

PLAN BREEDING INNOVATION

Técnica / Conocimiento, Acceso y Ambiente Regulatorio

Dr. Miguel Rapela

Cartagena, 6 de septiembre 2017

Correction of a pathogenic gene mutation in human embryos

Hong Ma^{1,*}, Nuria Martí-Gutiérrez^{1,*}, Sang-Wook Park^{2,*}, Jun Wu^{3,*}, Yeonmi Lee¹, Keiichiro Suzuki³, Amy Tomonari Hayama¹, Riffat Ahmed¹, Hayley Darby¹, Crystal Van Dyken¹, Ying Li¹, Eunju Kang¹, A.-Reum F Sang-Tae Kim², Jianhui Gong^{5,6,7,8}, Ying Gu^{5,6,7}, Xun Xu^{5,6,7}, David Battaglia^{1,9}, Sacha A. Krieg⁹, David M. Don P. Wolf¹, Stephen B. Heitner¹⁰, Juan Carlos Izpisua Belmonte^{2,§}, Paula Amato^{1,9,§}, Jin-Soo Kim^{2,4,§}, Sanj Shoukhrat Mitalipov^{1,§}

Genome editing has potential for the targeted correction of germline mutations. Here we describe the heterozygous MYBPC3 mutation in human preimplantation embryos with precise CRISPR-C accuracy and high homology-directed repair efficiency by activating an endogenous, germline-response. Induced double-strand breaks (DSBs) at the mutant paternal allele were predominant homologous wild-type maternal gene instead of a synthetic DNA template. By modulating the cell the DSB was induced, we were able to avoid mosaicism in cleaving embryos and achieve a high y embryos carrying the wild-type MYBPC3 gene without evidence of off-target mutations. The efficacy of the approach presented suggest that it has potential to be used for the correction of heritable embryos by complementing preimplantation genetic diagnosis. However, much remains to be considered applications, including the reproducibility of the technique with other heterozygous mutations.

More than 10,000 monogenic inherited disorders have been identified, affecting millions of people worldwide. Among these are autosomal dominant mutations, where inheritance of a single copy of a defective gene can result in clinical symptoms. Genes in which dominant mutations manifest as late-onset adult disorders include BRCA1 and BRCA2, which are associated with a high risk of breast and ovarian cancers¹, and MYBPC3, mutation of which causes hypertrophic cardiomyopathy (HCM)². Because of their delayed manifestation, these mutations escape natural selection and are often transmitted to the next generation. Consequently, the frequency of some of these founder mutations in particular human populations is very high. For example, the MYBPC3 mutation is found at frequencies ranging from 2% to 8%³ in major Indian populations, and the estimated frequency of both BRCA1 and BRCA2 mutations among Ashkenazi Jews exceeds 2%⁴.

HCM is a myocardial disease characterized by left ventricular hypertrophy, myofibrillar disarray and myocardial stiffness; it has an estimated prevalence of 1:500 in adults⁵ and manifests clinically with heart failure. HCM is the commonest cause of sudden death in otherwise healthy young athletes. HCM, while not a uniformly fatal condition, has a tremendous impact on the lives of individuals, including physiological (heart failure and arrhythmias), psychological (limited activity and fear of sudden death), and genealogical concerns. MYBPC3 mutations account for approximately 40% of all genetic defects causing HCM and are also responsible for a large fraction of other inherited cardiomyopathies, including dilated cardiomyopathy and left ventricular non-compaction⁶. MYBPC3 encodes the thick filament-associated cardiac myosin-binding protein C (cMyBP-C), a signalling node in cardiac

myocytes that contributes to the maintenance and regulation of both contraction and relaxation.

Current treatment options for HCM provide relief without addressing the genetic cause. Development of novel strategies to prevent founder mutations is desirable. One second-generation transmission is preimplantation genetic diagnosis (PGD) followed by selection of non-mutant embryos in the context of an *in vitro* fertilization (IVF) cycle. PGD carries a heterozygous mutation, 50% of the embryos are free and available for transfer, while the remainder are discarded. Gene correction would rescue the number of embryos available for transfer and pregnancy rates.

Recent developments in precise genome editing have found successful applications in animal models for correcting human germline mutations. In particular, a versatile tool for recognizing specific genomic DSBs⁷⁻¹⁰. DSBs are then resolved by endogenous mechanisms, preferentially using a non-homologous pathway. Obviously, NHEJ is inappropriate for germline editing because it introduces additional mutations or deletions at the DSB site, commonly referred to as indels. In some cases, however, targeted cells activate an alternative DNA repair pathway called homology-directed repair (HDR) that rebuilds the DSB site using the non-mutant homologous chromosome or a supplied exogenous DNA molecule as a template, leading to correction of the

27/07/2017 - 15:09 | Clarín.com | Sociedad

Ciencia

Investigadores en EE.UU. logran modificar genéticamente embriones humanos

Hasta ahora sólo lo habían hecho científicos chinos. El avance supone un paso fundamental para tratar enfermedades congénitas.



¹Center for Embryonic Cell and Gene Therapy, Oregon Health & Science University, 3303 Southwest, Bond Avenue, Portland, Oregon 97239, USA. ²Center for Genome Engineering, Institute for Basic Science, 70, Yusong-daero 1689-gil, Yusong-gu, Daejeon, 34047, Republic of Korea. ³Gene Expression Laboratory, Salk Institute for Biological Studies, 10010 North Torrey Pines Road, La Jolla, California 92037, USA. ⁴Department of Chemistry, Seoul National University, 599 Gwanak-ro, Gwanak-gu, Seoul, 151-747, Republic of Korea. ⁵BGI-Shenzhen, Build 11, Beishan Industrial Zone, Yantian District, Shenzhen, 518083, China. ⁶China National GeneBank, BGI-Shenzhen, Jinhua Road, Dapeng District, Shenzhen, 518210, China. ⁷BGI-Qingdao, 2877 Tianshan Road, Sinc-German Expat, Qingdao, 266000, China. ⁸Shenzhen Engineering Laboratory for Innovative Molecular Diagnostics, BGI-Shenzhen, Build 11, Beishan Industrial Zone, Yantian District, Shenzhen, 518083, China. ⁹Division of Reproductive Endocrinology and Infertility, Department of Obstetrics and Gynecology, Oregon Health & Science University, 3303 Southwest, Bond Avenue, Portland, Oregon 97239, USA. ¹⁰Night Cancer Institute, Oregon Health & Science University, 3181 Southwest, Sam Jackson Park Road, Portland, Oregon 97239, USA.

El salto del laboratorio a los medios



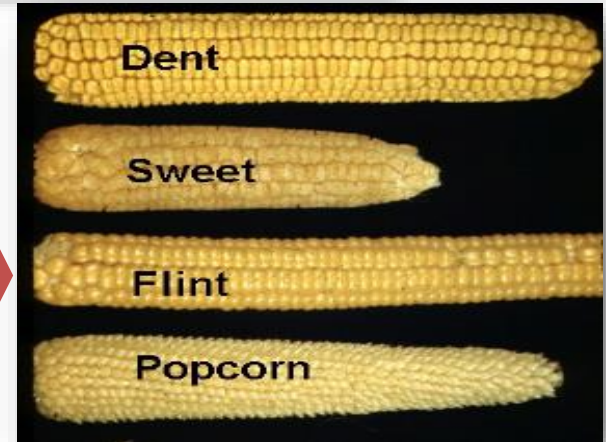
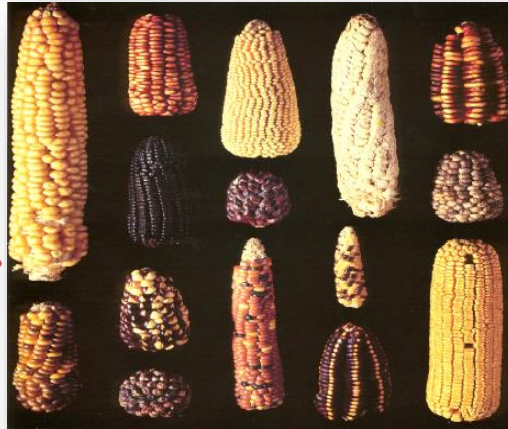
PBI: factores claves en el mejoramiento vegetal

1. Técnica / Conocimiento
2. Acceso
3. Ambiente Regulatorio

PBI: factores claves en el mejoramiento vegetal

1. Técnica / Conocimiento
2. Acceso
3. Ambiente Regulatorio

El contexto del mejoramiento vegetal



El contexto del mejoramiento vegetal



Brócoli



Coliflor



Collard Greens



Brassica oleraceae

selección

artificial



Repollito de
Bruselas



Colirrábano



Repollo



Col Berza



Brassica oleracea

<http://lsyl.la.asu.edu/plb598/kpigg/Brassica.htm>
http://www.fishing-in-wales.com/_pics/plantpic/seaspics/wildcabb.jpg

El contexto del mejoramiento vegetal

Mejoramiento por mutagénesis inducida (al azar)

Crisantemo:
rayos gamma



Pomelo Rosado: *neutrones*



Lino: *etilmetanosulfonato (EMS)*



Incorporación de tecnologías al mejoramiento vegetal

**¿Proceso continuo y
aditivo?**

- 
- Domesticación
 - Selección de los mejores ejemplares
 - Cruza entre individuos
 - Introgresión de genes de otras especies
 - Mejoramiento de líneas
 - Híbridos
 - Mutagénesis inducida (al azar)
 - Marcadores moleculares
 - Transgénesis
 - Silenciamiento de genes (RNAi)
 - “Ómicas”
 - Técnicas de edición génica/genómica
 - Biología sintética
 - ¿?

Incorporación de tecnologías al mejoramiento vegetal

¿Proceso disruptivo?



- Domesticación
- Selección de los mejores ejemplares
- Cruza entre individuos
- Introgresión de genes de otras especies
- Mejoramiento de líneas



- Híbridos
- Mutagénesis inducida (al azar)
- Marcadores moleculares



- Transgénesis
- Silenciamiento de genes (RNAi)
- “Ómicas”

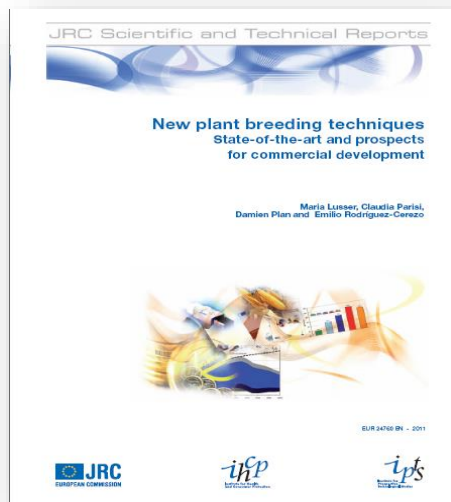


- Técnicas de edición génica/genómica
- Biología sintética
- ¿?

¿Qué son las New Breeding Techniques (NBT)?

2007 - Creación del Grupo de Trabajo sobre NBTs de la CE

2011 – informe del Joint Research Center + Reunión en Sevilla



- Zinc finger nuclease technology (ZFN-1, 2, 3)
- Oligonucleotide directed mutagenesis (ODM)
- Cisgenesis and intragenesis
- RNA-dependent DNA methylation (RdDM)
- Grafting (on GM rootstock)
- Reverse breeding
- Agro-infiltration, agro-inoculation, floral dip
- Synthetic genomics/biology

Agrupación “forzada” de las técnicas

Algunas técnicas no son nuevas

Algunas técnicas con definición incierta

Algunas técnicas de dudosa aplicación

Plant Breeding Innovation

- EDICIÓN GÉNICA
 - CRISPR-Cas

EL DESCUBRIMIENTO

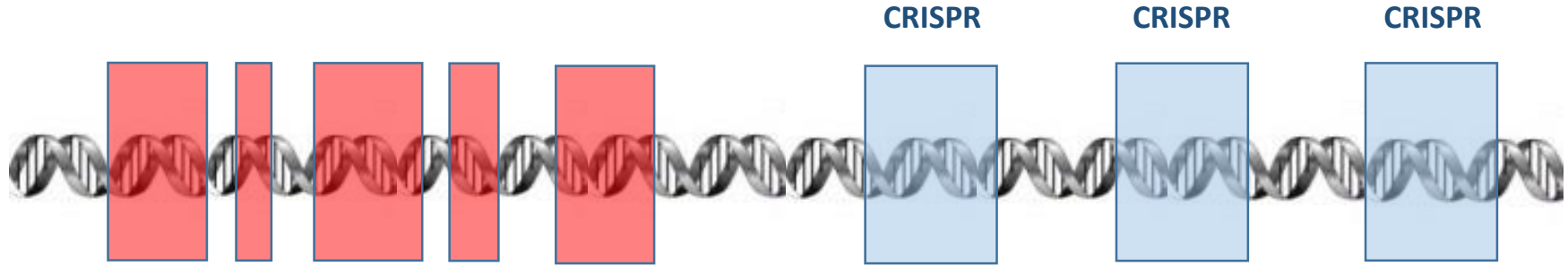


El descubrimiento



Dr. Francisco MOJICA

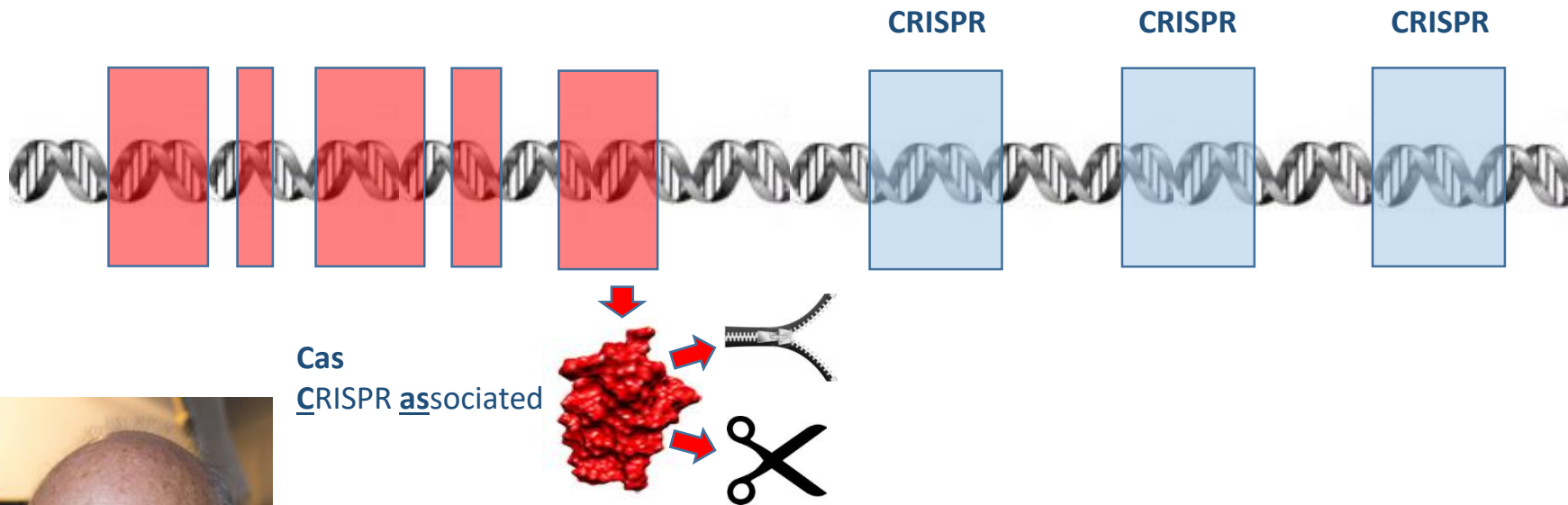
El descubrimiento



C (Clustered / Agrupadas)
R (Regularly / Regularmente)
I (Interspaced / Interespaciadas)
S (Short / Cortas)
P (Palindromic / Palindrómicas)
R (Repeats / Repeticiones)

Dr. Francisco MOJICA

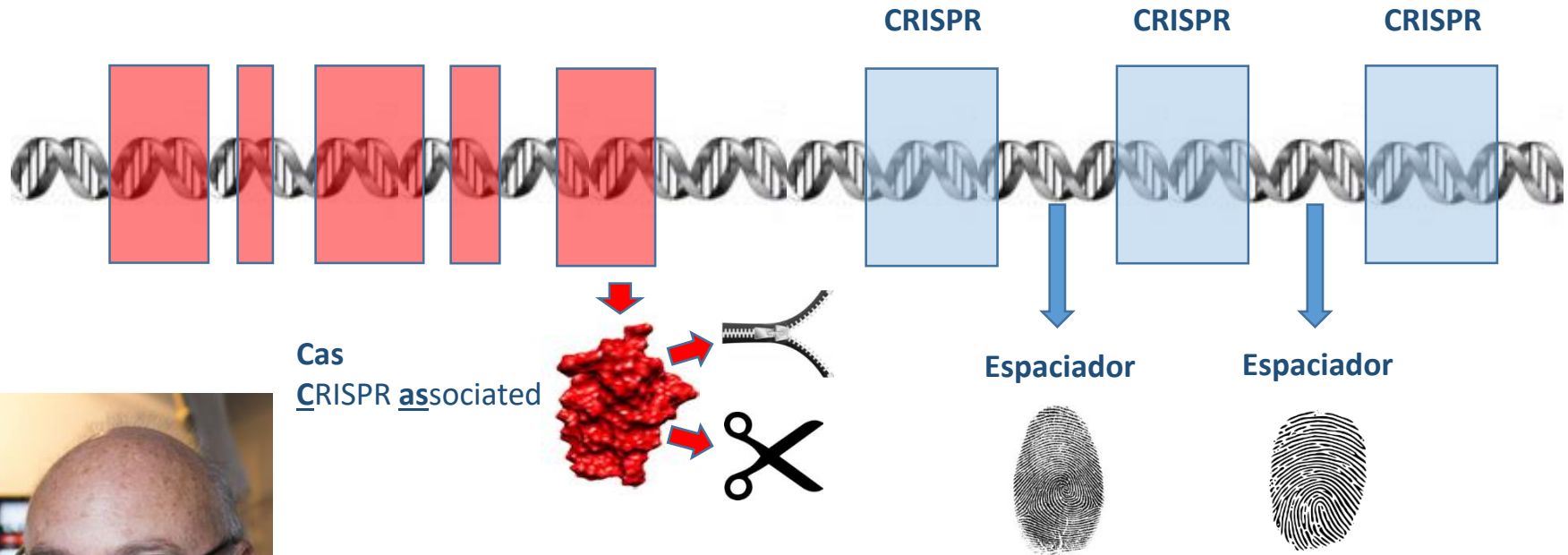
El descubrimiento



Cas
CRISPR associated

Dr. Francisco MOJICA

El descubrimiento



Cas
CRISPR associated

CRISPR

CRISPR

CRISPR

Espaciador

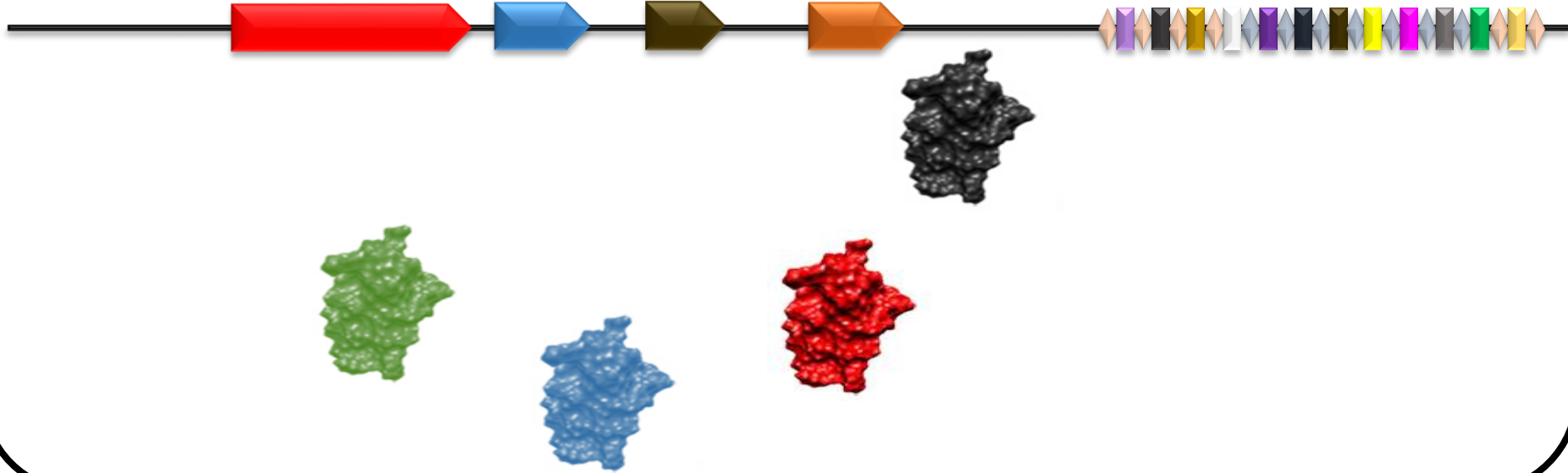
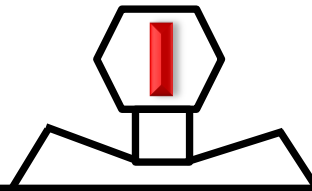
Espaciador

BACTERIAS + ARQUEAS

Sistema Inmuno-adaptativo defensivo

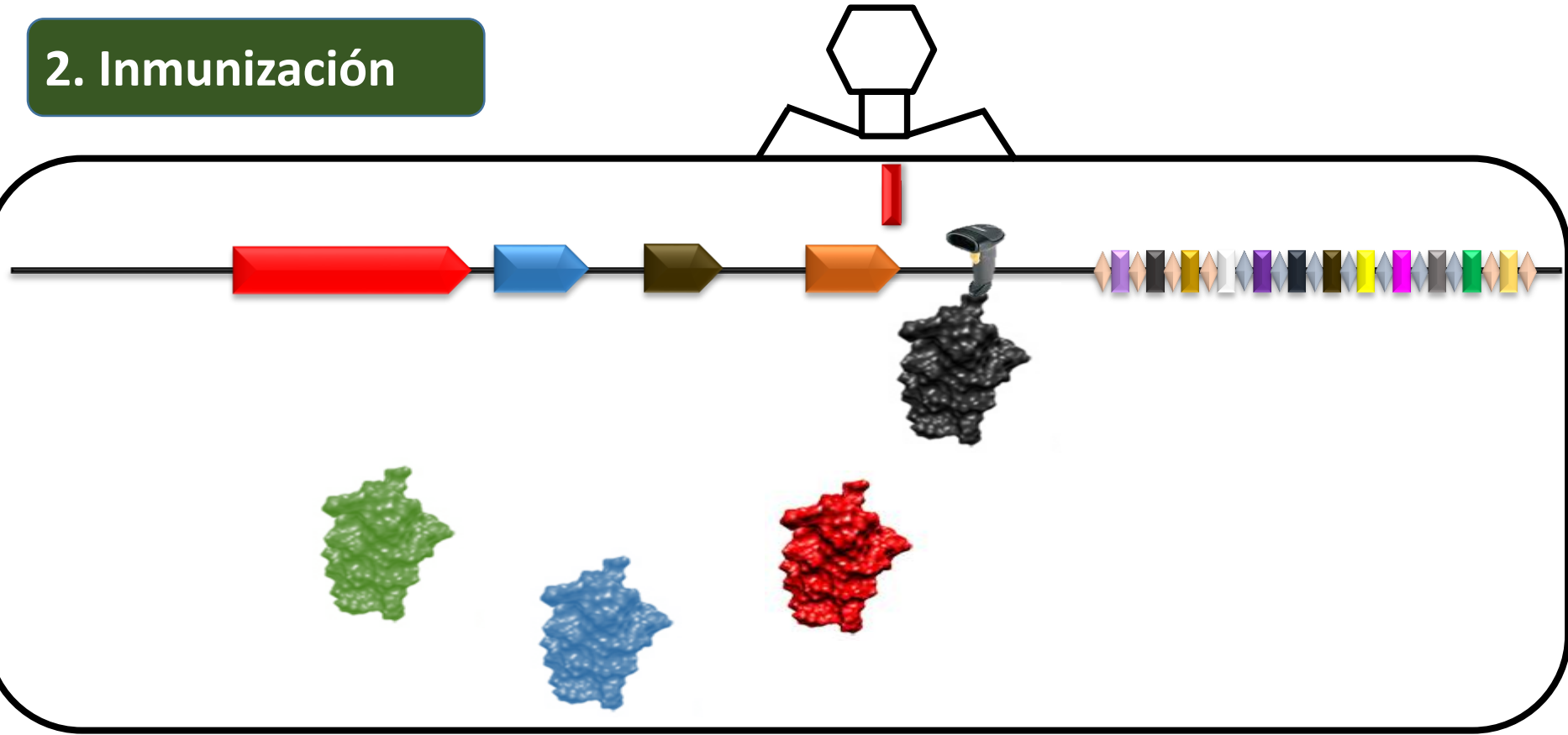
Dr. Francisco MOJICA

1. Infección



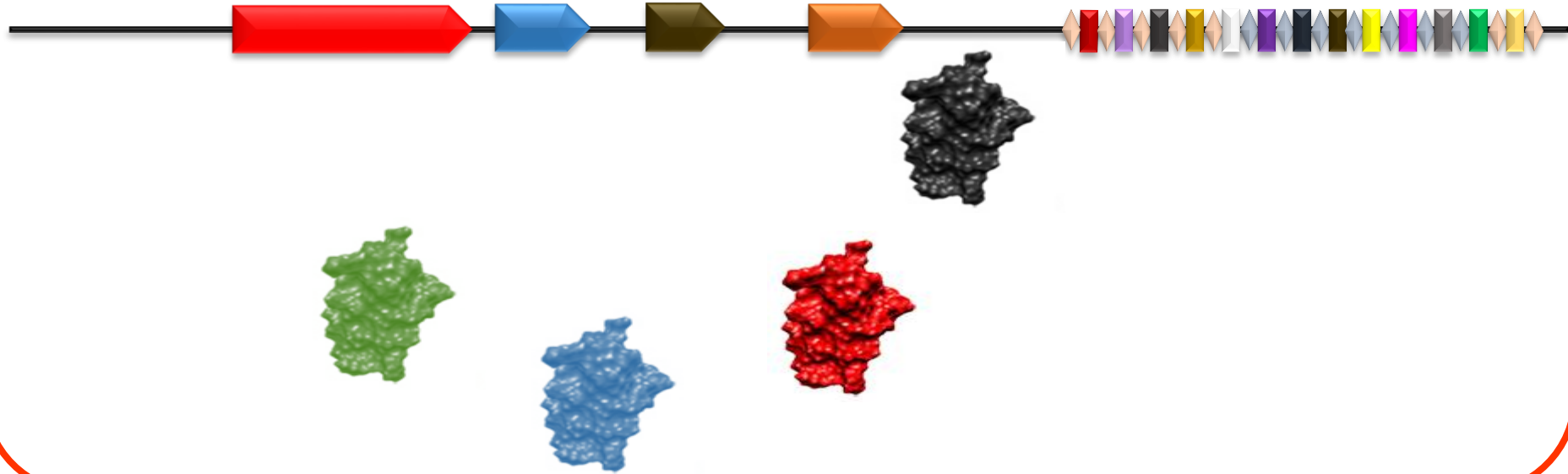
Animación: F. Mojica, con autorización

2. Inmunización



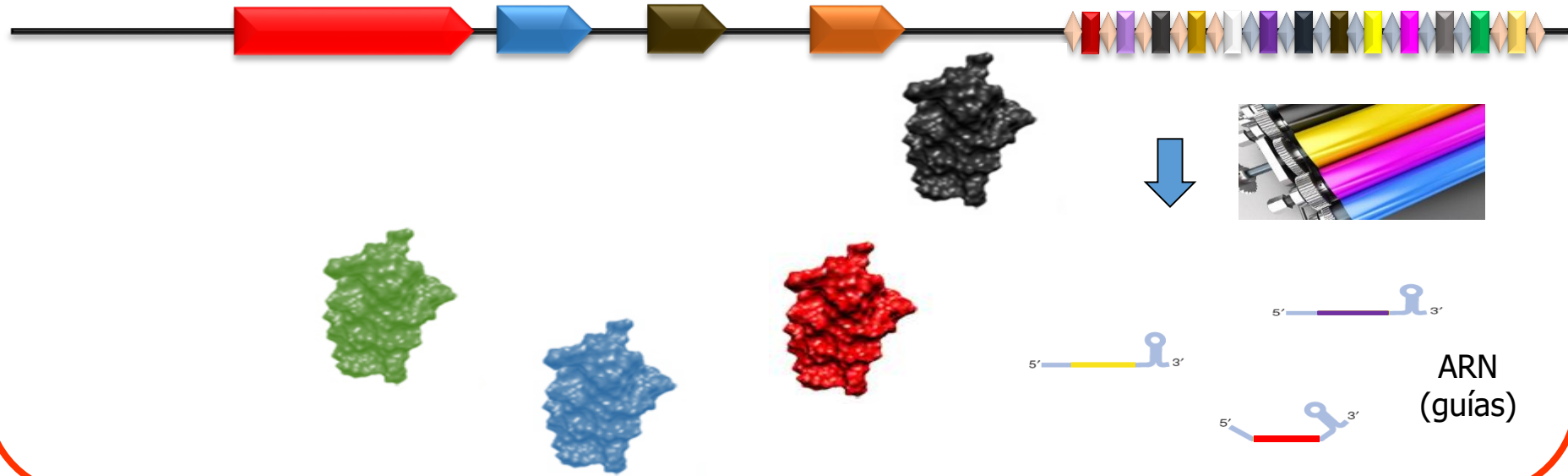
Animación: F. Mojica, con autorización

3. Bacteria inmunizada



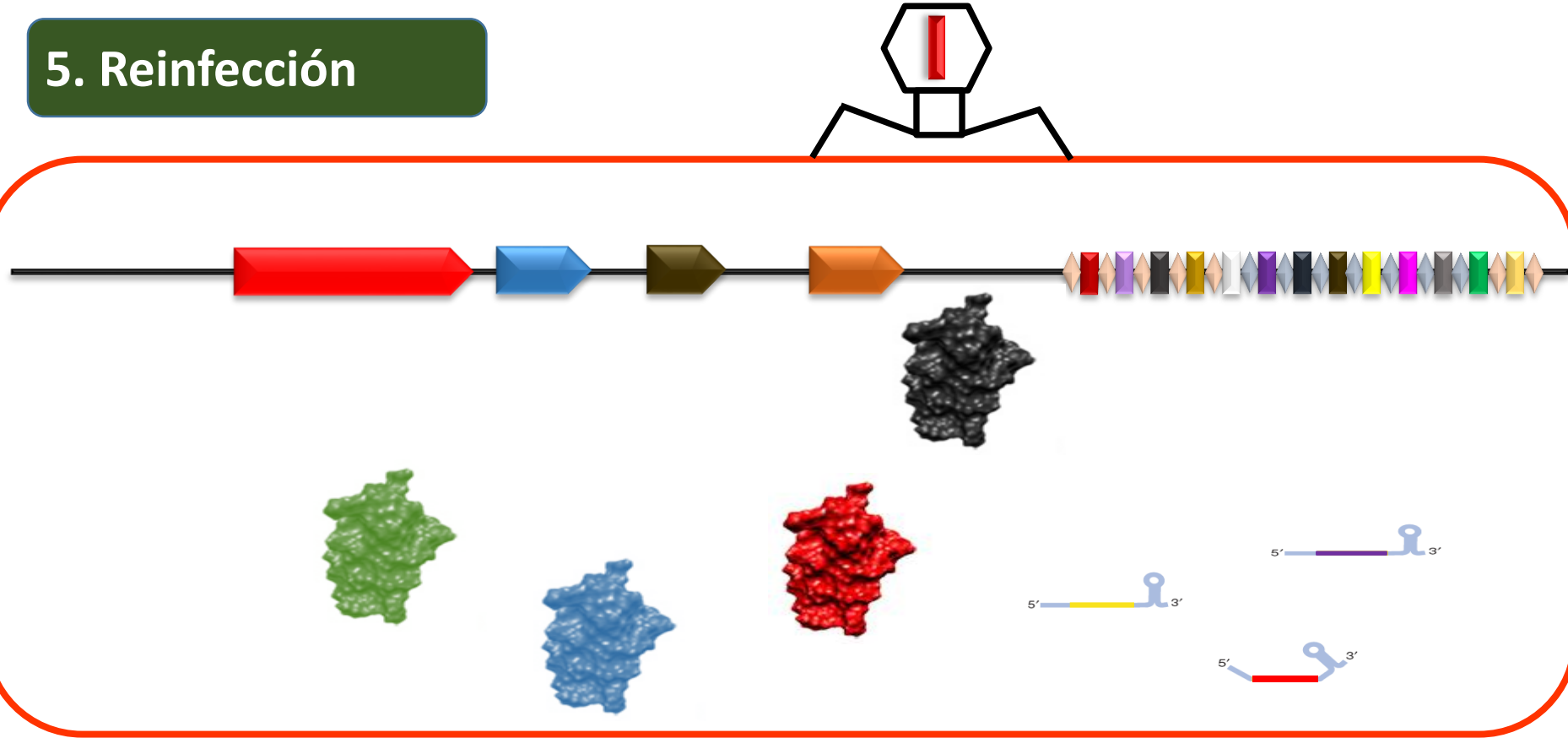
Animación: F. Mojica, con autorización

4. Producción de defensas



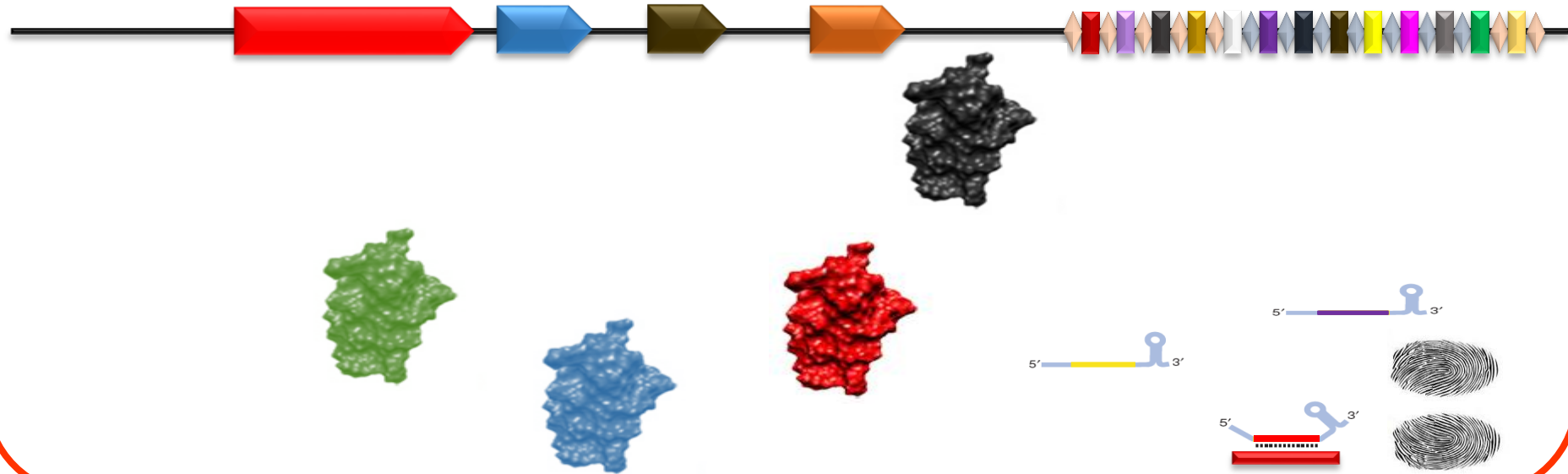
Animación: F. Mojica, con autorización

5. Reinfección



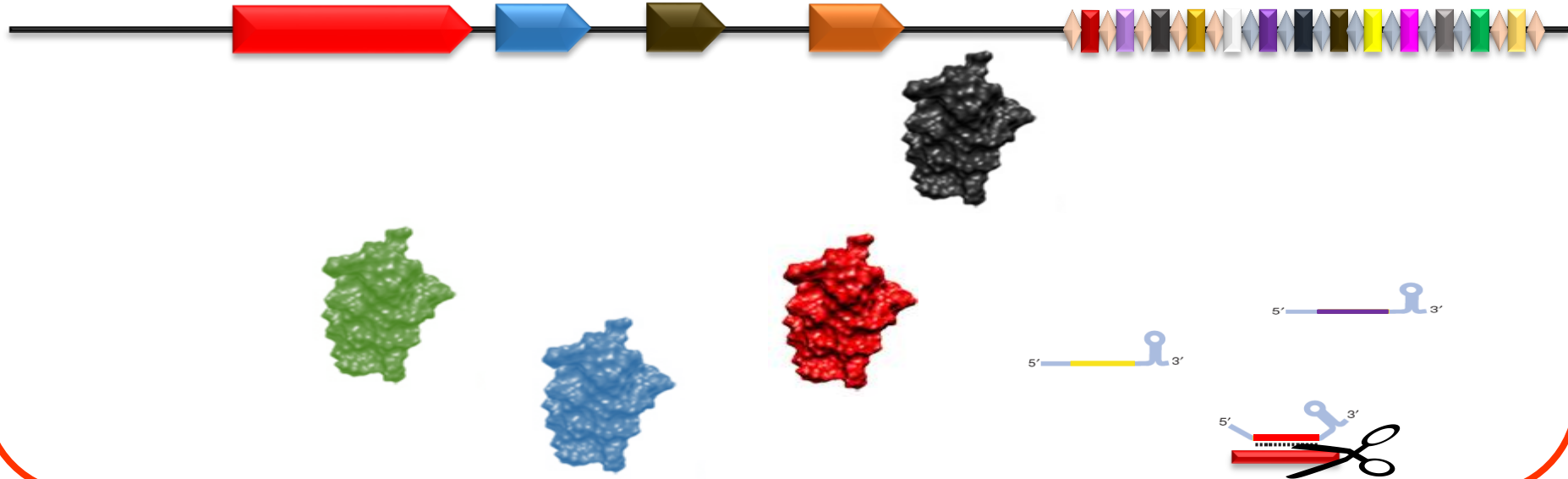
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6. Reconocimiento



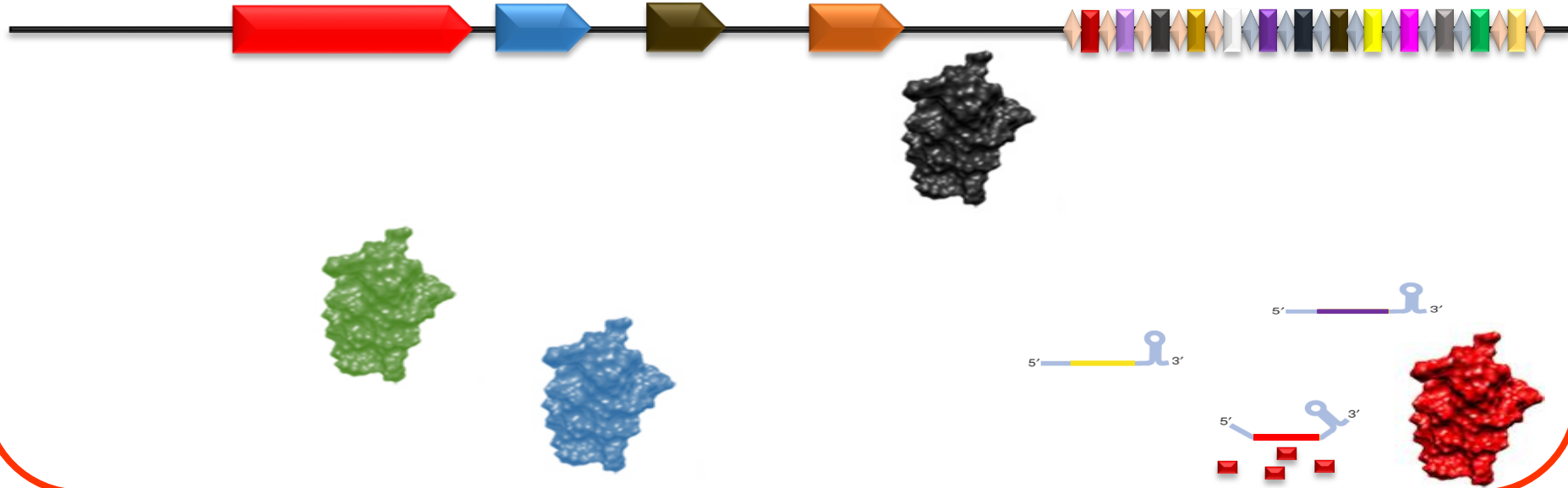
Animación: F. Mojica, con autorización

7. Destrucción



Animación: F. Mojica, con autorización

8. Sistema de Inmunidad Adquirida



Animación: F. Mojica, con autorización

La demostración experimental



Philippe Horvath

CRISPR Provides Acquired Resistance Against Viruses in Prokaryotes

SCIENCE VOL 315 23 MARCH 2007

Rodolphe Barrangou,¹ Christophe Fremaux,² Hélène Deveau,³ Melissa Richards,¹
Patrick Boyaval,² Sylvain Moineau,³ Dennis A. Romero,¹ Philippe Horvath^{2*}

LA INVENCION



De los procariotas a los eucariotas



Luciano Marraffini

Erik Sontheimer

CRISPR Interference Limits Horizontal Gene Transfer in Staphylococci by Targeting DNA

Luciano A. Marraffini and Erik J. Sontheimer*

Horizontal gene transfer (HGT) in bacteria and archaea occurs through phage transduction, transformation, or conjugation, and the latter is particularly important for the spread of antibiotic resistance. Clustered, regularly interspaced, short palindromic repeat (CRISPR) loci confer sequence-directed immunity against phages. A clinical isolate of *Staphylococcus epidermidis* harbors a CRISPR spacer that matches the *nickase* gene present in nearly all staphylococcal conjugative plasmids. Here we show that CRISPR interference prevents conjugation and plasmid transformation in *S. epidermidis*. Insertion of a self-splicing intron into *nickase* blocks interference despite the reconstitution of the target sequence in the spliced mRNA, which indicates that the interference machinery targets DNA directly. We conclude that CRISPR loci counteract multiple routes of HGT and can limit the spread of antibiotic resistance in pathogenic bacteria.

SCIENCE VOL 322 19 DECEMBER 2008

De los procariotas a los eucariotas



Jennifer Doudna



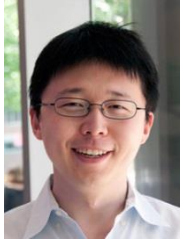
Emmanuelle Charpentier

A Programmable Dual-RNA–Guided DNA Endonuclease in Adaptive Bacterial Immunity

Martin Jinek,^{1,2*} Krzysztof Chylinski,^{3,4*} Ines Fonfara,⁴ Michael Hauer,^{2†}
Jennifer A. Doudna,^{1,2,5,6‡} Emmanuelle Charpentier^{4‡}

17 AUGUST 2012 VOL 337 SCIENCE

De los procariotas a los eucariotas



Feng Zhang

Science. 2013 February 15; 339(6121): 819–823. doi:10.1126/science.1231143.

Multiplex Genome Engineering Using CRISPR/Cas Systems

Le Cong^{1,2,*}, F. Ann Ran^{1,4,*}, David Cox^{1,3}, Shuailliang Lin^{1,5}, Robert Barretto⁶, Naomi Habib¹, Patrick D. Hsu^{1,4}, Xuebing Wu⁷, Wenyan Jiang⁸, Luciano A. Marraffini⁸, and Feng Zhang^{1,†}



Luciano Marraffini

Nature Biotechnology (2013) 31: 233–239 (2013)

RNA-guided editing of bacterial genomes using CRISPR-Cas systems

Wenyan Jiang, David Bikard, David Cox, Feng Zhang and Luciano Marraffini

Science. 2013 February 15; 339(6121): 823–826. doi:10.1126/science.1232033.

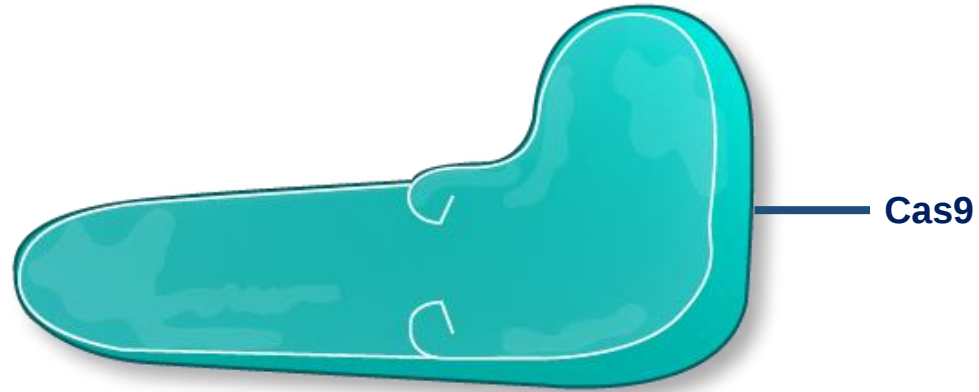
RNA-Guided Human Genome Engineering via Cas9

Prashant Mali^{1,5}, Luhan Yang^{1,3,5}, Kevin M. Esvelt², John Aach¹, Marc Guell¹, James E. DiCarlo⁴, Julie E. Norville¹, and George M. Church^{1,2,*}

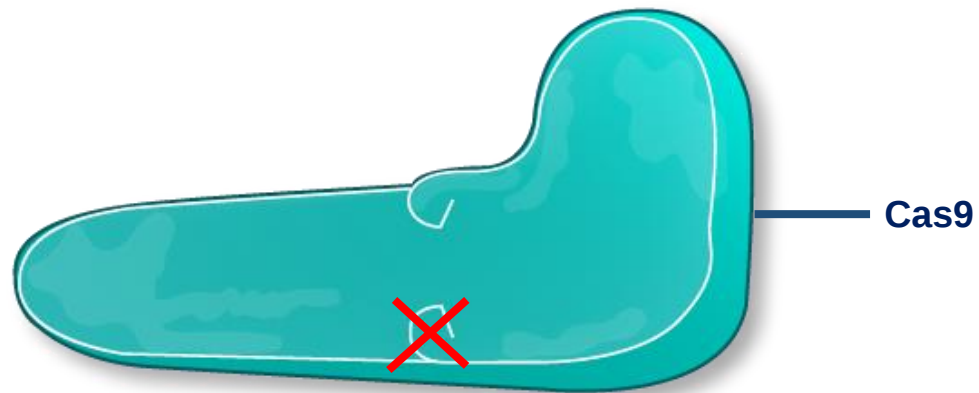


George Church

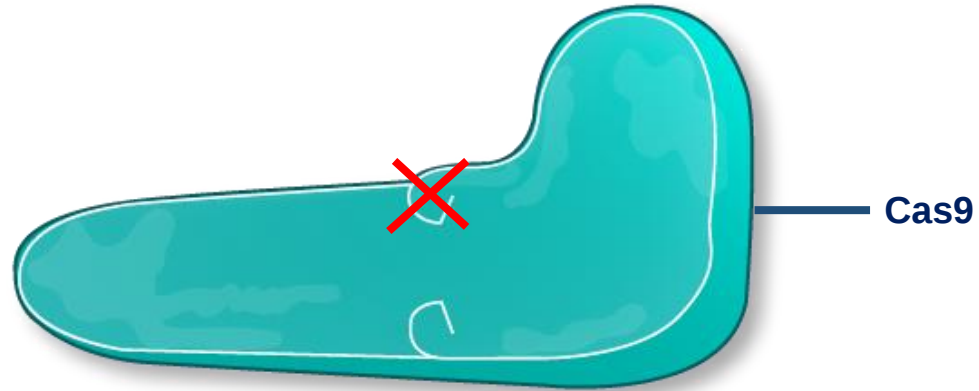
De los procariotas a los eucariotas



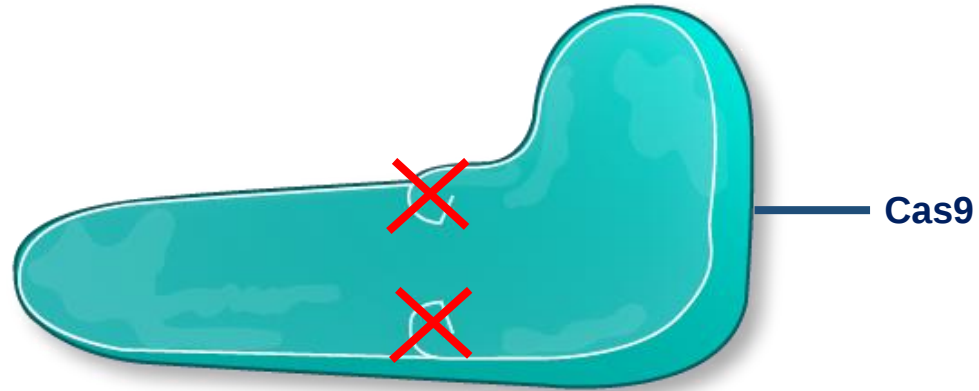
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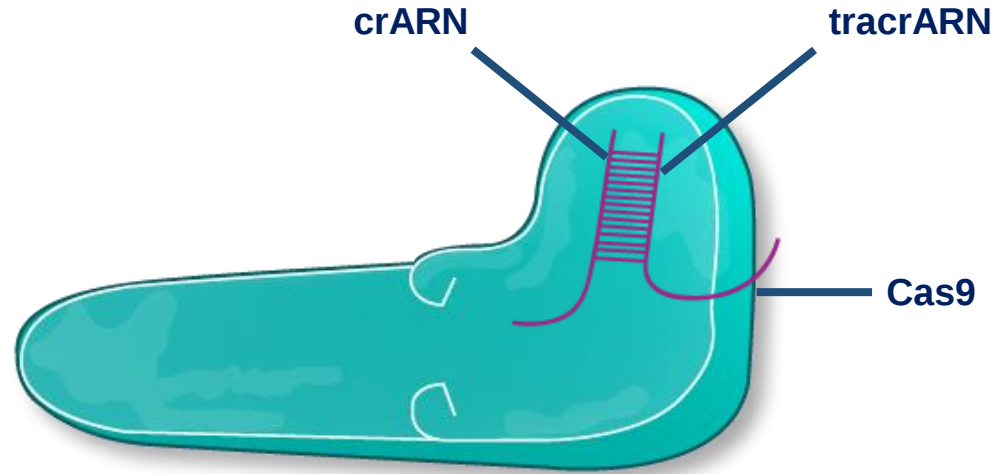
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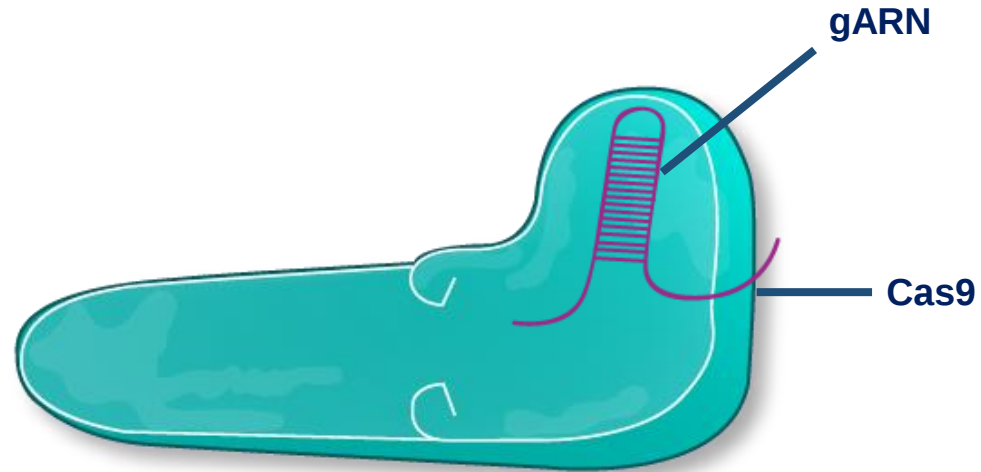
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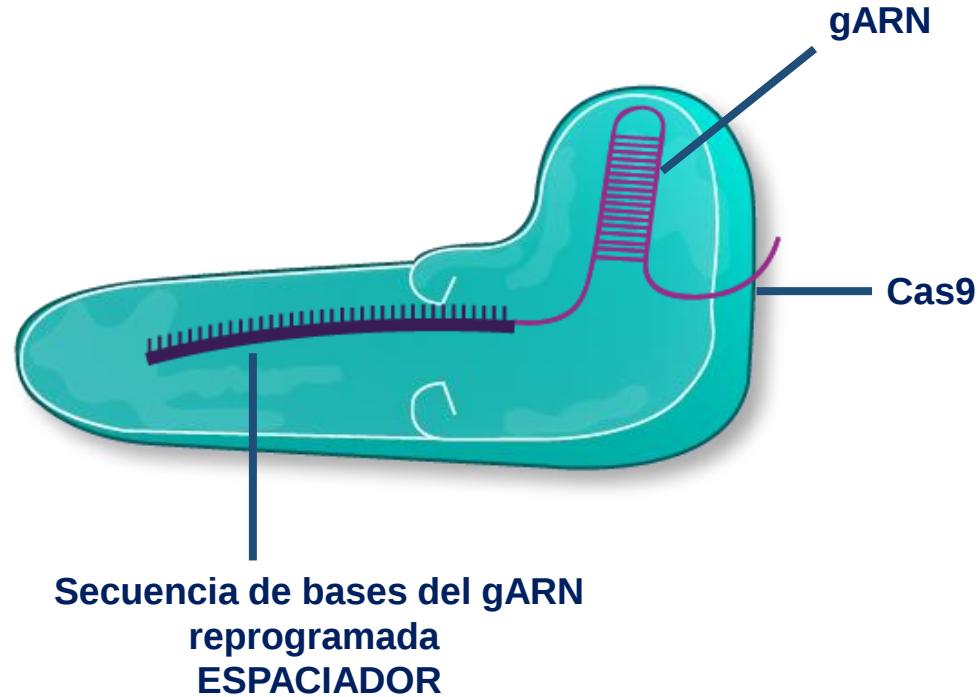
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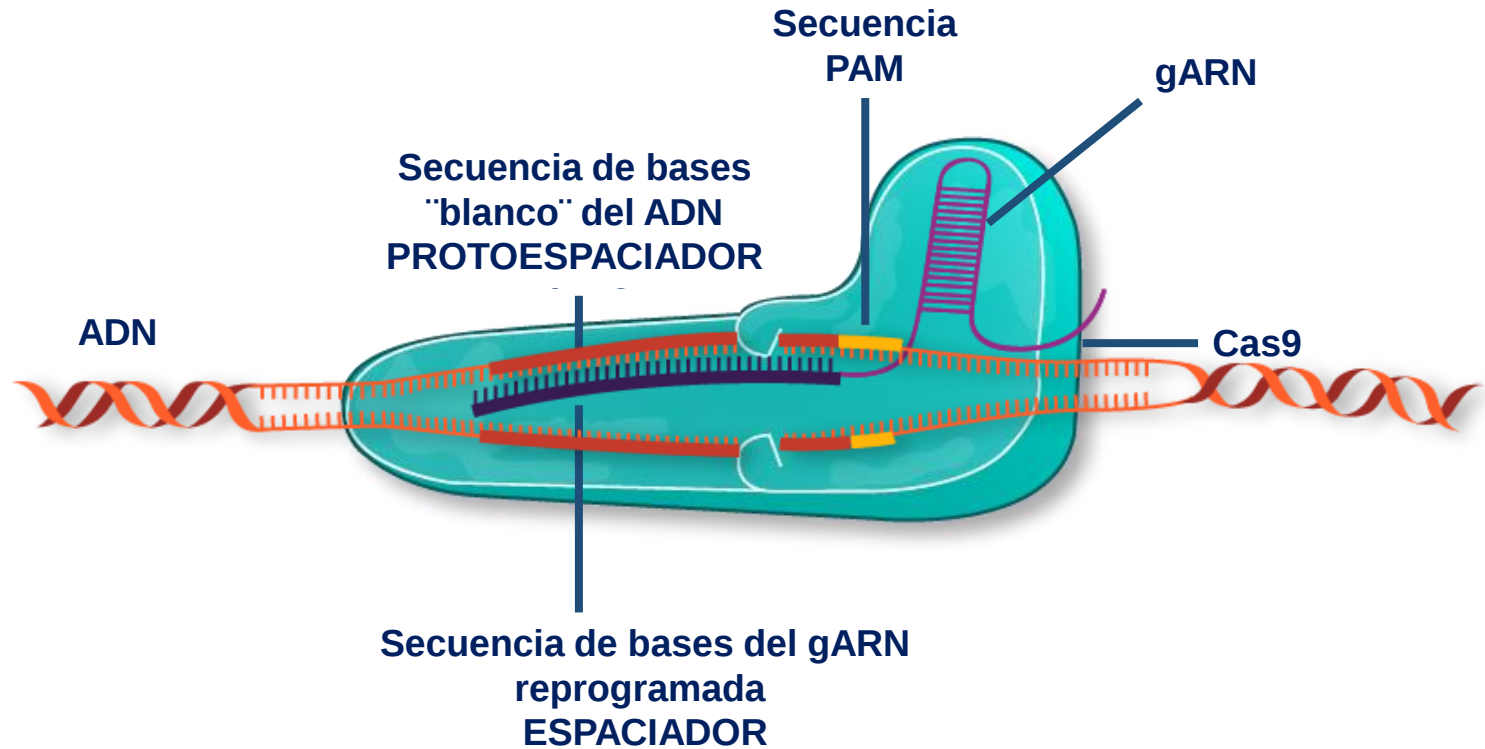
De los procariotas a los eucariotas



De los procariotas a los eucariotas



De los procariotas a los eucariotas

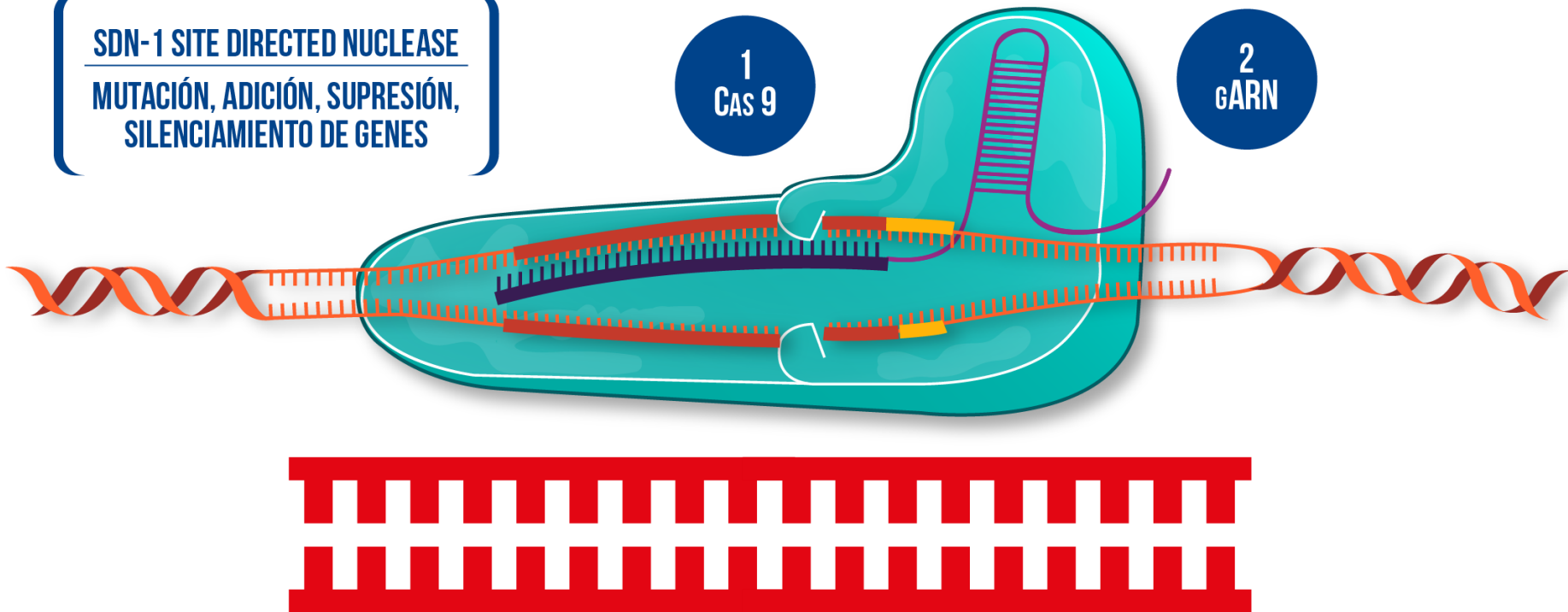


Edición de Genomas mediante CRISPR-Cas9

SDN-1 SITE DIRECTED NUCLEASE
MUTACIÓN, ADICIÓN, SUPRESIÓN,
SILENCIAMIENTO DE GENES

1
Cas 9

2
gARN

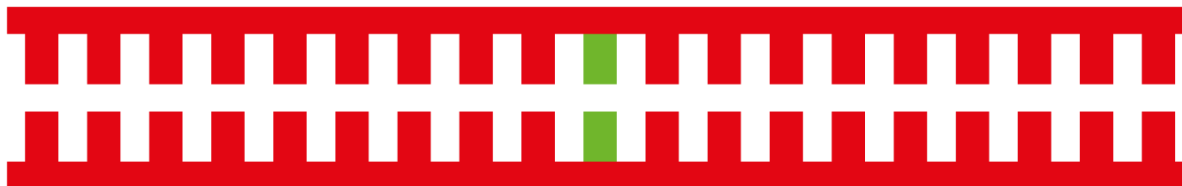
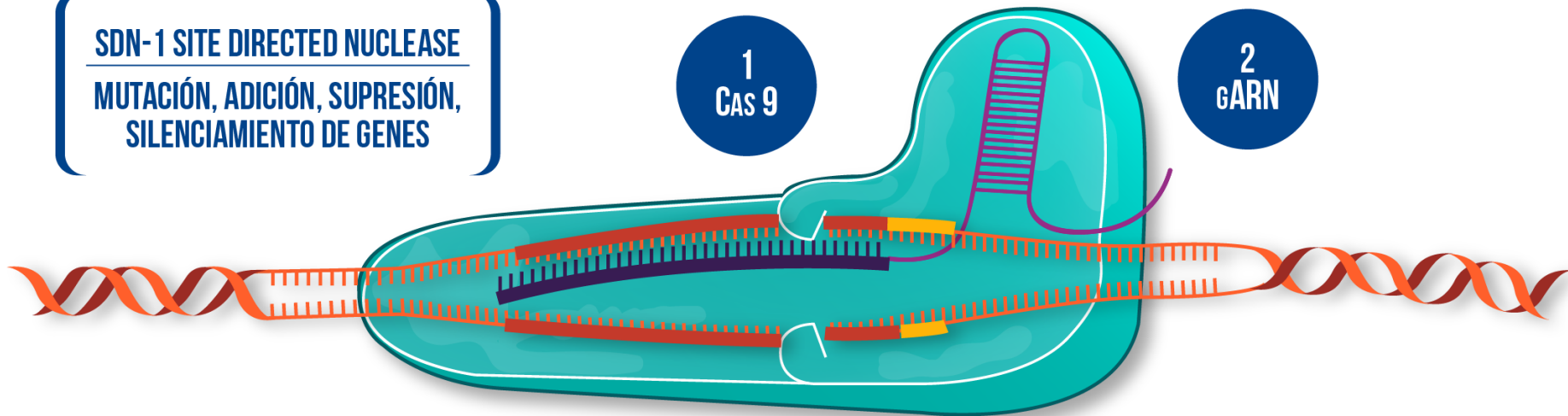


Edición de Genomas mediante CRISPR-Cas9

SDN-1 SITE DIRECTED NUCLEASE
MUTACIÓN, ADICIÓN, SUPRESIÓN,
SILENCIAMIENTO DE GENES

1
Cas 9

2
gARN



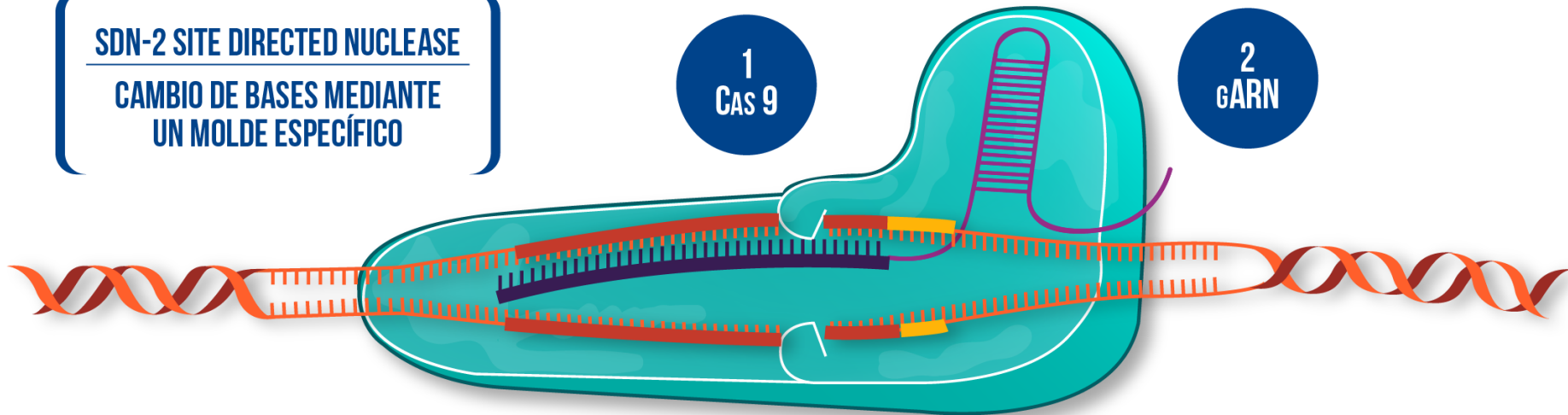
NHEJ

Edición de Genomas mediante CRISPR-Cas9

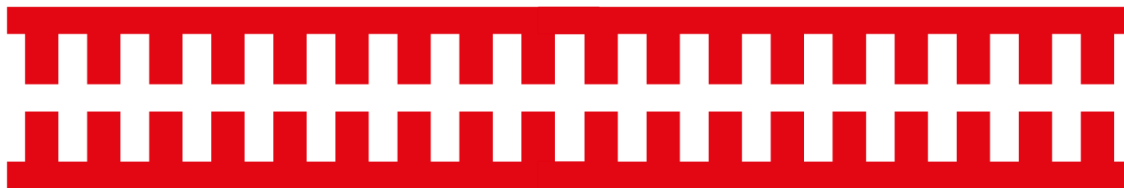
SDN-2 SITE DIRECTED NUCLEASE
CAMBIO DE BASES MEDIANTE
UN MOLDE ESPECÍFICO

1
Cas 9

2
gARN



3
MOLDE

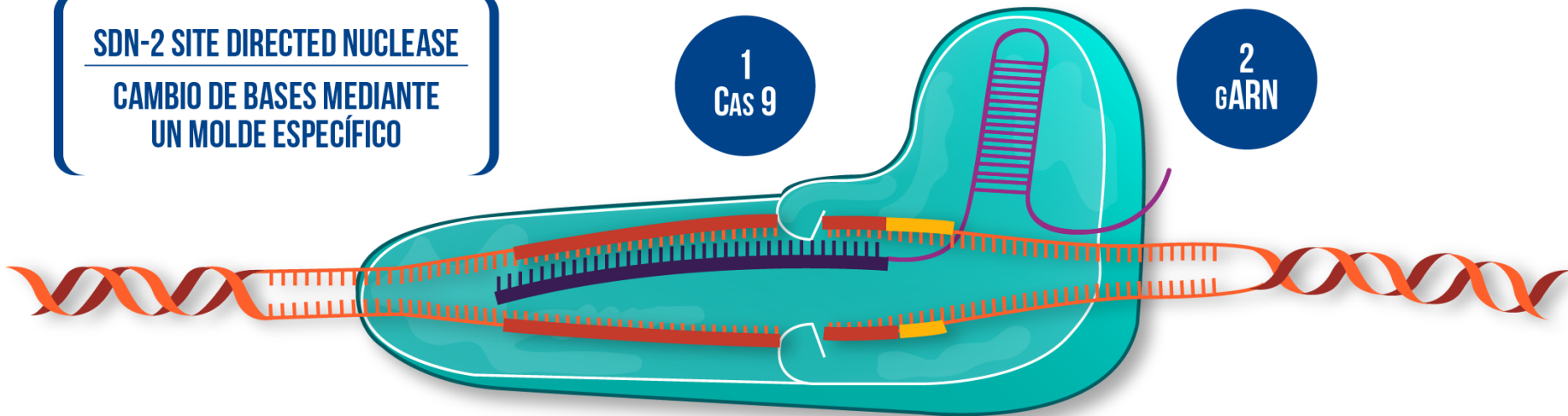


Edición de Genomas mediante CRISPR-Cas9

SDN-2 SITE DIRECTED NUCLEASE
CAMBIO DE BASES MEDIANTE
UN MOLDE ESPECÍFICO

1
Cas 9

2
gARN



HDR

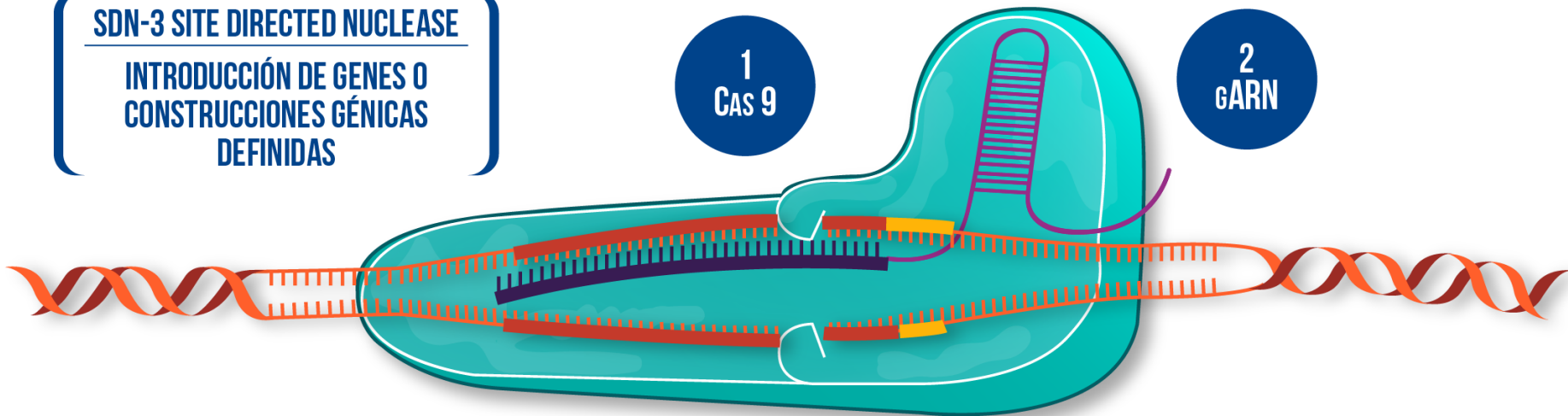
Edición de Genomas mediante CRISPR-Cas9

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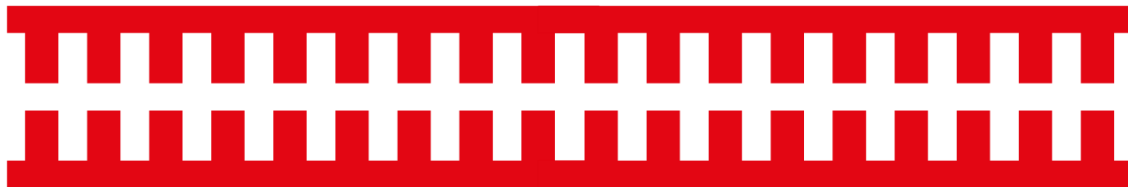
INTRODUCCIÓN DE GENES O
CONSTRUCCIONES GÉNICAS
DEFINIDAS

1
Cas 9

2
gARN



3
GEN



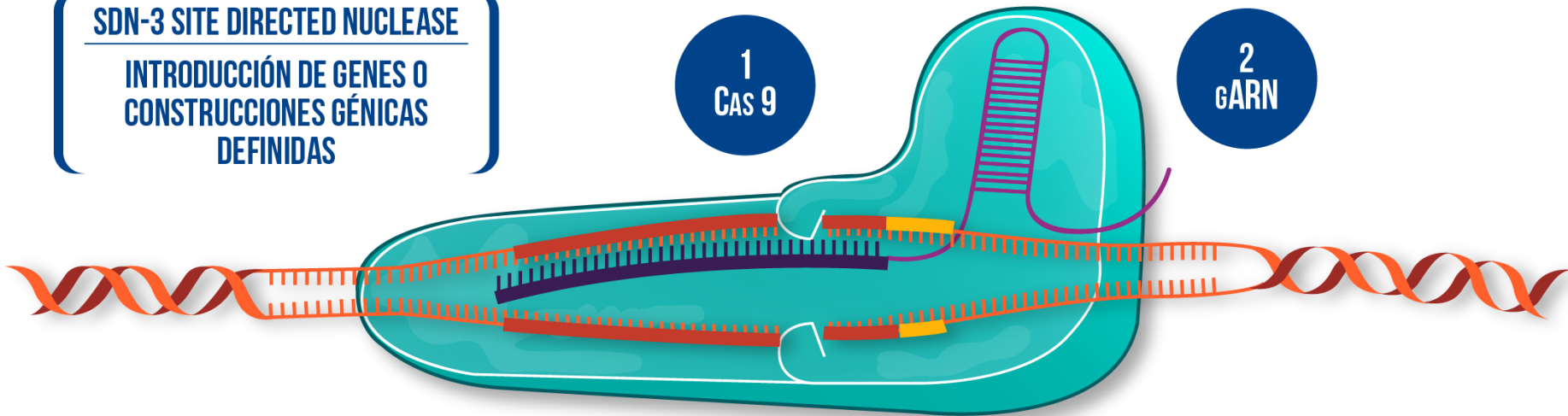
Edición de Genomas mediante CRISPR-Cas9

SDN-3 SITE DIRECTED NUCLEASE

**INTRODUCCIÓN DE GENES O
CONSTRUCCIONES GÉNICAS
DEFINIDAS**

**1
Cas 9**

**2
gARN**



- REEMPLAZO ALÉLICO
- CISGÉNESIS
- INTRAGÉNESIS
- TRANSGÉNESIS



HDR

Aplicaciones CRISPR-Cas9

- **Levaduras**
- **Protozoos: leishmaniasis, toxoplasmosis, malaria...**
- **Plantas: arroz, naranjo, trigo, soja, maíz, melón, patata, tomate, tabaco...**
- **Insectos**
- **Moluscos**
- **Reptiles**
- **Anfibios**
- **Peces**
- **Aves**
- **Mamíferos: ratón, conejo, cabra, rata, cerdo, perro, primates, humanos...**

Edición de Genomas con Nucleasas Sintéticas

Ventajas del sistema CRISPR sobre todas las anteriores técnicas de edición génica

- Versátil;
- Sencillo;
- Económico;
- Preciso;
- Rápido;
- Eficiente
- Predecible

PBI: factores claves en el mejoramiento vegetal

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Conflicto por Patentes

CRISPR-Cas9 no puede patentarse.

Las unidades CRISPR con sus secuencias repetidas y los espaciadores no repetidos, junto con los genes que codifican para las proteínas Cas están presentes en la naturaleza y son parte del sistema inmunológico de las bacterias.

Sí se pueden patentar:

- gARN diseñados para el sistema CRISPR-Cas9
- Modificaciones del sistema llevadas a cabo para editar el genoma de las células de mamífero u otros organismos, en los que normalmente no se encuentran los componentes del sistema.

¿De quién es CRISPR?

The Scientist » News & Opinion » News Analysis

Who Owns CRISPR?

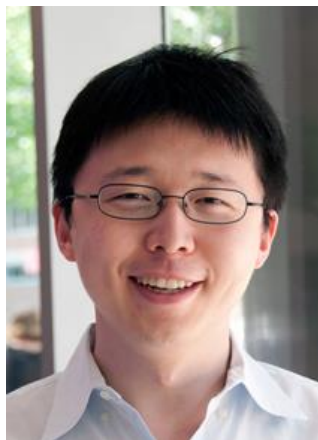
With one US patent awarded and many other applications under consideration for the popular genome-editing technology, companies are adopting multiple strategies to navigate the complex intellectual property landscape.



Jennifer Doudna



Emmanuelle Charpentier

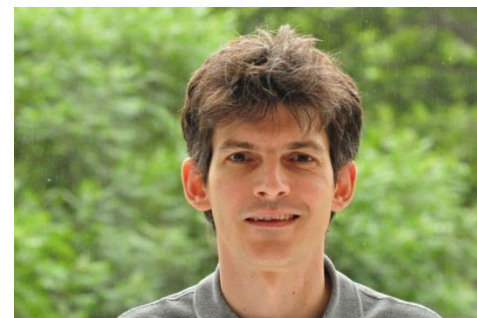


Feng Zhang

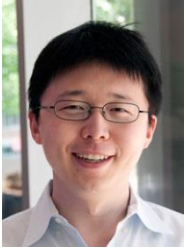


Francisco Mojica

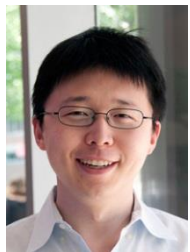
Luciano Marrafini



Acceso



Acceso



MONSANTO 
04-01-17
Worldwide, non-exclusive rights to
agricultural applications of the
CRISPR/Cpf1 system.
BROAD INSTITUTE



27-06-17
Exclusive rights to the **ERS** patent portfolio
covering CRISPR-Cas genome editing technology
for all agricultural uses and applications in plants.

February 17, 2017

The CRISPR patent battle spans two continents

Isobel Finnie and Catherine Williamson, GEN Exclusives, 6 February 2017, <http://www.genengnews.com/gen-exclusives/crispr-patent-wars/77900842>

The CRISPR/Cas9 patent battle has been closely watched in the United States with a decision expected in the next few months. Less attention has been paid to the ongoing European patent battle. Like in the US, both UC-Berkeley and The Broad Institute have submitted competing patent applications. Currently the Broad Institute has received all granted patents over UC-Berkeley, however the Broad is facing challenges to these decisions.

February 24, 2017

Broad Institute prevails over UC-Berkeley in patent battle

Heidi Ledford, Nature News, 15 February

2017 <http://www.nature.com/news/broad-institute-wins-bitter-battle-over-crispr-patents-1.21502>

The US patent office judges have ruled that the Broad Institutes and UC-Berkeley's patents do not interfere, providing a win for the Broad. This effectively allows both UC-Berkeley and the Broad to have patents covering portions of the CRISPR intellectual property landscape, possibly requiring companies to license patents from both institutions. This decision may be appealed to the circuit courts by UC-Berkeley.

April 21, 2017

University of California Appeals CRISPR Patent Decision

Sharon Begley, 13 April 2017, STAT

News, <https://www.statnews.com/2017/04/13/crispr-patent-uc-appeal/>

UC-Berkeley has filed an appeal with the federal Court of Appeals. UC-Berkeley was joined in its appeal by the University of Vienna and Emmanuelle Charpentier. Previously, the US Patent office had ruled that UC-Berkeley's and the Broad Institute's patents did not interfere, leaving them both able to pursue unique patents. In this appeal, UC-Berkeley hopes to establish that the teams led by Doudna and Charpentier were the first to engineer CRISPR/Cas9 in all cell types.

April 13, 2017

UC-Berkeley Awarded CRISPR Patents in Europe

Jef Akst, The Scientist, 24 March 2017, <http://www.the-scientist.com/?articles.view/articleNo/48987/title/UC-Berkeley-Receives-CRISPR-Patent-in-Europe/>

The European patent office has announced its intention to award broad CRISPR patents to the University of California-Berkeley and the University of Vienna. The awarded patents will cover the use of the CRISPR technology in both prokaryotic and eukaryotic cells/organisms, contrasting with the US patent office which denied UC-Berkeley the rights to eukaryotic cells.

July 16, 2017

Intellia Therapeutics Wins China CRISPR Patent

GEN News Highlights, 19 June 2017, <http://www.genengnews.com/gen-news-highlights/intellia-holder-of-rights-to-ucs-crispr-technology-to-win-china-patent/81254529>

Intellia Therapeutics, founded by Jennifer Doudna, has been awarded a broad patent for the CRISPR/Cas9 single guide gene editing system. Intellia has licensed the CRISPR technology developed by Jennifer Doudna at the University of California-Berkeley. This latest announcement comes on the tails of the European Patent Office's announcement favoring UC-Berkeley as well.

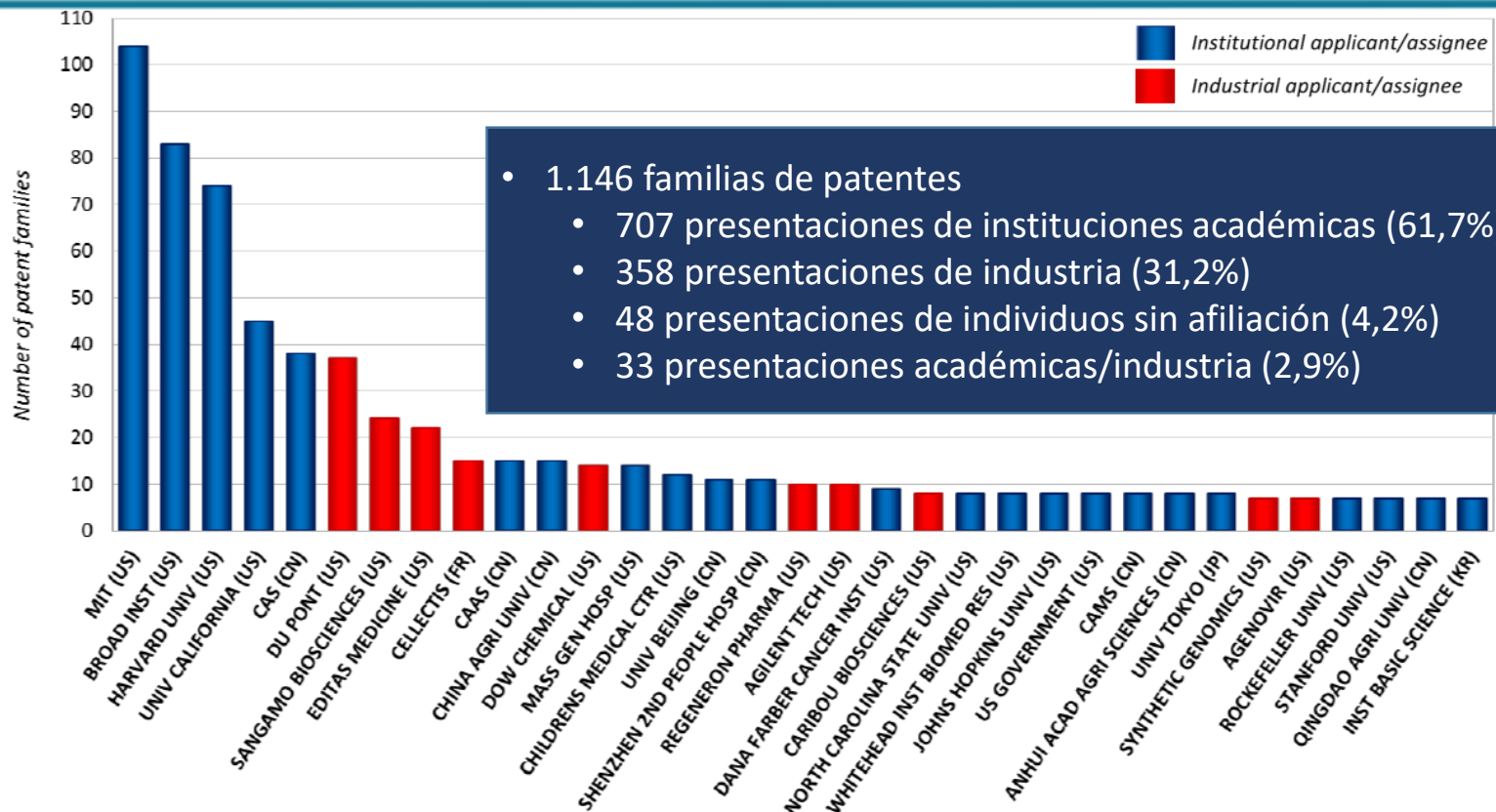
August 4, 2017

Collectis Wins CRISPR Patent in Europe

Jonathan Wosen, GEN News Highlights, 25 July 2017, <http://www.genengnews.com/gen-news-highlights/collectis-granted-t-cell-crispr-patent-in-europe/81254707>

French biotech company Collectis has been granted a European patent to use CRISPR in T cells valid until 2034. Collectis hopes to use this technology to edit T cells for cancer therapy. While other companies are pursuing similar treatments, Collectis hopes to develop a universal CAR-T cell line that can be widely used without tailoring treatment to individuals.

Principales solicitantes



- 1.146 familias de patentes
 - 707 presentaciones de instituciones académicas (61,7%)
 - 358 presentaciones de industria (31,2%)
 - 48 presentaciones de individuos sin afiliación (4,2%)
 - 33 presentaciones académicas/industria (2,9%)

Antecedentes



Harvard Oncomouse



Tecnología PCR – PCR/Taq patent war

Plataforma Global de Licencias Conjuntas

The screenshot shows a web browser window displaying the homepage of The Scientist. The browser's address bar shows the URL: www.the-scientist.com/?articles.view/articleNo/49835/title/Major-CRISPR-Patent-Holders-Agree-to-Patent-Pool/. The website header features the logo "TheScientist" with the tagline "EXPLORING LIFE, INSPIRING INNOVATION". Below the logo is a navigation bar with links for News, Magazine, Multimedia, Subjects, Surveys, and Careers. A search bar is also present. The main content area displays the article "Major CRISPR Patent-Holders Agree to Patent Pool" by Aggie Mika, dated July 10, 2017. The article text states: "The Broad Institute and others sign on to participate in a platform designed to streamline the licensing process." To the right of the article is a sidebar with a "The One-Stop Life Science Shop" section featuring icons for Antibodies, ELISAs, Chemicals, Enzymes, and Proteins. Below this is a promotional banner for "TheScientistExpo A FIRST OF ITS KIND EVENT" with a "REGISTER NOW" button. At the bottom of the page, there are social media sharing icons (Facebook, LinkedIn, Instagram, Twitter, YouTube) and a Windows taskbar showing the time as 06:58 a.m.

- Broad Institute
- MIT
- Harvard University
- Rockefeller University

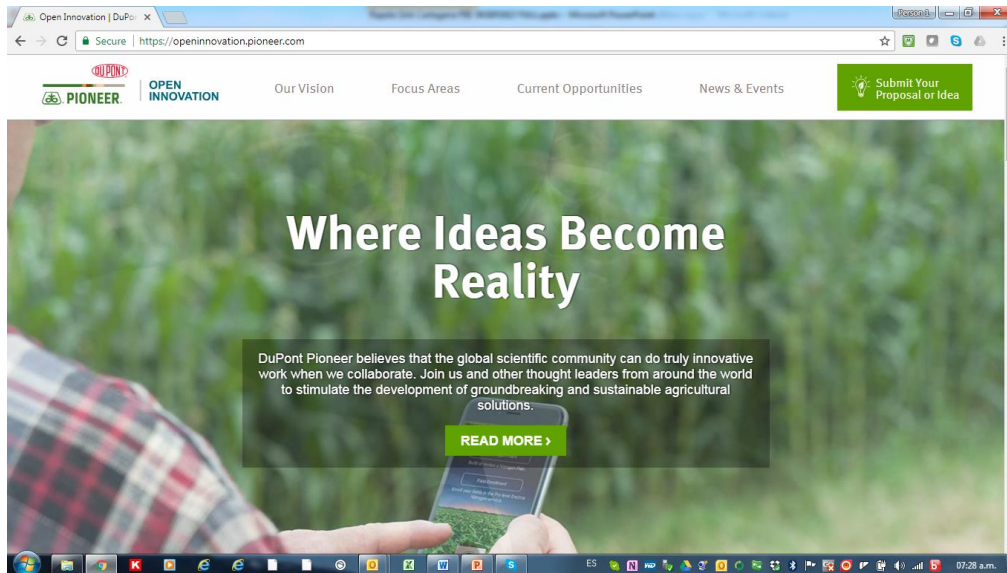
Plataforma Global de Licencias Conjuntas



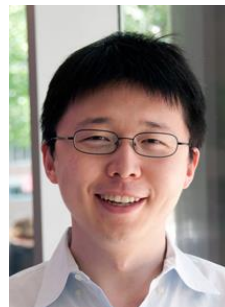
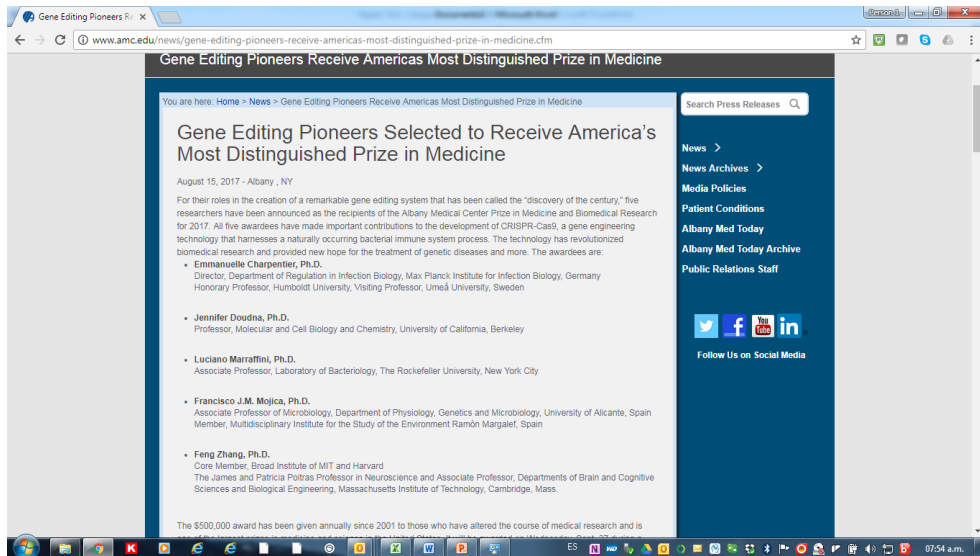
MPEG LA

Mecanismo de licencias no exclusivo mantenido y manejado por una entidad independiente de los poseedores de las patentes

Iniciativas de Open Innovation



Reconocimiento



17 de Agosto 2017
Albany Medical Center Prize in Medicine and Biomedical Research for 2017

PBI: factores claves en el mejoramiento vegetal

1. Técnica / Conocimiento
2. Acceso
3. Ambiente Regulatorio

Ambiente regulatorio

- Los productos editados, ¿son organismos genéticamente modificados?
- ¿Regular por proceso o por producto?
- ¿Es necesario un marco regulatorio especial para los productos editados?
- ¿Es necesario crear una nueva categoría de producto regulado?
- ¿Es necesario mencionar las técnicas?
- Si las modificaciones también pueden ser logradas mediante mejoramiento convencional, ¿el producto debe ser regulado?
- ¿La cantidad de nucleótidos modificada es el criterio central? ¿Es un criterio secundario? ¿No es un criterio?
- ¿Cuál es entonces el criterio?

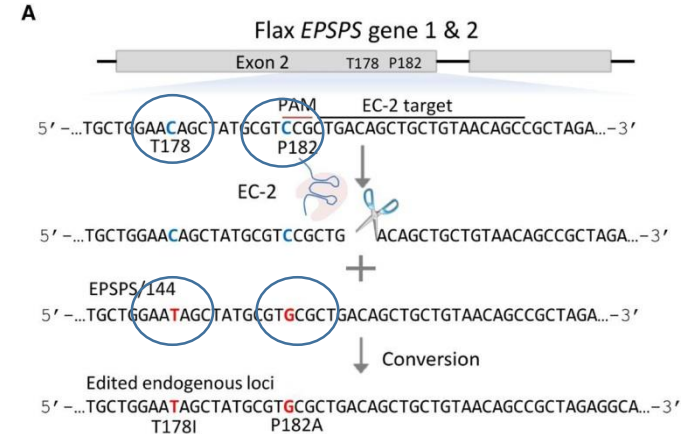
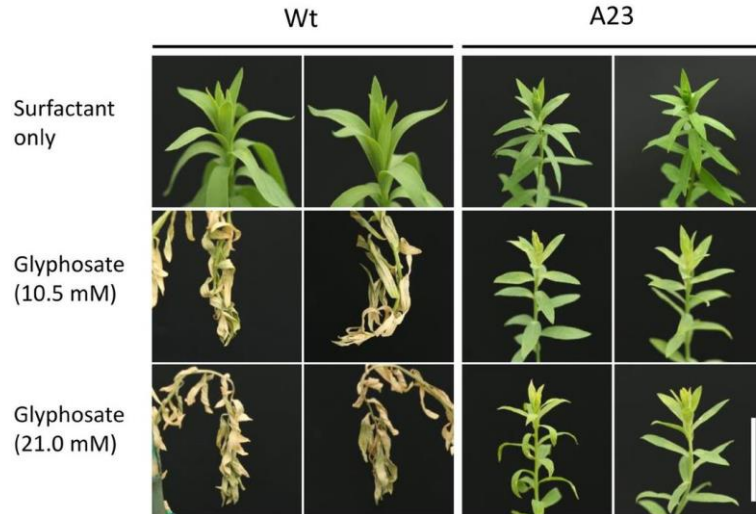
Ambiente regulatorio

- Canadá
 - Argentina (2015)
 - Israel (2016)
 - Chile (2017)
 - US (2017 – propuesta)
- } Regulación por producto
- Caso a caso
 - No crear una 3ª categoría de producto
 - El producto final está fuera del alcance del marco regulatorio si NO contiene una nueva combinación de material genético (= *la inserción en el genoma en forma estable y conjunta de uno o más genes o secuencias de ADN que forman parte de una construcción genética definida*).

Y los productos, ¿cómo se protegen?



Caso 1



Oligonucleotide-mediated genome editing provides precision and function to engineered nucleases and antibiotics in plants

Noel J Sauer (nsauer@cibus.com), Javier Narváez-Vásquez (jnarvaez@cibus.com), Jerry Mozoruk (jmozoruk@cibus.com), Ryan B Miller (rmiller@cibus.com), Zachary J Warburg (zwarburg@cibus.com), Melody J Woodward (mwoodward@cibus.com), Yohannes A Mihiret (ymihiret@cibus.com), Tracey A Lincoln (tlincoln@cibus.com), Rosa E Segami (rsegami@cibus.com), Steven L Sanders (ssanders@cibus.com), Keith A Walker (kwalker@cibus.com), Peter R Beetham (pbeetham@cibus.com), Christian R Schöpke (cschopke@cibus.com) and Greg FW Gocal (gogcal@cibus.com)

Plant Physiology. February 10, 2016

Caso 1

Compañía A



Compañía C



Compañía B



Variedad 1
Convencional



¿Definición de Variedad?

Variedad 3
No Transgénica
CRISPR-Cas9
Tol. glfosato

Ley 20147/73
Ley 24376/94

Variedad 2
Transgénica
Tol. glfosato

Caso 2

En maíz, el gen ARGOS8 es un regulador negativo de la respuesta al etileno. Las plantas con sobreexpresión de ARGOS8 muestran una reducida sensibilidad al etileno y mejoran la producción de grano bajo condiciones de stress hídrico.

En el año 2016 científicos de la compañía Pioneer utilizaron CRSPR-Cas9 tanto para editar el promotor nativo del gen ARGOS8 como para reemplazar al promotor nativo de este gen.

Las plantas regeneradas presentaron una alta expresión de ARGOS8, lo cual fue detectable en todos los tejidos de la planta, y en ensayos a campo incrementaron significativamente su producción de grano bajo condiciones de stress hídrico en floración, no mostrando a la par ninguna disminución de rendimiento en condiciones de adecuada humedad. Las nuevas variedades no son transgénicas.

(a) ARGOS8-v1

```
GOS2 5'-UTR
-----CTCAA CAACCAAGTT TCCATGAGCG CTGGCGCGCG GGTCCGCGG GCGGCTCTGT GAGGCAAAAT TTATATAGTT CTAGTGGTA CCCGGCTACG
GATAGATATG ATGCTGCAT GCACATTGGC TATATCTGAG GCTCTGCGC GCGCCTTGGC CAGGTGTCTG TCATGCGGGCGATGCCGAGGAAGAGGA--
M R A M P Q E E E
```

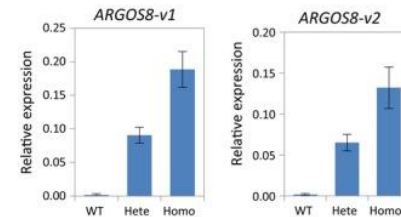
ARGOS8-v2

```
GOS2 5'-UTR
-----CTCAA CAACCAAGTT TCCATGGTAC GGATAGATAT GATGCTGCAC TGCACATTGG CTATATCTGA GGCTCTGCG GCGCCTTGG CCAGGTGTCT
GTCATGCGGG CGATGCCGCA GGAAGAGGAA ---
M R A M P Q E E E
```

ARGOS8-v3

```
CTS3 CTS1
---AAATAAA GAGTTACTTC TCTAAGCAGCT CGCTGGCGCG CGGTCCGCG GGGCGGTCT GTGAGGGCAA ATTTATATAG GTCTAGTGGG TACCCGGCTA
CGGATAGATA TGATGTGCTCA CTGCACATTG GCTATATCTG AGGCTCTCTG GCGCGCCTTG GCCAGGTGTC TGTCATGCCG GCGATGCCGC AGGAAGAG---
M R A M P Q E E E
```

(b)



Shi J, Gao H, Wang H, Lafitte HR, Archibald RL, Yang M, Hakimi SM, Mo H, Habben JE (2016). ARGOS8 variants generated by CRISPR-Cas9 improve maize grain yield under field drought stress conditions. Plant Biotechnol. J., doi: 10.1111/pbi.12603

Caso 2



Variedad 1



Variedad 2

*Tolerante stress hídrico por
modificación de un gen
promotor nativo*

¿Patente sobre un gen nativo modificado?

¿DOV sobre el híbrido?

¿DOV sobre la línea paterna?

Caso 3

El tomate tiene su origen en los Andes sudamericanos. Un equipo de investigadores liderado por Zachary Lippman en el Cold Spring Harbor Laboratory de los Estados Unidos analizó una colección de 4.193 variedades silvestres de tomate, buscando aquellos con patrones de ramificación inusuales, identificando dos genes de elevada aptitud comercial (Lippman y col, 2008).

Con estos genes descubiertos, su equipo utilizó la edición génica de CRISPR-Cas9 para eliminar su actividad en una variedad de tomate comercial, así como la de un tercer gen que también afecta el número de flores, en varias combinaciones. Esto generó una gama de arquitecturas en la planta, desde largas y delgadas ramas con racimos de flores, hasta tupidos ramitos de flores con una arquitectura similar a la coliflor; incluyendo algunos con rendimientos mejorados (Soyk y col, 2017). En otros términos, para este desarrollo, no se hizo uso ni se tomó acceso físico al material que conforma el recurso genético, sino solo información del mismo.

DEMATERIALIZACIÓN

GENETICS

CRISPR editing seeks the perfect tomato

Geneticists correct harmful interaction of two desirable plant mutations.

BY HEIDI LEFORD

From giant fruit to compact plants, today's tomatoes have been sculpted by thousands of years of breeding. But mutations linked to prized traits — including one that made the fruit easier to harvest — yield an undesirable plant when combined, geneticists have found.

It is a rare example of a gene harnessed during domestication that later hampered crop-improvement efforts, says geneticist Zachary Lippman of Cold Spring Harbor Laboratory in New York. After identifying the mutations, he and his colleagues used CRISPR gene editing to engineer more-productive plants — a strategy that plant breeders are eager to adopt.

"It's pretty exciting," says Rod Wing, a plant geneticist at the University of Arizona

in Tucson. "The approach can be applied to crop improvement, not just in tomato, but in all crops."



Tomatoes have been bred for thousands of years.

Lippman knows his way around a tomato farm. As a teenager, he spent his summers picking the fruit by hand — a chore he hated. "Rotten tomatoes. The smell lasts all day long," he says. "I would always pray for rain on tomato-harvest day."

But years later, his interest in the genetics that control a plant's shape led him back to tomato fields, to untangle the genetic changes that breeders had unknowingly made.

In the 1950s, researchers found a new trait in a wild relative of tomatoes growing in the Galapagos Islands: it lacked the swollen part of the stem called the joint.

Joints are weak regions of the stem that allow fruit to drop off the plant. Wild plants benefit from dropping fruit because it helps seed dispersal. But with the advent of mechanical tomato pickers, farmers wanted their fruit

PHILIPPE HUGENY/GETTY

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Lippman ZB, Cohen O, Alvarez JP, Abu-Abied M, Pekker I, Paran I, et al. (2008) The Making of a Compound Inflorescence in Tomato and Related Nightshades. PLoS Biol 6(11): e288. <https://doi.org/10.1371/journal.pbio.0060288>

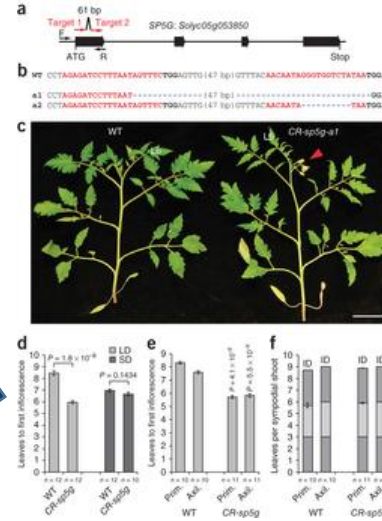
Soyk S, Lemmon ZH, Oved M, Fisher J, Liberatore KL, Park SJ, Goren A, Jiang K, Ramos A, van der Knaap E, van Eck J, Zamir D, Eshed Y, Lippman ZB (2017). Bypassing Negative Epistasis on Yield in Tomato Imposed by a Domestication Gene. Cell DOI: <http://dx.doi.org/10.1016/j.cell.2017.04.032>

Caso 3

Variedad 1



Edición génica a partir
de información sobre
un RRGG



Información
genética



Silvestre

¿Se hizo utilización
del recurso genético?

Ley 27182/15 TIRFAA
Ley 27246/15 PN

Conclusiones

■ CRISPR-Cas

- Es una plataforma multifuncional para la edición génica de todo tipo de organismo procariota o eucariota;
- Es el avance tecnológico en mejoramiento vegetal más significativo desde la transgénesis;
- Es una técnica versátil, sencilla, económica, rápida, precisa, muy eficiente y predecible;
- Podría reemplazar a varias de las técnicas de mejoramiento convencional (ej, back cross);
- Podría reemplazar a toda la transgénesis en tanto el carácter a modificar esté presente en la especie;
- Permite transgénesis a sitios definidos.

Conclusiones

- **Marco Regulatorios**
 - **Probable:** productos SDN-1 y SDN-2, no serán regulados
productos SDN-3, regulados, aunque no en todos los casos (¿tipos particulares de cisgénesis, reemplazo alélico?)
 - ¿Cómo generar doctrina?
- **Marco Propiedad Intelectual – Recursos Genéticos**
 - Cuestionamientos sobre la utilidad del alcance de los sistemas vigentes

Conclusiones

Potencial futuro y desafíos de la industria semillera argentina

- Las técnicas de edición génica constituyen un nuevo punto de ruptura y plantean la necesidad de un profundo ejercicio de armonización de la biotecnología, con aspectos regulatorios y de propiedad intelectual.

Thank you for your attention!

