Editorial

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Regulation of microRNAs and Transcription

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Editorial

Regulation of Transcription Factors and microRNAs (miRNAs) are coordinated in the cellular genomic responses. In general, the transcription of mRNAs is regulated by transcription factors binding to the promoter regions of the targeted mRNAs. The miRNAs regulate the transcription of mRNAs to suppress the expression. The miRNAs are regulated by transcription factors, followed by the regulation of mRNAs. In this editorial, the regulatory networks of mRNAs and miRNAs are described, mainly focused on the regulatory regions of the genome. The Transcription Factors (TFs) and microRNAs (miRNAs) regulate gene expression by its binding towards the regulatory regions of genome [1]. TFs and miRNAs share many features to regulate the gene expression, in which TFs bind to the promoter regions of mRNAs and miRNAs bind to the 3 prime regions of mRNAs [1]. TFs regulate the gene expression through promoter activation or repression. Epigenetic regulations of genes include the miRNA-driven gene suppression. There are several studies in which mutation and methylation in promoter regions of miRNAs playing important roles are identified [2-4]. The SNP in promoter region of *miR-10b* gene is associated with breast cancer risk [2]. CpG dinucleotide methylation of the promoter region of *miR-29c* gene is associated with breast cancer, where the inhibition of CpG methylation with 5-aza-CdR increases *miR-29c* expression in basal-like breast cancer cells [3]. Demethylation in SP1 sites within promoter region of miR-23a-27a-24-2 is associated with up-regulation of the expression, proliferation and apoptosis inhibition in laryngeal cancer cells [4]. The miRNA-target interactions contain the multiple targeting of the genes in which miRNA targets 3'-untranslated region (UTR) for several genes [5]. The *miR-27b* targets 3'-UTR of pyruvate dehydrogenase protein X (PDHX), leading to the repression of PDHX expression and promotion of growth in breast cancer [6]. The miRNA target sites in the 3'-UTRs of genes can be predicted using known mammalian miRNA sequences [7]. The 3'UTRs from the *Homo sapiens*, *Mus musculus* and *Rattus norvegicus* genomes were scanned with the algorithm based on sequence complementarity between the mature miRNAs and the target site, binding energy of the miRNA-target duplex, and evolutionary conservation of the target site sequence and target position in aligned UTRs of homologous genes [7]. The miRNA-dependent regulation of transcription is investigated using mRNA and miRNA expression correlation assessment [8]. The regulation of gene transcription by miRNAs in terms of the involvement to the changes in cellular phenotype in cancer would be interesting issues to be investigated. Previous finding indicated that gastric cancer-derived exosomal miR-21-5p induced the peritoneal metastasis *via* mesothelial-to-mesenchymal transition [9]. The mechanism in which miR-21-5p induces the cellular phenotypic change may be related to the miR-21-5p-directed targeting on SMAD family member 7 (SMAD7). SMAD7 is a molecule for TGFbeta/Smad pathway playing an important role in Epithelial-Mesenchymal Transition (EMT), which is the cellular phenotypic alteration related to cancer metastasis and drug resistance [9]. In hepatocellular carcinoma, *miR-197* activates Wnt/beta-catenin signaling, leading to promotion of EMT and metastasis [10]. It is described that miRNA genomics, biogenesis and function, as well as miRNA desregulation in the cellular pathways are important factors for the progressiveness of cancer cells [11]. A post-transcriptional mechanism of miRNA biogenesis regulation includes Epidermal Growth Factor Receptor (EGFR) regulation, which is one of the important factors for cancer [12]. The mutation of oncogenic miRNAs or tumor suppressor miRNAs, as well as dysregulation of miRNA, is linked to human cancer [13]. The gene and miRNA networks in stem cells and reprogramming play an important role for cancer signaling [14].

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The regulation of miRNAs in terms of EMT in stem cells and cancer cells is related to the abundant network pathways. Gene and miRNA networks would be important factors to elucidate the mechanism on cancer metastasis and epigenetic regulation.

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