



Computational identification and characterization of conserved miRNAs and their target genes in beet (*Beta vulgaris*)

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ABSTRACT. Highly conserved endogenous non-coding microRNAs (miRNAs) play important roles in plants and animals by silencing genes via destruction or blocking of translation of homologous mRNA. Sugar beet, *Beta vulgaris*, is one of the most important sugar crops in China, with properties that include wide adaptability and strong tolerance to salinity and impoverished soils. Seedlings of *B. vulgaris* can grow in soils containing up to 0.6% salt; it is important to understand the molecular mechanisms of salt tolerance to enrich genetic resources for breeding salt-tolerant sugar beets. Here, we report 13 mature miRNAs from 12 families, predicted using an *in silico* approach from 29,857 expressed sequence tags and 279,223 genome survey sequences. The psRNATarget server predicted 25 target genes for the 13 miRNAs. Most of the target genes appeared to encode transcription factors or were involved in metabolism, signal transduction, stress response, growth, and development. These results improve our understanding of the molecular mechanisms of miRNA in beet and may aid in the development of novel and precise techniques

for understanding post-transcriptional gene-silencing mechanisms in response to stress tolerance.

Key words: *Beta vulgaris*; Bioinformatics; EST; GSS; microRNA