

# Researchers develop interactive database for translatable circular RNAs based on multi-omics evidence

October 30 2020, by Liu Jia

---



Credit: Pixabay/CC0 Public Domain

A specialized database has been published online in *Nucleic Acids Research*. Called [TransCirc](#), the database provides comprehensive evidence supporting the translation potential of circular RNAs (circRNAs). This database was generated by integrating various direct

and indirect evidence to predict coding potential of each human circRNA and the putative translation products.

Recent studies indicated that some cytoplasmic circRNAs can be effectively translated into detectable peptides and many short sequences have been reported to function as internal ribosome entry site (IRES)-like elements to drive circRNA [translation](#). The translation of circRNA was upregulated during cellular stress, and some circRNA-encoded proteins were found to play key roles in regulating cancer cell growth.

However, the identification of circRNA-encoded protein has been a very difficult task, mainly because the sequences from circRNAs and their cognate linear mRNAs of host gene have a large overlap and differ only at the small window across the back-splice junction. As a result, while a large number of circRNAs have been identified through high-throughput transcriptome sequencing, a specialized and comprehensive [database](#) for translatable circRNAs is still lacking.

To meet this need, the researchers from the CAS-MPG Partner Institute for Computational Biology, Shanghai Institute of Nutrition and Health (SINH) of the Chinese Academy of Sciences (CAS) and the Bio-Med Big Data Center of SINH developed a comprehensive database, TransCirc, which contains information of ~300,000 circRNAs together with multi-omics evidence from published literatures to support circRNA translations.

Integrating seven types of evidence for circRNA translation, TransCirc provides an interactive data search engine and visualization interface for the translatable circRNAs and their translation products, as well as the regulatory elements that support its translation and analytic tools for potential function of circRNA encoded genes.

The TransCirc database is expected to facilitate further analysis of circRNA function and streamline the identification of circRNA translation product. All of the information and data is freely available at TransCirc.

circRNAs have recently been demonstrated as a class of abundant and conserved RNAs in animals and plants. Previous studies have revealed that circRNAs may play diverse biological roles by functioning as either no-coding or coding RNAs. Because circRNAs are more stable than their linear counterpart, they can naturally function as competitors of the linear RNAs to play regulatory roles in gene expression. Since most circRNAs contain exonic sequences and are localized in cytoplasm, many of these circRNAs may also function as mRNA to direct protein translation.

**More information:** Wendi Huang et al. TransCirc: an interactive database for translatable circular RNAs based on multi-omics evidence, *Nucleic Acids Research* (2020). [DOI: 10.1093/nar/gkaa823](https://doi.org/10.1093/nar/gkaa823)

Provided by Chinese Academy of Sciences

Citation: Researchers develop interactive database for translatable circular RNAs based on multi-omics evidence (2020, October 30) retrieved 11 July 2024 from <https://phys.org/news/2020-10-interactive-database-circular-rnas-based.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
--