Proceedings of the LXII SIGA Annual Congress
Verona, Italy – 25/28 September, 2018
ISBN **978-88-904570-8-1**

Poster Communication Abstract – 4.26

HIGH RUBBER PRODUCTION IN *TARAXACUM KOK-SAGHYZ* R. IS ASSOCIATED TO DOWN-REGULATION OF TRANSCRIPTS INVOLVED IN COMPETING BIOSYNTHETIC PATHWAYS IN THE ROOTS

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Natural rubber, Taraxacum kok-saghyz, Russian dandelion, transcriptomics

Taraxacum kok-saghyz R. (Tks) is a promising alternative species to *Hevea brasiliensis* for production of high quality natural rubber (NR). We carried out de novo root transcriptome sequencing, assembly, annotation and comparison of gene expression of plants with the low (LR plants) and high rubber content (HR plants) in their latex. Our results show that a higher amount of rubber in the latex in HR plants is positively correlated with higher expression levels of several genes directly involved in rubber synthesis showing that NR production is highly controlled at transcriptional level. Moreover, we observed an upregulation of genes involved in sesquiterpenoids, monoterpenoids and phenylpropanoid biosynthesis in LR plants. We hypothesize that the synthesis of the abovementioned secondary metabolites may compete towards NR biosynthesis. This dataset represents a fundamental genomic resource for the study of Tks and the comprehension of the synthesis of NR and other biochemically and pharmacologically relevant compounds in the *Taraxacum* genus.