Characteristics and function of non-coding RNAs involved in the development of kidney cells and their carcinogenesis

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Abstract

Genomic research has revealed that 80% of the genome undergoes transcription, but only 2% encodes proteins. The remaining portion of the transcriptome was long considered unimportant, and even referred to as "junk" RNA. As research has progressed and discoveries have been made, further fractions of non-coding RNA have been systematized and classified based on their function and structure. Non-coding RNA is a highly diverse fraction of RNA whose sequences do not encode protein information. Among non-coding RNAs, two groups are distinguished based on RNA function: structural and regulatory. Structural RNA including tRNA, rRNA, snRNA, and snoRNA. serves structural/play important roles in fundamental cellular processes. Regulatory RNAs influence cellular processes and are divided into two groups based on their length. These regulatory RNAs can be broadly divided into two main groups based on their length: small regulatory RNAs (snRNA) and long non-coding RNAs (lncRNAs). with the boundary between them being arbitrarily set at a length of 200 nt. The snRNA subgroup also differentiates based on length into siRNA, miRNA, piRNA, and tRF molecules, while among lncRNA, a fraction of circular RNAs (circRNA) can be distinguished. Changes in the presence of regulatory RNAs can affect cellular processes such as differentation and in consequence can lead to carcinogenesis. The significance of regulatory RNAs is so substantial that even modifications to individual nucleotides can lead to pathological conditions.

In this collection of publications, the significant impact of non-coding RNAs on function and pathological states has been demonstrated by examining the profiles of tRNA-derived fragments (tRFs) in two biological systems. The first involves various/several tissues from the model organism Sus scrofa (pig). The second is a cell model of human kidney development proposed by us, consisting of four cell lines illustrating kidney cell differentiation and carcinogenesis. To determine the tRF molecule profile, we employed next-generation RNAseq sequencing and membrane-based northern blot imaging techniques. To demonstrate function of ncRNA, we used Electrophoretic Mobility Shift Assay (EMSA) and bioinformatics tools like tRFTars by analyzing

databases. Finnaly, in comprehensive review articles, we summarized the latest knowledge regarding the interactions and modifications of lncRNAs, elucidating the mechanisms influencing cell differentiation and carcinogenesis.