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Abstract – SY05

GENOME-WIDE IDENTIFICATION OF Dof TRANSCRIPTION FACTORS IN CULTIVATED CARDOON (*CYNARA CARDUNCULUS* L. VAR *ALTILIS*)

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The plant DNA-binding with one finger (Dof) gene family is a class of plant-specific transcription factors that play key roles in many biological processes, including response to biotic and abiotic stresses. Genome-wide identification of the Dof transcription factor family has been reported for many plant species but not for cultivated cardoon (*Cynara cardunculus* L. var *altilis*), a traditional food crop closely related to globe artichoke and being also exploited for industrial uses in green chemistry, or for any other member of the Asteraceae family. Consequently, clues about the roles of Dof transcription factors in this important botanical group are still lacking. Here, using a genome-wide approach, we identified 37 Dof candidate genes in cardoon. Phylogenetic analysis showed that the CcDof proteins could be divided into four main groups (A, B, C and D) and eight subgroups (B1, B2, C1, C2.1, C2.2, C3, D1, and D2), as already shown in the par excellence model species *Arabidopsis thaliana*. However, differences in the number of one-to-one orthologs and paralogs between the two species were identified. A comprehensive investigation of the exon–intron organization of all candidates showed that 19 genes were intronless, whereas 14 had only one intron. Interestingly, members belonging to the same subgroup shared a similar exon–intron organization except for C1 and D1. Identification of conserved motifs in the 37 CcDof proteins showed a similar structure to the 36 AtDof proteins, with most of the conserved motifs that were in common between the two species, suggesting their functional conservation. However, exploring the cis-regulatory elements at promoter level of CcDof genes revealed several additional elements, which could be divided into six classes, including light responses, hormone responses, stress responses, tissue specific elements, circadian control and flavonoid biosynthesis regulation, suggesting that promoter regions might contribute to the functional differentiation of CcDof genes in cardoon in respect to *A. thaliana*. Our study provided for the first-time basic information on the potential function of the Dof genes in cardoon, allowing us to select seven candidates putatively involved in the regulation of abiotic stress response and flavonoid biosynthesis. The functional exploration of candidate genes is ongoing in order to confirm their role in the processes of interest. Furthermore, our findings could also provide an indication on the role of Dof genes in artichoke and members of Asteraceae in general.