

THE RESULTS OF GENETIC INVESTIGATIONS OF SUNFLOWER AT VIS

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Abstract

Fertility restoration of 20 CMS sources has been studied. Three groups of CMS sources were distinguished by their differences in restoration behavior from CMS PET1. Fertility restoration ability of 11 Rf lines was evaluated. A set of Rf genes was detected for all fertile lines investigated. The practical application of the results obtained for sunflower breeding was shown.

Introduction

The constant extension of sunflower popularity in the world stimulates widening and intensification of genetic investigations. The increase of sunflower production is connected largely to inclusion of genetic resources of the wild *Helianthus* genome into improving work on cultivated sunflower (Christov, 2003). According to numerous investigations the wild *Helianthus* species are a rich source of genetic determinants of desirable agronomic traits (Thompson et al., 1981; Seiler, 1992; Skoric, 1992; Christov, 1996, 2003).

The sunflower genetic collection of Veidelevka Institute of Sunflower (VIS) includes 35 *Helianthus* species, a collection of sources of cytoplasmic male sterility (CMS) and a set of fertility restorers for different germplasms. The study and evaluation of wild *Helianthus* species indicated the donors of important characters, including resistance to different sunflower diseases and parasites (Tavoljansky et al., 2002). But much attention is given to CMS investigations. The wide distribution of hybrids with a related type of cytoplasm (*Helianthus petiolaris* PET1) causes a potential risk for hybrid sunflower. Recent research programs have attempted to find new CMS sources and fertility restorer genes (Rf) for them (Series, 1999, 2002). Introduction of new CMS-Rf systems into hybrid production will permit enrichment of the genetic base of cultivated sunflower and avoidance of problems that occur with the CMS PET1.

In this connection the separate results of genetic studies on different CMS sources and fertility restorers with their further utilization in VIS Sunflower Breeding Programs are represented in this report.

Materials and Methods

Sixteen CMS sources from the Institute's sunflower genetic collection were used based on the following wild species: *Helianthus petiolaris* Nutt. (PET1), *H. argophyllus* T. and G. (ARG1, ARG3), *H. giganteus* L. (GIG1/141, GIG1/477, GIG1/647), *H. debilis* Nutt. (DEB1), *H. texanus* L. (ANT1/479, ANT1/645), *H. praecox* Engelm. and A. Gray (PRR1, PRH1), *H. fallax* (PEF1), *H. annuus* L. (wild) (ANN5), and *H. rigidus* (Cass.) Desf. (RIG1, RIG2, RIGL). Unidentified CMS sources DCS1, DCS2, DCS3 and DCS4 (Double-color sterile 1-4) obtained from ornamental sunflower were also used in the experiment. Eleven fertile lines carrying Rf genes for different germplasms were used as fertility restorers: RHA 274, SH-416/5, RJUG-1, RFT-1, DCF-1, DCF-2, DCF-3, DCF-4, RCMG-2, RPEF-1 and RARG-1. Three of them, RHA-274, RJUG-1 and RFT-1 were received from VNIIMK (Russia); others were obtained by a special scheme (Chepurnaya and Pershin, 2001). Hybrid analysis by the full top-cross scheme was used as a main research method. In order to determine the mechanism of fertility restoration fertile plants of obtained hybrid combinations were self-pollinated. Progenies of each plant were grown on a separate plot and individually observed. The segregation ratio in testing generations was evaluated by chi-square.

Results and Discussion

The CMS studies were performed at VIS according to following items: the investigation of fertility restoration response in combinations [CMS × Rf]; the determination of genetic control of the restoration; the search for new donors of Rf-genes to different germplasms; and the evaluation of restoration range of Rf-lines. The final objective of the experiment was to indicate new CMS Rf systems for sunflower breeding.

The results of genetic analysis and comparison of different CMS sources against the classical CMS PET1 used as a control permitted classification into three groups (Figure 1). The arrangement was performed according to the exhibited differences in restoration behavior of CMS sources. Genetic mechanism of fertility restoration was detected for all investigated CMS sources (Chepurnaya et al., 2003).

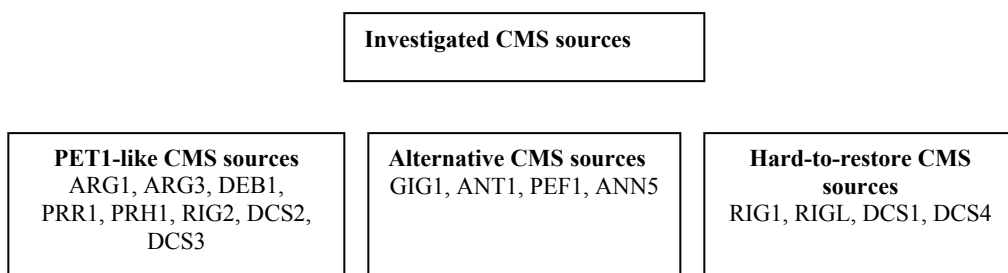


Figure 1. The classification of sunflower CMS sources.

The CMS sources with fertility restoration systems similar to CMS-PET1 were placed in a separate group of PET1-like CMS sources. The determination according to results of genetic analysis is confirmed by molecular studies (Horn and Friedt, 1999). The sources of CMS that

completely failed to restore with lines, donors of Rf PET1 genes (RHA 274, SH-416/5) but demonstrated fertility restoration in combination with the other fertile lines composed the group of alternative CMS sources. Different restoration responses within this CMS group indicate the existence of complex mechanisms of cytoplasm Rf genes interaction (Chepurnaya and Pershin, 2000). The CMS sources which possessed an extremely low fertility restoration reaction were classified as hard-to-restore CMS.

At present, all 20 CMS sources are maintained at VIS. Negative effects of CMS sources were not observed. All plants produced on the basis of these CMS sources showed normal development. Their seed productivity was equal to that of inbred lines, and they could be used in sunflower breeding programs.

At the same time the evaluation of developed fertility restorers was undertaken. The data obtained indicated that each of 11 investigated Rf lines possessed its own unique fertility restoration range (Chepurnaya, 2002). The morphobiological and immunological evaluations of all investigated Rf lines were conducted under the field conditions. These R-lines can be successfully used in heterotic sunflower breeding.

Significance of CMS-Rf investigations permitted the mobilization of obtained results in VIS Breeding Programs. Thus, 13 new sterile CMS analogues (A-lines) with different cytoplasmic backgrounds have been obtained and evaluation of main agronomic traits, including disease resistance, has been performed (Tavoljansky et al., 2003). The sterile inbred lines based on CMS ARG1, ARG3 and RIG2 seemed to be prospective for breeding purposes.

At present the complex evaluation of new hybrids (A × R) produced based on different non-PET-type CMS-Rf systems is finished. Some hybrid combinations are presented in Table 1.

Table 1. Characterization of hybrid combinations including the sources of CMS ARG3 and PRH1.

Hybrid combination	Vegetation period (days)	Seed yield (t/ha)	Yield to St (%)	Oil yield (t/ha)	Seed oil content (%)	Quantity of lvs (n)	Plant height(cm)	Head dia. (cm)
2002								
B-99St (control)	94	2.54	100.0	49.4	1.10	23	155	20
VB1002 _{ARG3} × VB2003R	96	2.81	110.6	49.3	1.22	25	170	22
VB1002 _{PRH1} × VB2003R	93	2.68	105.5	49.1	1.16	23	160	20
2003								
B-99St (control)	95	2.68	100.0	49.3	1.16	24	160	20
VB1002 _{ARG3} × VB2003R	95	2.86	106.7	49.5	1.24	25	175	21
VB1002 _{PRH1} × VB2003R	94	2.75	102.6	49.1	1.18	23	170	20

Conclusions

The classification of different CMS sources according to differences distinguished in their restoration behavior has been performed. Also, the fertility restoration ranges of Rf lines were determined. The results of genetic investigations exhibited a real opportunity to introduce new CMS-Rf systems in sunflower breeding.

References

- Chepurnaya, A. L. 2002. New CMS sources for sunflower hybrid breeding Dissertation. Moscow (Russia). 124 p. (In Russian).
- Chepurnaya, A. L., and Pershin, A. P. 2000. The mobilization of new cytoplasmic male sterility types in sunflower breeding. *Nauchno-tehnich. Bull. IMK UAAN.* 5:41-45. (In Russian).
- Chepurnaya, A. L., and Pershin, A. F. 2001. The search for new sources of fertility restoration genes in sunflower. *Vestnik ZGU.* 1:222-227. (In Russian).
- Chepurnaya, A. L., Sherstyuk, S. V., and Tikhomirov, V. T. 2003. CMS-Rf system for sunflower breeding. *Helia.* 26:59-66.
- Christov, M. 1996. Characterization of wild *Helianthus* species as sources of new features for sunflower breeding. *In: P. D. S. Caligari and D. J. N. Hind (eds). Compositae: Biology & Utilization. Proc. Int. Compositae Conference, Kew.* 2:547-570.
- Christov, M. 2003. *Helianthus* species in the improving research work on sunflower. *In: Proc. Int. Research Conference "Technological characteristics of new hybrids and varieties of oil and volatile-oil crops",* June 5-6, Krasnodar (Russia). p. 34-45.
- Horn, R., and Friedt, W. 1999. Molecular characterisation of CMS sources in sunflower. *In: FAO working group progress report 1996-1999: Identification, study and utilization in breeding programs of new CMS sources: Rep. from IX FAO Consultation on Sunflower, July 27-30, Dobrich (Bulgaria).*
- Seiler, G. J. 1992. Utilization of wild sunflower species for the improvement of cultivated sunflower. *Field Crops Research.* 30:195-230.
- Serieys, H. 1999. Identification, study and utilization in breeding programs of new CMS sources. *Helia* 22 (Special issue):71-84.
- Serieys, H. 2002. Identification, study and utilization in breeding programs of new CMS sources. Progress report 1999-2001 FAO Working group. European Cooperative Network on Sunflower, Montpellier (France).
- Skoric, D. 1992. Results obtained and future directions of wild species use in sunflower breeding. *Proc. 13th International Sunflower Conference, September 7-11, Pisa, Italy.* p. 1317-1348.
- Tavoljansky, N., Chepurnaya, A., and Sherstyuk, S. 2003. The obtaining of sunflower sterile CMS analogues on the base of different cytoplasmic backgrounds. *Proc. VI European Conference of Sunflower Biotechnology, October 5-9, Seville (Spain).*
- Tavoljansky, N., Yesaev, A., Yakutkin, V., Akhtulova, E., and Tikhomirov, V. 2002. Using the collection of wild species in sunflower breeding. *Helia.* 25-36:65-78.
- Thompson, T. E., Zimmerman, D. C., and Rogers, C. E. 1981. Wild *Helianthus*, as a genetic resource. *Field Crop Research.* 4(4):333-343.