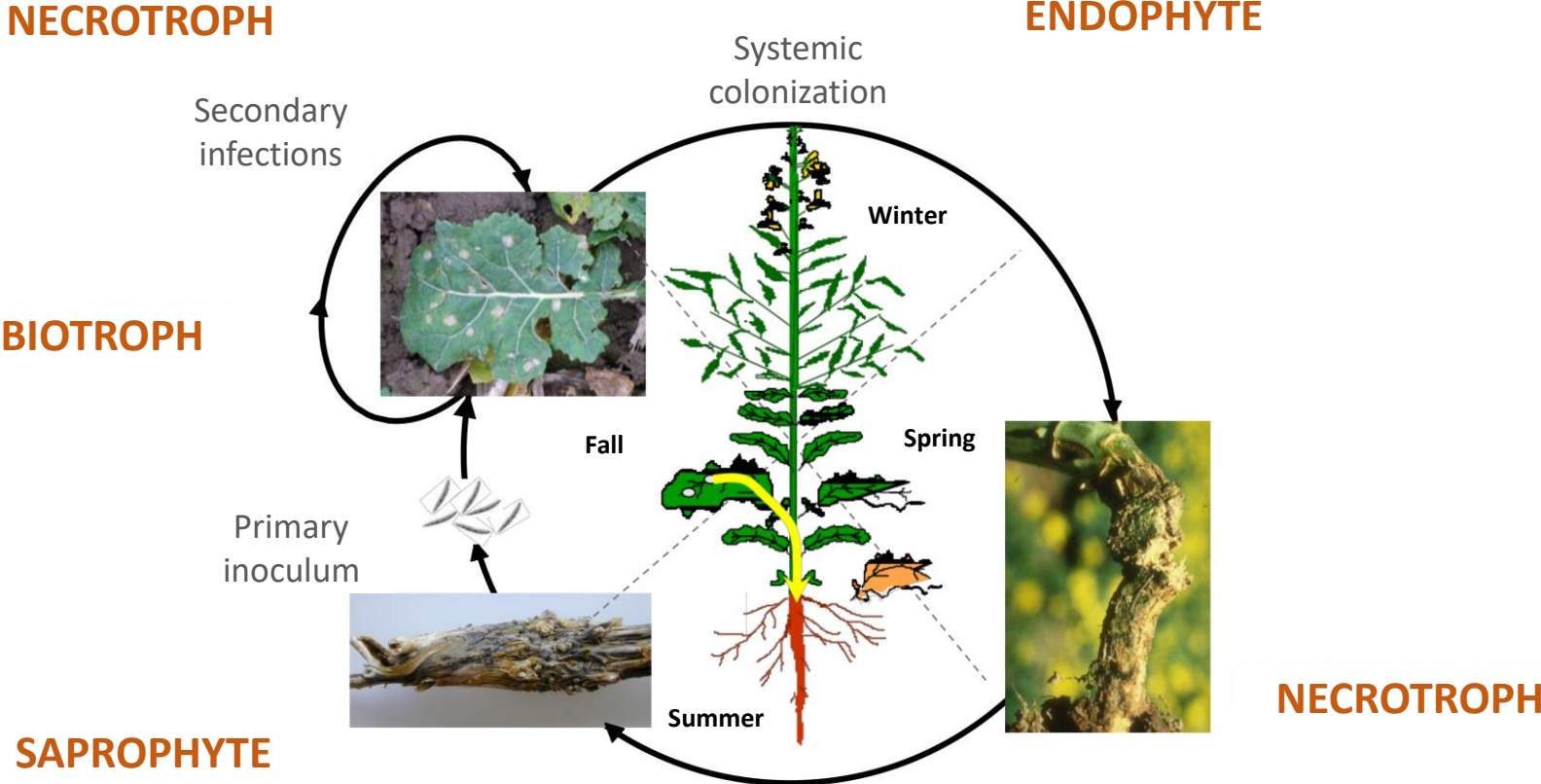




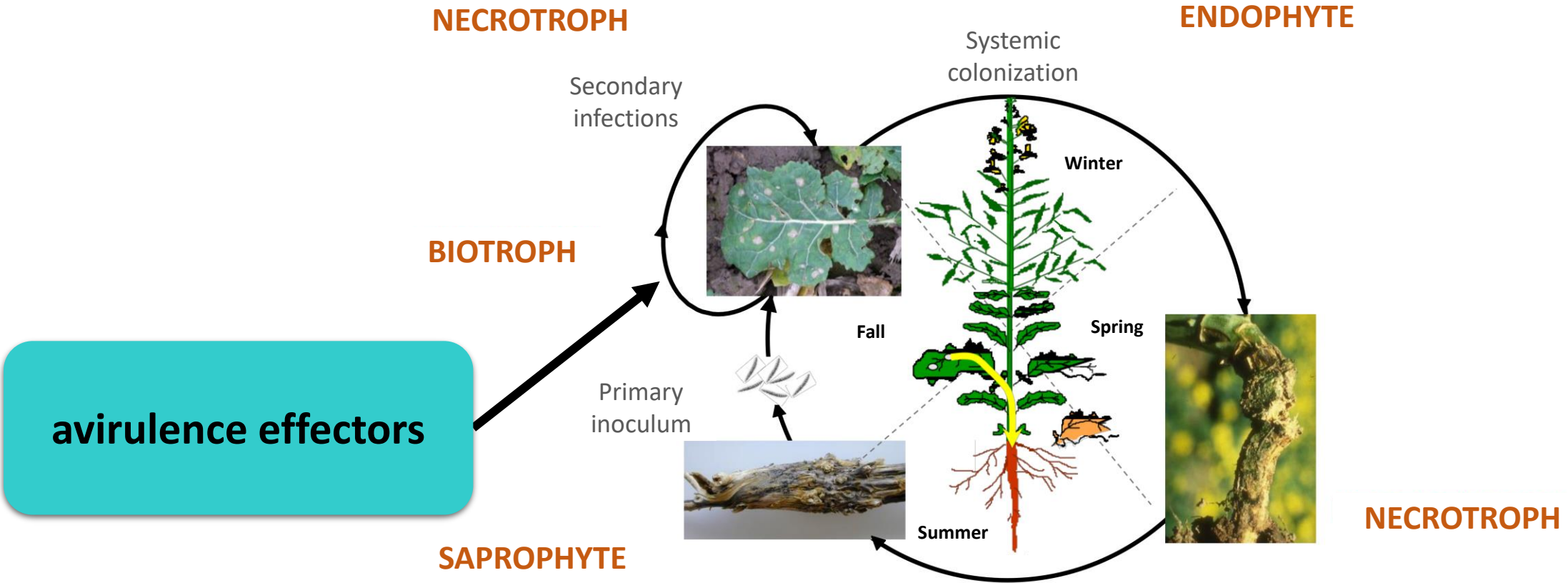
➤ Regulation of effector gene expression as concerted waves in *Leptosphaeria maculans*: a two-players game

GDR3E/REaction 2021_Antoine PORQUIER

Leptosphaeria maculans : a complex lifecycle

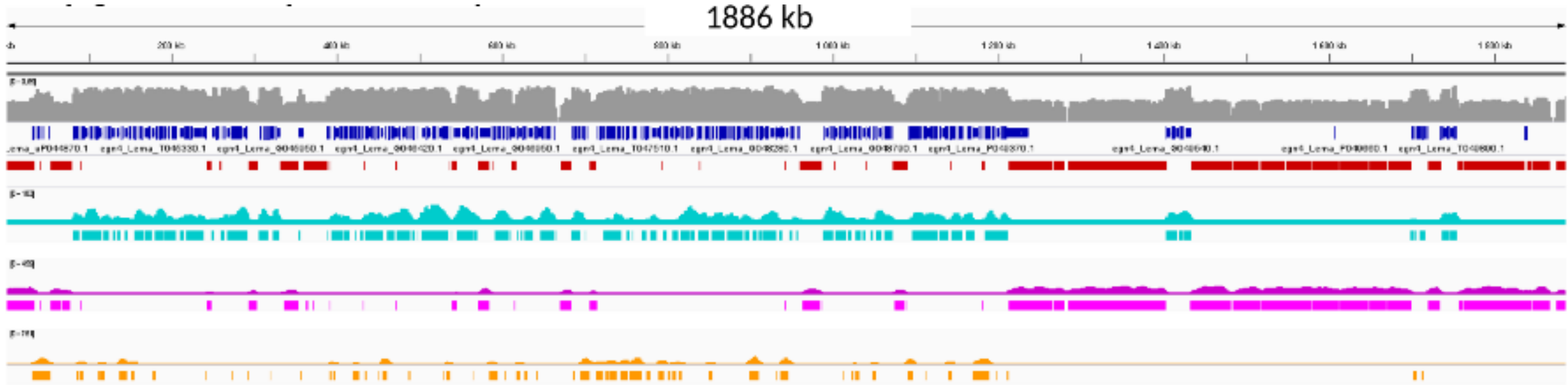


Leptosphaeria maculans : a complex lifecycle



Recognized effector leading to plant resistance = *AvrLm*

Leptosphaeria maculans epigenome *in vitro*



- % GC
- H3K4me2 = euchromatic mark
- H3K9me3 } Heterochromatic marks
- H3K27me3 }
- Repeats
- Genes

Leptosphaeria maculans epigenome *in vitro*

AT-isochores

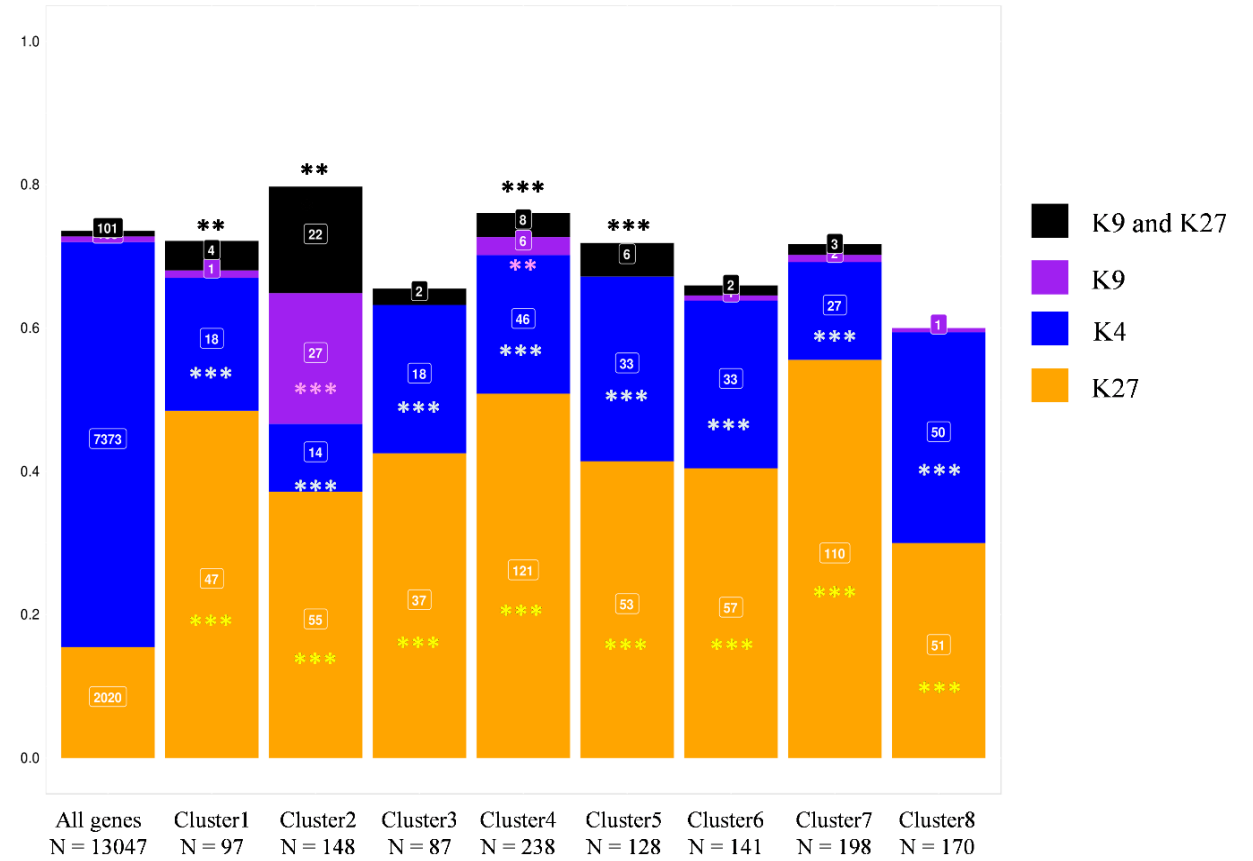
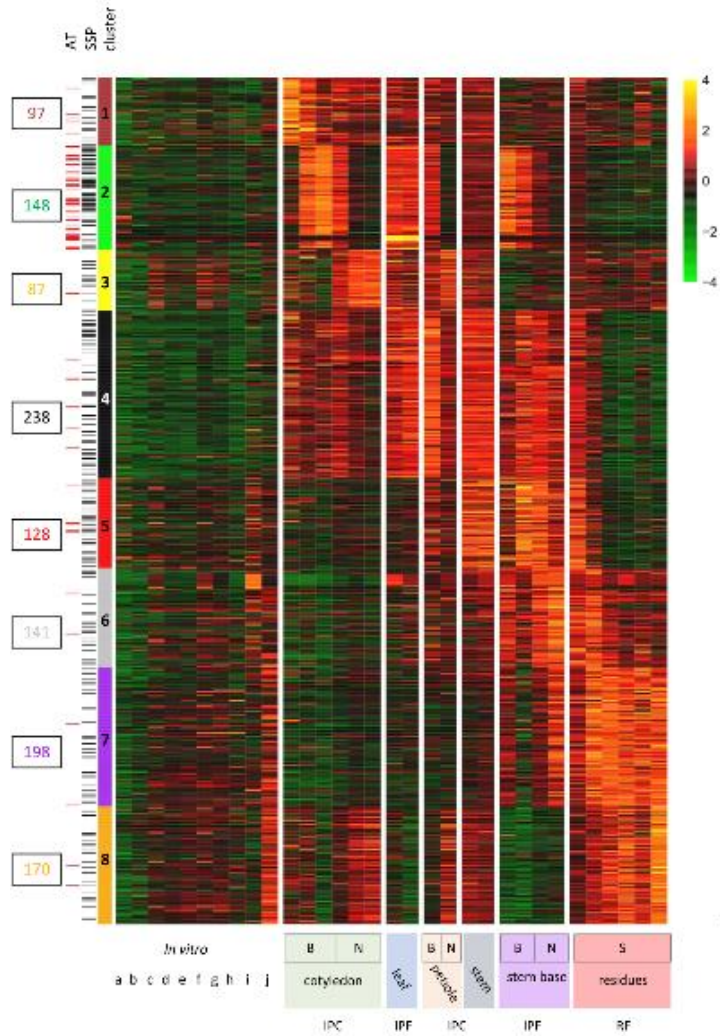


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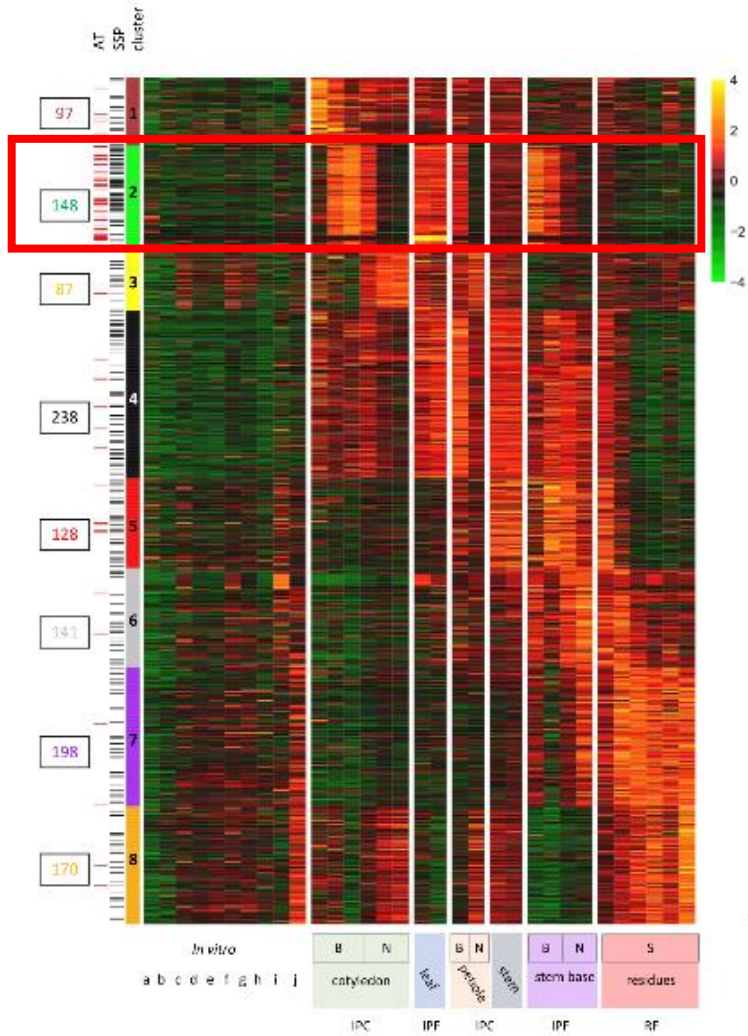
2 types of heterochromatin

Both are enriched in effector-encoding genes

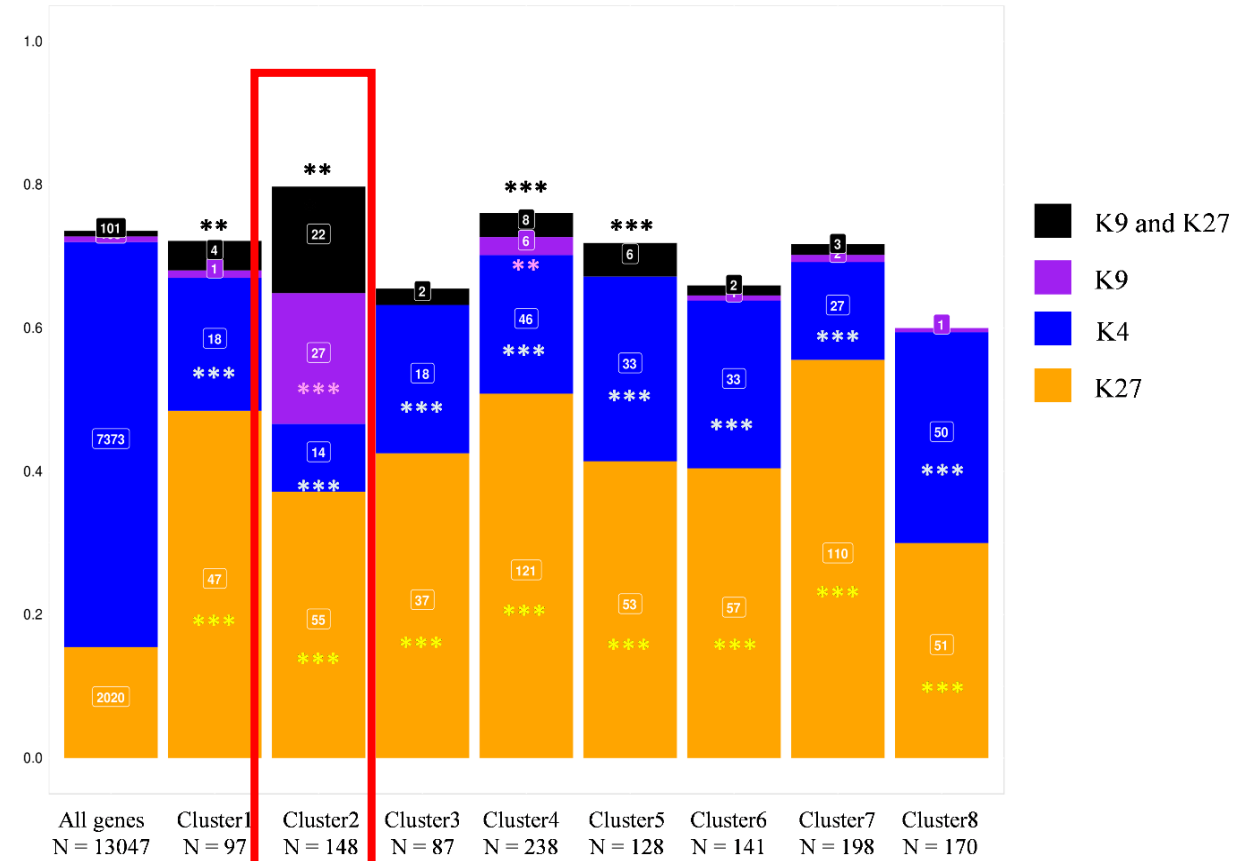
Link between the epigenome *in vitro* and gene expression *in planta*



Link between the epigenome *in vitro* and gene expression *in planta*



Cluster 2 all cloned avirulence genes



Up-regulated genes *in planta* are enriched in heterochromatin *in vitro*

Our working model

Axenic culture

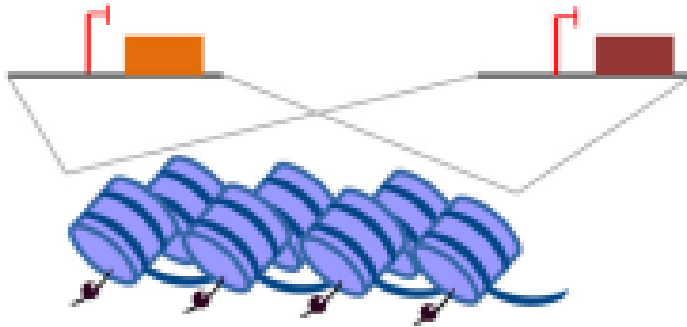


In planta infection

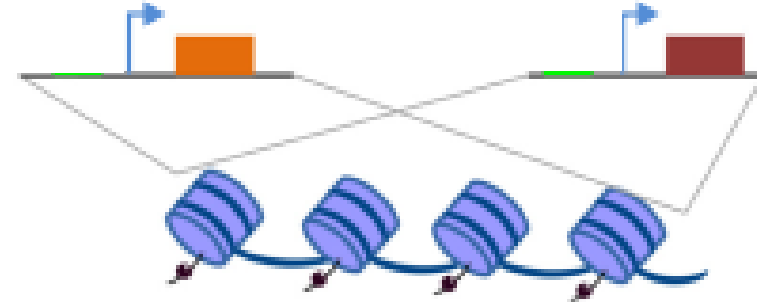


Our working model

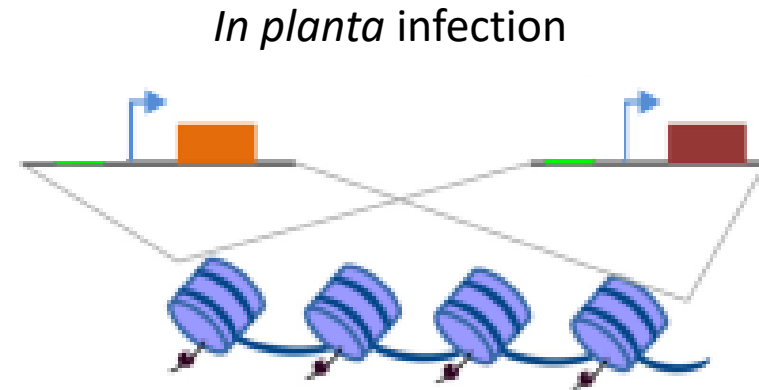
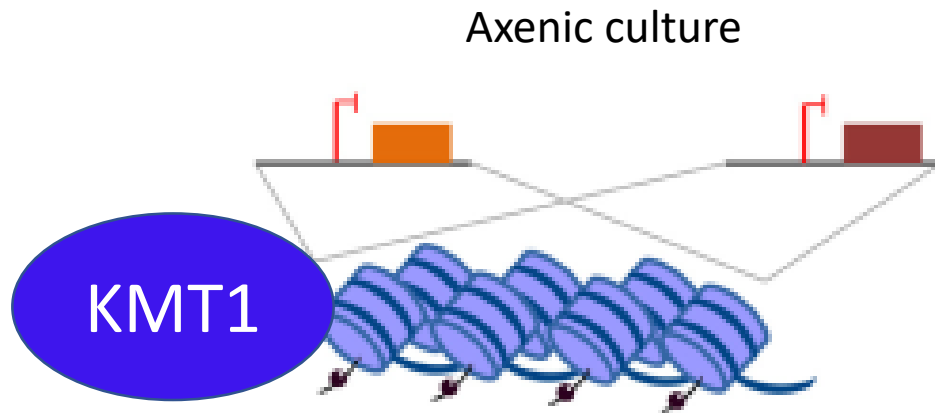
Axenic culture



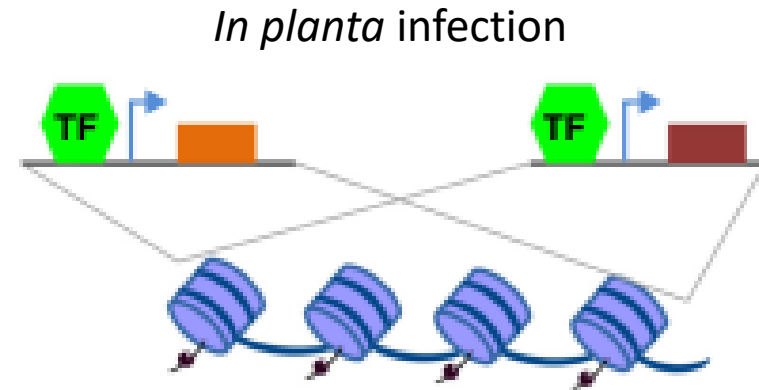
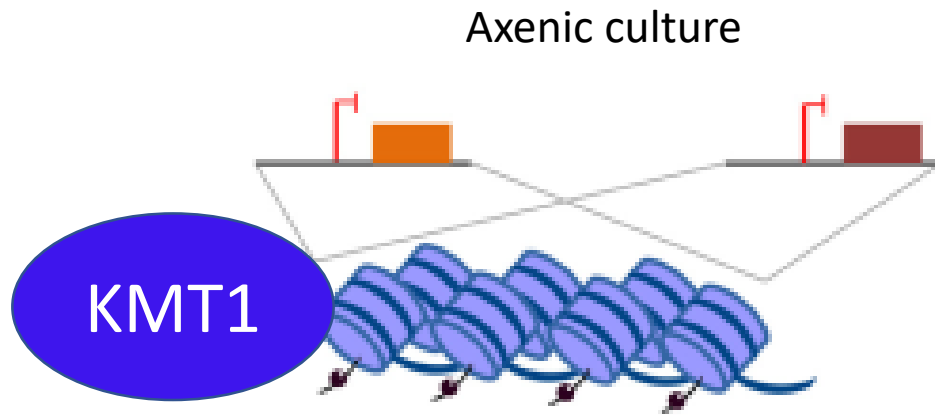
In planta infection



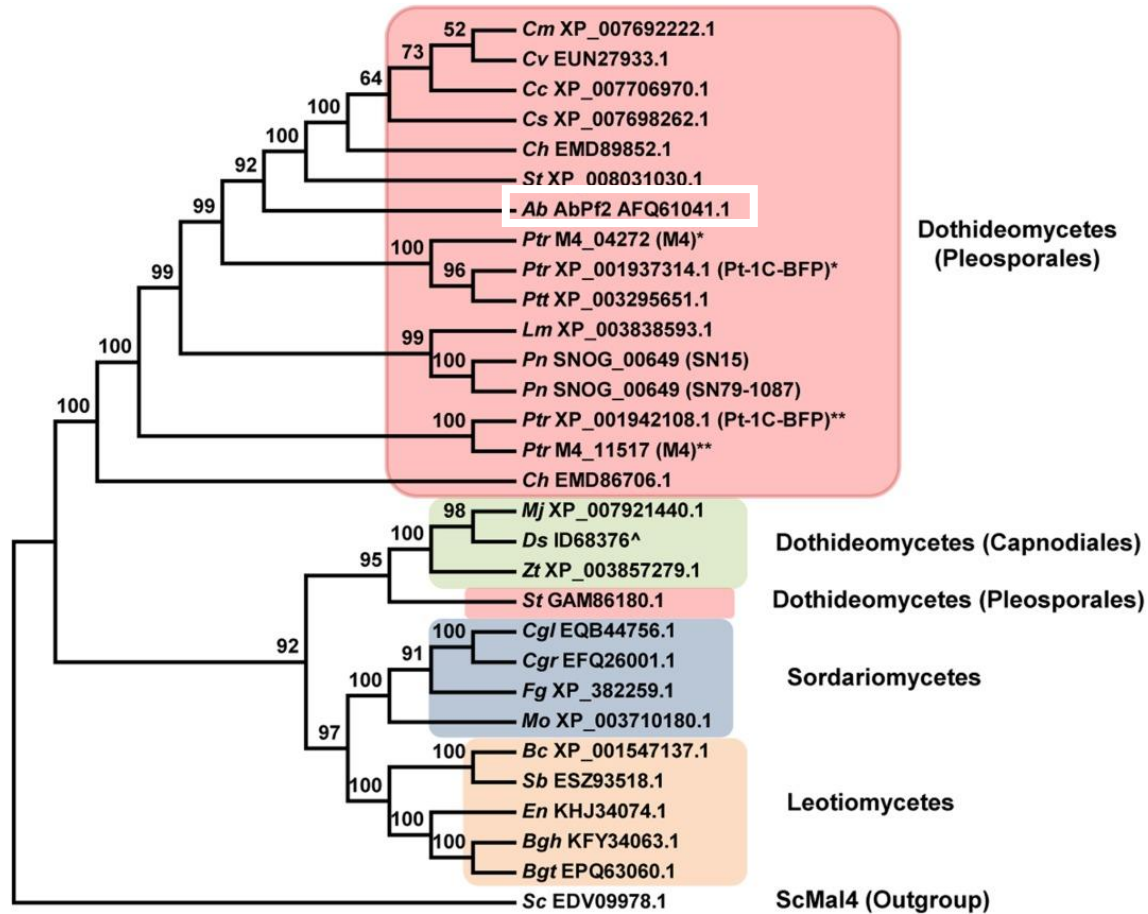
Our working model



Our working model

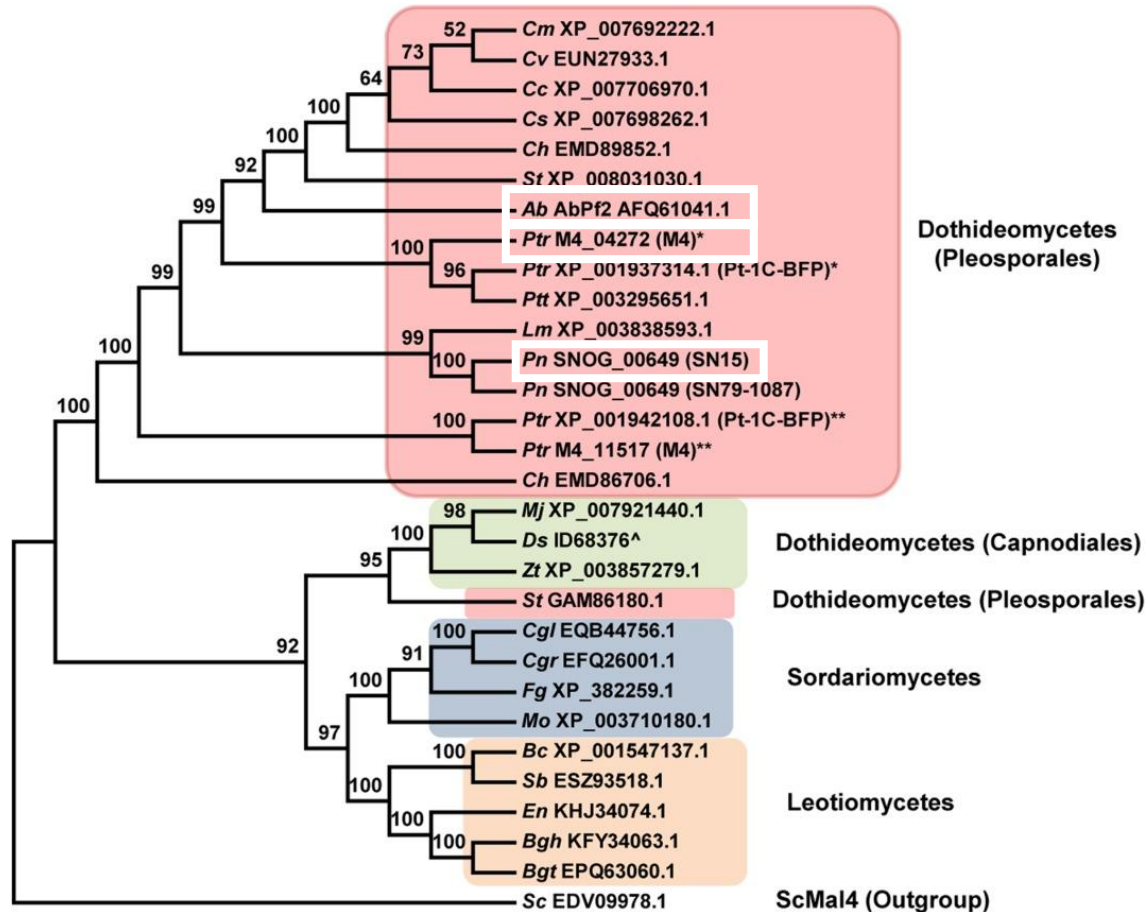


Our working model



Role of AbPf2 in *Alternaria brassicicola* virulence notably via the positive regulation of secreted proteins (Cho *et al.* 2013 and 2015)

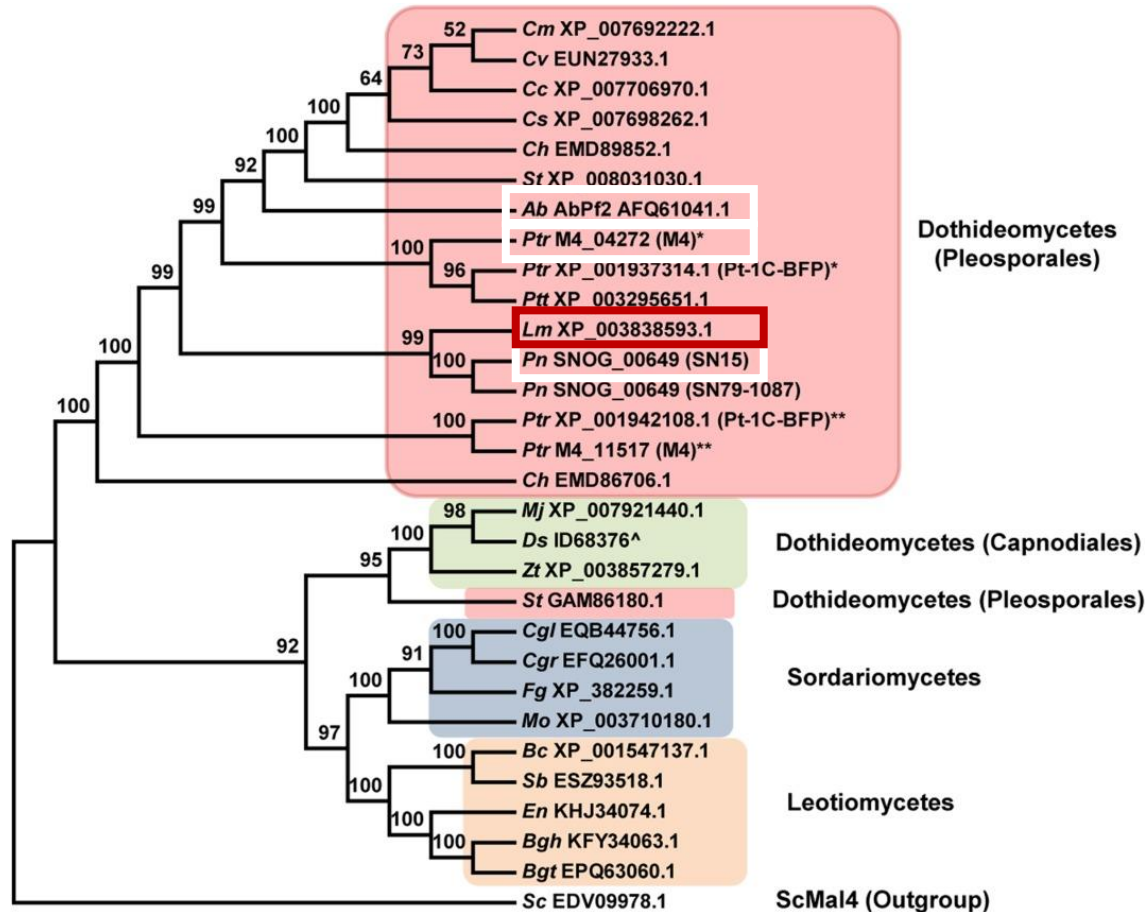
Our working model



Role of AbPf2 in *Alternaria brassicicola* virulence notably via the positive regulation of secreted proteins (Cho *et al.* 2013 and 2015)

Pf2 also characterized in *Parastagonospora nodorum* and *Pyrenophora tritici-repentis* → Role in virulence (Rybak *et al.* 2017) notably via regulation of effectors (Jones *et al.* 2019)

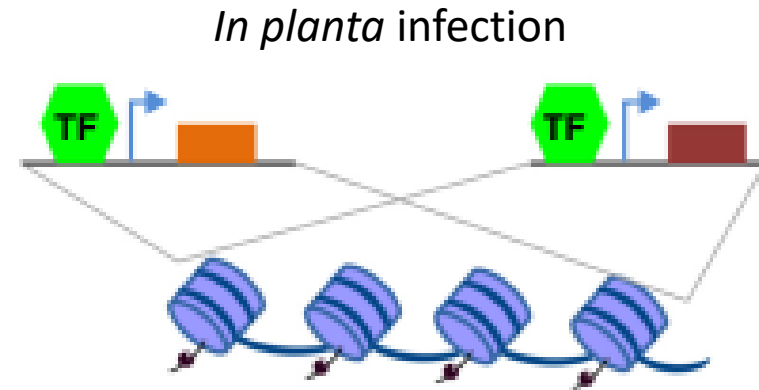
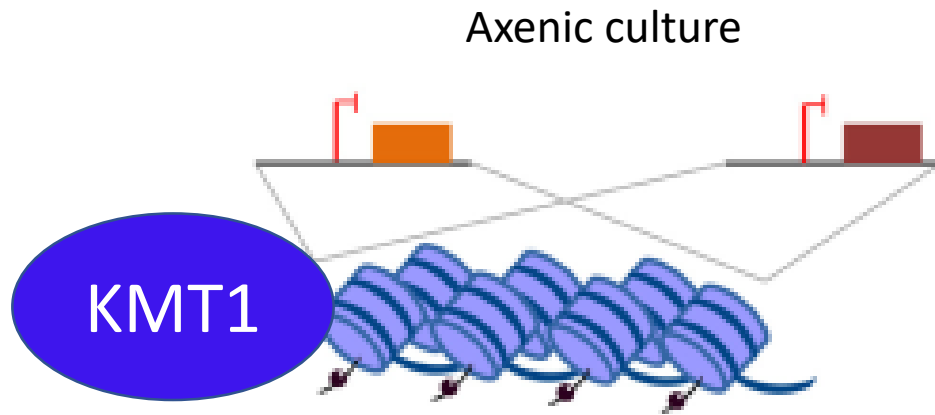
Our working model



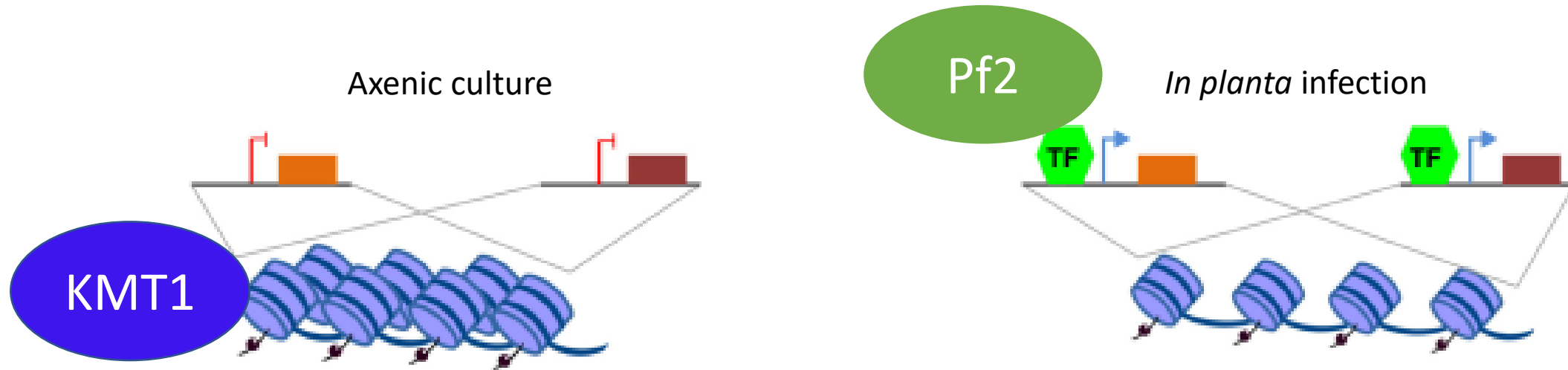
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Our working model



Our working model

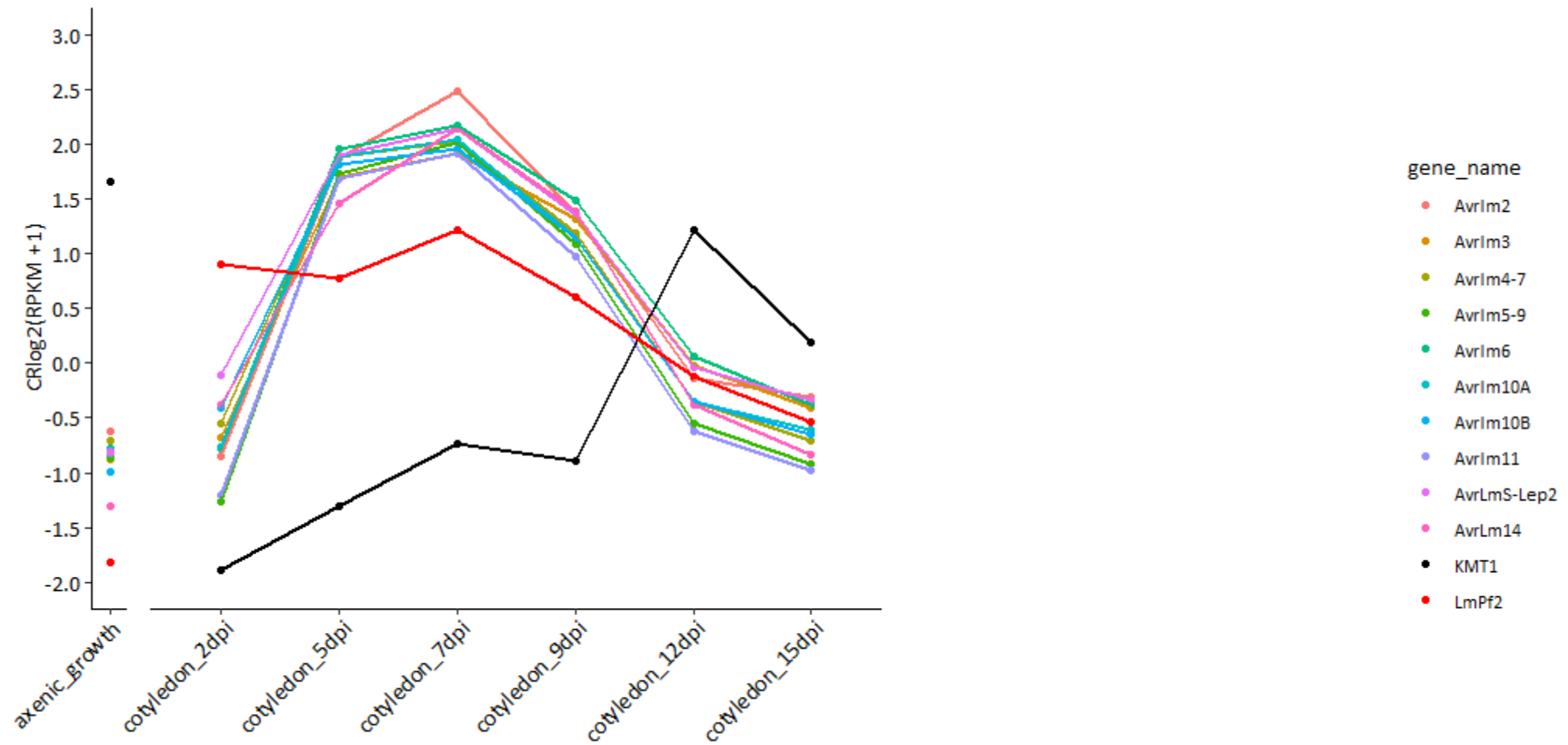


A two-layers regulatory mechanism ?

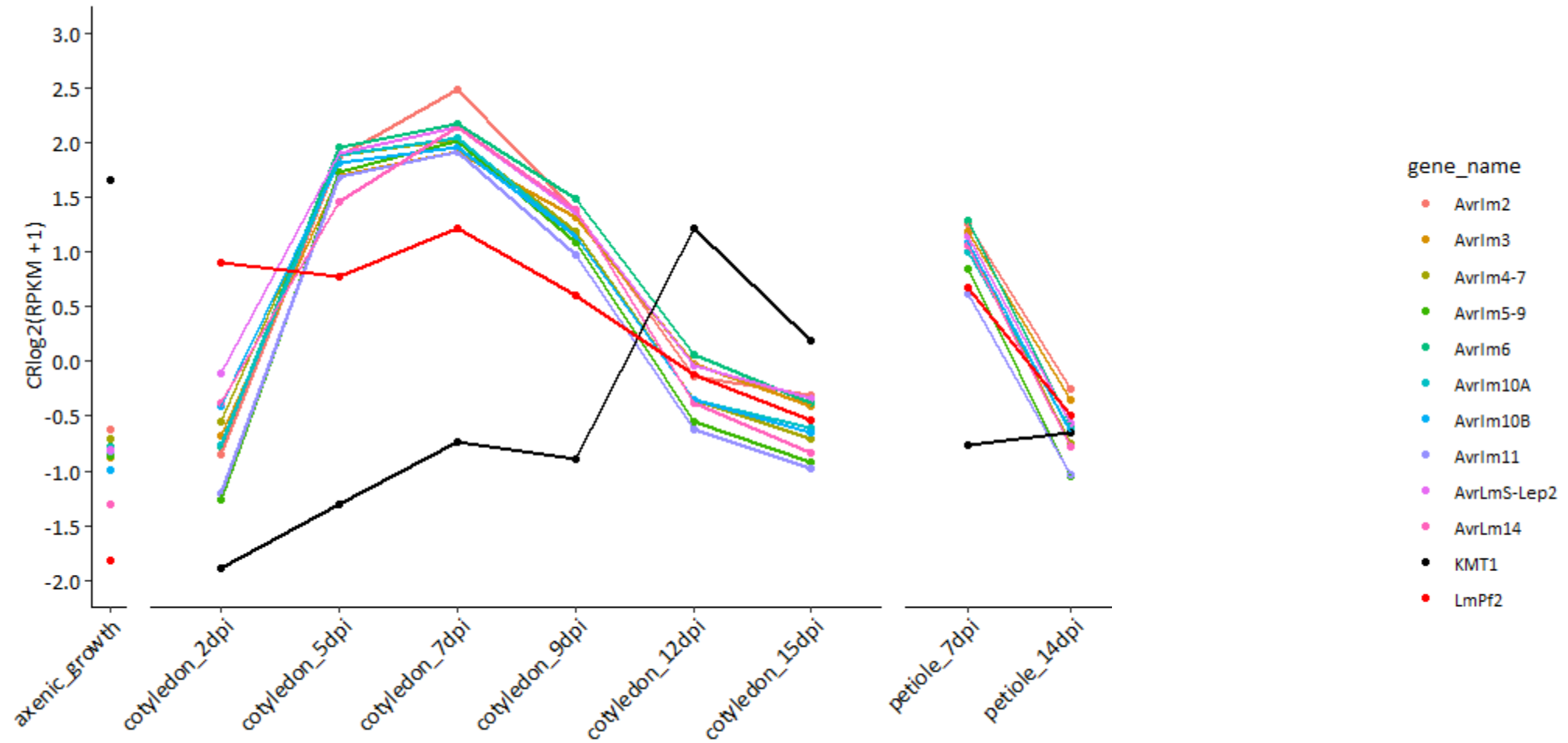
Expression kinetics of *KMT1*, *LmPf2* and known avirulence genes



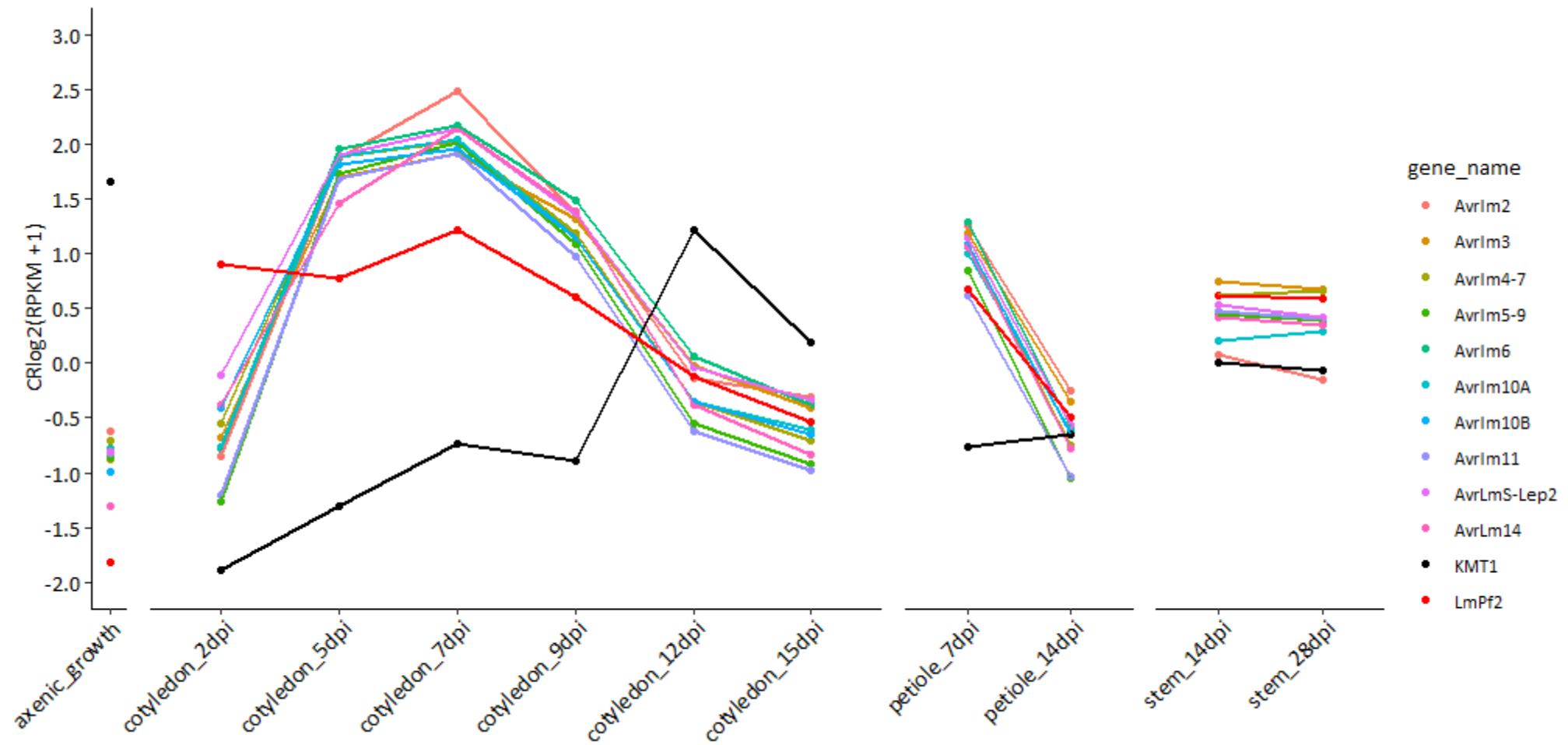
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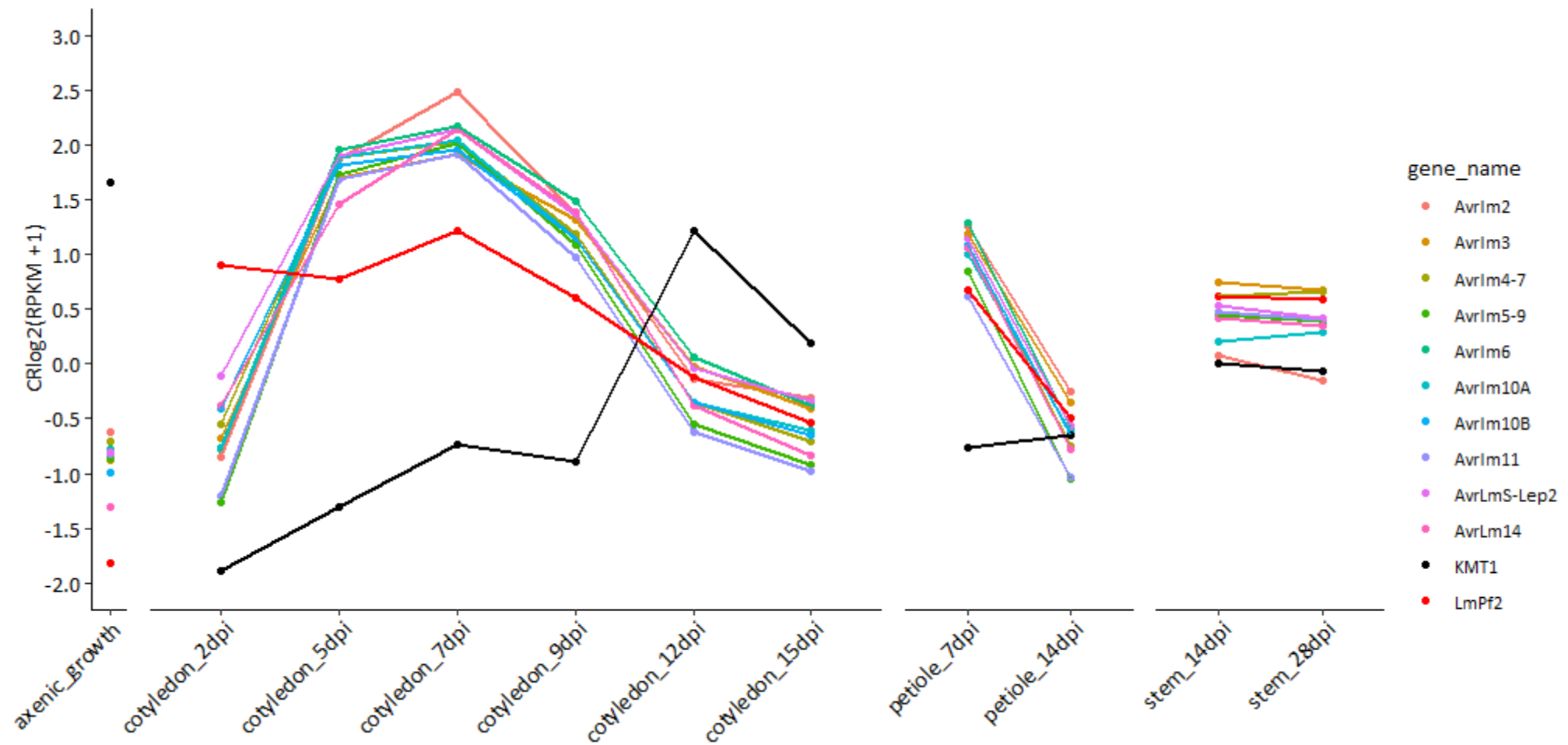
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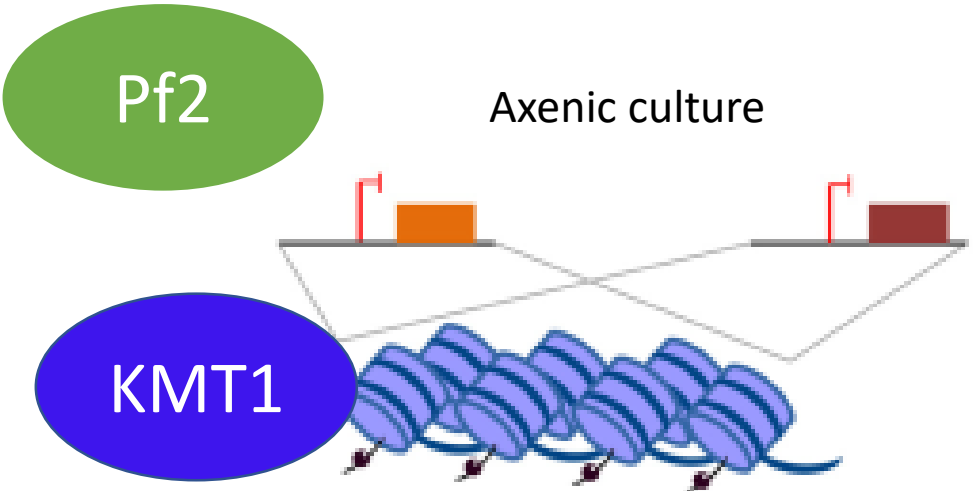


Expression kinetics of *KMT1*, *LmPf2* and known avirulence genes

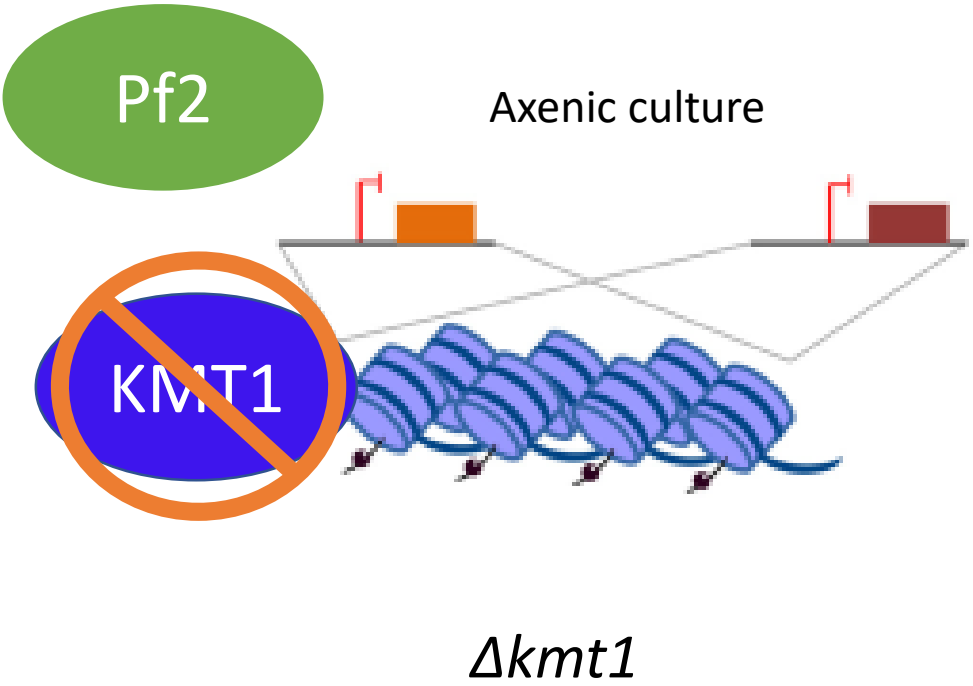


The expression of *LmPf2* follows the same pattern than *AvrLm* genes while *KMT1* seems regulated in an opposite manner

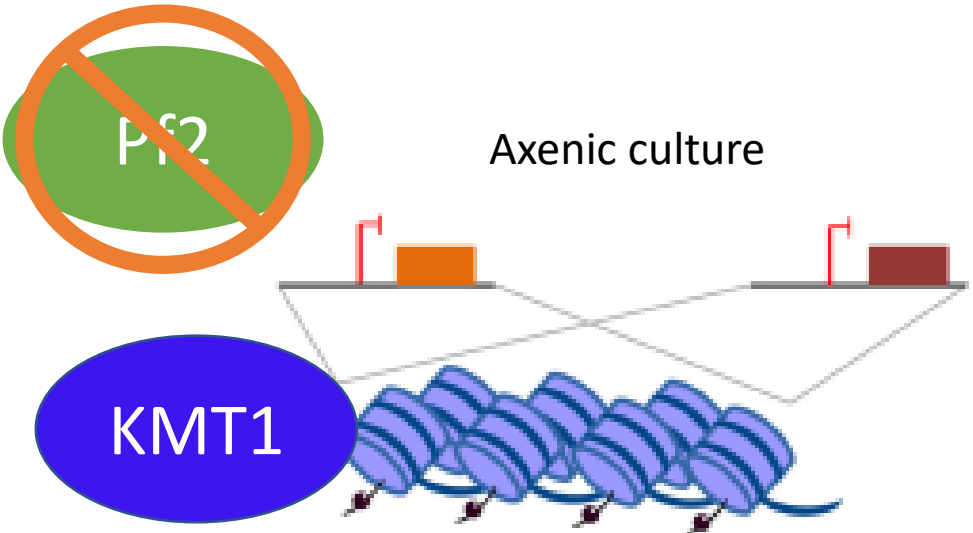
Generation of biological materials



Generation of biological materials

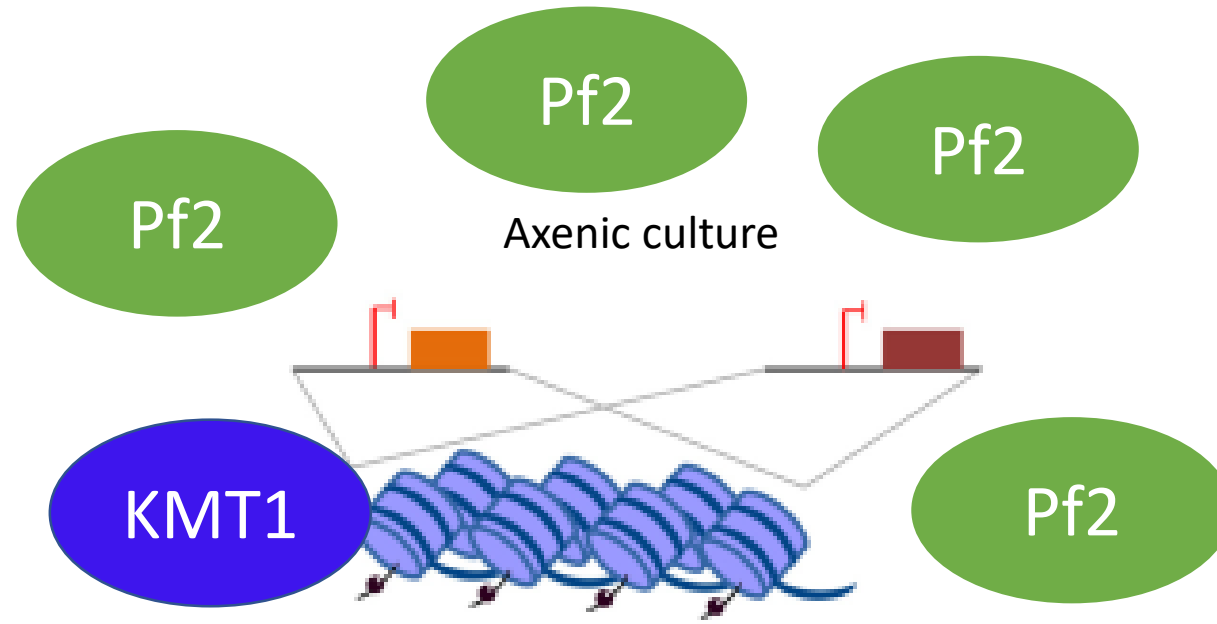


Generation of biological materials



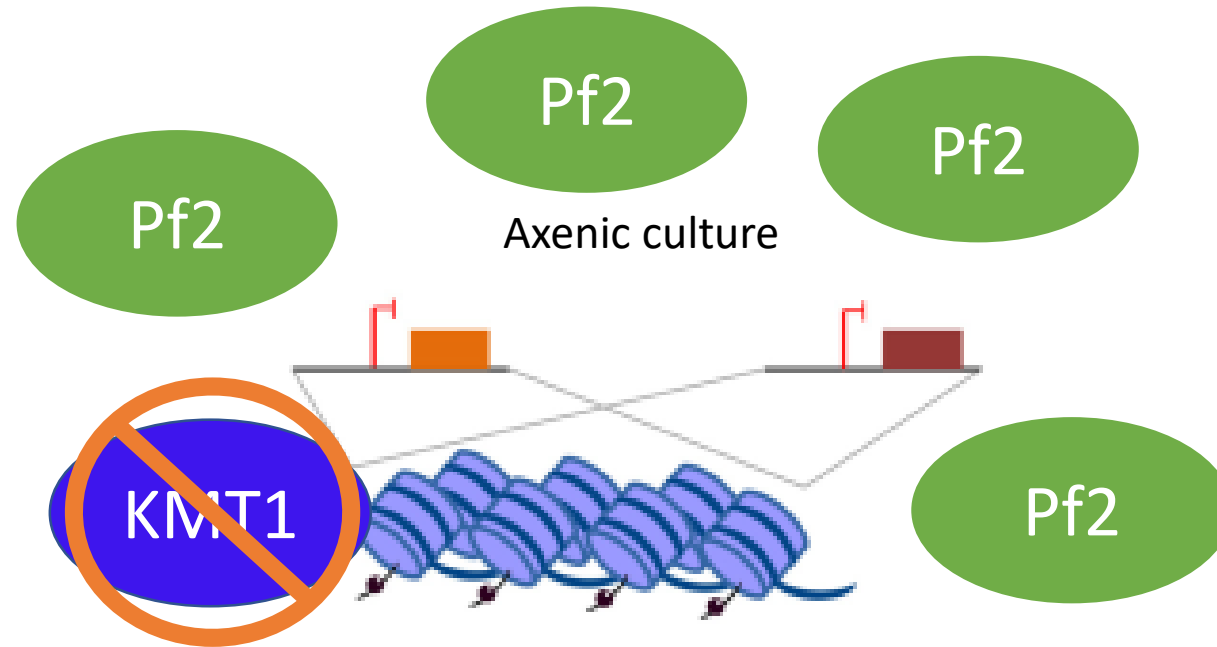
$\Delta kmt1$
 $\Delta LmPf2$

Generation of biological materials



$\Delta kmt1$
 $\Delta LmPf2$
 WT_oPf2

Generation of biological materials



$\Delta kmt1$
 $\Delta LmPf2$
WT_oPf2
 $\Delta kmt1_oPf2$

Characterization of transformant strains

Isolate /
transformants^a

WT

Δkmt1

ΔLmPf2_A

ΔLmPf2_B

WT_oPf2_A

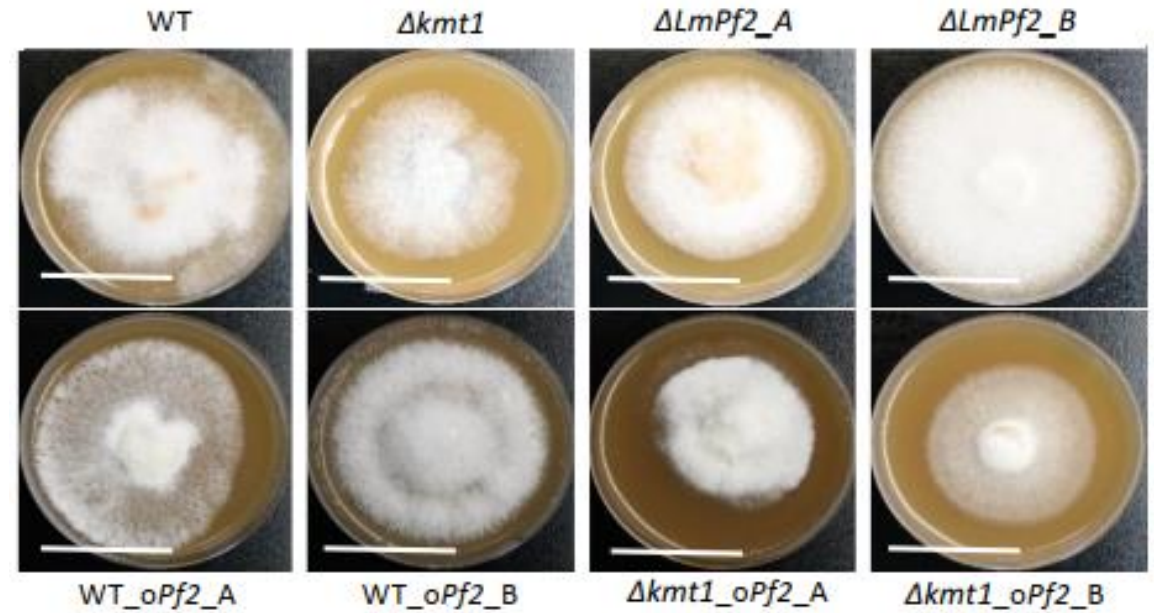
WT_oPf2_B

Δkmt1_oPf2_A

Δkmt1_oPf2_B

Characterization of transformant strains

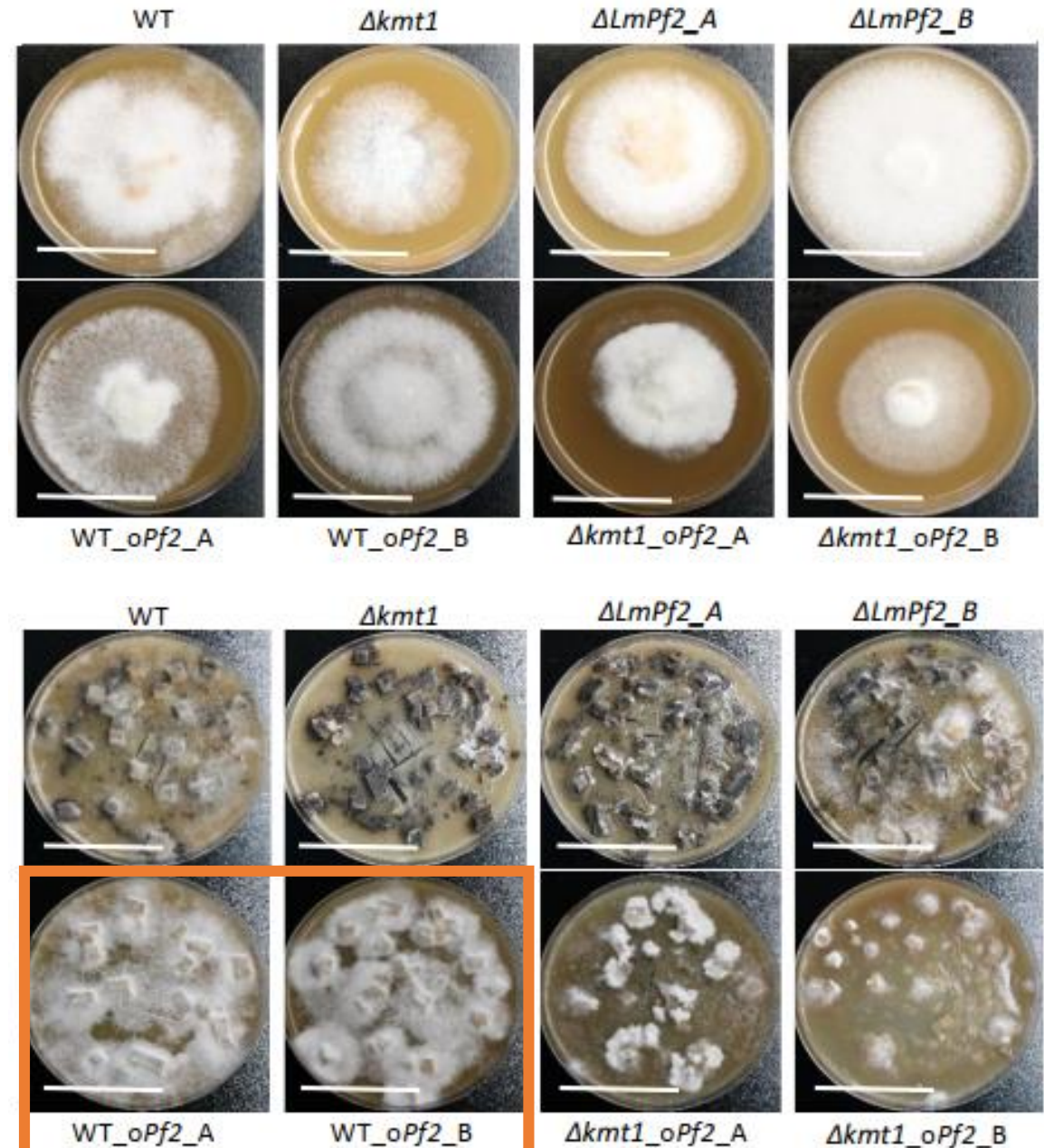
Isolate / transformants ^a	Radial growth 9 dpi on V8 medium (mm)
WT	60.5 (± 2.24)
$\Delta kmt1$	50.25 (± 1.94)
$\Delta LmPf2_A$	56.13 (± 0.9)
$\Delta LmPf2_B$	80 (± 0.8)*
WT_oPf2_A	77.38 (± 0.76)
WT_oPf2_B	73.5 (± 1.19)
$\Delta kmt1_oPf2_A$	68.38 (± 1.03)
$\Delta kmt1_oPf2_B$	53.75 (± 1.06)



Characterization of transformant strains

Isolate / transformants ^a	Radial growth 9 dpi on V8 medium (mm)	conidia/ml
WT	60.5 (± 2.24)	4.50.10 ⁷
<i>Δkmt1</i>	50.25 (± 1.94)	4.00.10 ⁷
<i>ΔLmPf2_A</i>	56.13 (± 0.9)	1.53.10 ⁸
<i>ΔLmPf2_B</i>	80 (± 0.8)*	1.08.10 ⁸
WT_oPf2_A	77.38 (± 0.76)	0
WT_oPf2_B	73.5 (± 1.19)	0
<i>Δkmt1_oPf2_A</i>	68.38 (± 1.03)	2.00.10 ⁷
<i>Δkmt1_oPf2_B</i>	53.75 (± 1.06)	1.25.10 ⁶

Denser and white mycelium
No conidiation



Characterization of transformant strains

Isolate / transformants ^a	Radial growth 9 dpi on V8 medium (mm)	conidia/ml	Pathogenicity assay (conidia)	Pathogenicity assay (mycelium plugs)
WT	60.5 (± 2.24)	4.50.10 ⁷	4.83 (± 0.28)	pathogenic
<i>Δkmt1</i>	50.25 (± 1.94)	4.00.10 ⁷	3.09 (± 0.35)	pathogenic
<i>ΔLmPf2_A</i>	56.13 (± 0.9)	1.53.10 ⁸	1 (± 0)	non pathogenic
<i>ΔLmPf2_B</i>	80 (± 0.8)*	1.08.10 ⁸	1 (± 0)	non pathogenic
WT_οPf2_A	77.38 (± 0.76)	0	not enough conidia	pathogenic
WT_οPf2_B	73.5 (± 1.19)	0	not enough conidia	pathogenic
<i>Δkmt1_οPf2_A</i>	68.38 (± 1.03)	2.00.10 ⁷	4 (± 0)	pathogenic
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While not affecting phenotype *in vitro*, *LmPf2* is required for virulence

On the contrary, deletion of *KMT1* decreases aggressiveness

Characterization of transformant strains

Isolate / transformants ^a	Radial growth 9 dpi on V8 medium (mm)	conidia/ml	Pathogenicity assay (conidia)	Pathogenicity assay (mycelium plugs)	Effector gene expression during axenic growth	
					<i>AvrLm6</i>	<i>AvrLm4-7</i>
WT	60.5 (± 2.24)	4.50.10 ⁷	4.83 (± 0.28)	pathogenic	1	1
<i>Δkmt1</i>	50.25 (± 1.94)	4.00.10 ⁷	3.09 (± 0.35)	pathogenic	9.70.10 ⁻² (± 0.22)	2.37.10 ² (± 27)
<i>ΔLmPf2_A</i>	56.13 (± 0.9)	1.53.10 ⁸	1 (± 0)	non pathogenic	4.60.10 ⁻² (± 0)	0
<i>ΔLmPf2_B</i>	80 (± 0.8)*	1.08.10 ⁸	1 (± 0)	non pathogenic	6.30.10 ⁻³ (± 0)	4.10.10 ⁻³ (± 0)
WT_0 <i>Pf2_A</i>	77.38 (± 0.76)	0	not enough conidia	pathogenic	3.05 (± 0.14)	2.50.10 ⁻¹ (± 0.20)
WT_0 <i>Pf2_B</i>	73.5 (± 1.19)	0	not enough conidia	pathogenic	2.68 (± 0.19)	7.00.10 ⁻² (± 0.02)
<i>Δkmt1_0Pf2_A</i>	68.38 (± 1.03)	2.00.10 ⁷	4 (± 0)	pathogenic	2.61.10 ¹ (± 3.4)	4.73.10 ² (± 8.6)
<i>Δkmt1_0Pf2_B</i>	53.75 (± 1.06)	1.25.10 ⁶	not enough conidia	non pathogenic	1.30.10 ⁴ (± 107.79)	2.31.10 ³ (± 24.64)

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Characterization of transformant strains

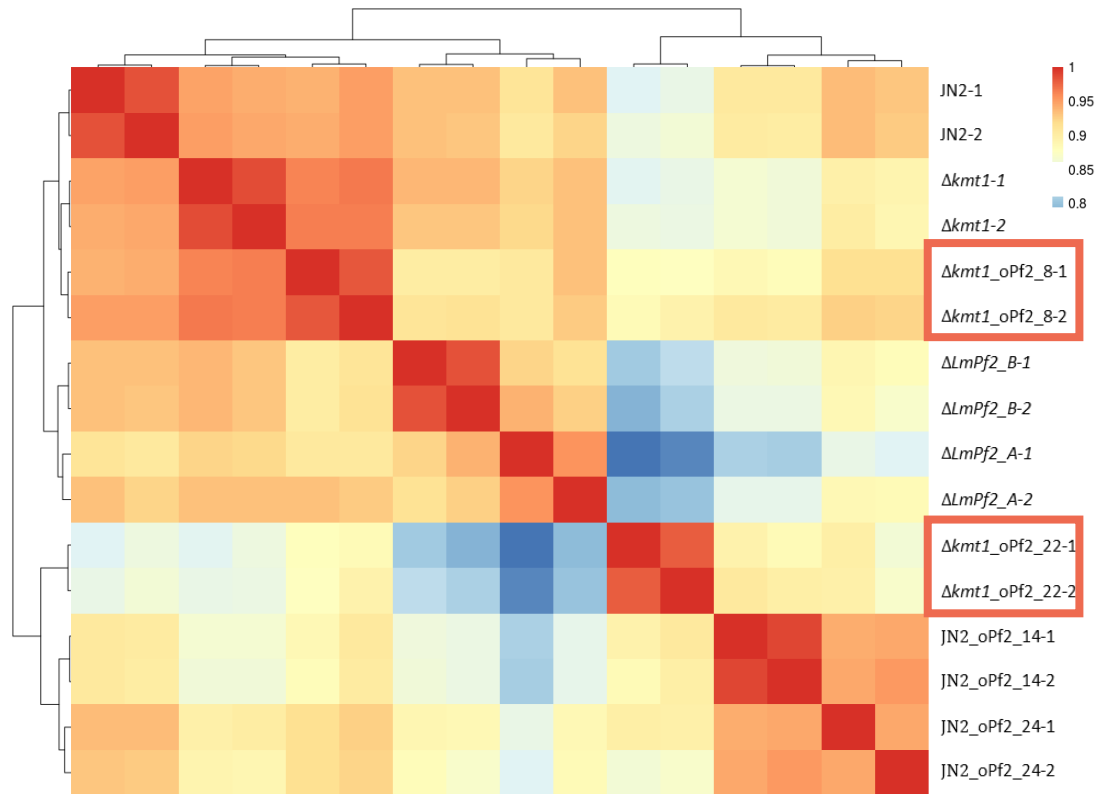
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The inactivation of *KMT1* and overexpression of *LmPf2* leads to higher derepression of *AvrLm* genes *in vitro*

Assessing the genome-wide expression differences by RNAseq



$\Delta kmt1$

$\Delta LmPf2$

WT_oPf2

$\Delta kmt1_oPf2_A$

$\Delta kmt1_oPf2_B$

1.8E+07 paired reads on average

Reproducibility OK for all the samples
except for $\Delta kmt1_oPf2$ mutants

Assessing the genome-wide expression differences by RNAseq

		Total genes
Up-regulated	<i>Δkmt1</i>	129
	<i>ΔLmPf2</i>	202
	<i>WT_oPf2</i>	247
	<i>Δkmt1_oPf2_A</i>	275
	<i>Δkmt1_oPf2_B</i>	931
Down-regulated	<i>Δkmt1</i>	143
	<i>ΔLmPf2</i>	225
	<i>WT_oPf2</i>	277
	<i>Δkmt1_oPf2_A</i>	158
	<i>Δkmt1_oPf2_B</i>	861

#genes statistically under-represented in a given category

*genes statistically enriched in a given category

Assessing the genome-wide expression differences by RNAseq

No GO enrichment

		Total genes
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	<i>ΔLmPf2</i>	202
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#genes statistically under-represented in a given category

*genes statistically enriched in a given category

Assessing the genome-wide expression differences by RNAseq

No GO enrichment

Carbohydrate uptake (primary metabolism)

		Total genes
Up-regulated	<i>Δkmt1</i>	129
	<i>ΔLmPf2</i>	202
	<i>WT_oPf2</i>	247
	<i>Δkmt1_oPf2_A</i>	275
	<i>Δkmt1_oPf2_B</i>	931
Down-regulated	<i>Δkmt1</i>	143
	<i>ΔLmPf2</i>	225
	<i>WT_oPf2</i>	277
	<i>Δkmt1_oPf2_A</i>	158
	<i>Δkmt1_oPf2_B</i>	861

#genes statistically under-represented in a given category

*genes statistically enriched in a given category

Assessing the genome-wide expression differences by RNAseq

		Total genes	
No GO enrichment			
Carbohydrate uptake (primary metabolism)	Up-regulated	<i>Δkmt1</i>	129
		<i>ΔLmPf2</i>	202
		<i>WT_oPf2</i>	247
		<i>Δkmt1_oPf2_A</i>	275
		<i>Δkmt1_oPf2_B</i>	931
Oxido-reduction processes	Down-regulated	<i>Δkmt1</i>	143
		<i>ΔLmPf2</i>	225
		<i>WT_oPf2</i>	277
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CAZymes			

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Assessing the genome-wide expression differences by RNAseq

No GO enrichment

Carbohydrate uptake (primary metabolism)

Oxido-reduction processes

CAZymes

		Total genes	Effector genes	H3K4me2 genes	H3K9me3 genes	H3K27me3 genes	H3K9me3/H3K27me3 genes
Up-regulated	<i>Δkmt1</i>	129	22*	22 [#]	3	64*	4*
	<i>ΔLmPf2</i>	202	20	68 [#]	4	57*	5*
	<i>WT_oPf2</i>	247	46*	46 [#]	2	101*	6*
	<i>Δkmt1_oPf2_A</i>	275	59*	38 [#]	11*	144*	15*
	<i>Δkmt1_oPf2_B</i>	931	154*	233 [#]	25*	329*	24*
Down-regulated	<i>Δkmt1</i>	143	27*	35 [#]	10*	42*	9*
	<i>ΔLmPf2</i>	225	40*	58 [#]	4	88*	10*
	<i>WT_oPf2</i>	277	19	110 [#]	1	60*	3
	<i>Δkmt1_oPf2_A</i>	158	23*	32 [#]	11*	47*	6*
	<i>Δkmt1_oPf2_B</i>	861	83	364 [#]	11	182*	14*

[#]genes statistically under-represented in a given category

*genes statistically enriched in a given category

Expression of *AvrLm* genes *in vitro* in the different strains

ID	name	TE	H3K4me2	H3K9me3	H3K27me3
Lmb_jn3_00001	<i>AvrLm3</i>	yes	-	all_included	-
Lmb_jn3_03262	<i>AvrLm4-7</i>	yes	-	all_included	-
Lmb_jn3_05547	<i>AvrLm14</i>	yes	-	all_included	-
Lmb_jn3_07862	<i>AvrLm6</i>	yes	-	all_included	-
Lmb_jn3_07863	<i>AvrLm2</i>	yes	-	5'_included	-
Lmb_jn3_07874	<i>AvrLm10_A</i>	yes	-	all_included	-
Lmb_jn3_07875	<i>AvrLm10_B</i>	yes	-	all_included	all_included
Lmb_jn3_08343	<i>AvrLm5-Lep2</i>	yes	-	all_included	-
Lmb_jn3_10106	<i>AvrLm5-9</i>	yes	-	all_included	-
Lmb_jn3_12994	<i>AvrLm11</i>	yes	-	all_included	-

Expression of AvrLm genes *in vitro* in the different strains

ID	name	TE	H3K4me2	H3K9me3	H3K27me3	<i>Δkmt1</i>
Lmb_jn3_00001	<i>AvrLm3</i>	yes	-	all_included	-	up
Lmb_jn3_03262	<i>AvrLm4-7</i>	yes	-	all_included	-	-
Lmb_jn3_05547	<i>AvrLm14</i>	yes	-	all_included	-	-
Lmb_jn3_07862	<i>AvrLm6</i>	yes	-	all_included	-	-
Lmb_jn3_07863	<i>AvrLm2</i>	yes	-	5'_included	-	down
Lmb_jn3_07874	<i>AvrLm10_A</i>	yes	-	all_included	-	down
Lmb_jn3_07875	<i>AvrLm10_B</i>	yes	-	all_included	all_included	-
Lmb_jn3_08343	<i>AvrLm5-Lep2</i>	yes	-	all_included	-	-
Lmb_jn3_10106	<i>AvrLm5-9</i>	yes	-	all_included	-	-
Lmb_jn3_12994	<i>AvrLm11</i>	yes	-	all_included	-	-

Expression of AvrLm genes *in vitro* in the different strains

ID	name	TE	H3K4me2	H3K9me3	H3K27me3	$\Delta kmt1$	$\Delta LmPf2$
Lmb_jn3_00001	<i>AvrLm3</i>	yes	-	all_included	-	up	-
Lmb_jn3_03262	<i>AvrLm4-7</i>	yes	-	all_included	-	-	-
Lmb_jn3_05547	<i>AvrLm14</i>	yes	-	all_included	-	-	-
Lmb_jn3_07862	<i>AvrLm6</i>	yes	-	all_included	-	-	-
Lmb_jn3_07863	<i>AvrLm2</i>	yes	-	5'_included	-	down	-
Lmb_jn3_07874	<i>AvrLm10_A</i>	yes	-	all_included	-	down	-
Lmb_jn3_07875	<i>AvrLm10_B</i>	yes	-	all_included	all_included	-	down
Lmb_jn3_08343	<i>AvrLm5-Lep2</i>	yes	-	all_included	-	-	-
Lmb_jn3_10106	<i>AvrLm5-9</i>	yes	-	all_included	-	-	-
Lmb_jn3_12994	<i>AvrLm11</i>	yes	-	all_included	-	-	-

Expression of AvrLm genes *in vitro* in the different strains

ID	name	TE	H3K4me2	H3K9me3	H3K27me3	$\Delta kmt1$	$\Delta LmPf2$	WT_ oPf2
Lmb_jn3_00001	<i>AvrLm3</i>	yes	-	all_included	-	up	-	-
Lmb_jn3_03262	<i>AvrLm4-7</i>	yes	-	all_included	-	-	-	-
Lmb_jn3_05547	<i>AvrLm14</i>	yes	-	all_included	-	-	-	-
Lmb_jn3_07862	<i>AvrLm6</i>	yes	-	all_included	-	-	-	-
Lmb_jn3_07863	<i>AvrLm2</i>	yes	-	5'_included	-	down	-	-
Lmb_jn3_07874	<i>AvrLm10_A</i>	yes	-	all_included	-	down	-	-
Lmb_jn3_07875	<i>AvrLm10_B</i>	yes	-	all_included	all_included	-	down	-
Lmb_jn3_08343	<i>AvrLm5-Lep2</i>	yes	-	all_included	-	-	-	-
Lmb_jn3_10106	<i>AvrLm5-9</i>	yes	-	all_included	-	-	-	-
Lmb_jn3_12994	<i>AvrLm11</i>	yes	-	all_included	-	-	-	-

Expression of AvrLm genes *in vitro* in the different strains

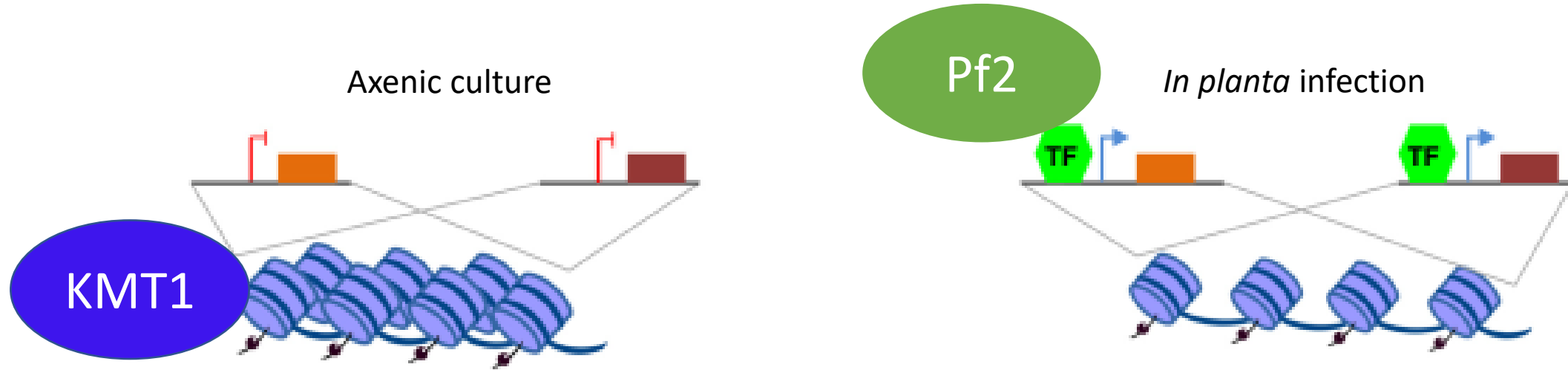
ID	name	TE	H3K4me2	H3K9me3	H3K27me3	$\Delta kmt1$	$\Delta LmPf2$	WT_ <i>oPf2</i>	$\Delta kmt1_oPf2_A$	$\Delta kmt1_oPf2_B$
Lmb_jn3_00001	<i>AvrLm3</i>	yes	-	all_included	-	up	-	-	up	up
Lmb_jn3_03262	<i>AvrLm4-7</i>	yes	-	all_included	-	-	-	-	up	up
Lmb_jn3_05547	<i>AvrLm14</i>	yes	-	all_included	-	-	-	-	up	up
Lmb_jn3_07862	<i>AvrLm6</i>	yes	-	all_included	-	-	-	-	up	up
Lmb_jn3_07863	<i>AvrLm2</i>	yes	-	5'_included	-	down	-	-	-	up
Lmb_jn3_07874	<i>AvrLm10_A</i>	yes	-	all_included	-	down	-	-	down	up
Lmb_jn3_07875	<i>AvrLm10_B</i>	yes	-	all_included	all_included	-	down	-	up	up
Lmb_jn3_08343	<i>AvrLm5-Lep2</i>	yes	-	all_included	-	-	-	-	up	up
Lmb_jn3_10106	<i>AvrLm5-9</i>	yes	-	all_included	-	-	-	-	-	-
Lmb_jn3_12994	<i>AvrLm11</i>	yes	-	all_included	-	-	-	-	-	-

Expression of AvrLm genes *in vitro* in the different strains

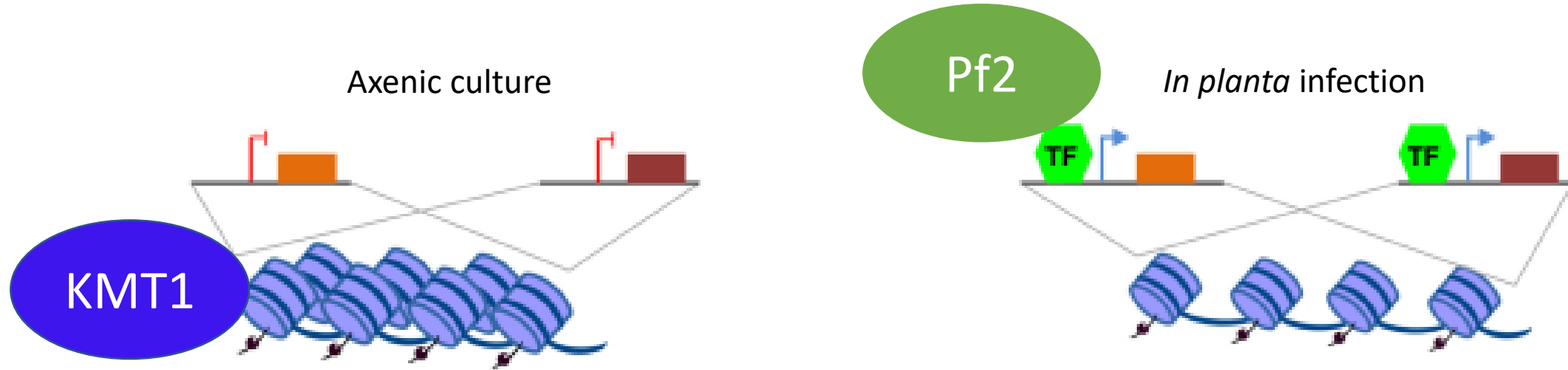
ID	name	TE	H3K4me2	H3K9me3	H3K27me3	<i>Δkmt1</i>	<i>ΔLmPf2</i>	WT_ <i>oPf2</i>	<i>Δkmt1_oPf2_A</i>	<i>Δkmt1_oPf2_B</i>
Lmb_jn3_00001	<i>AvrLm3</i>	yes	-	all_included	-	up	-	-	up	up
Lmb_jn3_03262	<i>AvrLm4-7</i>	yes	-	all_included	-	-	-	-	up	up
Lmb_jn3_05547	<i>AvrLm14</i>	yes	-	all_included	-	-	-	-	up	up
Lmb_jn3_07862	<i>AvrLm6</i>	yes	-	all_included	-	-	-	-	up	up
Lmb_jn3_07863	<i>AvrLm2</i>	yes	-	5'_included	-	down	-	-	-	up
Lmb_jn3_07874	<i>AvrLm10_A</i>	yes	-	all_included	-	down	-	-	down	up
Lmb_jn3_07875	<i>AvrLm10_B</i>	yes	-	all_included	all_included	-	down	-	up	up
Lmb_jn3_08343	<i>AvrLm5-Lep2</i>	yes	-	all_included	-	-	-	-	up	up
Lmb_jn3_10106	<i>AvrLm5-9</i>	yes	-	all_included	-	-	-	-	-	-
Lmb_jn3_12994	<i>AvrLm11</i>	yes	-	all_included	-	-	-	-	-	-

The absence of H3K9me3 and overexpression of *LmPf2* derepress a high proportion of *AvrLm* genes *in vitro*

Conclusions and perspectives



A two-layers regulatory mechanism ?

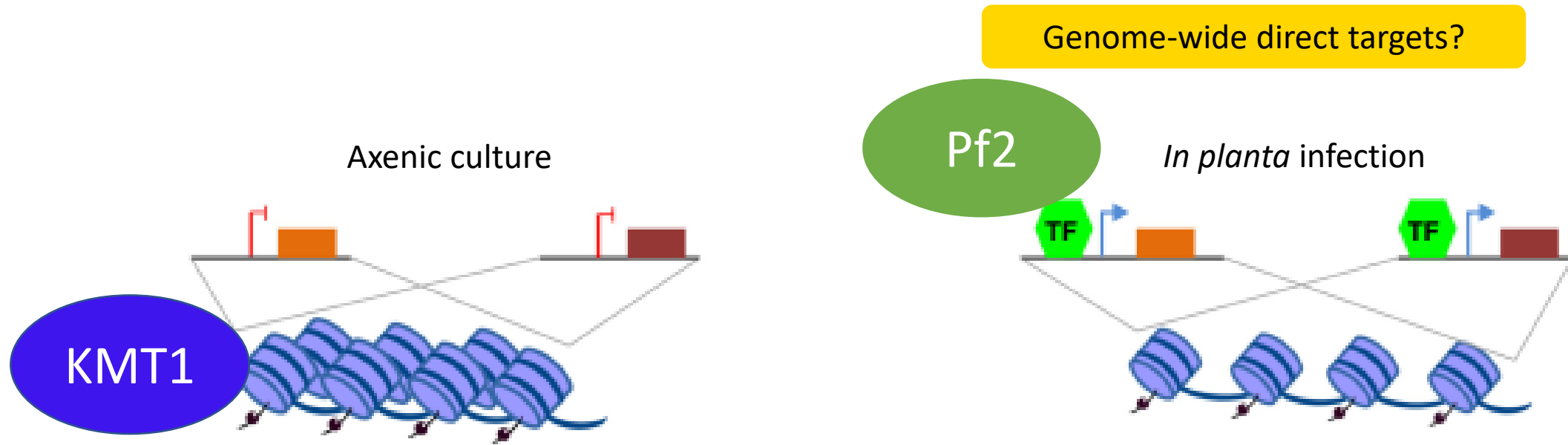


A two-layers regulatory mechanism ?



YES but there remain lots of opened questions

Conclusions and perspectives

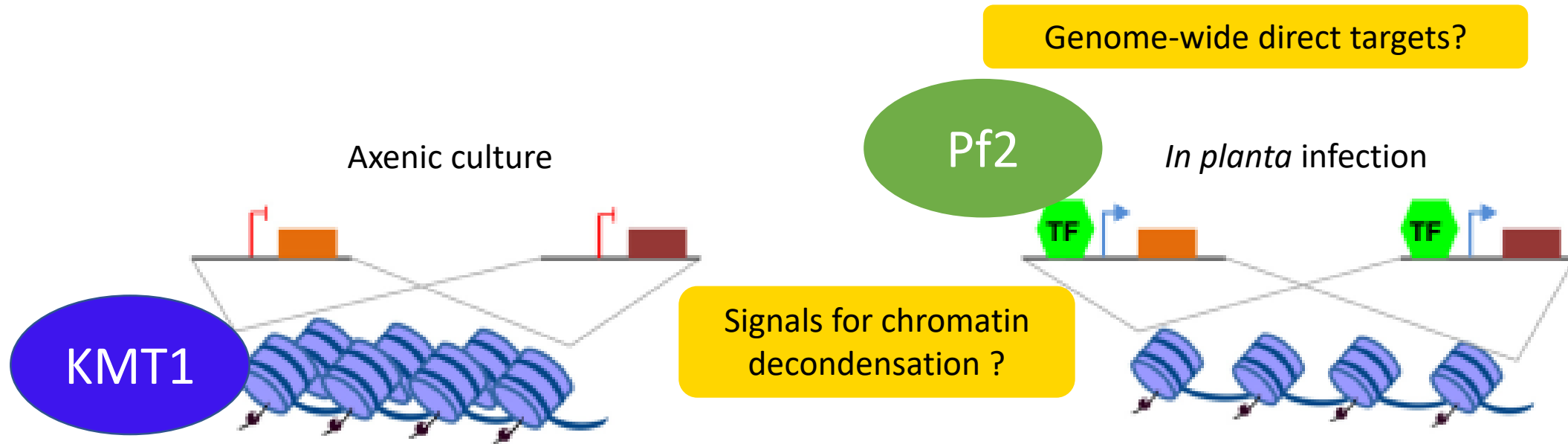


A two-layers regulatory mechanism ?



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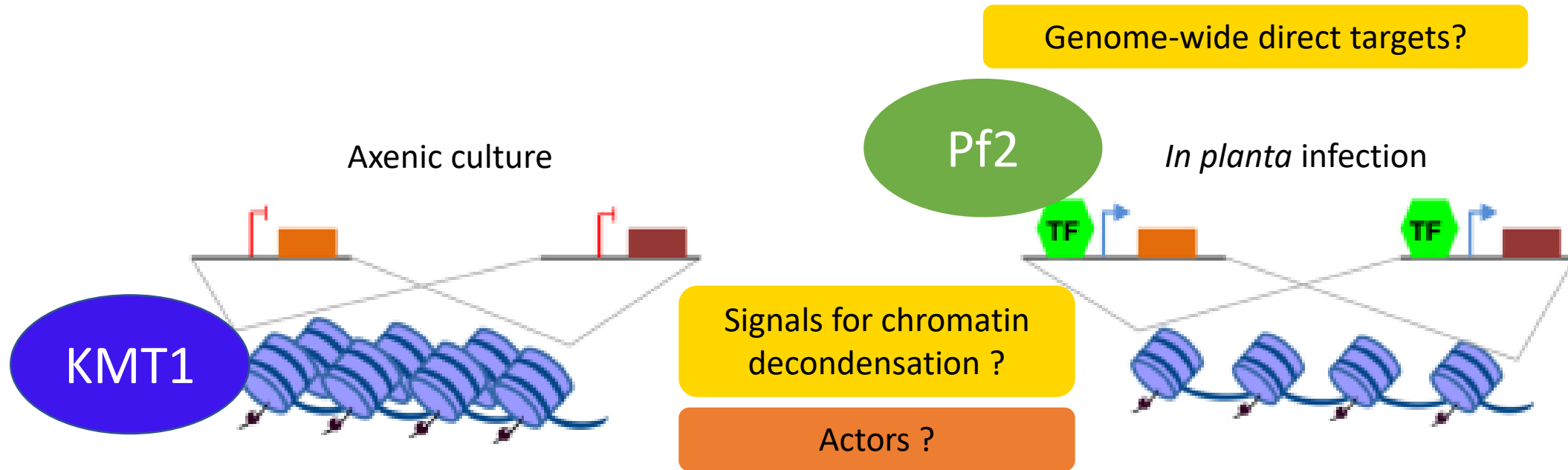
Conclusions and perspectives



A two-layers regulatory mechanism ?

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Conclusions and perspectives

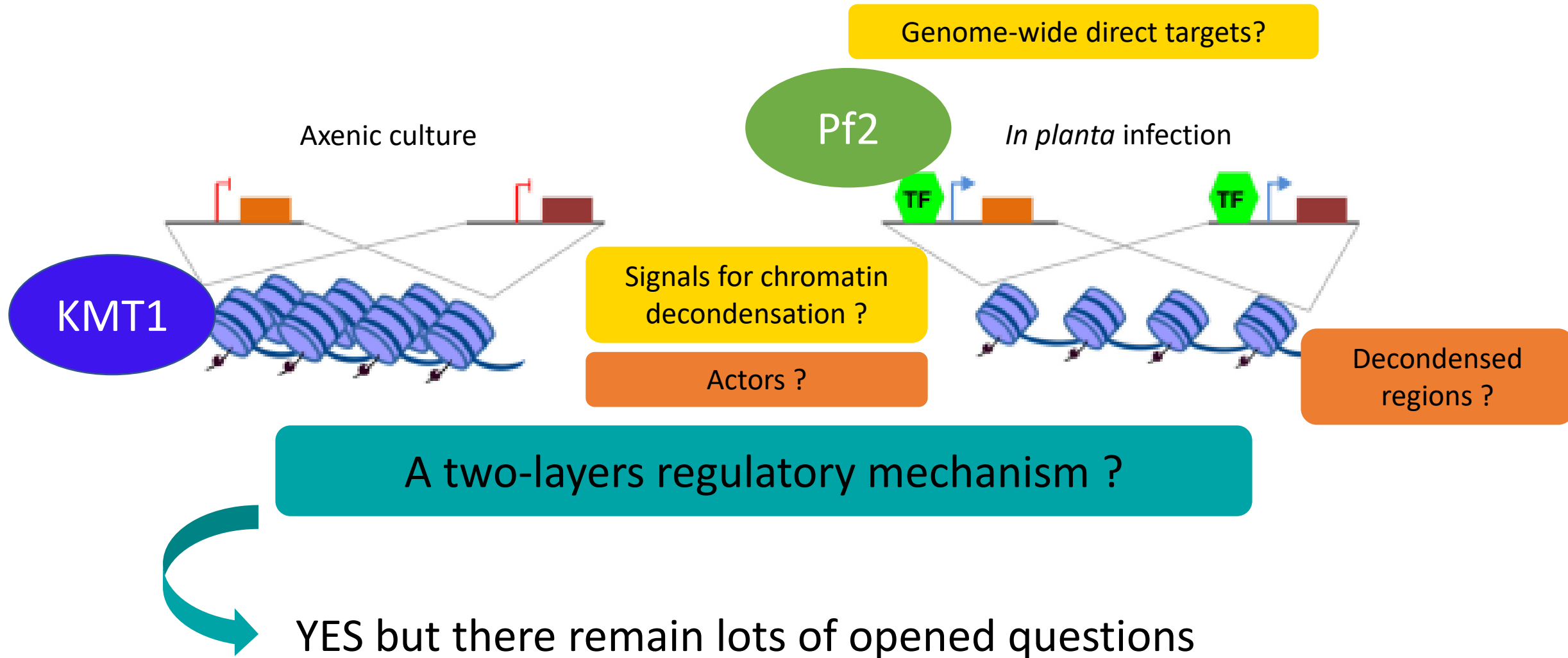


A two-layers regulatory mechanism ?



YES but there remain lots of opened questions

Conclusions and perspectives



EPLM team

Colin CLAIRET
Jessica SOYER
Isabelle FUDAL



BIOGER staff



SPE division
(Chromadyn project)



The background of the image is a classic marbled paper pattern. It features intricate, swirling designs in shades of light blue, pale green, and off-white, with occasional thin lines of red and orange. The overall effect is a textured, organic pattern that resembles watercolor or stone. Centered on this background is the text "THANK YOU" in a bold, black, sans-serif font.

THANK YOU

Characterization of transformant strains

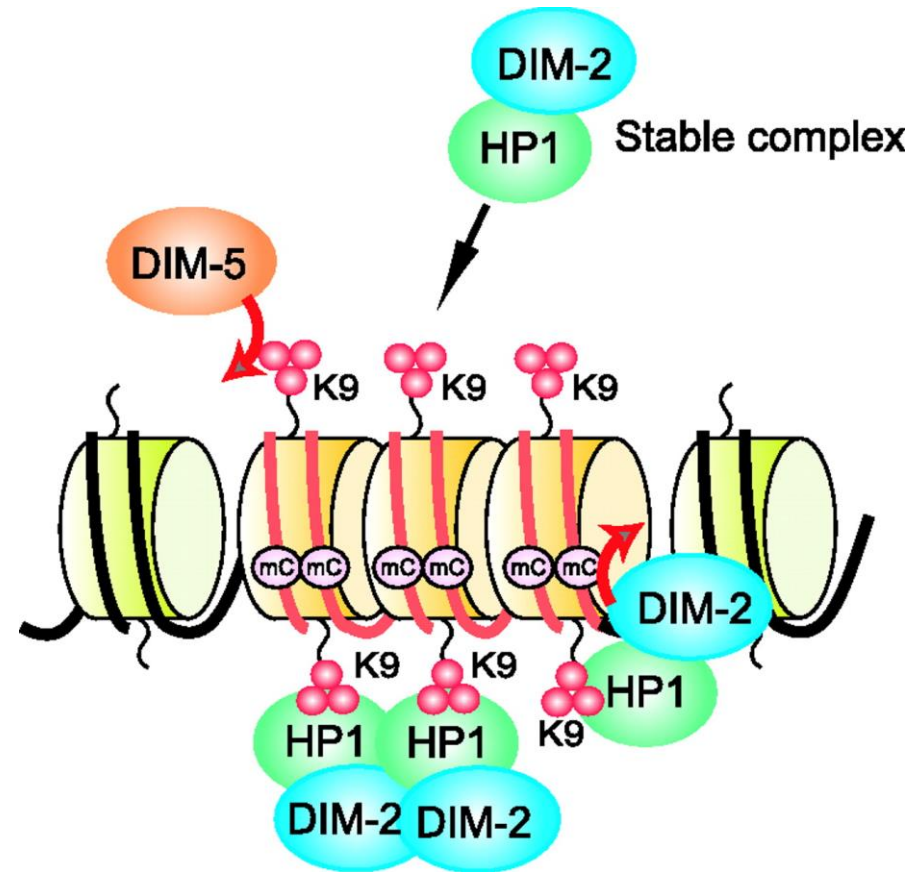
Isolate/ transformant	expression <i>in planta</i> 7 dpi			
	<i>AvrLm4-7</i>	<i>AvrLm6</i>	<i>AvrLm10A</i>	<i>AvrLm11</i>
WT	$3.25 \cdot 10^1$	$7.41 \cdot 10^1$	$2.92 \cdot 10^1$	$1.96 \cdot 10^2$
$\Delta LmPf2_A$	nd	$4.58 \cdot 10^{-2}$	$2.49 \cdot 10^{-2}$	$7.64 \cdot 10^{-2}$
$\Delta LmPf2_B$	$4.08 \cdot 10^{-3}$	$6.27 \cdot 10^{-3}$	$3.25 \cdot 10^{-2}$	$9.55 \cdot 10^{-2}$
$\Delta kmt1$	1.03	4.23	1.93	5.23

Characterization of transformant strains

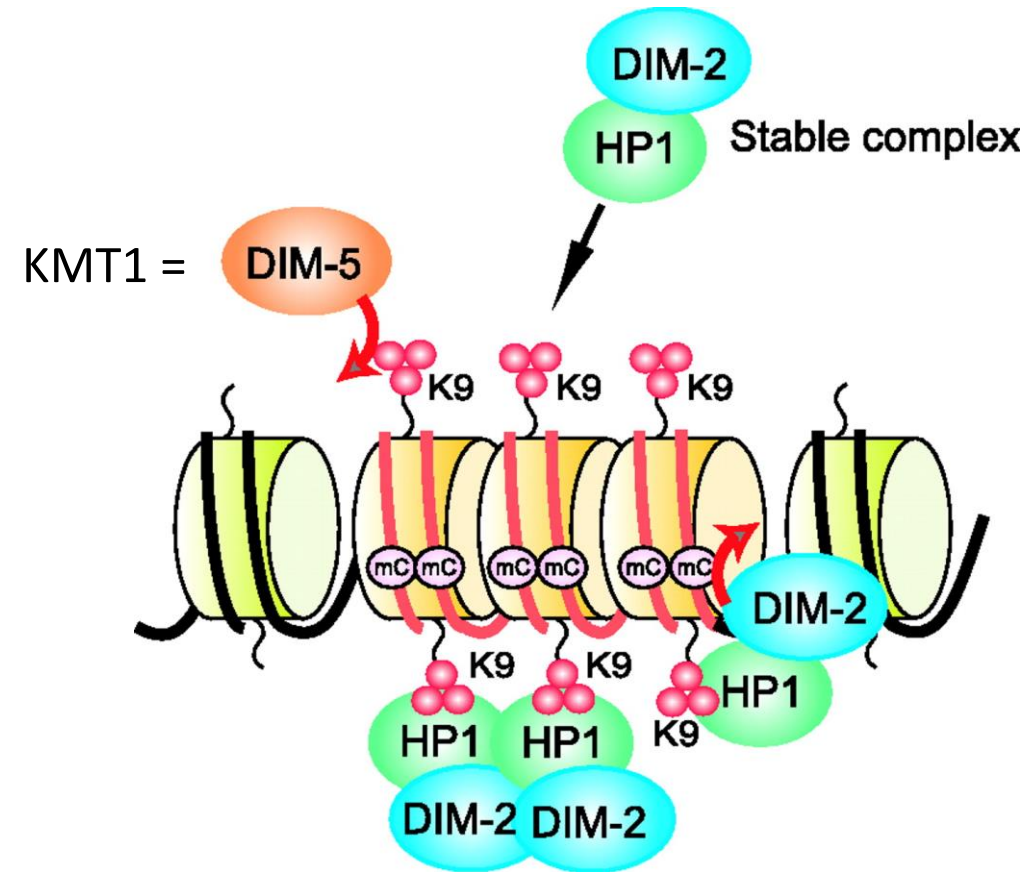
Isolate/ transformant	expression <i>in planta</i> 7 dpi			
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$\Delta kmt1$	1.03	4.23	1.93	5.23

Expression of AvrLm genes is decreased in $\Delta kmt1$ and even more $\Delta LmPf2$

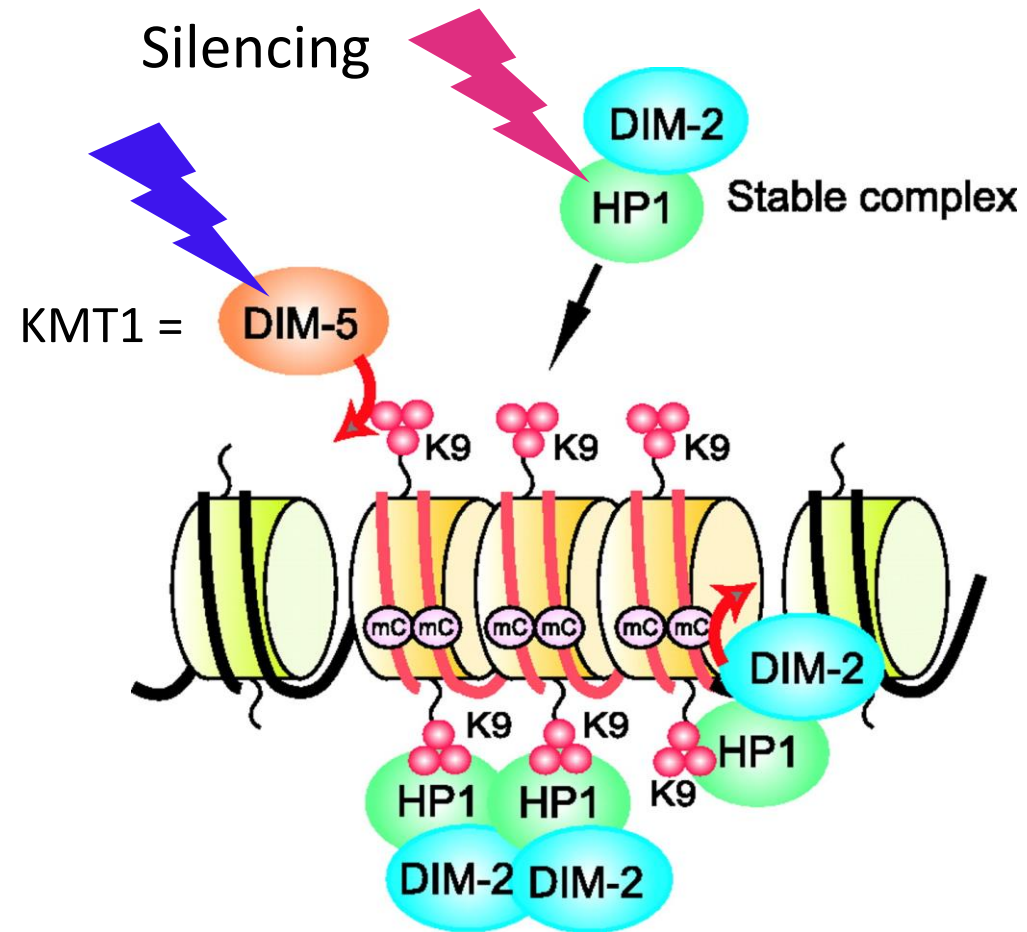
Regulation of effector genes by chromatin modifiers in *L. maculans*



Regulation of effector genes by chromatin modifiers in *L. maculans*



Regulation of effector genes by chromatin modifiers in *L. maculans*



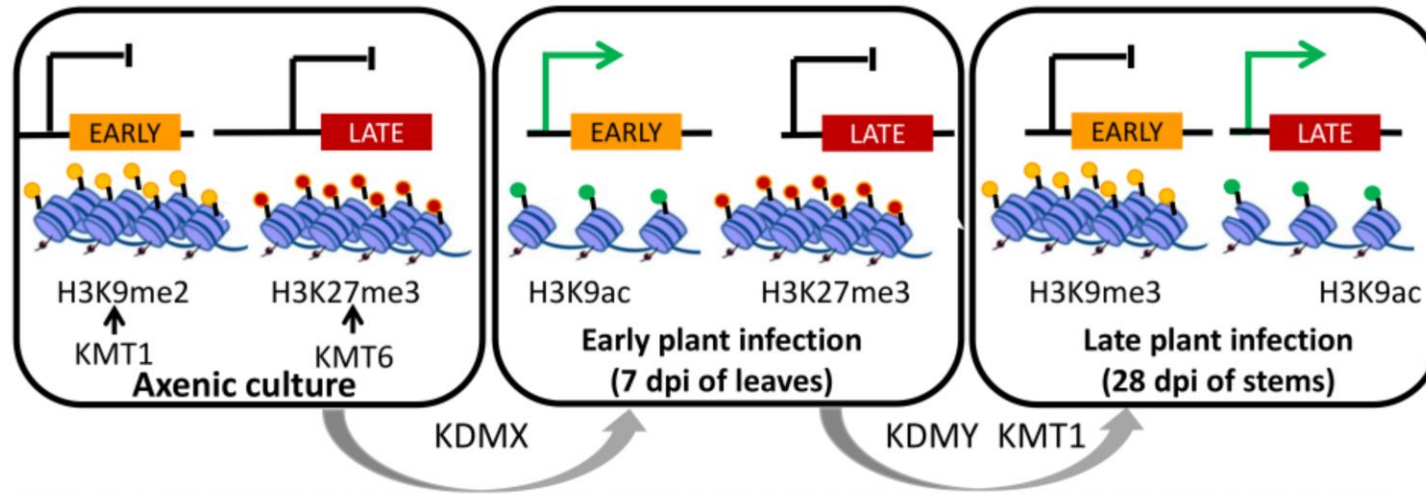
Regulation of effector genes by chromatin modifiers in *L. maculans*

SEQ_ID	Fold change in silenced- <i>LmHP1</i> ^a	Fold change in silenced- <i>LmDIM5</i> ^a	Function	Fold change 7 dpi ^b
lmctg_1626_v2_egn4_Lema_uP123840.1	1.63	2.24	predicted protein	7.38
AT10_ext_SuperContig_10_G00134	7.74	17.45	putative SSP-encoding gene	231.47
lmctg_1311_v2_T000008 ^c	2.24	8.98	predicted protein	#N/A
lmctg_0674_v2_egn4_Lema_P049660.1	5.95	14.58	similar to AvrLm1 protein	327.73
AT15_ext_SuperContig_5_3	5.97	11.45	putative SSP-encoding gene	189.62
lmctg_1229_v2_egn4_Lema_P086540.1	3.00	8.04	similar to Six5	163.23
lmctg_1459_v2_egn4_Lema_uP104510.1	8.59	4.52	predicted protein	67.64
AvrLm1	5.60	16.93	AvrLm1	313.63
lmctg_1214_v2_egn4_Lema_P086290.1	8.80	16.83	AvrLm4-7	182.85
lmctg_1539_v2_T000001 ^c	13.80	67.97	predicted protein	#N/A
lmctg_0562_v2_egn4_Lema_uP038240.1	1.77	2.14	predicted protein	3.99
lmctg_0550_v2_T000028 ^c	1.85	4.69	predicted protein	#N/A
lmctg_0898_v2_T000001 ^c	5.31	62.19	putative SSP-encoding gene	#N/A
lmctg_0001_v2_T000001 ^c	6.65	77.16	putative SSP-encoding gene	#N/A
lmctg_0105_v2_egn2_Lema_P012060.1	2.97	30.18	putative SSP-encoding gene	1.94

Regulation of effector genes by chromatin modifiers in *L. maculans*

SEQ_ID	Fold change in silenced- <i>LmHP1</i> ^a	Fold change in silenced- <i>LmDIM5</i> ^a	Function	Fold change 7 dpi ^b
lmctg_1626_v2_egn4_Lema_uP123840.1	1.63	2.24	predicted protein	7.38
AT10_ext_SuperContig_10_G00134	7.74	17.45	putative SSP-encoding gene	231.47
lmctg_1311_v2_T000008 ^c	2.24	8.98	predicted protein	#N/A
lmctg_0674_v2_egn4_Lema_P049660.1	5.95	14.58	similar to AvrLm1 protein	327.73
AT15_ext_SuperContig_5_3	5.97	11.45	putative SSP-encoding gene	189.62
lmctg_1229_v2_egn4_Lema_P086540.1	3.00	8.04	similar to Six5	163.23
lmctg_1459_v2_egn4_Lema_uP104510.1	8.59	4.52	predicted protein	67.64
AvrLm1	5.60	16.93	AvrLm1	313.63
lmctg_1214_v2_egn4_Lema_P086290.1	8.80	16.83	AvrLm4-7	182.85
lmctg_1539_v2_T000001 ^c	13.80	67.97	predicted protein	#N/A
lmctg_0562_v2_egn4_Lema_uP038240.1	1.77	2.14	predicted protein	3.99
lmctg_0550_v2_T000028 ^c	1.85	4.69	predicted protein	#N/A
lmctg_0898_v2_T000001 ^c	5.31	62.19	putative SSP-encoding gene	#N/A
lmctg_0001_v2_T000001 ^c	6.65	77.16	putative SSP-encoding gene	#N/A
lmctg_0105_v2_egn2_Lema_P012060.1	2.97	30.18	putative SSP-encoding gene	1.94

The CHOPIN project



WP1- Fungal epigenomic dynamics during oilseed rape infection

Strategy

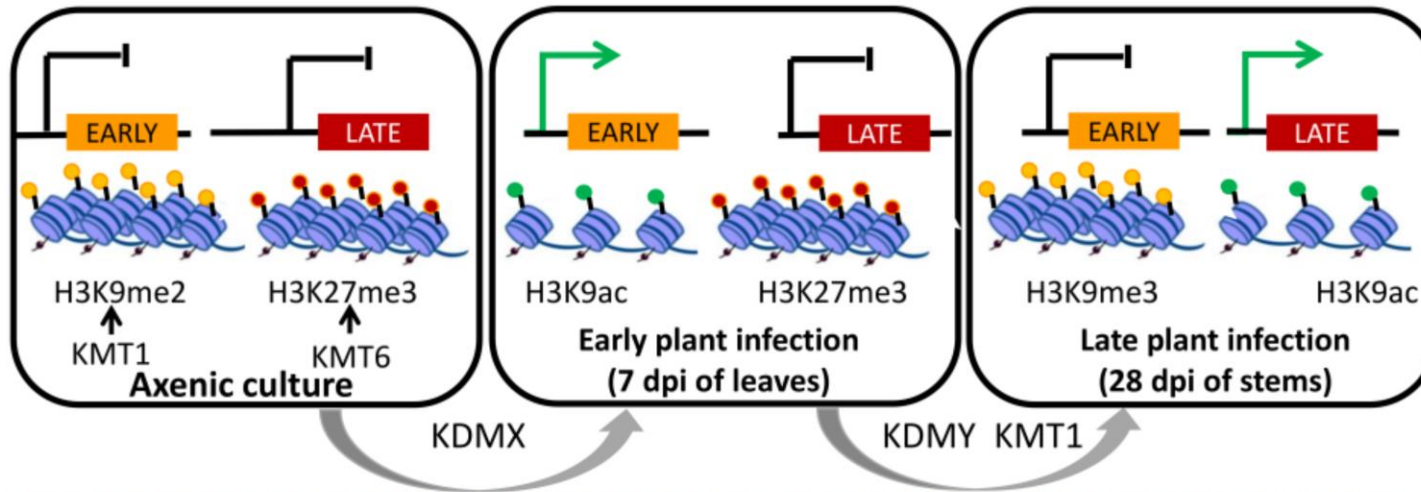
- Epigenomic analyses (ChIP-seq, Hi-C, ATAC-seq) *in vitro* & at two infection stages
- Transcriptomic analyses same conditions



WP1- Fungal epigenomic dynamics during oilseed rape infection

Strategy

- Epigenomic analyses (ChIP-seq, Hi-C, ATAC-seq) *in vitro* & at two infection stages
- Transcriptomic analyses same conditions



Strategy

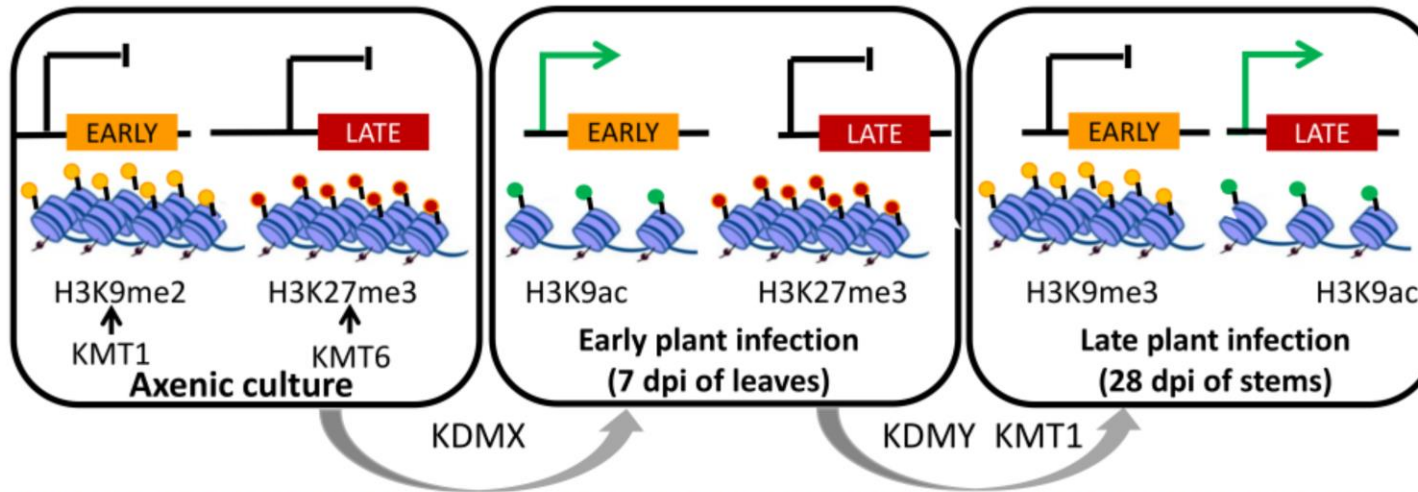
- CRISPR-Cas9 mutation of *KMT1*, *KMT6*, and candidate KDMs
- Transcriptomic analyses/ Epigenomic analyses *in vitro*
- Transcriptomic analyses during two infection stages
- Mutants deregulating expression of (effector) genes / impaired in pathogenicity selected for *in planta* targeted chromatin dynamics analyses

WP2- Role of the chromatin structure on the regulation of *L. maculans* gene expression

WP1- Fungal epigenomic dynamics during oilseed rape infection

Strategy

- Epigenomic analyses (ChIP-seq, Hi-C, ATAC-seq) *in vitro* & at two infection stages
- Transcriptomic analyses same conditions



Strategy

- CRISPR-Cas9 mutation of *KMT1*, *KMT6*, and candidate KDMs
- Transcriptomic analyses/ Epigenomic analyses *in vitro*
- Transcriptomic analyses during two infection stages
- Mutants deregulating expression of (effector) genes / impaired in pathogenicity selected for *in planta* targeted chromatin dynamics analyses

WP2- Role of the chromatin structure on the regulation of *L. maculans* gene expression

MAIN RESULTS

- Global picture of fungal chromatin dynamics during infection
- Role of chromatin dynamics and selected chromatin modifiers on the regulation of gene expression and pathogenicity