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ABSTRACTS











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BIOMASS YIELD AND RELATED TRAITS IN Cynara cardunculus: TOWARDS A GENOMIC APPROACH

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Bioenergy represents a promising source of renewable energies, which may reduce the dependency on fossil fuels. Energy can be produced from plant biomass that can be directly used for combustion, gasification or for the production of biofuels. Previous studies demonstrate that both cultivated and wild forms of Cynara cardunculus can be exploited for biomass production, however, the yield expressed in total energy obtainable by 1 ha of crop is greater for cultivated cardoon due to its higher biomass production, which can reach up to ~19t/ha (energy value ~ 17 MJ/kg) with a moisture content from 10 to 15%. First studies reveal the feasibility of cultivated cardoon to be deployed in biomass gasifier with particular care about ash management which has shown tendency of slagging and some corrosive potential. Among 9 varieties and ecotypes of cultivated cardoon, showing a within large phenotypic and molecular variation, we identified genotypes which were assessed over years, and subjected to a selection program aimed at increasing biomass yield and reduce genetic variability. Biomass yield is directly related to traits such as stem height, number of stems and capitula, which are quantitatively controlled by several genes. This makes it difficult their evaluation and selection, owing to the influence of the interactions between the environment and the genotype in all the growth and development stages. Recently, we generated the first high-quality draft genome of C. cardunculus, structured in 17 pseudo-molecules and, thanks to a low-coverage genotyping-by-sequencing of 163 F1 progeny, we developed ultra-dense genetic maps. The population, highly segregating for ligno-cellulosic biomass, was used for the identification of related QTL (quantitative trait loci). The scan highlighted genomic regions influencing biomass related traits which are scattered in 16 linkage groups. Our results represent an applicative standpoint for setting up new omics-based breeding programs for the increase of C. cardunculus biomass production.

Keywords: cultivated cardoon, genome, sequencing, biomass, QTL