New techniques improve specificity of CRISPR/Cas9 genome editing tools

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To overcome the off-target mutations that commonly occur with CRISPR/Cas9 genome editing methods, researchers at Harvard Medical School and Massachusetts General Hospital have developed two strategies that greatly improve the specificity of RNA-guided nucleases for the DNA region targeted to be cut and repaired. A description of these new techniques and their successful use to modify human cancer cells and embryonic stem cells is described in a special issue on genome editing in *Human Gene Therapy*.

In the special issue led by Guest Editor Feng Zhang, PhD, Broad Institute of MIT and Harvard, and McGovern Institute for Brain Research, MIT (Cambridge, MA), ?Nicolas Wyvekens, Ved Topkar, Cyd Khayter, J. Keith Joung, and Shengdar Tsai present their work in the article "Dimeric CRISPR RNA-Guided FokI-dCas9 Nucleases Directed by Truncated gRNAs for Highly Specific Genome Editing 9." They introduce two new strategies to reduce the off-target effects of current CRISPR genome editing methods: the use of truncated guide RNA molecules (gRNAs), creating shorter binding sites between the gRNAs and targeted DNA regions; and the addition of a FokI domain to the Cas9 protein, resulting in the formation of a nuclease dimer instead of monomer (the RNA-guided FokI-dCas9 Nuclease, or RFN).

More information: Wyvekens Nicolas, Topkar Ved V., Khayter Cyd, Joung J. Keith, and Tsai Shengdar Q.. Human Gene Therapy. July 2015, 26(7): 425-431. DOI: 10.1089/hum.2015.084.

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