

P007 Evolutionary genomics of microRNA and regulatory elements

Yoko Fukuda¹, Masanobu Tanabe² and Taro Fukao³

¹University of Tokyo, Japan ²Keio University, Japan,

³Max-Planck-Institute of Immunobiology, Germany

Although thousands of miRNAs have been identified in mouse, human and other species so far, few studies reported precise mechanisms for transcriptional regulation of primary miRNA transcripts (pri-miRNAs), which would be crucial to confer the specificity of spatiotemporally restricted miRNA expression. Providing that genes are regulated by various miRNAs in a combinatorial manner, another question is what regulates the expression of miRNAs themselves and triggers the whole process of complex gene regulatory networks. We have found various candidates of pri-miRNAs based on genome mapping of mouse full-length cDNA and conserved precursor sequences (pre-miRNA). Comparison with other species of some those screened-out miRNAs elucidated that the predicted regulatory elements are often conserved as observed on precursor sequences in spite of long genomic distances separating those two regions. Sequences of regulatory elements give us the information about their roles in spatial and temporal specific expression of pri-miRNA, and co-evolution of their sequence and miRNAs. Moreover our result suggested that miRNA genes can be a new hallmark of evolution because of its characteristic structure in the genome.