

Integrative networks analysis based on RNAseq data to elucidate a presence of B chromosome

Rafael Takahiro Nakajima¹, Ivan Rodrigo Wolf², Guilherme Targino Valente³,
Rodrigo de Oliveira Almeida², Rafael P. Simões³, Cesar Martins¹

1 IBB-UNESP

2 FCA-UNESP

3 UNESP - STATE USP

Abstract

B chromosomes occur in about 2000 species, including animals, insects and plants. Several works have been conducted with the aim of understanding their distribution, frequency, transmission mechanisms, structure and origin. Cichlid fish receive great scientific interest, since many species are under rapid and extensive adaptive radiation. *Astatotilapia latifasciata* is one of the species of African cichlids that presents B chromosomes. In this species, Bs, although heterochromatic, present genes with high integrity and interfere in the transcriptional profile of the cells. Thus, the present work aims to characterize possible candidate genes of *A. latifasciata* specific tissues to elucidate the influence of the presence of B chromosomes in specific metabolic pathways from data obtained from RNASeq. For this purpose, networks were constructed by concatenating co-expression and protein-protein interaction networks, which obey the expected degree-distribution for biological networks. Ontologically enriched domains were extracted from the network for important biological processes to be compared with differential expression data of mRNAs in gonads. Results of the intersection between networks and differential expression, presented an important role in the regulation of cellular activity, mainly to an anti-inflammatory response, the presence of cellular membrane processes and components that may be related to the defense mechanism.

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