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Poster Abstract - C.37

INTRA- AND INTER-SPECIFIC VARIABILITY IN THE GENUS HELIANTHUS AS ASSESSED BY IRAP MARKERS

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Sunflower breeding began in Russia in the 19th century using relatively few American genotypes introduced into Europe by early Spanish explorers and in Russia by Peter the Great in the 18th century. This small number of genotypes was the starting material for subsequent breeding, as has been shown by pedigree analysis of modern cultivars, even in North America. The narrow genetic background of cultivated sunflower has been a concern for its potential for improvement, and efforts to widen its genetic base are underway. Wild *Helianthus* species often constitute the basic genetic stock from which cultivated sunflower originated, and they are used for variability rescue and the introgression of important traits in *H. annuus*. The 49 North American wild *Helianthus* species have long survived extreme environments and possess resistance or tolerance genes to salt, drought, insects, diseases, as well as cytoplasmic male sterility. Gene transfer from wild species into the cultivated background largely depends on the success of interspecific hybridisation, F1 fertility, chromosome pairing for genetic recombination, efficient screening methods and a sufficient number of progenies for selection. When used in crosses with *H. annuus*, wild annual *Helianthus* species generally produce F1 seeds, perennial species do not. Such difficulties are obviously absent in crosses involving wild *H. annuus*. If wild populations of *H. annuus* indeed show large genetic variability, they could be the best genetic resources for sunflower improvement, together with or alternative to interspecific crosses.

Microsatellite and dehydrin-encoding sequence analyses suggest a remarkable genotype variability among wild sunflowers. In our experiments we have analysed genetic variability as related to retrotransposon sequences within *H. annuus* using the IRAP technique. According to IRAP (Inter-Retrotransposon-Amplified-Polymorphism, Kalendar et al. 1999) protocol, one or two primers designed on retrotransposon LTRs are used for PCR amplification of fragments of adjacent retrotransposons.

We have analysed IRA polymorphism in 30 accessions of wild sunflowers (*H. annuus*), 7 sunflower cultivars randomly chosen according to their different provenance (one for each country in which sunflower is a major crop, hence presumably not deriving from the same inbred lines), 18 *Helianthus* species, and *Viguiera multiflora e Tithonia rotundifolia.* Larger variability was observed, as expected, among wild *H. annuus* accessions compared to sunflower cultivars. Interestingly, the extent of variability of wild sunflowers was similar or even larger to that among *Helianthus* species, i.e. intraspecific was larger than interspecific variability. Phylogenetic analysis showed that *H. annuus* accessions do not belong to a single clade. On the contrary, they are in loose order among *Helianthus* species in the tree.

The large extent of retrotransposon variability within *Helianthus* observed in our experiments indicates lack of coevolution between retrotransposons related to selected primers and the host species. Such a lack of coevolution is probably due to massive activity of retrotransposons after *Helianthus* speciation. It is known that different environmental conditions can activate retrotransposons. The massive activity of

retrotransposons could be related to the different geographic distribution of wild *H. annuus* and *Helianthus* species in North America.