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TOWARDS UNDERSTANDING MOLECULAR DYNAMICS AND RIBOREGULATORS INVOLVED IN THE COLD STRESS TOLERANCE OF WILD *SOLANUM COMMERSONII*

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The cultivated potato is classified as frost-sensitive, whereas some of its wild relatives useful for breeding are tolerant. Among them, *Solanum commersonii* is the one displaying the highest tolerance to low temperatures and it is also the first wild potato relative whose genome has been deciphered. Taking advantage from its DNA sequence, we determined the transcriptome profile (via RNAseq) and the small non-codingRNAome (via smallRNAseq) of two clones contrasting in their cold response (tolerant cmm1T and sensitive cmm6-6). Our analysis revealed a lower number of differentially expressed genes (DEGs) in cmm1T rather than cmm6-6 (1.001 vs 8.054 DEGs), of which 241 were unique in the former, 7.294 in the latter and 761 were common between them. Ontology analysis through AGRIGO revealed genes involved in "lignin catabolic process", "lignin biosynthetic process" and "plant type secondary cell wall biogenesis" highly associated to DEGs of tolerant cmm1T. We also identified a prevalence of 21- and 24-nt small non-codingRNAs yielding three classes of mature miRNAs (273), tasiRNA (5.737) and other smallRNA (134.868). Among miRNAs, 44 were identified as conserved (i.e. similar to those identified in other species) while 229 were *S. commersonii*-specific (i.e. not previously reported in any database). Fifteen cold-inducible miRNAs (4 up-regulated and 11 down-regulated) were identified through differentially expressed miRNAs analysis and verified by real-time RT-PCR. Among miRNAs differentially expressed, and in agreement with RNAseq, we established the role of conserved miR408 as important player in enhancing cold tolerance in cmm1T by inhibiting its target genes (laccases), confirming the hypothesis that lignin deposition is reduced under cold stress. Further functional studies aimed at elucidating the functions of these miRNAs and their targets are ongoing through virus-induced gene silencing (VIGS) and CRISPR/CAS9 approaches.