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Transcriptome assembly for non-model Apinae bees: reference or de novo approach?

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RNA-Seq is a cost-effective method to characterize the gene set of species under interest. Initially it is required the reconstruction of all full-length transcripts based on short nucleotide reads, which represents a substantial computational challenge. Basically there are two strategies for transcriptome assembly, the Mapping-first and the Assembly-first (de novo). The first one is based on the alignment of all reads to a reference genome. It is less intensive computationally and, in principle, provides maximum sensitivity. However it demands an accurate mapped genome as reference. Conversely, the Assembly-first assemble the reads in contigs not using a reference genome as a guide. Herein we compare the success of both methods for assembling the transcriptome of the solitary bee *Tetrapedia diversipes*. This species belongs to the subfamily Apinae and is native of the American Tropics. The total RNA from 9 adults was extracted. These RNA samples were grouped in 3 pools and sequenced by Illumina HiSeq2000. Approximately 90 million paired reads of 100bp were generated. After quality trimming steps the reads were aligned to *Apis mellifera* genome using Bowtie2 (Mapping-first). The Trinity program was used for the normalization and the de novo assembly, the resulting contigs were then aligned to the reference genome using Bowtie2 (Assembly-first). In general, the alignment of the de novo transcriptome against the genome of reference recovered larger similar regions. It is worth to note that the contigs were previously combined (Trinity assembly) whereas for Mapping-first the alignment was done with smaller reads. To our understanding the de novo assembly strategy seems to be more effective to study non-model species, here *T. diversipes*. This is the first transcriptome generated for a Neotropical solitary species. The transcripts data will be analyzed under the perspective to better understand fundamental questions about evolution of the social behavior.