Poster Abstract - B.29

A SURVEY OF LTR-RETROTRANSPOSONS IN *HELIANTHUS ANNUUS* AND RELATED SPECIES

V. FERRILLO*, L. NATALI*, T. GIORDANI*, I. JURMAN**, A. ZUCCOLO**, M. MORGANTE**, A. CAVALLINI*

*) Department of Crop Plant Biology, Genetics Section, Via del Borghetto 80, 56124 Pisa, Italy – veropos@virgilio.it **) Department of Crop and Environmental Sciences, Via della Science 208, 22100 Uding, Italy

**) Department of Crop and Environmental Sciences, Via delle Scienze 208, 33100 Udine, Italy

Asteraceae, genome, Helianthus, LTR-retrotransposon, sunflower

Retrotransposons (REs) and their remnants represent a major fraction of interspersed repetitive DNA in eukaryotes, especially in plant species. It is generally accepted that REs have played an important role in plant genome evolution. Their amplification and dispersion contributed to genome structure with important consequences on gene activity regulation. Among REs, elements with long-terminal-repeats (LTRs) and without LTRs can be distinguished. LTRs are direct repeats situated at the extremities of the retrotransposon. LTR-retrotransposons are the most common in plant genomes and are distinguished into two major groups, Ty1/*copia* and Ty3/*gypsy*, according to sequence similarity and to gene order.

Due to their large number, a comprehensive analysis of LTR-REs within a species needs a genomic approach. Though their large number, Asteraceae are still relatively unexplored at genomic level. We used randomly sheared (nebulised) genomic DNA of sunflower (*H. annuus*) to construct a library, representing a random sample of the genome. Sunflower genome is large (nearly 4,300 Mbp per diploid genome); more than 1700 sequences were obtained, corresponding to nearly 860 Kbp, i.e. 1.8% of the genome. Blastn and Blastx analyses of sequences indicated that 17.9% sequences are similar to LTR-REs: of these, 8.1% presumably belong to *gypsy*-like REs, 2.6% to *copia*-like REs, and 7.2% to REs of uncertain nature.

A clustering analysis was carried out to assess the amount of LTR-REs in sunflower: 603 sequences were arranged in 137 contigs using the software cap3; 40/137 contigs showed some similarity to LTR-REs. Six *gypsy*-like and three *copia*-like related contigs, chosen among contigs formed by the highest number of sequences, hence presumably corresponding to most numerous REs, were analysed by slot-blot and Southern hybridisations. The frequencies of six selected *gypsy* REs ranged from 7,100 to 37,000 copies per haploid genome, and those of three *copia* REs from 2,100 to 16,000 copies. Whenever possible, RE-contig portion corresponding to LTR was used also as probe in comparison to its coding portion, in order to investigate the occurrence of solo-LTRs: the occurrence of solo-LTR elements is strongly supported only for one *copia*-like related contig.

Finally, the sunflower library was spotted onto membranes and hybridised to genomic DNAs of ten *Helianthus* species (4 annuals and 6 perennials) and of twelve non-*Helianthus* Asteraceae species. As to the most frequent REs in *H. annuus*, conservation in the other species was observed in specific domains of the RE. Moreover, some REs were especially frequent in *Helianthus* annuals, other in all *Helianthus* species. Some of these were numerous also in *Viguiera* and, at a lesser extent, in *Tithonia*, two genera strictly related to *Helianthus*. Occasionally, different RE clones hybridized to genomic DNA of other Asteraceae, however the vast majority of RE clones revealed specificity to the *Helianthus* genus,

especially *gypsy*-like REs, suggesting a more recent reproduction of these REs compared to *copia*-like ones.