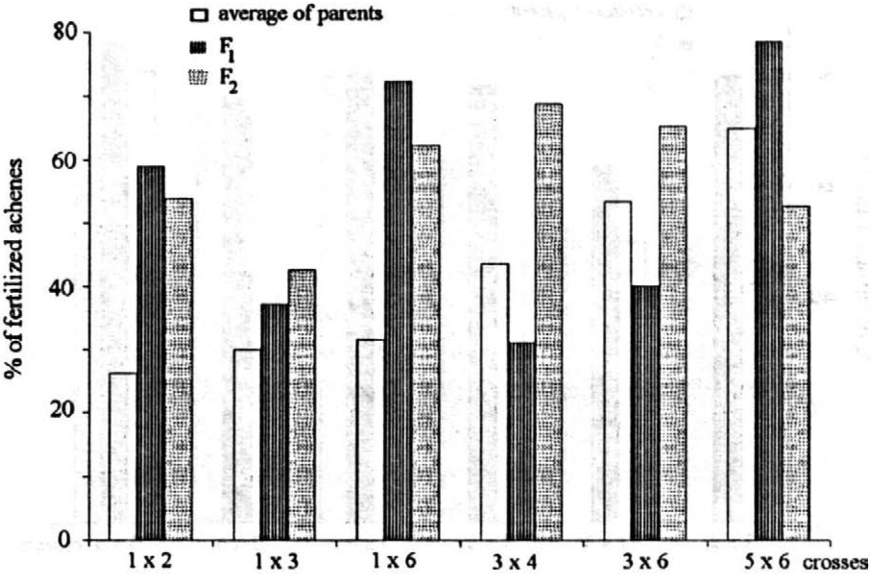
A comparison of the average of parents with hybrids presented in Fig. 4 shows that after geitonogamy most hybrids (except combination 3 x 6) exceeded the average of parents in achene set (significant differences in combinations 1 x 2, 1 x 3 and 1 x 6). This can be explained either by the expression



4. Comparison of hybrid generations with the average of parents after geitonogamy

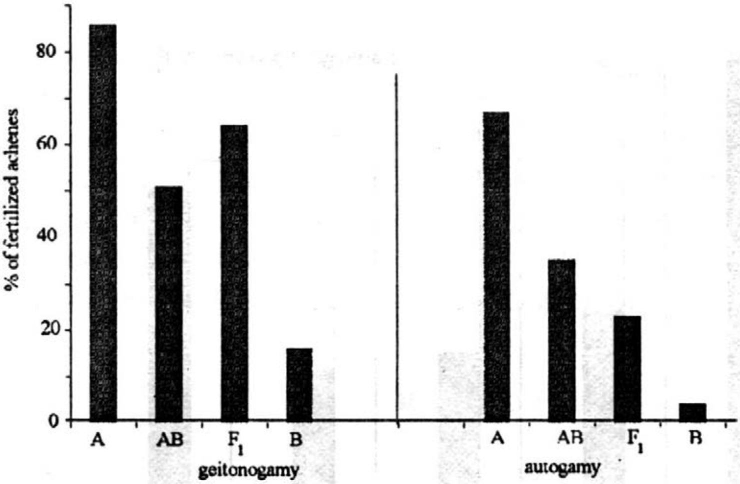
of hybrid vigour, or by dominance of the more efficient parent. In comparison with the more efficient parent, hybrid vigour manifested itself only in combinations 1 x 2 (25%; significant difference) and 3 x 4 (10%). A comparison of the average of parents with the F_2 generation shows that even in these cases the set of achenes is influenced also by dominance of the more efficient parent aside from hybrid vigour. It is obvious that in the inheritance of achene set after geitonogamy the prevailing principle is incomplete dominance, in fewer cases intermediarity (combination 3 x 6). Hybrid vigour contributes to the expression of the trait particularly when parents show a lower level of self-fertility.

After autogamy the situation is slightly different, as presented in Fig. 5. In the two combinations 3 x 4 and 3 x 6 (significant differences), achene set in the hybrid was lower than in both parental lines; in combination 1 x 3 the decrease is noticeable in comparison with the more efficient parent. In these cases the level of achene set in the F_2 is also higher than in F_1 (significantly), which shows dominance of the parent that inclines to a low level of self-fertility. Rather close to dominance of the self-fertile line or the effect of hybrid vigour is manifested in other combinations (significant difference in combinations 1 x 2, 1 x 6, 5 x 6).



5. Comparison of hybrid generations with the average of parents after autogamy

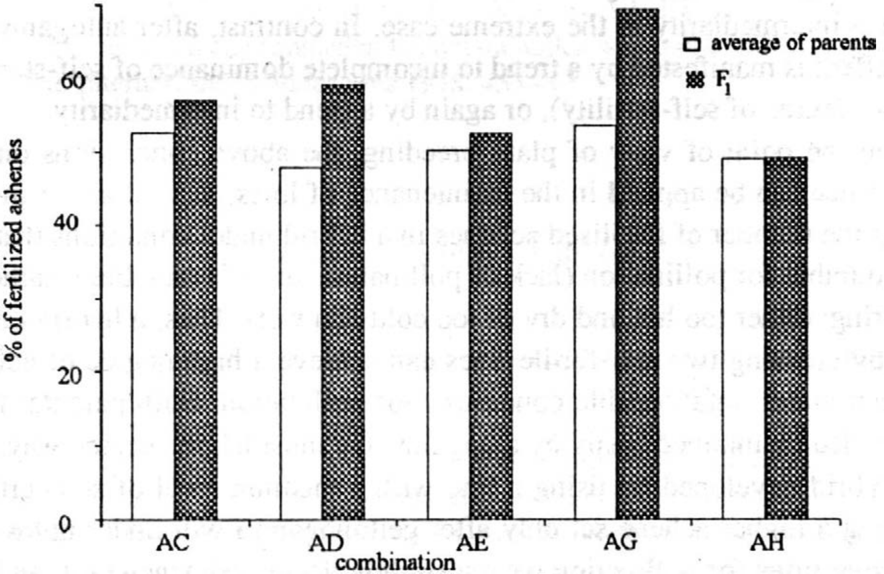
To confirm the above conclusions, an additional experiment was carried out in which only extreme categories of lines were crossed. Results of the cross of line A (86 % self-fertility after geitonogamy and 67% after autogamy) with line B (showing an achene set of 16% after geitonogamy and 4% after autogamy) are presented in Fig. 6. The same self-fertile line was further crossed with five other, almost self-sterile lines (achene set after autogamy 2–6%, after geitonogamy 11–22%). Fig. 6 shows that the level of the hybrid in the F_1 corresponds to incomplete dominance of self-fertility after geitonogamy, and incomplete dominance of sterility after autogamy (differences between parents, their mean value and F_1 in geitonogamy as well as in autogamy are statistically significant). Fig. 7 shows that incomplete dominance of self-fertility after geitonogamy is manifested in two out of five cases (differences in combination AD as well as AB are significant). The remaining three cases are closer to the expression of intermediarity. Fig. 8 presents the expression of the same trait after autogamy, but with a reversed trend. Two out of five crosses show more or less intermediarity, three other crosses show a trend to dominance of the self-sterile line (differences in combinations AD, AE and AG are significant).



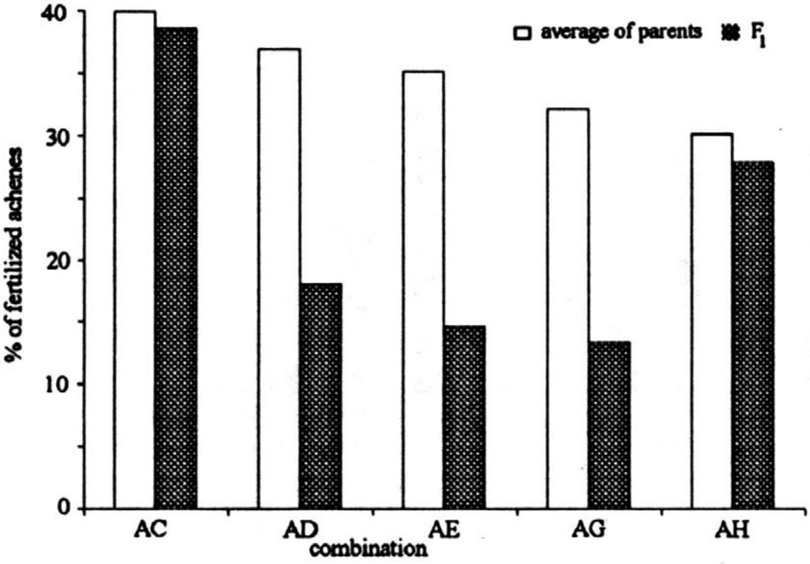
6. Results of crosses of two lines with extreme levels of self-fertility after geitonogamy and autogamy

DISCUSSION

The inheritance of self-fertility is governed by a higher number of genes. In their interactions two basic principles prevail, dominance and additivity. The degree of trait expression largely depends upon the way of pollination



7. Results of crosses of highly self-fertile lines with low self-fertile lines after geitonogamy



8. Results of crosses of highly self-fertile lines with low self-fertile lines after autogamy

eventually form of self-pollination. After geitonogamy, the interactions between genes that determine the inheritance of self-fertility are expressed in various degrees of incomplete dominance of self-fertility, absence of dominance – intermediarity is the extreme case. In contrast, after autogamy the final effect is manifested by a trend to incomplete dominance of self-sterility (or low degree of self-fertility), or again by a trend to intermediarity.

From the point of view of plant breeding, the above conclusions on the inheritance can be applied in the maintenance of lines, as well as for in-fluencing the number of fertilised achenes in a hybrid under conditions that are unfavourable for pollination (lack of pollinators, or unfavourable weather at flowering: either too hot and dry or too cold and wet). Thus, a hybrid developed by crossing two self-fertile lines can achieve a high degree of achene set even under unfavourable conditions for pollination. Both parental lines can be also maintained easily by autogamy, the most labour-saving way.

A hybrid developed by using a line with a medium level of self-fertility (offering a higher achene set only after geitonogamy) will under unfavourable conditions for pollination have a slightly decreased achene set, and the parental line must be maintained by more laborious geitonogamy. Only in an exceptional case should a line with a high trend to self-sterility be used in the development of hybrids; this exception applies if such a line is an exclusive donor of necessary genes. A hybrid developed with participation of an almost self-sterile line faces the risk of a very low achene set under unfavourable conditions for pollination, and is able to give high yields only under optimal conditions for pollination. The line itself is difficult to maintain; successful self-fertilisation can be usually achieved only when a laborious way of pollination-adelphogamy (see Fig. 1) is used.

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Received June 26,1996

Hodnocení autofertility u linií slunečnice

Z různých způsobů opylení bylo v pokusech použito autogamie, geitonogamie a volného opylení. Vzájemná křížení linií s různými hladinami autofertility po autogamii a geitonogamii ukazují, že dědičnost autofertility je řízena větším počtem genů. V jejich interakcích převládají dva základní principy – dominance a aditivita. Stupeň projevu znaku do značné míry závisí na způsobu opylení, případně na způsobu samoopylení. Po geitonogamii se interakce mezi geny určujícími dědičnost autofertility projevují různým stupněm neúplné dominance autofertility, nepřítomností dominance, přičemž intermediarita je extrémní případ. Naopak po autogamii ukazuje konečný efekt trend k neúplné dominanci autosterility (případně nízkou úroveň autofertility), nebo opět trend ke stavu blízkému k intermediaritě. Užití linií s různými hladinami autofertility pro tvorbu hybridů je významné pro šlechtění, pro různé nároky udržování rodičovských linií a pro schopnost hybrida poskytovat vysoký výnos i za horších podmínek pro opylení.

křížení linií; autofertilita; dědičnost znaku; slunečnice

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Genet. a Šlecht., *32*, 1996 (4) : 275-286

TRANSFER OF NEW CHARACTERS FROM WILD *Helianthus* SPECIES TO CULTIVATED SUNFLOWER

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Abstract: Through interspecific hybridization between cultivated sunflower and wild *Helianthus* species, forms with the potential of use for new characteristics in sunflower were produced. Genetic material from 94 accessions of 6 annual and 20 perennial species was transferred into hybrid material. Transfer of resistance to pests, early maturity and fertility-restorer genes (*Rf*-genes) was apparent in the F_1, and of other traits in the next generations. Application of single and double backcross, sib-pollination and self-pollination made possible not only to overcome the barrier of sterility of the interspecific hybrids, but to create forms with interesting new characteristics. New material with resistance to *Plasmopara helianthi*, *Phomopsis helianthi*, *Phoma helianthi*, *Erysiphe cichoracearum* and *Orobanche cumana*, with high seed oil content, early maturity and large seed size was produced by involving a large number of annual and perennial species. Twelve new CMS-sources were obtained from five annual and one perennial species. A significant number of forms that are carriers of fertility-restorer genes was obtained from 6 annual and 20 perennial species. R-lines were created from these forms with high combining ability and resistance to pests.

sunflower; *Helianthus*; wild species; resistance; R-lines; CMS

Heterosis breeding has been the main direction in sunflower breeding during the last few years. The wild *Helianthus* species offer great and valuable opportunities for utilization of heterosis selection. According to Thompson et al. (1978), wild *Helianthus* germplasm, besides contributing the basic stock from which cultivated sunflower originated, continues to contribute specific characteristics for sunflower improvement. A number of investigations show that *Helianthus* species are a rich genetic source for disease and pest resistance, cytoplasmic male sterility, fertility restoration, increased seed protein content, high oil quality and other features.

Saziperov (1916) was the first who reported that genetic material had been transferred from wild *Helianthus* species into cultivated sunflower. Marchenko (1975), Pustovoit (1960), Leclercq et al. (1970), Pustovoit (1975), Georgieva-Todorova (1976), Tsvetkova (1976), Škorić (1985), Jan and Chadler (1985), Christov (1990) and others also reported a transfer of genetic material and development of new sunflower forms using wild *Helianthus* species. The discovery of cytoplasmic male sterility (CMS) in sunflower (Leclercq, 1969) was very important for heterosis breeding. Equally significant was the fertility restoration gene (Leclercq, 1971; Fick et al., 1974; Škorić et al., 1978).

The present paper examined the results of studies on the transfer of genetic material from wild *Helianthus* species into sunflower, and the development of new cultivated sunflower forms.

MATERIALS AND METHODS

New cultivated sunflower forms have been created and investigated for 12 years. Interspecific hybrids were used. They were obtained with the participation of 26 wild *Helianthus* species and cultivated sunflower, using reciprocal hybridization. From the annual species *H. annuus* (w.f.), *H. debilis*, *H. neglectus*, *H. petiolaris* and *H. praecox* (diploid, $2n = 34$) were included. From the perennial species we used *H. divaricatus*, *H. giganteus*, *H. glaucophyllus*, *H. grosseserratus*, *H. maximiliani*, *H. mollis*, *H. nuttallii*, *H. salicifolius*, *H. smithii* (diploid, $2n = 34$); *H. decapetalus*, *H. hirsutus*, *H. laevigatus*, *H. scaberimus*, *H. tomentosus* (tetraploid, $2n = 68$); *H. eggertii*, *H. ciliaris*, *H. pauciflorus* (*H. rigidus*), *H. resinosus*, *H. strumosus* and *H. tuberosus* (hexaploid, $2n = 102$). Material involving *H.* x *laetiflorus* ($2n = 102$) was also studied. Cultivated sunflower was represented by fertile and male sterile forms.

The material was investigated under field conditions. Phenological and biometric observations were taken. Female fertility of the plants was determined by the quantity of seeds obtained under open pollination. The 1000 seed weight was calculated by weighing two samples of 250 seed each. Seed oil content and fatty-acid composition of the oil were determined according to standard methods. The resistance to pests and parasites was established by methods approved and used in IWS (Panchenko, 1965, 1975; Pustovoit et al., 1976; Saliman et al., 1982; Tourvieille et al., 1988).

For most of the material the selection started in F_1. Self-pollination, sib-pollination and backcrosses were used to obtain the next generations. The male sterile plants obtained from interspecific hybrids (wild species x cultivated sunflower) were pollinated with pollen from different sunflower inbreds and cultivars with the aim to establish the type of sterility and to maintain it. If fertile plants were produced from crosses between sunflower A lines (sterile analogues) and different accessions of wild *Helianthus* species, self-pollination was performed. At the same time new male sterile plants were pollinated with pollen of F_1, F_2 or F_3 plants. This was done to confirm the presence of fertility restorer genes. After repeated self-pollination the degree of restoring ability was determined for the newly obtained forms. Much of this material was included in heterosis breeding for the production of new hybrid combinations.

RESULTS AND DISCUSSION

1. Some characteristics of the work with hybrid progenies

The progenies of interspecific hybrids could be characterized by an extremely wide formative process, which makes it possible that new sunflower forms are produced. The first hybrid generation is usually uniform in morphological features. The plants are intermediate in phenotype, with dominating features of the wild parent. The F_1 hybrids, obtained with the participation of annual species, give sufficient seed set if they are backcrossed or sib-pollinated once and sometimes even self-pollinated. It is possible that F_1 plants are pollinated with pollen of just one line or variety and sufficient quantity of seeds and F_2 plants are produced. These ways of reproduction and production of the next generation help to obtain forms which could combine useful characters of both parents.

There are some difficulties connected with producing the second hybrid generation of hybrids that involve perennial species, such as partial or total sterility of the F_1 plants. It is useless to self-pollinate them, because it is almost impossible to obtain seed set in this way. Most of the F_1 plants do not set seed even if they are open-pollinated. This is especially true for hybrids with *H. decapetalus*, *H. hirsutus* and *H. scaberimus*. We found that backcrossing (pollination with cultivated sunflower pollen) is the most successful procedure for overcoming this barrier. The pollen is collected from a group of lines and varieties. Part of it is mixed with pollen of F_1 plants (that produce pollen) of the same combination. Those F_1 plants are pollinated with the new pollen mixture. In this way a sufficient quantity of seeds and plants of the next hybrid generation are produced. The partial sterility of the F_2 hybrids is similarly overcome.

Evaluation of disease and parasite resistance of the F_2 hybrids is done mainly to determine the character of the genes which control a particular resistance. At the same time, plant selection is done, especially if a resistance is combined with some other useful features. The heterogeneous character of the hybrids for some features favors selection even in the first hybrid generation. When the generation number increases, selection becomes more purposeful. Sterile analogues of cultivated sunflower lines are used once or twice as maternal parents to produce materials that are carriers of fertility-restoring (*Rf*) genes. In the latter case it is preferable to use sterile analogues of two sunflower lines.

The specificity of obtaining F_2 (BC_1) and F_3 (BC_2) in some cases complicates the maintenance and evaluation of the useful characters that were transferred from wild *Helianthus* species. Nevertheless, it gives the opportunity to eliminate the undesired ones. Successive and repeated self-pollination to produce the next generations makes it possible to reduce many of the traits to a homozygous state and leads to a more effective selection of desired forms. These will thus have better self-fertility, higher seed oil content, and other desirable traits.

2. Development of new sunflower forms

Sunflower forms were developed from the crosses of cultivated sunflower x wild Helianthus species in which the cytoplasm and half or the greater part of the nuclear material originated from cultivated sunflower. Some of these forms had in their nuclear material *Rf*-genes, transferred from the wild parent. Thus, lines with normal cytoplasm without Rf nuclear genes, and lines with normal cytoplasm with *Rf* nuclear genes, called R-lines, have been developed from this type of crosses.

Lines were produced from the crosses of CMS sunflower lines x wild *Helianthus* species in which the cytoplasm belonged to the wild species (*H. petiolaris* or *H. annuus* (w.f.), *H. argophyllus*, *H. debilis*, *H. praecox*, *H. rigidus*). A half or the greater part of their nuclear material originated from cultivated sunflower, while the *Rf*-genes came from the wild parent. The cytoplasm in this case is called sterile cytoplasm, because the plant material is male sterile. R-lines with sterile cytoplasm and *Rf*-genes have been produced from wild species.

New sunflower forms have been developed from reciprocal crosses of wild *Helianthus* species x cultivated sunflower, these are called alloplasmic lines. Their cell cytoplasm came from the wild species, and the greater part of the nuclear material from cultivated sunflower. By using these crosses, genetic material was transferred into cultivated sunflower from both the nuclear and cytoplasm of the wild parent. Some alloplasmic forms had *Rf*-genes in their nuclear material. If male sterile plants were obtained in the progenies and the male sterility was maintained, this type of crosses allowed to develop forms which had the cell cytoplasm of the wild parent and the nuclear material only from cultivated sunflower. New CMS-sources were produced.

By the above-mentioned methods and successive aimed selection a great diversity of sunflower forms has been produced which would be useful mainly for heterosis breeding. Most valuable are those forms that combine genes for resistance to some diseases or *Orobanche cumana* with high seed oil content, good combining ability and other traits.

There are five trends for development of initial breeding material:

a) Development of new sunflower forms with complete or high resistance to mildew, *Phoma*, *Phomopsis*, *Sclerotinia*, powdery mildew and broomrape

Emphasis is put on the development of forms that are carriers of resistance. The other characters, such as high seed oil content, high 1000 seed weight, vegetation period etc. remain in the background. The already obtained resistant forms have been crossed with other forms which had other valuable features to combine all these characters in one form and to develop lines with normal cytoplasm or R-lines. Eighty-seven accessions of 5 annual and 20 perennial species were used in the development of resistant forms (Table I).

I. Characters, transferred from wild *Helianthus* species into the cultivated sunflower

Characters	Species
Full resistance to	
Plasmopara helianthi	*H. annuus* (w.f.), *H. agrophyllus*, *H. debilis*, *H. petiolaris*, *H. praecox*, *H. divaricatus*, *H. giganteus*, *H. glaucophyllus*, *H. grosseserratus*, *H. mollis*, *H. maximiliani*, *H. nuttallii*, *H. salicifolius*, *H. smithii*, *H. decapetalus*, *H. hirsutus*, *H. laevigatus*, *H. scaberimus*, *H. eggertii*, *H. ciliaris*, *H. pauciflorus*, *H. resinosus*, *H. strumosus*, *H. tuberosus*, *H.* x *laetiflorus*
Phomopsis helianthi	*H. annuus* (w.f.), *H. argophyllus*, *H. eggertii*, *H. pauciflorus*, *H. glaucophyllus*
Erysiphe cichoracearum	*H. decapetalus*
Orobanche cumana	*H. tuberosus*, *H. argophyllus*, *H. pauciflorus*, *H. strumosus*
High percent resistance to	
Phoma helianthi	*H. argophyllus*, *H. laevigatus*
Sclerotinia sclerotiorum (infection with mycelium)	*H. praecox*, *H. argophyllus*, *H. annuus* (w.f.)
Earliness	*H. praecox*, *H. scaberimus*, *H. glaucophyllus*, *H. giganteus*, *H. rigidus*, *H. nuttallii*, *H. ciliaris*, *H. annuus* (w.f.)
Seed size	*H. annuus* (w.f.), *H. agrophyllus*, *H. tuberosus*, *H. strumosus*
High oil content	*H. annuus* (w.f.), *H. debilis*, *H. petiolaris*, *H. praecox*, *H.* x *laetiflorus*
Genes, controlling CMS	*H. annuus* (w.f.), *H. argophyllus*, *H. debilis*, *H. petiolaris*, *H. praecox*, *H. pauciflorus*
***Rf*-genes**	*H. annuus* (w.f.), *H. argophyllus*, *H. debilis*, *H. neglectus*, *H. petiolaris*, *H. praecox*, *H. divaricatus*, *H. glaucophyllus*, *H. giganteus*, *H. grosseserratus*, *H. maximiliani*, *H. mollis*, *H. nuttallii*, *H. salicifolius*, *H. smithii*, *H. decapetalus*, *H. hirsutus*, *H. laevigatus*, *H. scaberimus*, *H. tomentosus*, *H. eggertii*, *H. ciliaris*, *H. resinosus*, *H. pauciflorus*, *H. tuberosus*, *H.* x *laetiflorus*

b) Development of new sunflower forms that are outstanding in early maturity, short stem, seed size and kernel size, high seed oil content

The species from which these characters have been transferred into the newly obtained sunflower forms are presented in Table I. It is difficult to combine all these features in just one form, but nevertheless some new forms have been produced which combined two, three and even the four features together. At the same time forms were obtained with transferred resistance to some of the pathogens noted in Table I. Several of these forms represent already fixed lines that were directly included in heterosis breeding.

c) Development of inbred sunflower lines with normal cytoplasm ("B" lines)

The newly obtained "B" lines originated from crosses of cultivated sunflower x wild *Helianthus* species and wild Helianthus species x cultivated sunflower. The total number of the already fixed "B" lines that had been developed until 1994 was 36. Stem height varied from 80 to 170 cm, and the

II. Characteristics of "B" lines, obtained from interspecific hybridization

No	Origin	Plant height (cm)	Head diameter (cm)	Seed oil content (%)	Vegetation period (days)
93–1159	*H. pauciflorus* – M-028	155	15	48.79	105
93–1170	*H. strumosus* – M-056	110	12	47.82	110
93–1191	*H. decapetalus* – M-043	150	16	52.54	109
93–1202	*H. hirsutus* – M-029	105	12	45.25	105
93–1215	*H. salicifolius* – M-045	180	18	51.15	107
93–1217	*H.* x *laetiflorus* – M-005	120	17	49.72	110
93–1224	*H. annuus* – E-002	160	20	51.60	115
93–1275	*H. argophyllus* – E-007	140	23	49.96	105
93–1291	*H. debilis* – E-011	155	24	47.10	108
93–1305	*H. debilis* – E-014	150	21	52.68	108
93–1310	*H. petiolaris* – E-034	135	16	49.67	105
93–1330	*H. praecox* – E-029	125	16	45.34	113

vegetation period from 92 to 125 days. The 1000 seed weight varied from 35 to 118 g, and oil content from 37 to 53%. Some "B" lines had a high level of *Phomopsis* resistance; others had complete resistance to downy mildew and broomrape. The characteristics of some "B" lines are presented in Table II.

d) Development of inbred sunflower lines that are carriers of *Rf*-genes (R-lines)

R-lines originated from crosses of cultivated sunflower x wild *Helianthus* species, CMS cultivated sunflower x wild *Helianthus* species, and wild *Helianthus* species x cultivated sunflower. Ninety-four accessions of 26 species were used for their development, and 81 R-lines have been fixed till now. Except for two, all of them had complete resistance to downy mildew. Some R-lines have also been resistant to *Phomopsis* and broomrape. Those that had no resistance to *Mildew* were completely resistant to *Phomopsis*. Line R-7006 was remarkable for its high resistance to *Sclerotinia* (under artificial inoculation with sclerotia). Two lines were notable for their high resistance to *Phoma*. All R-lines had a high combining ability. Data for some R-lines is given in Table III.

III. Characterization of R-lines, obtained from interspecific hybridization

No	Origin	Plant height [cm]	Head diameter [cm]	Vegetation period [days]	Seed oil content [%]	Gene ratio
7004R	*H. praecox* – E-028	145	16	112	52.64	10*
7006R	*H. praecox* – E-028	120	18	98	46.71	12
7009R	*H. tuberosus* – M-037	80	13	92	45.99	12*
7011R	*H. annuus* – E-004	145	15	103	46.85	11*
7015R	*H. debilis* – E-011	120	15	102	52.73	10*
7017R	*H. praecox* – E-028	145	16	110	52.10	12*
7024R	*H. tuberosus* – M-004	140	25	105	48.95	11
7026R	*H. smithii* – M-008	140	14	106	45.34	11*
7027R	*H. x laetiflorus* – M-005	135	17	102	48.86	11*
7041R	*H. eggertii* – M-001	120	15	101	47.21	11*
7042R	*H. pauciflorus* – M-028	130	15	106	49.13	11*

e) Development and investigation of new CMS-sources.

The search for new CMS-sources was combined with the development of alloplasmic sunflower lines based on the cytoplasm of different wild species. It was established that sterile forms could be obtained in different generations, from F_1, BC_1 to F_5. It became necessary to use a greater number of pollinators. Twelve CMS-sources have been obtained until 1994 (Table IV). In none of the CMS-sources a negative effect of the cytoplasm was observed. The plants produced with these CMS-sources developed normally. The seed productivity of the sterile analogues that were based on the new CMS-sources was equal to that of inbred lines ("B" lines).

IV. New CMS-sources, obtained from interspecific hybridization until 1995 in IWS "Dobroudja", Bulgaria

New CMS-sources	Numbering according to FAO	Origin	Obtained in year:
AN-67	ANN-10	*H. annuus* – E-067	1986
AN-58	ANN-11	*H. annuus* – E-058	1988
AN-2-91	ANN-12	*H. annuus* – E-002	1991
AN-2-92	ANN-13	*H. annuus* – E-002	1992
ARG-1	ARD-1	*H. argophyllus* – E-006	1985
ARG-2	ARG-2	*H. argophyllus* – E-007	1985
ARG-3	ARG-3	*H. argophyllus* – E-006	1987
DV-10	DEB-1	*H. debilis* – E-010	1990
PHIR-27	PRH-1	*H. praecox* – E-027	1990
PRUN-29	PRR-1	*H. praecox* – E-029	1989
Pet-34	PET-4	*H. petiolaris* – E-034	1991
Rig-28	RIG-2	*H. rigidus* – M-028	1991

CONCLUSION

The methods of interspecific hybridization and the hybrid material production made possible to develop a range of forms that are valuable for the sunflower crop quality. New forms were produced with resistance to diseases and parasites, with economical importance for cultivated sunflower; new forms that are remarkable for their short vegetation period, short or medium hight of stem, high oil content. On this basis 36 "B" lines and 81 R-lines have been developed and were included as parents in heterosis breeding. Twelve new CMS-sources have been obtained from the hybrid material.

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Received June 26, 1996

Přenos nových genových znaků z planě rostoucích druhů *Helianthus* na kulturní slunečnici

Mezidruhovou hybridizací mezi kulturní slunečnicí a planě rostoucími druhy *Helianthus* byly vytvořeny nové formy s užitečnými vlastnostmi. Do hybridního materiálu byl přenesen genetický materiál tvořený 94 přírůstky (6 jednoletých a 20 vytrvalých druhů). Přenos znaků zahrnujících odolnost ke škůdcům, ranost a geny obnovy fertility (geny *Rf*) byl zaznamenán již v generaci F_1 spolu s dalšími znaky také v následných generacích. Použití jednoduchého a dvojitého zpětného křížení, příbuzenského opylení a autogamie umožnilo nejen překonání bariéry sterility mezidruhových hybridů, ale také vytvoření forem slunečnice se zajímavými vlastnostmi pro šlechtění. Byl získán nový materiál s odolností k *Plasmopara helianthi*, *Phomopsis helianthi*, *Phoma helianthi*, *Erysiphe cichoracearum* a *Orobanche cumana*, s vysokým obsahem oleje v nažkách, s raností a velkými nažkami, který obsahuje velký počet jednoletých a vytrvalých druhů. Z pěti jednoletých a jednoho vytrvalého druhu jsme získali dvanáct nových zdrojů CMS. Významný počet forem jako nosičů genů-obnovitelů fertility jsme získali ze šesti jednoletých a 20 vytrvalých druhů. Z těchto forem byly vytvořeny R-linie s vysokou kombinační schopností a odolností ke škůdcům.

slunečnice; *Helianthus*; planě rostoucí druhy; rezistence; R-linie; CMS

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Genet. a Šlecht., *32*, 1996 (4) : 287-296

NEWS

ELMI – AN INFORMATION SYSTEM TO USE PLANT BREEDING DATA EFFICIENTLY

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Modern variety development has to focus on many traits. Not only parameters about yield and agronomic performance have to be considered, but all kinds of data on disease resistance or quality. In some cases even biochemical data like enzympolymorphisms, RFLP or AFLP etc. must be used to distinguish between genotypes.

Therefore, almost all European plant breeding establishments are equipped with computers to manage the many data gained during the development of a variety.

From the plant breeding point of view, breeding work consists of four stages (adapted from Schnell, 1982):

I – choice of parents to create new variation
II – development of varieties
III – test of experimental varieties
IV – maintenance of variety

The selection work is mainly performed by the breeder, whereas the technical work like design and planting of the experiments or taking data is done by the technical personnel.

From the technical point of view the features shown in Table I have to be performed:

This means that an information system for plant breeding (ISP) on one hand has to support the technical personnel in the daily routine work, and on the other hand it has to efficiently support the breeder in his selection procedures. Therefore, the collected data have to be prepared so that they can be evaluated by the relevant statistical methods. A complete ISP therefore consists of a data bank management system, a bank of evaluation methods, and an interface between these two (Fig. 1).

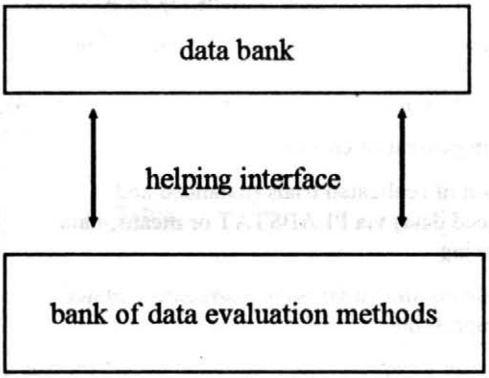
For managing the databank we found it best to use an already existing relational database management system. Many of them are available (like dBase, FOXpro etc.).

Examples of programmes usable for data evaluation which could be integrated into the bank of data evaluation methods for breeding stages II and III are

I. Features that have to be performed by data processing in a plant breeding company

Work		Feature
general		– evaluate and check of external data (e.g. varietal admission and registration)
		– put data into the archives
		– protect data against unauthorisized use
		– protect data against unwanted lost
trial technic		– set up of sowing lists
		– set up of sowing plans
		– set up of lists e.g. for weighing
		– set up of field books
		– print field labels
		– take and manage data
		– process pedigrees and data from one generation to the next
selection work in stage	I	– put into the archives the parents for creating new variation
		– put into the archives the created populations
		– choice of parents
		– maintenance of parents
	II	– design and evaluate single locus trials by standard or neighbourhood trials
		– design and evaluate multiple locus yield trials
		– collect and evaluate data of one candidate from previous seasons
		– set up of lists where candidates are sorted according to different aspects
		– calculate selection indices
		– evaluate the performance of families
		– calculate means and variability parameters of candidate groups
	III	– design and evaluate multifactorial balanced or unbalanced trials
		– set up of lists where candidates are sorted according to different aspects
		– calculate selection indices
		– documentation of a candidate's genealogy

e.g. GEN-STAT, SAS, SPSS or BMDP. Programmes to support stage I (choice of parents) are created e.g. by Pešek (1983), Osborne and Mathern (1990), Styles et al. (1985) or Coe (1991). At least one method for each breeding stage should be part of an ISP.



1. Elements of an ISP (Information System for Plant Breeding)

Meanwhile, there are many PC-Programmes available to help the breeder in his work. Most of them deal at least with the evaluation of field trials (e.g. VERA, VESAM, PLANTA, FTAB/ANOFT, PLABSTAT, SAS). The work of Brehm (1991) or Schott (1989) was devoted to create an ISP for the segregating populations of autogamous crops or beets, respectively. Other programmes allow to print field labels and field books (e.g. Andrews, Hardwick, 1982), but these programmes cannot be considered as ISPs since they deal with only parts of the work. Very few programmes cover the total range of work at a plant breeding institution from harvest to harvest, and for all aspects and stages of the breeding process (e.g. MSTAT C, AGRO-BASE 4.0, STRUBE). With ELMI we have tried to offer a comprehensive ISP which can be run by the technical personnel without being computer specialists.

ELMI up to now shows a main menu which reflects parts of the breeding work and evaluation (Table II).

Before creating an ISP one has to decide on the keys for retrieving the data of a candidate variety. In combining technical and theoretical breeding aspects we decided to use the annual candidate number combined with the pedigree information. In trial plots the candidate number plus replication number results in the fieldnumber. For multilocation experiments the candidate has the same fieldnumbers at each location, thus facilitating retrieval of the candidate over locations (Weissmann, 1992).

Most of the programmer's work is devoted to creating a link between database and methods of data evaluation. This link has to talk in the same "language" as the

II. Main menu options of ELMI

Menu option	Feature
1 trial plots	design and evaluation of replicated lattices and randomized complete block designs via PLABSTAT
2 segregating generations	data management and evaluation of segregating material, design and evaluation of unreplicated standard trials after Schuster and Lochow (1964)
3 crosses	data management of crosses
4 archives of trial plots	evaluation of replicated trials (balanced and unbalanced data) via PLABSTAT or means, data compressing
5 archives of segregating generations	family means and variation of segregating material, data compressing
6 special evaluations	on company's request (e.g. evaluation of test crosses etc.)
7 system survey	create information about the data of trial plots for fast data retrieval (which experiments are in which file, or how many data has been taken for experiment no. *x* at location no. *y*)
8 installation	set up of parameters for company specific hardware
9 exit to DOS	quick exit to dos for one prompt

breeding personnel and shall reflect the known structure of breeding work (e.g. Schlinggmann, 1994). The menu of ELMI's helping interface rather reflects the technical part of the work.

It is separated into the chapters:

- setup of trials and fieldbook
- selection of candidates
- data input (via keybord, interface from a handheld PC, disk, or ASCII-file)
- data output (fieldbooks, lists, labels, to interface or to ASCII-file)
- evaluation of data (link e.g. to ANOVA via PLABSTAT)
- manipulation of traits (add or delete traits, rename, calculate, describe)
- file management (select, copy, rename, describe, backup, restore)

Figs. 2 and 3 show examples of printouts generated by ELMI. Fig. 2 shows a page of a fieldbook. Even though field data like scores could now be recorded at once in the field by mobile hand held microcomputers, many breeders still prefer to have a printed fieldbook. The example shows a lattice of 16 candidates. As an option, the first replication is printed with larger spacing than the second replication. The candi-

2. Printout of a fieldbook: candidates of a 5x5 lattice, first and second replication (truncated)

Fieldbook of TI93HP
Triticale Hauptprüfung
Location: Hohebuch

page 1

1. replication

FENR	name (pedigree)	youth develop	plant height	sclero-tinia	mil-dew1	mil-dew2	winter hard		
1501-1	Lasko								
1502-1	Lukas								
1503-1	Salvo								
1504-1	Alamo								
1505-1	692/89 Salvo x Cin-13-E1-E2-								
1506-1	692/89 Salvo x Cin-13-E1-E2-								
1507-1	694/89 Salvo x Cin-13-E1-E2-								
1508-1	704/89 Salvo x Cin-13-E1-E2-								
1509-1	714/89 Salvo x 78PN-6655-E2								
1510-1	715/89 Salvo x 78PN-6655-E2								
1511-1	719/89 Wintri x 6TA-876H								
1512-1	28/89 Wintri * Cin-13-E1-E2								
1513-1	35/89 Salvo x Cin-13-E1-E2-E								
1514-1	14/89 LT404 x (274-320PjPol								
etc.									

Fieldbook of TI93HP
Triticale Hauptprüfung
Location: Hohebuch

page 2

2. replication

FENR	name (pedigree)	youth develop	plant height	sclero-tinia	mil dew1	mil dew2	winter hard		
1524-2	701/90 (4/11/87)								
1509-2	714/89 Salvo x 78PN-6655-E2								
1504-2	Alamo								
1514-2	14/89 LT404 x (274-320PjPol								
1519-2	03/22/90 LT696 * 274-320								
etc.									

3. Printout of means of a 5x5 lattice, trials at four locations. The important trait (yield) is given in detail: means over locations (mean abs), means relative to check varieties (means rel) and LSD 5% score (significantly better + or worse – than check mean) and rank. Additionally the means relative to checks are given for each location. All other traits are chosen to be given as absolute means over locations. LSD 5% is only given, when the number of data per trait allows analysis of variance. The lower part shows how many data values have been available for the evaluation

	TI91HP	yield dt/ha mean				relative yield dt/ha locations				winter hard	ear-emerge
no	name (pedigree)	abs	rel	t	rank	HB	HH	HI	OL		
1501	*Lasko	77.6	98		12	95	97	97	101	6.2	5.2
1502	*Lukas	71.5	90	–	23	90	85	94	95	5.1	5.2
1503	*Salvo	78.1	98		8	104	101	95	94	3.5	7.3
1504	*Alamo	90.3	114	+	1	112	116	117	109	0.9	1.5
1505	692/89 Salvo x Cin-13-E1-E2-	75.0	94		17	96	97	89	95	3.6	6.2
1506	692/89 Salvo x Cin-13-E1-E2-	71.0	89	–	24	89	88	89	91	3.6	5.8
1507	694/89 Salvo x Cin-13-E1-E2-	74.0	93	–	18	97	91	91	94	2.4	6.3
1508	704/89 Salvo x Cin-13-E1-E2-	72.2	91	–	22	93	95	85	90	5.1	5.9
1509	714/89 Salvo x 78PN-6655-E2	73.7	93	–	20	93	98	92	88	5.6	5.2
1510	715/89 Salvo x 78PN-6655-E2	75.8	95		15	100	97	94	91	6.3	6.3
1511	719/89 Wintri x 6TA-876H	68.7	87	–	25	95	77	86	91	3.6	5.5
1512	28/89 Wintri * Cin-13-E1-E2	81.4	103		5	102	107	97	104	1.8	4.2
1513	35/89 Salvo x Cin-13-E1-E2-E	77.2	97		14	100	104	95	90	1.0	4.8
1514	14/89 LT404 x (274-320PjPol	81.7	103		4	108	102	101	102	4.4	4.0
1515	07/89 Pull18F5479 * Basalt *ff	81.9	103		3	111	104	100	99	3.6	6.8
1516	03/09/90 Salvo * Cin-13-E1-E2	75.3	95		16	98	93	90	99	3.6	5.8

1517	03/10/90 Salvo * Cin-13-E1-E2	78.0	98		9	104	99	92	99	3.1	4.5
1518	03/20/90 (Clevix x Okapi) x lll	88.0	111	+	2	115	114	104	111	4.4	4.0
1519	03/22/90 LT696 * 274-320 * Y	73.9	93	–	19	88	100	89	96	3.7	6.8
1520	TIW 66 (5/14/87)	80.5	101		6	102	101	97	107	1.8	6.7
1521	TIW 83 (5/19/87) HO 502-504/	77.7	98		11	103	102	89	97	4.4	6.5
1522	602/90 (1/04/86)	77.5	98		13	96	105	87	102	4.4	7.0
1523	603/90 (1/04/86)	72.3	91	–	21	97	88	87	94	3.7	6.5
1524	701/90 (4/11/87)	77.8	98		10	104	100	92	97	5.7	4.3
1525	702/90 (4/11/87)	79.6	100		7	105	107	86	104	3.7	6.5
	mean across locations	77.2	97			100	99	93	98	3.8	5.6
	mean across check vareties (*)	79.4	100			69	62	81	76	3.9	4.8
	LSD 5 over locations	5.2	7			11	7	0	9	0	0
data taken at:		amount of data									
1 HB Hohebuch		75								75	75
4 HI Hildesheim		75								0	25
6 HH Hohenheim		50								0	0
7 OL ObererLindenhof		75								0	0

dates can be printed in the same order as they are planted on the field. Fig. 3 shows a table of means as a result of evaluating a trial of four locations via PLABSTAT. On the operator's request only means can be printed. Additionally, the original values or the analysis of variance, stability parameters, and coefficients of correlations between traits are given.

First steps have been taken to integrate methods for evaluating statistical parameters like general and specific combining ability of topcrosses, diallels etc., or for the evaluation of the candidate's performance during all the years of varietal development. More work needs to be done in the field of choice of parents by integrating not only the known programmes (e.g. Pešek, 1983), but also other modern methods of data evaluation for separating parents e.g. based on RFLP and cluster analysis.

All these efforts of programming are undertaken since we are aware of the fact that the most expensive and valuable part of breeding work is data. ELMI is designed to use even more efficiently the large capital of data in plant breeding. Up to now, ELMI is used by some German and one Czech breeding company, including their different international breeding stations. ELMI can talk German and English.

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Received June 29, 1996

ELMI – informační systém

Moderní šlechtění odrůd se musí zaměřovat na mnoho vlastností důležitých pro rostliny. Musí být zohledňovány nejen výnosové parametry, ale i všechny druhy dat vztahujících se k odolnosti k chorobám nebo ke kvalitě. Velké množství dat vztahují-

cích se ke každé potenciální odrůdě nutí šlechtitelské firmy využívat počítačové techniky ke zpracování dat. Vedle rostlinného materiálu jsou dnes data nejcennějšími objekty šlechtitelské firmy. Proto byl vytvořen systém ELMI, informační systém pro šlechtění rostlin, jímž se má docílit zvýšení efektivity získávání dat, jejich managementu a vyhodnocování.

informační systém; management dat; databanka; metody vyhodnocování; šlechtění rostin

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Genet. a Šlecht., *32*, 1996 (4) : 297-306

REVIEWS

GERMPLASM IN SUNFLOWER BREEDING IN THE NEXT TEN YEARS

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Sunflower (*Helianthus annuus* L.) is one of the most important crop plants to have been domesticated in what is now the United States. Wild sunflower was an important food source to seed gatherers in western North America, and was apparently carried as a weed to the central U.S.A., where it became domesticated sometime before 3 000 BC. Native Americans esteemed the sunflower seeds as food and a source of oil, but also found many other uses for the plant (Seiler, 1992).

The domesticated sunflower has narrow genetic variability, especially with respect to important agronomic characters. Diseases are a limiting factor in the production in most sunflower-growing countries. Different diseases prevail in different regions because of various agroecological conditions. Cultivated sunflower is deficient in resistance genes, but sources of resistance have been sought and found in wild species. Some of these have rendered genes of resistance to *Plasmopara helianthi*, *Puccinia helianthi*, *Verticillium alboatrum*, *Verticillium dahliae* and *Orobanche cumana*. Still, there remains a large number of diseases for which sources for resistance have yet to be found (Škorić, 1988).

Of all field crops, sunflower has the highest number of wild relatives. The genus *Helianthus* is composed of 49 species and 19 subspecies with 12 annual and 37 perennial species. These diverse species represent considerable genetic variability which can be utilized for the improvement of cultivated sunflower (Seiler, 1992).

Significant results have been achieved using wild species in sunflower breeding programs, especially regarding disease and pest resistance. Another significant contribution of wild species has been in the discovery of cytoplasmic male sterility (CMS) sources and restorer (*Rf*) genes by interspecific hybridization, which has enabled the manifestation of heterosis by hybrids (Škorić, 1993).

Germplasm in sunflower breeding

The existing genetic variability of cultivated sunflower enables the development of hybrids with a genetic seed yield potential of as much as 7 t/ha. Unfortunately, large-scale production gives yields which are most often not higher than 2 to 3 t/ha. Yields higher than 3 t/ha are much less frequent than those lower than 2 t/ha. There are various reasons that the genetic potential of sunflower is so underexploited, but most often they are high susceptibility of hybrids to diseases, insects and stress (drought) as well as inadequate application of technological measures in the production.

This raises the question of how to realize the full genetic potential of this crop. Certainly, this cannot be done by simple means and quickly. Disease and insect resistance should be improved first, which is a complex and long-term task. At the same time an effort should be made to improve other agronomic traits, such as drought resistance and attractiveness to pollinators, as well as to increase self-fertility and fully optimize the utilization of soil nutrients. All this requires a certain level of genetic variability, i.e. germplasm, in the sunflower. The limitations of the cultivated sunflower's genetic variability can be overcome in a variety of ways, but primarily through interspecific hybridization with wild species.

A prerequisite for increasing this variability is a germplasm collection comprised of diverse cultivated and wild sunflower genotypes. Since the cultivated sunflower originated in North America, it is natural that the greatest genetic variability exists there, especially in the wild relatives. The National Plant Germplasm Plant Introduction Station at Ames, Iowa, has the worlds largest collection of wild sunflower species as well as of cultivated sunflower genotypes. According to Seiler (1992), the collection now contains over 2 000 accessions. The active collection contains approximately 1 000 annual and 500 perennial accessions. Since 1976, 4 200 accessions of wild sunflower have been distributed to 30 different countries, and have become the basis of several wild species collections throughout the world.

The worlds second largest collection of wild species is undoubtedly at our Institute. To collect wild sunflower species, our experts have participated in a number of explorations across the U.S.A., which were financed by the International Board for Plant Genetic Resources (IBPGR), European Cooperative Program for Genetic Resources (ECP/GR). In addition, our Institute has a collection of over 5 000 inbred lines from various sources.

In North America, there is a plenty of wild populations yet to be collected – something to be done in the years to come. In addition to collecting wild sunflower species, great attention should be paid also to their maintainance and study.

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Using interspecific hybridization to increase genetic variability of cultivated sunflower

Wild *Helianthus* species constitute the basic genetic stock from which the cultivated sunflower originated. They have contributed specific characteristics for sunflower improvement (Seiler, 1992). Knowledge of a particular habitat and adaptation of the species often help to identify potential sources of desirable genes for specific traits.

The correct choice of wild species is very important when increasing the genetic variability of cultivated sunflower by means of interspecific hybridization. In making this choice, the habitat of a wild species should be considered foremost. According to Seiler (1992), genetic diversity in the genus *Helianthus* is reflected by habitat diversity among the species. Thus, he argues, dry, sandy soils are inhabited by such species as *H. anomalus*, *H. deserticola*, *H. neglectus* and *H. niveus*, while very moist ones are the habitat of *H. angustifolius*, *H. agrestis*, *H. californicus*, *H. giganteus*, *H. nuttallii* ssp. *nuttallii*, *H. paradoxus* and *H. tuberosus*. Deep woods are the habitat of *H. decapetalus*, and prairies of *H. maximiliani*, *H. grosseserratus* and *H. pauciflorus* ssp. *subrhomboideus*. Some species inhabit moist, heavy and very saline soils. *H. paradoxus* has a high tolerance to salt and a great potential as a source of genes for salt tolerance in cultivated sunflower.

In addition to habitat, another important characteristic in choosing the right wild species for interspecific hybridization is their tolerance or resistance to diseases and insects.

The utilization of wild species in breeding is a long and complex process. Interspecific hybridization is often hampered by different numbers of chromosomes (in addition to diploid species there are also tetraploid and hexaploid ones) and incompatibility with cultivated species. Abortion of the hybrid embryo is a further mechanism that prevents hybridization of perennials. Chandler and Beard (1983) successfully made 53 interspecific *Helianthus* combinations using an embryo culture system. a number of other authors have also managed to overcome abortion in F_1 generations of interspecific hybrids by using the embryo culture system.

Another problem in interspecific hybridization is insufficient knowledge of the genome character of the genus *Helianthus*, since genes responsible for desirable characters and traits can in the process of hybridization be lost. Interspecific hybridization introduces into the cultivated form not only desirable but also negative traits, especially in the case of trait linkage.

Yet another problem is presented by seed dormancy in wild species and interspecific hybrids. Moreover, utilization of many species is limited by poor crossability and the high degree of F1 sterility in interspecific hybrids. Chromosome doubling of interspecific hybrids is generally effective in improving fertility when sterility is associated with meiotic abnormalities in sunflower (Jan et al., 1983).

All of these problems, as well as a number of others, sufficiently illustrate the complexity accompanying the use of wild sunflower species. Still, numerous interspecific hybrids between wild species and cultivated sunflower genotypes have been created by means of conventional crossing methods as well as biotechnological ones. In future, as many crosses as possible should be made through conventional crossing methods in order to develop a range of interspecific hybrids. It should be stressed that this is one of the best approaches to increasing and widening of the germplasm of this oil crop. Another way that can be advised is intergeneric hybridization.

Breeding for disease and insect resistance

Sunflower breeding around the world has made significant progress in producing new high-yielding sunflower hybrids resistant to different major diseases, resulting in an increase on a permanent basis of the areas and yields of this important oil crop. In order to be more stable, new sunflower genotypes should incorporate new genes for resistance to a number of pathogens and other forms of stress, such as drought (Škorić, 1995).

Diseases are a limiting factor in the production in the majority of sunflower-growing countries. Different diseases prevail in different regions because of various agroecological conditions. Cultivated sunflower has a narrow genetic base and is deficient in resistance genes. So far, sources of resistance have been sought and found in wild sunflowers. Certain wild species have rendered genes of resistance to *Puccinia helianthi*, *Plasmopara helianthi*, *Verticillium dahlia*, *Phomopsis/Diaporthe helianthi*, *Erysiphe cichoracearum* and *Orobanche cumana*. There is still a large number of diseases for which resistance sources remain to be found. Among these, the most important are *Sclerotinia sclerotiorum*, *Macrophomina phaseolina*, *Phoma macdonaldi*, *Alternaria helianthi*, *Botryis cinerea*, *Rhizophus* spp., etc. (Škorić, 1988). Wild *Helianthus* species constitute the basic genetic stock from which the cultivated sunflower originated. The diverse species are adapted to a wide range of habitats and possess considerable variability for most economic and agronomic characteristics, disease and insect resistance and seed quality factors (Seiler, 1992).

Thus, the genetic variability of the cultivated sunflower can be increased by crossing it with numerous wild *Helianthus* species as potential sources of genes for disease resistance. Breeding for resistance is the most economical and effective way to control diseases (Seiler, 1991). To accomplish that, breeders should include all available wild species in their programs of breeding for resistance to pathogens.

However, the occurrence of new races in some pathogens requires permanent breeding efforts on enriching the sunflower germplasm through wild species, as in the example of downy mildew. For many years, breeders needed resistance to race 1 in Europe and race 2 of downy mildew in North America (Miller, 1992). Vranceanu et al. (1978) reported a new race in Romania. In North America, rapid changes have occured since 1980 with the occurrence of new races. Races 3, 4, 6 and 7 were discovered and are now prevalent in North America (Gulyua et al., 1991). The existence of new races 3, 4 and 6 in Europe was stated by Gulyua et al. (1991) and Tourvielle et al. (1988), while Gulyua et al. (1991) found races 3 and 7 in Argentina. Miller (1992) concludes that sources of resistance to all downy mildew races have been discovered, the genetics of inheritance of the resistance determined and the genes incorporated into commercial lines. This is a perfect example of good utilization of wild species in increasing the variability of cultivated sunflower germplasm.

Similarly, wild sunflowers are effectively used in breeding for resistance to *Orobanche cumana* which frequently develops new races (Škorić, 1988).

According to Škorić (1988), there are no genes for resistance to *Sclerotinia sclerotiorum* in the genus *Helianthus*. It is still uncertain whether the current level of 'genetic engineering' (gene transfer) will enable the detection of genes for resistance to *Sclerotinia* in a monocotyledonous plant and incorporate them into cultivated sunflower. The answer will perhaps be found in the following period.

Certain insects present a great problem in sunflower production in North America as well as some regions of South America, Africa, Asia and Australia. The greatest success in breeding for resistance to insects has been the discovery of genotypes that have a phytomelanin layer in the husk providing resistance to the sunflower moth (*Homeosoma nebullella* and *Homeosoma electellum*). Researchers in the U.S.A. have extensively studied wild sunflower species in terms of resistance to certain insects. Their results have been more modest than those of research aimed at resistance to diseases. Instead of being unduly pessimistic, however, we should bear in mind that "host resistance in cultivated sunflower via incorporation of germplasm from wild *Helianthus* offers a tremendous potential for long-lasting economical management of several insect pests. For the short term, knowledge of the bionomics of pests on native *Helianthus* hosts will promote ecologically sound strategies which could be developed for management of insects on cultivated sunflower" (Rogers, 1988).

Successfull application of the new methods of 'biotechnology' can contribute to overcoming the problems of a narrow genetic base, and at the same time accelerate the breeding process. These methods are also significant for avoiding or alleviating the numerous problems that can occur in interspecific hybridization. Various techniques, such as embryo culture ('embryo rescue'), meristem culture, anther and microspore culture, protoplast culture and cell fusion, and molecular techniques including gene transfer should be applied (Friedt, 1992).

Oil and seed quality

Sunflower oil ranks among the best oils of plant origin. The food industry demands fats and oils with more specific fatty acid compositions. Consequently, there is an increasing interest in producing modifications in the oil composition to offer the food and non-food industry oils for specific purposes (Friedt, 1994).

The most extensive studies of the variability of wild sunflower and possibilities of its utilization in changing the quality of both seed and oil in sunflower have been done by Seiler (1992). He showed that the wild species can significantly contribute to those changes.

In this field the best results on a world scale have been achieved by induced mutations. Soldatov (1976) made a particularly significant contribution to a change of oleic acid ($C_{18:1}$) composition, and developed a high oleic genotype by means of induced mutation in the variety Pervenets. It served as the source for producing lines that, by virtue of hybrids, had a high oleic acid content in the oil.

Induced mutations also produced hybrids with a high palmitic ($C_{16:0}$), stearic ($C_{18:0}$) and palmitoleic ($C_{16:1}$) acid content. Genotypes thus produced enable further manipulation of the fatty acid composition of sunflower oil composition as well as the process of getting new germplasm in terms of oil quality.

The manipulation of oil quality on an even larger scale, this time of the type of tocopherol, was made possible through the development of isogenic lines (LG-15, LG-17 and LG-24) by Demurin (1993). It is known that standard sunflower oil contains predominantly type α tocopherol. The isogenic line LG-15 contains gene *tph1*, which causes sunflower oil to have equal contents of α and σ tocopherols. Line LG-17 contains gene *tph2*, with which μ tocopherol predominates, while in line LG-24 the genes *tph1 tph2* secure the following tocopherol composition: 8% α, 84% μ and 8% σ.

The combined effect of *Ol* genes and the genes *tph1*, *tph2* and *tph1 tph2* increases the stability of sunflower oil by as much as 16 times in comparison to its standard form, allowing its use to be significantly widened. It is very likely that the next ten years will see a significant enrichment of sunflower germplasm based on those genes, and a consequent development of hybrids with various oil quality.

The existing genetic variability of wild and cultivated sunflower permits the manipulation of other seed and oil characteristics as well. New germ-plasm will be developed on the basis of market demand and the genetic potentials of sunflower and its wild relatives.

Utilization of wild species in changing the idiotype of cultivated sunflower

The variability existing within the cultivated form of sunflower enables the development of inbred lines with an insufficiently high heterosis effect on seed yields. An increase in the productivity of future hybrids can only be brought about by an increase in the genetic variability of cultivated sunflower based on wild species of the genus *Helianthus* (Škorić, 1989; Seiler, 1992).

The change of sunflower germplasm should not be focussed solely on seed productivity, but one of its objectives should also be the incorporation of genes from wild species that would allow the use of other plant organs for commercial purposes (Seiler, 1992), including the use of the sunflower head for pectines, forage, and fuel, the use of the stem for silage (green stems), fuel, and as raw materials for the production of gum, and the use of the leaves for forage and various phyto-pharmaceutical preparations.

One of the primary goals of sunflower breeders should be a change in the architecture of the photosynthetic apparatus. The change should be directed toward shortening the period which precedes the formation of the maximum leaf area of parental lines, as well as their hybrids. Furthermore, green leaf area duration (LAD) should be prolonged and the efficiency of NAR increased. The number and disposition of leaves on the stem should be modified so as to provide maximum exploitation of CO_2 from the air and as much aeration as possible. These changes of the photosynthetic apparatus should exploit the high genetic variability existing within wild species, as shown by the diverse photosynthetic apparatuses of *H. mollis*, *H. argophylus*, *H. salicifolius*, *H. radula*, *H. maximiliani* and other species. This illustrates how extensive the genetic possibilities for the manipulation of leaf number, form, activity and other traits are (Škorić, 1989).

There has been a rapid expansion of sunflower in the dry regions of the world, but the cultivated sunflower form used does not always provide an economically justified production. Wild sunflower species existing in extreme drought conditions provide a basis for an increase in drought resistance of cultivated sunflower. Drought resistance is complex in nature; it includes resistance to arid soil and dry air, a more efficient root system, early maturity, resistance to *Sclerotinia bataticola* (*M. phaseoli*), as well as better utilization of soil water and more efficient use of soil nutrients.

The use of wild species in breeding programs has been well under way in the world for some time now. Serieys (1980) suggests *H. argophyllus* in breeding for drought resistance because of its "leathery" leaves covered with numerous hairs. Another species recommended for drought resistance is *H. deserticola* with its deep and powerful root system. France, Spain, the U.S.A., Romania and Italy are the countries with the most extensive use of wild species in breeding for drought resistance.

The expansion of cultivated sunflower will also include more saline soils. An increase in resistance to the high pH value of such soils can again be brought about through wild species. Current research in the U.S.A. seems to suggest that the most resistant species to high salinity is *H. paradoxus*, but this should not preclude investigations of other species (Seiler, 1992).

Sunflower is known to be a particularly open-pollinated species. The success of its cultivation under stress conditions depends largely on self-fertility, the level of which can be greatly increased via wild species. The findings of Heiser et al. (1969) and other authors suggest to use *H. agrestis*, *H. radula* and some other species.

Conclusions

The existing genetic divergence of cultivated sunflower enables the development of hybrids with a genetic seed yield potential of as much as 7 t/ha. Unfortunately, large-scale production renders yields which are most often not higher than 2 to 3 t/ha, the reason being a deficiency in genes for disease, insect and stress (drought) resistance. The richness of wild species in the genus *Helianthus* enables germplasm of the cultivated sunflower to be enriched by means of interspecific hybridization. The difficulties associated with this process can be surmounted by means of modern biotechnological methods.

Wild species should also be used to change the idiotype of cultivated sunflower and to increase the level of commercial exploitation of all plant organs.

Induced mutations should be used for increasing the genetic variability of the parameters of oil and protein quality as well as other seed traits.

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Received June 26, 1996

Genofond ve šlechtění slunečnice v příštích deseti letech

Jedna ze čtyř významných olejnin na světě, slunečnice (*Helianthus annuus* L.), je v Jugoslávii hlavní olejninou. Její genetická variabilita je poměrně nízká zejména s ohledem na geny pro odolnost k chorobám. Pomocí mezidruhové hybridizace s planě rostoucími druhy došlo k určitému zvýšení její divergence. Rod *Helianthus* se skládá ze 46 druhů (37 vytrvalých a 12 jednoletých) a z 19 poddruhů. Pro rod *Helianthus* je typická značná variabilita uvnitř každého druhu a poddruhu. Tato variabilita nabízí perspektivy pro zvýšení genetické variability kulturní slunečnice v příštích deseti letech. Mezidruhovou hybridizaci však často brzdí polyploidie planě rostoucích druhů (2*n*, 4*n*, 6*n*) a inkompatibilita. Tuto potíž lze překonat použitím nových biotechnologických metod. Úsilí zaměřené na zvýšení genetické variability slunečnice prostřednictvím planě rostoucích druhů bude mít za cíl zvýšení kvality oleje, odolnosti proti chorobám, škůdcům a stresu (způsobenému většinou suchem), přičemž dojde k využití mezirodové i mezidruhové hybridizace. Současná sbírka našeho ústavu obsahuje více než 5 000 inbredních linií a 1 000 populací planě rostoucích druhů a je zárukou úspěchu šlechtění slunečnice v příštích deseti letech.

slunečnice; genofond; planě rostoucí druhy; mezidruhová hybridizace; genetická divergence

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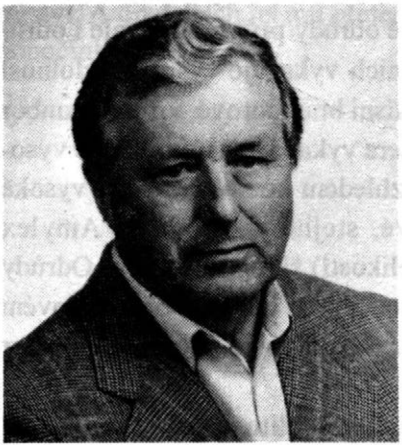
ŽIVOTNÍ JUBILEA

70 let Ing. Miroslava Majora, CSc.



V letošním roce dosáhl význačného životního jubilea – 70 let – jeden z našich velmi úspěšných šlechtitelů brambor, Ing. Miroslav Major, CSc., šlechtitel známý a uznávaný nejen v České republice, ale i v zahraničí.

Narodil se 31. března 1926 v Horním Prysku na Děčínsku. Je absolventem Zemědělského institutu – oddělení šlechtění v Oděse v bývalém SSSR (1950–1955). V roce 1964 získal vědeckou hodnost kandidáta věd.

V roce 1955, po ukončení vysokoškolského studia, nastoupil do šlechtitelské stanice Vyklantice u Pacova, náležející v té době Výzkumnému ústavu bramborářskému v Havlíčkově Brodě (od roku 1956 Šlechtitelskému a semenářskému podniku v Havlíčkově Brodě a po územní reorganizaci v roce 1960 Šlechtitelskému a semenářskému podniku v Táboře), kde pracoval nejprve jako šlechtitel a od roku 1958 jako vedoucí šlechtitel. V roce 1968, po převodu novošlechtění brambor z Vyklantic do Šlechtitelské stanice Hrádek u Pacova (náležející v té době rovněž k ŠSP Tábor), přešel jako vedoucí šlechtitel na tuto stanici. Po začlenění šlechtitelské stanice Hrádek ke stanici Pacov (v roce 1973) zodpovídal i za udržovací šlechtění brambor na stanici Pacov.

Díky svému širokému odbornému rozhledu v oblasti šlechtitelských metod a organizačním schopnostem vytvořil na stanici Hrádek moderní šlechtitelské pracoviště, které ve své práci využívalo nejnovějších poznatků šlechtitelského bramborářského výzkumu jak našeho, tak i zahraničního. V tom mu byly nápomocny jak úzké kontakty s pracovníky Výzkumného ústavu bramborářského v Havlíčkově Brodě, tak i četné studijní cesty do obdobných zahraničních ústavů a šlechtitelských stanic (zejména v bývalé NDR a v bývalém SSSR, v Polsku, ale i v jiných zemích). To vše ve spojení s velmi dobrými půdními a povětrnostními podmínkami stanice (jakož i celého Pacovska s nadmořskou výškou 550–650 m) se promítlo v úspěšnosti jeho práce. Nutno však poznamenat, že význačnou pomocnicí v jeho práci mu byla manželka Ing. Blažena Majorová, která – rovněž šlechtitelka brambor – mu byla cennou spolupracovnicí ve šlechtění brambor (zabývala se tvorbou výchozích materiálů a laboratorními testy), jemuž se věnoval až do odchodu do důchodu v roce 1987.

Ing. Miroslav Major, CSc., je hlavním šlechtitelem (příp. spolušlechtitelem) 17 odrůd brambor: Doubrava (povolená v roce 1958), Orlík (1962), Jizera (1963), Kamýk (1974), Otava (1981), Svatava (1983), Oreb (1983), Zvíkov (1984), Šárka (1985), Lukava (1988), Zlata (1989), Tara (1994), Amylex (1994), Tegal (1995), Ornella (1995), Pacov (1995) a Tábor (1996). Jedná se o odrůdy různých užitkových směrů – odrůdy konzumní i vysoce škrobnaté odrůdy průmyslové, ale i odrůdy vhodné pro potravinářské výrobky. Většina z nich vykazuje vysokou odolnost proti obecné strupovitosti, dobrou odolnost proti plísni bramborové, virům brambor a proti mechanickému poškození. Např. odrůda Jizera vykazovala mimořádně vysokou rezistenci proti virům, odrůda Tegal náleží vzhledem ke své ranosti a vysoké škrobnatosti mezi špičkové odrůdy průmyslové, stejně jako odrůda Amylex svou vysokou stabilní škrobnatostí a kvalitou (velikostí) škrobových zrn. Odrůdy Lukava, Tara, Tegal, Pacov a Tábor vykazují rezistenci proti háďátku bramborovém – patotypu Ro 1, odrůda Tegal dále rezistenci proti 6 patotypům rakoviny brambor (patotypy D1, P2, N1, M2, V1, S3).

Obdobně jako odrůdy průmyslové, vykazují vysokou kvalitu i odrůdy konzumní. Důkazem toho je, že čtyři odrůdy byly na výstavě Země Živitelka v Českých Budějovicích oceněny Zlatým klasem: konzumní odrůdy Svatava (1983), Šárka (1985), Lukava (1988) a průmyslová odrůda Cornella (1995). Za nejzávažnější úspěch mnohaleté šlechtitelské práce Ing. M. Majora je nutné vyzvednout zvýšení škrobnatosti u průmyslových odrůd hrádeckého šlechtění o 1,5–2,0 % proti standardu.

Ing. M. Major, CSc., pracoval též výzkumně, zejména v oblasti škrobnatosti brambor, a výsledky dosažené v této oblasti využil především ve své vlastní šlechtitelské práci, ale i ke zpracování své kandidátské disertační práce na téma Škrobnatost brambor (1963) a ideotypu průmyslové odrůdy brambor (1978). Dále je publikoval v několika vědeckých a odborně populárních pracích a přednesl na několika konferencích. Podílel se také na zpracování odrůdové agrotechniky pěti odrůd brambor: Blaník (1977), Svatava (1987), Šárka (1987), Oreb (1985) a Zvíkov (1987). Pro potřebu šlechtitelské stanice Hrádek zpracoval Analýzu současného stavu a výhledové programy ve šlechtění brambor (1980), jež se stala programem pro další šlechtitelskou práci stanice.

Výzkumný ústav bramborářský v Havlíčkově Brodě využíval odborných znalostí Ing. Majora k oponování závěrečných zpráv a metodik úkolů s geneticko-šlechtitelskou problematikou, zařazovaných do plánu výzkumu ústavu.

Ing. Major byl též členem vědecké rady Výzkumného ústavu bramborářského v Havlíčkově Brodě (1976–1987) a členem šlechtitelské rady pro brambory (1977–1987), v letech 1984–1987 byl jejím předsedou

Za velmi úspěšnou práci obdržel řadu uznání a vyznamenání. Tak např. obdržel čestné uznání ČSAZ Za zásluhy o úspěšnou realizaci výsledků výzkumu (1981), státní vyznamenání Za vynikající práci (1984) a řadu různých podnikových uznání.

Vysoce oceňujeme svědomitou práci Ing. Miroslava Majora, CSc., která byla završena tolika cennými odrůdami brambor, práci, kterou vykonal pro naše bramborářství. A do dalších let mu přejeme mnoho zdraví a zaslouženého důchodcovského odpočinku.

Ing. Josef Zadina, CSc.

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Z VĚDECKÉHO ŽIVOTA

5. mezinárodní konference o pšenici 10.–14. června 1996, Ankara, Turecko

Konference byla pořádána ke 30. výročí činnosti CIMMYT (International Maize and Wheat Improvement Centre) a k 25 letům jeho úspěšné pomoci tureckému zemědělství. Zasedání se účastnilo 350 odborníků z celého světa.

Hlavními náměty přednesených referátů byly perspektivy šlechtění pšenice v 21. století i jeho současný stav, metody a cíle. Z výzkumných programů byly prezentovány poznatky z genetiky, fyziologie, jakosti, fytopatologie pšenice aj. Složení referujících umožnilo účastníkům získat přehled o stavu šlechtění, výzkumu i pěstování pšenice z celého světa, od Austrálie přes Ameriku, Evropu až po Asii. Prof. W. E. **Kronstadt** (Oregon State University, USA) uvedl, že v roce 1994 tvořila produkce obilovin svými 1 950 mil. tun 42 % zemědělské produkce, pšenice se vyrobilo 528 mil. tun (11,6 %), kukuřice 570 mil. tun (12,4 %). Největším světovým producentem pšenice je Čína, kde je pšenicí oseto kolem 35 mil. hektarů (výroba 100 mil. tun). Na druhém místě je Kanada s roční produkcí 27 mil. tun. Šlechtěním a zlepšenou pěstební technologií se výnosy pšenice zvýšily za posledních 50 let o 136 % a produkce pšenice vzroste v každém desetiletí o 100 mil. tun.

Prof. R. G. **Sears** (Kansas University, USA) se zaměřil na metody šlechtění. Zdůraznil velký vliv osobnosti šlechtitele a jeho důkladné znalosti materiálu v polních podmínkách. Doporučil tři stupně šlechtitelského postupu: 1. křížit na jakost, 2. vybírat na odolnost k chorobám, 3. testovat na výnos a jakost. Za základní potřebu pro další rozvoj šlechtění označil zachování možnosti volné výměny odrůd a zdrojů.

Celkový pohled R. **Brunse** (AGRIPRO Seeds Inc., USA) na perspektivy hybridní pšenice nebyl příliš optimistický. Přes průkazné zvýšení výnosu hybridních odrůd proti odrůdám klasickým (až o 13,8 %; nejčastěji kolem 11 %) není jejich pěstování díky vysokým nákladům na výrobu osiva rentabilní. Podal však důkazy o tom, že v oblasti USA Great Plains najde hybridní pšenice své uplatnění na větších plochách vzhledem k výrazně vyšší výkonnosti a stabilitě výnosu v porovnání s liniovým materiálem.

Dr. R. **McIntosh** (University of Sydney, Austrálie) měl klíčový referát ke šlechtění na rezistenci k chorobám. Biotické stresy vyvolává zhruba 20 nejdůležitějších chorob a škůdců. Poukázal na význam zdrojů rezistence, které lze získat v rámci druhu, rekombinacemi z příbuzných druhů nebo pomocí genetického inženýrství z druhů vzdálených. Selekci je možné vést přímo pomocí screeningu nebo nepřímo využíváním vazby s markerovacími znaky. Zdůraznil potřebu stanovení tolerovatelné hranice napadení chorobami, protože šlechtění na úplnou rezistenci není nutné ani účelné (zvyšuje navíc selekční tlak na populaci patogena, vedoucí k rozšíření virulence).

Dr. R. Singh (CIMMYT, Mexiko) přednesl výsledky výzkumu, ve kterém srovnával účinnost 4 odlišných šlechtitelských postupů u pšenice s cílem zvýšit kvantitativní odolnost ke rzi pšeničné (Puccinia recondita tritici): 1. klasický rodokmenový postup (pedigree) se zahájením selekce rostlin od F_2 generace; 2. neselektovaný ramš (bulk) s přesevy bez výběru až do generace F_4 a výběry rostlin od generace F_5; 3. modifikovaný ramš (hromadný výběr rostlin v F_2, přesevy ramše v F_3, F_4, výběr rostlin v F_5); 4. selektovaný ramš – výběr rostlin a jejich přesevy ve směsi (hromadný výběr) v každé generaci od F_2 do F_4, od F_5 rodokmenový postup.

V zásadě se prokázal minimální vliv vybraného šlechtitelského postupu. Nejvyšší selekční zisk byl u klasické metody pedigree, ale tento postup byl nejnákladnější. Z ekonomického pohledu byl nejpříznivější selektovaný ramš, neboli hromadný výběr. Za nejkritičtější bod úspěchu ve šlechtění označil Dr. Singh výběr vhodných rodičovských odrůd.

V sekci zaměřené na šlechtění pšenice na odolnost k abiotickým stresům se v úvodním referátu Dr. A. Blum (ARO Bel Dagan, Izrael) zaměřil na optimalizaci nalévání zrna za stresových podmínek. Vedle dosažení delšího trvání listové plochy (LAD) má v tomto směru klíčový význam šlechtění na optimální využití rezerv ze stonku. V CIMMYT Mexiko (S. Rajaram) je testován liniový materiál na odolnost k časnému, pozdnímu a kontinuálnímu suchu. S ohledem na zmíněné různé typy stresu ze sucha jsou důležitými ukazateli vysoká rychlost růstu a produkce biomasy, osmotická přizpůsobivost, vodivost průduchů a teplota listů v porostu. Dr. L. A. Hunt (University of Guelph, Kanada) uvedl přednosti vytvořeného dynamického simulačního modelu predikce vývoje porostu v závislosti na průběhu počasí (software package DSSAT 3). Dr. E. El. Bassam (FRC Braunschweig, SRN) představil koncept šlechtění odrůd pro snížené vstupy. Ukázal, že moderní německé odrůdy se vyznačují vyšší efektivitou v příjmu živin, přičemž existují odrůdové rozdíly (nejlepší výsledky u odrůdy Hermes).

Dr. W. Bushuk (University of Manitoba, Canada) shrnul význam i šlechtitelské perspektivy z hlediska konečného využití pšenice – tj. její jakosti. V lidské výživě je kryta energetická potřeba z 20 % pšenicí. Pšenice obecná (*Triticum aestivum* L.) se pěstuje na 95 % ploch ve světě, *Triticum durum* L. na 4 % a ostatní druhy (včetně např. špaldy) na 1 % ploch. Pekařskou jakost ovlivňuje zejména obsah a jakost proteinů. Zdůraznil závislost obsahu proteinů na vlivu prostředí a teprve až na druhém místě na genotypu, tj. odrůdě. U jakosti proteinů je tento vztah obrácený. Rozhoduje odrůda (jakost bílkovin je geneticky podmíněná) a v menší míře je jakost bílkovin ovlivňována prostředím. Poukázal i na odlišné požadavky na odrůdy z hlediska jejich využití a na významné korelace gluteninových podjednotek k pekařské jakosti.

Dr. B. Borghi (ISC S. Angelo Lodigiano, Itálie) ve své studii k jakosti pšenice uvedl své výzkumy, podle nichž má negativní vliv na pekařskou jakost dlouhodobější působení (nad 80 hodin) vysokých teplot (nad 30 °C) v období dozrávání. Jakost odrůd dělí do tří kategorií (zlepšující, pekařské a ostatní). Třídu jakosti může potvrdit pouze komplex: rozbor bílkovin a pekařský pokus.

Dr. J. W. Snape (JIC Norwich, Anglie) pojednal o přínosu nových biotechnologií šlechtění. Z technik dihaploidizace jmenoval na prvním místě metodu křížení pšenice s kukuřicí a dále využívání pylové embryogeneze. Velký pokrok slibuje vývoj genetické mapy u pšenice s využitím molekulárních technik spolu s komparativními studiemi genomů. V genovém inženýrství jsou nejvíce využívány biolistické metody.

V sekci věnované genetickým zdrojům pšenice zdůraznil Dr. A. F. Merežko (VIR, St. Petersburg, Rusko) význam genetických zdrojů pro šlechtění pšenice. Při šlechtění rostlin hledá šlechtitel optimálně přijatelný kompromis mezi požadavky člověka, genotypy dané plodiny a prostředím. K řešení tohoto problému využívá šlechtitel genetické zdroje. Nutnost interdisciplinárního přístupu při využívání genetických zdrojů zdůraznil Dr. B. Skovmand (CIMMYT, Mexiko). Předpokladem pro to je účinná výměna informací. S cílem pokrýt tuto potřebu u tak významné plodiny jako je pšenice byl vyvinut v CIMMYT International Wheat Information Sytem (IWIS). Ten bude rozšířen na ICIS (International Crop Information System). V závěrečném vystoupení této sekce seznámil přítomné Dr. H. J. Braun (CIMMYT, Turecko) s mezinárodní spoluprací při šlechtění a hodnocení ozimé pšenice, do které je zahrnuto 170 spolupracovníků.

Kromě referátů bylo prezentováno 291 posterů. Např. 80 sdělení se týkalo šlechtitelských postupů a přehledů nejnovějších odrůd a jejich vlastností od Anglie přes Maďarsko, Rusko až po Čínu a Nepál či Egypt. Dalších 78 sdělení bylo zaměřeno na problémy biotických a abiotických stresů u pšenice. U rezistentního šlechtění bylo možné z těchto zpráv zaznamenat, že se větší kapacity soustřeďují na výzkum a šlechtění odrůd odolných k houbám *Septoria nodorum* i *S. tritici* a k fuzariózám klasu. Z abiotických stresů dominovala odolnost k suchu, mrazu, tolerance k low input aj.

Další cykly posterů byly o jakosti, agronomii a fyziologii, biotechnologiích, genetických zdrojích a o mezinárodní spolupráci. Velmi zajímavé bylo vyhodnocení dotazníku, který zaslali z CIMMYT šlechtitelům ve všech zemích světa, ve kterém se subjektivně hodnotil význam šlechtitelských cílů, používané postupy, význam chorob, rezistentního šlechtění apod. Za prioritní šlechtitelské cíle označili šlechtitelé výnos, jakost a rezistentní šlechtění. Velký podíl nakřižovaných rodičů tvoří vlastní šlechtitelské linie.

Poslední den účastníci podepisovali petici, která měla podpořit možnost volné výměny šlechtitelských zdrojů. Závěrečným slovem uzavřel zasedání prof. S. Borojevič s tím, že zhodnotil význam nových biotechnologických postupů jako důležitého doplňku. Rozhodující úloha i nadále bude patřit klasickým šlechtitelským postupům, které zůstanou páteří šlechtění.

Celá konference vyzněla ve prospěch mezinárodní šlechtitelské spolupráce, jejímiž hlavními současnými nositeli jsou mezinárodní organizace CIMMYT a ICARDA. Konference umožnila i navázání nebo obnovení kontaktů mezi šlechtiteli a výměnu odrůd, šlechtitelských linií i praktických poznatků.

Ing. Alena Hanišová, Ing. Václav Šip, CSc., Ing. Ladislav Dotlačil, CSc., Ing. Pavel Bartoš, DrSc., Ing. Zdeněk Stehno, CSc.

Konference EUCARPIA
1.–5. července 1996, Brno

Na Mendelově zemědělské a lesnické univerzitě v Brně se konala konference EUCARPIA (skupina Medicago). Odborným a organizačním garantem tohoto vědeckého jednání věnovaného fertilitě vojtěšky byl profesor Oldřich Chloupek, DrSc., prorektor MZLU v Brně a člen výboru Eucarpie pro tuto skupinu.

Konference se zúčastnilo 63 odborníků z České a Slovenské republiky, Polska, Litvy, Maďarska, Chorvatska, Bulharska, Itálie, Francie, Německa, Kalifornie, Wyomingu, Quebecku a Saskatchevanu. Jednání probíhalo ve čtyřech odborných sekcích. Sekci zaměřenou na biologii opylení a vývoj semen vojtěšky řídil dr. C. Huyghe z INRA (Francie) a referovali dr. J. Nedělník z Výzkumného ústavu pícninářského v Troubsku a prof. F. Veronesi z Univerzity v Perugii (Itálie). V sekci Produkce semen a šlechtění na stabilitu fertility, kterou řídil prof. Chloupek, vystoupili s referáty prof. U. Simon z Univerzity v Mnichově, prof. I. Bócsa z Výzkumného ústavu v Kompoltě, prof. Staszewski z Výzkumného ústavu v Radzikowě a prof. A. Svirskis z Výzkumného ústavu v Donutvě (Litva). Prof. F. Gray z Univerzity ve Wyomingu hovořil o šlechtění vojtěšky na rezistenci ve vztahu k fertilitě. O semenářství vojtěšky jakožto dobře organizovaném průmyslovém odvětví v Severní Americe přednášeli prof. V. Marble z Univerzity v Davisu (Kalifornie) a dr. R. Michaud, prezident North American Alfalfa Improvement Conference (NAAIC) z Výzkumného institutu St. Foy (Quebeck) v Kanadě.

Bylo prezentováno přes čtyřicet posterových sdělení, ke kterým byla vedena v rámci sekcí odborná diskuse. Diskutovány byly další postupy ve šlechtění vojtěšky včetně šlechtění na vyšší symbiotickou fixaci dusíku, která uspoří v osevních postupech hnojení minerálními hnojivy.

Součástí konference byly i odborné exkurze na pokusné plochy pracovišť, které se na organizaci konference podílely: Výzkumného ústavu pícninářského v Troubsku, Šlechtitelské stanice v Želešicích, Výskumného ústavu rastlinnej výroby v Piešťaeoch a Šľachtitelské stanice v Špačincích.

Podrobně byl diskutován návrh prof. P. Rotili, prezidenta této skupiny Eucarpia, aby se sloučila s Mediteránní skupinou pro vojtěšku, zahrnující asi deset evropských, afrických a asijských zemí. Většina účastníků se však domnívá, že na každé konferenci se může zúčastnit kdokoliv, a proto bylo doporučeno název Eucarpia zachovat. Příští konference by měla být v evropské, mediteránní zemi.

Ing. Jaroslava Ehrenbergerová, CSc.

Barley-Wheat Chromosome Rationalization

Ve dnech 30. 7. až 6. 8. 1996 se uskutečnilo VIIth International Barley Genetics Symposium (spojené s Vth International Oat Conference). Obě akce byly uspořádány ve světově významné obilnářské oblasti v areálu University of Saskatchewan v Saskatoon, Kanada. Sympozia se účastnilo celkem šest pracovníků z České republiky (všichni s profesním zaměřením na ječmen). Z jednání byl vydán třídílný sborník.

V rámci doplňkového programu se uskutečnila řada satelitních jednání (workshops/meetings), jejichž tematika není ve sborníku obsažena. Zvláště užitečné jsou snad informace z workshopu nazvaného Barley-Wheat Chromosome Rationalization. Návrh projednávané tematiky Recommendations for the designation of the barley chromosome and their arms zpracovali I. Linde-Laursen, J. S. Heslop-Harrison, K. W. Shepherd a S. Taketa. Jednání řídil první z uvedených autorů.

Na tomto workshopu byly posuzovány nové návrhy na označování chromozomů ječmene. Vycházejí z poznatků pracovníků působících na molekulární úrovni výzkumu. Hlavní obilní druhy (pšenice, rýže, ječmen) mají každý v základní sadě sedm ($n = 7$) chromozomů. Jejich obsah a řazení odpovídajících lokusů je u čeledi *Triticeae* podobné. U každé z těchto plodin však bylo (do přijetí návrhu) jejich označení jiné. Bylo dohodnuto, že číslování chromozomů ječmene bude pozměněno podle pšenice (názor, že ječmen je diploid a že by tedy bylo logičtější číslovat chromozomy pšenice a rýže podle něj, nebyl projednáván).

Aby bylo zřejmé, že jde o nové číslování, bude za číslem chromozomu (bez mezery) uvedeno velké počáteční písmeno rodu "H" = *Hordeum* (chromozom s dosavadním označením 1 = 7H, chromozom 5 = 1H a chromozom 7 = 5H; čísla chromozomů 2, 3, 4 a 6 se nemění, i u nich však bude užit symbol "H"). Po přechodnou dobu (do příštího BGS) může být vedle nového značení použito v závorce i označení dosavadní, např. chromozom 1H (5). Nové značení chromozomů ječmene (v závorce dosavadní značení): 1H (5); 2H (2); 3H (3); 4H (4); 5H (7); 6H (6); 7H (1)

Bylo dohodnuto, že symbol „H" bude psán standardním písmem (nikoli tučným – jeden z nepřijatých návrhů). Nebude používáno rozlišení mezi *H. vulgare* ssp. *vulgare* (H^v) a *H. vulgare* ssp. *spontaneum* (H^s). Pro označení chromozomů genomu ječmene nebude nadále používáno písmeno "I". Pro označení ramen chromozomů byla ponechána velká písmena "S" a "L", i když jejich původní význam (krátké a dlouhé rameno) je jen relativví. Alternativní návrh na používání symbolů "+" (p) místo "S" a "-" (q) místo "L" nebyl přijat. Symboly označující rameno chromozomu budou psány (bez mezery) za označení chromozomu, tedy např. 1HS (písmena "p" a "q" jsou užívána pro označení příslušných ramen chromozomů člověka).

Hostitelská University of Saskatchewan je také pořadatelem International Wheat Genetics Symposium v roce 1998. Příští (VIIIth) International Barley Genetics Symposium se uskuteční v srpnu roku 2000 v Austrálii.

Ing. Antonín Dreiseitl, CSc.

Instructions for authors

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