IX International Symposium on Artichoke, Cardoon and their wild relatives

ABSTRACTS
THE GLOBE ARTICHOKE GENOME

Lanteri, S.1; Scaglione, D.1; Acquado, A.1; Portis, E.1; Tirone, M.1; Mauro, R.2; Lo Monaco A.2; Mauronicale G.2; Froenicke, L.3; Reyes Chin Wo S.3, Michelmore R.3

1DISAFA Plant Genetics and Breeding, University of Torino, Largo P. Braccini 2, I-10095 Grugliasco (Torino), Italy, 2Di3A, Dipartimento di Agricoltura, Alimentazione e Ambiente, University of Catania, via Valdisavola 6, I-95123 Catania, Italy, 3The Genome Center, UC Davis (USA).
E-mail: sergio.lanteri@unito.it

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 (S3) 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