# CHARACTERISTICS OF THE GENOMIC NEIGHBOURING REGIONS OF MICRORNAS IN *D. MELANOGASTER* AND *C. ELEGANS*

*Fagundes-Lima, D.[1], Guerra-Sá, R.[1], Castro e Silva, A.[2], Machado, R. F.[2] and Weber, G.[2]*

[1]Departament of Biological Sciences, and [2]Departament of Physics, Federal University of Ouro Preto, Ouro Preto, Brazil

MicroRNAs are noncoding genes that regulate the expression of target genes by binding to partially complementary sites in mRNA. In animals, miRNAs (microRNAs) are derived from two cleavages of the primary RNA transcript by the action of Ribonuclease III, resulting in characteristic stem-loop structures (hairpins). Further to these cleavages, the hairpins are processed by the Drosha enzyme close to the base of the stem to generate miRNAs precursors (pre-mRNAa), usually of 70-80 nucleotides in lenght. Recently, Ruby et al (Nature, v. 448, p. 83, 2007) showed that certain number of pre-miRnas *D. melanogaster* in are originated from intronic regions and bypass the Drosha processing altogether, and termed then as mirtrons. To better understand the miRNA biogenesis it is important to analyse the neighbouring regions of the genome from where the miRNA precursors originate. We have developed a set of Perl scripts to retrieve and analyse the genomic neighbourhood of known precursor miRNAs for *D. melanogaster* and *C. elegans.* These regions were analysed for disctinctive features, starting from simple CG content analysis to thermodynamic stability. Our results indicate important differences between mirtrons and ordinary miRNAs. For instance, we found that the neighbouring regions of mirtrons all have higher CG content than the mirtrons themselves. In contrast, of all known miRNAs of *D. melanogaster* and *C. elegans* 66% and 81%, respectively, have neighbouring regions with lower CG content. We discuss how our findings can be used for the bioinformatic discovery of new precursor miRNAs. Support: Fapemig.