

FIRST INSIGHTS INTO THE POPULATION STRUCTURE, LINKAGE DISEQUILIBRIUM AND ASSOCIATION MAPPING IN A GLOBE ARTICHOKE GERMPLASM COLLECTION

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Globe artichoke (*Cynara cardunculus* var. *scolymus*, $2n = 2x = 34$, haploid genome size ~ 1.08 Gbp) is an allogamous, highly heterozygous Asteraceae species which contributes significantly to the agricultural economy of the Mediterranean basin. Globe artichoke is mainly used in human nutrition: its immature inflorescence (capitulum, or more commonly ‘head’ or ‘bud’) represents the edible part of the plant and is consumed fresh, canned or frozen. It is also a promising source of biopharmaceuticals, such as mono-/ di-caffeoylquinic acids, sesquiterpene lactones and inulin.

Unravelling the genetic basis of phenotypic traits is helpful for the design of breeding strategies directed at improved yield and end-use quality. The genome-wide association (GWA) mapping approach represents an alternative to bi-parental linkage mapping for the genetic dissection of quantitative traits in crops. In a GWA approach the number of polymorphisms is determined by the genetic diversity of the entire germplasm panel, and the *linkage disequilibrium* is determined not only by recombination frequency, but also by genetic drift, by the mating system of the plant and by the history of selection. Advances in “next generation sequencing” (NGS), through multiplexed sequencing of barcoded samples in a single sequencing run, have driven the costs down to the point so that it is now feasible to perform the re-sequencing of entire germplasm collections with the aim to provide a comprehensive resource on species variation.

Here we present the first insights on a genome-wide association approach in globe artichoke, based on an association panel composed of 111 varietal types deriving from the living collection maintained at AGRIS (Sardinia, Italy). The collection has been investigated through two complementary molecular approaches: (i) microsatellite genotyping, using 34 loci uniformly distributed throughout the genome to investigate the population structure of the core germplasm set; and (ii) genotyping by sequencing, using a two-enzymes RADseq (restriction-site associated DNA sequencing) technology, as a basis for an association mapping approach.

An extensive phenotyping of the collection for key breeding traits is in progress. Moreover, the availability of the globe artichoke genome sequence, recently developed at the DISAFA group, represents an invaluable resource which will speed up the detection of alleles underpinning phenotypic diversity and will expedite studies in comparative genomics providing new insights into *genotype x environment* interactions.