

Genomewide Analysis of Expression of Genes Located near miRNAs in Humans and Mice

Hidenori Inaoka*, Yutaka Fukuoka^{1,**} and Makoto Noshiro

School of Allied Health Sciences, Kitasato University,
1-15-1, Kitasato, Minami, Sagamihara, Kanagawa 252-0373, Japan

¹Graduate School of Biomedical Science, Tokyo Medical and Dental University,
Yushima, Bunkyo, Tokyo, 113-8510, Japan

(Received October 3, 2011; accepted January 24, 2012)

Key words: MicroRNA (miRNA), transcription

MicroRNAs (miRNAs) are 20- to 22-nucleotide RNAs that regulate the transcription and translation of genes. In our previous studies, we reported that a miRNA has the potential to affect the transcription of genes located near it. The number of miRNAs recorded in databases continues to increase. However, the effects of the miRNAs, including newly found miRNAs, on the transcription of genes located near them have not yet been analyzed. In this study, we investigated the effects in humans and mice. The average expression levels are increased in the 10⁴ bp vicinity of miRNA in all the datasets investigated. Many of the newly found miRNAs are located in an intron, exon or untranslated region (UTR) of host genes. When a host gene is transcribed, the miRNA located in such a region of the host gene is also transcribed. In addition, recent reports indicate that some noncoding RNAs, including miRNAs, can upregulate the expression of genes that have the complement sequences of the noncoding RNA in their promoter regions. Therefore, if genes having complement sequences of miRNAs are located around these miRNAs, the expression levels of these genes could be increased. These phenomena may be the reasons for the increased average expression levels around miRNAs.

*Corresponding author: e-mail: inaoka@kitasato-u.ac.jp

**Present affiliation: Department of Electrical Engineering, Kogakuin University, Tokyo, Japan