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## SOME CHARACTERS INHERITED BY SUNFLOWER

The VNIIMK sunflower breeding laboratory has been conducting genetic studies of sunflower male sterility and sunflower resistance to most dangerous pathogens.

In most cases sunflower male sterility is known to be determined by nucleus genes and does not depend on cytoplasm. In the sources suspected of cytoplasmic male sterility (CMS) the exact type of sterility heritability (nucleus or CMS) was studied considering that unlike nucleus genes plasmogenes are not inherited in the paternal line (Table 1). The sterility type was studied: in the sterility source singled out from an American interlinear hybrid which, according to further research, turned out to be identical to the P-21 ms source; the source 9G2 ms singled out from interspecific hybrids (H. tuberosus x H. annuus); the 1970 R Composited source from the USA in which the sterility proportion was 40% and the K 088-S from Kenya. The type sterility inheritance was judged by the results of the segregation of the whole population F<sub>2</sub> obtained thanks to the introduction of recessive celleles, facilitating ms manifestation, into diverse cytoplasm sources.

The sources P-21 ms and 9G2 ms pass male sterility along the paternal line. The ratio obtained between fertile and sterile plants of total sampling in F2 fully corresponds to the theoretical relation 7:1 for monogenous heritability. Consequently, male sterility of these sources is stipulated by one nucleus and does not gene depend on cytoplasm.

The CMS was found in the sources 1970 R Composite and the K 038-S. In these sources the male sterility character is not inherited in the paternal line when normal (fertile) cytoplasm sources are used in crossings as the maternal

Table 1

Four Sources Inheriting Male Sterility in the Paternal Line in Combinations F2 (Ms Ms x Ms mx)

l D		>0.20	>0.05	>0°06	0.11 \$0.50
$\mathbf{x}_2$ designed for theoretical	7:0 1:0	1.50 -	2.04	0	0
Character of segregation in F2	plants fertile/ste- rile ratio	6.06:1	8.04:1	1:0	112:1
Character cf	Number of plants fertile sterile fertile/ste-	509 84	957 119	1202 0	672 6
Number of com-	binations	7	<b>\omega</b>	ις.	۵
Sources of steri- Number lity of com-		P-21 ms	9G2 ms	1970 R Compositea	K 088-S

form. For the source 1970 R Composite in  $F_2$  the ratio between fertile and sterile plants exactly corresponds to the 1:0 ratio, and for the K 088-S the ratio 112:1 quite agrees with the theoretical one 1:0 (P > 0.50).

Four different genes were found in experiments on the identification of sterility nucleus factors and each of them taken separately causes paternal sterility. This allowed to group the sources according to the general sterility genes and to number them from the first to the fourth for convenience (Table 2). In the progenies from brother-sister crossings these sources have segregation of these gens in the ratio close to the theoretically expected 1:1.

CMS sources were sent to us from the USA, Kenya and Bulgaria.

It turned out that the reaction of these CMS sources to sterility fixatives and fertility restorers received from the USA, Kenya and Bulgaria and to those singled out from interspecific hybrids is the same. This confirmed our conjecture of the identity of the sources studied. A conclusion can also be drawn that ecological and other factors have not changed the nature of CMS sources obtained by P. Leklerk in 1968.

The CMS source can be successfully used in the selection of interspecific hybrids (H. tuberosus x H. annuus). When lines were assessed as regards their fixing-restorative ability towards a CMS source both sterility fixatives and fertility restorers were identified. Out of 512 lines assessed bred from interspecific hybrids 308 are sterility fixatives, 143 fertility restorers and 61 are split according to this feature. Thirty-three lines coming from VNIIMK varieties turned out to be sterility fixatives. A high recurrence of data on assessing lines according to this feature (correlation coefficient r = 0.8723) testifies to the stability of the nucleus-cytoplasm system employed.

It is possible to single out fertility restorers from cultivated sunflower varieties because there

Table 2

Splitting According to Male Sterility in Progenies from Brother-Sister Crossings in Sources of Nucleus Male Sterility

р	4	>0.50	>0.05	>0.05	>0.05
<b>4</b> 2	₹	0.25	3.59	3.00	2.34
Fertile/sterile plants ratio	expected	1:1	T: T	<b>:</b> -T	 
e e	actual	1.04:1	1,31:1	1,25:1	1.19:1
Character of segregation	Number of plants fertile sterile	326	88	108	197
Characte reg	Number fertile	339	115	125	235
Number of sour-	ces	5	7	Н	W
Genes		MS	MS,	MS	MS <sub>4</sub>

are fertile plants in progenies from crossing the CMS sources with the VNIIMK bred varieties.

In the completeness of fertility restoration, restorers singled out from interspecific hybrids are not worse than restorers homozygous in the gene Rfl of the 1970 R Compositea. The hybridological analysis shows that the restoration of fertility of interspecific hybrids is determined by one dominant gene (Table 3). There were 403 fertile and 120 sterile in the sampling in F2 obtained from CMS plants with fertility restored in Fl. The actual ratio 3.36:1 fully corresponds to the expected one 3:1 (P > 0.20). The results of analysing crossings also testify to the monofactorial nature of this character. The ratio 1.17:1 obtained corresponds to the expected one 1:1 (P > 0.20).

The gene Rf<sub>1</sub> splitting, as was expected, follows the monofactorial scheme. The ratio 3.74:1 in  $F_2$  fully corresponds to the expected 3:1 (P > 0.20). The actual ratio 1.20:1 in  $F_2$  also corresponds to the expected 1:1 (P > 0.50).

Studies were made of the inheritance of interspecific hybrids resistance (H. tuberosus x H. annuus) towards downy mildew (Plasmopara helianthi Novot) with the use in crossings of homozygous resistant eines (9Gl, 9G2-320 ms, 9G2-210 ms) and susceptible (SLB-II and P-21 ms) lines. Irrespective of the direction if crossing predominant resistance in F1 has been established.

Assessment of the splitting results in  $F_2$  by means of  $\mathbf{X}^2$  has shown that all combinations are split according to the resistance trait in keeping with the expected ratio 3:1 (Table 4). The results of splittings in the analysing crossings ( $F_B$ ) confirmed the monofactorial nature of the interspecific hybrids' resistance towards downy mildew. The actual ratio 1.07:1 fully corresponds to the theoretical 1:1 (P > 0.05). In case when  $F_1$  is back-crossed with resistant

Table 3

Heritability of the Fertility Restoration Character in CMS and in Progenies from Analysing Crossings  $(\mathbf{F}_{\mathbf{B}})$ Sources in F2

Sources of restorer Gene- genes ration	Gene- ration		Character of splitting	Fertile/sterile ratio	sterile	<b>x</b> 2	ር
		fertile plants	fertile sterile plants plants	actual	actual expected		
H. tuberosus x H. annuus	면	403	120	3,36:1	3:1	1.18	>0.20
H. tuberosus x H. annuus	F E	64	42	1.17:1	1:1	· 72	>0.20
1970 R Compositea 1970 R Compositea	т т 2 п	71	19	3.74:1	3:1	0.73	>0.20 >0.50

Character of Splitting in  $\mathbb{F}_2$  and  $\mathbb{F}_B$  According to Resistance Towards Mildew

Combinations	Gene-	Character of splitting	er of	Healthy/deseased plants ratio	seased	<b>%</b>	<u>Ω</u>
		healthy plants	healthy diseased plants plants	actual	expect-		
9GlxSLB-II	币 2	928	304	3.05:1	3:1	0.07	<b>&gt;0.50</b>
9G2-320ms x P-21ms	면 C)	689	200	3.45:1	3:1	2.97	<b>&gt;</b> 0.05
9G2-210ms x P-21ms	FP 23	119	200	3.90:1	3:1	1.65	×0.05
P-21ms x F1	्र प्र प्र	1289	1206	1.07:1	1:1	2.76	>0.05
9G2-320ms x F,	ξή 1 Ω	577	W	192:1	1:0	0.03	>0.95
9G2-210ms x F1	स्य J प्र	287	9	98:1	1:0	0.12	×0.50

parents no diseased plants are expected in  $F_{B^{\bullet}}$ . Though our experiment saw a few affected plants, the actual ratio 129:1 fully corresponds to the theoretical 1:0 (P > 0.50).

Hence interspecific hybrids (H. tuberosus x H. annuus) resistance to downy mildew is caused by one dominant gene. It is unclear whether the gene is identical to the earlier known Pl<sub>1</sub>, Pl<sub>2</sub>, and Pl<sub>3</sub>.

In the USA there is another downy mildew race, Red river, which affects the S-37-388 RR, AD-66 and CM 90RR lines, but to which HA-61 is resistant. These lines have proved resistant both in our experiments and in France and Romania. Taking these lines as indicators of this disease races one can draw a conclusion that one and the same race Plasmopara helianthi exists in France, Romania, the Krasnodar Territory and possibly in the whole of Europe.