Analysis of Distinctive microRNA Conservation Patterns as Markers for Unique microRNA Processing Mechanisms

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MicroRNAs (miRNA) are an emerging class of non-coding RNA that enable post-transcriptional regulation through repression and degradation of target mRNA. Dysregulation of miRNAs has been associated with cancer and other forms of malignancy, highlighting their critical role in gene regulation. Biogenesis of miRNAs involves multiple proteins that utilize well-conserved structural motifs to enable greater processing efficiency. In this study, the conservation of 30 randomly-selected miRNAs well-expressed within the Euarchontoglires superorder was analyzed with respect to the mouse (Mus musculus) in order to classify their divergence patterns. Genomic data from the UCSC Genome Browser was aligned with Mirbase in order to calculate a divergence score for the guide strand, star strand, terminal loop, and flanking regions of each miRNA. Through the analysis, selected miRNAs were categorized into five distinct classes based on divergence of motifs that highlighted common evolutionary patterns shared between them which suggest differences in contribution to important gene regulatory networks in certain divergent species. Investigating the patterns of the miRNAs found in this study serves as the basis of future research in order to better understand the functional mechanisms of non-canonical and lesser-studied miRNAs in addition to the evolution of the structure and function of miRNAs as a general class.

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