Hitos y aplicaciones de la tecnología CRISPR-Cas

Aplicaciones de la Ingeniería Genética

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Máster en Genética y Evolución

(Especialidad Agroalimentaria)

IMPLICACIONES EN LA MEJORA ANIMAL Y VEGETAL

POPULAR MECHANICS

Science

China Used Gene-Editing To Make Hulked-Out Goats and Dogs. Where Does It End?

The latest advancements in CRISPR gene-editing tools have created livestock with more muscle mass and hair. What's next? And what is the limit?

BY JAY BENNETT PUBLISHED: NOV 18, 2015 9:00 AM EST

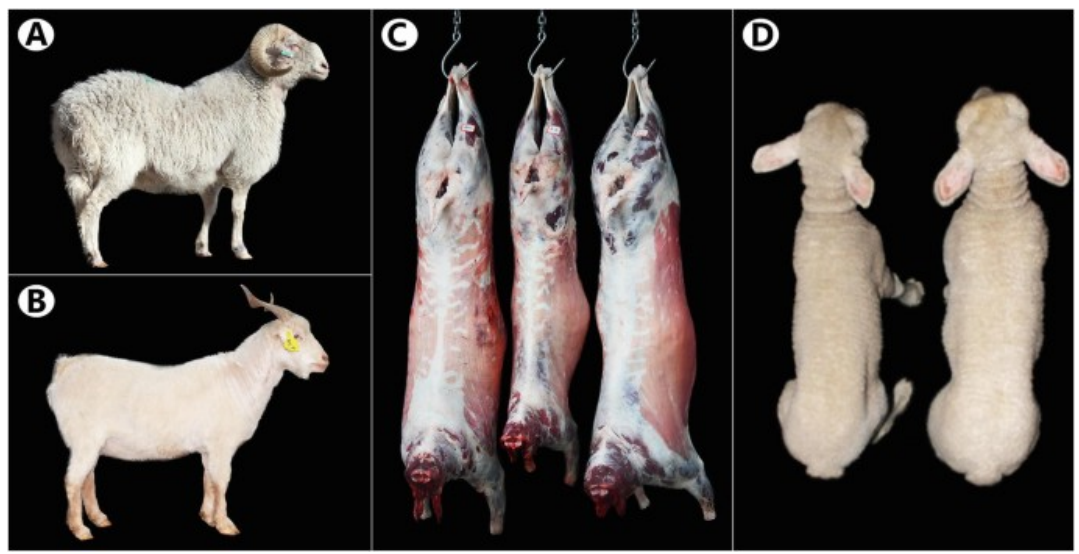
Christina Larson's **article for*Scientific American*** describes how the Shaanxi Provincial Engineering and Technology Research Center has used the gene-editing tool CRISPR to manufacture a new type of goat—one that has larger muscles, produces more meat, and grows longer hair that can be sheared into wool.

Generation of Double-Muscled Sheep and Goats by CRISPR /Cas9-Mediated Knockout of the Myostatin Gene

Protocol | First Online: 14 June 2022

pp 295–323 | Cite this protocol

The *myostatin* (*MSTN*) gene has shown to play a critical role in the regulation of skeletal muscle mass, and the translational inhibition of this gene has shown increased muscle mass, generating what is known as "double-muscling phenotype." Disruption of the *MSTN* gene expression using the CRISPR/Cas9 genome-editing system has shown improved muscle development and growth rates in livestock species, including sheep and goats.



EL PAÍS

GENÉTICA >

Un equipo de genetistas descubre la tecla para aumentar el sabor de los tomates sin reducir su tamaño

Los investigadores han logrado incrementar un 30% el nivel de azúcares del fruto, un sueño perseguido por otros científicos desde hace décadas

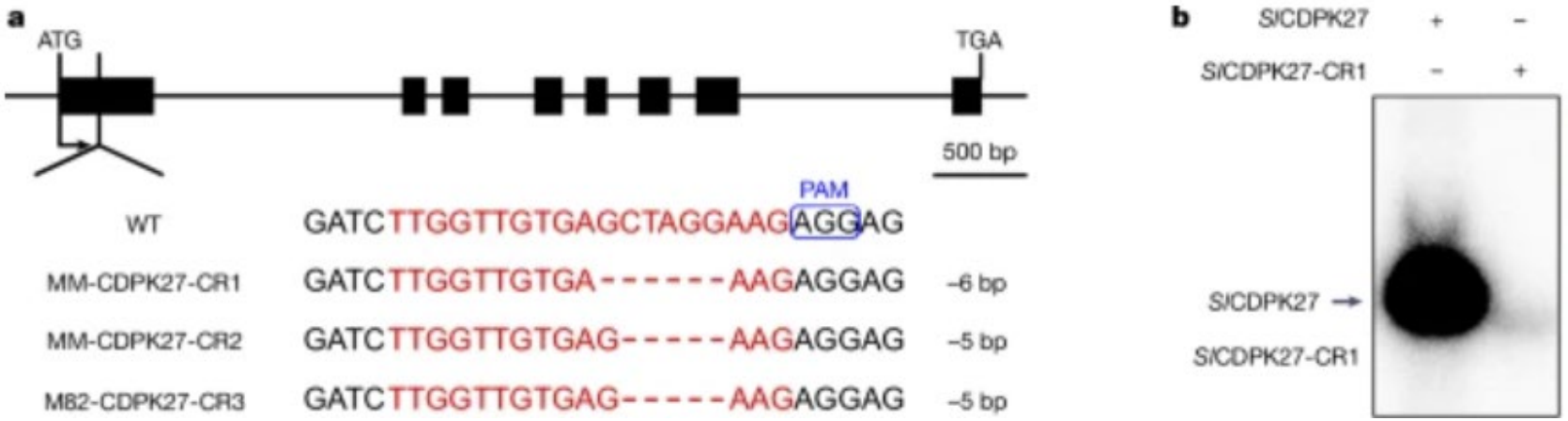
Este miércoles, el equipo de Jinzhe Zhang anuncia que ha empleado las tijeras CRISPR para inactivar dos genes, Sl*CDPK27* y Sl*CDPK26*, que actúan como frenos en la producción de azúcares durante la maduración del fruto, probablemente para asegurar un suministro adecuado de energía para el desarrollo posterior de las semillas. El resultado es un aumento del 30% en los niveles de fructosa y glucosa, sin reducir ni el tamaño ni la cosecha. Su estudio se publica en la revista *Nature*.

Releasing a sugar brake generates sweeter tomato without yield penalty

Jinzhe Zhang, Hongjun Lyu, Jie Chen, Xue Cao, Ran Du, Liang Ma, Nan Wang, Zhiguo Zhu, Jianglei Rao, Jie Wang, Kui Zhong, Yaqing Lyu, Yanling Wang, Tao Lin, Yao Zhou, Yongfeng Zhou, Guangtao Zhu, Zhangjun Fei, Harry Klee & Sanwen Huang

Nature **635**, 647–656 (2024) | Cite this article

Sl*CDPK27* regulates tomato fruit sugar content.



IMPLICACIONES EN LA SALUD HUMANA

POPULAR MECHANICS

Science

Gene-Editing Creates Malaria-Resistant Mosquitoes

If we can use the same CRISPR technique on other species and flood the population, we might be able to eliminate the infection entirely.

BY JAY BENNETT PUBLISHED: NOV 24, 2015 3:59 PM EST

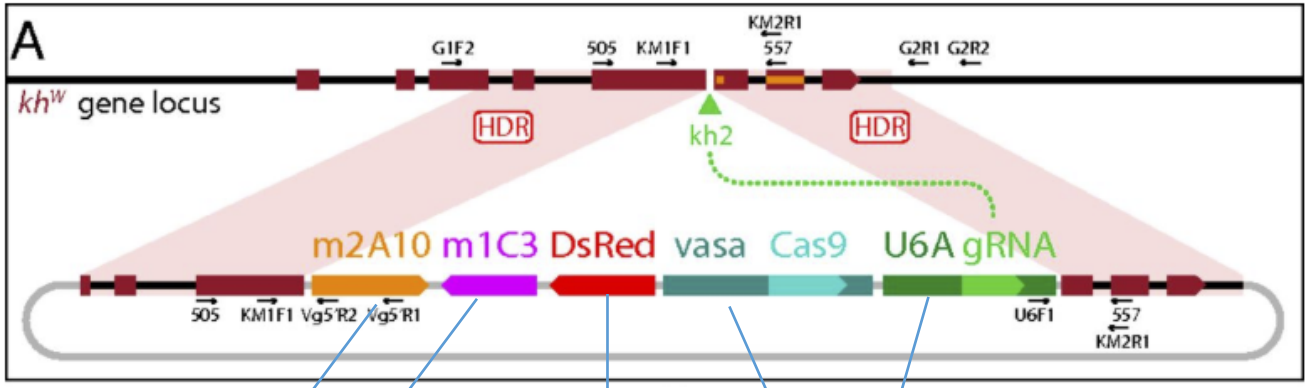
RESEARCH ARTICLE | APPLIED BIOLOGICAL SCIENCES |

Highly efficient Cas9-mediated gene drive for population modification of the malaria vector mosquito *Anopheles stephensi*

Valentino M. Gantz, Nijole Jasinskiene, Olga Tatarenkova, +3, and Anthony A. James Authors Info & Affiliations

Contributed by Anthony A. James, October 26, 2015 (sent for review October 11, 2015; reviewed by Malcolm Fraser and Marcelo Jacobs-Lorena)

November 23, 2015 | 112 (49) E6736-E6743 | https://doi.org/10.1073/pnas.1521077112



Cassette de genes que confieren resistencia a *P. falciparum*

Proteína fluorescente

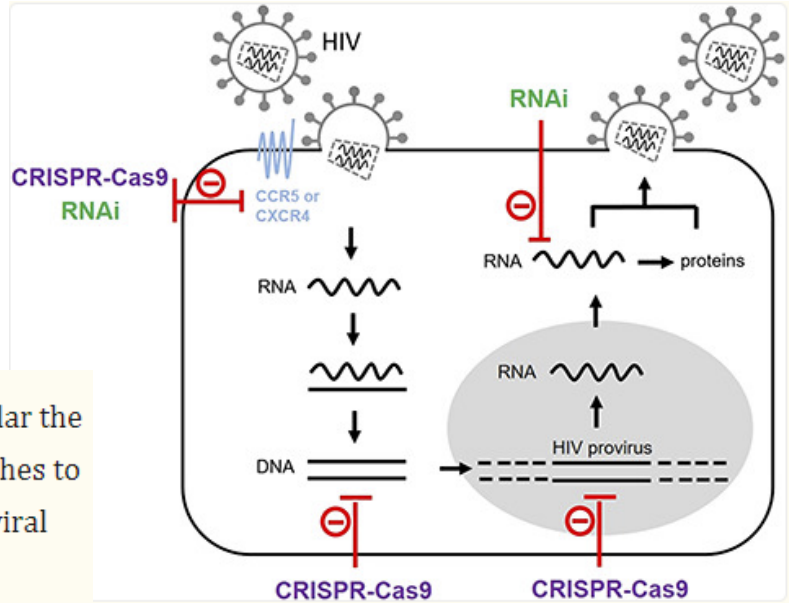
Promotores

UMass Chan MEDICAL SCHOOL News

Editing HIV out of our genome with CRISPR

UMass Chan scientists seek ways to use powerful gene editing tool to excise latent HIV virus

By Jim Fessenden and Bryan Goodchild | April 13, 2015



HIV targeting by RNAi or CRISPR-Cas9. HIV infects cells of the immune system, in particular the CD4-positive T cells. The HIV particle contains two genomic RNA copies. The virion attaches to the membrane of target T cells by binding to the CD4 and CCR5/CXCR4 receptors. Upon viral entry, the viral RNA genome is converted into double-stranded DNA (dsDNA) by the HIV reverse transcriptase. The resulting DNA is actively transported into the nucleus and integrated in the host cell genome. This integrated DNA or provirus uses the host cell transcription machinery to produce new viral RNAs, which serve as mRNA for protein production or as genomic RNAs that are packaged into new viral particles, which are released from the cell by budding. RNAi can target the RNA transcripts that encode the HIV receptors to block viral entry. In addition, RNAi can target the viral RNA produced during HIV replication. The receptor-encoding genes can be targeted by CRISPR-Cas9, which can also target the HIV dsDNA that is formed upon reverse transcription of the viral RNA and the integrated proviral DNA.

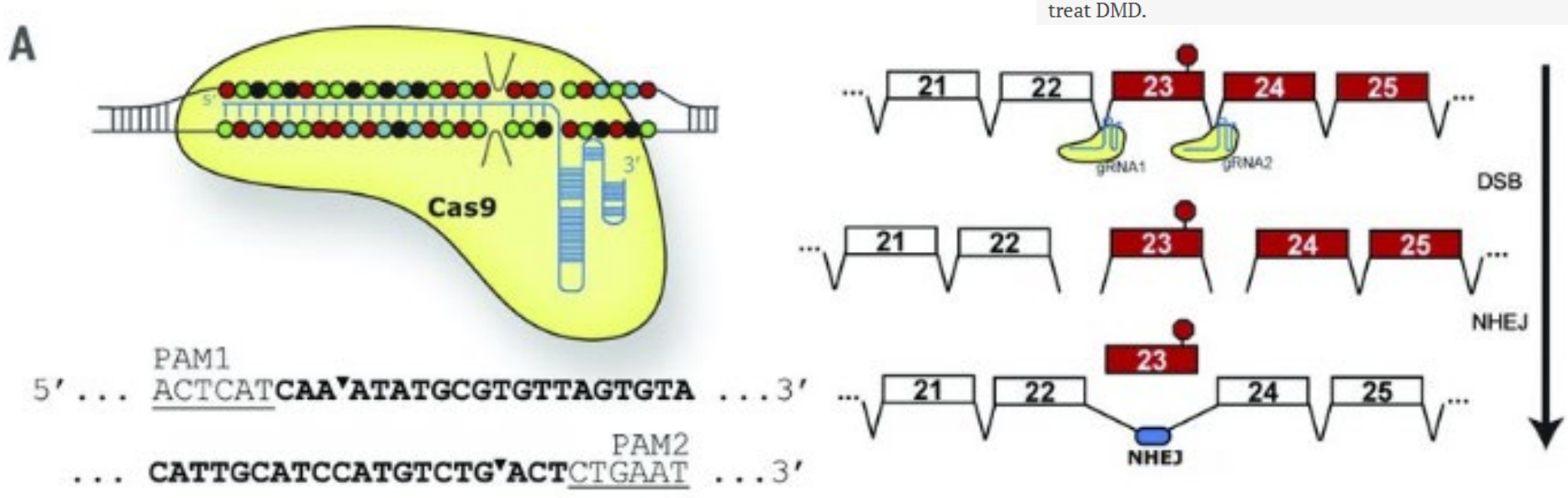
Science

In vivo genome editing improves muscle function in a mouse model of Duchenne muscular dystrophy

CHRISTOPHER E. NELSON, CHADY H. HAKIM, DAVID G. OUSTEROUT, PRATIKSHA I. THAKORE, EIRIK A. MOREB, RUTH M. CASTELLANOS RIVERA, SARINA MADHAVAN, XIUFANG PAN, F. ANN RAN, [...], AND CHARLES A. GERSBACH +4 authors Authors Info & Affiliations

SCIENCE • 31 Dec 2015 • Vol 351, Issue 6271 • pp. 403-407 • DOI: 10.1126/science.aad5143

Duchenne muscular dystrophy (DMD) is a devastating disease affecting about 1 out of 5000 male births and caused by mutations in the dystrophin gene. Genome editing has the potential to restore expression of a modified dystrophin gene from the native locus to modulate disease progression. In this study, adeno-associated virus was used to deliver the clustered regularly interspaced short palindromic repeats (CRISPR)–Cas9 system to the *mdx* mouse model of DMD to remove the mutated exon 23 from the dystrophin gene. This includes local and systemic delivery to adult mice and systemic delivery to neonatal mice. Exon 23 deletion by CRISPR-Cas9 resulted in expression of the modified dystrophin gene, partial recovery of functional dystrophin protein in skeletal myofibers and cardiac muscle, improvement of muscle biochemistry, and significant enhancement of muscle force. This work establishes CRISPR-Cas9–based genome editing as a potential therapy to treat DMD.



(**A**) The Cas9 nuclease is targeted to introns 22 and 23 by two gRNAs. Simultaneous generation of double-stranded breaks (DSBs) by Cas9 leads to excision of the region surrounding the mutated exon 23. The distal ends are repaired through nonhomologous end joining (NHEJ). The reading frame of the dystrophin gene is recovered and protein expression is restored.

POPULAR MECHANICS

New Technology

Chinese Scientist Discusses Human Cloning, Lays Out Plans for Massive Cloning Factory

The largest cloning factory in the world will break ground in China in 2016, and the man behind it is not shy about discussing the future of cloning humans.

BY JAY BENNETT PUBLISHED: DEC 01, 2015 3:07 PM EST

EL PAÍS

CÓDIGO ABIERTO > | COLUMNA

El regreso de la eugenesia

Mejorar genéticamente a una persona sana evoca unos escenarios de ciencia ficción que pocos expertos están dispuestos a asumir por ahora

Una investigadora lleva a cabo pruebas genéticas animales en el laboratorio del Servicio Regional de Investigación y Desarrollo Agroalimentario de Asturias, en Gijón.
ÁLVARO FUENTE

JAVIER SAMPEDRO
11 ENE 2025 - 05:00 CET

La comunidad científica manda un contundente mensaje al creador de los humanos modificados genéticamente

Se trata de una de las mayores irresponsabilidades del siglo XXI.

HUFFPOST

Por Redacción HuffPost

Publicado el 09/09/2024 a las 11:20

OTRAS FUNCIONES DE CRISPR

Regulación de la expresión génica

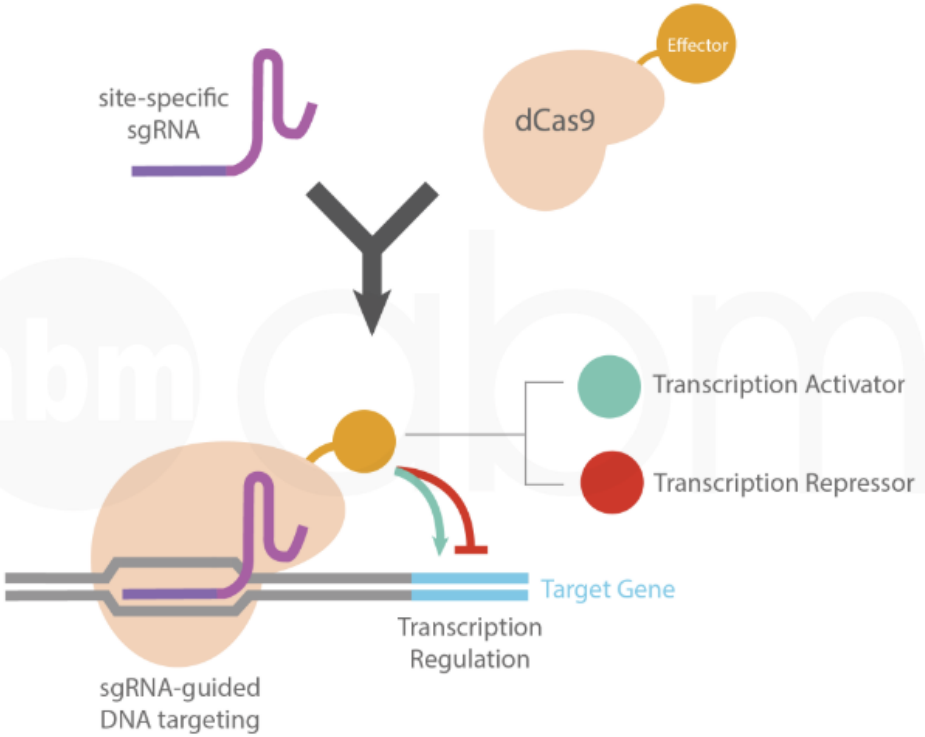


Figure 1 – dCas9 as a modular system for attachment of transcriptional regulators. dCas9 can easily be fused to effectors (either transcription activators or repressors) for targeted gene regulation. Adapted from Figure 1a of Gilbert et al. (2013).

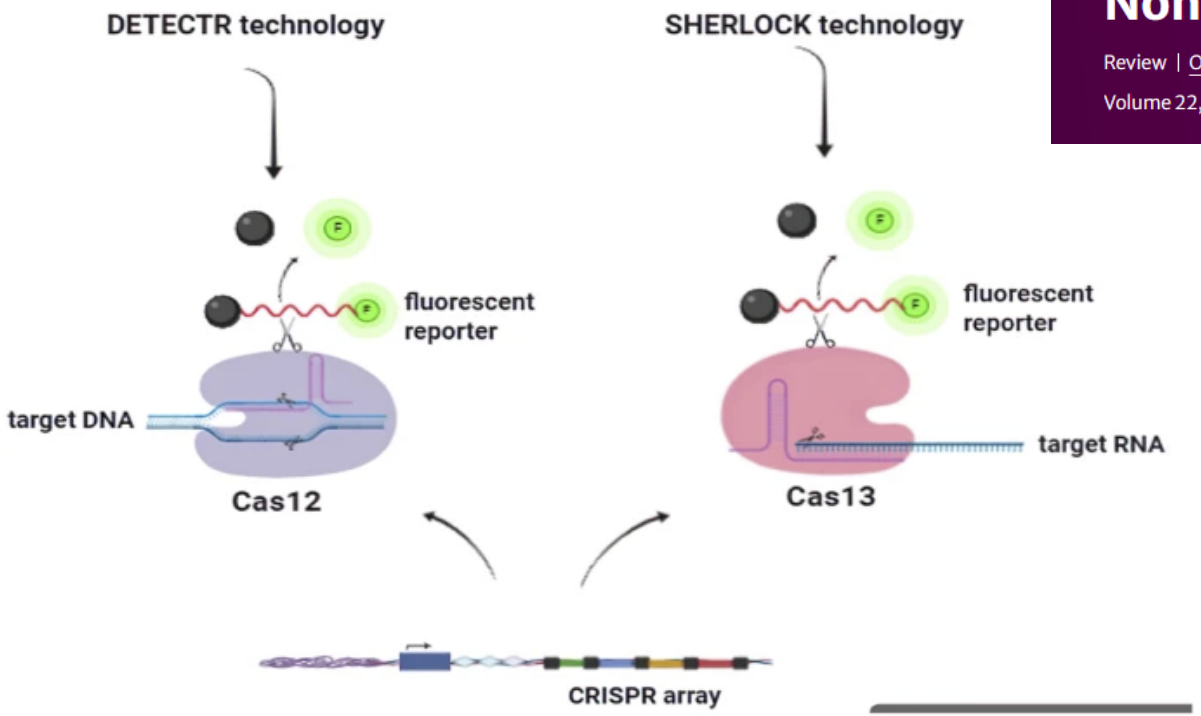
Sistema de detección molecular

Home > Biological Procedures Online > Article

CRISPR-Based Diagnosis of Infectious and Noninfectious Diseases

Review | Open access | Published: 14 September 2020

Volume 22, article number 22, (2020) Cite this article



Cas12 and Cas13 Cleavage Activity. In the DETECTR technology, after binding the Cas12-crRNA complex to its target (dsDNA) the collateral nuclease activity of the Cas12 leads to cleavage of the reporter molecule nonspecifically after which the fluorescent signal is detectable. In the SHERLOCK technology, Cas13a guided by the single CRISPR RNA (crRNA) to cleave ssRNA or mRNA and the same process occurs

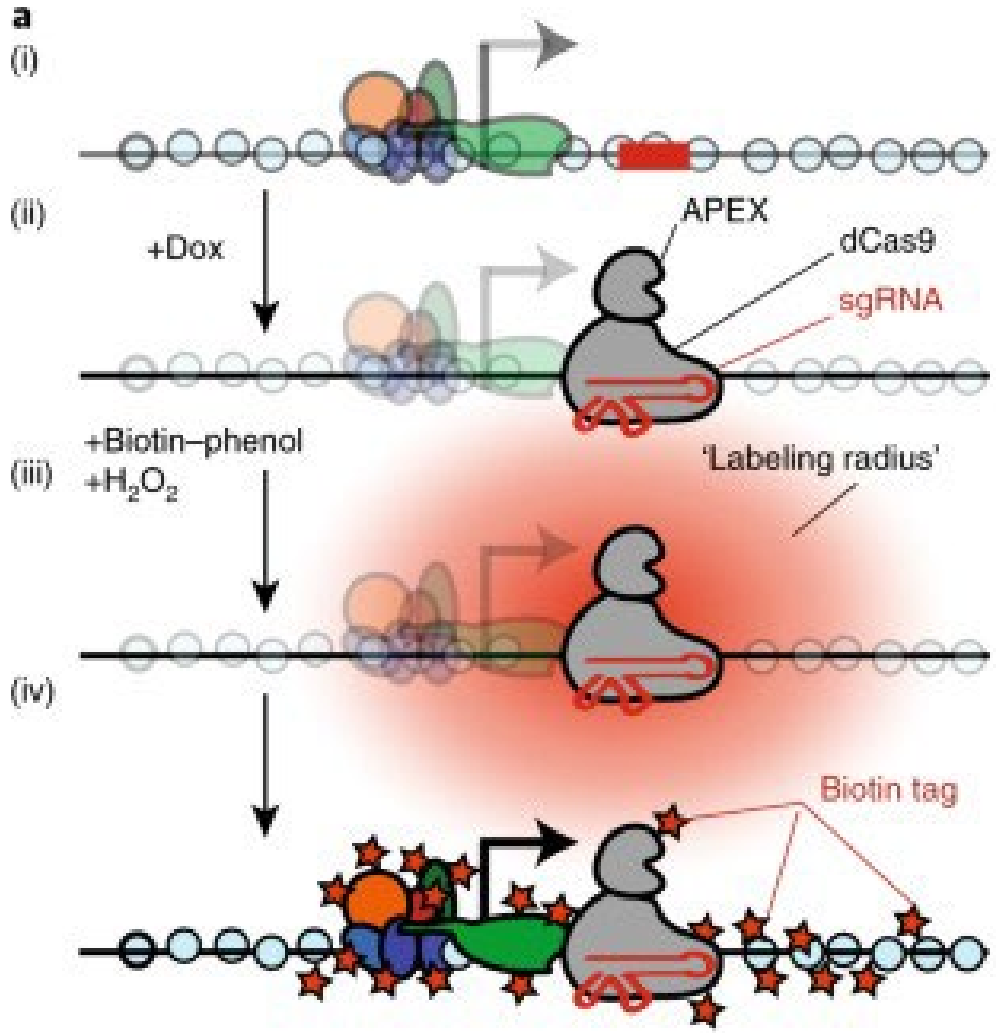
Estudio de la interacción ADN-proteína

Brief Communication | Published: 07 May 2018

Discovery of proteins associated with a predefined genomic locus via dCas9–APEX-mediated proximity labeling

Samuel A. Myers, Jason Wright, Ryan Peckner, Brian T. Kalish, Feng Zhang & Steven A. Carr

Nature Methods **15**, 437–439 (2018) | Cite this article



APEX2 es una peroxidasa modificada genéticamente que cataliza la adición de biotina (**biotinilación**) de moléculas cercanas en presencia de **peróxido de hidrógeno** y un precursor de biotina.

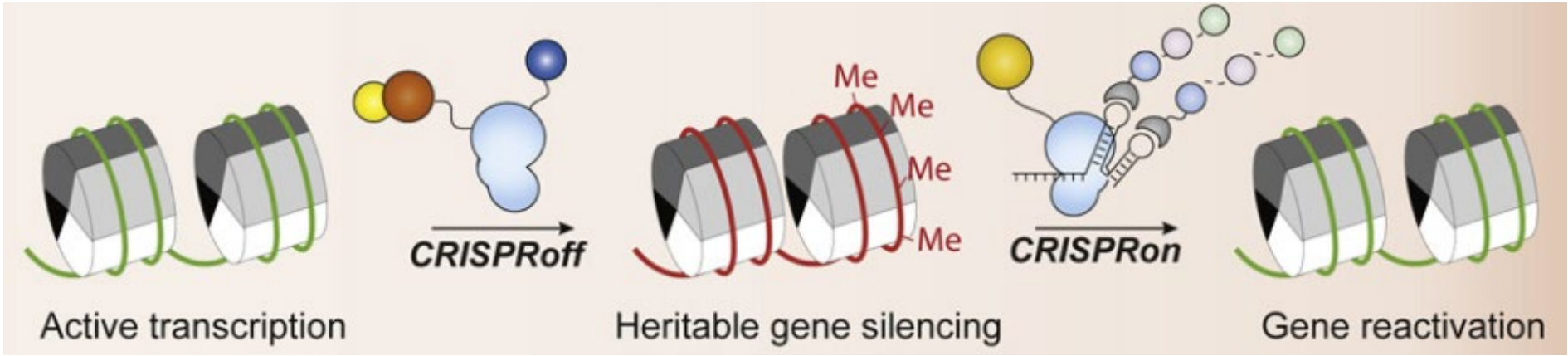
Modificación epigenética

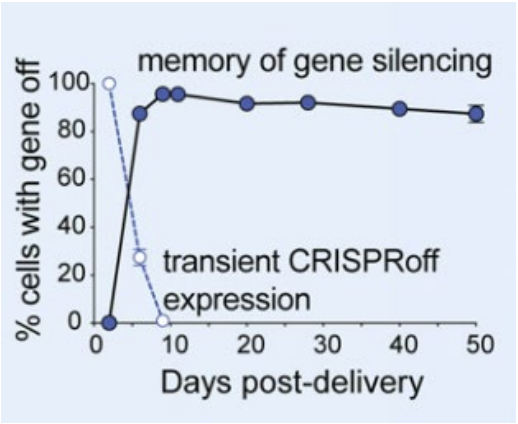
RESOURCE · Volume 184, Issue 9, P2503-2519.E17, April 29, 2021 · *Open Archive* Download Full Issue

Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing

James K. Nuñez [1,2] · Jin Chen [1,2,18] · Greg C. Pommier [3,4] … · Volker Hovestadt [9,16,17] · Luke A. Gilbert [1,3,4] · Jonathan S. Weissman [1,2,7,19] … Show more

Affiliations & Notes · Article Info





A general approach for heritably altering gene expression has the potential to enable many discovery and therapeutic efforts. Here, we present CRISPRoff—a programmable epigenetic memory writer consisting of a single dead Cas9 fusion protein that establishes DNA methylation and repressive histone modifications. Transient CRISPRoff expression initiates highly specific DNA methylation and gene repression that is maintained through cell division and differentiation of stem cells to neurons. Pairing CRISPRoff with genome-wide screens and analysis of chromatin marks establishes rules for heritable gene silencing. We identify single guide RNAs (sgRNAs) capable of silencing the large majority of genes including those lacking canonical CpG islands (CGIs) and reveal a wide targeting window extending beyond annotated CGIs. The broad ability of CRISPRoff to initiate heritable gene silencing even outside of CGIs expands the canonical model of methylation-based silencing and enables diverse applications including genome-wide screens, multiplexed cell engineering, enhancer silencing, and mechanistic exploration of epigenetic inheritance.