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Poster Abstract – D.03

CHARACTERIZATION OF THE CHROMOSOME COMPLEMENT OF *HELIANTHUS ANNUUS* BY *IN SITU* HYBRIDIZATION OF A TANDEM REPEATED DNA SEQUENCE

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Due to its high yield and adaptation to certain environmental conditions, sunflower (*Helianthus annuus* L.) is cultivated all over the world and is the fourth major annual crop grown for edible oil. In spite of this, a satisfactory characterization of the chromosome complement of this species is lacking. The large number (2n=34) and small size of the chromosomes and the striking similarity of their morphology are factors that have impaired a reliable identification and classification of the pairs. Contradictory data have been reported after studies carried out by using different methods of chromosome investigation, and several chromosome pairs are still not discriminated. A more precise characterization of the chromosome complement of the sunflower would be of great interest. Identification of each chromosome pair would greatly benefit genetic improvement by increasing the understanding of phylogenetic relationships between cultivated sunflowers and their related wild forms, which can be exploited as a donor-source of genes for agronomically-important traits. Moreover, pair recognition would make it possible to construct physical gene maps by assigning genetically-mapped linkage groups of molecular markers to the single chromosomes. Currently, this is impossible.

In situ hybridization using repeated DNA sequences has been used successfully to characterize other difficult chromosome complements. A repetitive DNA sequence, which was isolated in a previous study of the *H. annuus* genome and termed HAG004N15, has been shown to be a tandem array of 369 bp-long repeats, having a redundancy of about 7,800 copies per haploid genome in line HOR. HAG004N15 repeats and the wheat ribosomal DNA probe pTa71, containing 18S-5.8S-26S rDNA, were used to study the metaphase chromosomes of lines HA89, RA20031 and HOR by fluorescence in situ hybridization. After hybridization of HAG004N15 repeats, signals were observed at the end of both chromosome arms in four pairs, and at the end of only one arm in eight other pairs. Signals were also observed at the intercalary (mostly subtelomeric) regions in all the pairs, in both arms in eight pairs and in only one arm in the other nine pairs. The shorter arm of one pair was labelled entirely. The localization of hybridization signals was the same in all the chromosome complements studied, but appreciable differences were seen between complements

concerning the relative intensity of labelling at given chromosome sites. In all lines, four chromosome pairs bore ribosomal cistrons at the end of their shorter arm, but a satellite was only seen in three pairs. The patterns of chromosomal localization of HAG004N15-related sequences allowed all of the complement pairs to be distinguished from each other with certainty.