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SEQUENCE AND ANNOTATION OF THREE GENOMIC LOCI OF SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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The sunflower (*Helianthus annuus* L.) has a large-sized genome because of a high content of repetitive DNA. To date, the knowledge of the repetitive component of the sunflower genome is based on the sequence and analysis of a small-insert genomic DNA library, that allowed the discovery of many repetitive DNA families (especially transposable elements). However, such an approach did not allow isolating full-length elements and studying dynamic and structural aspects of the sunflower genome evolution. For example, since the scarcity of long range genomic sequences, it is not known how repetitive elements are arranged in the chromosomes and the extent of dispersion of genes among non-coding sequences.

We report the annotation of three large regions from the genome of the sunflower, screened from a BAC library by hybridization using three putative single-copy genes, encoding a lipid-transfer-protein (LTP), a Z-carotene desaturase (Z-DES), and a dehydrin (DHN). The three BAC clones account for 136, 97, and 131 contiguous Kb, respectively.

Beside LTP, Z-DES, and DHN, other protein encoding genes were identified, accounting on their whole for 27 over 363 Kb. The BAC clone carrying the LTP gene revealed that this gene is present in five copies of different length and sequence.

Several families of repetitive DNA were identified. *Gypsy* retroelements were by far the most represented, followed by *Copia* retrotransposons. Four non-autonomous LTR-retrotransposons (the so-called LARDs) were found for the first time in the sunflower. Other repetitive families included non-LTR retrotransposons and DNA transposons. In many cases, complete elements were discovered.

Our analyses also provided the first insight into the local organization of the sunflower genome showing nests of retrotransposons inserted into each other and allowing the estimation of retroelement insertion ages. Different waves of retroelement mobilization during the evolution of this species and the occurrence of very recent retroposition events are suggested.