



The genome of the solitary bee *Tetrapedia diversipes*

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The advances in sequencing technology expanded the possibilities of investigating the molecular basis of complex phenotypes in non-model organisms. Genome sequencing data have enabled the description of the genetic content and its organization, likewise the types and abundance of transposable elements and other regulatory components, the acquisition of new genes and modification in the existent ones, and to perform evolutionary and functional studies. Several genomes have been deposited in databanks during last decade. Considering just bees one finds 17 genomes. However this number is far from representing the high diversity of this group. It is known that the vast majority of bee species are solitary nonetheless only three genomes of those species are available and none of them are from Neotropics. Here we present the draft genome of the solitary oil-collecting bee *Tetrapedia diversipes*. This species is endemic of the Neotropical region and is one of the most abundant species found in trap-nests. This species presents some intriguing characteristics: 1) bivoltinism; 2) diapause solely present during the development of individuals from the second generation; and 3) the nests are parasitized by a sister group cleptoparasite species *Coelioxoides waltheriae*. *T. diversipes* is an excellent model to study general aspects of ecology, development, species interaction, responses to environmental changes, physiology among others. The genome will contribute to explore all these features in a molecular manner. We will present the first draft of the genome assembly, the statistics obtained and insights about its content in a comparative analysis with other bee genomes.