



# IX International Symposium on Artichoke, Cardoon and their wild relatives

## ABSTRACTS



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## ■ THE GLOBE ARTICHOKE GENOME

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Globe artichoke ( $2n=2x=34$ ) has a medium-sized genome, estimated by flow cytometry, of 1.07 Gb. At present the few genomics information available for this crop include a restriction associated DNA sequencing (RADseq) genome analysis, a specific miRNA database and a RNAseq analysis, which provided a reference transcriptome of 38K unigenes. In addition, several *C. cardunculus* genetic maps, based on a two-way pseudo test cross strategy, have been developed and QTL analyses for key breeding traits have been conducted. Recently the complete chloroplast genome has been sequenced (PlosOne 10.1371/journal.pone.0120589). We performed Illumina HiSeq2000 whole-genome sequencing (133X) of an inbred genotype (S<sub>3</sub>) and assembled the first high-quality draft genome assembly (13 K scaffolds, 725 Mb, N50 = 123 Kb), with *de novo* prediction of 27,196 gene models. Through re-sequencing (30X) of a globe artichoke and a cultivated cardoon parental genotypes, and low-coverage genotyping-by-sequencing of their 163 F1 progeny, a total of 5,322 scaffolds (525 Mb, 73% of the assembly) were assigned to the maps and more than 2,000 successfully oriented in 17 reconstructed pseudo-molecules. To facilitate this, we developed and applied a novel algorithm (SOILoCo - Scaffold Ordering by Imputation with Low Coverage) to detect heterozygous regions with low sequencing depth in phase-unknown, pseudo-test cross populations. The sequence of globe artichoke genome provides information on its organization and gene content, along with structural and functional annotation, and represents a key tool for the molecular deciphering of complex traits. We also gathered insights on timing of speciation, whole genome duplication and mobile elements expansion.

○ **Keywords:** globe artichoke, genome, sequencing, assembly, annotation