

INSIGHT INTO THE ORGANIZATION OF THE *CYNARA CARDUNCULUS* GENOME

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Deep sequencing offers new possibilities to improve knowledge on genome composition producing a huge amount of sequence information in a short time. We used Illumina platform to explore artichoke genome with the aim of characterize in particular its repetitive component, highlighting remarkable features and generating information for further research applications.

Globe artichoke (*Cynara cardunculus* var. *scolymus*) is an important Mediterranean crop largely cultivated in the area from where it originated.

In this study we provide a first report on the organization of the artichoke genome using Illumina technology, which allowed to obtain a 2.3 x coverage of the variety Brindisino genome. Reads were assembled into contigs and characterized. A short insert plasmid library was constructed from the same genotype, and produced about 1700 clones sequenced using Sanger technology, for a total length of 2.74 Mbp. Moreover, twelve BAC clones belonging to a random sheared library were also sequenced and annotated.

All these sequences were BlastN and BlastX searched against the non redundant nucleotide and protein GenBank databases and against transposable elements databases. Pairwise BlastN comparison of each sequence was performed against all sequences to determine the genome repetitiveness. *Copia*, *Gypsy* and LINE were the most abundant retrotransposable elements; CACTA repetitive elements were also numerous in the artichoke genome. However, a large fraction of the repetitive component seems to be unknown.

A comparison with the repetitive fraction of the genome from other *C. cardunculus* taxa (i.e. wild and cultivated cardoon) was performed.

Results regarding repetitive component of artichoke genome generates important insight in its local organization and will serve in both theoretical and applied research, e.g. to improve strategies for genetic and physical mapping and for the development of molecular markers. Moreover, it represents a prerequisite for the annotation steps in sequencing projects.