

FUNCTIONAL AND MOLECULAR ANALYSIS OF *an1* MYB TRANSCRIPTIONAL FACTOR INVOLVED IN ANTHOCYANIN PRODUCTION IN POTATO

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Anthocyanins are generally accepted to be enhancers of plant reproductive success as well as plant defence mechanisms. A member of R2R3 MYB TFs (transcriptional factors) gene family, named *an1* in potato, seems to have a key role in the anthocyanin accumulation in potato tissues. The aim of this study was to identify *an1* allelic variants and their expression pattern in potato leaves in order to better understand *an1*MYB mechanism in anthocyanin production in this tissue. For this purpose, *an1* was amplified from 17 of genotypes of cultivated *Solanum tuberosum* and two wild potato species, *S. commersonii* and *S. bulbocastanum*. The fragments were sequenced and analysed through bioinformatics tools. Real-time PCR assay was run on selected genotypes. We detected 26 polymorphic sites due to SNP mutations in all genotypes. Nucleotide deletions in *an1* sequence were also found in cultivar Spunta and Adora. Protein prediction revealed important amino acid substitutions in the hydrophobic *core* of R2 domain. Real-time analysis showed a different pattern of expression relative to *an1* gene among the different genotypes. HOT02-700 resulted to be the genotype with the maximum expression and S8617 the one with the lowest. The amino acid substitutions found could play an important role in R2R3 MYB TFs activity modulating the expression of structural genes and the interactions with other TFs. The function of alleles and the promoter sequences will be investigated.