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Abstract MicroRNAs are single-stranded regulatory RNAs of 18–25 nucleotides that generate from endogenous transcripts that form local hairpin structures. The processing of microRNA transcripts involves the activities of two RNases, III and Drosha and Dicer. In this study we analyzed structural features of human microRNA precursors that make these transcripts Drosha and Dicer substrates. We identified minimal functional primary processors (pri-microRNAs) and secondary processors (pre-microRNAs) sites produced. The frequency, nucleotide content, and the localization of various structure destabilizing motifs was studied. We identified numerous pri-microRNAs which structure strongly depart from the consensus structure and their processing is hard to explain by the existing model of the Microprocessor complex. We also found a biased distribution of symmetric and asymmetric motifs along the pre-microRNA hairpin stem and an over-representation of bulges on its 5' arm ($p < 0.00001$), which may have considerable functional implications.

Keywords: miRNA biogenesis, Dicer, Drosha, RNA structure prediction, pri-miRNAs, pre-miRNA structural motifs

1. Introduction

MicroRNAs (miRNAs) are a family of short single-stranded noncoding RNAs described in many eukaryotes from simple organisms to humans [1, 2]. It is estimated that hundreds of miRNAs regulate the expression of thousands of protein genes [3–5]. MiRNAs regulate gene expression at the posttranscriptional

Received 12 November 2008; revised 10 December 2008; accepted 10 December 2008.

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