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THE GLOBE ARTICHOKE GENOME SEQUENCE

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Cynara cardunculus (*Asteraceae*, 2n=2x=34, genome = 1,06 Gb) is an out-crossing perennial species which includes two cultivated forms, globe artichoke (var. scolymus) and domesticated cardoon (var. altilis). Globe artichoke is an important vegetable crop that is grown worldwide with an annual production of 750 million Mt and a gross production of 580 million US\$ (FAOSTAT, 2011). Italy is the leading world producer (475 Mt/year, 2011), followed by Egypt and Spain, but in recent years the production of the crop has spread to South America, USA, and China. The primary product of globe artichoke is the immature inflorescence (head or *capitulum*), which is consumed fresh, preserved or frozen, while the edible part of cultivated cardoon is the fleshy young stems. The species also represents a source of various biopharmaceuticals and can be exploited to produce lignocellulosic biomass and seed oil, the latter being suitable for both edible and biofuel purposes. Globe artichoke improvement through breeding has been limited and, unlike some other Asteraceae species (e.g. sunflower and lettuce), its genome remains largely unexplored. The species is highly heterozygous and does not tolerate self-fertilization; thus, a double pseudo-testcross approach has been adopted for mapping studies. We used an inbred (S_3) globe artichoke genotype to generate the first high-quality draft genome assembly (13 K scaffolds, 725 Mb, N50 = 123 Kb), with *de novo* prediction of 27,196 gene models. Re-sequencing (30X) of parental genotypes (globe artichoke and cultivated cardoon) and genetic anchoring of scaffolds, through low-coverage genotyping-bysequencing of 163 F₁ progeny, allowed the construction of ultra-dense genetic maps. We developed and applied a novel algorithm to detect heterozygous regions with low sequencing depth in phaseunknown, pseudo-test cross populations. A total of 5,322 scaffolds (525 Mb, 73% of the assembly) were assigned to the maps and more than 2,000 successfully oriented.