



Genomic tools provide insights to Agave fructan metabolism

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Key words: Agave, fructans, genomics

Traditionally in Mexico agave species are grown to produce tequila and mescal by exploiting the high concentration of fructans that accumulate in stem tissue but more recently agave species have also been proposed as raw material for biofuel production. Biochemically, the structure of agave fructan polymers have been well described, and some of the genes and enzymes involved have been characterized. However in order to optimize the use of agaves for commercial applications, an understanding of fructan metabolism in these species at the molecular and genetic level is necessary. We have previously reported the characterization of genes encoding fructosyltransferases and invertases from *A. tequilana* (Cortes-Romero et al., 2012) but were unable to obtain data for a complete set of enzymes involved in Agave fructan metabolism. We have therefore employed the analysis of RNAseq data to identify different isoforms of enzymes involved in agave fructan metabolism and the expression patterns of the genes encoding these enzymes in different tissues and plant organs. Transcriptome data for *A. tequilana* and *A. deserti* is already available (Gross et al., 2013) and we have also developed transcriptome databases for 3 Agave species: *A. tequilana*, *A. striata* and *A. victoria-reginae* using the Illumina Myseq method. Based on this analysis we identified 31 new isoforms in agave species for members of plant glycoside hydrolase family 32 (invertases, fructosyltransferases and fructanexohydrolases) which could be classified based on conserved amino acid motifs and comparison with previously characterized sequences from other monocotyledonous and dicotyledonous species. These isoforms include a novel invertase that may be specific to a particular sub-genus of *Agave* and data support the hypothesis that separate 1FFT type enzymes may not be necessary in *Agave* and closely related species. Differential expression patterns were observed for different isoforms in particular in relation to floral tissue, indicating the importance of fructan metabolism not only for energy storage in stem tissue but potentially also in producing the osmotic variations leading to flower opening. These findings open the door for the optimization of fructan metabolism for the production of bioenergy, alcoholic beverages and specific types of fructans that could be exploited in the food industry.

Cortes-Romero, C., Martinez-Hernandez, A., Mellado-Mojica, E., Lopez, M.G., and Simpson, J. (2012). Molecular and functional characterization of novel fructosyltransferases and invertases from *Agave tequilana*. *PLoS One* 7, e35878. doi: 10.1371/journal.pone.0035878.

Gross, S.M., Martin, J.A., Simpson, J., Abraham-Juarez, M.J., Wang, Z., and Visel, A. (2013). De novo transcriptome assembly of drought tolerant CAM plants, *Agave deserti* and *Agave tequilana*. *BMC Genomics* 14, 563. doi: 10.1186/1471-2164-14-563.