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THE FAD2 GENE FAMILY IN *SILYBUM MARIANUM*

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Silybum marianum (L.) Gaertn. (Asteraceae; common name: milk thistle) is an annual plant species native to the Mediterranean area and cultivated as medicinal plant in Europe and Asia. Its fruits contain silymarin, a high-value complex of flavonolignans with health beneficial properties, mainly used for the treatment of liver diseases. The S. marianum oil, a by-product of silymarin production, is rich in linoleic acid. Increasing S. marianum fruit quality traits represents one of the main targets for breeding in this species and high oleic acid fruit content is an important characteristic for different food and industrial applications. For this reason, an Ethyl Methanesulfonate (EMS)-induced mutagenesis programme was implemented and a High oleic (Ho) mutant line showing 68.8 ±0.92% (±SE) oleic acid content was identified. Interestingly, this trait is not present in wild type (WT) germplasm and might boost the exploitation of *S. marianum* as multipurpose crop for industrial bioproducts and food production. In lipid biosynthetic pathway, the enzyme Fatty Acid Desaturase 2 (FAD2) is responsible for the conversion of oleic acid (C18:1) to linoleic acid (C18:2) in developing seeds and it is by far the most studied plant fatty acid desaturase gene family in both molecular and biochemical investigations. Although only a single representative gene was identified in Arabidopsis, FAD2 usually is a complex multigenic family in other plant genomes, with 13 members in Carthamus tinctorius and 26 in *Artemisia sphaerocephala*. Knocking out or silencing this gene results in a higher content of C18:1 and/or a lower content of polyunsaturated fatty acid in many oil crops. In this work, we have characterized the FAD2 family in S. marianum at genomic and transcriptional level. The family is composed of 21 members therefore representing the second larger FAD2 gene family so far described. Moreover, we identified a Single Nucleotide Polymorphism (SNP) in a fruit specific gene of the Ho mutant genotype and in the F2 progeny derived from Ho X WT backcrosses, thus hypothesizing the direct implication of this gene in the synthesis of linoleic acid. The characterization of this large FAD2 gene family in S. marianum and the newly identified mutation highlight interesting novelties with respect to other oleaginous crops species and it will provide useful information for directing further breeding programmes towards new *S. marianum* varieties suitable for the production of high oleic oil.