

COMMENTARY

Open Access



circRNAs shed light on cancer diagnosis and treatment

Christophe Nicot*

Circular RNAs (circRNAs) are a subgroup of single-stranded endogenous RNAs which exert differential expression pattern between normal and cancerous tissues and function as important regulators in cancer initiation and progression. However, comprehensive characterization of circRNA landscape across cancer types is still lacking. In a recent article published in *Molecular Cancer*, Wang and his colleagues have now placed seven types of tumors in a unified analytic framework [1], all with matched tumors and corresponding normal tissues. This work illustrated the detailed picture of circRNA expression signatures among solid tumors and highlighted the significance of these dysregulated circRNAs in cancer pathogenesis as well as their utility as potential indicators or therapeutic agents.

Through rRNA depleted transcriptome sequencing, the authors identified a total of 59,056 circRNAs, the majority of which were lowly expressed, while a subset of circRNAs exhibited much higher abundance than their cognate linear transcripts, indicating their biological significance in homeostasis. Using stringent criteria, the authors pictured the distinct circRNA expression signatures among seven types of solid tumors. The dysregulated circRNAs exhibited cancer-specific expression or shared common expression pattern across cancers, implying their diverse functions in cancer progression and their diagnostic potential in multiple cancers. Among the aberrant circRNAs, circLIFR showed an overall downregulation in tumors. Significantly, circLIFR was experimentally validated as a bona fide circRNA which

inhibited tumor metastasis in vitro and in vivo, demonstrating circLIFR may serve as a therapeutic target in metastatic cancer. Consistently, the RNA-seq results suggested the ability of circLIFR to alter the expression pattern of some metastasis-related genes involved in cell adhesion and epithelial-mesenchymal transition (EMT). Collectively, this study by Wang et al. certainly illustrates the comprehensive circRNA profiles in multiple solid tumors and highlights the potential of circRNAs as important diagnostic tools or therapeutic targets.

Author's contributions

Christophe Nicot wrote the commentary. The author(s) read and approved the final manuscript.

Competing interests

The author declares no financial conflict of interest. Christophe Nicot is Editor-in-Chief of *Molecular Cancer*.

Published online: 29 April 2022

Reference

1. Wang C, Liu WR, Tan S, Zhou JK, Xu X, Ming Y, et al. Characterization of distinct circular RNA signatures in solid tumors. *Mol Cancer*. 2022;21(1):63.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

*Correspondence: cnicot@kumc.edu

Department of Pathology and Laboratory Medicine, University of Kansas Medical Center, 3901 Rainbow Boulevard, Kansas City, KS 66160, USA



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.