

# EPICATCH5

## THE 5<sup>TH</sup> EPI-CATCH MEETING

Epi-biology of the mycotoxin producer *Fusarium graminearum* vs. host plant defense mechanisms

By Nadia PONTS

anr<sup>®</sup>

INRAE

July 11<sup>th</sup> 2024

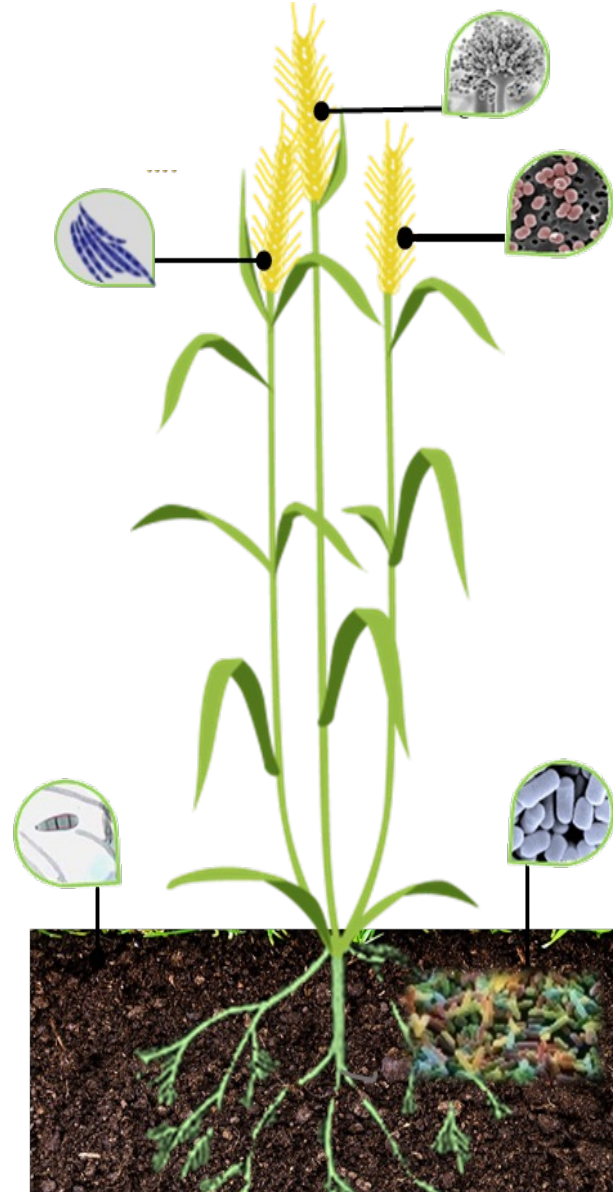
  
RÉPUBLIQUE  
FRANÇAISE  
Liberté  
Égalité  
Fraternité



# ➤ One plant vs. the rest of the world

## Who?

- Fungi
- Oomycetes
- Bacteria
- Viruses
- Insects
- Nematodes
- Other plants



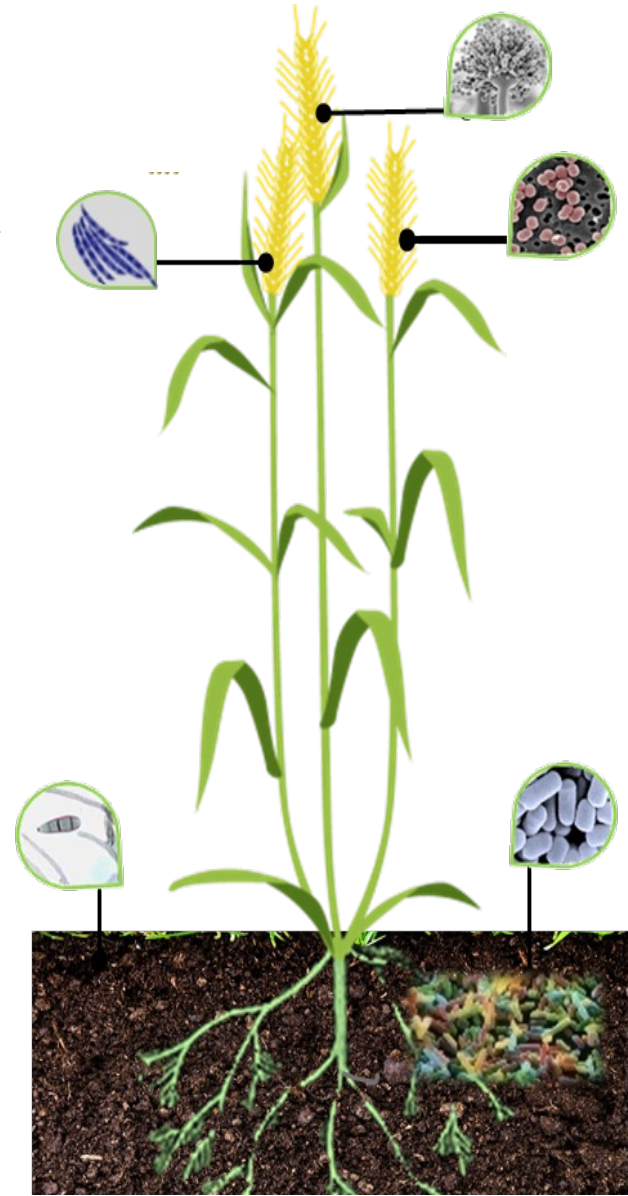
## Outcome

- Beneficial
- Neutral
- Unfavorable
- All of the above

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➤ Fungal pathogen: attack



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Outcome

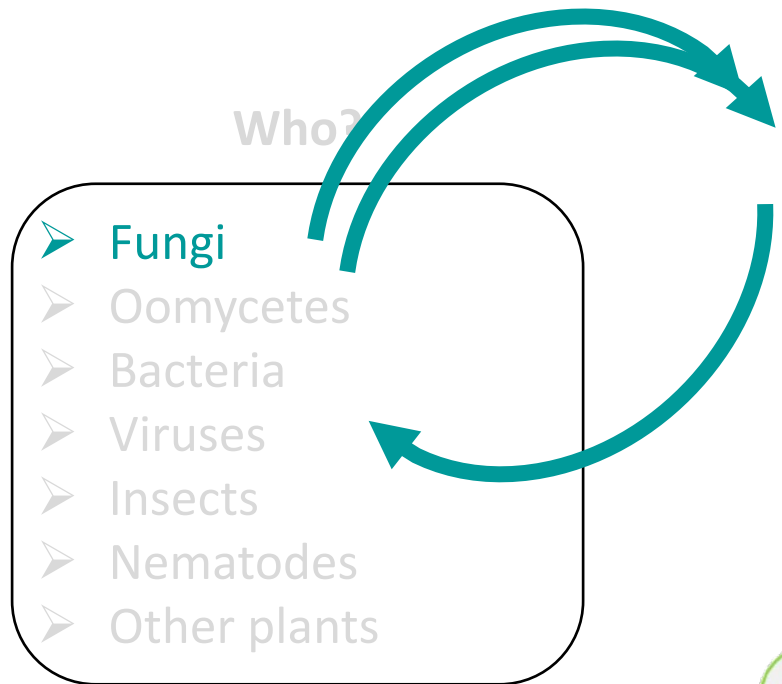
- Beneficial
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- Fungal pathogen: attack
- The plant: defense / counter attack mechanisms

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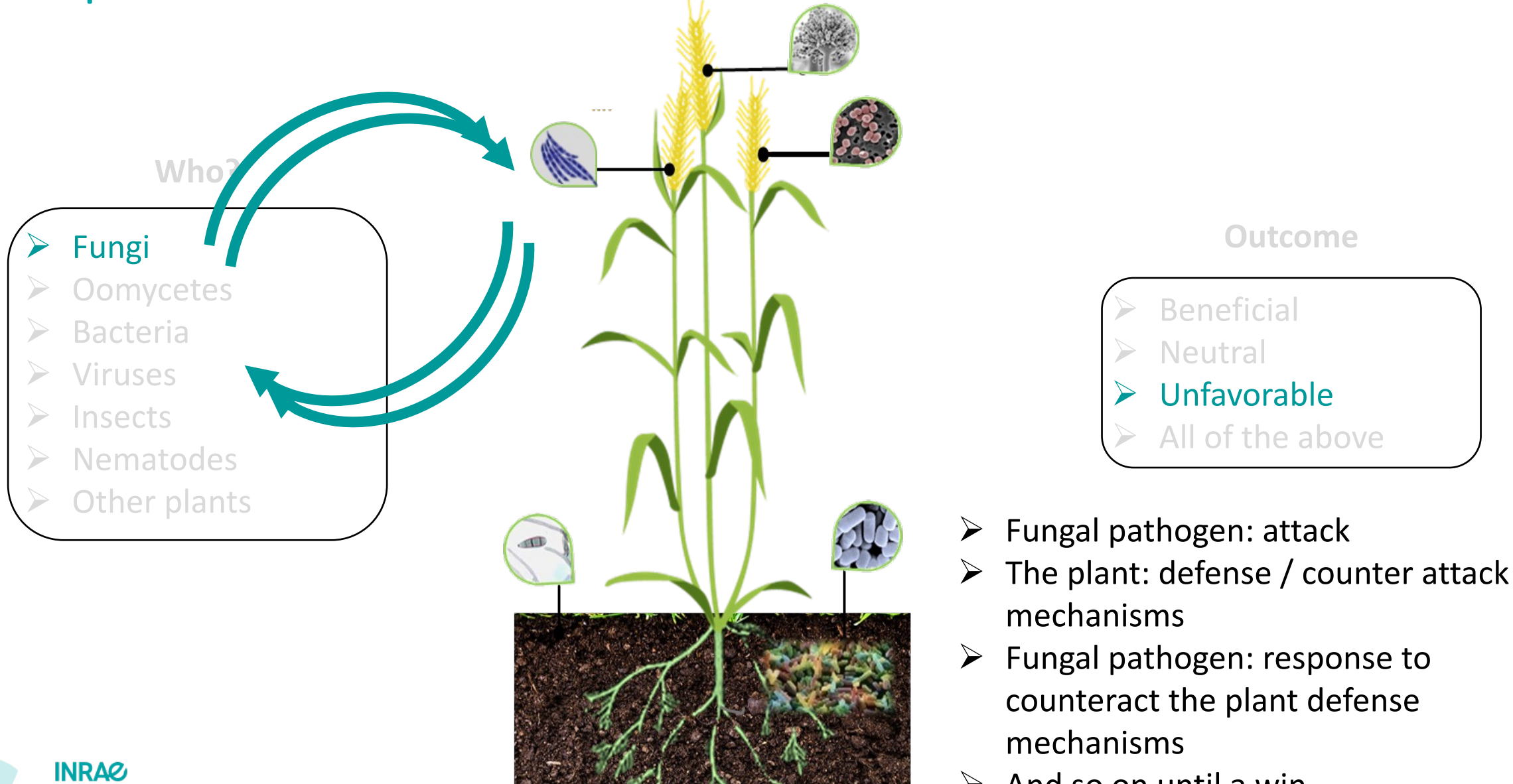

Outcome

- Beneficial
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- **Unfavorable**
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- Fungal pathogen: attack
- The plant: defense / counter attack mechanisms
- Fungal pathogen: response to counteract the plant defense mechanisms

Credit: L. Pinson-Gadais@INRAE-MycSA

# ➤ One plant vs. the rest of the world



Credit: L. Pinson-Gadais@INRAE-MycSA

The Epi life of the plant pathogen *Fusarium graminearum*

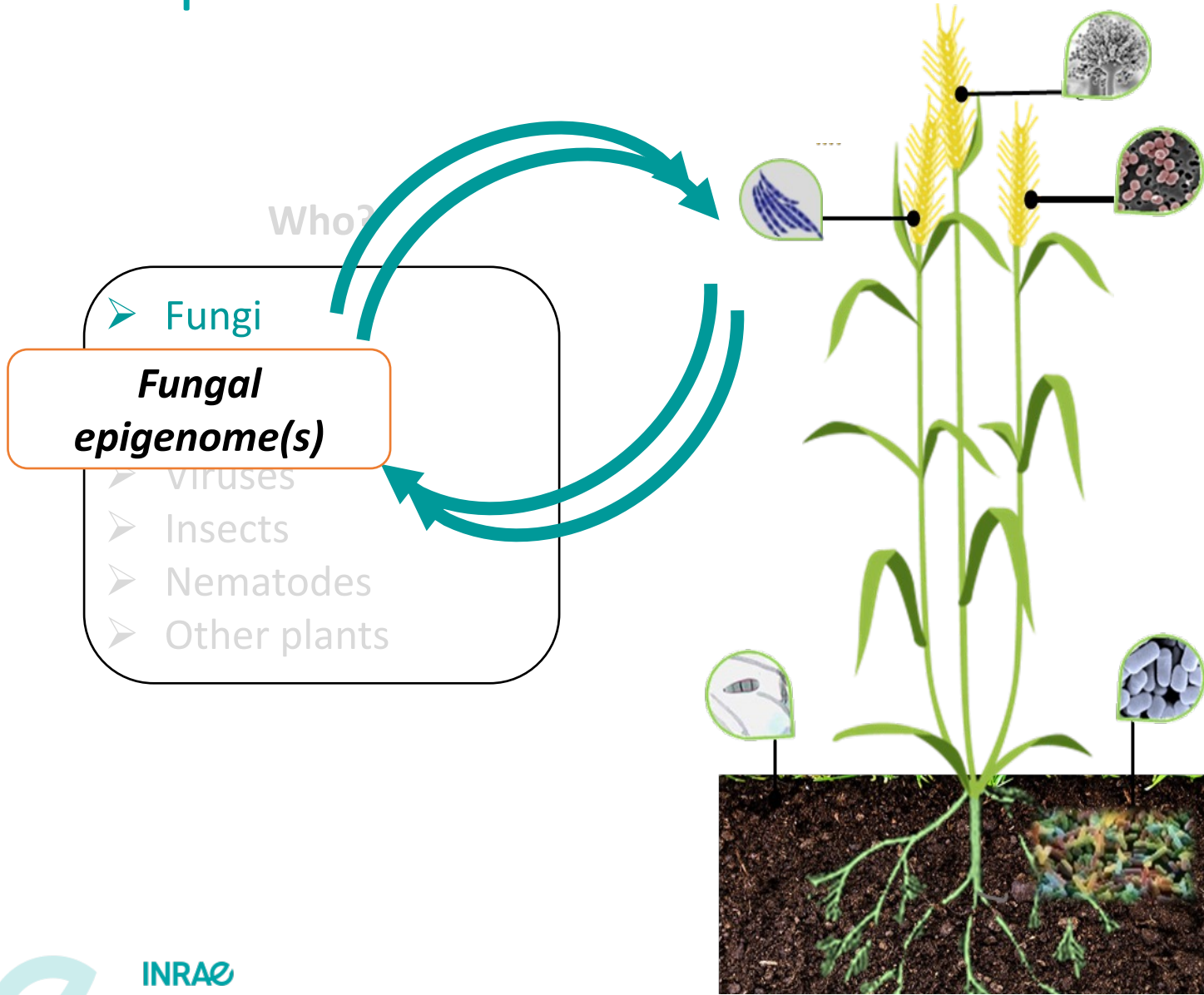


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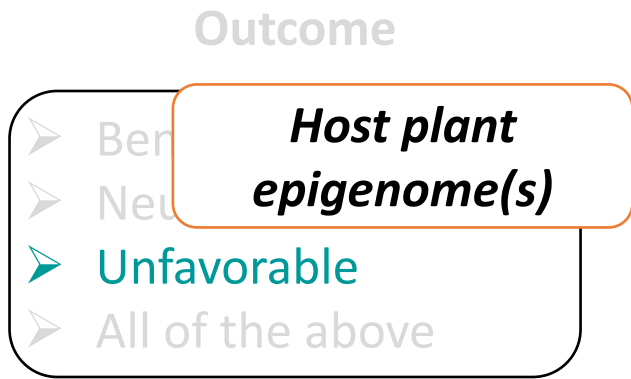
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July 11th 2024

# ➤ One plant vs. the rest of the world



## Epigenetics of the biotic interactions



- Fungal pathogen: attack
- The plant: defense / counter attack mechanisms
- Fungal pathogen: response to counteract the plant defense mechanisms
- And so on until a win...

Credit: L. Pinson-Gadais@INRAE-MycSA

# ➤ One plant vs. the rest of the world

## Epigenetics of the biotic interactions

### The Epigenetic Language

DNA methylation  
Histone marks  
Small RNAs\*



Modulation of  
chromatin accessibility



Modifies gene  
expression

*Fungal  
epigenome(s)*

*Host plant  
epigenome(s)*





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## Epigenetics of the biotic interactions

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*Fungal epigenome(s)*

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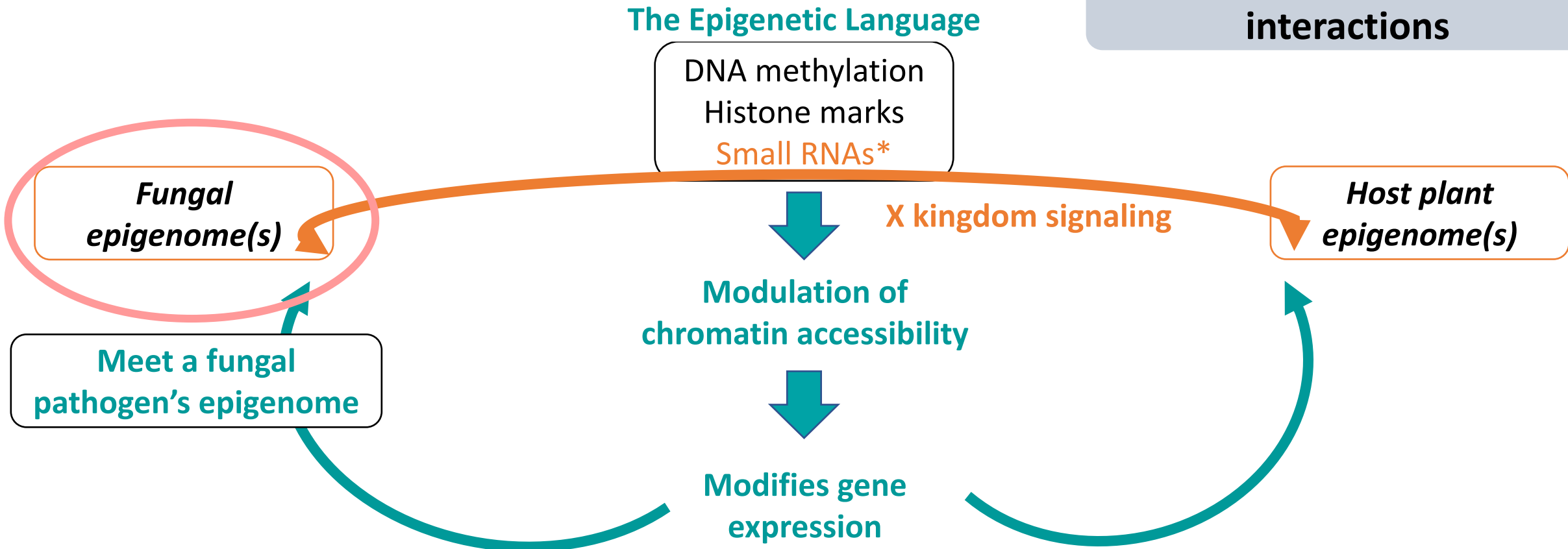
X kingdom signaling

Modulation of chromatin accessibility

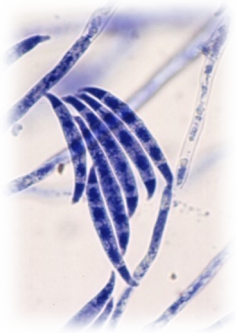
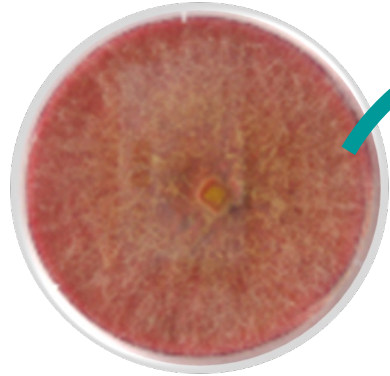
Modifies gene expression

# ➤ One plant vs. the rest of the world

## Epigenetics of the biotic interactions



# ➤ The plant pathogen *Fusarium graminearum*

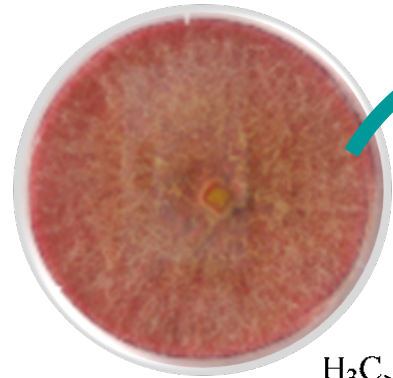


**Problem #1:**  
Dramatic  
yield losses  
worldwide  
\$\$\$\$

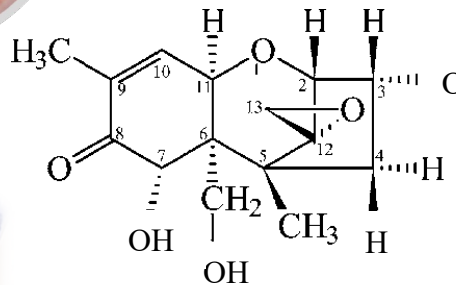
*Fusarium graminearum*

Fusarium Head Blight (FHB) on wheat ears

# ➤ The plant pathogen *Fusarium graminearum*



**MYCOTOXINS**



**Deoxynivalenol (DON)**

**Virulence factor on wheat**



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**Problem #1:**  
Dramatic yield losses worldwide  
\$\$\$\$

**Problem #2:**  
Public health concerns

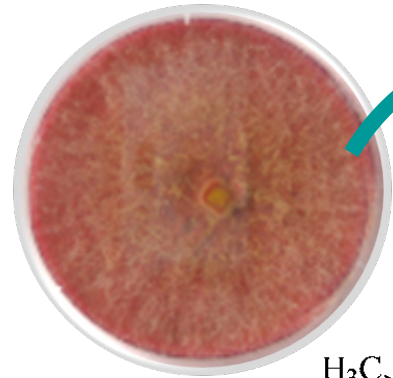


(and more \$\$\$)

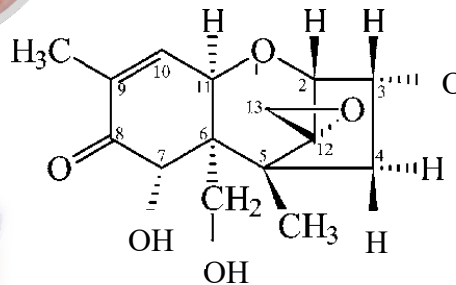
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# ➤ The plant pathogen *Fusarium graminearum*



**MYCOTOXINS**



**Deoxynivalenol (DON)**

**Virulence factor on wheat**



**Problem #1:**  
Dramatic yield losses worldwide  
\$\$\$\$

**PREVENTION**

**Problem #2:**  
Public health concerns



(and more \$\$\$)

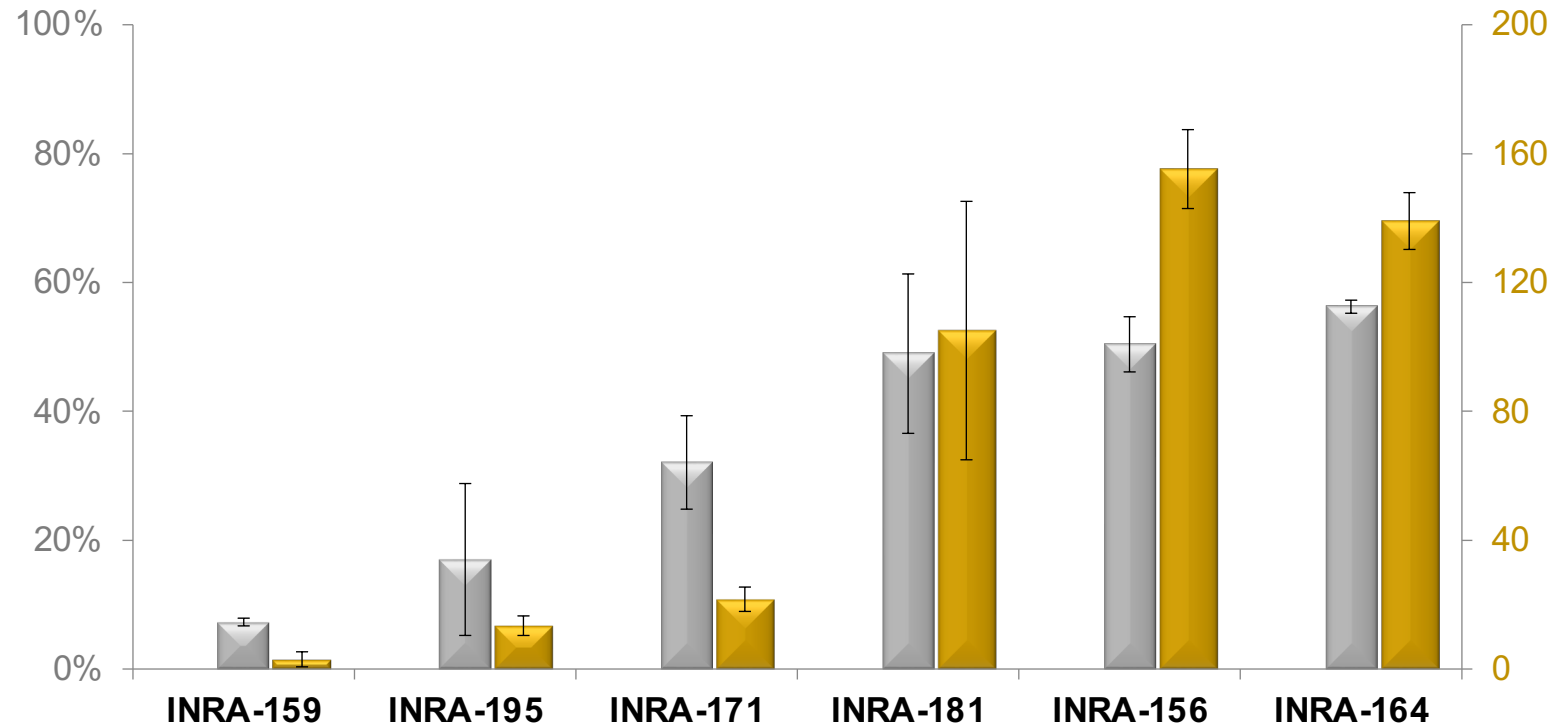
*Fusarium graminearum*

Fusarium Head Blight (FHB) on wheat ears

# ➤ Different isolates have different abilities to...

## ... Infect wheat

% of infected ear



## ... produce mycotoxins

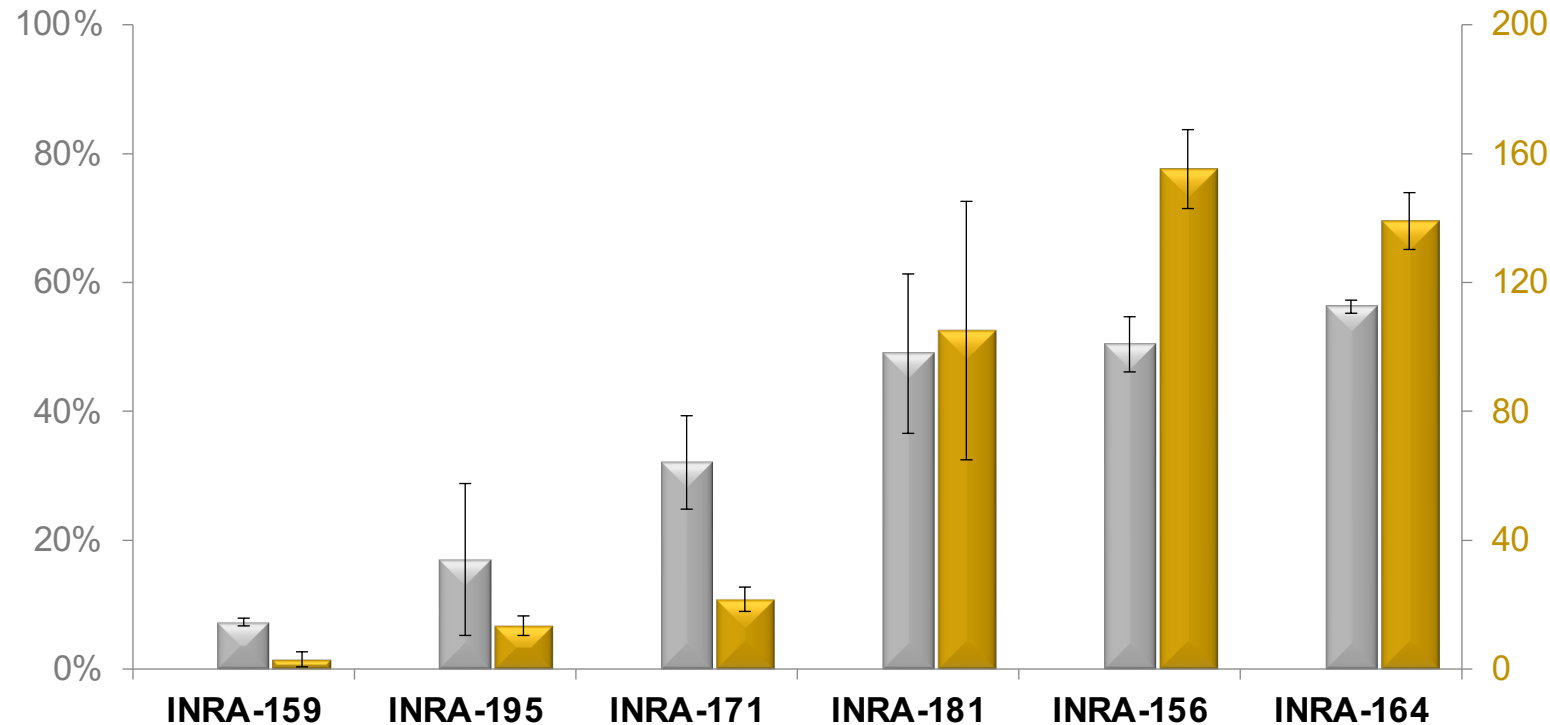
[DON] µg/g of dry weight

What bases for such differences?

# ➤ Different isolates have different abilities to...

## ... Infect wheat

% of infected ear



## ... produce mycotoxins

[DON] µg/g of dry weight

What bases for such differences?

Genetics ?

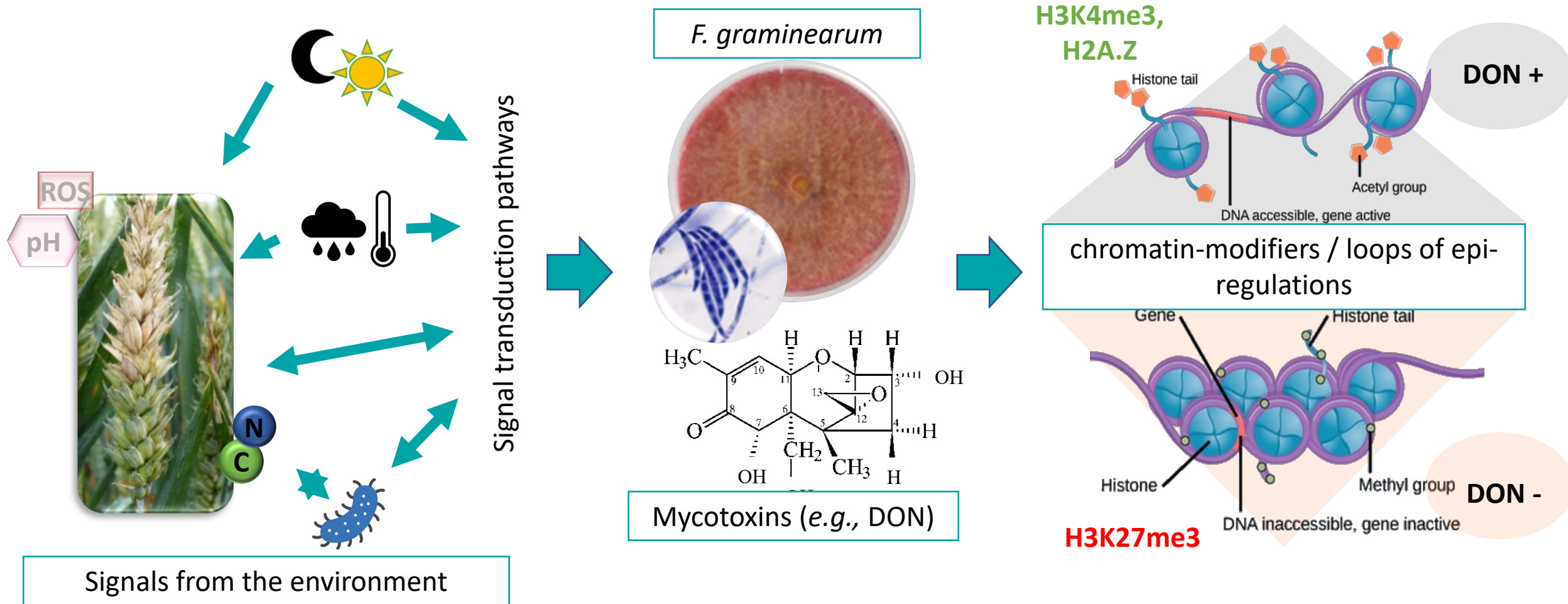


All isolates have the « same » potential to produce DON

High genetic diversity at other *loci*, but no association found (yet?)

# ➤ Role of chromatin structure in *F. graminearum*

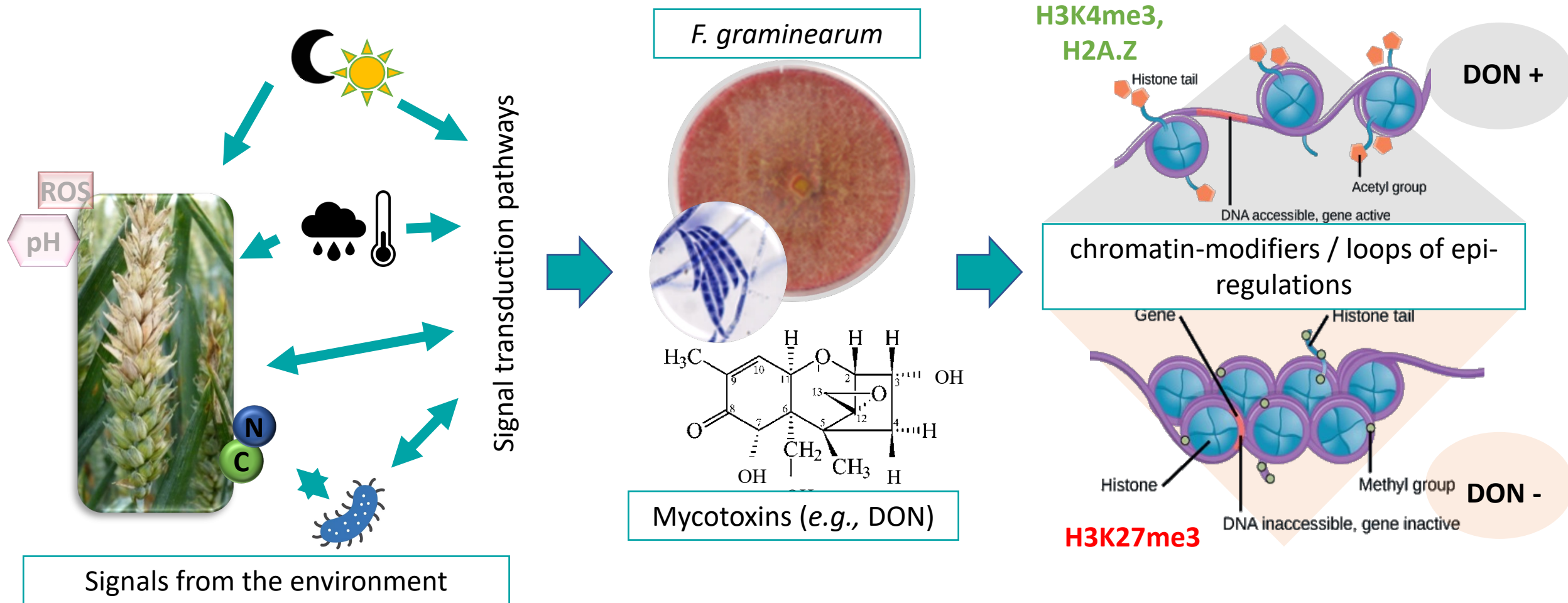
Ecophysiology + targeted functional analyses approaches





# ➤ Role of chromatin structure in *F. graminearum*

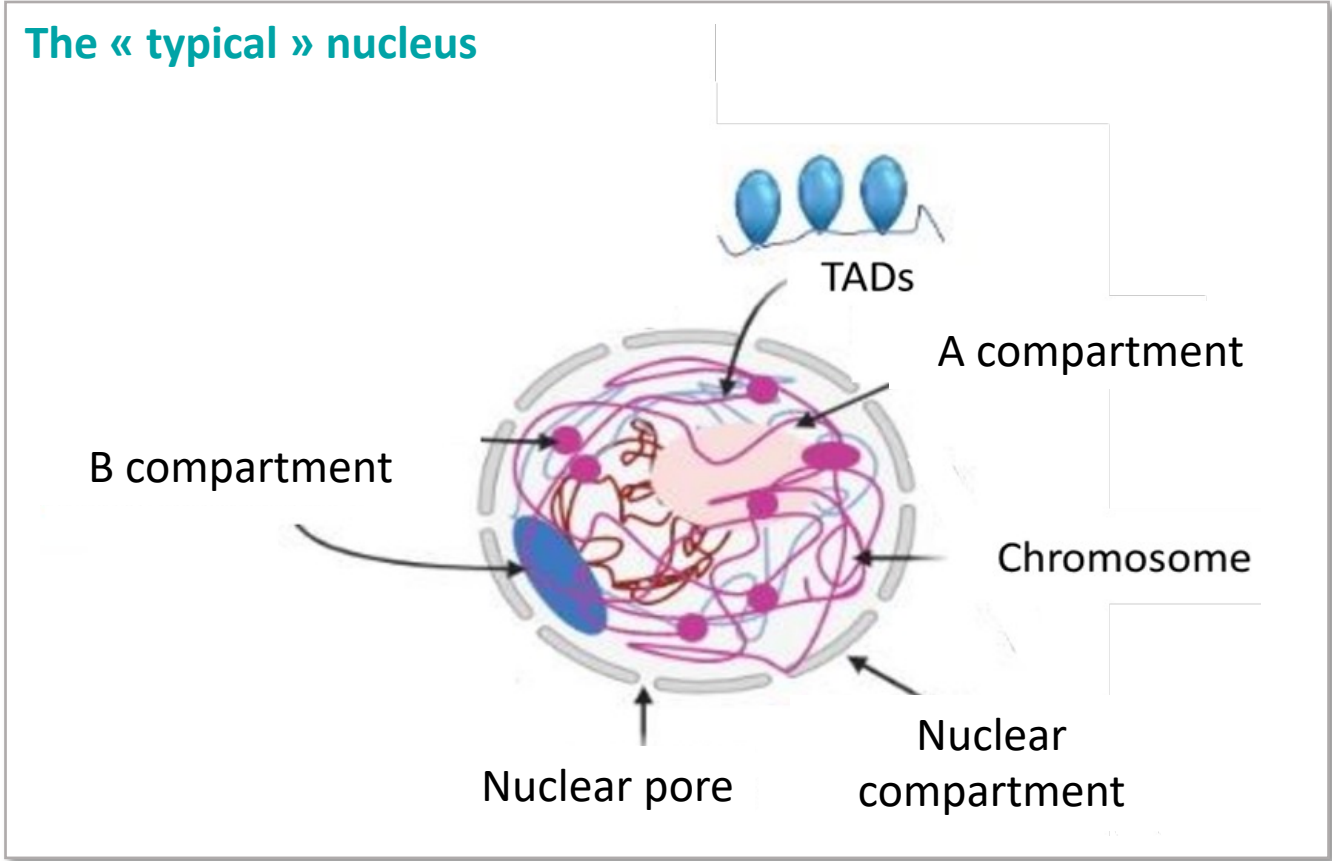
Ecophysiology + targeted functional analyses approaches



**How does the genome structure relates to the epibiology of the *Fusarium graminearum*?**

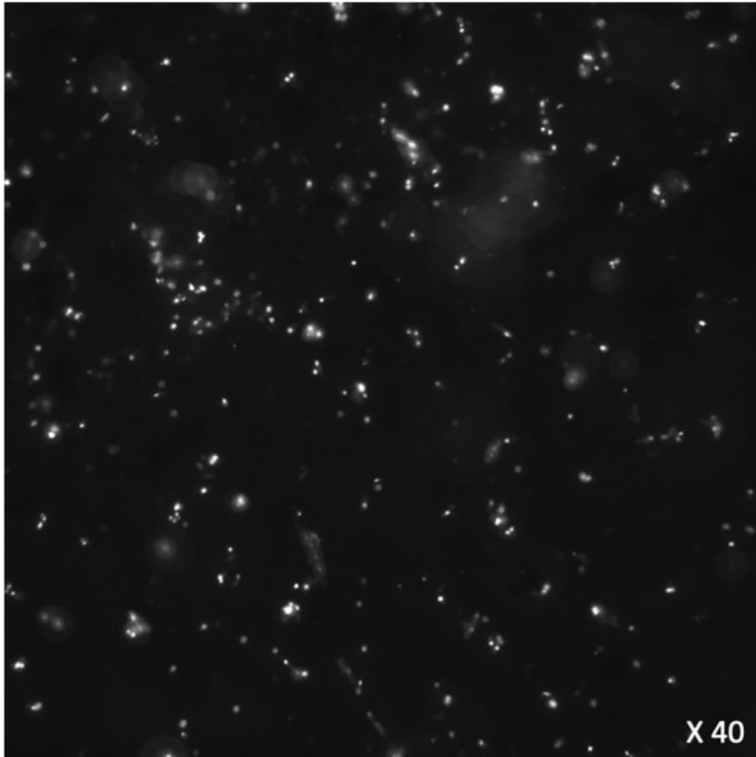
# ➤ Topology of the *Fusarium graminearum* genome

~37 Mb; >14k genes; 4 chromosomes

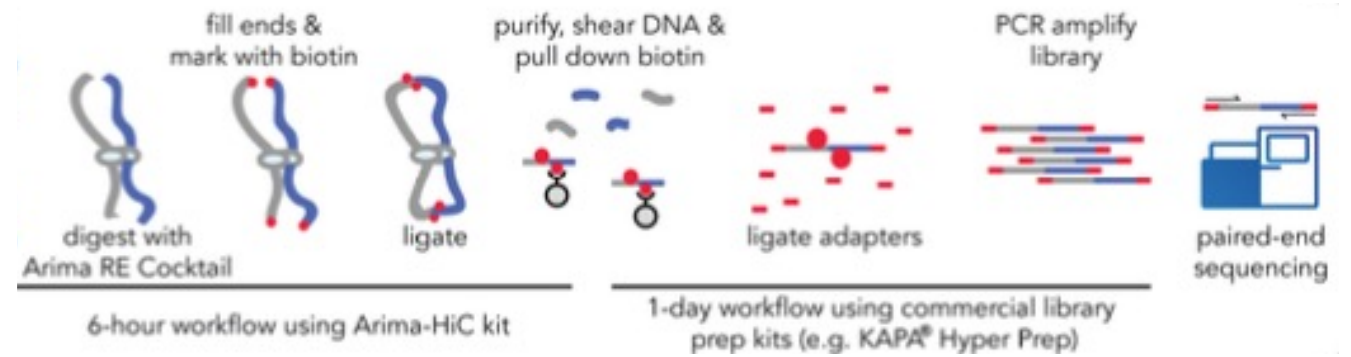
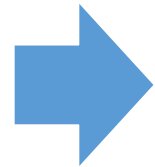


# ➤ Topology of the *Fusarium graminearum* genome

*In situ* Hi-C



**1 – Isolating intact nuclei**

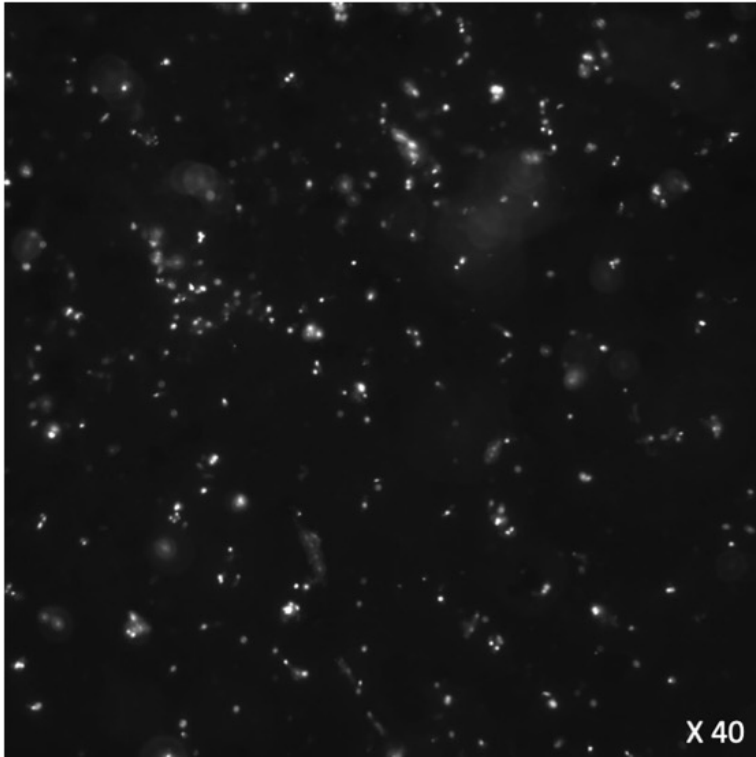


**2 – Preparation of sequencing-ready chimeric fragments**

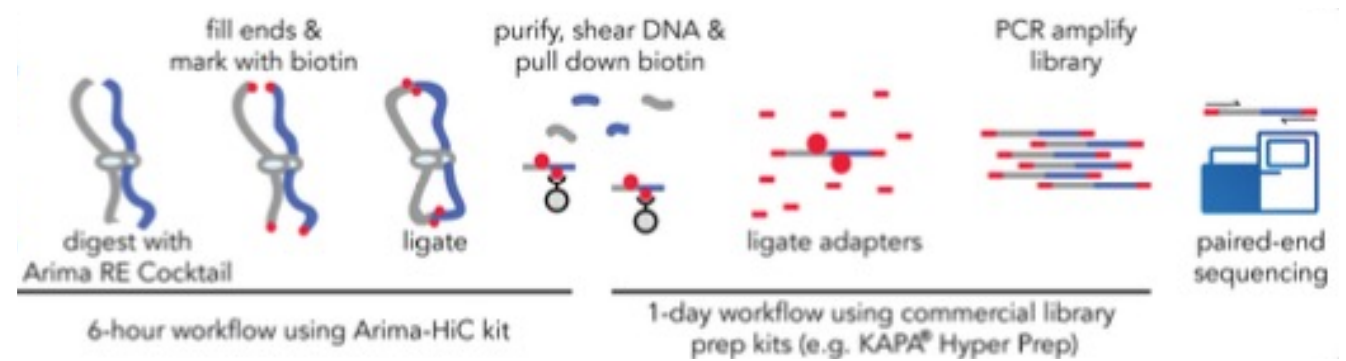
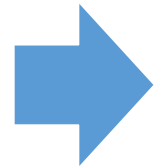
**3 – Illumina® paired-end sequencing**

# Topology of the *Fusarium graminearum* genome

*In situ* Hi-C



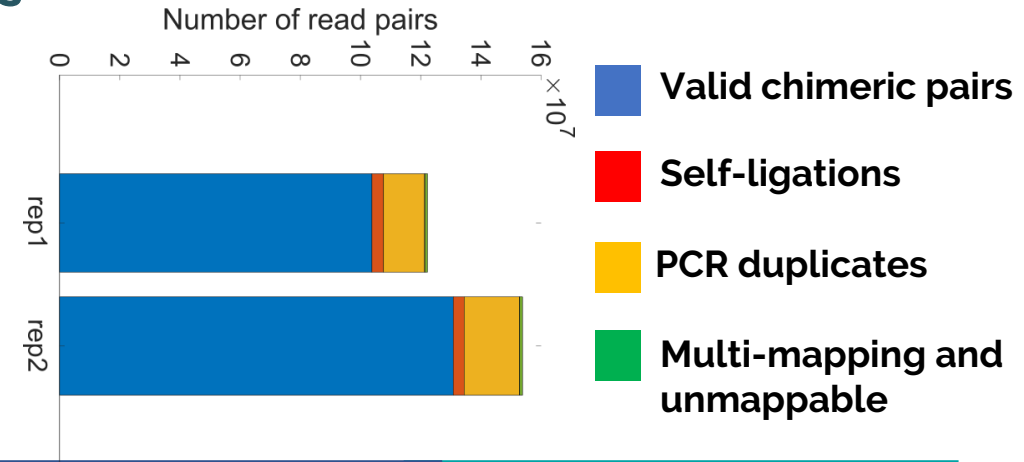
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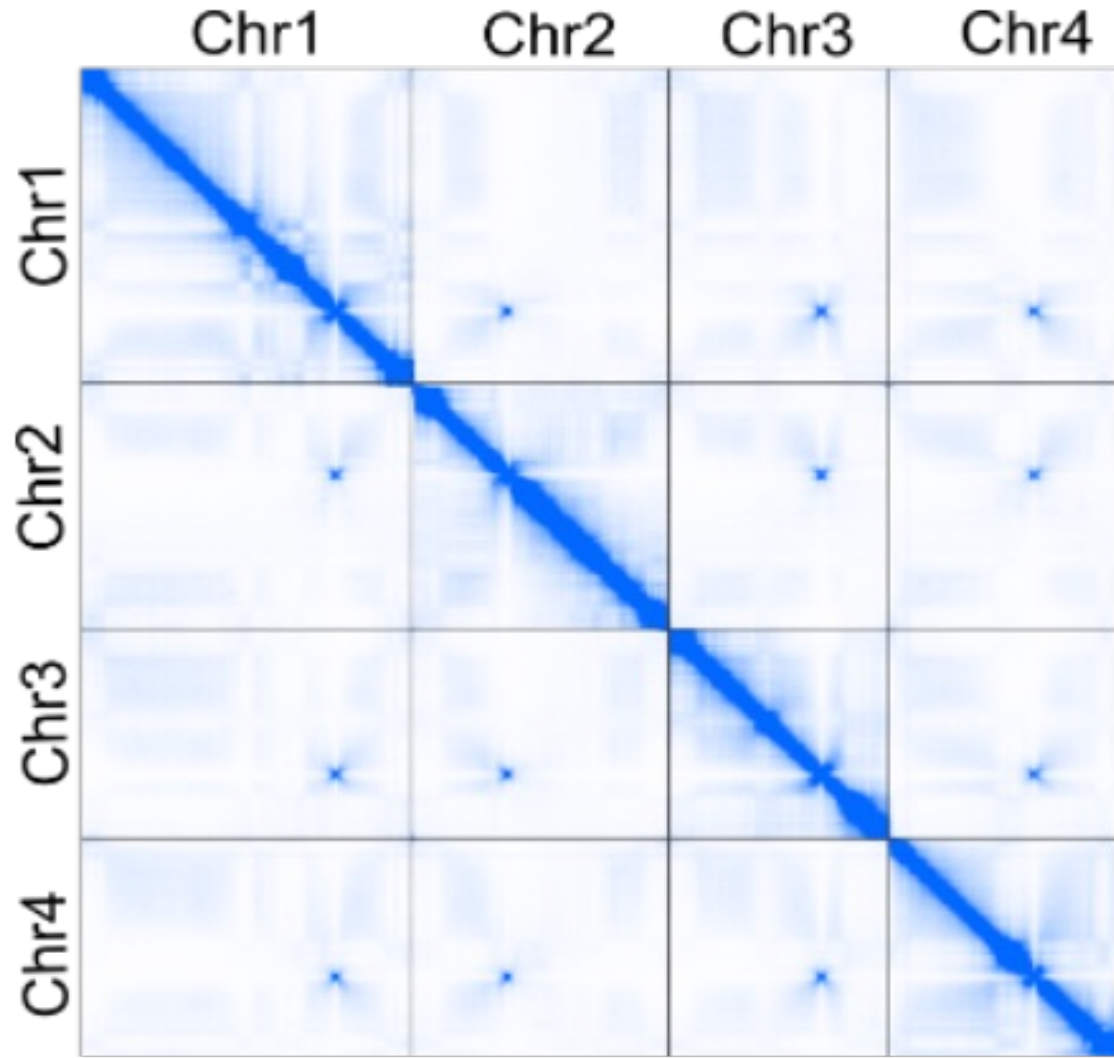
**3 – Illumina® paired-end sequencing**

**4 – Read processing and data analysis.**



# ➤ Topology of the *Fusarium graminearum* genome

*In situ* Hi-C



**1 pixel = 1 contact**

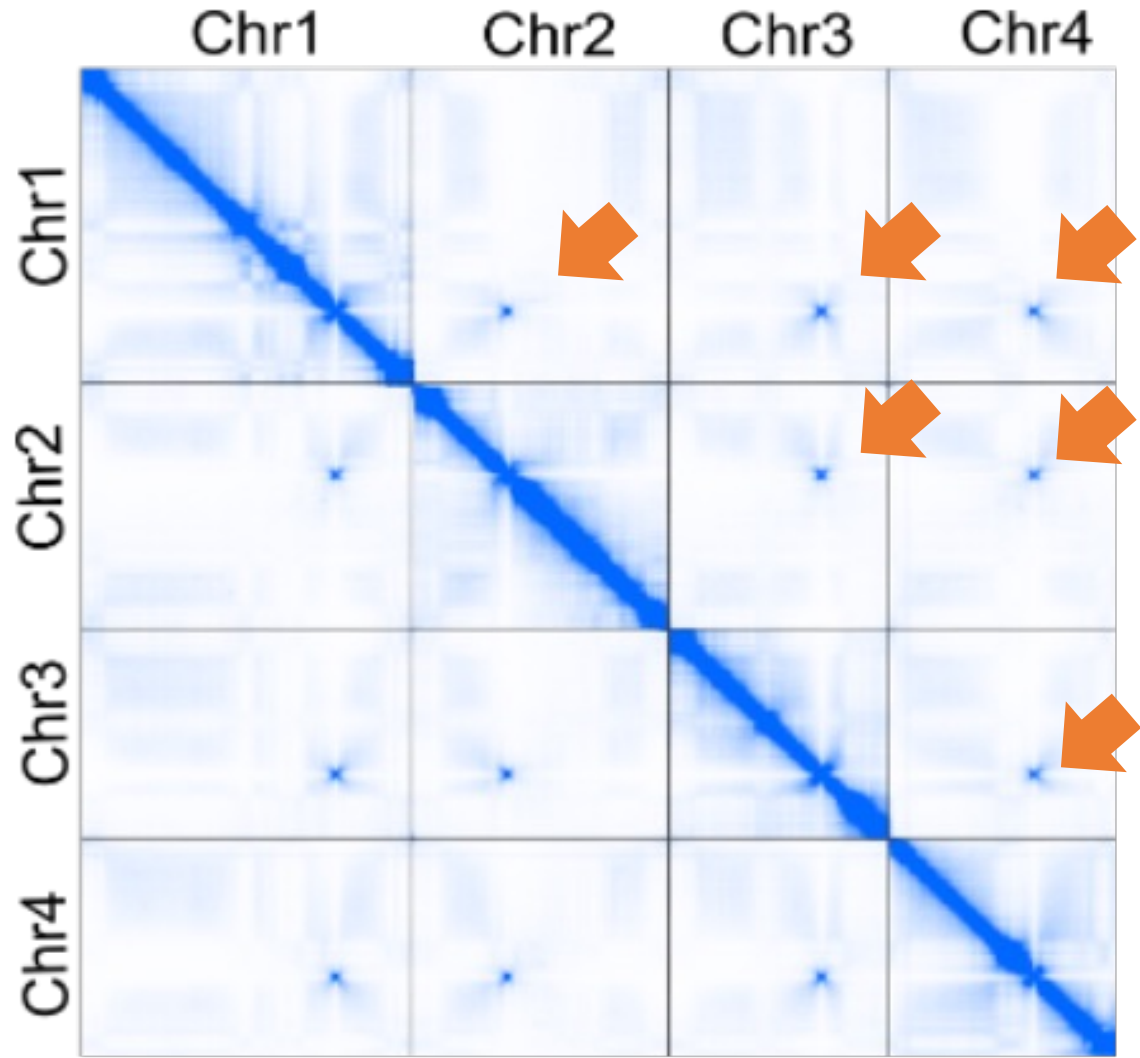
**Intensity ⇔ contact frequency**

**What we expect vs. what we observe**

# ➤ Topology of the *Fusarium graminearum* genome

*In situ* Hi-C

Trans-interactions at centromere *loci*



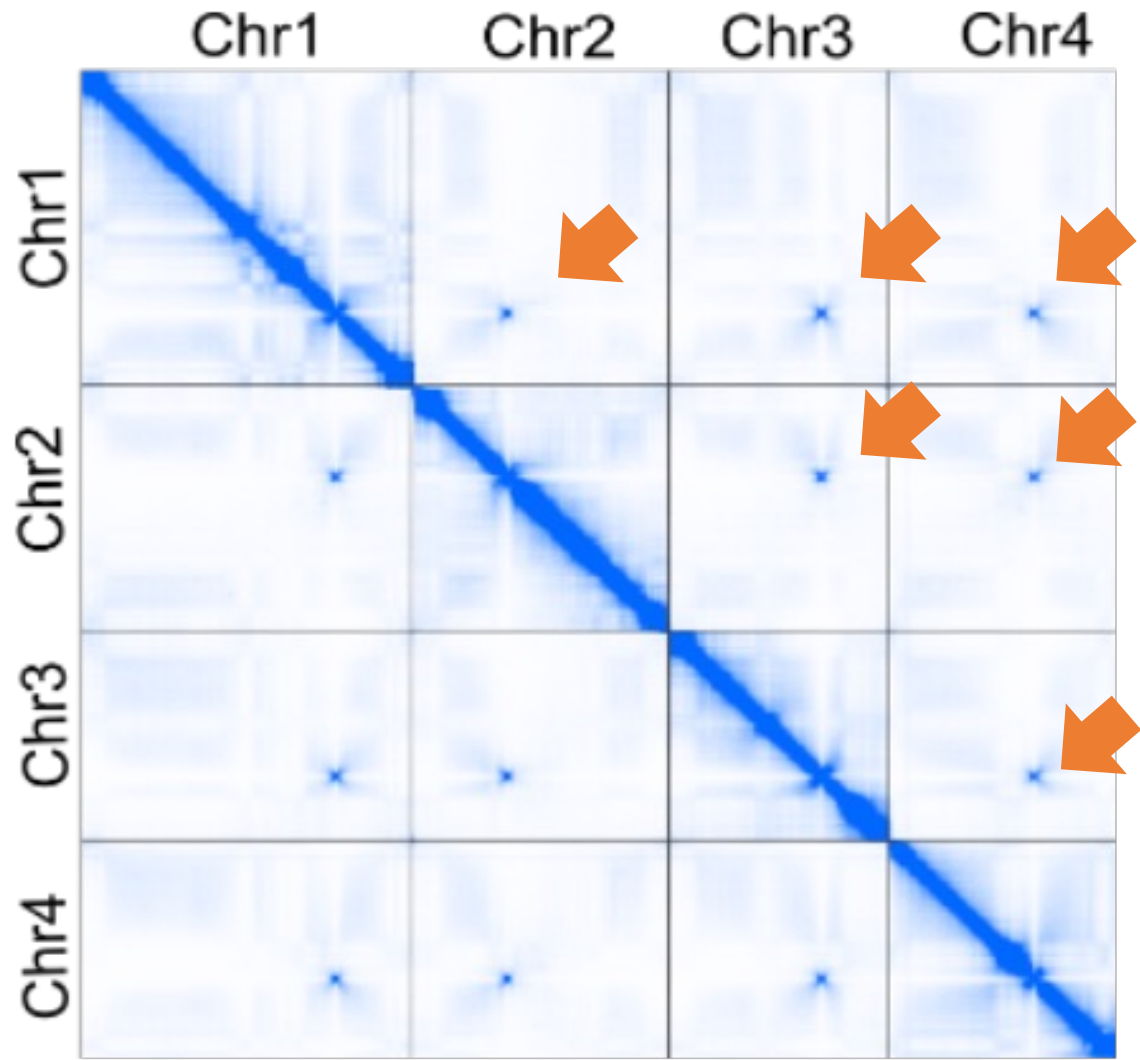
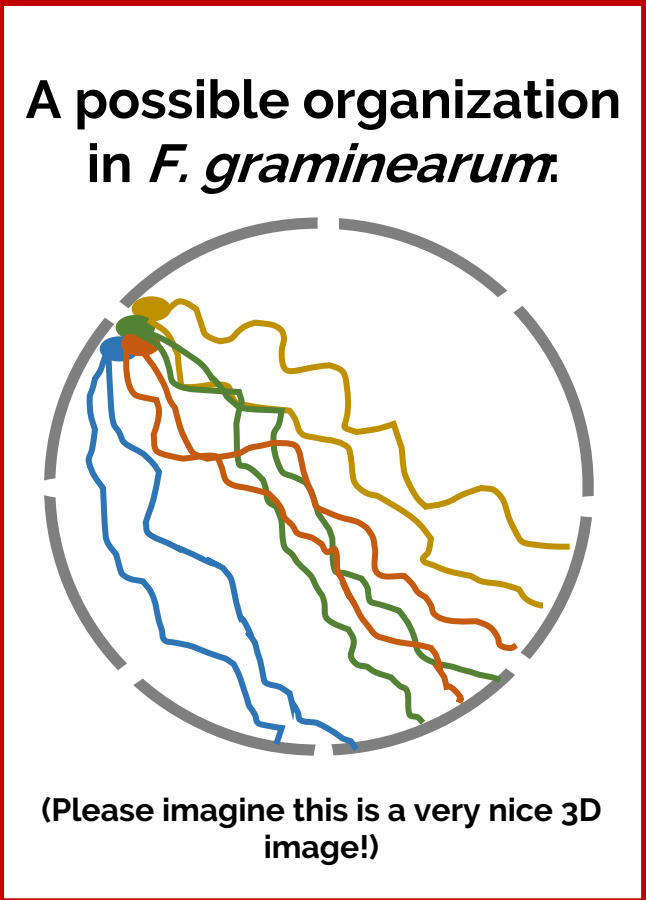
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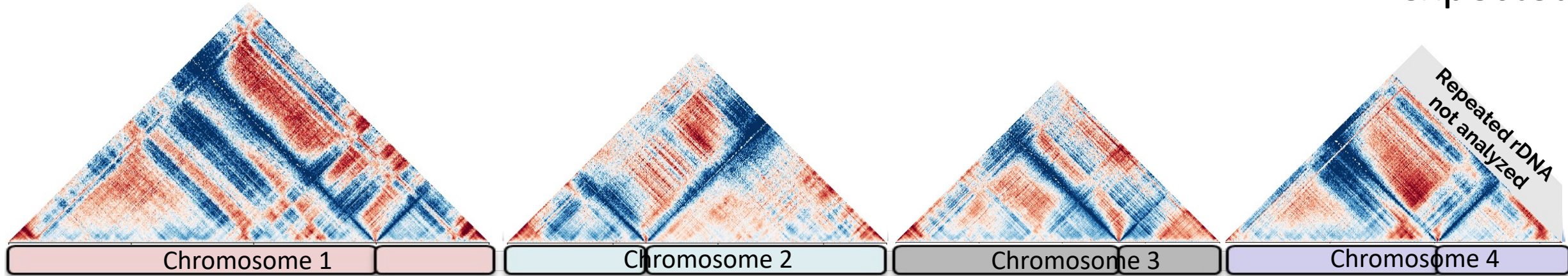
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# Topology of the *Fusarium graminearum* genome

Observed vs.  
expected

*In situ* Hi-C



**Cis-regulatory  
structures visible**

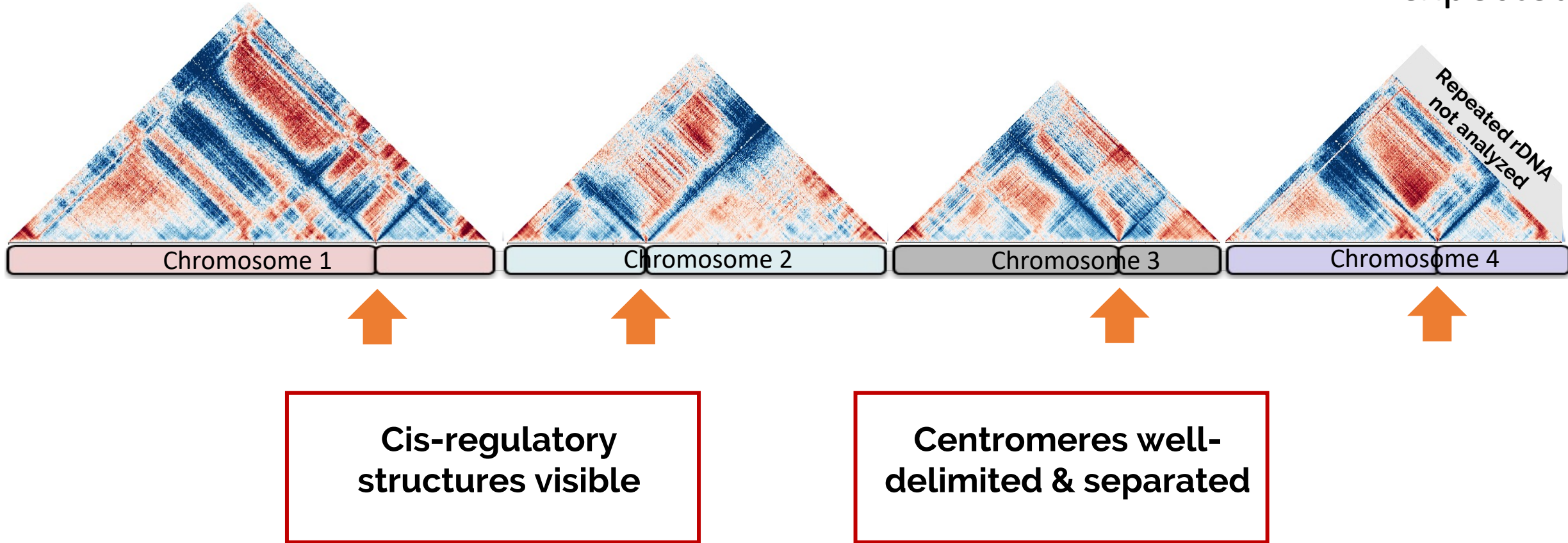
Pearson correlation between distances



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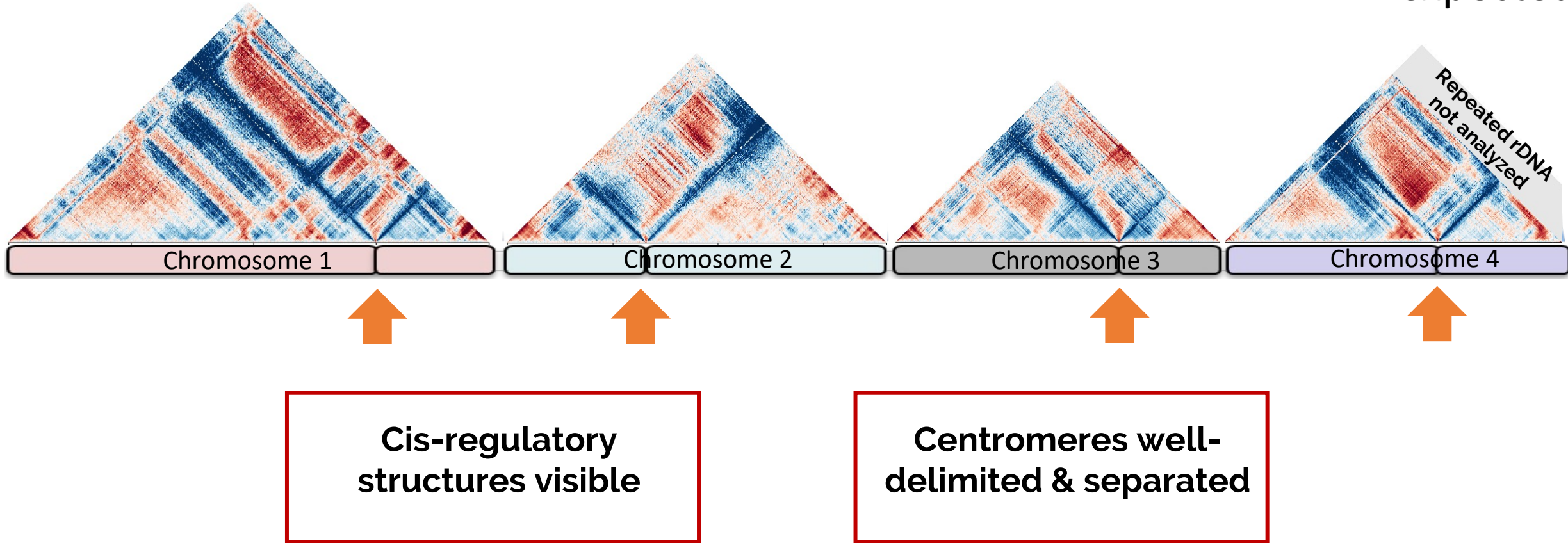


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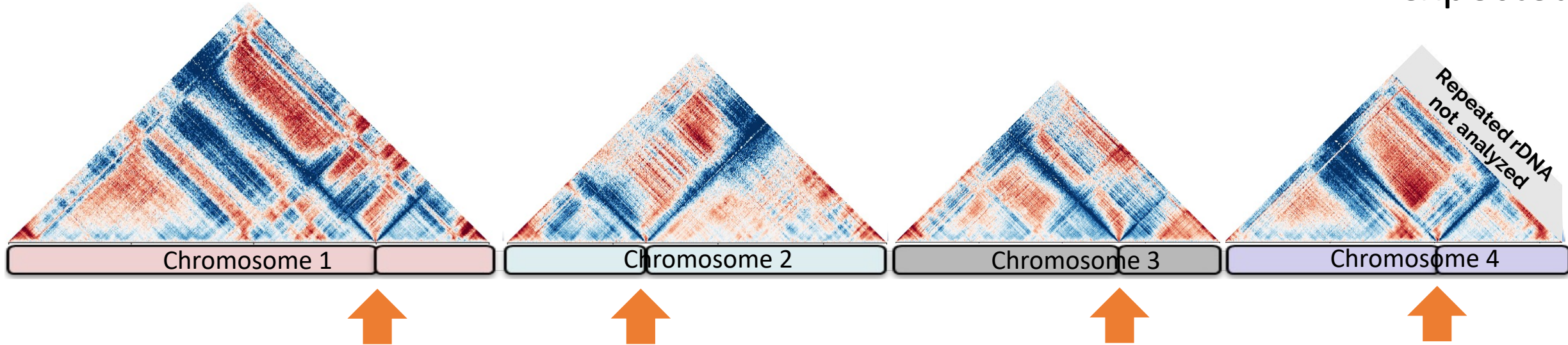


Pearson correlation between distances

# Topology of the *Fusarium graminearum* genome

Observed vs.  
expected

*In situ* Hi-C



Cis-regulatory  
structures visible

Centromeres well-  
delimited & separated

Compartments of  
active vs. inactive  
chromatin?

Pearson correlation between distances



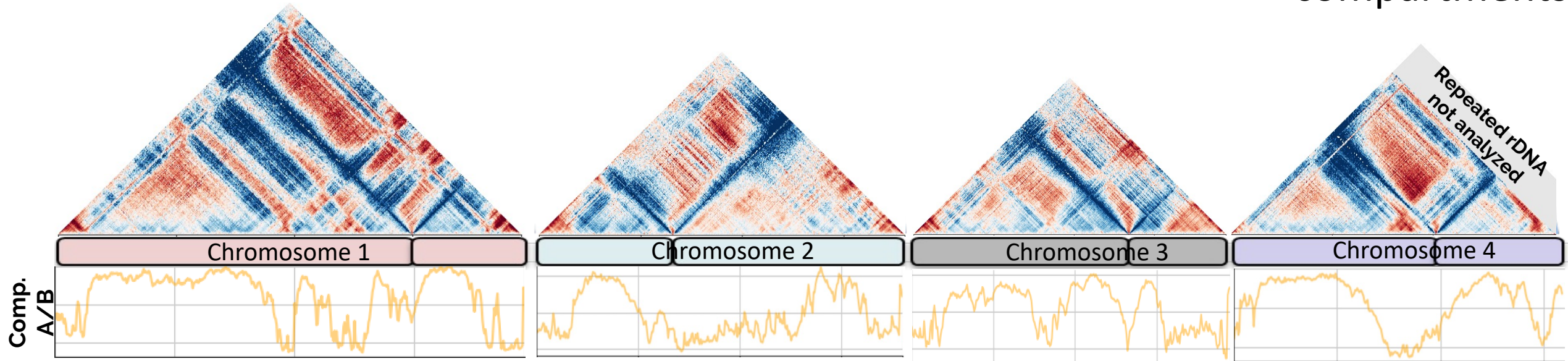
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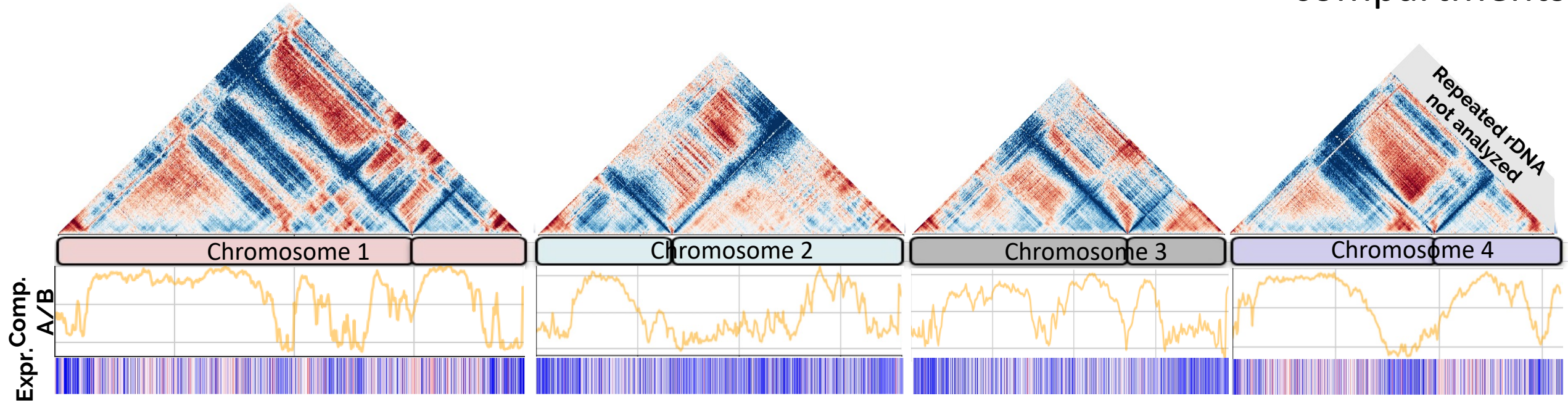
*In situ* Hi-C



A “active”  
compartments  
interspersed with “B”  
inactive

# Topology of the *Fusarium graminearum* genome

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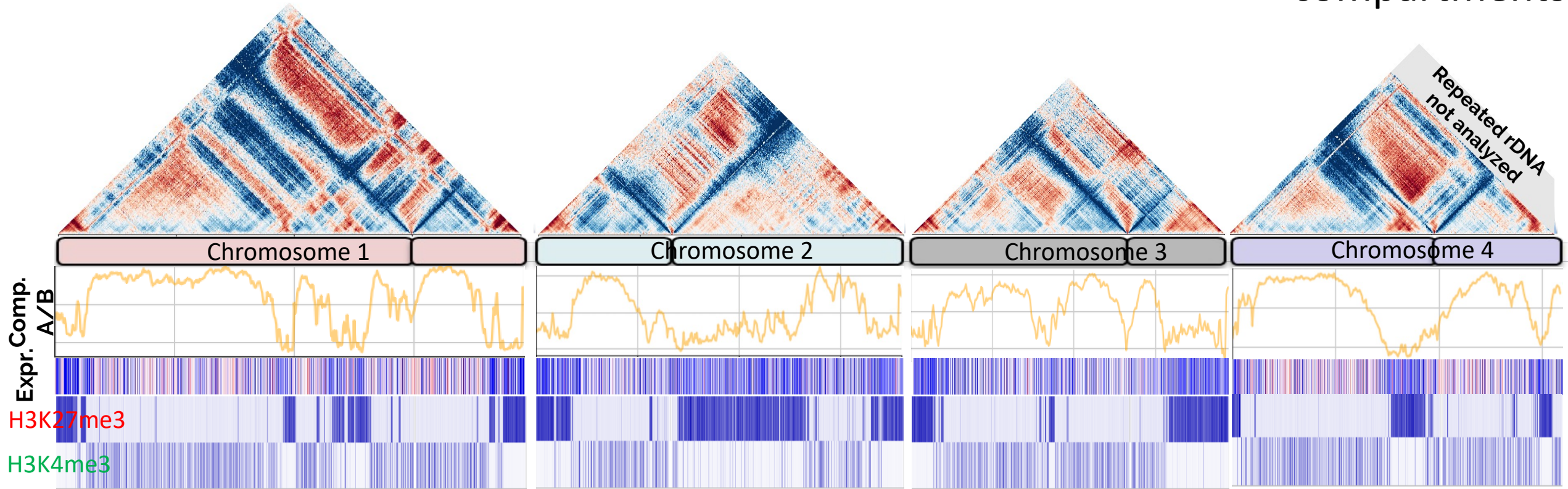


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(roughly speaking...)

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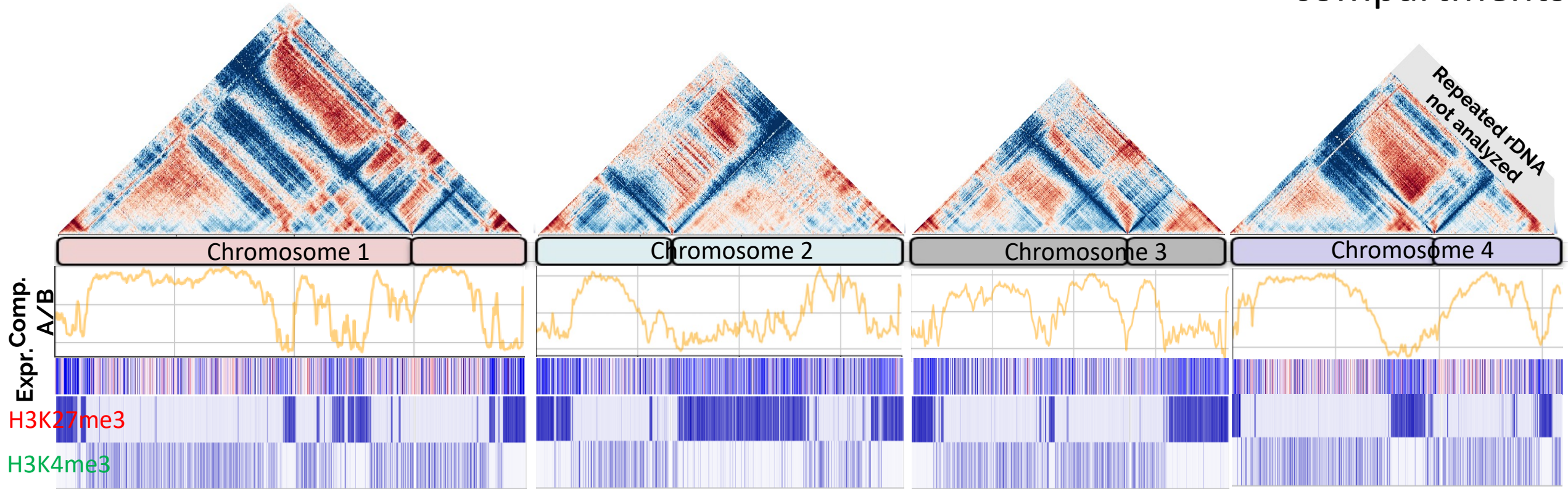


**H3K4me3 is associated with A compartments, H3K27me3 with B**

(also roughly speaking...)

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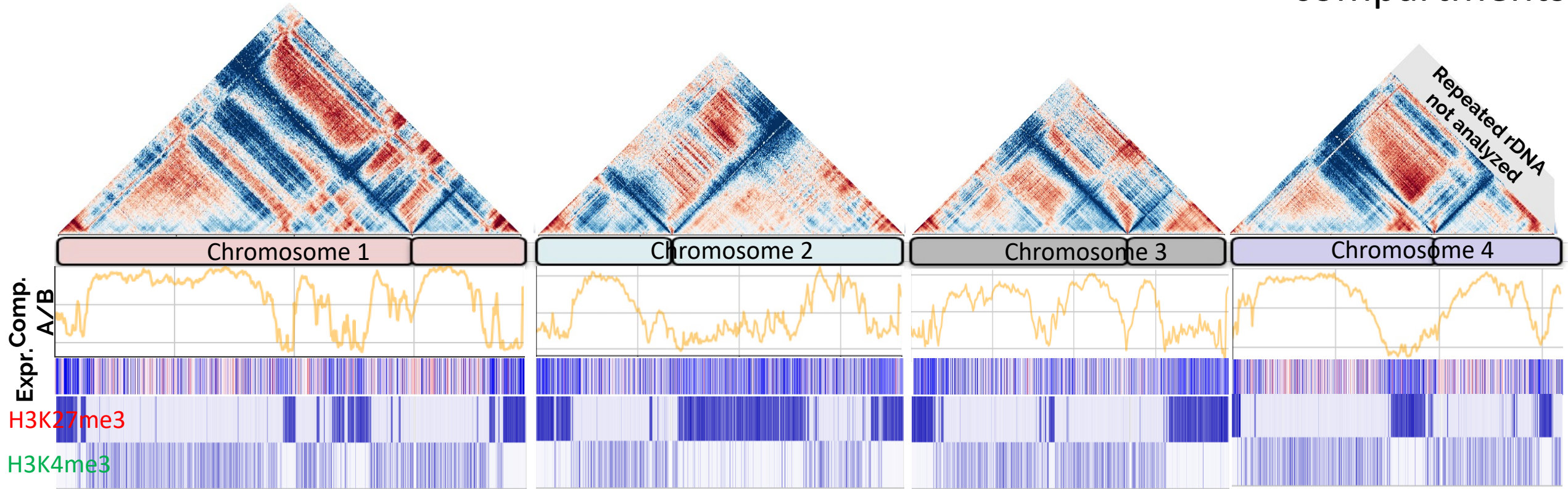


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# Topology of the *Fusarium graminearum* genome

*In situ* Hi-C



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**Topologically-associated domains?**

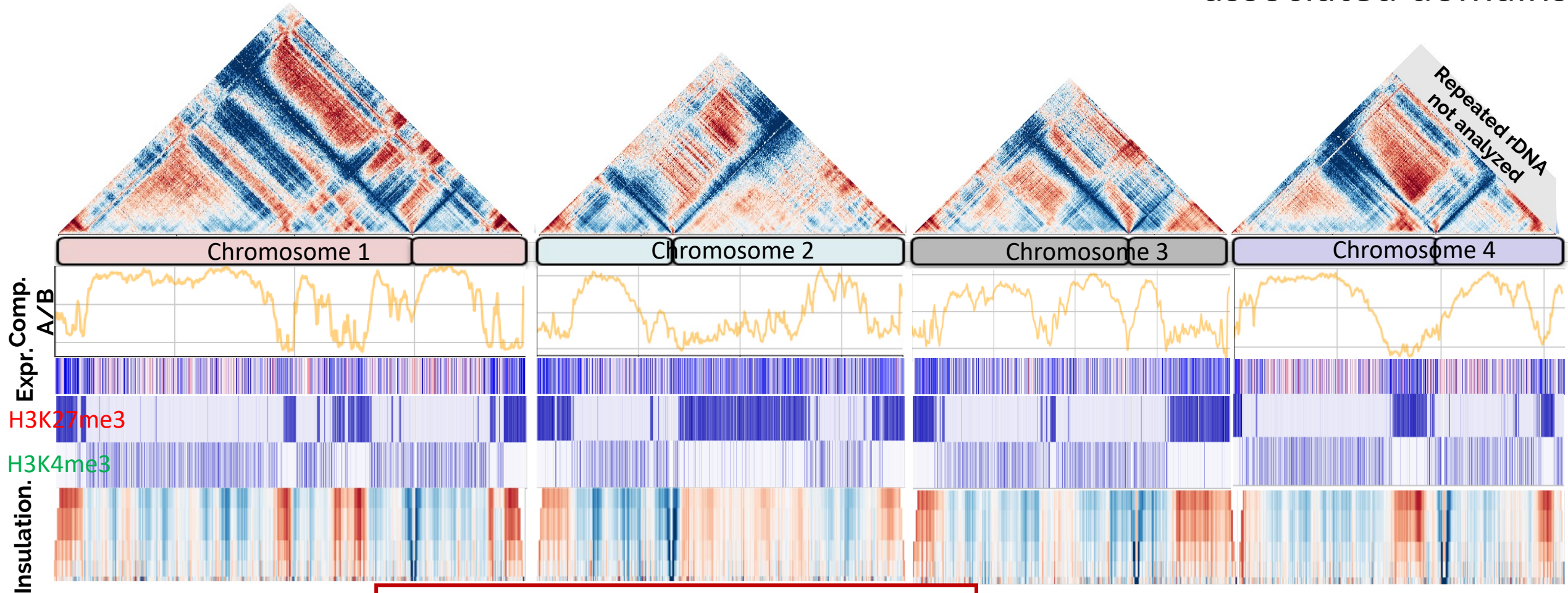
(also roughly speaking...)



# Topology of the *Fusarium graminearum* genome

*In situ* Hi-C

Topologically-associated domains



**H3K4me3/H3K27me3 mark different topologically associated domains**

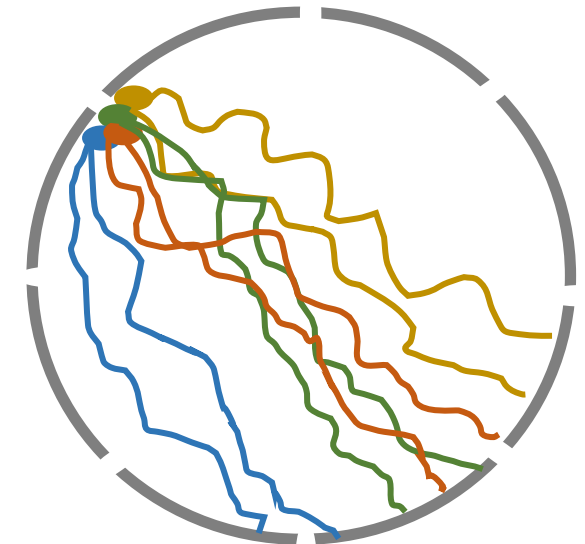
(but not TADs...)

## ➤ To remember...

- *In situ* Hi-C successfully applied to *F. graminearum* – it's easy provided Xlinked nuclei can be purified;
- Centromeres interact together, leaving telomeres and the rest of the chromosomes at a distance;
- A/B compartments can be delineated but do not necessarily correlate with no/low gene expression;
- Topologically-associated domains parallel to H3K27me3H3K4me3

(but not TADs...)

A possible organization in *F. graminearum*:



(Please imagine this is a very nice 3D image!)

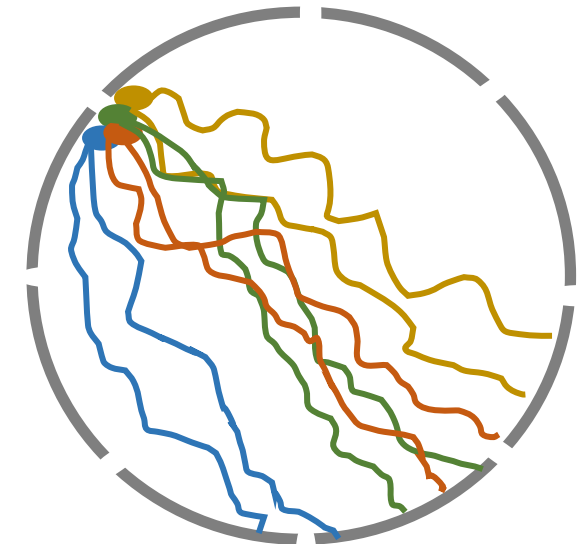
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(but not TADs...)

**Let's do it again in interaction  
with the host plant!**

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(Please imagine this is a very nice 3D image!)

➤ Thank you all!



Special thanks to:

Aurelie Etier  
Fabien Dumetz

Gael Le Trionnaire &  
Nathalie Prunier-Leterme (INRAE Rennes)

