

Genomic annotation and gene expression analysis related to oil production of the non-model crop *Plukenetia volubilis*

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Plukenetia volubilis L. (also known as Sacha inchi) is a crop from the family Euphorbiaceae of considerable economic interest given the nutritional properties of its seeds: high content of edible oils, protein and tocopherols. Sacha inchi's seed oil is characterized by a predominant proportion of polyunsaturated fatty acids (PUFAs), which is favorable from a health perspective. In this work, the genome annotation of a previously generated draft-genome assembly was performed. Later, genome-guided transcriptome analyses, including differential expression and co-expression network analyses, were carried out to identify potential regulators of FA and TAG biosynthesis. A total of 51757 genes models were predicted, from which 47531 were functionally annotated. Differential expression dynamics of genes related to FA and TAG biosynthesis is described. From the co-expression network analysis, important putative regulators of FA and TAG biosynthesis were found. In particular, WRI1, FUS3, and LEC1 stand out given their regulatory roles. The identification of regulatory genes involved in FA and TAG biosynthesis pathways will provide useful resources for further research and efforts in the genetic improvement of Sacha Inchi.