論 文 の 内 容 の 要 旨

論文題目　Studies on ribosome-associated lncRNAs using ribosome profiling data
(リボソームプロファイリングデータを用いたリボソーム関連長鎖ノンコーディングRNAに関する研究)

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Although the number of discovered long non-coding RNAs (lncRNAs) has increased dramatically, their biological roles have not been established. Many recent studies have used ribosome profiling data to assess the protein-coding capacity of lncRNAs. However, very little work has been done to identify ribosome-associated lncRNAs, here defined as lncRNAs interacting with ribosomes related to protein synthesis as well as other unclear biological functions.

On average, 39.17% of expressed lncRNAs were observed to interact with ribosomes in human and 48.16% in mouse. We developed the ribosomal association index (RAI), which quantifies the evidence for ribosomal associability of lncRNAs over various tissues and cell types, to catalog 691 and 409 lncRNAs that are robustly associated with ribosomes in human and mouse, respectively. Moreover, we identified 78 and 42 lncRNAs with a high probability of coding peptides in human and mouse, respectively. Compared with ribosome-free lncRNAs, ribosome-associated lncRNAs were observed to be more likely to be located in the cytoplasm and more sensitive to nonsense-mediated decay. Furthermore, we tried to investigate the sequence features involved in the ribosomal association of lncRNA. We have extracted ninety-nine sequence features corresponding to different biological mechanisms (i.e., RNA splicing, putative ORF, k-mer frequency, RNA modification, RNA secondary structure, and repeat element). An L1-regularized logistic regression model was applied to select these features. Finally, we obtained fifteen and nine important features for the ribosomal association of human and mouse lncRNAs, respectively.

To our knowledge, this is the first study to characterize ribosome-associated lncRNAs and ribosome-free lncRNAs from the perspective of sequence features. These sequence features that were identified in this study may shed light on the biological mechanism of the ribosomal association and provide important clues for functional analysis of lncRNAs. Our results suggest that RAI can be used as an integrative and evidence-based tool for distinguishing between ribosome-associated and free lncRNAs, providing a valuable resource for the study of lncRNA functions.