Basic Research

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Re: MicroRNA-210-3p Depletion by CRISPR/Cas9 Promoted Tumorigenesis through Revival of TWIST1 in Renal Cell Carcinoma

Yoshino H[1], Yonemori M[1], Miyamoto K[1], Tatarano S[1], Kofuji S[2], Nohata N[3], Nakagawa M[1], Enokida H[1]

[1]Kagoshima University, Graduate School of Medical and Dental Sciences, Department of Urology, Kagoshima, Japan
[2]Vontz Center, University of Cincinnati College of Medicine, Department of Internal Medicine, Ohio, USA
[3]Moores UCSD Cancer Center, La Jolla, USA

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EDITORIAL COMMENT

Recently, a new tool based on a bacterial clustered regularly interspaced short palindromic repeats (CRISPR)-associated protein-9 (Cas9) nuclease from *Streptococcus pyogenes* has created a new hope for scientific researches. This new approach can modify targeted permanent mutations on the genome. The functions of CRISPR and CRISPR-associated genes are essential in adaptive immunity in some bacteria and archaea, enabling the organisms to respond to and eliminate invading genetic material. The CRISPR/Cas9 system requires only the redesign of the crRNA to change target specificity. This contrasts with other genome editing tools, including zinc finger and transcription activator-like effector nucleases, where redesign of the protein-DNA interface is required. In the urology literature, previous studies showed that five miRNAs (miR-885-5p, miR-1274, miR-210-3p, miR-224 and miR-1290) were upregulated the most in clear cell renal cell carcinoma (RCC). In this research, the authors identified twist-related protein 1 (TWIST1) as a key target of miR-210-3p. They utilized the CRISPR/Cas9 gene editing system to deplete miR-210-3p in RCC cell lines (786-o, A498 and Caki2). They suggested that high TWIST1 and low miR-210-3p expression was associated with poorer overall and disease-free survival as compared to low TWIST1 and high miR-210-3p expression. According to this research, CRISPR/Cas9 system to study specific miRNAs and other non-coding RNAs in areas of cancer can be useful as a targeted genome-editing tool. This tool will be crucial in urooncology researches in the near future.

Fehmi Narter, MD, PhD