Kurokawa, Transcriptomics 2013, 1:1
DOI: 10.4172/2329-8936.1000e102

Transcriptomics: Open Access

Editorial Open Access

Transcriptomics Inspires Long Noncoding RNA

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Now, the OMICS group has launched "Transcriptomics", Open Access Electric Journal. Transcriptomics is one of young field of bioinformatics that deals with transcriptome, dynamics of transcripts, messenger RNA, ribosomal RNA, transfer RNA, small RNA like microRNA, and long noncoding RNA (lncRNA). Such kind of the field grows rapidly. Scientific outcomes of transcriptomics are divergent and flow swiftly. Therefore, the open access format fits the field well.

One of remarkable achievements in transcriptomics is to identify noncoding RNA in the human genome. Coding regions of the human genome occupy less than 5% of the genome, while rest of the genome comprises noncoding regions that generate noncoding RNAs. Most of noncoding RNAs are categorized into lncRNAs (that are longer than two hundred nucleotides). More than 35,000 lncRNAs have been documented, while less than 180 lncRNAs have been annotated. We are focusing on a fraction of lncRNAs, bound with RNA binding protein TLS. Our deep sequencing analysis of the TLS-bound fraction of RNA indicated that approximately 5,000 lncRNAs bind to TLS. Many of these lncRNAs could possess biological function, because the RNAs bound to TLS have been found to induce repression of transcription.

Recently, we demonstrated that promoter associated lncRNA (pncRNA) repress transcription,upon its binding TLS through inhibition ofhistone acethyltransferase activity [1]. The pncRNA might exert inhibitory effecton cancer growth. Recently, our 5' race analysis determined the length of the pncRNA (pncRNA-D) as a 600 nucleotides transcript, with a predicted secondary structure. Our biochemical analysis showed that the core consensus GGUG sequence of the pncRNA-D with only 25 nucleotides has the HAT inhibitory activity. The 25 mer RNA oligonucleotides have full activity of the HAT inhibition through binding to TLS, and also induction of a conformational change on TLS. Now, lncRNA has been getting attention regarding target for nucleic acid medicine. The GGUG RNA is a possible candidate for the RNA medicine. TLS has been found to be methylated, at least at four arginine residues, PRMT1 (protein argininemethyltransferase 1) and PRMT5 methylatethese Arg residues. Our preliminary data showed that this Arg methylation could play a role inregulation of the binding of TLS to lncRNAs. Taken together, these data indicate that functions of lncRNAs could be regulated by their diversity of sequences, and chemical modification of their cognate RNA binding proteins. These pncRNAs are just one group of the lncRNAs. Others have divergent structures and functions.

The lncRNA could be comparable to messenger RNA, being recognized as a traditional gene expression mediator. Transcriptomics, analysis of transcriptome uncovers hidden layer of the human genome. The filed could provide more fruitful achievement near future.

References

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Received January 29, 2013; **Accepted** January 31, 2013; **Published** February 02, 2013

Citation: Kurokawa R (2013) Transcriptomics Inspires Long Noncoding RNA. Transcriptomics 1: e102. doi:10.4172/2329-8936.1000e102