

TITLE: ANALYSIS OF miRNA EXPRESSION IN *Paracoccidioides brasiliensis* DURING IRON DEPRIVATION

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ABSTRACT:

The *Paracoccidioides* genus is composed of thermodynamophilic fungi that cause paracoccidioidomycosis (PCM), an endemic human systemic mycosis of Latin America. Iron is an essential micronutrient for all eukaryotes since it participates in several essential biological processes. However, the bioavailability of this metal within the host is low. The ability to uptake iron ions is extremely important for the establishment of infection. Since iron deprivation is imposed by the host, pathogenic fungi developed mechanisms of high affinity for the capture of this metal. Among the processes regulated by iron restraint, changes in the transcription pattern of genes involved in iron uptake are one of the most evident responses. miRNAs are short sequences of RNA that act as transcriptional regulators in several processes, including genes associated to the systemic iron homeostasis. The present study aims to identify miRNAs expressed in *P. brasiliensis* (Pb18) during iron deprivation. Using qRT-PCR, we evaluated the expression levels of transcripts encoding proteins involved in the silencing machinery mediated by miRNAs (dicers and argonautes). We observed that both dicer and argonautes are differentially expressed in the 24 hour period of iron deprivation in *P. brasiliensis*. Furthermore, next generation sequencing (NGS) of total RNA extracted during this condition revealed 18 differentially expressed miRNAs. Further studies, including sequence characterization and miRNA expression, are required to understand the potential impact of iron on miRNA processing and determine the role of miRNAs in the regulation of iron metabolism in *Paracoccidioides* spp.

Keywords: *Paracoccidioides*, iron, miRNA.

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