

GENOME-WIDE IDENTIFICATION AND SPATIAL EXPRESSION ANALYSIS OF HISTONE MODIFICATION GENE FAMILIES IN THE RUBBER DANDELION *TARAXACUM KOK-SAGHYZ*

PANARA F.*, FASANO C.*, LOPEZ L.*, PORCEDDU A.***, FACELLA P.*, FANTINI E.*, DADDIEGO L.*, PERRELLA G.***

*) Trisaia Research Center, Italian National Agency for New Technologies Energy and Sustainable Economic Development

**) Department of Agriculture, University of Sassari,

***) Department of Biosciences, University of Milan

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Taraxacum kok-saghyz (*Tks*), also known as the Russian dandelion, is a recognized alternative source of natural rubber quite comparable, for quality and use, to the one obtained from the so-called rubber tree, *Hevea brasiliensis*. In addition to that, *Tks* roots produce several other compounds, including inulin, whose use in pharmaceutical and dietary products is quite extensive. Histone Modifying Genes (HMGs) catalyse a series of post-translational modifications that affect chromatin organisation and conformation which, in turn, regulate many downstream processes, including gene expression. In this study, we present the first analysis of HMGs in *Tks*. Altogether we identified 154 putative *Tks* homologs: 60 HMTs, 34 HDMs, 42 HATs and 18 HDACs. Interestingly, whilst most of the classes showed similar numbers in other plant species, including *M. Truncatula* and *A. thaliana*, HATs and HMT-PRMTs were indeed more abundant in *Tks*. Composition and structure analysis of *Tks* HMG proteins showed, for some classes, the presence of novel domains, suggesting a divergence from the canonical HMG model. Analysis of publicly available transcriptome datasets, combined with spatial expression of different developmental tissues, allowed to identify several HMGs with a putative role in metabolite biosynthesis. Overall, our work describes HMG genomic organisation and sets the premises for functional characterisation of epigenetic modifications in rubber-producing plants.

