

# RNA-based mechanisms in the human pathogen *Clostridioides difficile*: focus on CRISPR-Cas system

Olga Soutourina, February 7<sup>th</sup>, 2024

université  
PARIS-SACLAY

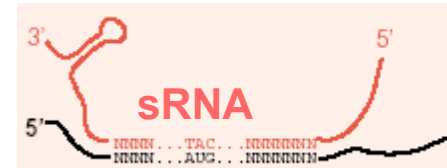
*I2BC, Microbiology department*  
*« Regulatory RNAs in Clostridia » Group*  
*Professor, Paris-Saclay University*



# Widespread regulatory mechanisms based on RNAs in bacteria

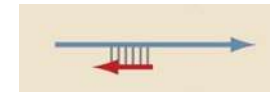
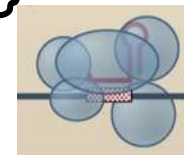
- Adaptive responses
- Metabolic, physiological processes
- Virulence in major pathogens

*Staphylococcus aureus*, *Listeria monocytogenes*, *Streptococcus pyogenes*

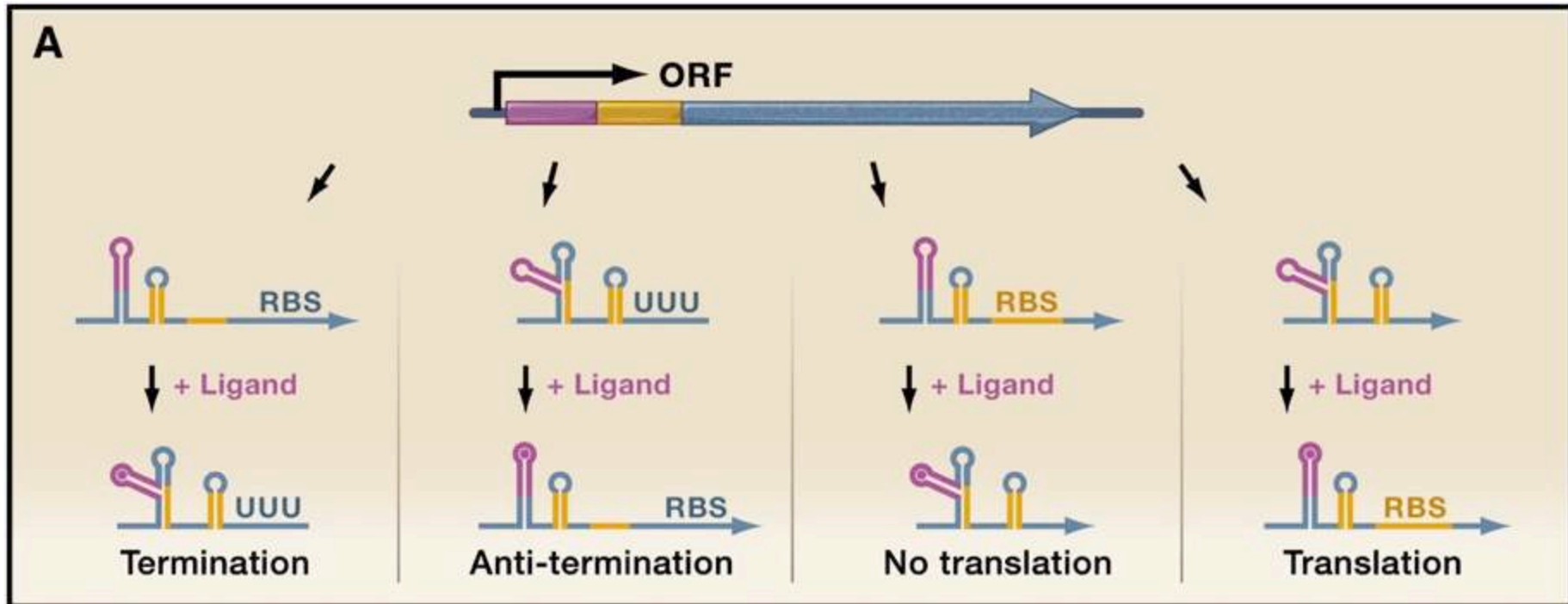
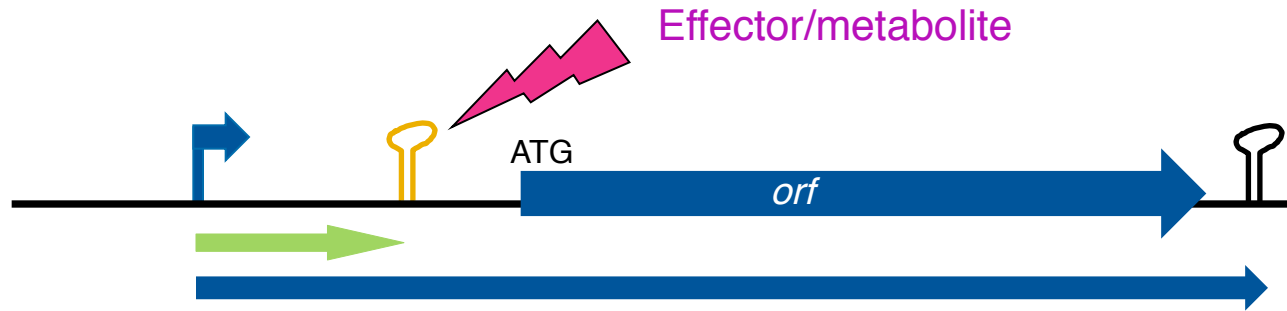


## Diversity of regulatory mechanisms

- Direct effector binding (« **riboswitch** ») (c-di-GMP)
- **Protein** binding (RNAP, CsrA, Hfq, ProQ)
- Foreign **DNA/RNA** binding (CRISPR RNA)
- sRNA-**mRNA** duplex formation (*trans* and *cis* riboregulators)

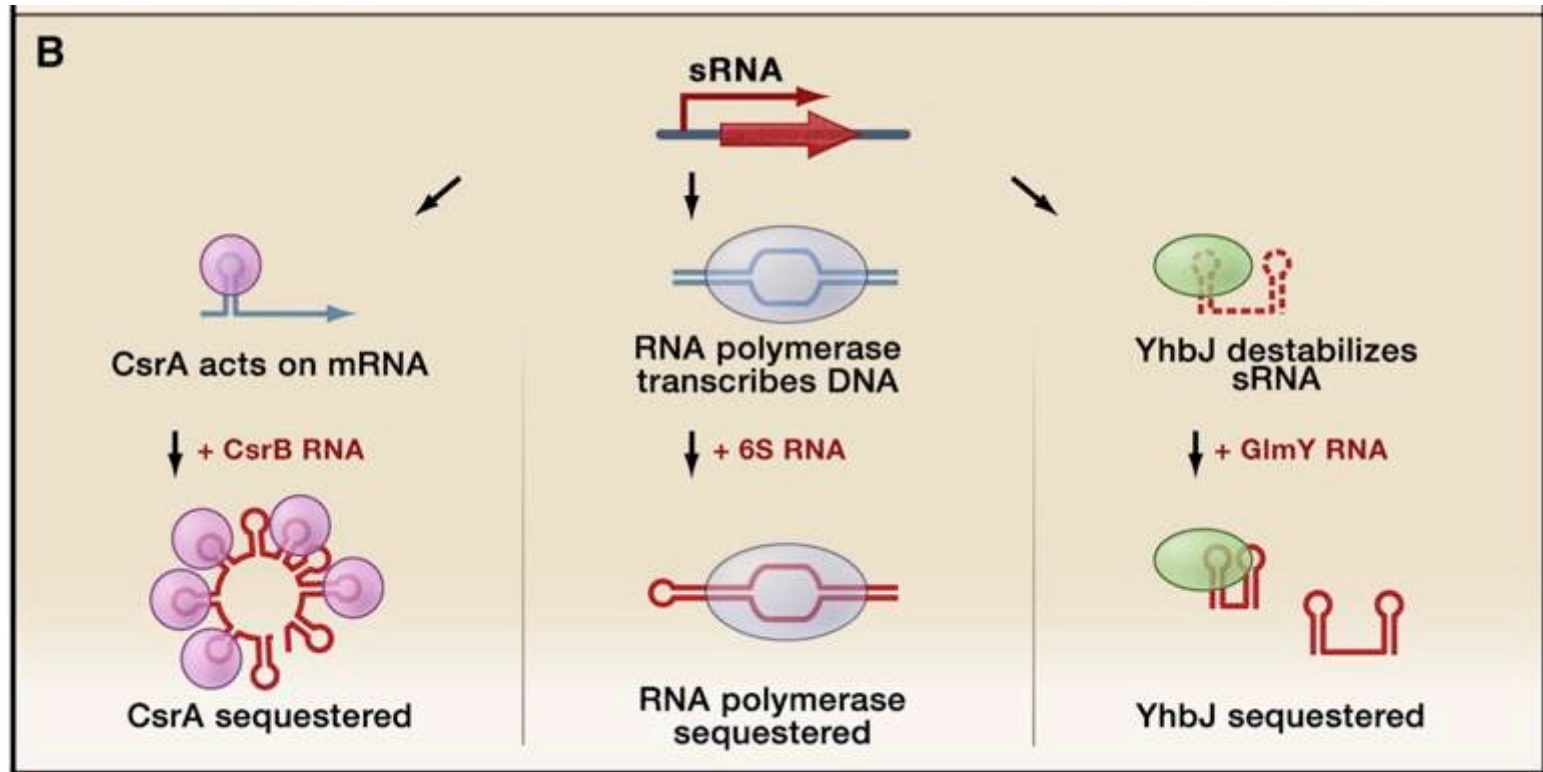


# Direct effector binding by riboswitches



L. Waters and G. Storz. *Cell*. 2009

# Regulatory RNA acting by protein binding



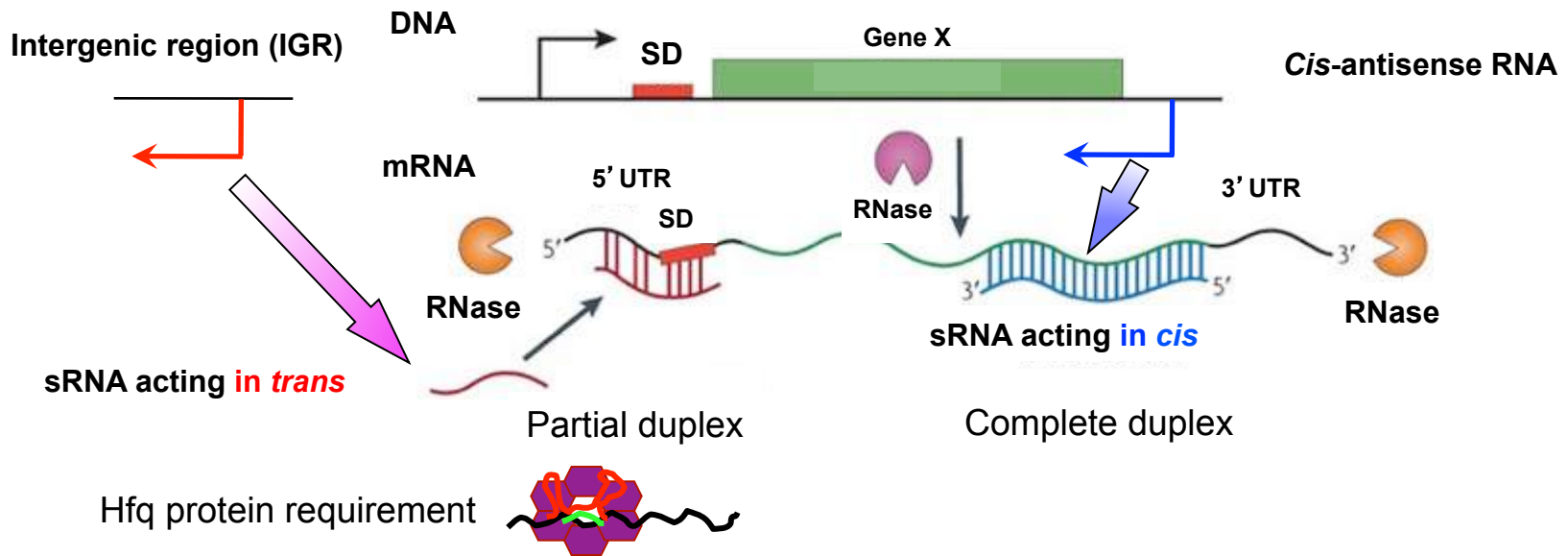
L. Waters and G. Storz. *Cell*. 2009

# Regulatory RNA acting by duplex formation



**Trans localisation**

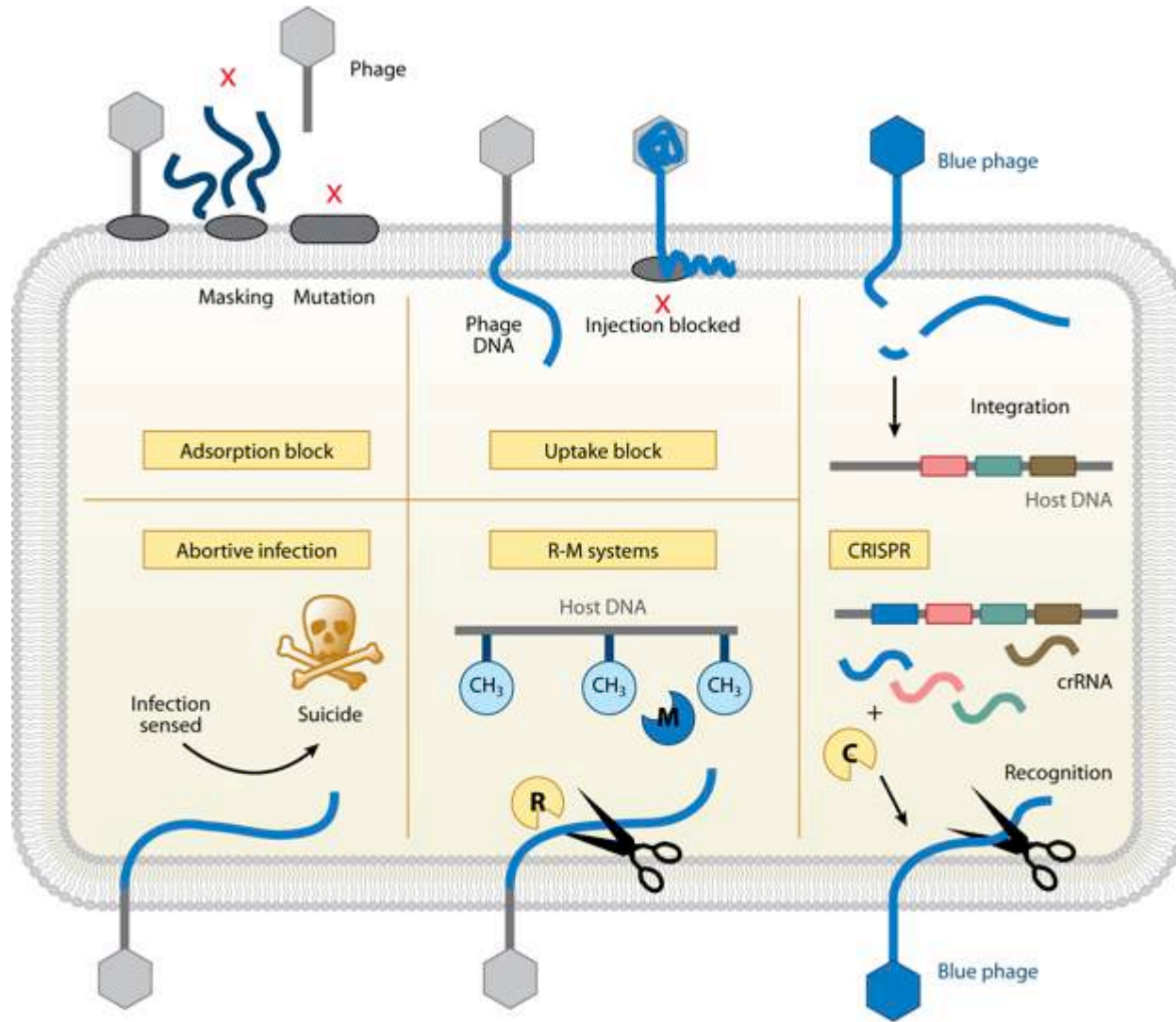
**Cis localisation**



**RNA duplex formation – negative or positive effect on target mRNA**

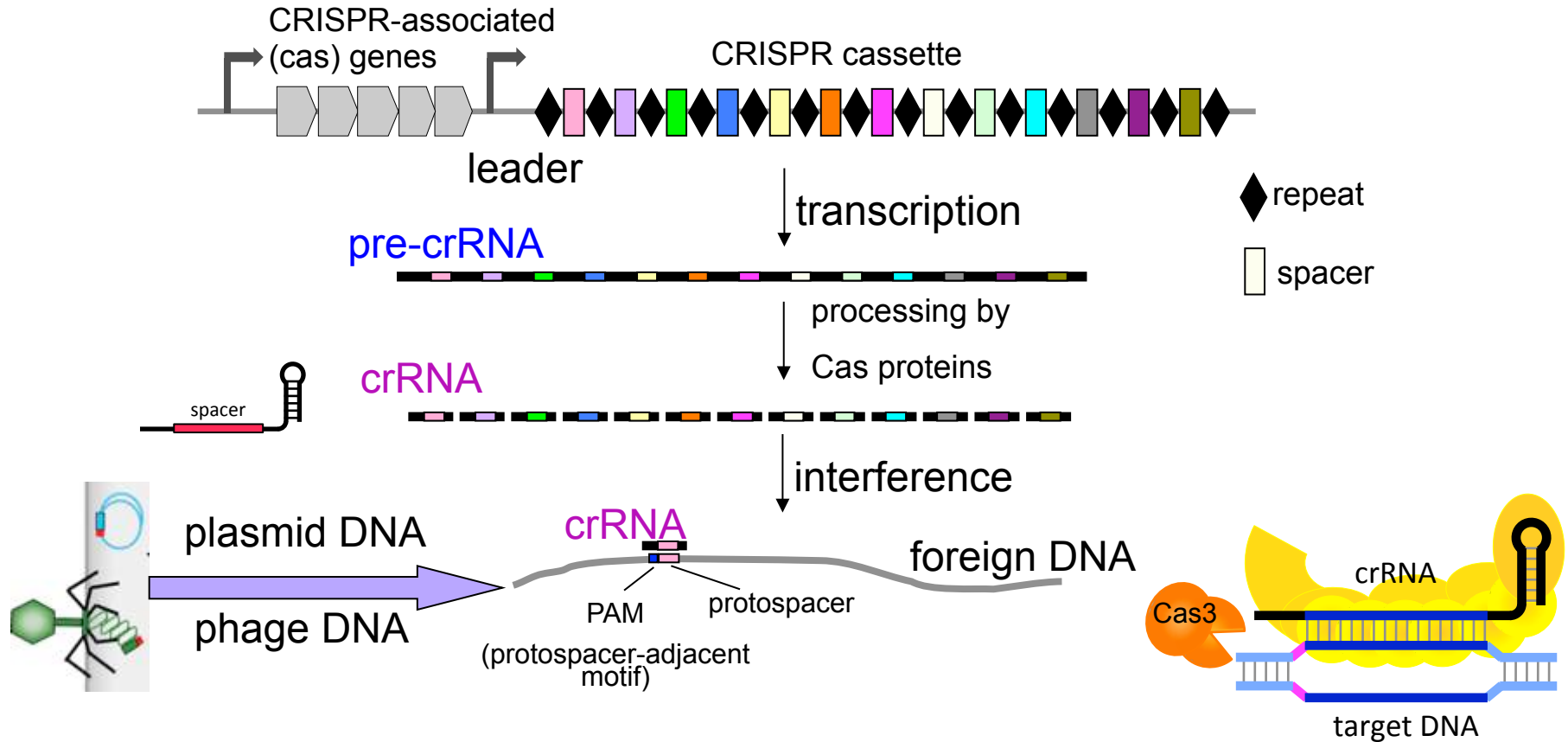
*J. Gripenland. et al. Nature reviews. Microbiology. 2010*

# Prokaryotic defense systems



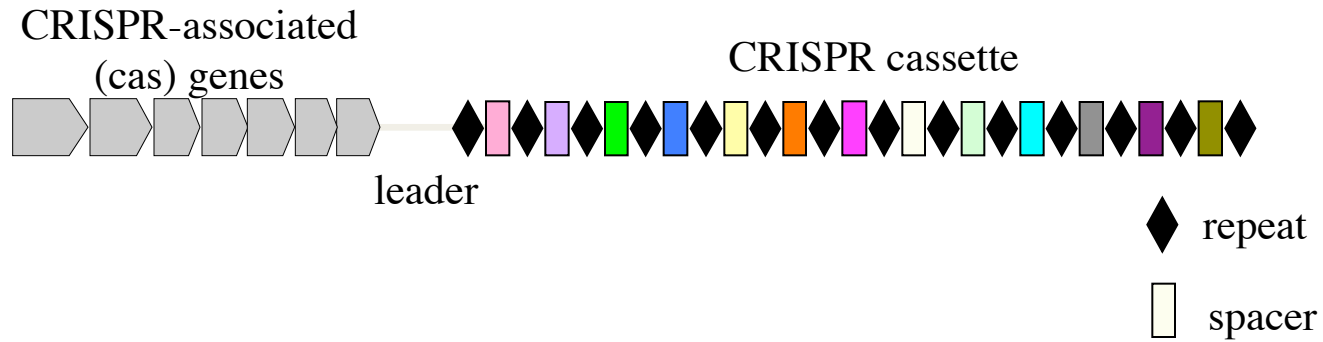
# CRISPR-Cas system

**CRISPR (clustered regularly interspaced short palindromic repeats)-Cas system**  
found in 90% of archaeal and 40% of bacterial genomes, prokaryotic immune system



Bhaya et al. *Annu. Rev. Genet.* 2011

# CRISPR-Cas system



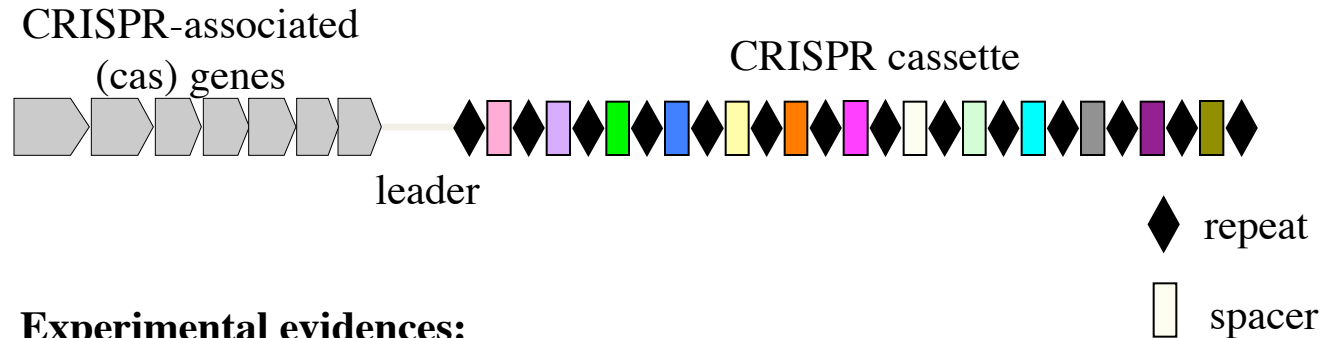
2005 - some spacer sequences match plasmid or viral DNA



CRISPR-Cas - prokaryotic immune system?



# CRISPR-Cas system



## Experimental evidences:

[CRISPR provides acquired resistance against viruses in prokaryotes.](#)

Barrangou *et al.*, Science. 2007, 315(5819):1709-12.

*Streptococcus thermophilus*:

phage infection → new spacer incorporation → phage resistance

[Small CRISPR RNAs guide antiviral defense in prokaryotes.](#)

Brouns *et al.*, Science. 2008, 321(5891):960-4.

*Escherichia coli*:

artificially engineered CRISPR locus containing  $\lambda$  phage DNA-matching spacer →  $\lambda$  phage resistance

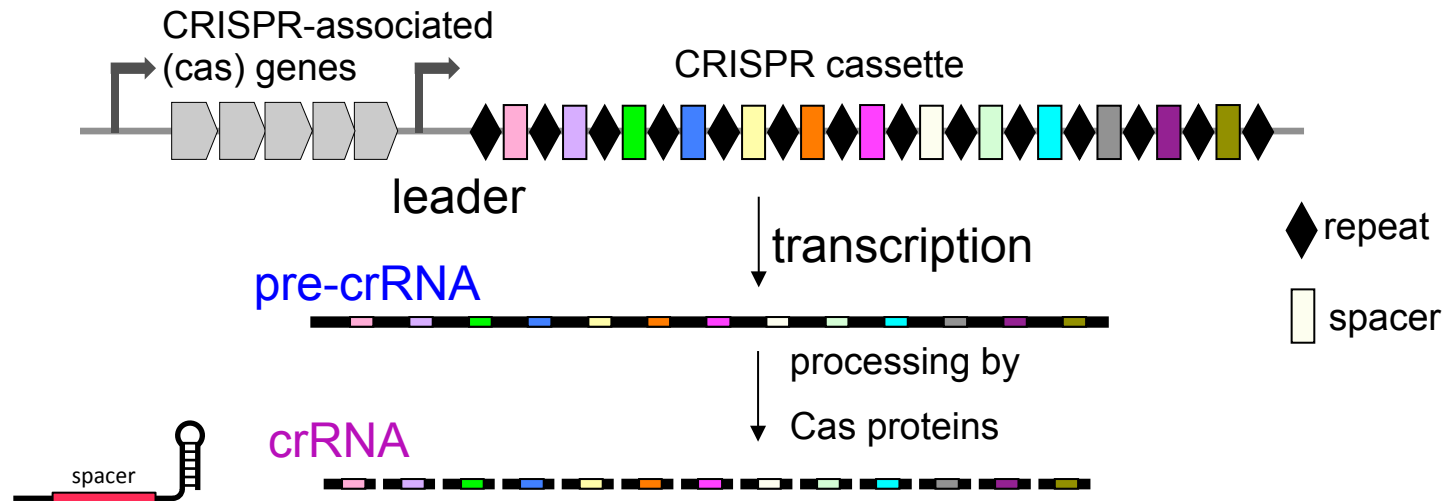
[CRISPR interference limits horizontal gene transfer in staphylococci by targeting DNA.](#)

Marraffini & Sontheimer, Science. 2008, 322(5909):1843-5.

*Staphylococcus epidermidis*:

CRISPR-Cas system provides a barrier against plasmid conjugation/transformation

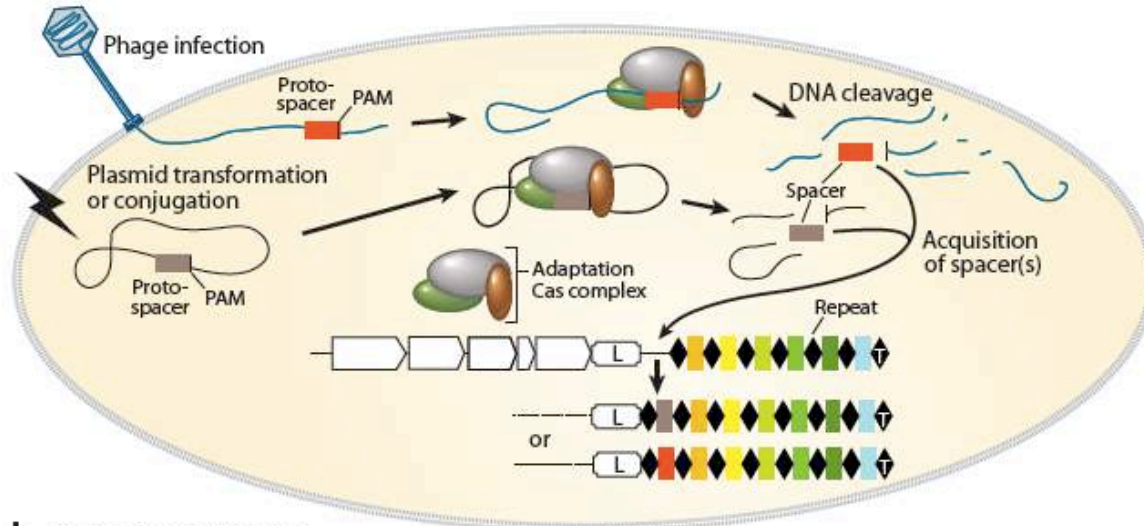
# CRISPR-Cas system expression



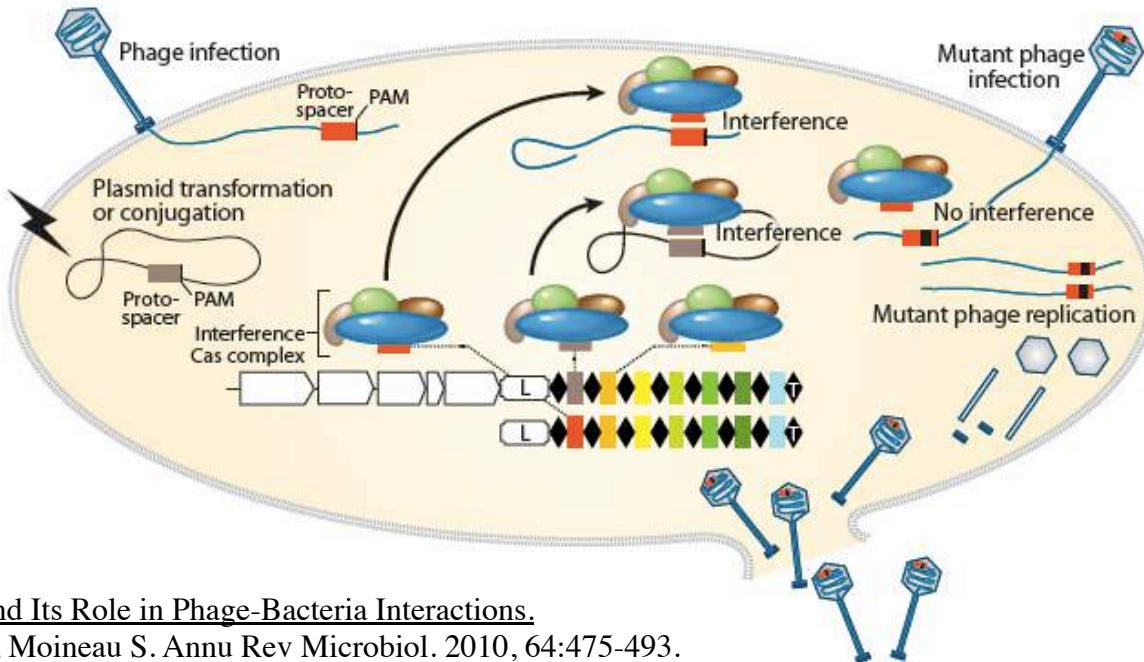
Bhaya et al. *Annu. Rev. Genet.* 2011

# CRISPR-Cas system function

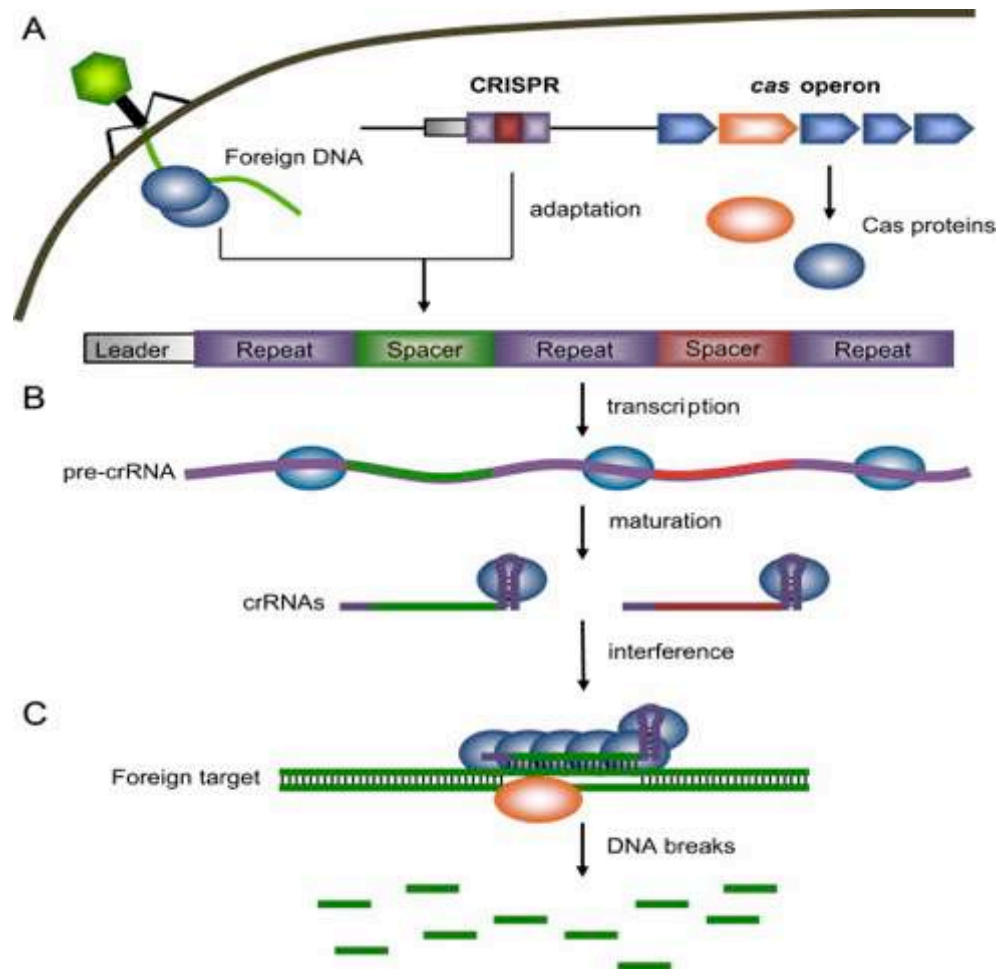
## a Stage I: Adaptation



## b Stage II: Interference



# CRISPR-Cas system function: interference

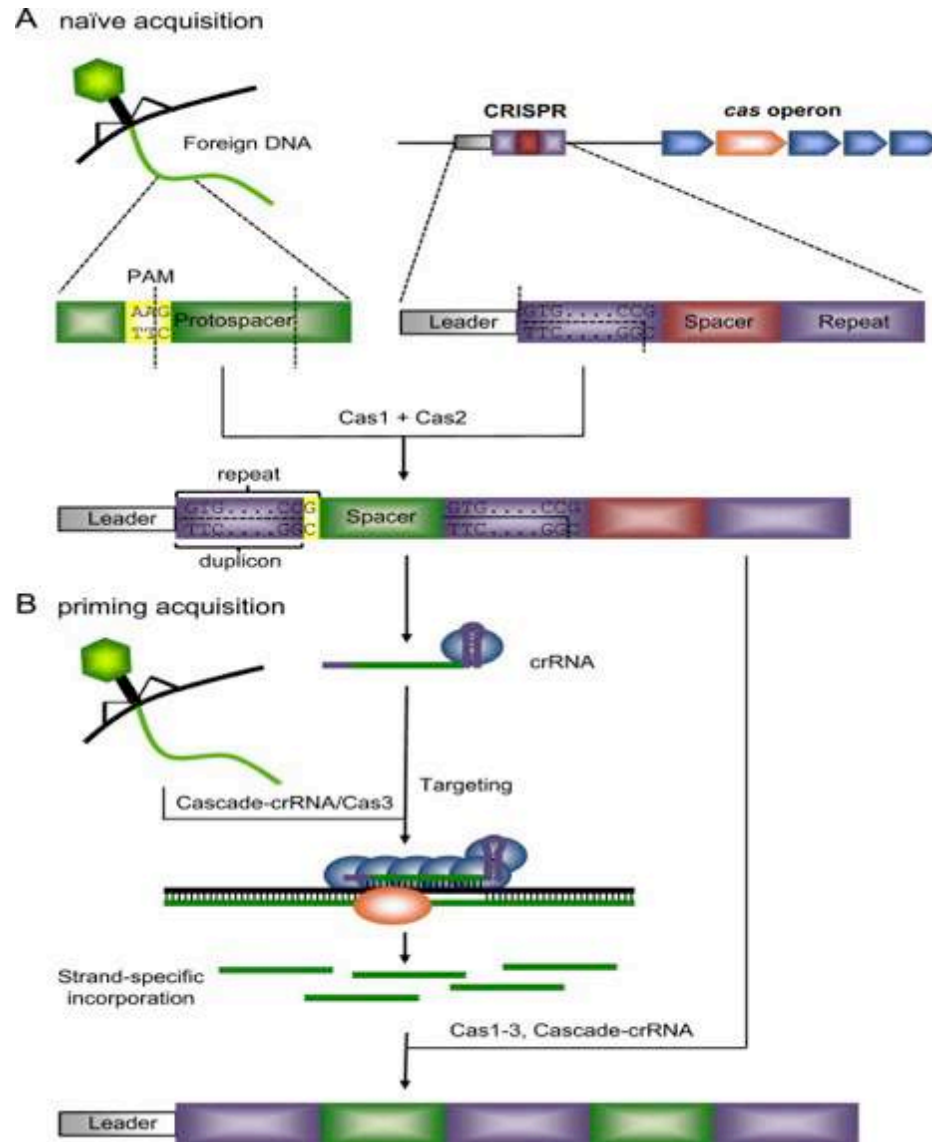


Peter C. Fineran , Emmanuelle Charpentier

**Memory of viral infections by CRISPR-Cas adaptive immune systems: Acquisition of new information**

Virology Volume 434, Issue 2 2012 202 - 209

# CRISPR-Cas system function: adaptation



Peter C. Fineran , Emmanuelle Charpentier

**Memory of viral infections by CRISPR-Cas adaptive immune systems: Acquisition of new information**

Virology Volume 434, Issue 2 2012 202 - 209

# Distinctive features of strict anaerobes

## Anaerobic metabolism (ancient group, Clostridia)

- ✓ Fe-S enzymes for energy metabolism
- ✓ Amino acid fermentations (Stickland reactions)
- ✓ Oxidative stress response mechanisms (absence of SOD, catalase)
- ✓ Establishment of sporulation
- ✓ Link between metabolism and virulence

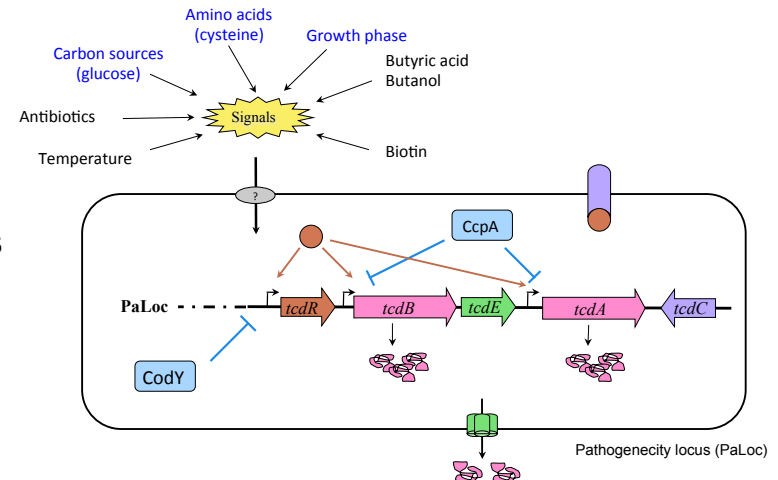
## Biotechnological applications

- ✓ Solvents production, biosynthesis of biofuels (*C. acetobutylicum*, *C. thermocellum*)



## Regulation

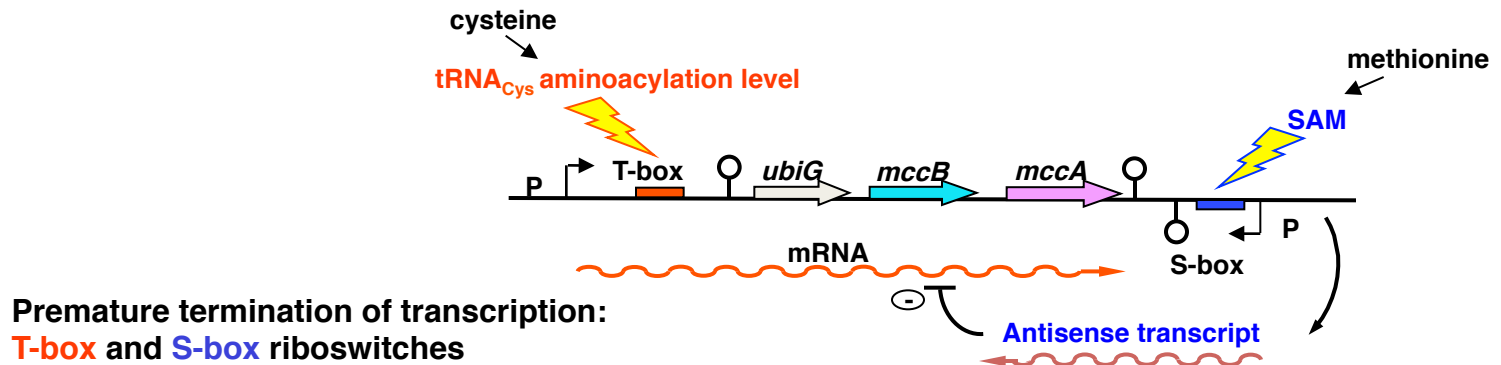
- ✓ Specific regulators, particular pathways
- ✓ Toxin production control by glucose and amino acids (cysteine)
- ✓ RNA-based mechanisms



# RNA-based regulation in Clostridia

*Clostridium acetobutylicum*

Control of sulfur metabolic operon by an **antisense RNA**  
(André ... Soutourina, NAR 2008)



*Clostridium perfringens*

Control of toxin-encoding genes by **4 non coding RNAs**  
(Okumura et al, 2008; Ohtani et al, 2010)

*Clostridium difficile*

Control of virulence determinants ?

**sRNAs contributing to regulatory networks governing *C. difficile* physiology and pathogenesis ?**





## Regulatory RNAs in Clostridia team Microbiology Department

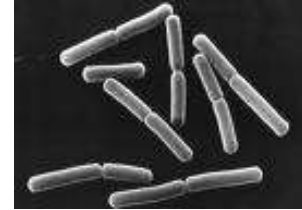
<https://www.i2bc.paris-saclay.fr/>





# *Clostridioides (Clostridium) difficile*

- ✓ Gram positive spore forming
- ✓ strictly anaerobic bacterium
- ✓ colonization of intestinal tract
- ✓ **a major nosocomial enteropathogen**



## ***C. difficile* became a public health issue**

- ✓ 95% cases of pseudomembranous colitis (PMC)
- ✓ 10-25% cases of antibiotic-associated diarrhoea (AAD)



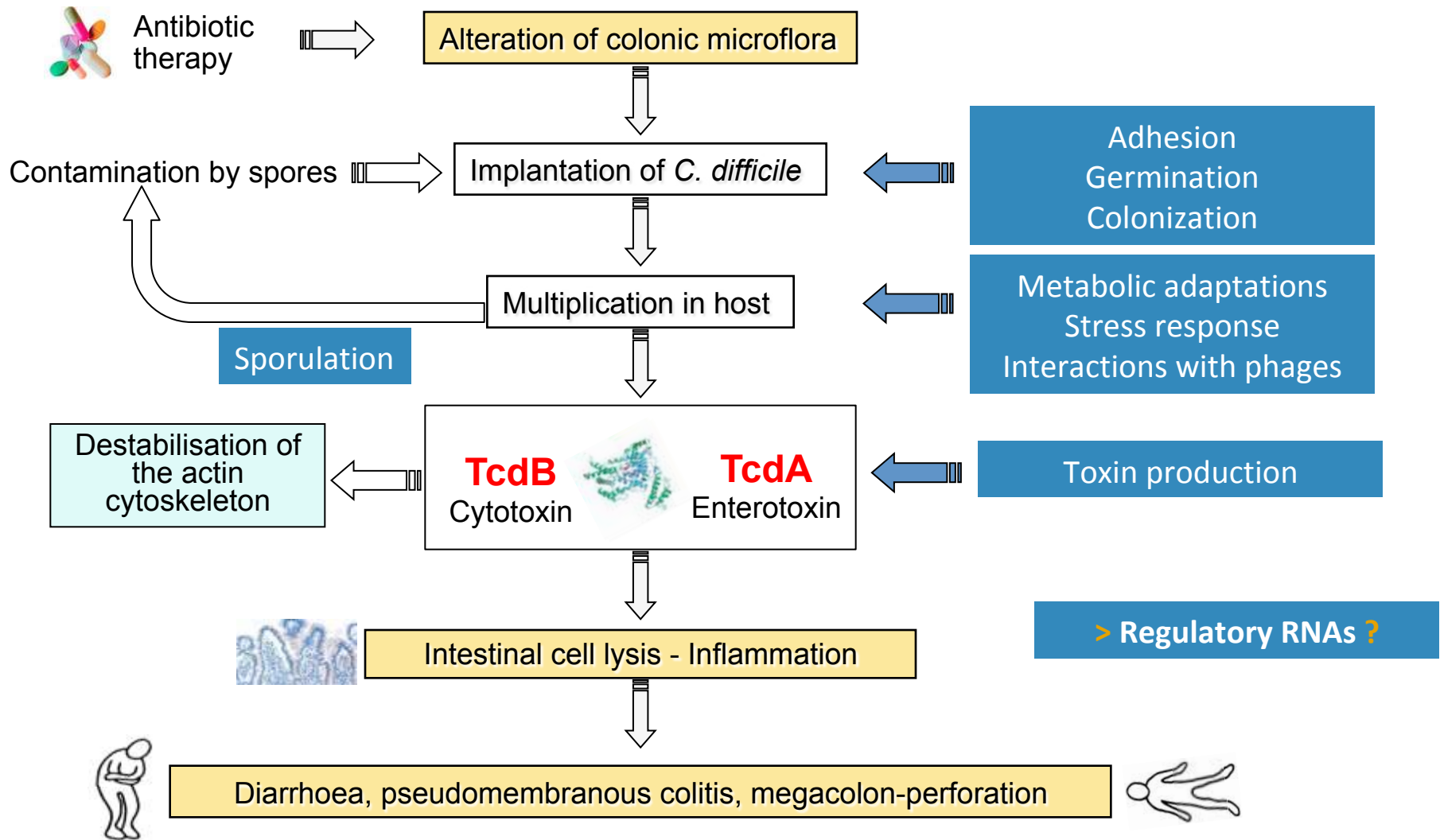
- ✓ **Most common cause of nosocomial infectious diarrhoea in adults**

**Emergence of hypervirulent and epidemic strains** (as 027 strain)

**Economic burden** in the developed countries (3 billions € or \$ of costs in US and EU)

**Risk factors of *C. difficile* infection (CDI): Antibiotic exposure and old age** (over 65)

# Infection cycle of *C. difficile*

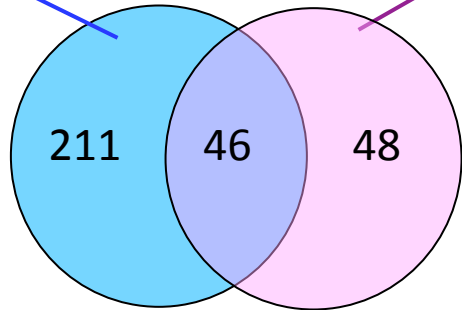


**Regulatory RNAs could be involved in several stages of the infection cycle**

# Genome-wide identification of sRNAs in *C. difficile*

Comparative genomics  
and bioinformatics

RNA-seq, dRNA-seq

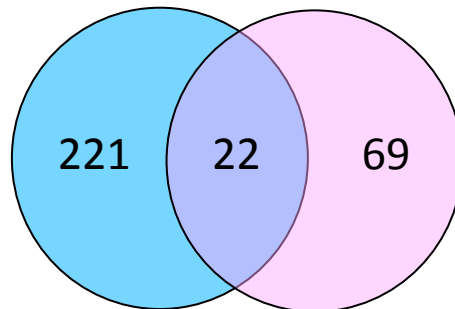


**94 intergenic region (IGR) sRNAs**

Potential *trans* riboregulators



**12 CRISPR RNAs**



**91 Antisense sRNAs**

Potential *cis* riboregulators



**66 riboswitches**

**16 cyclic di-GMP riboswitches**



About **185** sRNAs (**35/40** detected by Northern blot)

Soutourina et al. PLoS Genetics. 2013

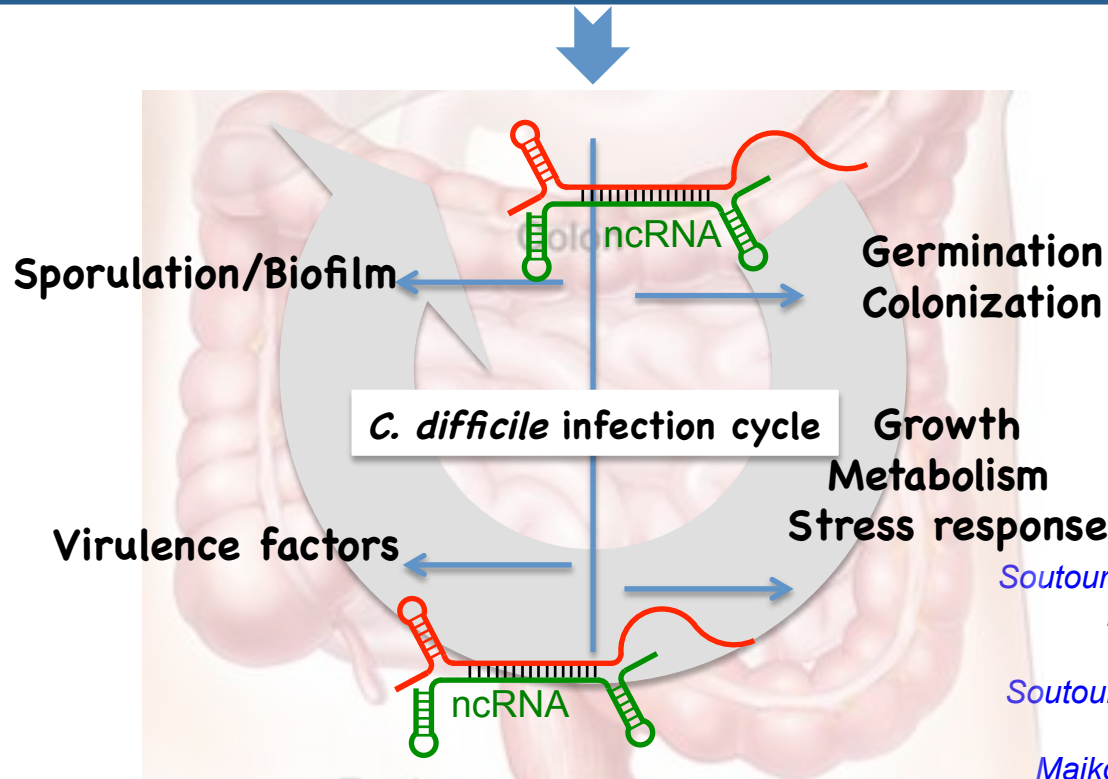
# Role of the regulatory RNAs in *C. difficile* physiology

More than **250 ncRNA** & **large diversity** of mechanisms in *CD* (CRISPR RNAs, *trans* and *cis* antisense RNAs and riboswitches)

TSS-mapping

RNA-seq

*In silico*



[Soutourina et al. PLoS Genetics. 2013](#)

[Boudry et al. J. Bacteriol. 2014](#)

[Boudry et al. mBio. 2015](#)

[Soutourina. Curr Opin Microbiol. 2017](#)

[Maikova et al. NAR. 2018](#)

[Maikova et al. Front Microbiol. 2018](#)

[Soutourina. Toxins. 2019, Maikova et al AEM. 2019](#)

[Soutourina et al. Frontiers in Microbiol. 2020](#)

[Peltier et al. Communications Biol 2020](#)

[Piattelli et al. Genes 2020, Kreis & Soutourina Current Opinion Microbiol 2022](#)

[Boudry et al. RNA Biol. 2021, Maikova et al. mBio 2021](#)

[Muzyukina et al. mSphere 2023, Muzyukina & Soutourina. Biochimie. 2023](#)

# Role of the regulatory RNAs in *C. difficile* physiology

More than **250 ncRNA** & **large diversity** of mechanisms in *CD* (CRISPR RNAs, *trans* and *cis* antisense RNAs and riboswitches)



## Original aspects of RNA-based control in regulatory function



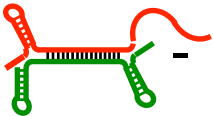
- **Riboswitches** responding to **c-di-GMP** involved in cellular processes



- **RNA chaperone protein Hfq** in the ncRNA network



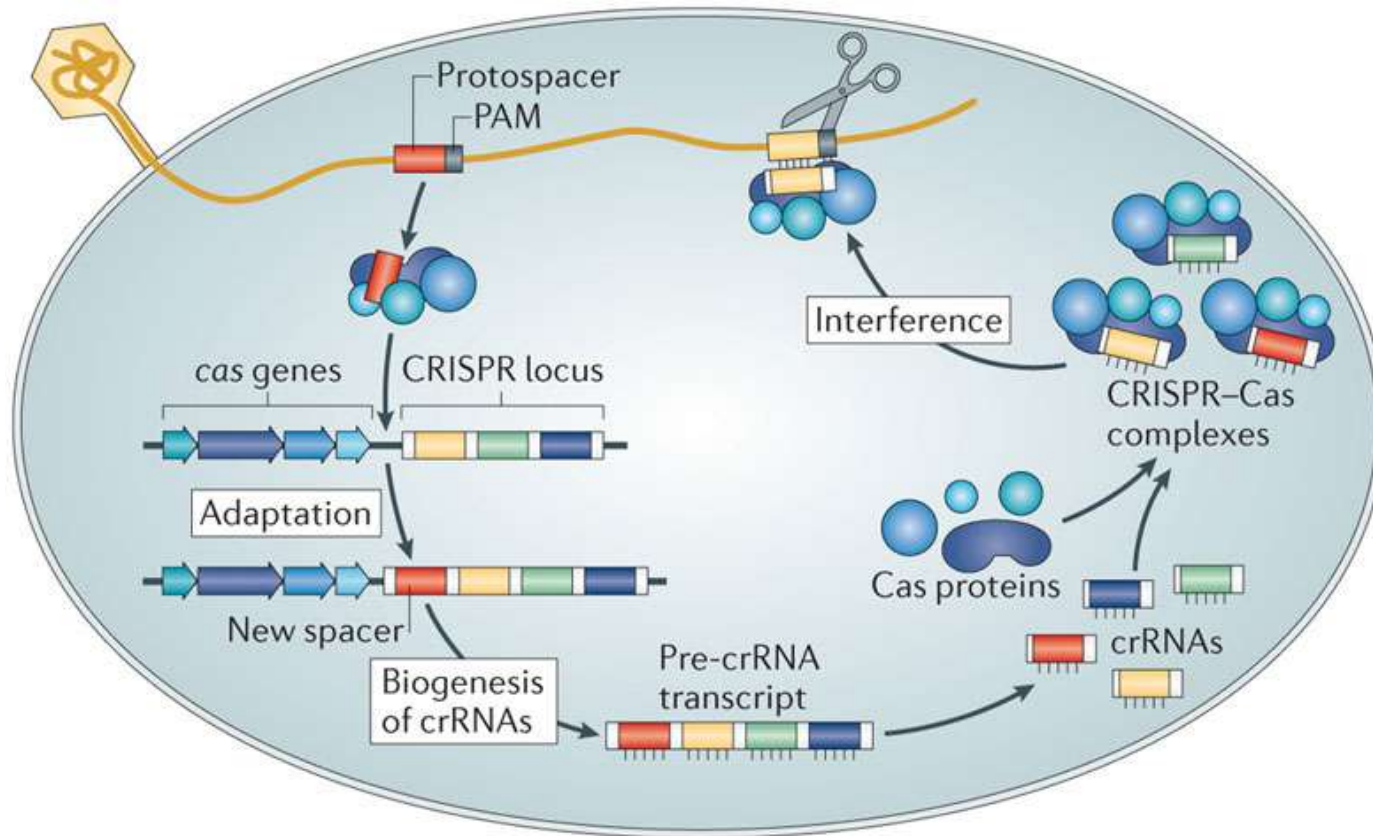
- Function and regulation of **CD CRISPR-Cas system**



- Antisense RNAs within **type I toxin-antitoxin systems**

# CRISPR-Cas system

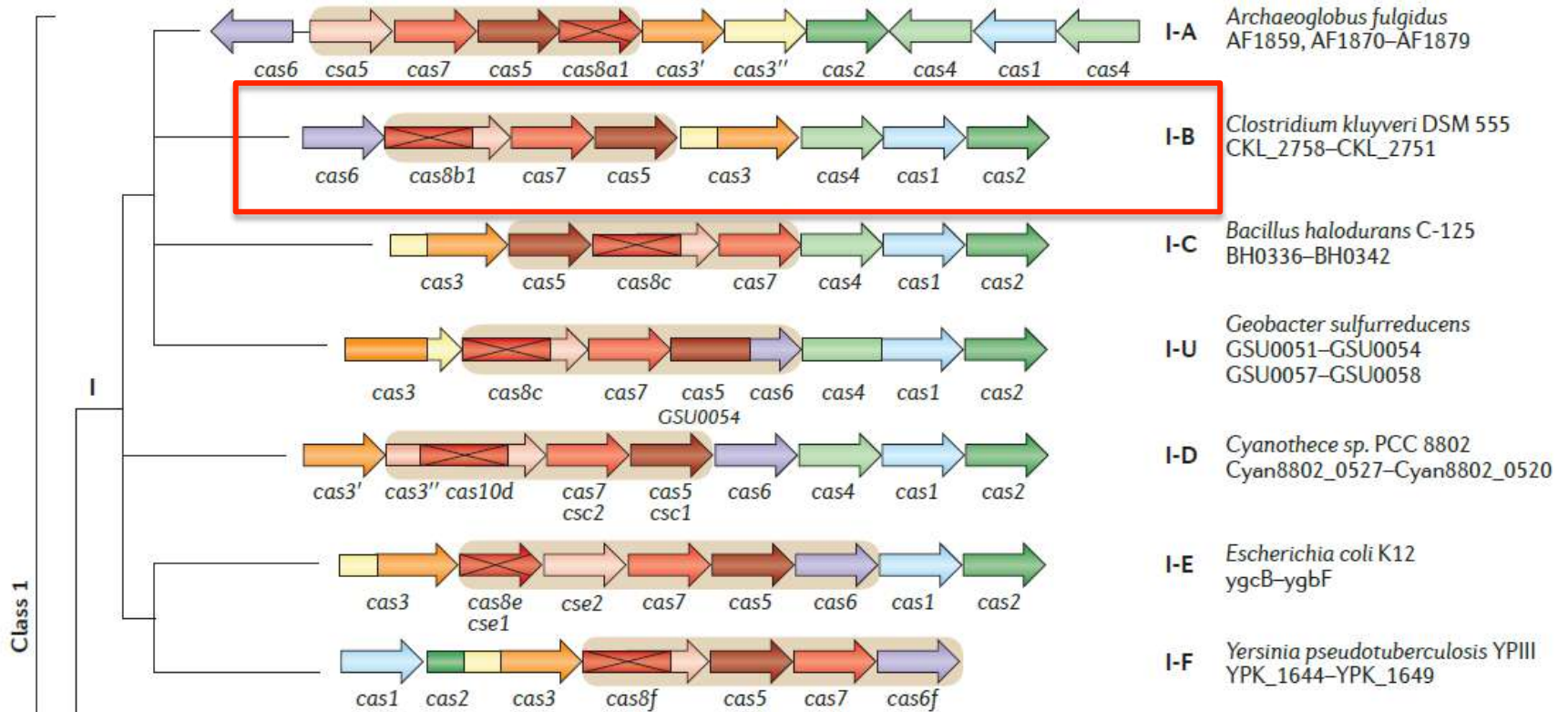
clustered regularly interspaced short palindromic repeats





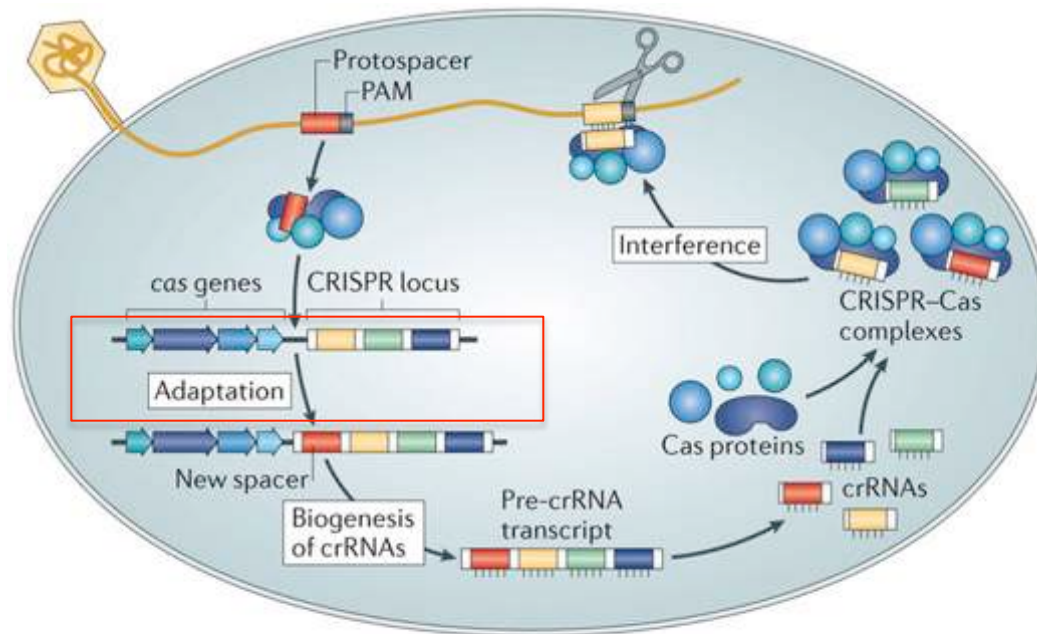


# Class 1 type I CRISPR-Cas systems





# Function and regulation of *C. difficile* CRISPR-Cas system



Nature Reviews | Microbiology

In *CD* strain 630 : 12 CRISPR regions exist and are expressed

In epidemic *CD* strain 027: 9 active CRISPR arrays

.... A total of 819 spacers from nine *CD* strains

**Large defence capacity within phage-rich gut communities**

# CRISPR RNAs identified by dRNA-seq

CRISPR (clustered regularly interspaced short palindromic repeats)-Cas system

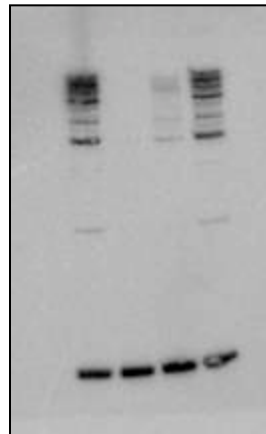


## CRISPR16

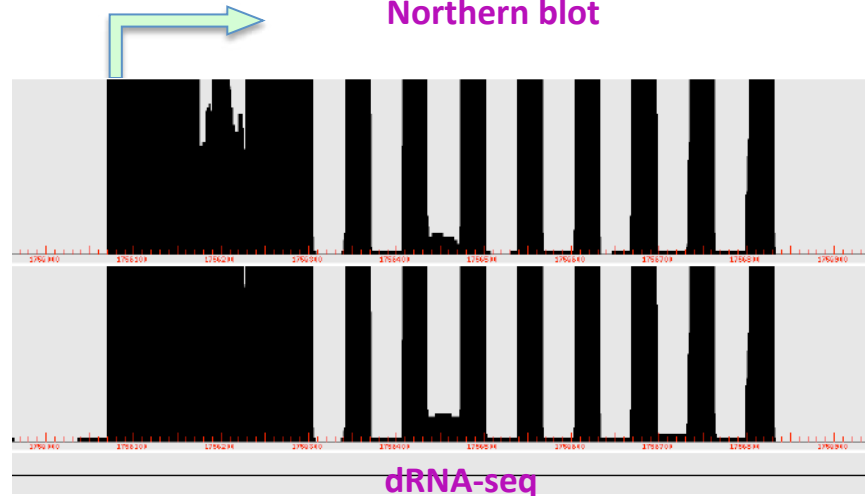
≈1000 nt  
≈700 nt  
pre-crRNA

≈130 nt  
Processed  
pre-crRNA

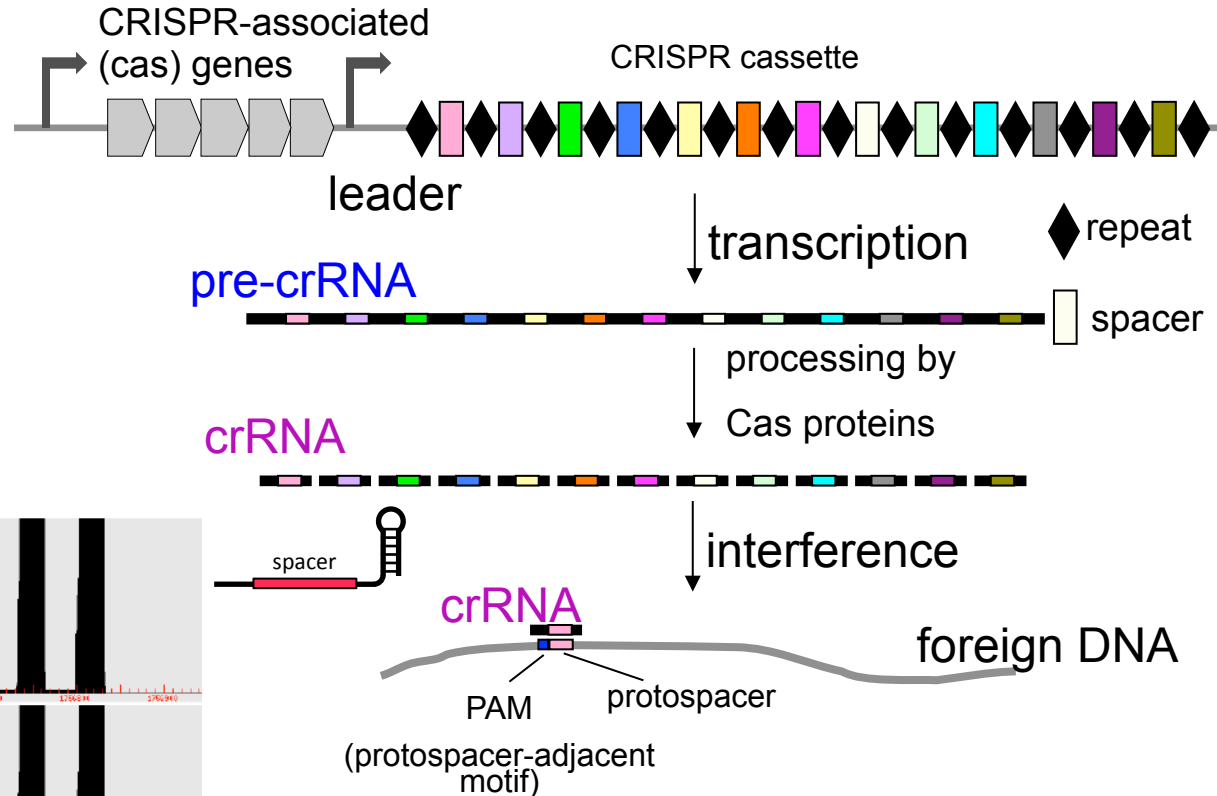
≈66 nt  
crRNA



Northern blot



dRNA-seq



# Project 1: CD CRISPR-Cas system function and regulation

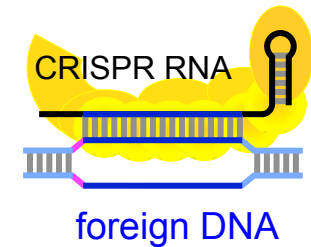
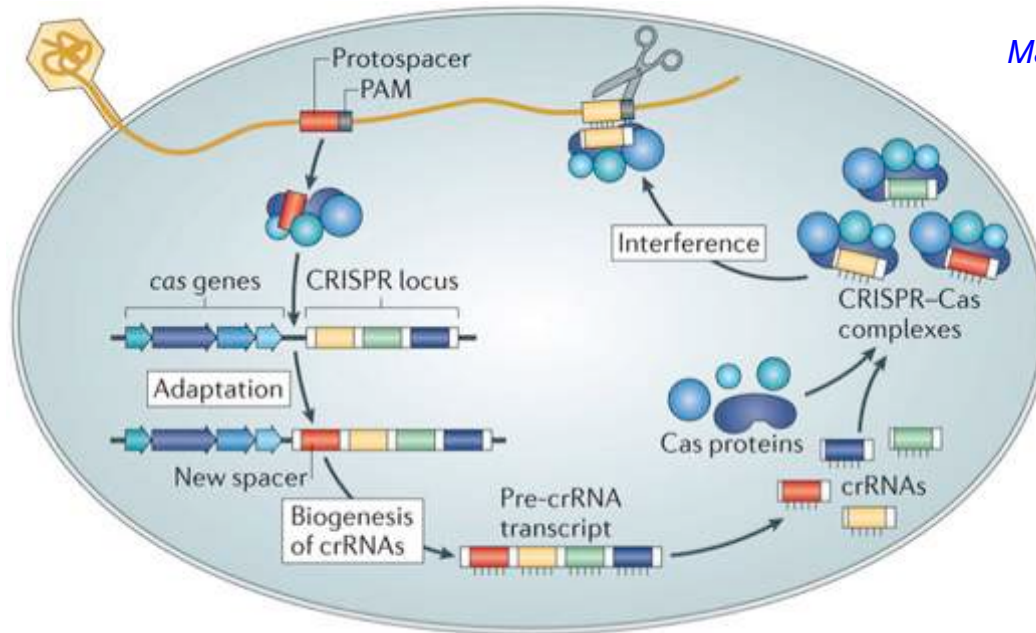
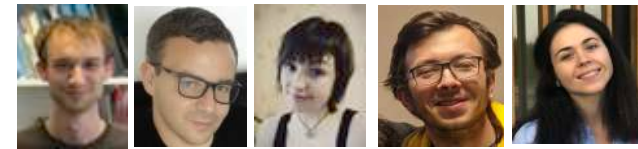
ARNCLO



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Universitaires  
Est Parisien

SAINT-ANTOINE

UNIVERSITÉ DE  
SHERBROOKE



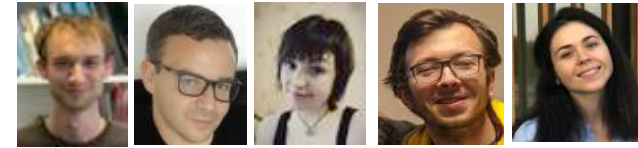
*Boudry et al. mBio. 2015*  
*Maikova et al. NAR. 2018*  
*Maikova et al. Frontiers Microbiol. 2018*  
*Maikova et al. AEM. 2019*  
*Maikova et al. PhD thesis*

Endogenous system for CD genome editing

Sensitive high-resolution CRISPR-based typing for epidemiology & CD microevolution survey

Self-targeting, autoimmunity

**Great potential for genome editing and therapeutic applications**



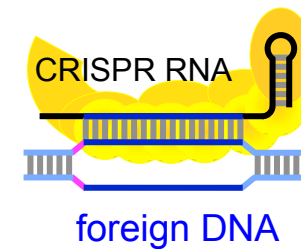
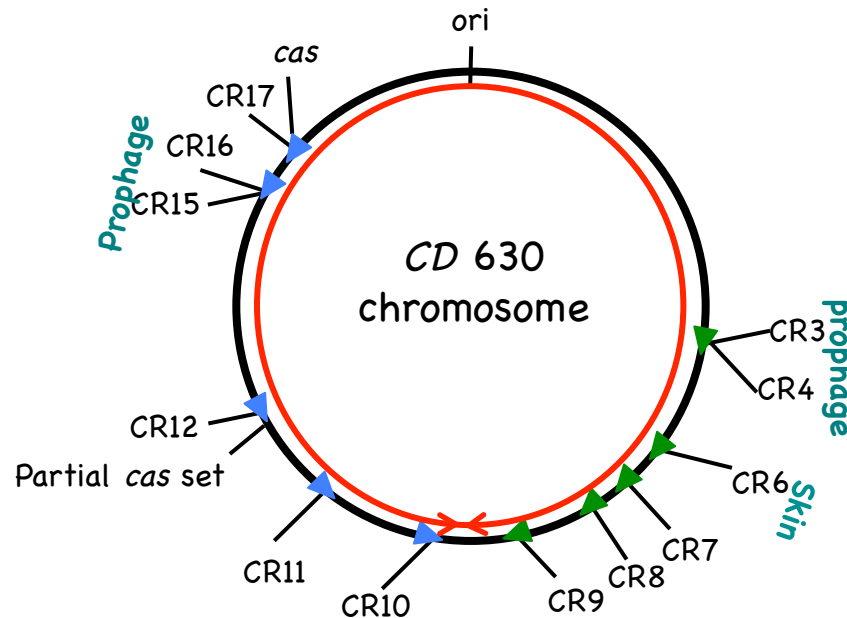
Boudry et al. *mBio*. 2015

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Maikova et al. *Frontiers Microbiol.* 2018

Maikova et al. *AEM*. 2019

Maikova et al. *PhD thesis*



In CD strain 630 : **12 CRISPR regions** exist and are expressed  
In epidemic CD strain 027: **9 active CRISPR arrays**



.... A total of 819 spacers from nine CD strains  
**Large defense capacity within phage-rich gut communities**

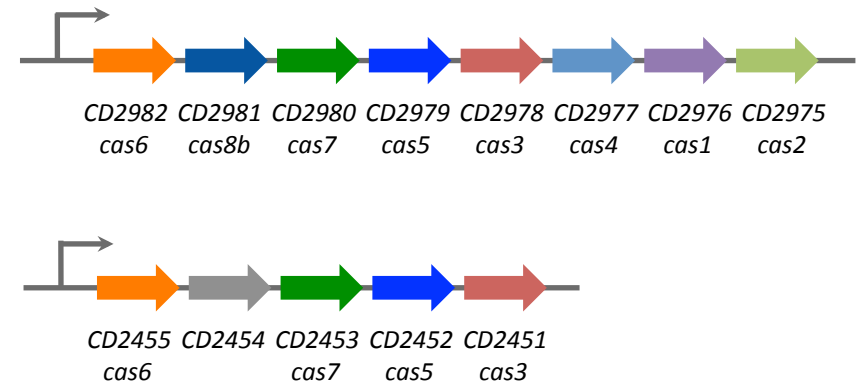
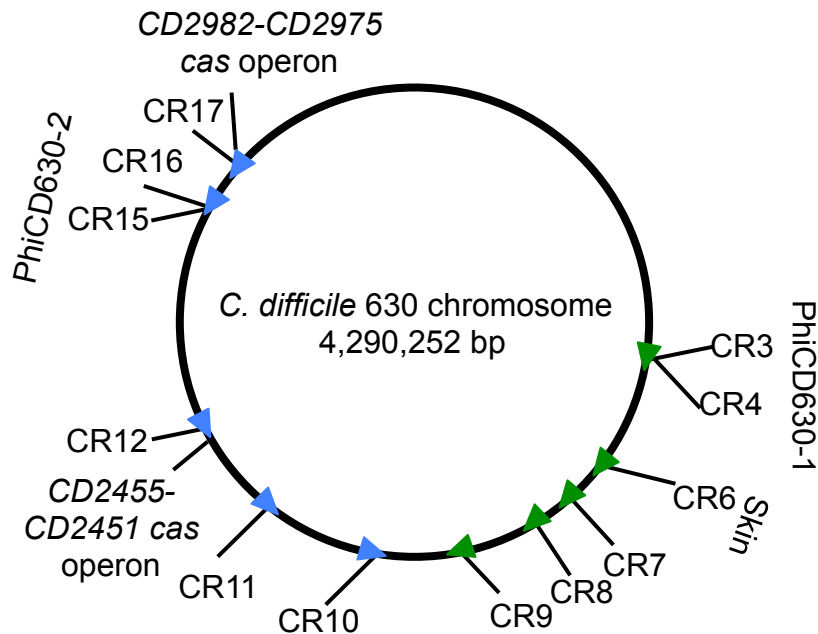
# CRISPR analysis in *C. difficile*



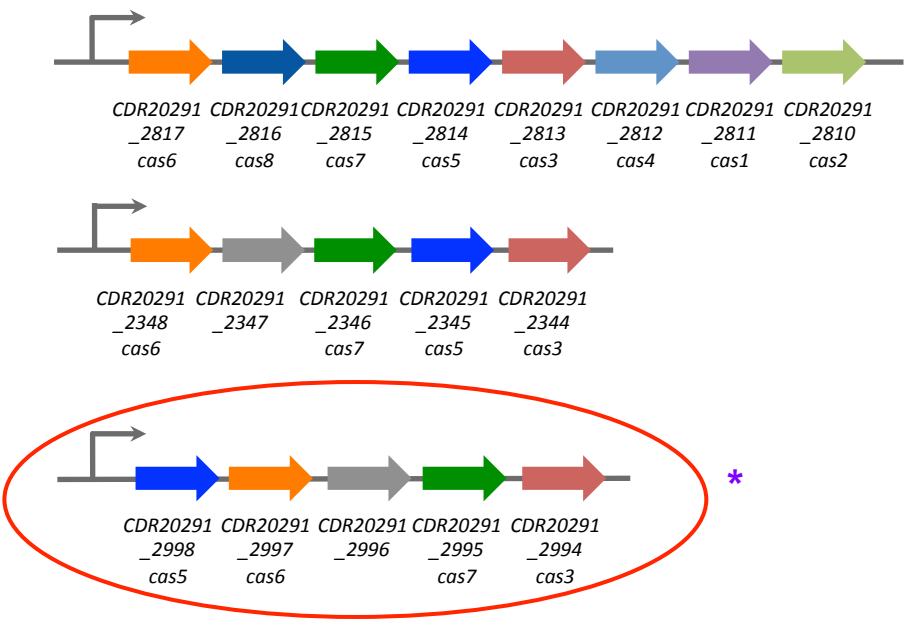
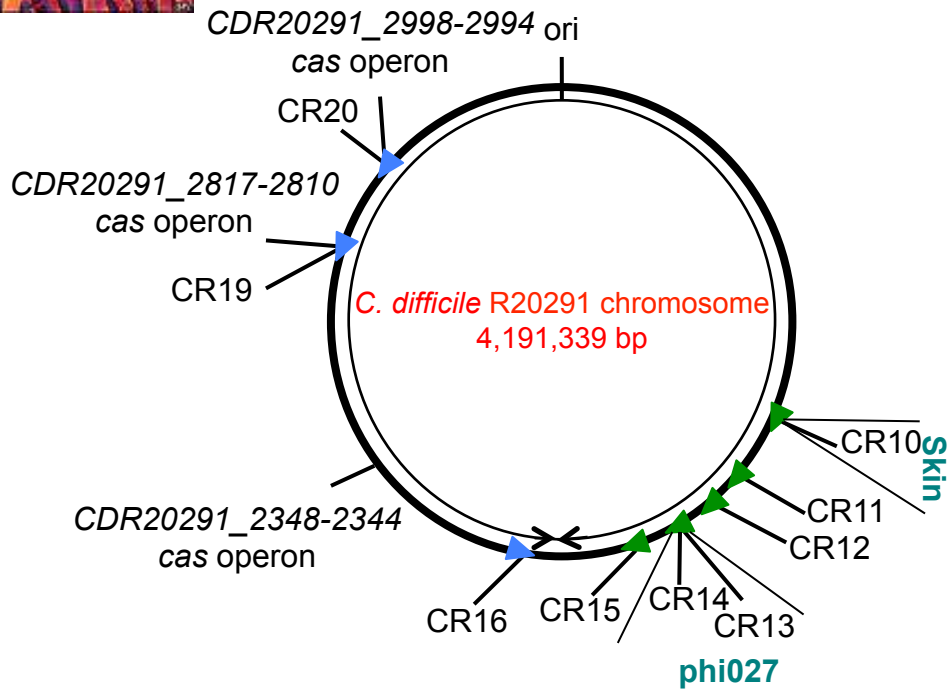
dRNA-seq/ RNA-seq: expression of all **12 CRISPR RNAs**:

**2** associated with **cas genes (type I-B)**

**5** in **phage** regions (**3** highly expressed), strategy for limiting competing phages ?  
complex **regulation** by stress- and biofilm-related stimuli, link with TA systems



# CRISPR analysis in epidemic *C. difficile* strain of 027 ribotype



## RNA-seq: expression of all 9 CRISPR RNAs:

- transcriptional orientation in the direction of replication
- 2 associated with cas genes (type I-B)
- additional cas operon specific to 027 ribotype strains\*
- 3 in phage regions

Boudry et al. mBio. 2015

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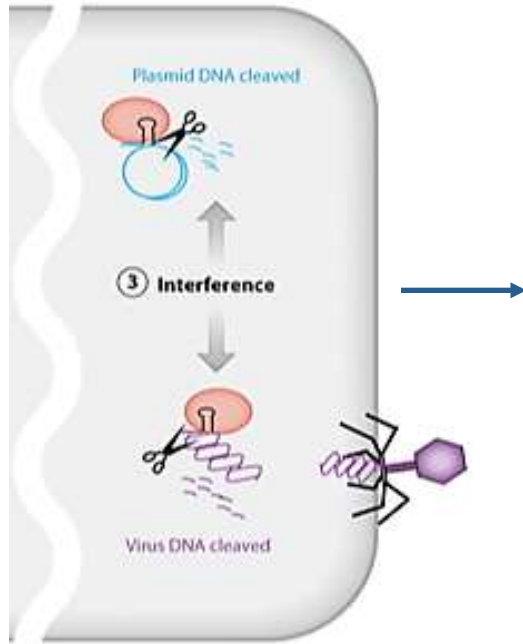
## Results:

### I. **Functionality** of CRISPR-Cas system in *C. difficile*

# Function of *C. difficile* CRISPR-Cas system



## Functionality of CRISPR system



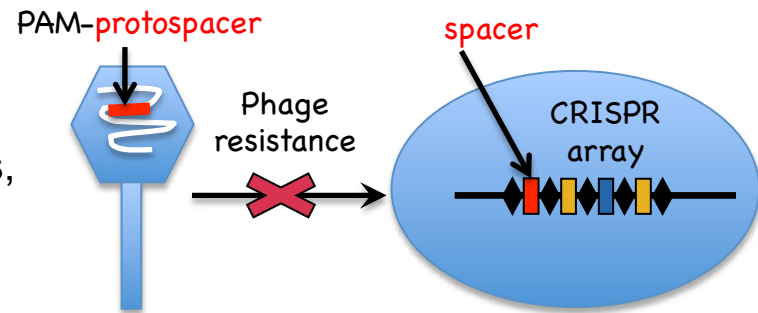
| Phage     | Strain | CRISPR Spacer match | Phage sensitivity |
|-----------|--------|---------------------|-------------------|
| PhiCD27   | 630    | +                   | R                 |
|           | 027    | +                   | R                 |
| PhiCD38-2 | 630    | +                   | R                 |
|           | 027    | -                   | S                 |

Correlation between **phage resistance** phenotype and CRISPR spacer match



**Large *in silico* CRISPR spacer homology analysis** (9 strains/22 phages, 11 new phage genome sequencing):

- extensive targeting of clostridial phages;
- multiple targeting of conserved homologous genes within related phages



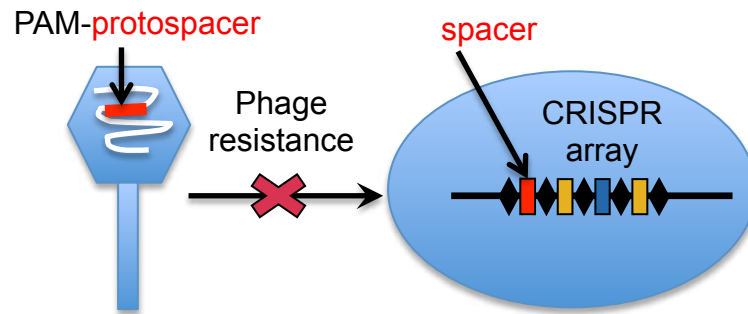
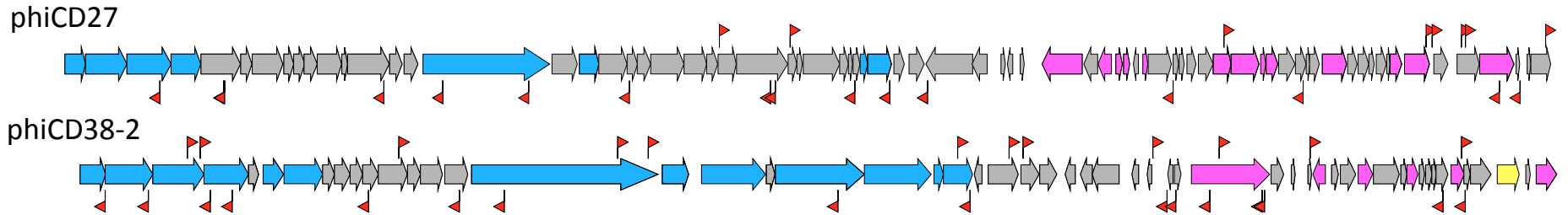
Boudry et al. *mBio*. 2015





# Functionality of CRISPR system in *C. difficile*: interactions with phages

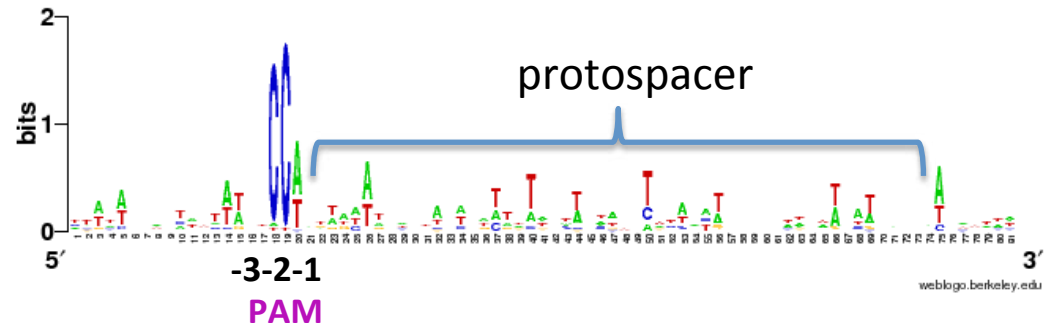
## Example of CRISPR spacer targeting of *C. difficile* phages



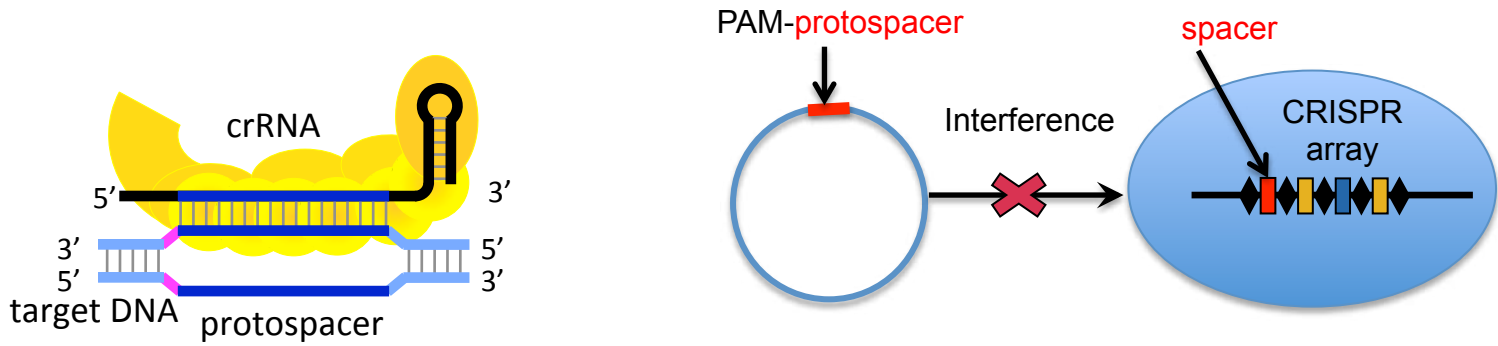
Boudry *et al.* mBio. 2015.

# Functionality of CRISPR system in *C. difficile*: plasmid interference

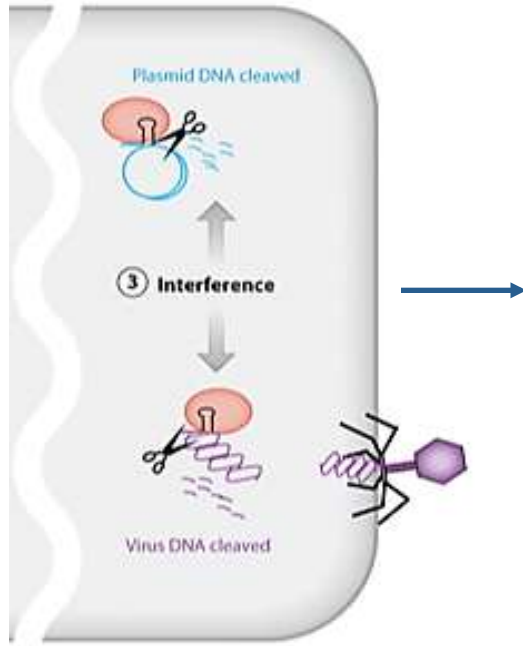
## PAM identification by protospacer alignment



Identification of 5' **CCA/CCT** protospacer-adjacent motif



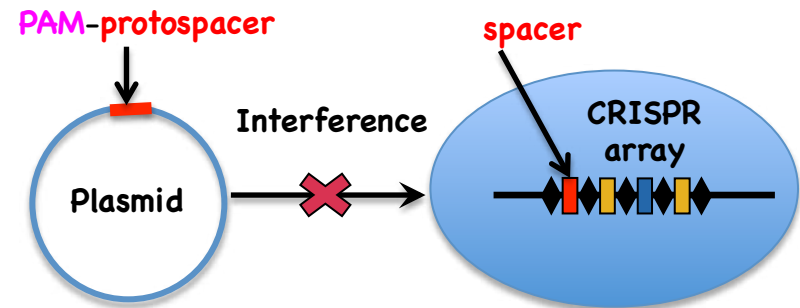
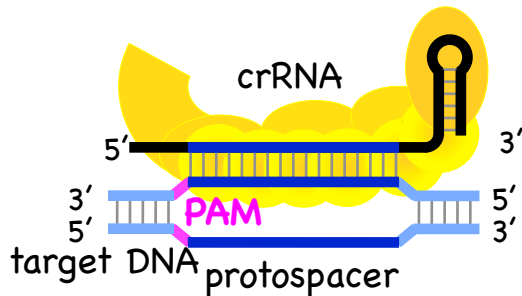
Boudry *et al.* mBio. 2015.



## Functionality of CRISPR system

Active interference process in **plasmid conjugation** efficiency assays in *CD* and in heterologous host *E. coli*

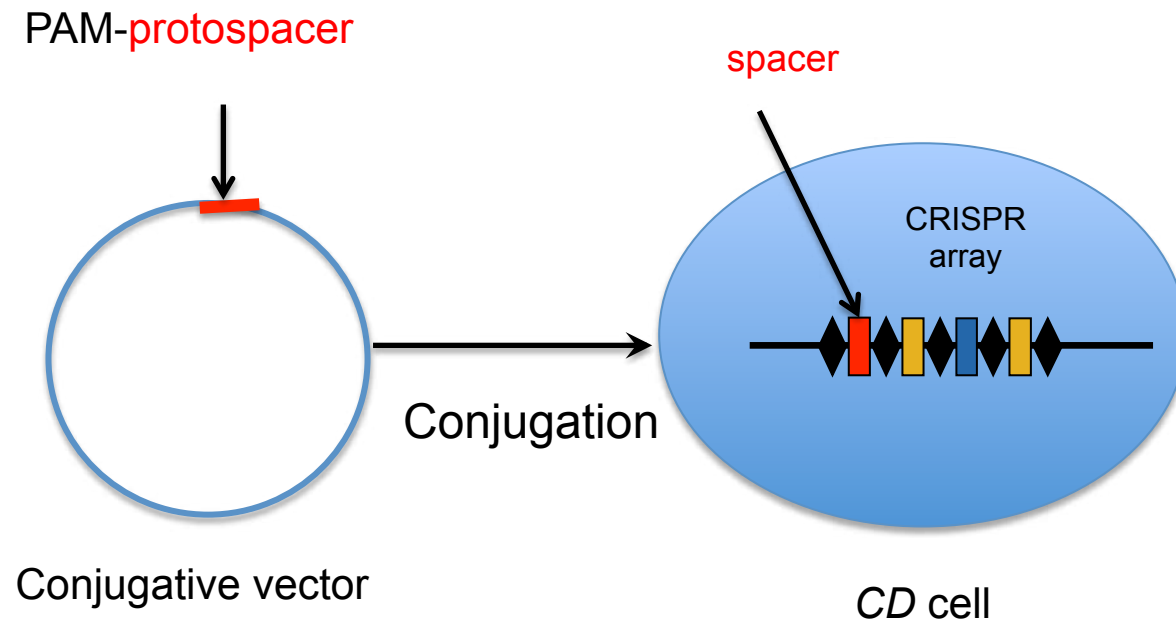
*Boudry et al. mBio. 2015*



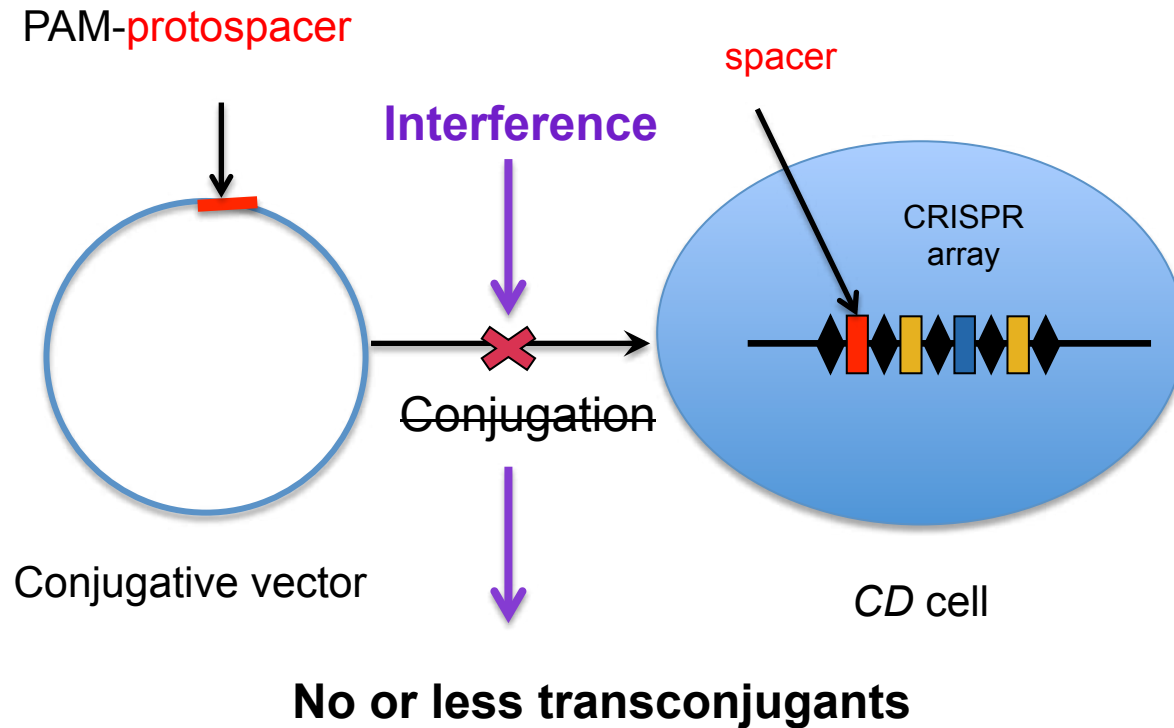
Almost all CRISPR arrays are active for interference !

*Maikova. PhD thesis; Maikova et al. mBio 2021*

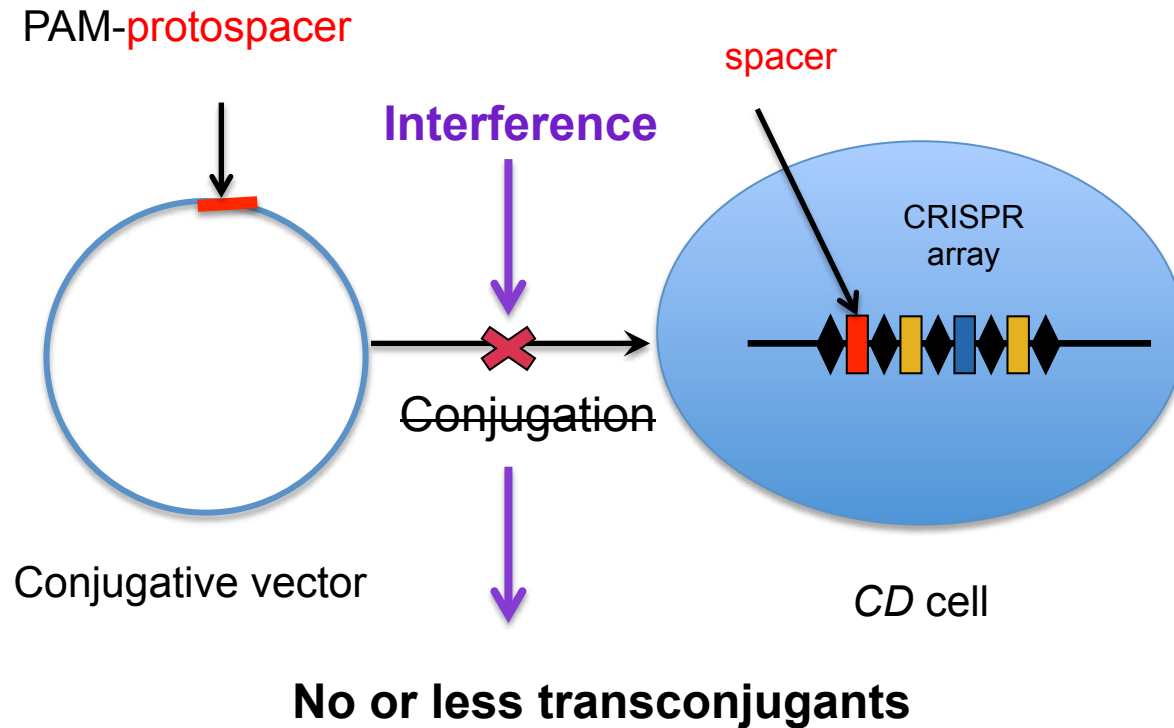
# Functionality of CRISPR-Cas system in *C. difficile*: plasmid interference



# Functionality of CRISPR-Cas system in *C. difficile*: plasmid interference

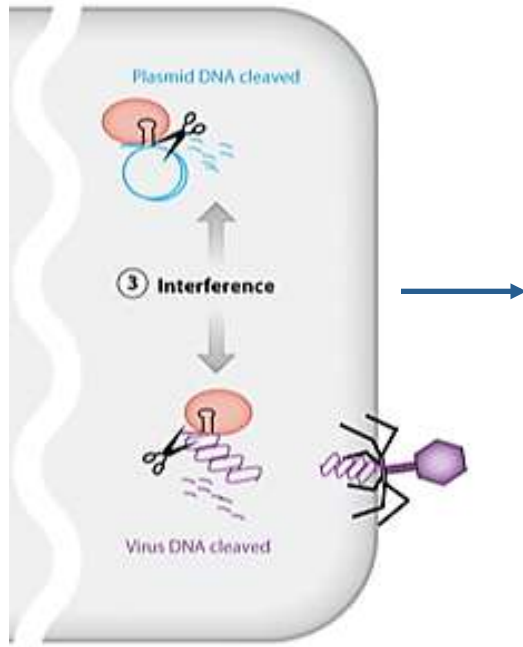


# Functionality of CRISPR-Cas system in *C. difficile*: plasmid interference



Strategy for interference experiments

# Function of *C. difficile* CRISPR-Cas system

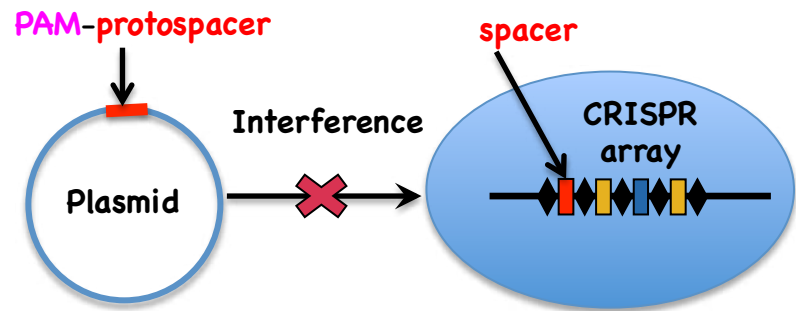
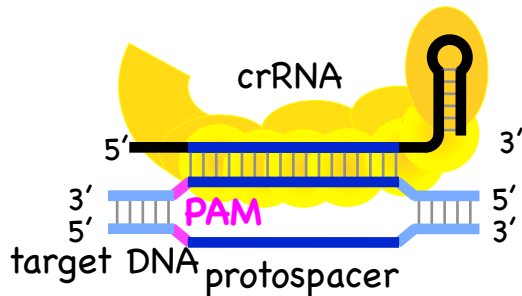


## Functionality of CRISPR system

Experimental evidence for **PAM 5'CCW**:  
plasmid conjugation efficiency

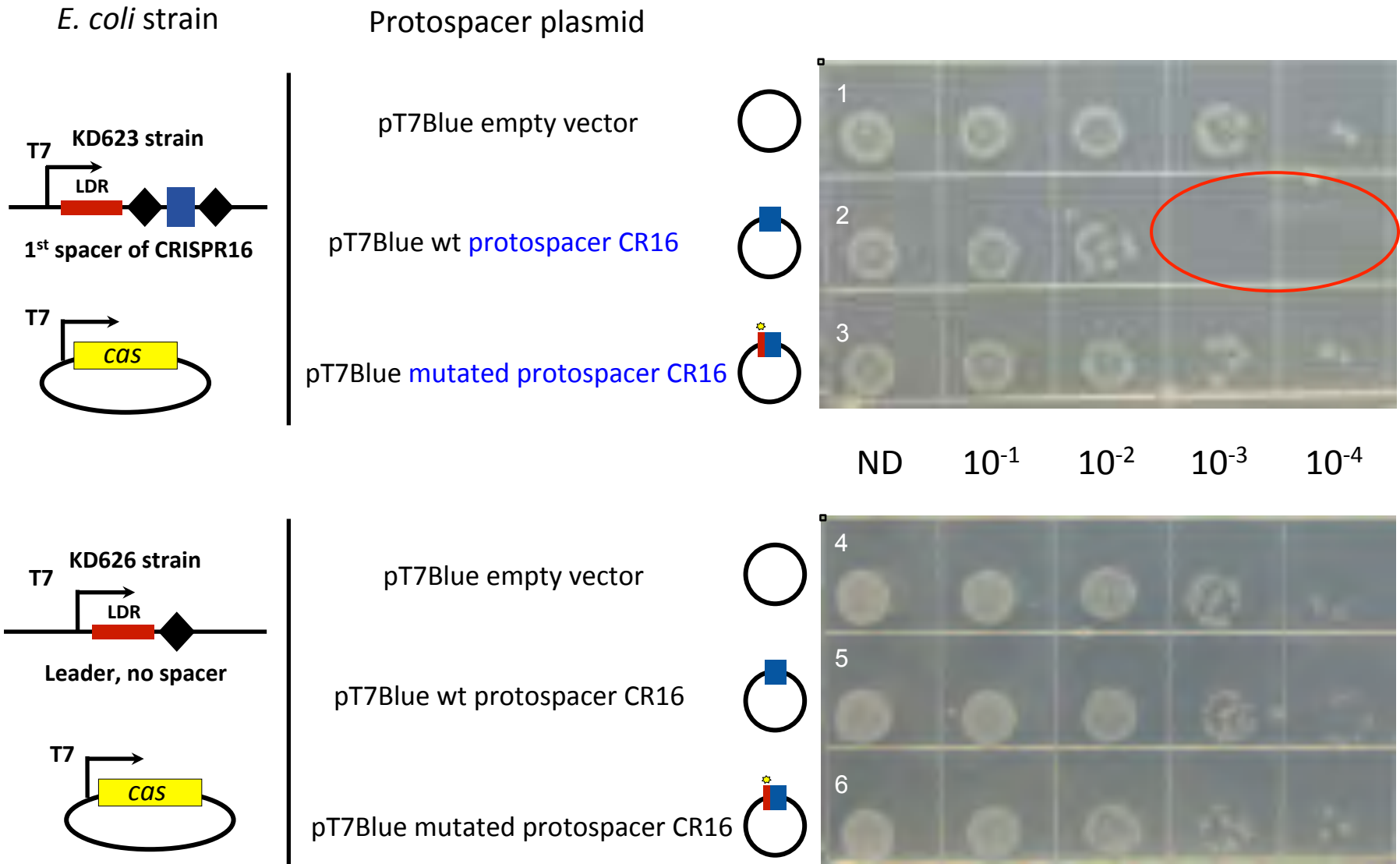
| PAM            | Number of transconjugants | Conjugation efficiency       |
|----------------|---------------------------|------------------------------|
| <b>CCA PAM</b> | 0                         | less than $1 \times 10^{-9}$ |
| <b>CCT PAM</b> | 0-1                       | $1 \times 10^{-9}$           |
| <b>GAG</b>     | 138                       | $5 \times 10^{-7}$           |
| <b>AAT</b>     | 178                       | $6 \times 10^{-7}$           |

1<sup>st</sup> protospacer of CRISPR12



Boudry et al. mBio. 2015

# Functionality of *C. difficile* cas genes for plasmid interference in *E. coli*



Boudry et al. mBio. 2015

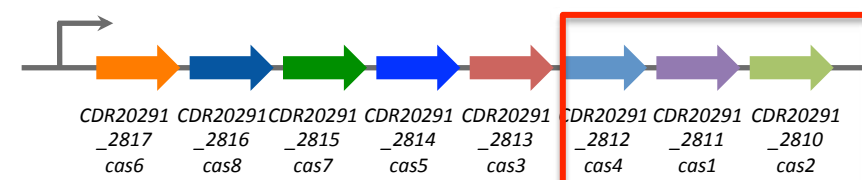
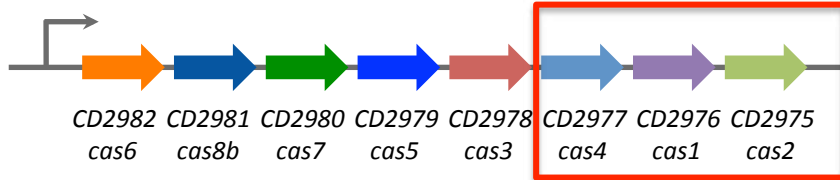


# Functionality of CRISPR-Cas system in *C. difficile*: adaptation assays

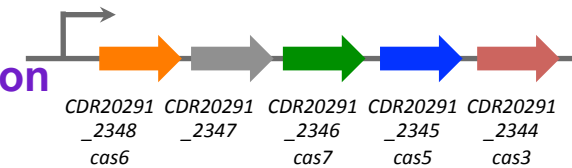
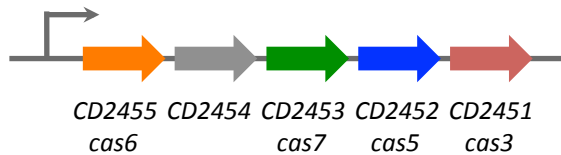
## *C. difficile* 630E R20291

## *C. difficile*

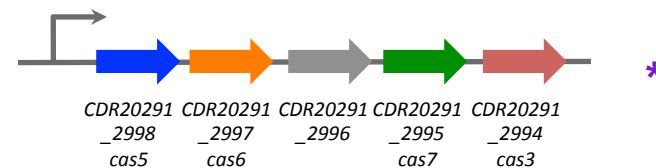
Full operon



Partial operon

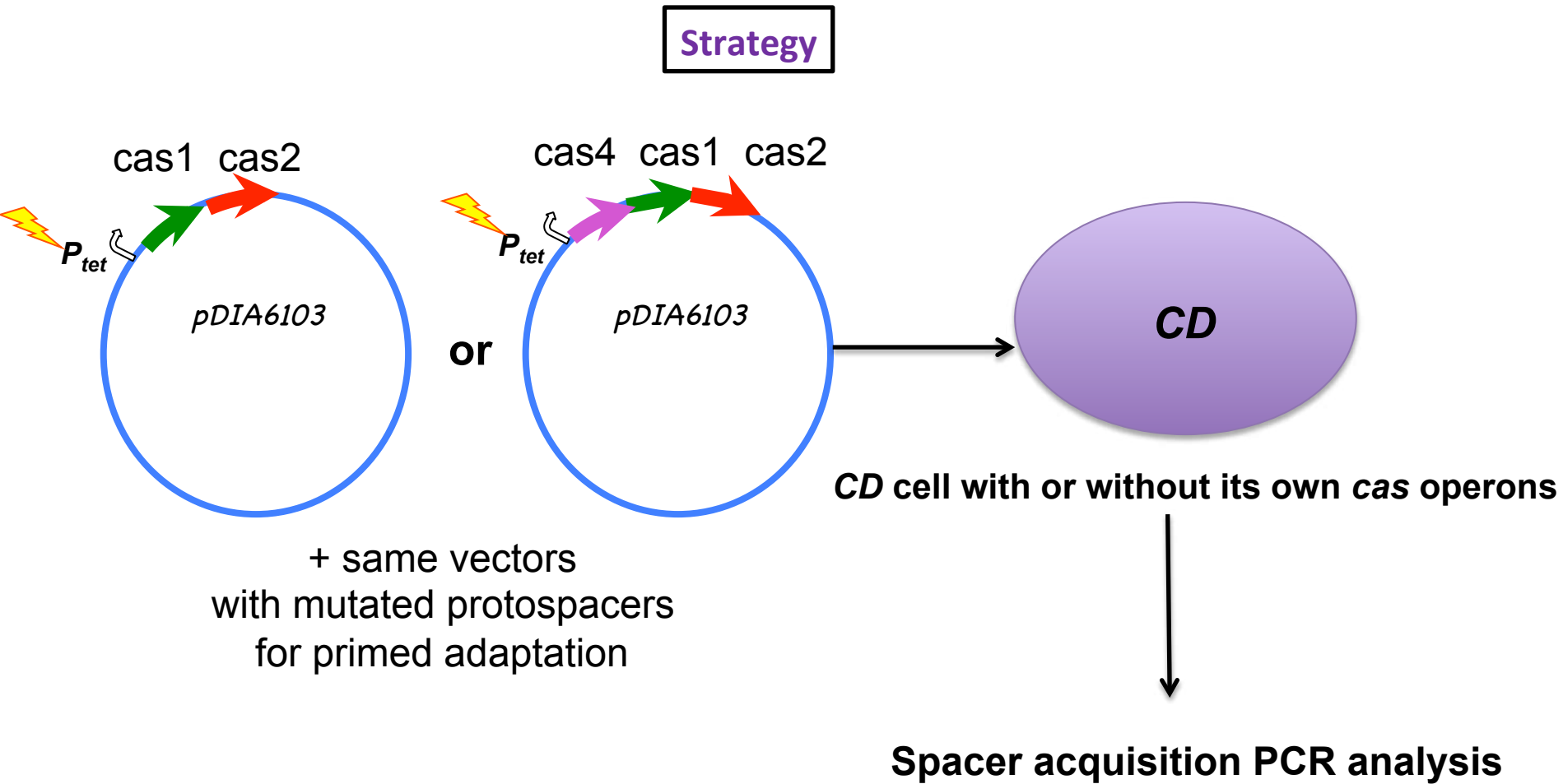


- **Cas1** and **Cas2** are essential for new spacer acquisition on **all** CRISPR-Cas system types
- Potential role of **Cas4** in CRISPR-adaptation is actively discussed



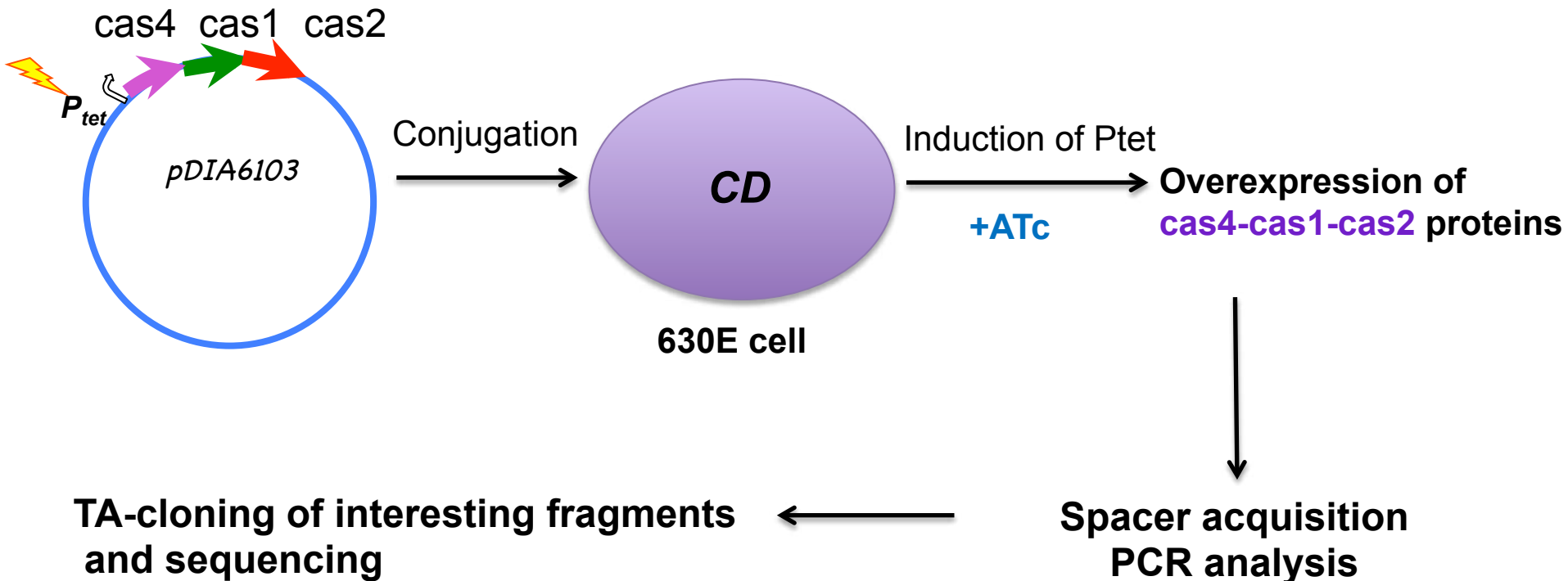
cas operon specific to 027 ribotype strains\*

# Functionality of CRISPR-Cas system in *C. difficile*: adaptation assays



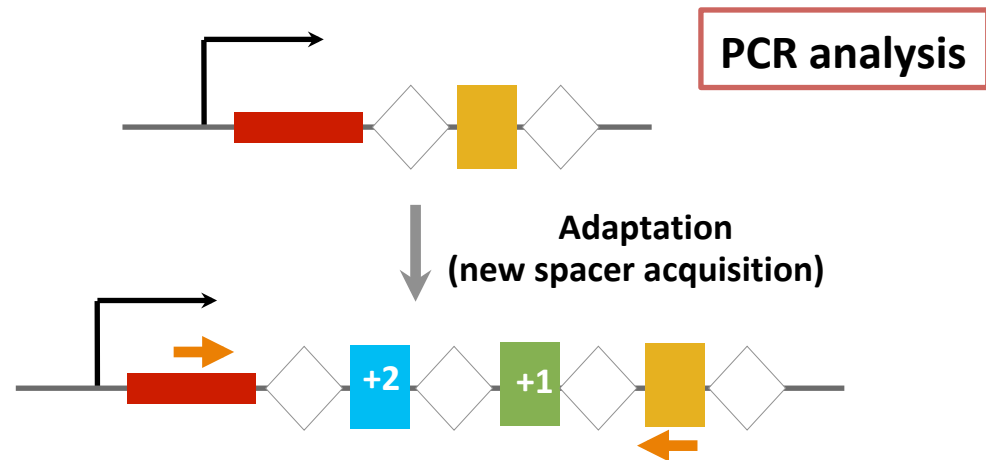
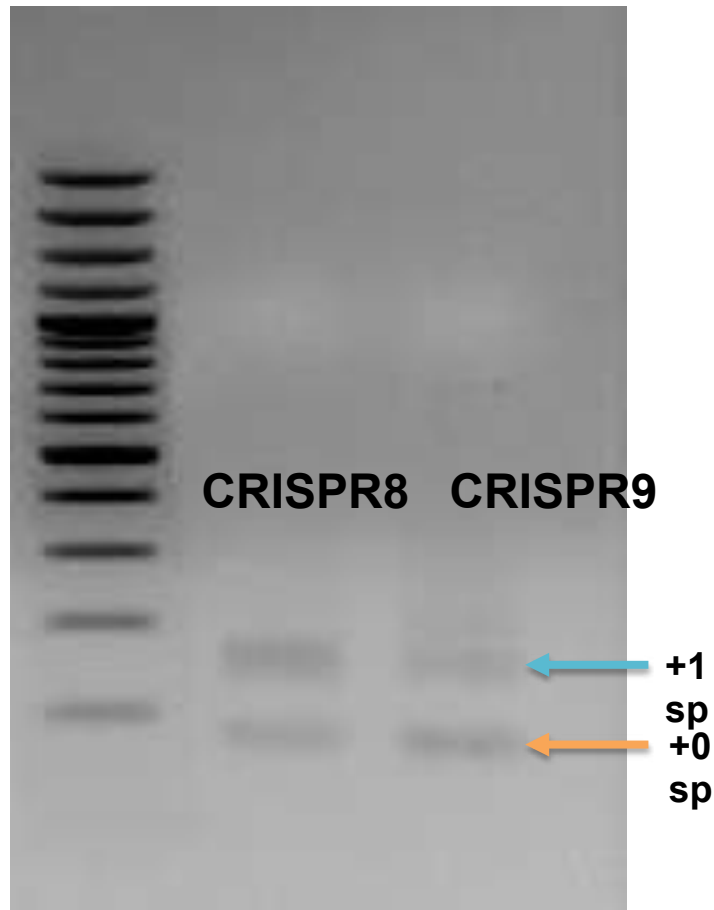
# Functionality of CRISPR-Cas system in *C. difficile*:

## naïve adaptation assays



# Functionality of CRISPR-Cas system in *C. difficile*:

## naïve adaptation assays

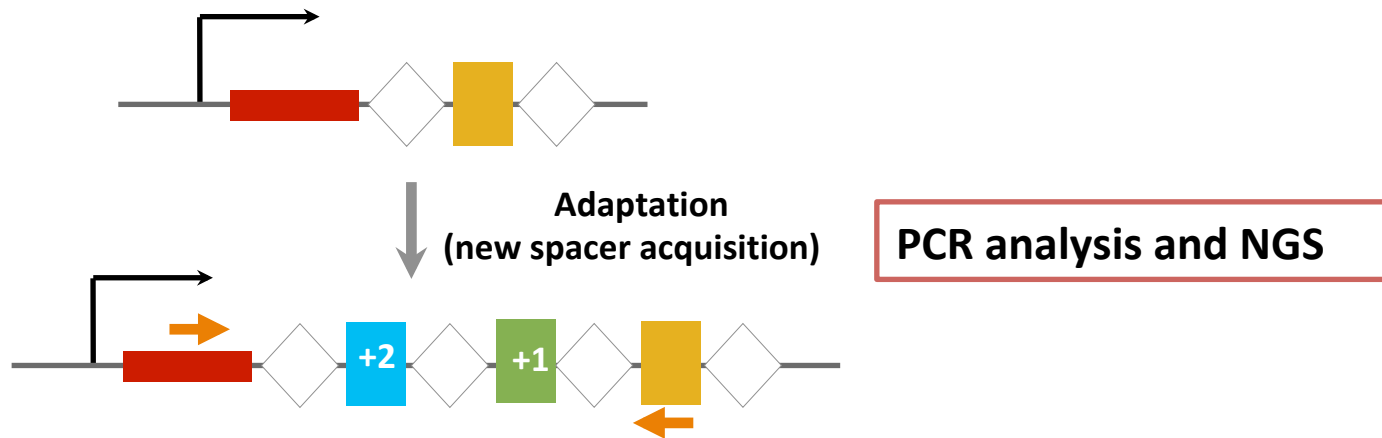


- CRISPR-Cas system in *CD 630E* **is functional for adaptation**
- New spacer acquisition was detected in **CR8** and **CR9** arrays
- These arrays are also **active for interference**
- All new acquired spacers were from the **plasmid**

# Functionality of CRISPR-Cas system in *C. difficile*:

## naïve adaptation assays

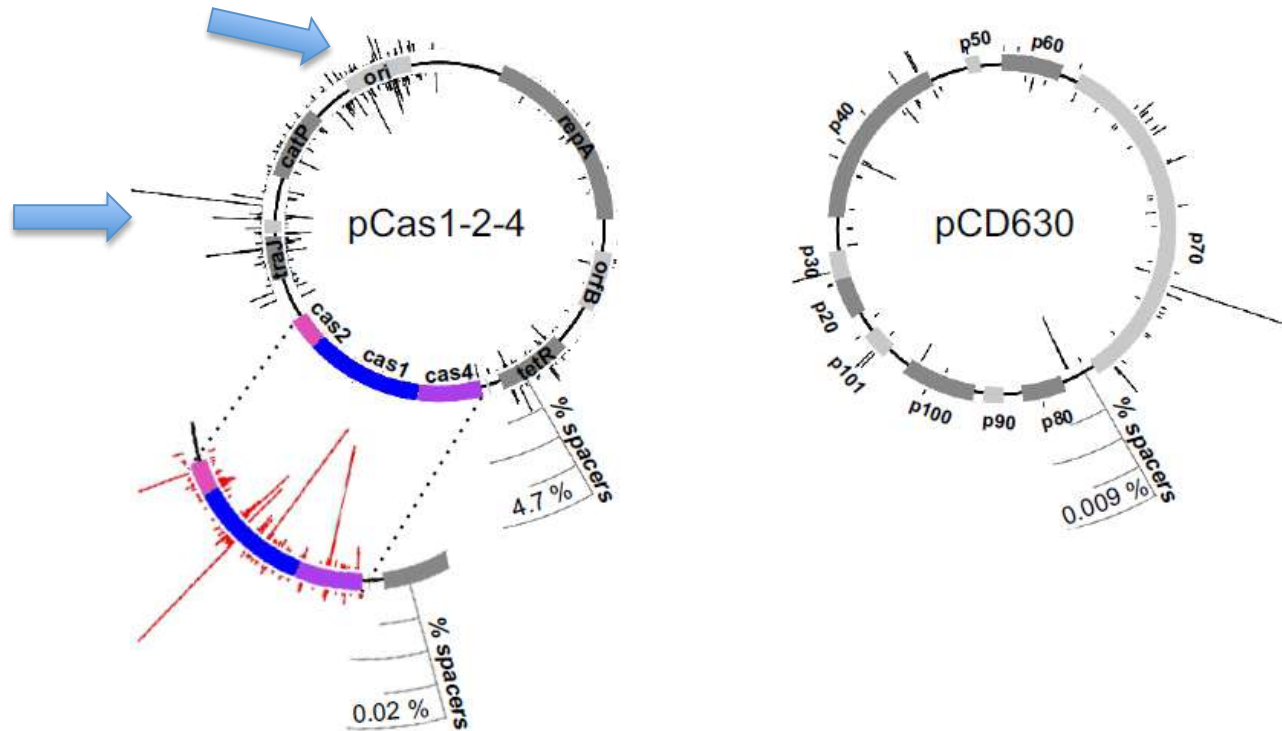
Maikova. PhD thesis  
Maikova et al. mBio 2021



### Uniquely aligned spacers CRISPR8

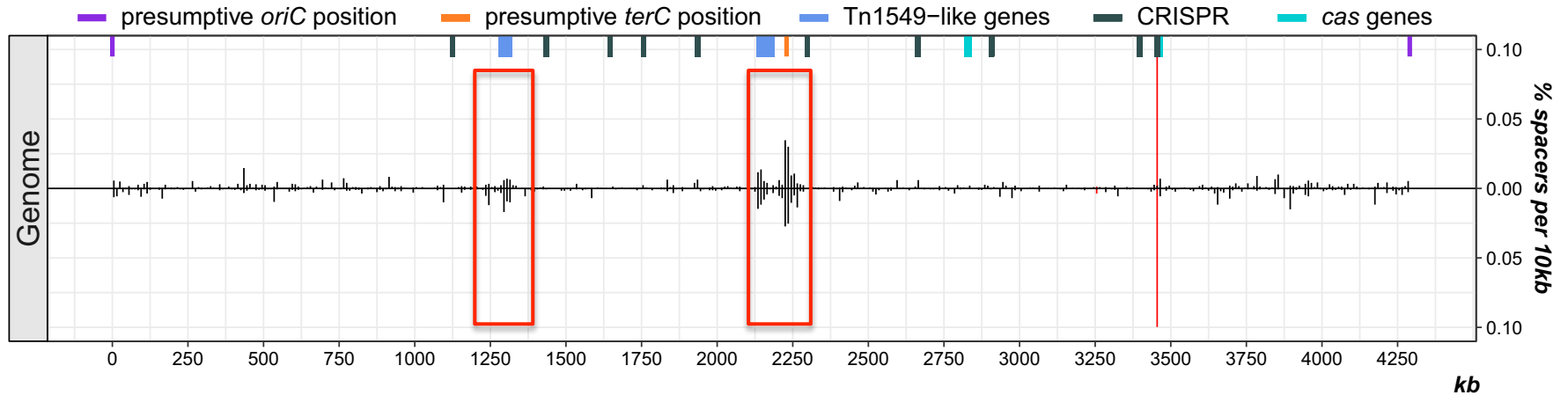
| Genome     |            | Plasmid      |              |
|------------|------------|--------------|--------------|
| dir strand | rev strand | dir strand   | rev strand   |
| 2474       | 1884       | 119274       | 111496       |
| 1.1%       | 0.8%       | <b>50.7%</b> | <b>47.4%</b> |

# Spacer acquisition hot spots in *C. difficile*



- Adaptation hot spots on **pCas1-2-4 plasmid** are located in ***traJ*** and ***ori*** regions

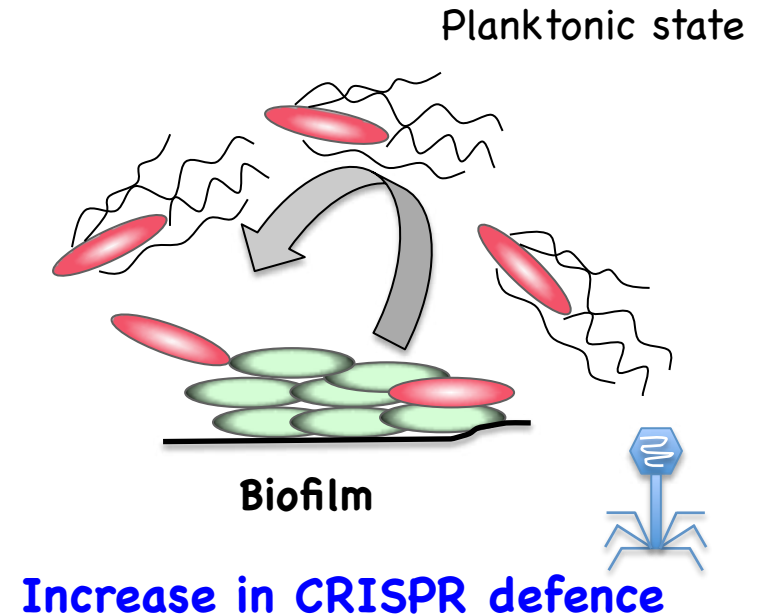
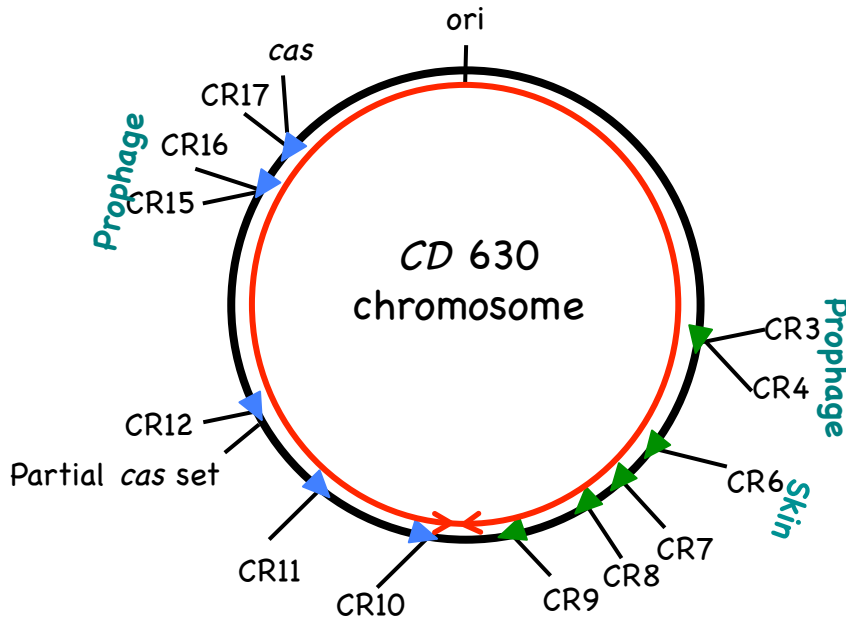
# Spacer acquisition hot spots in *C. difficile*



- Adaptation hot spots on **genome** are located in ***terC*** and **Tn1549-like gene** regions

Maikova. PhD thesis  
Maikova et al. mBio 2021

# Function and regulation of *C. difficile* CRISPR-Cas system



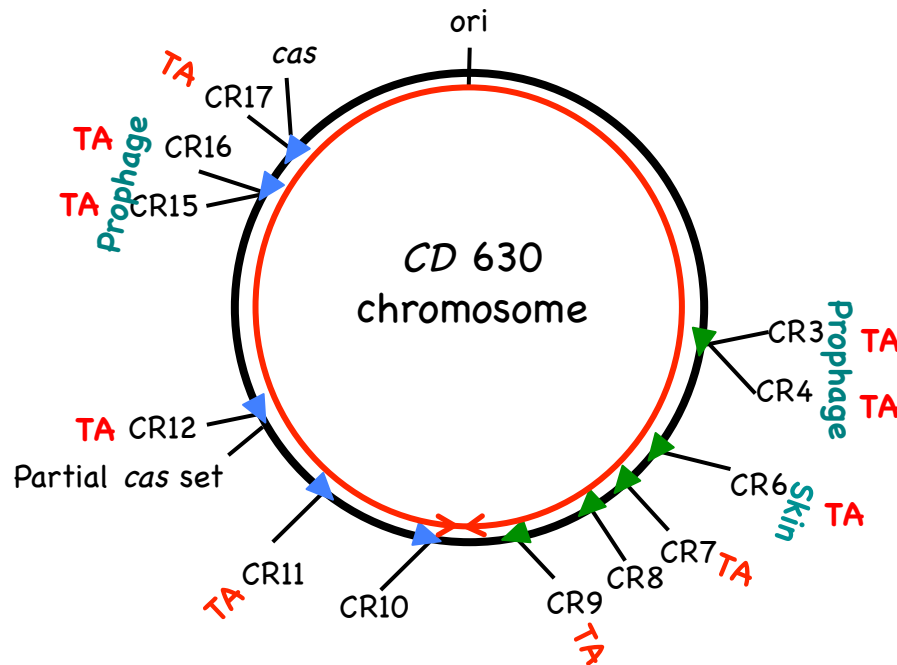
## Perspectives: Role of the CRISPR-Cas during infection

- Regulation of **CRISPR-Cas expression** in response to stress-related factors (phages-biofilm)

Maikova A. PhD thesis



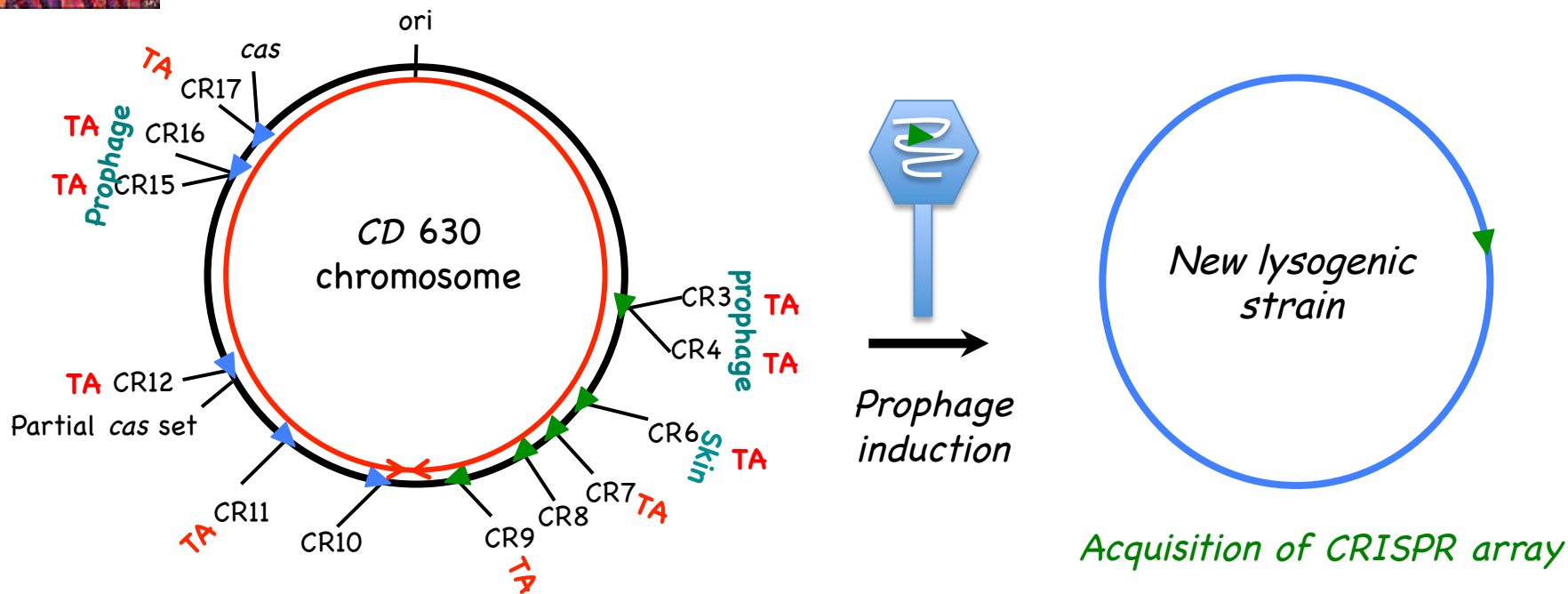
# Function and regulation of *C. difficile* CRISPR-Cas system



## Perspectives: Role of the CRISPR-Cas during infection

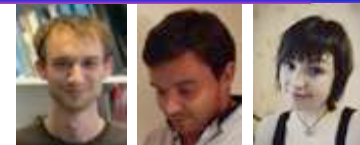
- Regulation of **CRISPR-Cas expression** in response to stress-related factors (phages-biofilm)
- Link with **Toxin/antitoxin (TA) systems of type I** (**defence islands**)
- Mechanism of **CRISPR array transfer** (adaptation)

# Evolution of CRISPR-Cas system in *C. difficile*

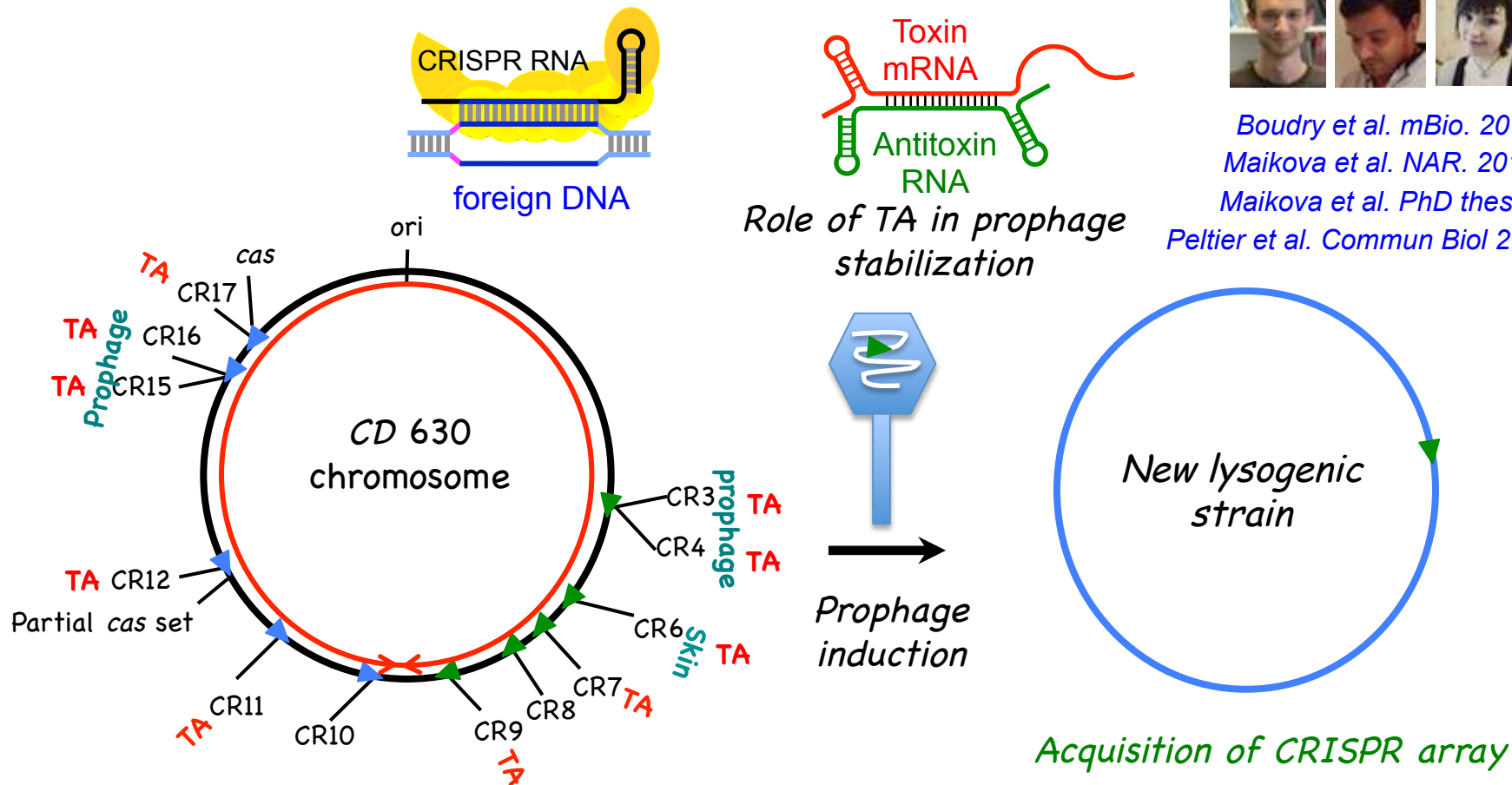


## Genomic analysis of 3,000 *C. difficile* strains

- **Conservation of cas operons**, identification of 027-specific operon
- **Co-localisation of CRISPR and TA** (defence islands)
- Prophage localisation of **CRISPR arrays** (evolution)



*Boudry et al. mBio. 2015*  
*Maikova et al. NAR. 2018*  
*Maikova et al. PhD thesis*  
*Peltier et al. Commun Biol 2020*



In CD strain 630 : **12 CRISPR regions** exist and are expressed  
In epidemic CD strain 027: **9 active CRISPR arrays**



.... A total of 819 spacers from nine CD strains  
**Large defense capacity within phage-rich gut communities**

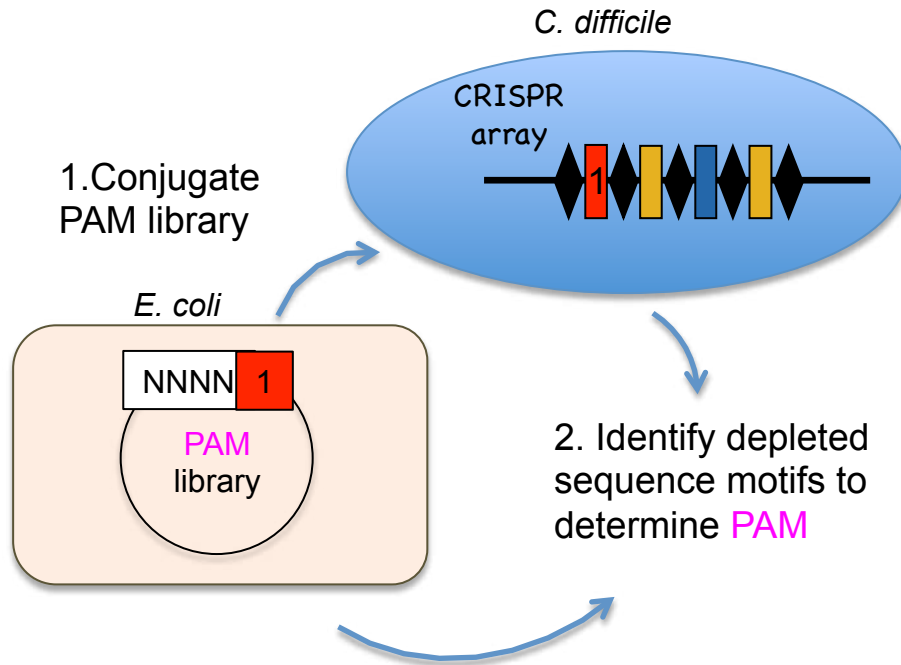
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## Results:

II. **Using** of CRISPR-Cas system in *C. difficile* for genome editing

# PAM sequences in *C. difficile* 630E and R20291 strains

Maikova. PhD thesis  
Maikova et al. mBio 2021

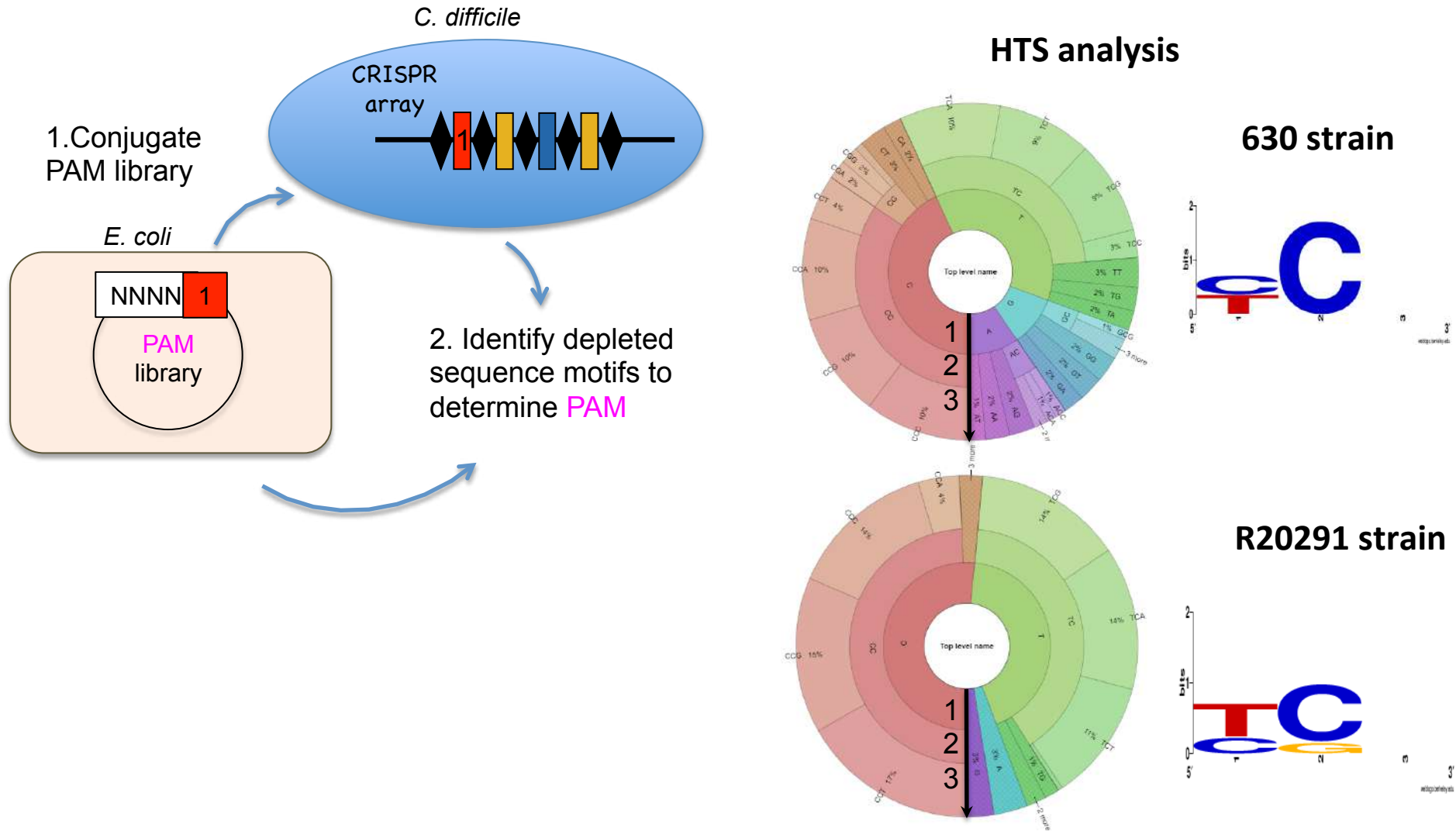


## Two PAM plasmid libraries:

1. Vector-NNNN (PAM)-protospacer 1  
CRISPR16 CD 630
2. Vector-NNNN (PAM)-protospacer 1  
CRISPR13 CD R20291

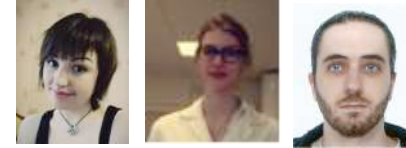
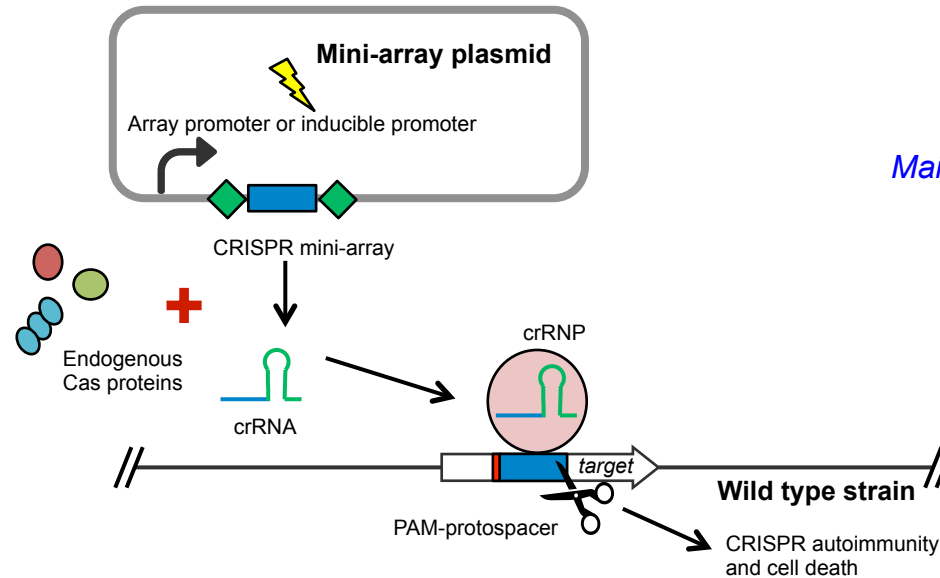
# PAM sequences in *C. difficile* 630E and R20291 strains

Maikova. PhD thesis  
Maikova et al. mBio 2021



Functional PAMs **CCN/TCN** in accordance with interference efficiency experiments

# Genome editing in *C. difficile* using the endogenous CRISPR-Cas system

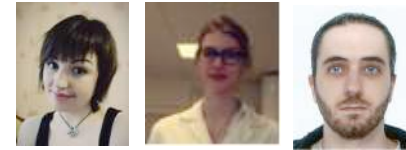


Maikova et al. *Frontiers Microbiol.* 2018

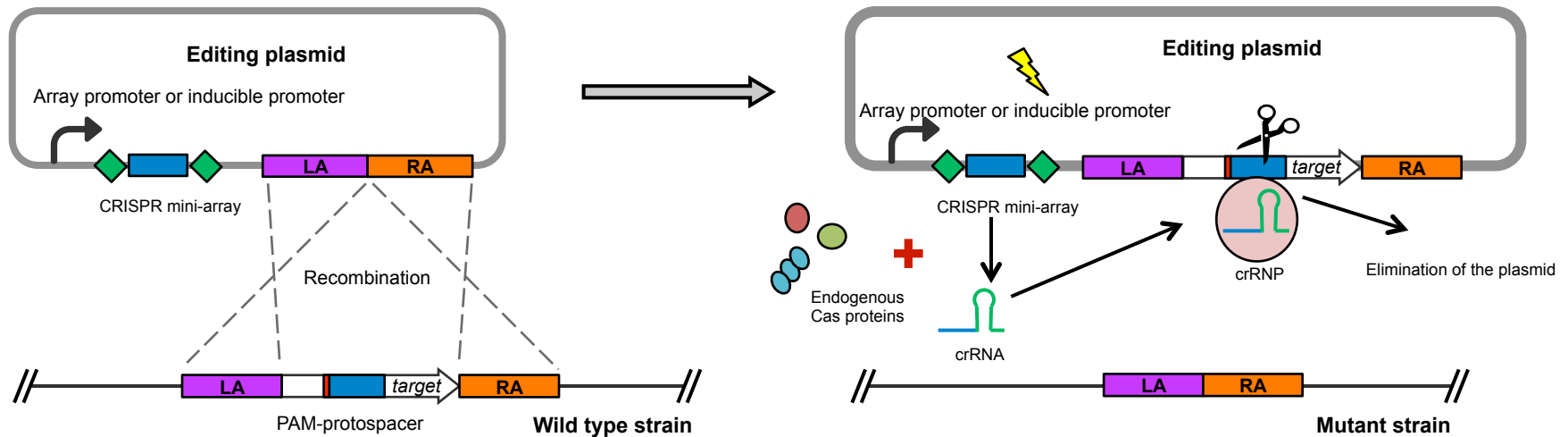
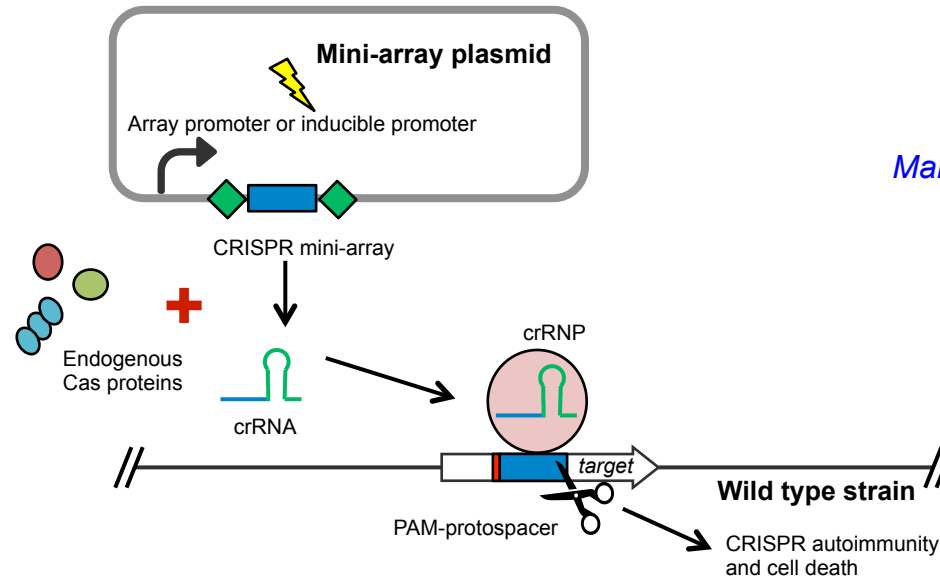
Maikova. *PhD thesis*

Maikova et al. *AEM.* 2019.

# Genome editing in *C. difficile* using the endogenous CRISPR-Cas system



Maikova et al. *Frontiers Microbiol.* 2018  
Maikova. PhD thesis  
Maikova et al. *AEM.* 2019.

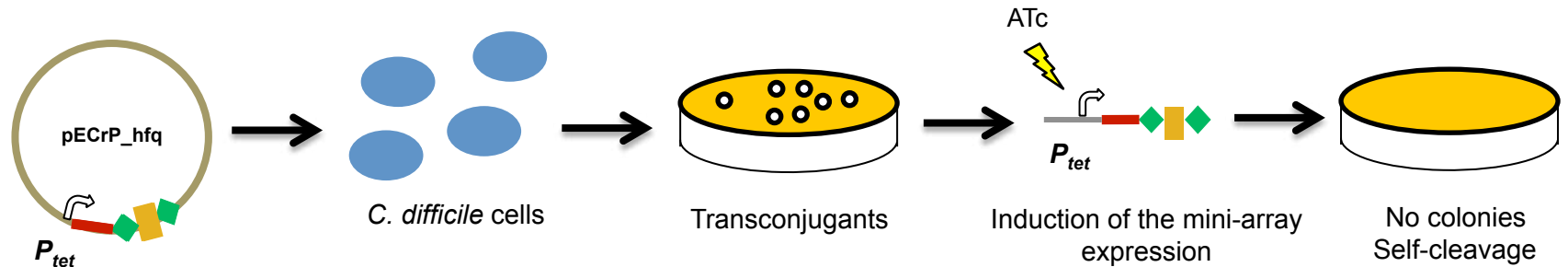




# Genome editing in *C. difficile* using the endogenous CRISPR-Cas system

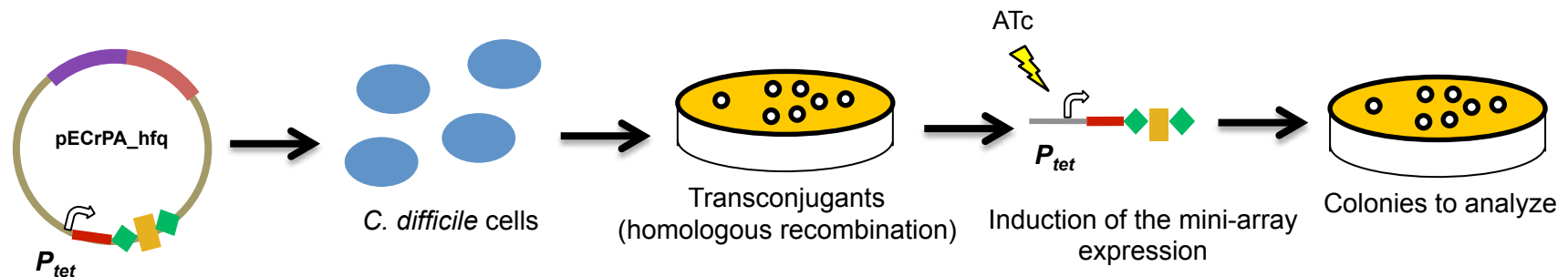
Maikova et al. *Frontiers Microbiol.* 2018  
Maikova. PhD thesis  
Maikova et al. *AEM.* 2019.

## Induced endogenous CRISPR-Cas autoimmunity

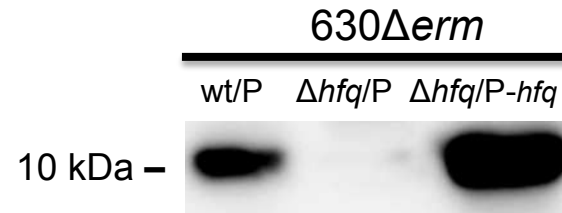
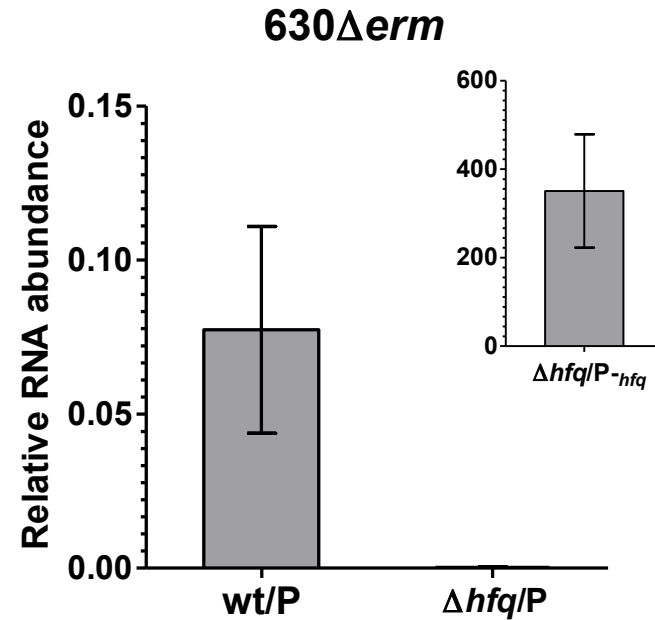
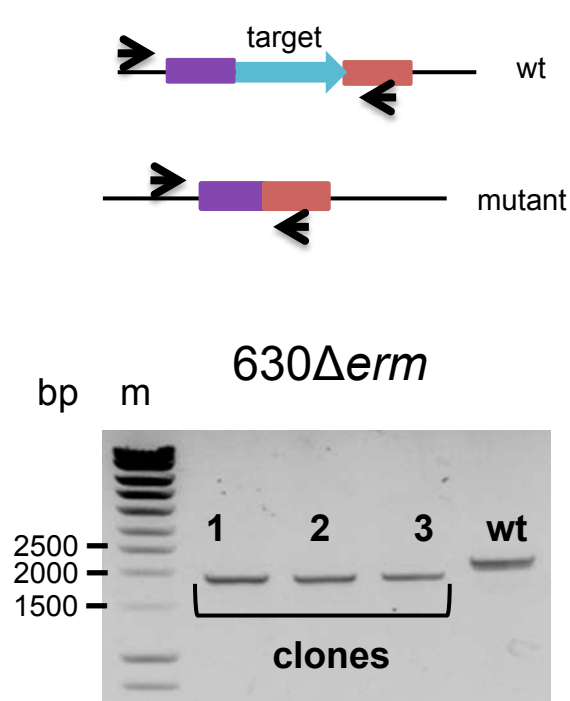


new type of drugs against *CD* ?

## Mutant construction using plasmid with homologous arms



# Genome editing in *C. difficile* using the endogenous CRISPR-Cas system



- **Δhfq mutants** in 630 and R20291 strains
- **Could not be obtained** using **other** genome editing methods (*codA* allele exchange and Clostron)
- **Efficient plasmid loss**

Maikova. PhD thesis  
Maikova et al. AEM. 2019.

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## Results:

### III. Regulation of CRISPR-Cas system in *C. difficile*

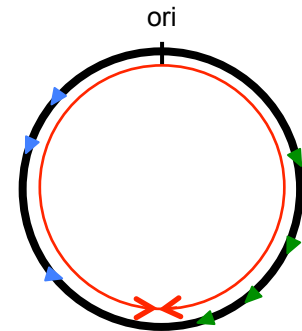
# Complex regulation of CRISPR system in *C. difficile*

➤ Optimization of CRISPR loci transcription (conserved orientation in direction of replication)

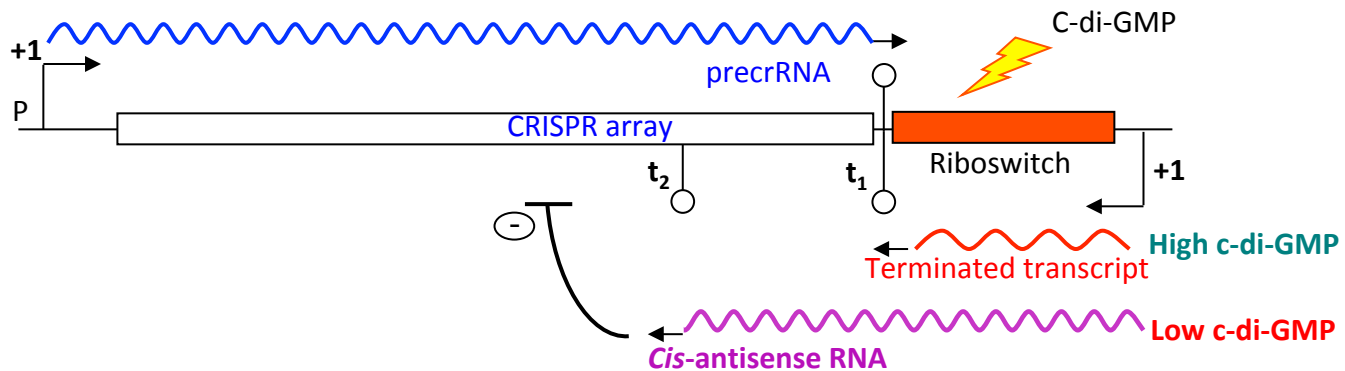
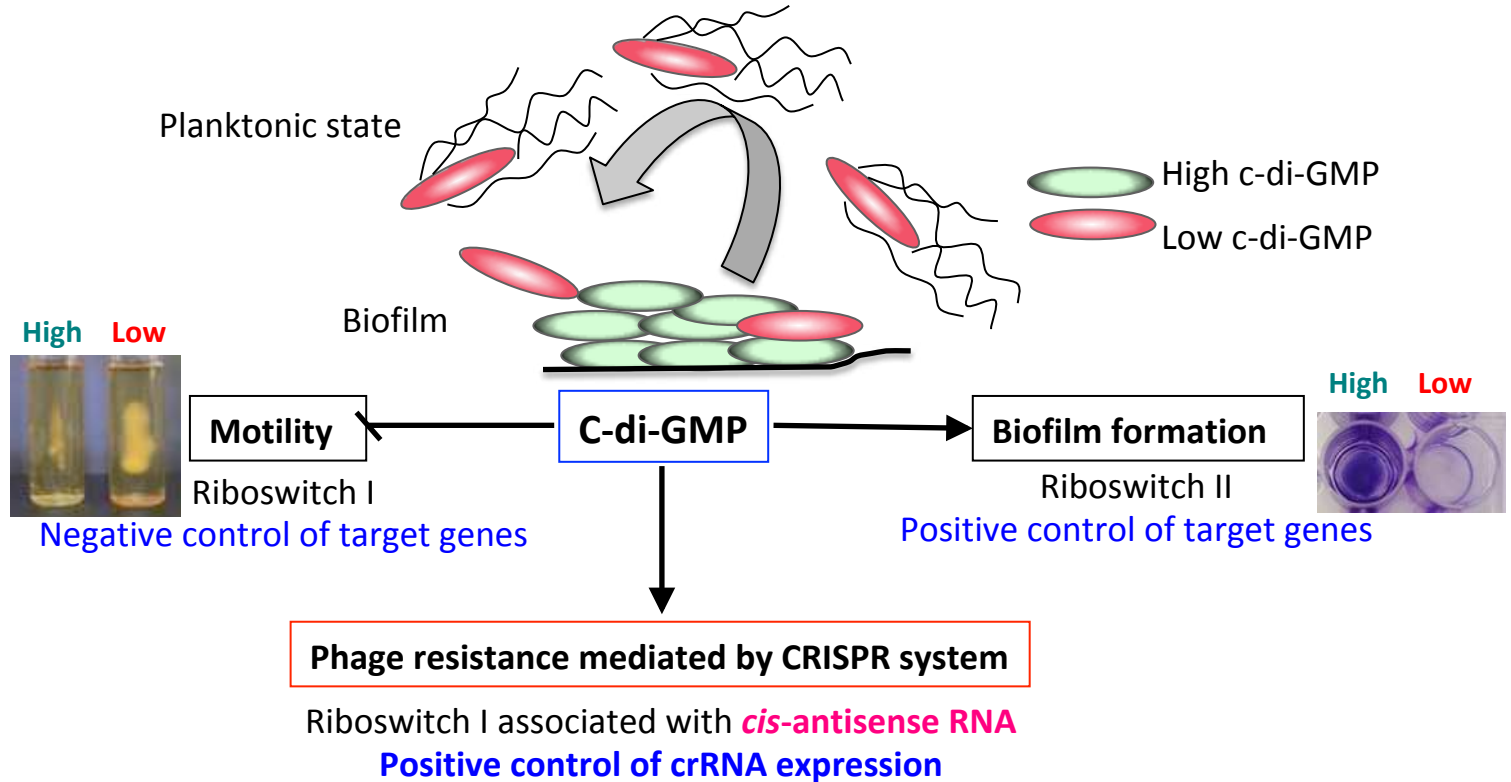
➤ **Induction within biofilm** communities for efficient defence against foreign DNA, role of biofilm-related signalling molecules (**c-di-GMP**)

➤ Control in response to **stress-related factors** relevant for *C. difficile* infection cycle (sigma B control, interactions with **phages**, stress conditions inside the host)

➤ Link with Toxin/antitoxin (TA) systems of type I, co-localization and co-regulation of CRISPR and TA systems within “defence islands” in *C. difficile* chromosome



# Regulation of *C. difficile* CRISPR system within biofilms

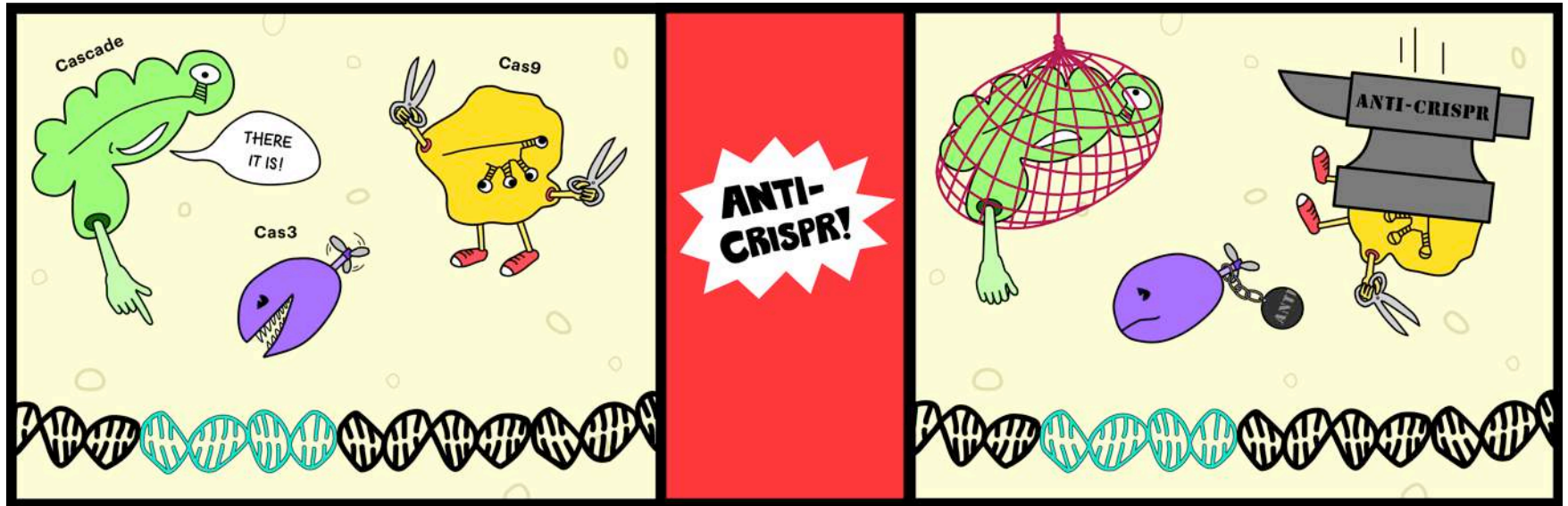


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## Results:

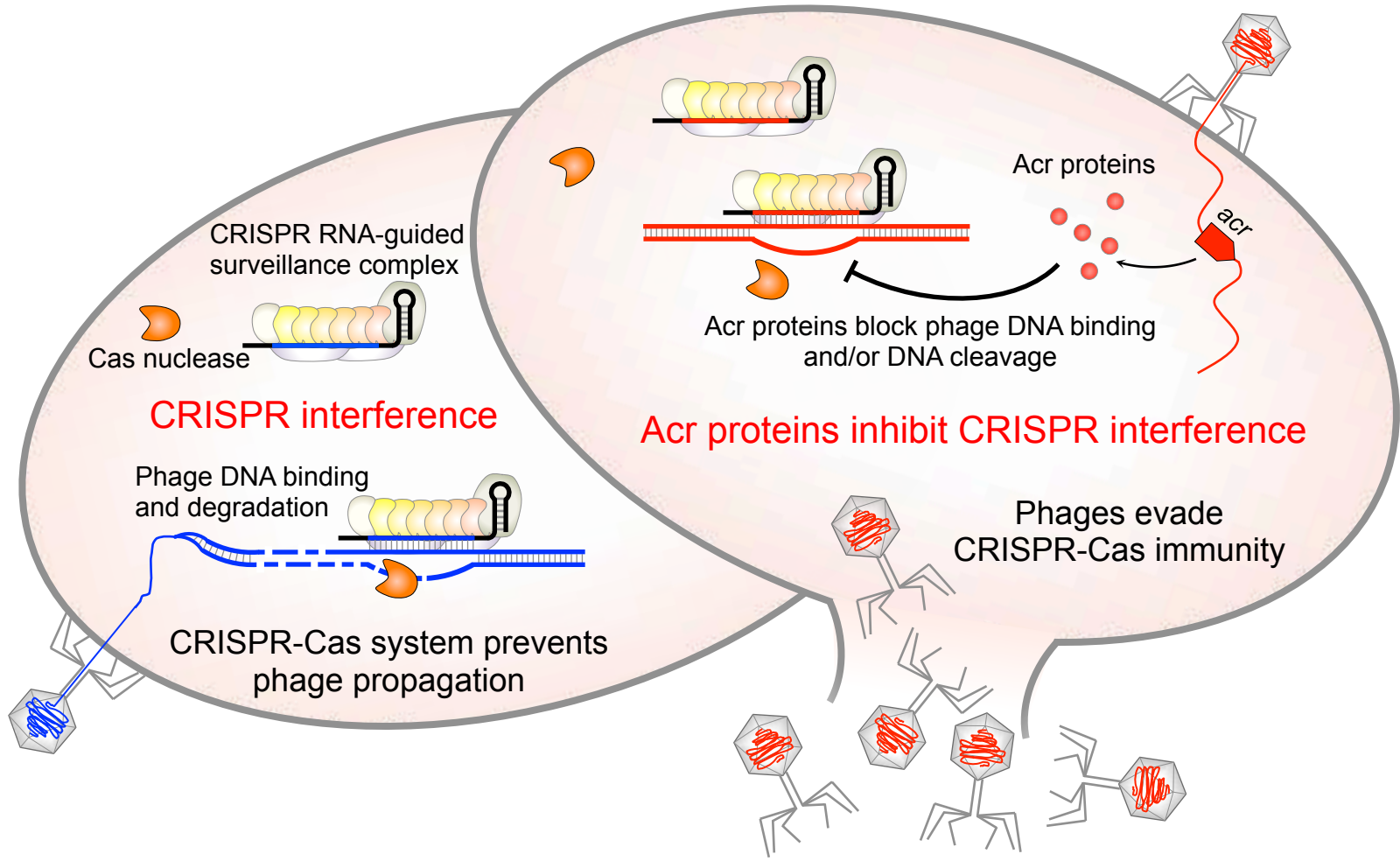
### IV. Inhibitors of CRISPR-Cas system in *C. difficile*

# Potential inhibitors of CRISPR-Cas system in *C. difficile*

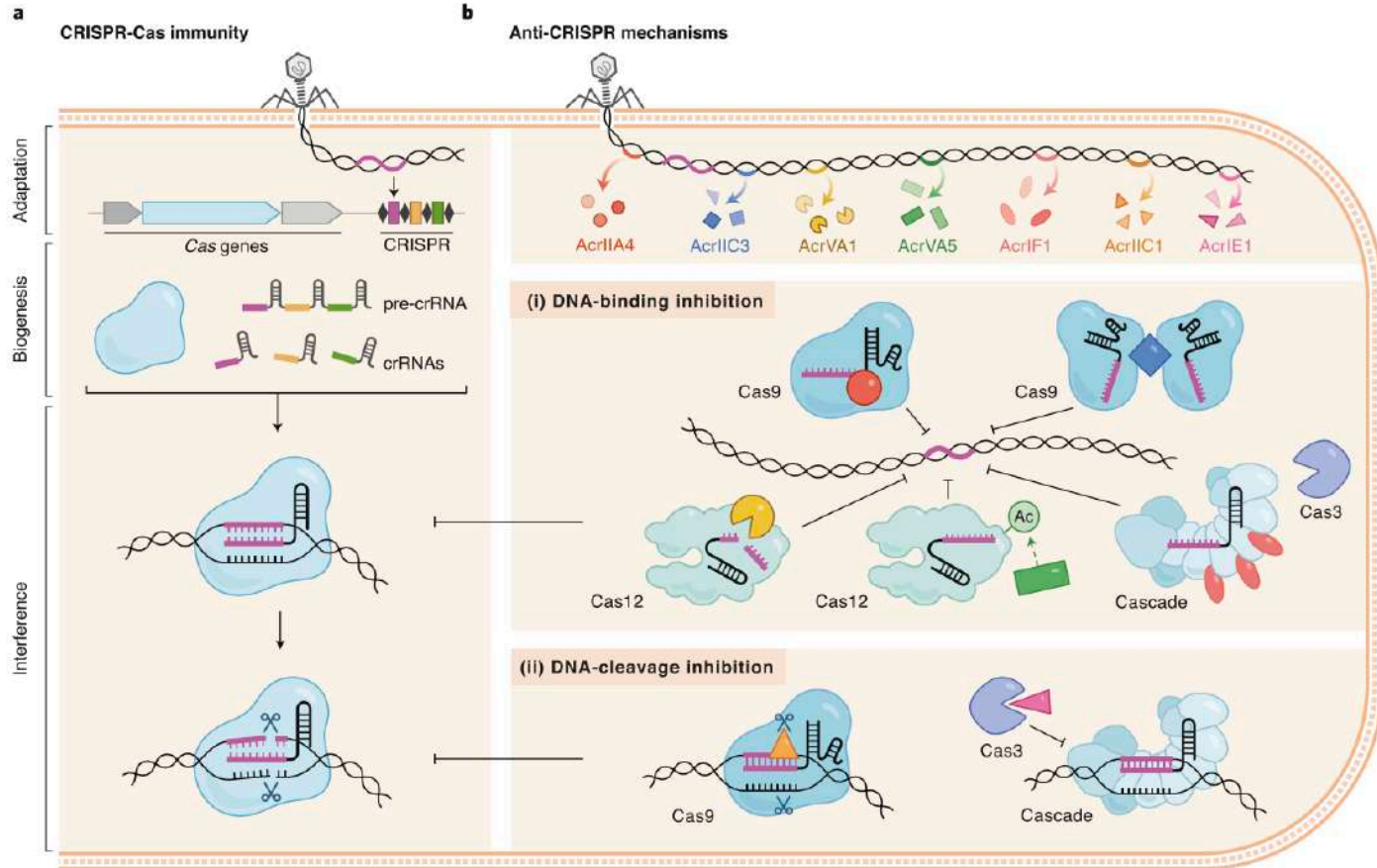




# Acr proteins in suppression of CRISPR-mediated immunity

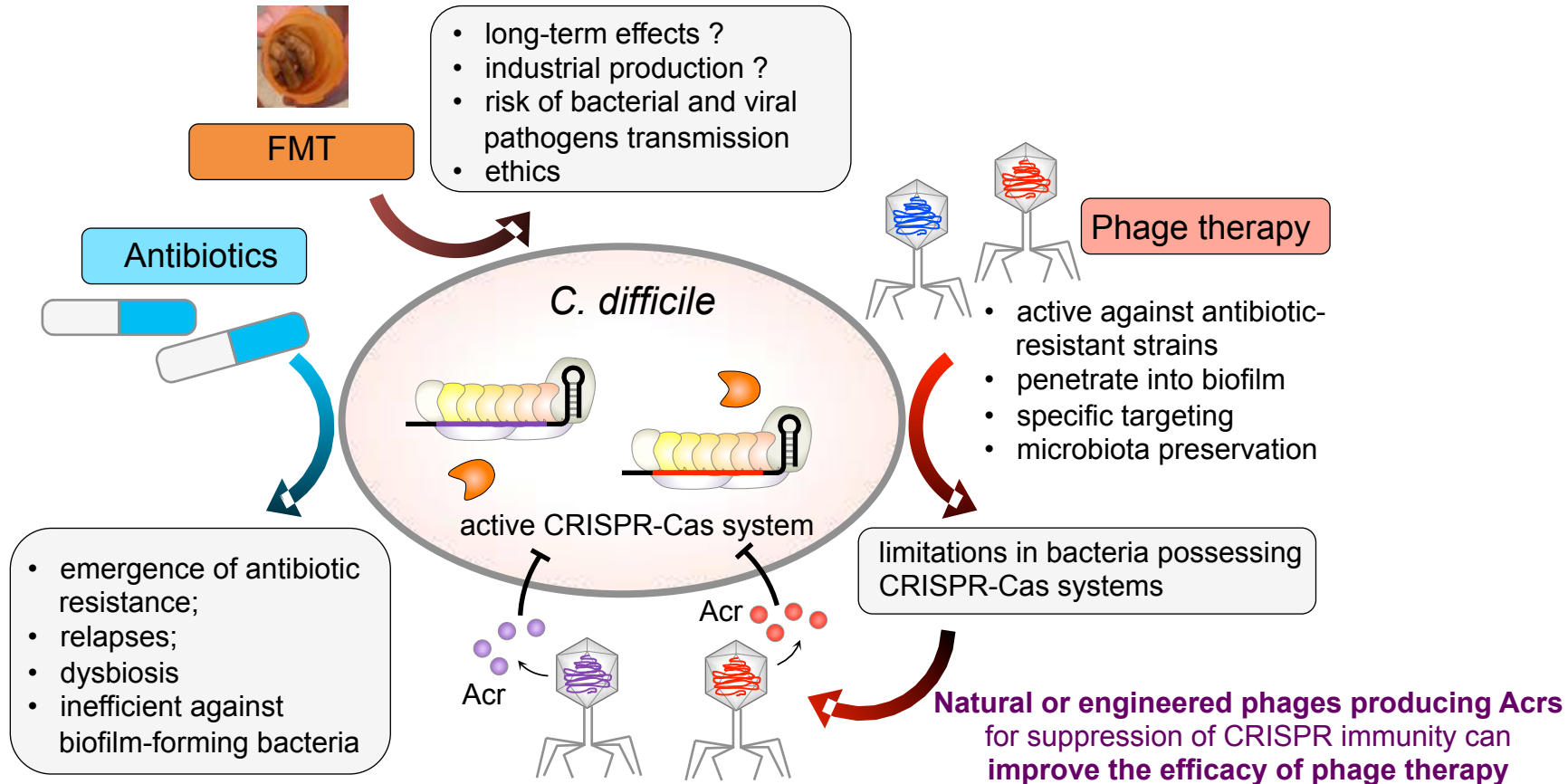


# Mechanisms of anti-CRISPR protein activity



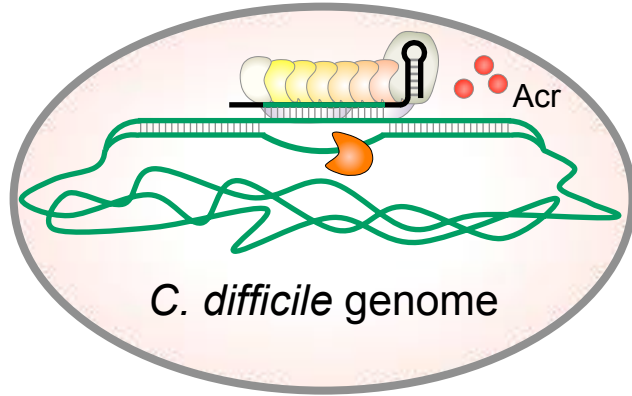
# Potential applications of Acr proteins in *C. difficile* for phage therapy

## Treatment of *C. difficile* infection



# Potential applications of Acr proteins in *C. difficile* for genome editing

Genome editing in *C. difficile* using endogenous CRISPR-Cas system





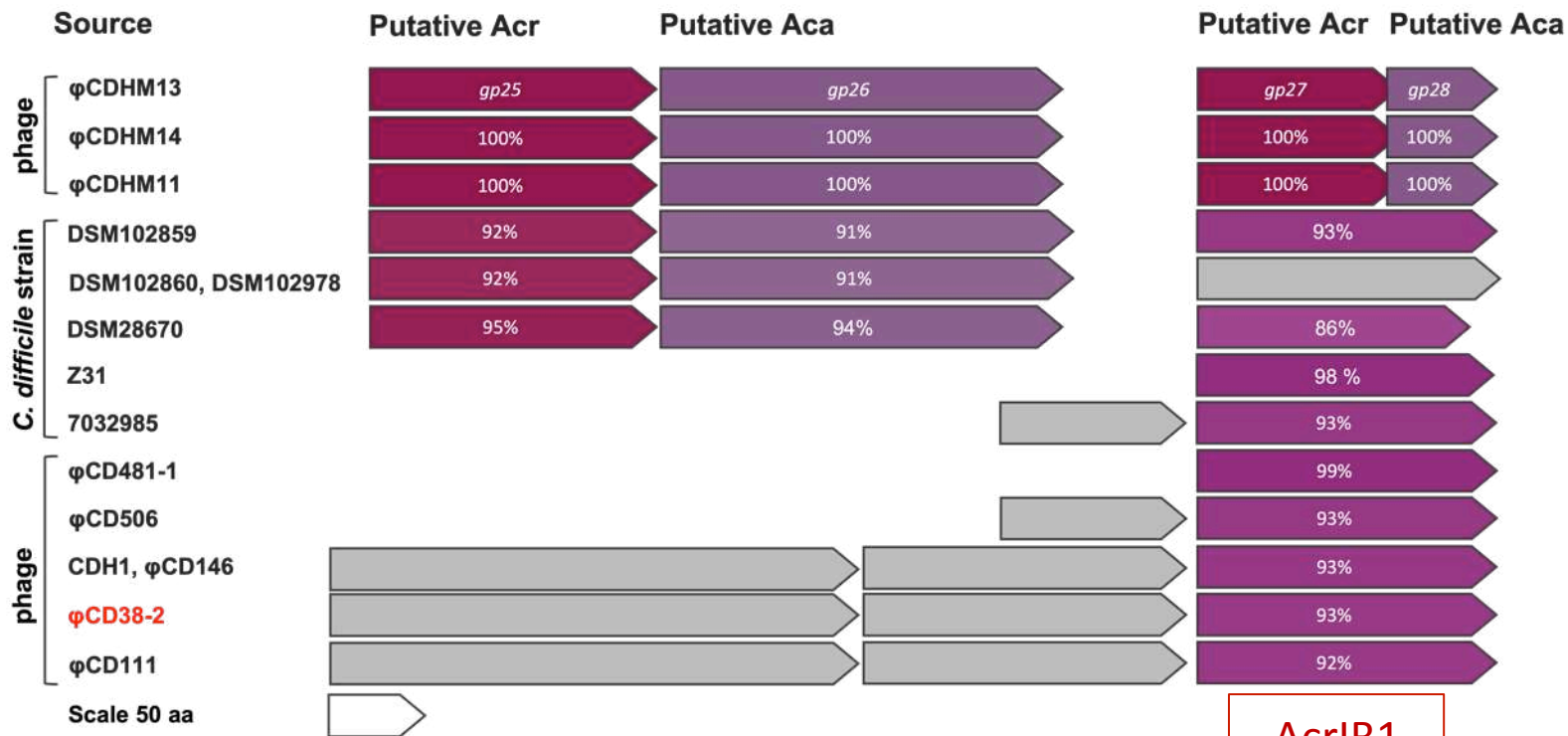
The use of Acr proteins in genome editing can provide:

- precise temporal control of CRISPR-Cas activity through “ON-OFF” regulation
- decreasing off-target effects
- reducing the toxicity of self-targeting CRISPR-Cas system

# Putative anti-CRISPR loci of *C. difficile* phages

A. Borges, J. Bondy-Denomy

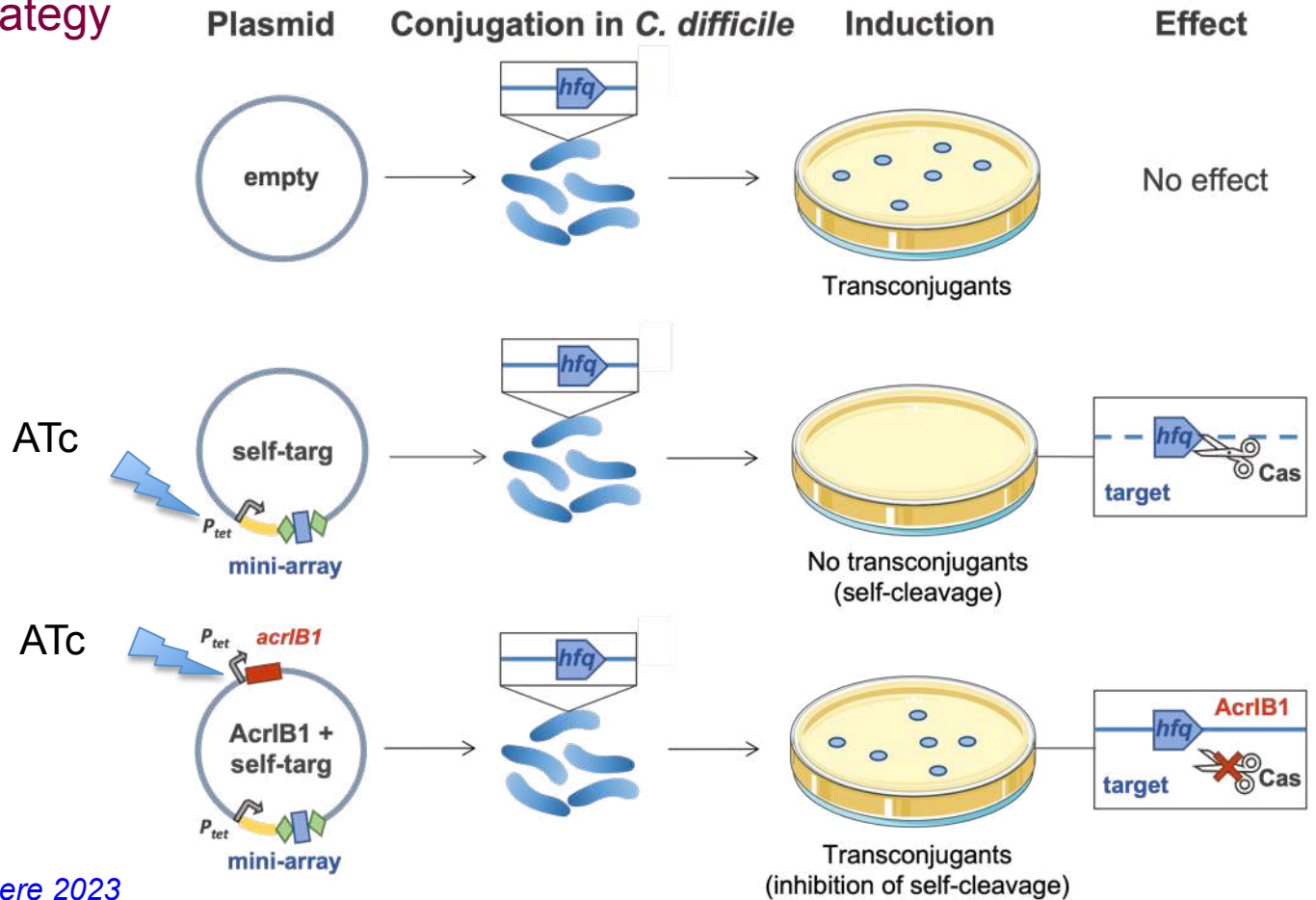
 - putative anti-CRISPR (Acr)  
 - putative anti-CRISPR associated (Aca)



**AcrIB1**

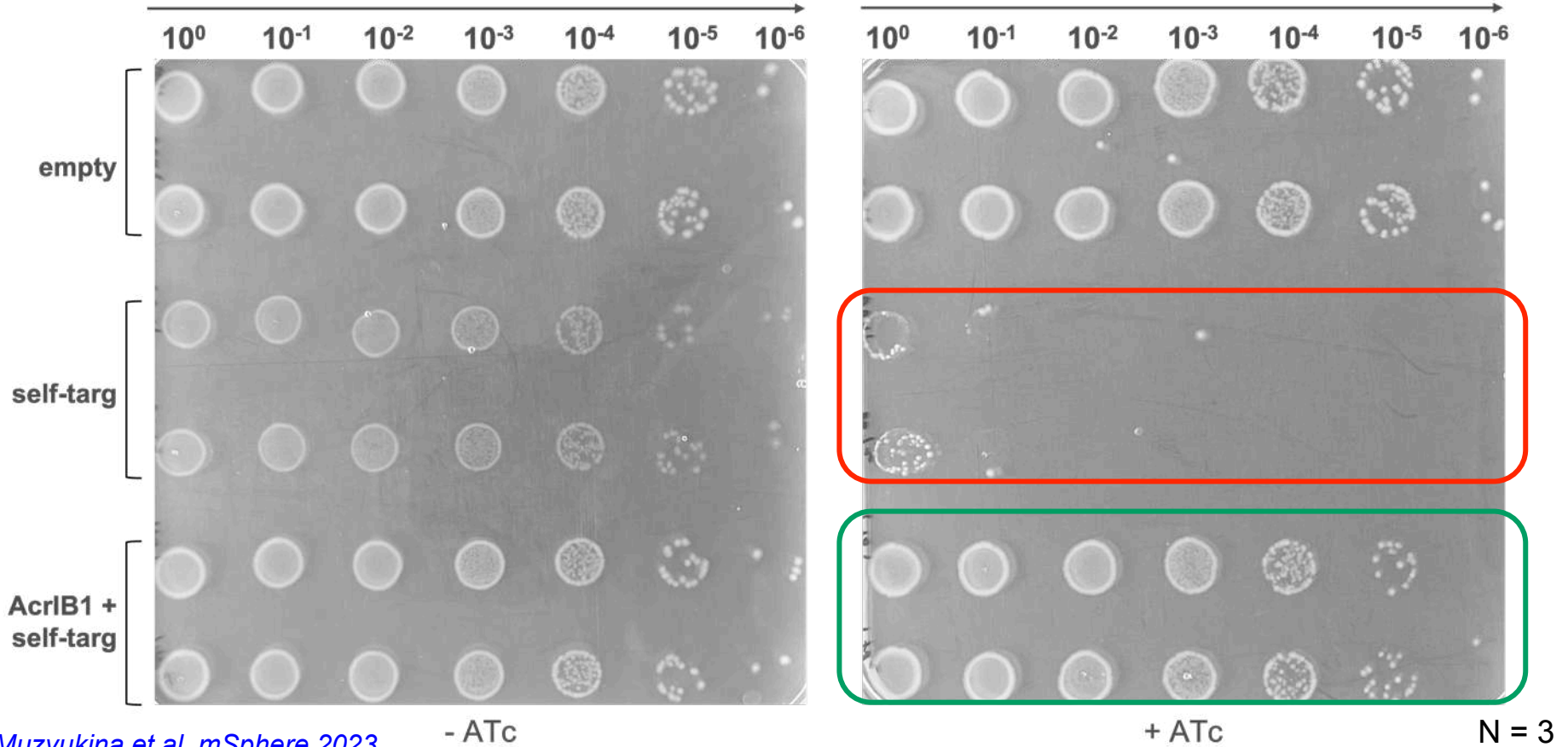
# *C. difficile* conjugation experiment for AcrIB1 efficiency testing

## Self-targeting strategy



# *acrIB1* gene expression inhibits CRISPR interference in *C. difficile*

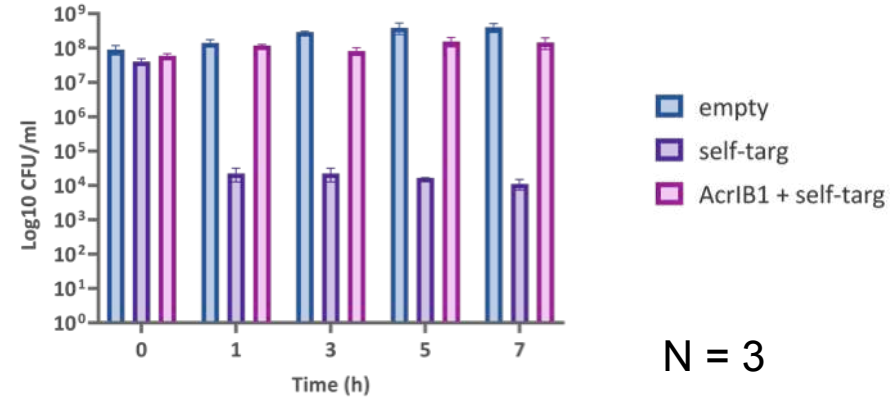
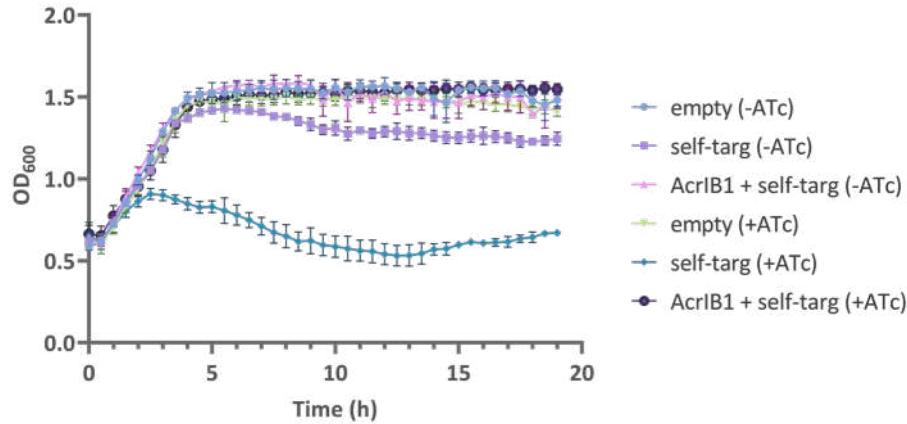
## Self-targeting strategy





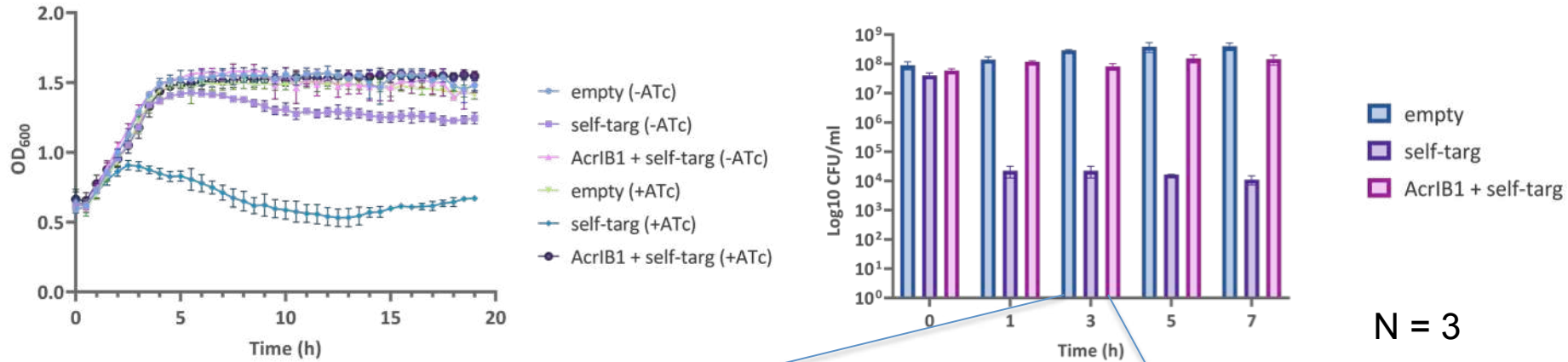
# *acrIB1* gene expression inhibits CRISPR interference in *C. difficile*

Effect of anti-CRISPR self-targeting inhibition on bacterial growth in BHI liquid medium

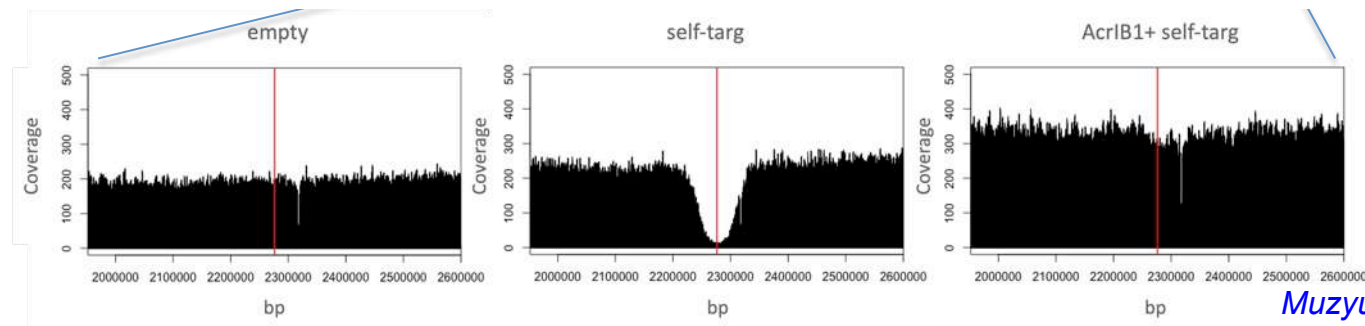


# *acrIB1* gene expression inhibits CRISPR interference in *C. difficile*

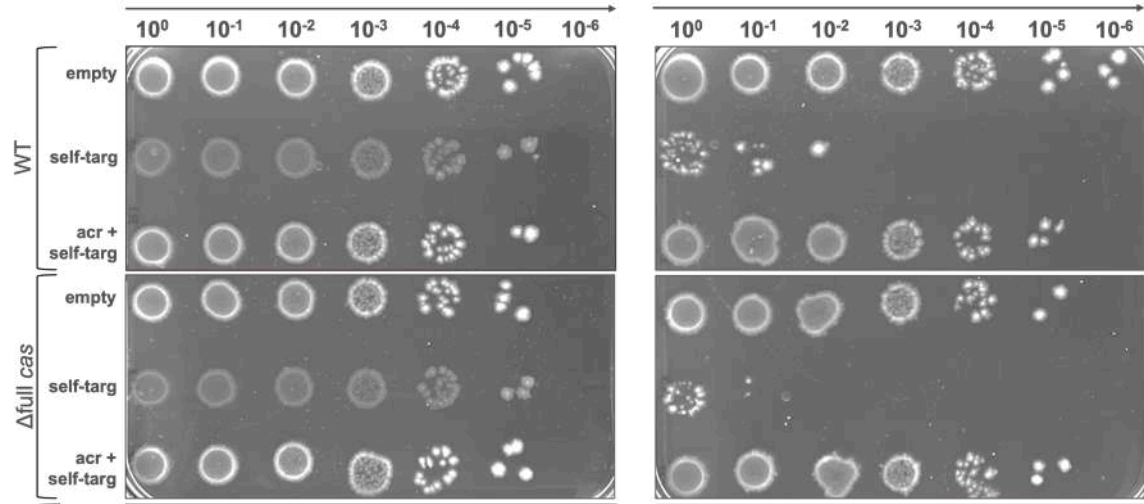
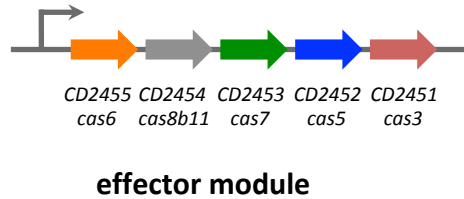
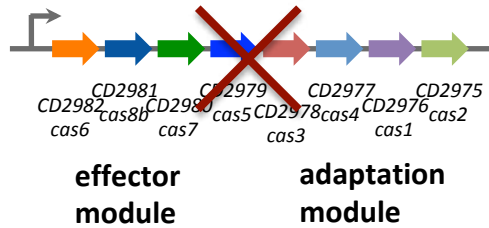
Effect of anti-CRISPR self-targeting inhibition on bacterial growth in BHI liquid medium



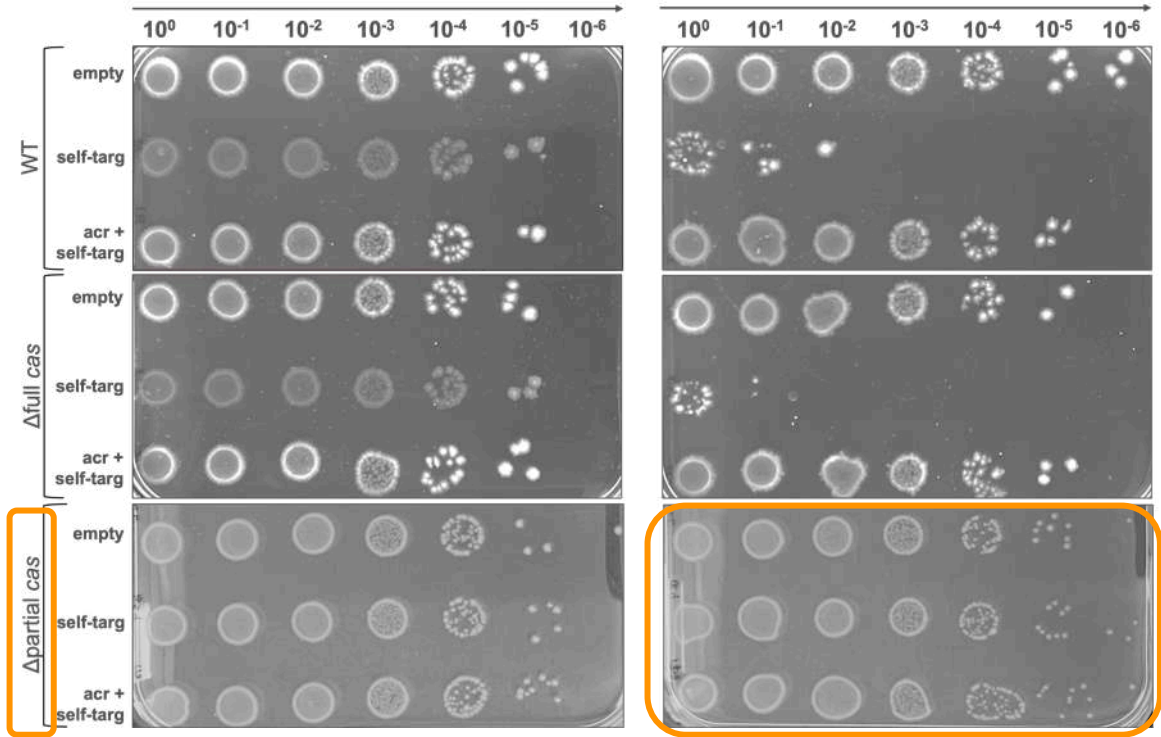
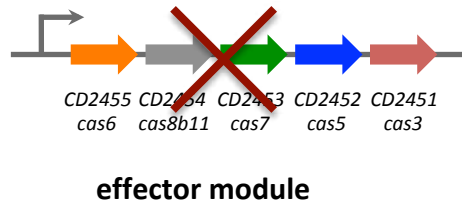
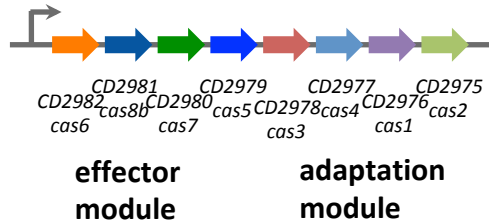
Effect of self-targeting and anti-CRISPR inhibition of self-targeting on genomic DNA content



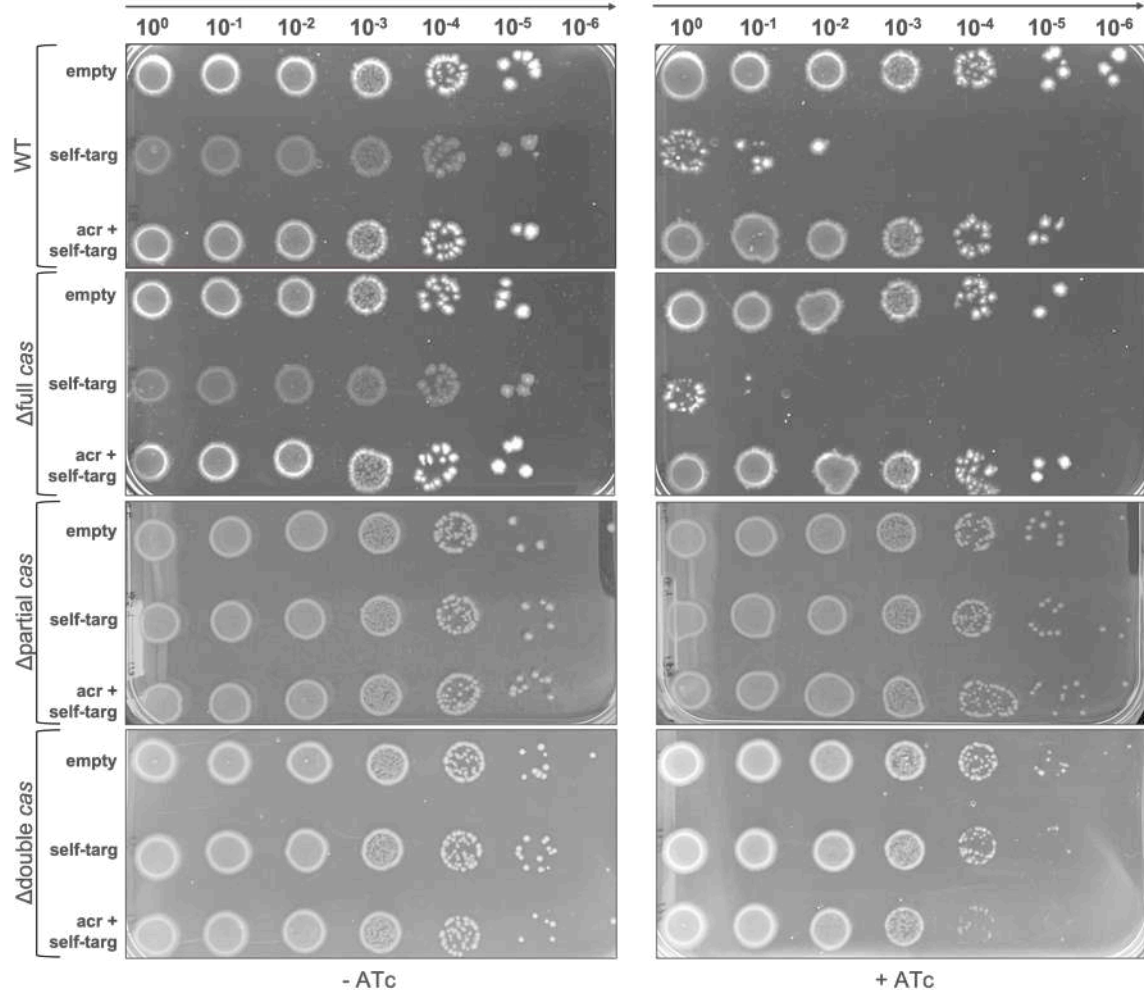
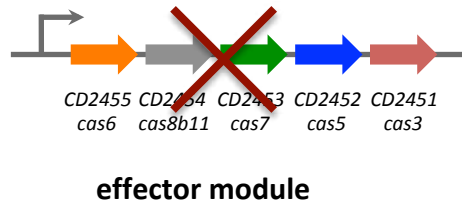
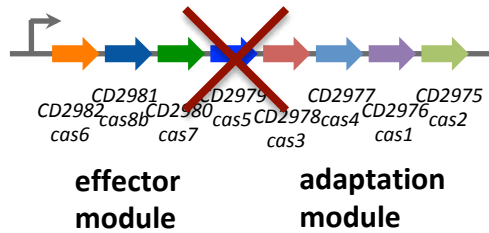
# Deletion of partial *cas* operon disables CRISPR inhibitory activity



# Deletion of partial *cas* operon disables CRISPR inhibitory activity

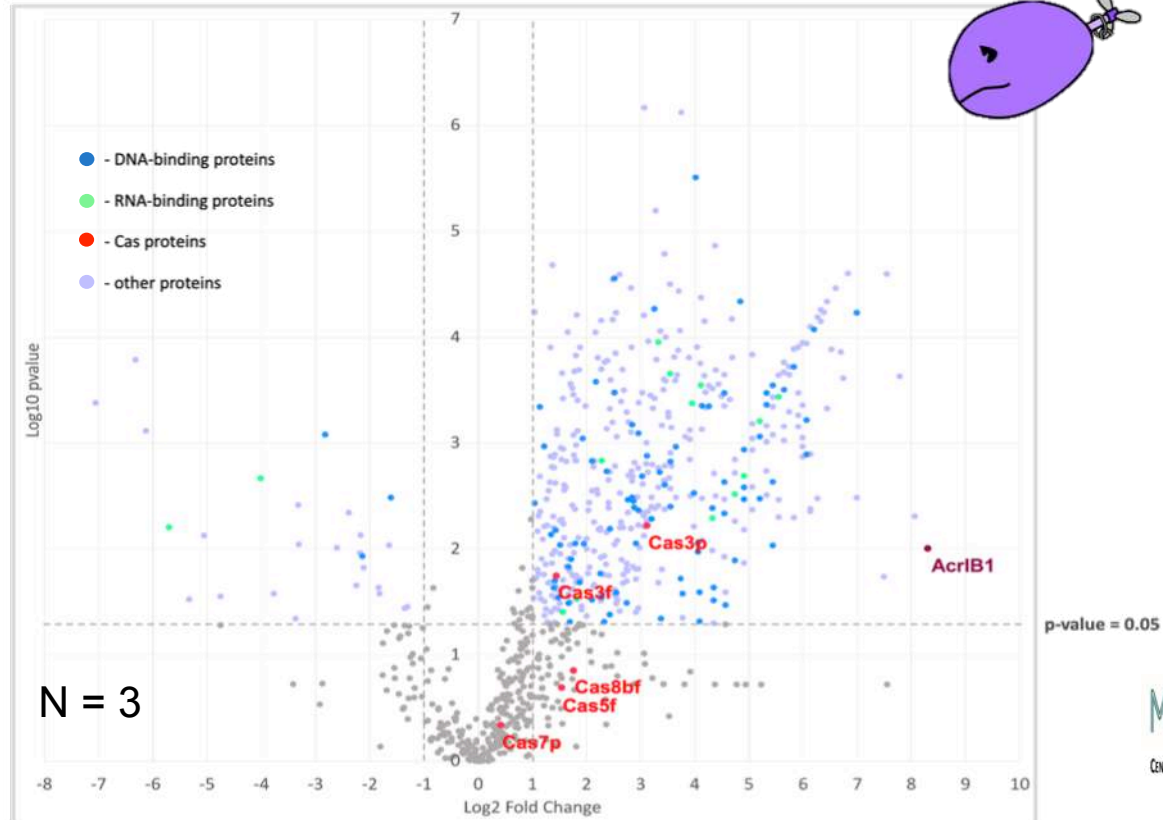
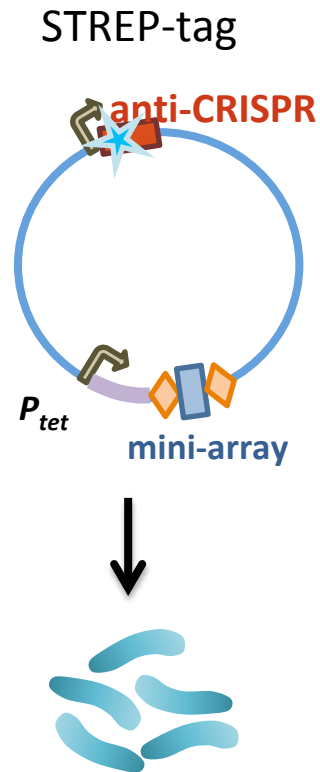


# Deletion of partial *cas* operon disables CRISPR inhibitory activity



# Identification of AcrIB1 interacting proteins

Pull-down results for AcrIB1-N-Strep sample by LC-MS/MS



# Potential DNA mimicry mechanism of action of AcrIB1

**Negatively charged** amino acids (**D** – aspartic; **E** – glutamic acid)

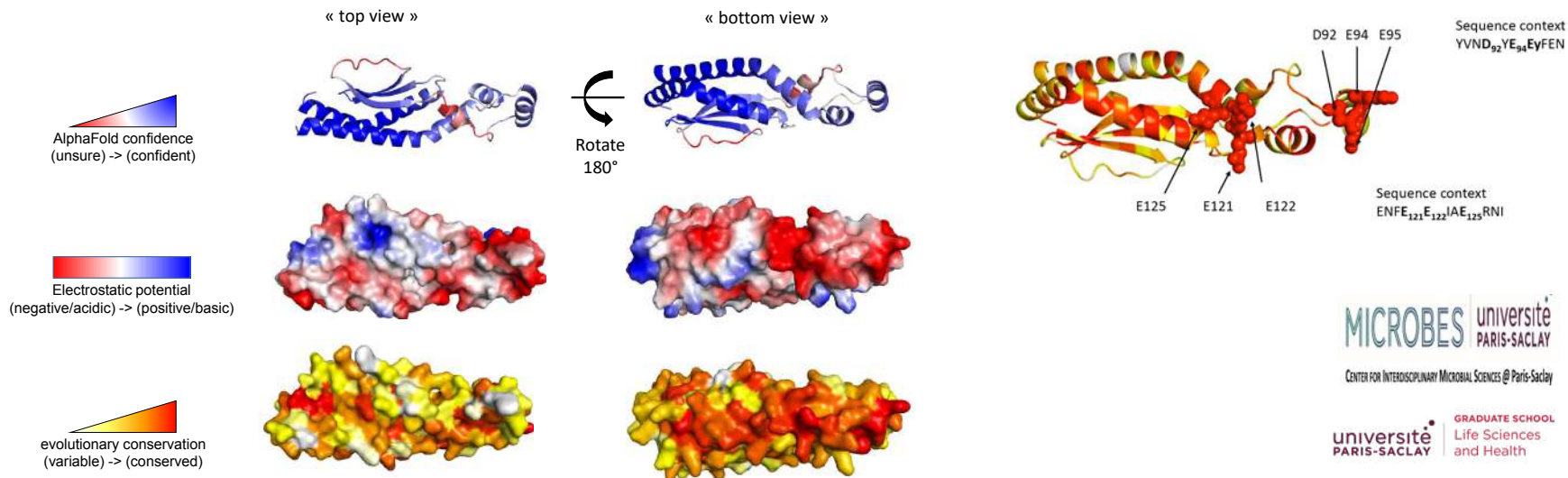
**Aromatic** amino acids (**F** – phenylalanine; **Y** – tyrosine; **W** - tryptophan)

**J. Andreani**



>AcrIB1

MWSHPQ**FE**KNKQKARR**F**LRVID**DM**NI**DK**IE**EE**AIKA**FKE**SCLIK**E**TNNIKI**Y**DI**Q**GK**VE**AI**AV**Q**T**WAKLLG  
**DD**K**E**INI**F**TLN**Q**AP**TH**LN**D**ML**GE**IC**Y**VN**D****YEEFE****N**WC**E****N****E****W****E****N****L****D****W****D****S****Y****K****K****F****N****K****E****N****F****E****E****I****A****E****R****N****I****DD****S****T****S****V**  
**F****L****E****E****L****Q****K****G****I****E****S****C****K****Q****E****L****Q****N****V****I****E****N**



Alpha Fold predictions

Muzyukina et al. mSphere 2023

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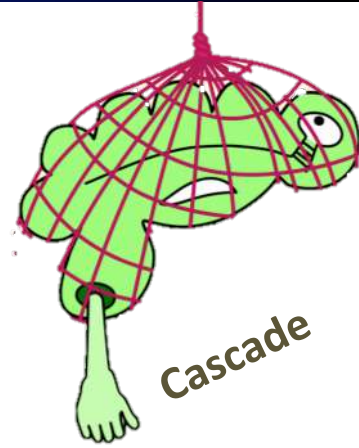
CENTER FOR INTERDISCIPLINARY MICROBIAL SCIENCES @ Paris-Saclay

universit  PARIS-SACLAY GRADUATE SCHOOL Life Sciences and Health



# Conclusions

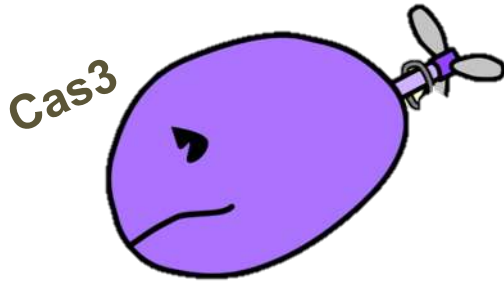
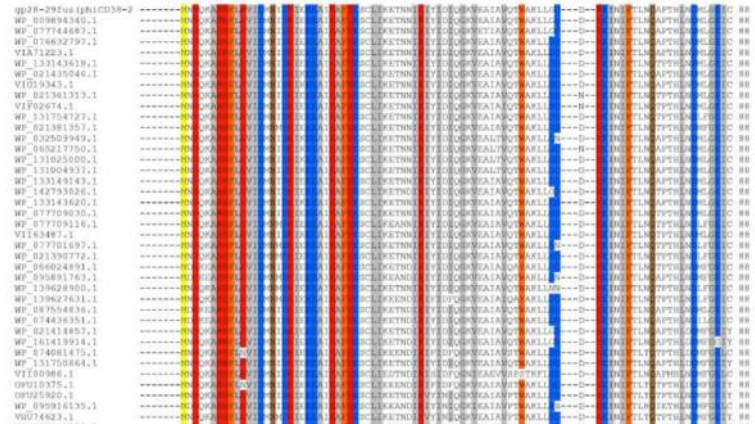
- Identification of first anti-CRISPR protein that inhibits subtype I-B CRISPR-Cas system in the human pathogen *C. difficile*
- DNA mimicry mechanism of AcrIB1 from structure predictions



## Perspectives

- Analysing AcrIB1 partner protein(s) and mechanism of action
- Testing new Acr candidates

Protein alignment of 79 homologs of AcrIB1

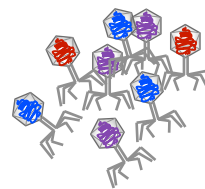




From molecules to infection

Signals

Dynamic model



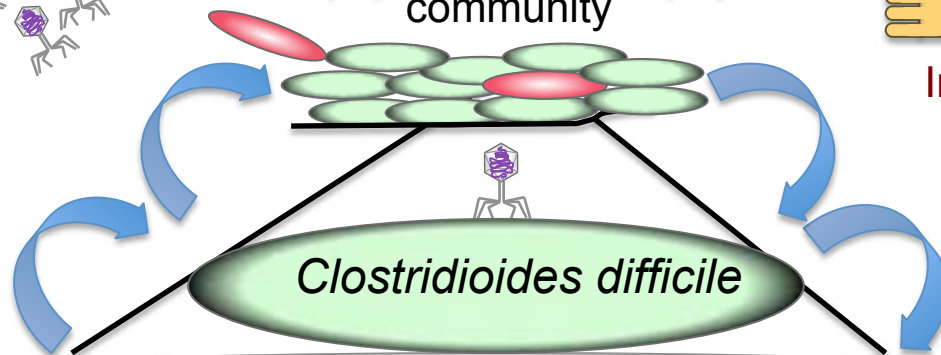
Phages

Bacterial community

Host

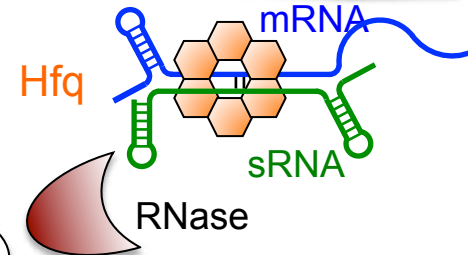
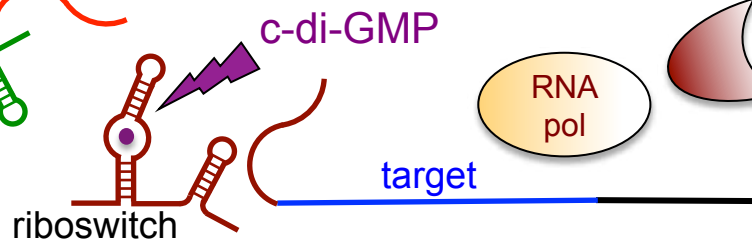
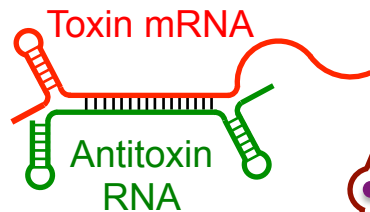
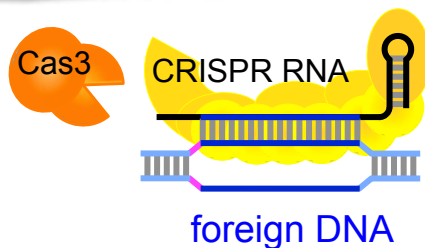


Inflammatory response



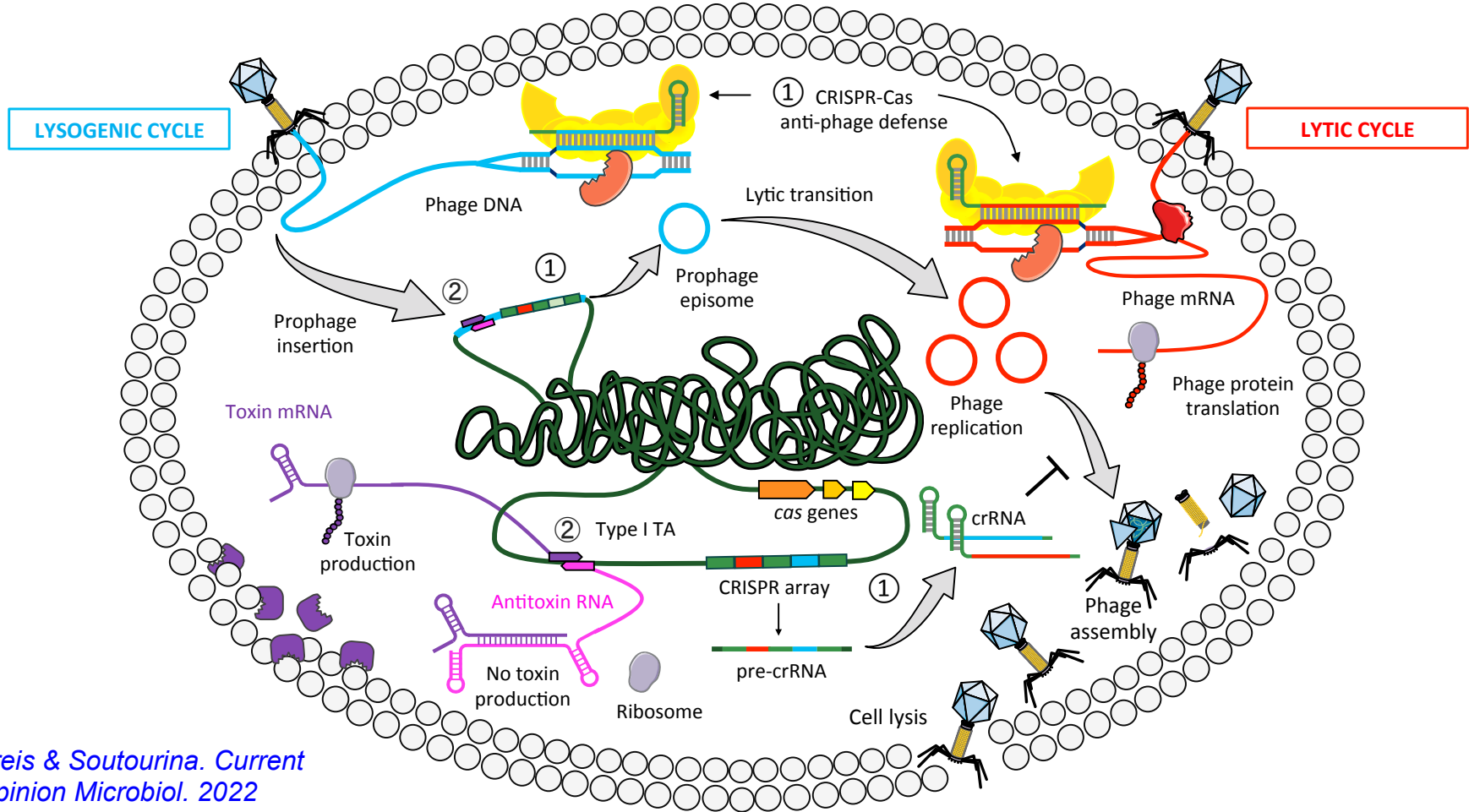
*Clostridioides difficile*

### Molecular mechanisms

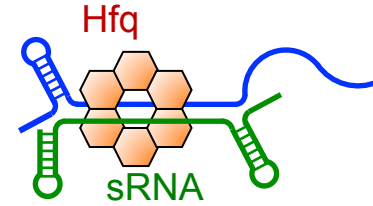
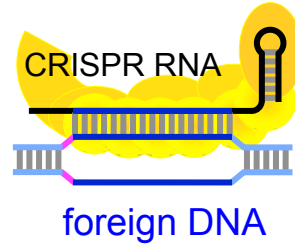
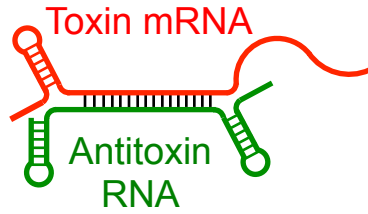


Pathogenesis, metabolism, defence systems, biofilm, sporulation, stress response

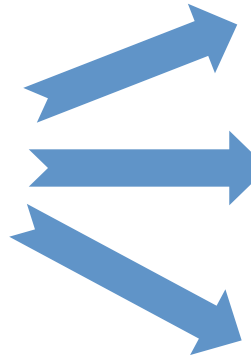
# Summary of RNA-based mechanisms in *C. difficile*-phage interactions



# Potential RNA applications in *C. difficile*



## ➤ Applications



### ➤ **Biotechnology**

(endogenous **CRISPR editing** & **TA-based** tools, **Anti-CRISPR**)

### ➤ **Epidemiology**

(**CRISPR typing**, ncRNA markers for epidemic strains)

### ➤ **New antimicrobials**

(**Antisense RNA**, **sRNAs as drug targets**)

**CRISPR autoimmunity**, **TA induction for self-targeting**  
**Anti-CRISPR for phage therapy**

**Riboswitches targeting**, **Secreted RNAs ...)**