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Cross-Kingdom Similarity of Transcriptional Regulation in Innate Immunity

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Bundesministerium
für Bildung
und Forschung

From the Greening of the TRANSFAC Database.....



ISPMB

Québec
l'an 2000

6th International Congress
of Plant Molecular Biology

Québec, Canada
June 18 - 24, 2000



organized by
The International Society
for Plant Molecular Biology
and
Université Laval

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THE GREENING OF THE TRANSFAC DATABASE

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1- Institute for Genetics, Technical University at Braunschweig, Germany.

2- BIOBASE GmbH, Braunschweig, Germany.

3- German Research Centre for Biotechnology, Braunschweig, Germany.

TRANSFAC is a database on transcription factors, their genomic binding sites and DNA-binding profiles (<http://transfac.gbf.de/TRANSFAC/>). Its content has been enhanced in particular by data on plant sites and factors. During the last year the number of plant FACTOR entries has been more than trebled, amounting now to 325 entries (as of March 2000). The volume of binding sites for plant transcription factors in the SITE table has been more than doubled, now comprising 154 genomic and 245 artificial sites. The latter come mostly from random selection studies to identify the DNA-binding specificity of individual factors and are used to generate binding profiles. Correspondingly, the number of plant-related entries in the MATRIX table has been more than trebled (from 8 to 30 matrices; March 2000). These matrices, together with a total of 18 consensus strings stored in the SITE table, can serve as a basis to identify potential plant transcription factor binding sites in genomic sequences using the search routines provided by the TRANSFAC server. During the year 2000 significant additional resources have been devoted to updating and complementing the TRANSFAC database with plant transcription factors. Therefore it is expected that the number of FACTOR and SITE entries will increase at least ten times during this year. Furthermore, the databases TRANSPATH, about signal transduction, and CYTOMER, about organs and cell types, will be extended and integrated with the TRANSFAC plant data sources.



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.....to a Rich Harvest

Trends in Plant Science



Volume 6, Issue 6, 1 June 2001, Pages 251–255

Opinion

Database-assisted promoter analysis

Reinhard Hehl^a, Edgar Wingender^b

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[https://doi.org/10.1016/S1360-1385\(01\)01954-9](https://doi.org/10.1016/S1360-1385(01)01954-9)

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316–319 *Nucleic Acids Research*, 2000, Vol. 28, No. 1

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TRANSFAC: an integrated system for gene expression regulation

E. Wingender^{1,*}, X. Chen^{1,2}, R. Hehl³, H. Karas⁴, I. Liebich¹, V. Matys^{1,4}, T. Meinhardt¹,
M. Prüß^{1,4}, I. Reuter¹ and F. Schacherer¹

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Nucleic Acids Research, 2001, Vol. 29, No. 1 281–283

The TRANSFAC system on gene expression regulation

E. Wingender^{1,*}, X. Chen^{1,2}, E. Fricke³, R. Geffers³, R. Hehl⁴, I. Liebich¹, M. Krull³, V. Matys³,
H. Michael¹, R. Ohnhäuser³, M. Prüß³, F. Schacherer¹, S. Thiele³ and S. Urbach³

374–378 *Nucleic Acids Research*, 2003, Vol. 31, No. 1
DOI: 10.1093/nar/gkg108

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TRANSFAC[®]: transcriptional regulation, from patterns to profiles

V. Matys^{1,*}, E. Fricke¹, R. Geffers¹, E. Gößling¹, M. Haubrock¹, R. Hehl², K. Hornischer¹,
D. Karas¹, A. E. Kel¹, O. V. Kel-Margoulis¹, D.-U. Kloos¹, S. Land¹, B. Lewicki-Potapov¹,
H. Michael², R. Münch¹, I. Reuter¹, S. Rotert¹, H. Saxel¹, M. Scheer¹, S. Thiele¹ and
E. Wingender^{1,3}



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..... and to our own Databases like AthaMap

AthaMap



- Home
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 - Colocalization
 - Gene Analysis
 - Gene Identification
 - Small RNA Targets
 - MicroRNA Targets
- Description
- Documentation
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AthaMap

AthaMap provides a genome-wide map of potential transcription factor and small RNA binding sites in *Arabidopsis thaliana*. Please refer to the [description](#) page for detailed instructions on how to use the AthaMap [tools](#). Please cite the corresponding [publications](#) when using AthaMap.

The screenshot displays the AthaMap web interface with two main panels. The left panel shows search results for a small RNA (smRNA) with the following details:

- Name:** smRNA()
- Description:** small RNA from inflorescence library
- Species:** *Arabidopsis thaliana*
- Family:** small RNAs
- Sequence:** TGGGGATGATGATCAAT
- Corresponding smRNAs:** smRNA(): [Chromosome 1_11911](#), smRNA(): [Chromosome 3_10329766](#)
- Reference(s):** Lu C, Tej SS, Luo S, Haudenschild CD, Meyers BC, Green PJ. 2005. Elucidation of the small RNA component of the transcriptome. *Science* 309: 1567-9. [PubMed](#)

The right panel shows search results for a transcription factor (TF) with the following details:

- Name:** MYC_MYB
- Distance between sites:** 3-40bp
- Factor binding sites employed:** Element 1: TGA1a, Element 2: AtMYB15, AtMAB77, AtMYB84, CDC5, MYB-Ph3(1), MYB-Ph3(2), P, GAMYB
- Number of combinatorial elements annotated:** 38065

Below these panels, a sequence alignment view is shown with various motifs (TEIL, DOF2, AGL15, MYB84, AGP1, ALFIN1, PIF3) and their corresponding scores. A matrix is also displayed for the AGL15 motif, showing scores for different nucleotides (A, C, G, T) at various positions.



Steffens et al., (2004) *Nucleic Acids Res.* **32**: D368-372.
 Hehl et al., (2016) *Plant Cell Physiol* **57**: e4

.....and PathoPlant

PathoPlant



Home

Search

- accession no
- plant
- pathogen
- molecule
- interaction

Microarray expression

In silico expression analysis

cis-elements

Signaling pathways

Description

Documentation

Contact

Disclaimer

PathoPlant is a database on plant-pathogen interactions and components of signal transduction pathways related to plant pathogenesis. PathoPlant also harbors gene expression data from *Arabidopsis thaliana* microarray experiments to enable searching for specific genes regulated upon certain stimuli like pathogen infection, elicitor treatment, or abiotic stress. Validation of short DNA sequences as *cis*-elements responsive to different stimuli can also be performed in PathoPlant.

Current database content:

Table	No. of records
plants	99
pathogens	107
interactions	350
molecules	638
reactions	370
stimuli	173
references	619
comments	22
hyperlinks	2588

Last database update: 01.04.2016 18:07:46



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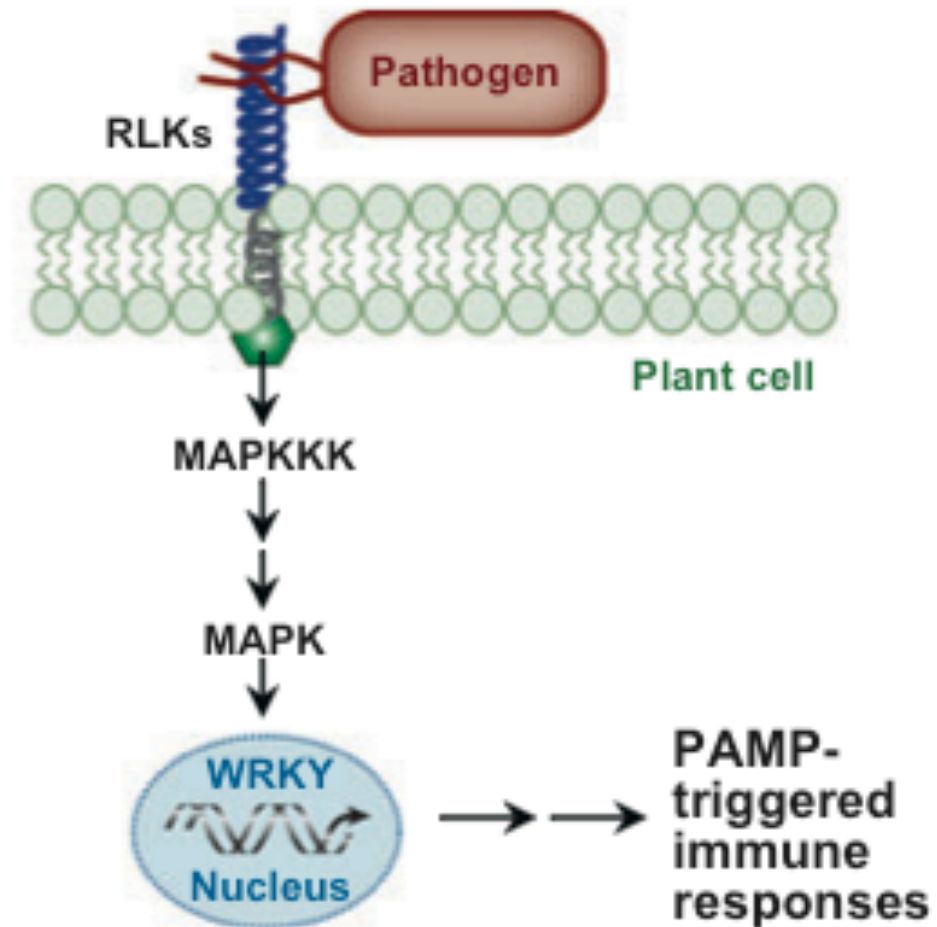
Bülow et al., (2004) *In Silico Biol.* 4: 529–536
Bolívar et al., (2014) *Database (Oxford)* 2014: bau030

Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity

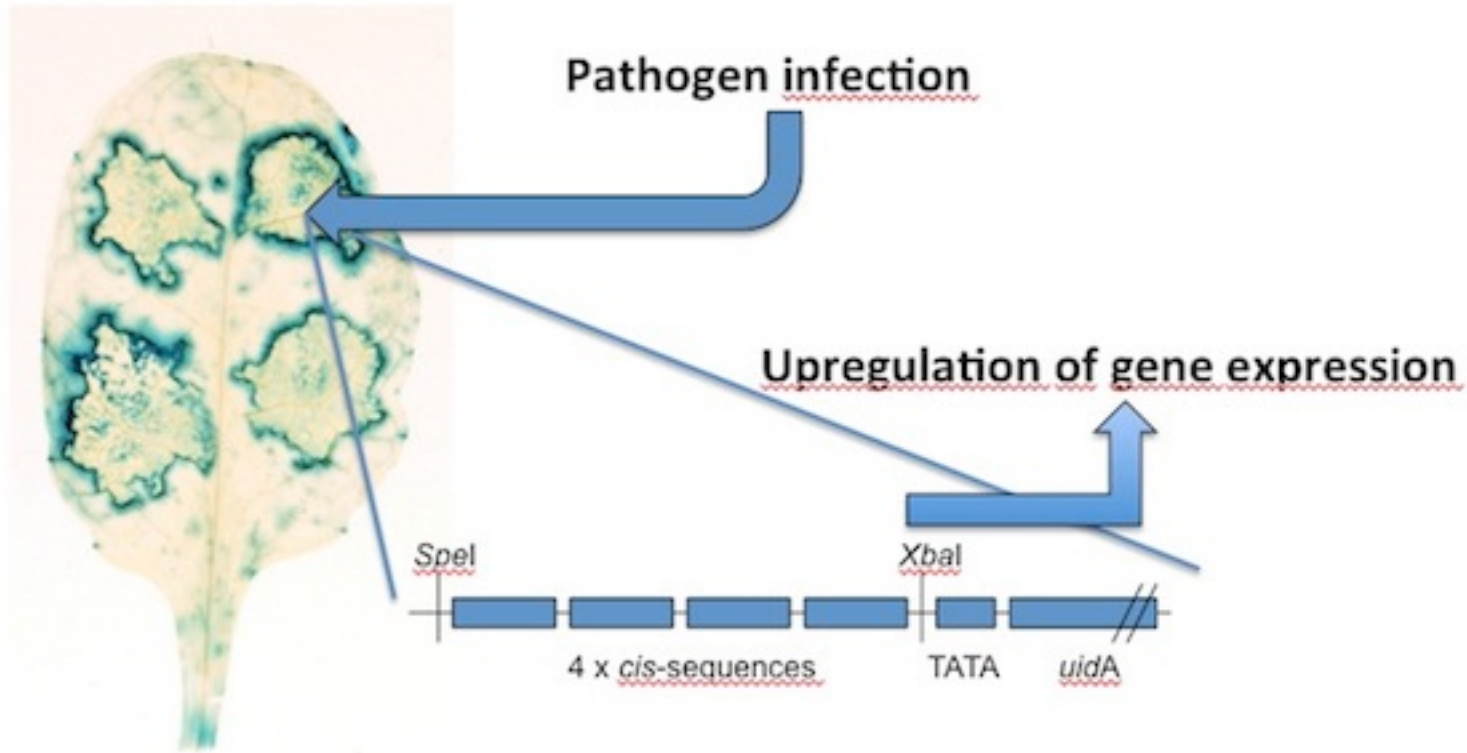
a

PAMP recognition triggers immunity

Resistance



Novel *Cis*-Regulatory Sequences for Synthetic Pathogen-Responsive Promoters

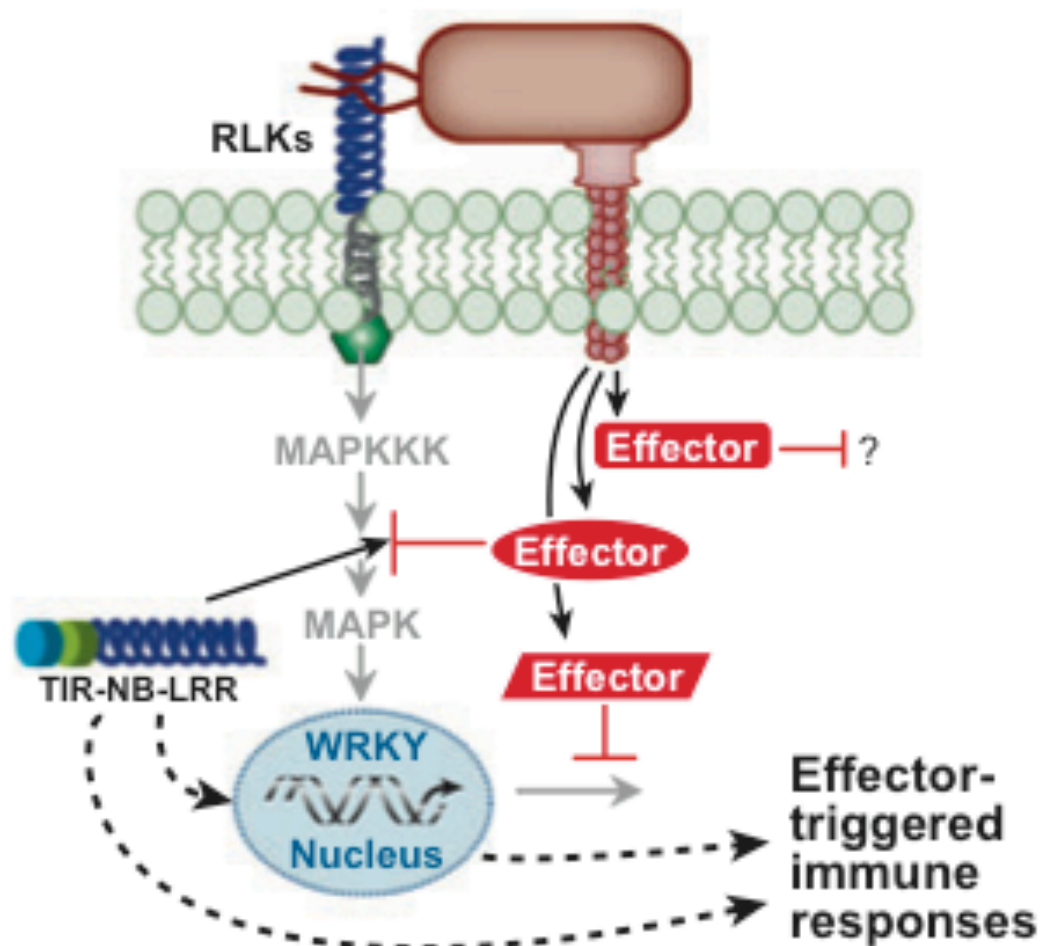


Application of Synthetic Pathogen-Responsive Promoters

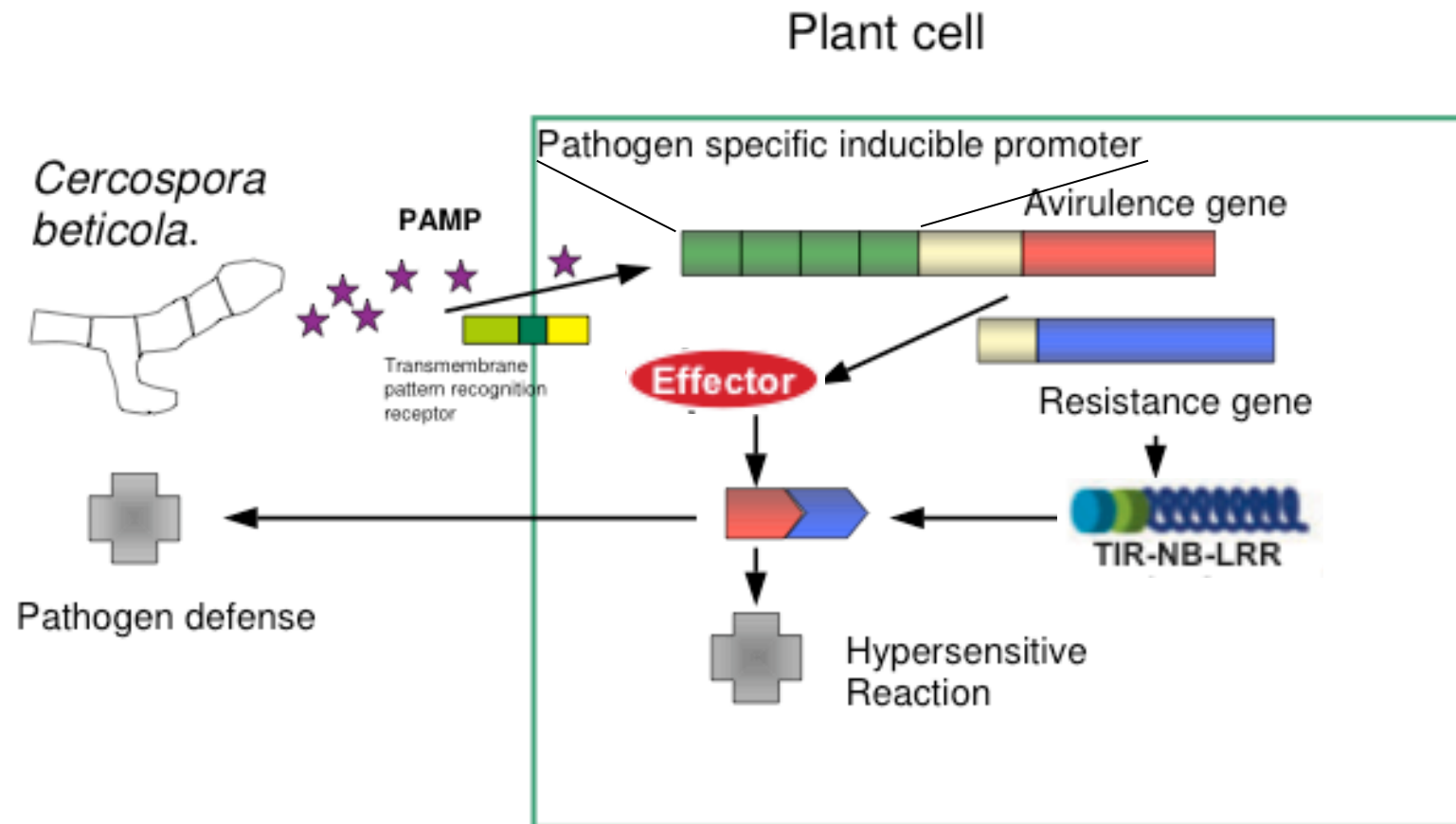
C

R proteins recognize effector activities

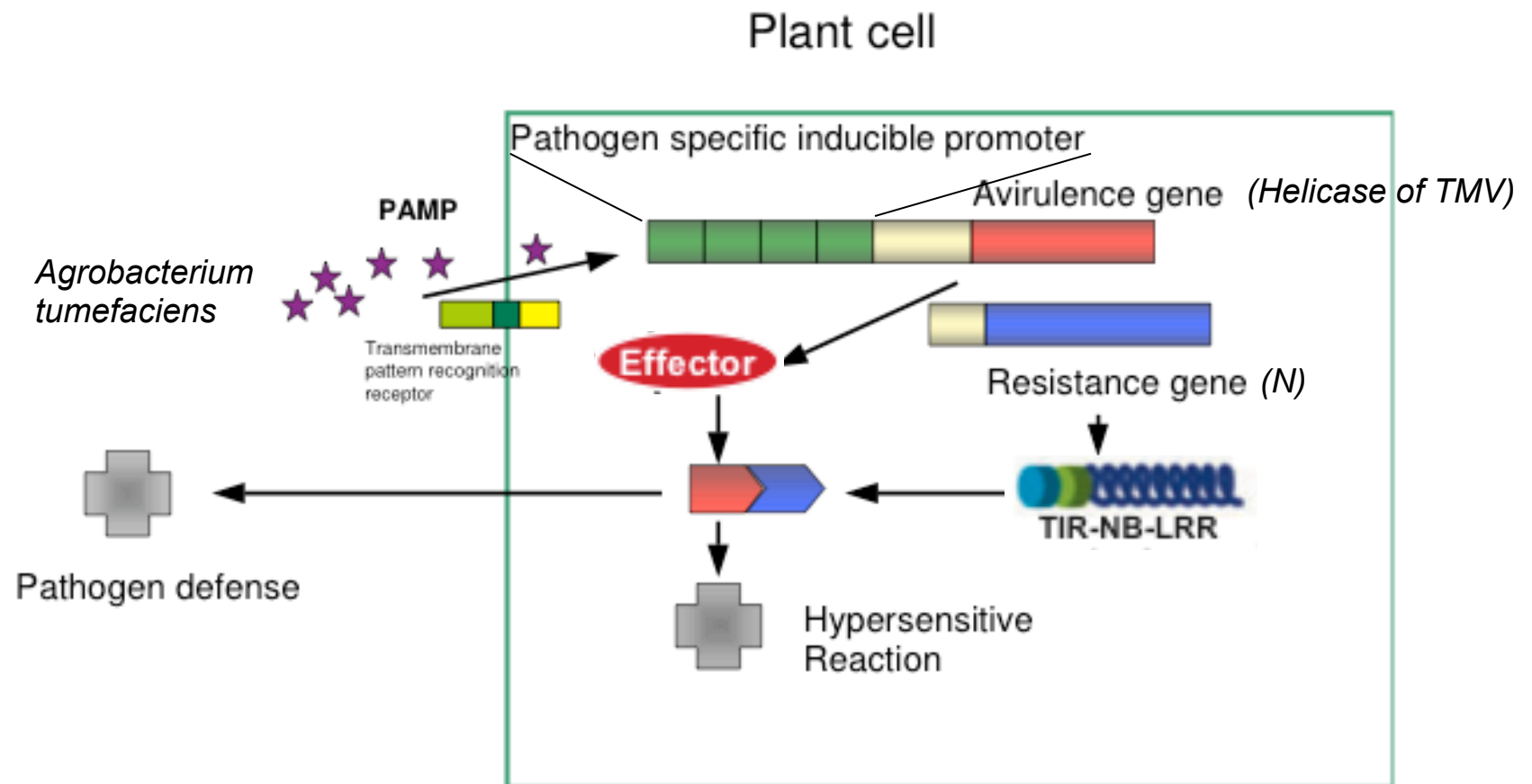
Resistance



Application of Synthetic Pathogen-Responsive Promoters



Application of Synthetic Pathogen-Responsive Promoters



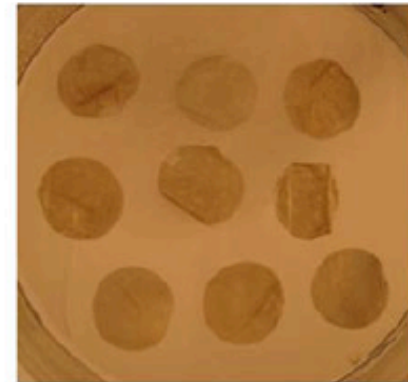
Application of Synthetic Pathogen-Responsive Promoters



Nn



TATA::p50-g1 *Nn*



2S2D::p50-g1 *Nn*



Nn



TATA::p50-g1 (*Nn*)



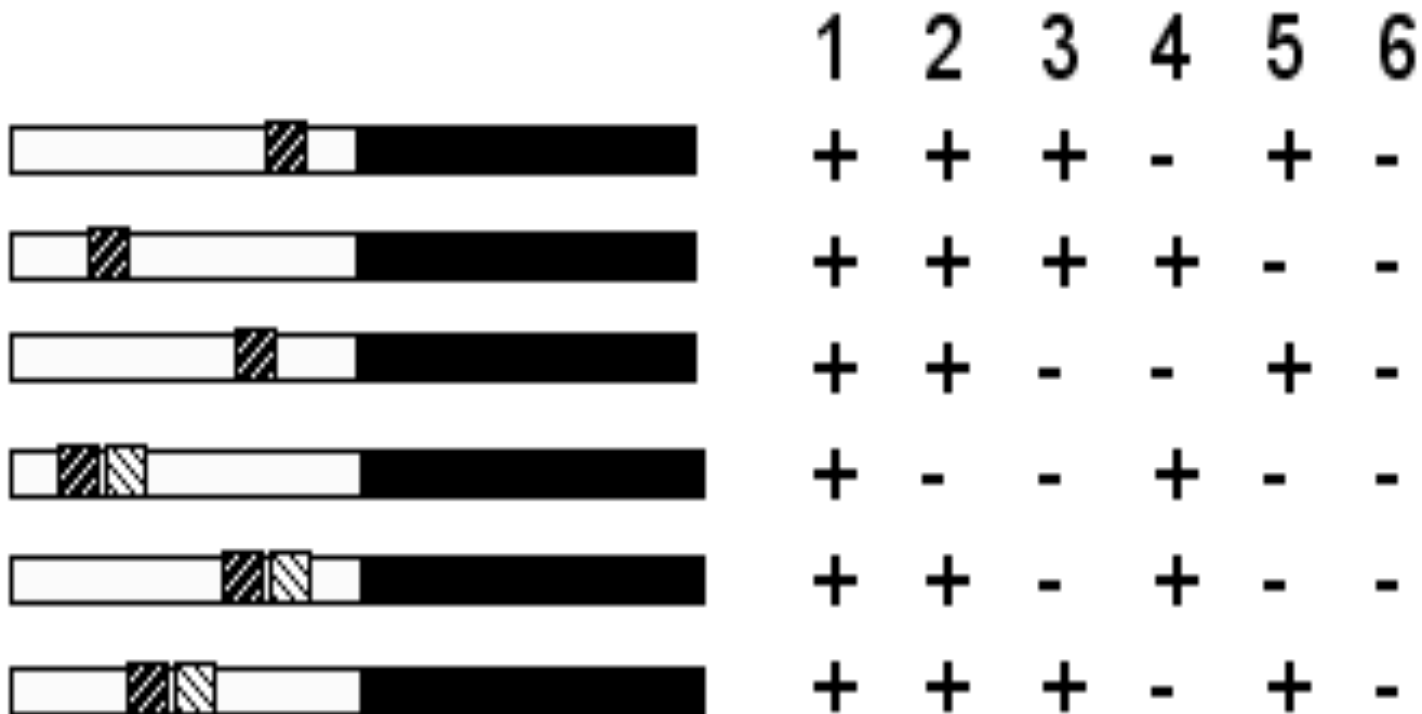
2S2D::p50-e1 *Nn*



2S2D::p50-g1 *Nn*



Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity



Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity

1. Step

732 PathoPlant database queries for genes
Upregulated more than twofold by
pathogen related stimuli

510 upregulated gene
groups identified

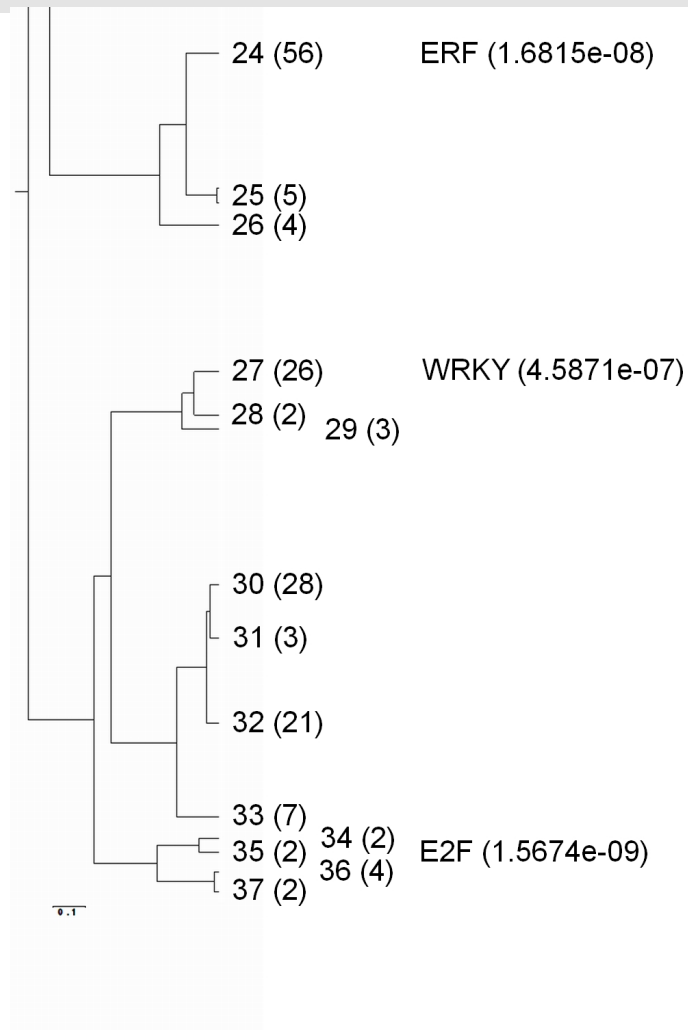
2. Step

Identification of conserved sequence motifs within
1,000 bp upstream sequence of 510 upregulated
gene groups using BEST

443 motifs identified



Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity

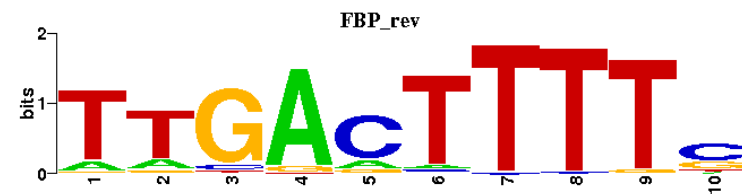


3. Step

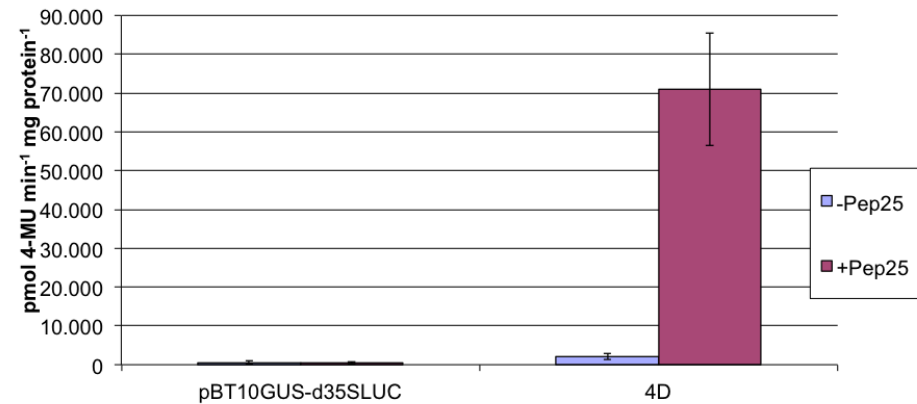
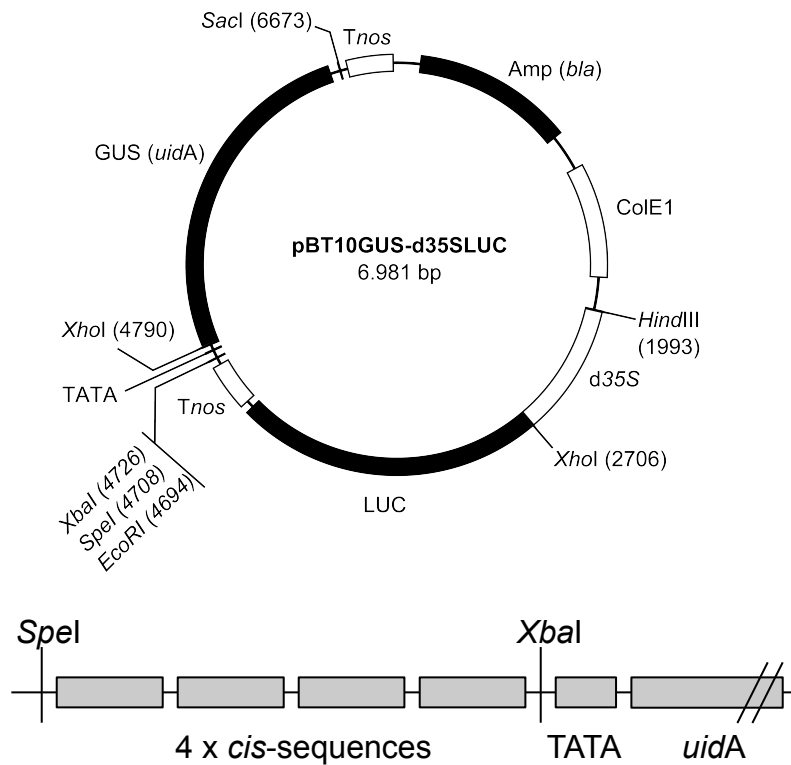
Motif classification using STAMP



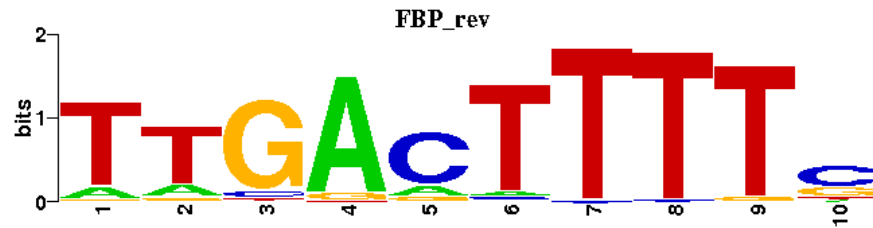
37 motif groups identified



Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity

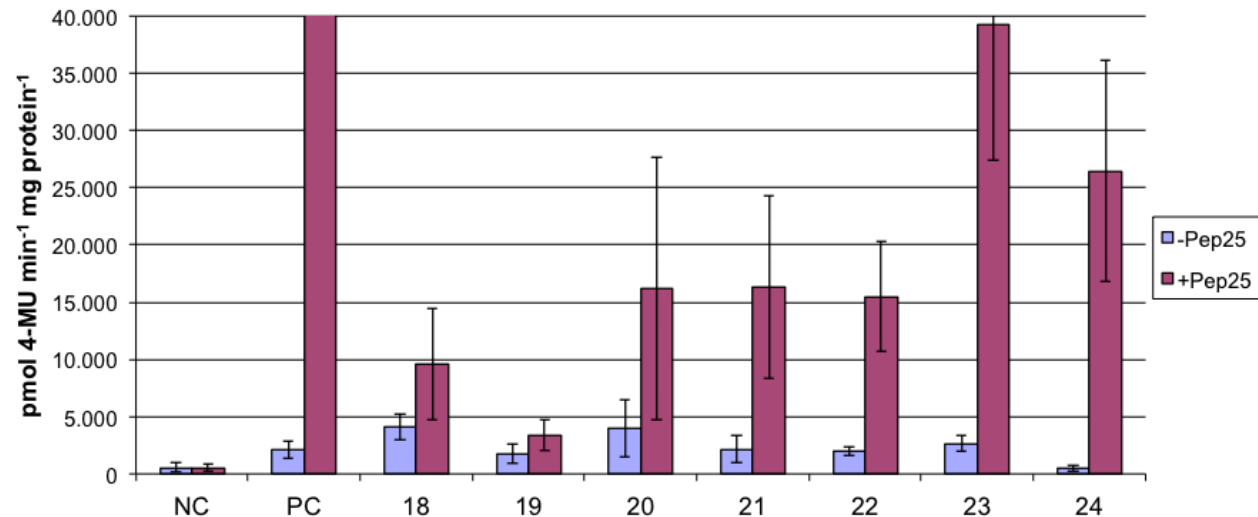


Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity



```

18   CTTCCCGATCAGACTTTTCTACGCAAGAGAAATTA
19       CGATCAGACTTTTCTACGCAAGAGAA
20   ACAACAGACGACTTTTCATAATTCA
21   TTTATGTTTGACTTTTGTTCATATAG
22   GAGAGAGATAGTTTGACTTTTGGACTGAAGAACGA
23   CTCAAAGAATACTTTTCAAAGTGAACA
24   TGGTCAGCATGTTGGACTTTCCAAATTCATTGACC
  
```

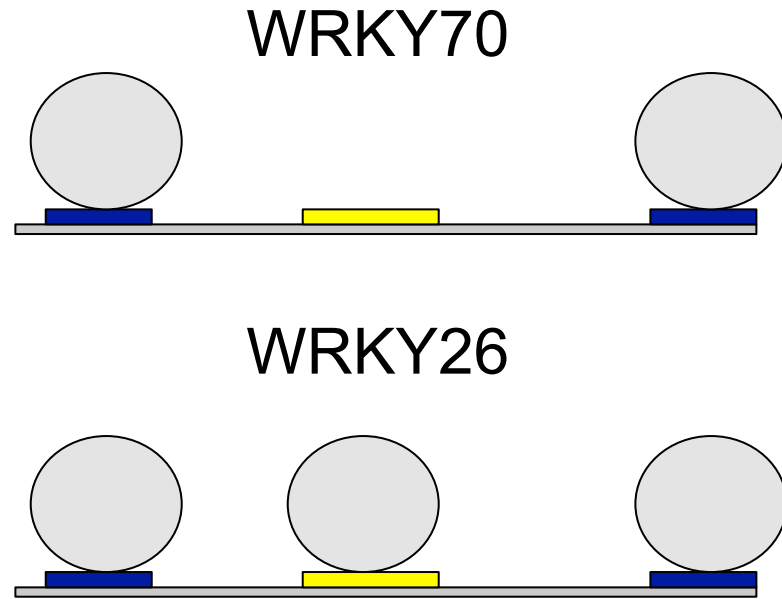
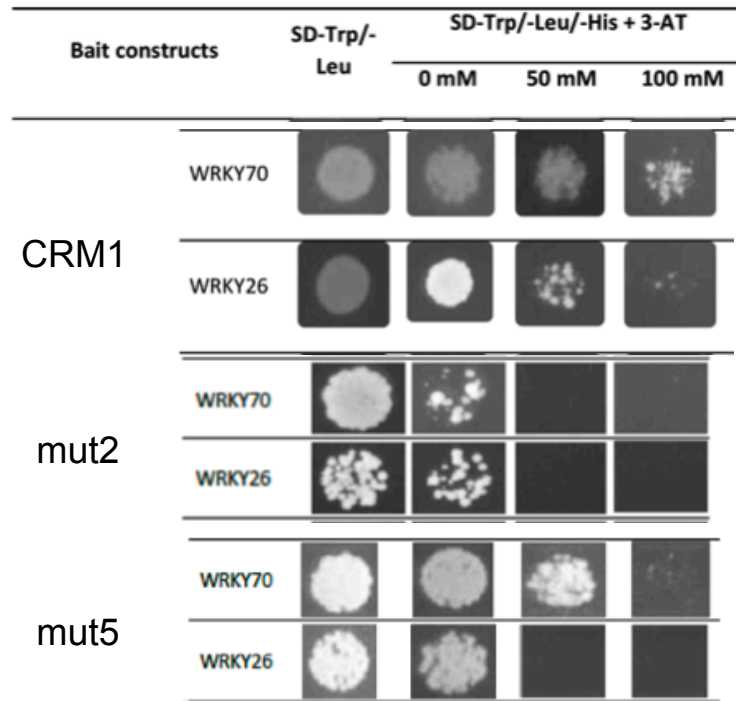


Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity

WT-box	Type	Binding TF
CGACTTTT	I	WRKY70
TGACTTTT	I	WRKY70
GGACTTTT	II	?
GGACTTTG	II	?
GGACTTTC	II	?



Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity

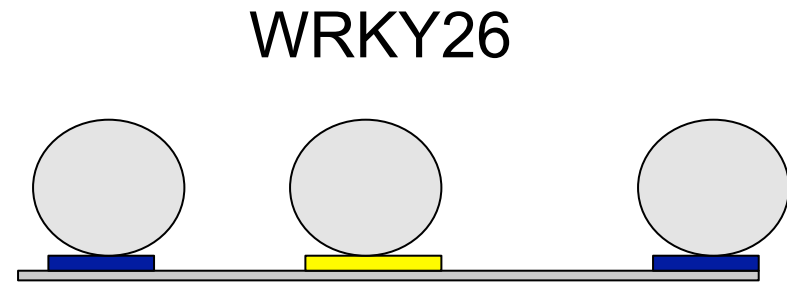
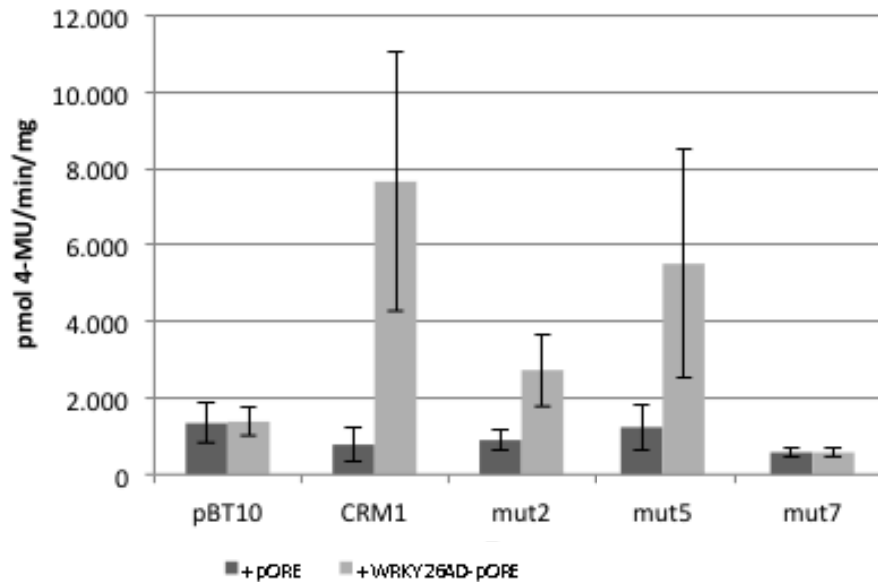


CRM1	<u>TGGTCAGCATGTTGGACTTTCCAAATTCATTGACC</u>
mut2	-AACTG-----CCAGTT
mut5	-----AAGTCCCTT-----

W-box
WT-box
W-box



Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity



CRM1	<u>TGGTCAGCATGTTGGACTTTCCAAATTCATTGACC</u>
mut2	-AACTG-----CCAGTT
mut5	-----AAGTCCCTT-----
mut7	-AACTG-----AAGTCCCTT-----CCAGTT

■	■	■
W-box	WT-box	W-box



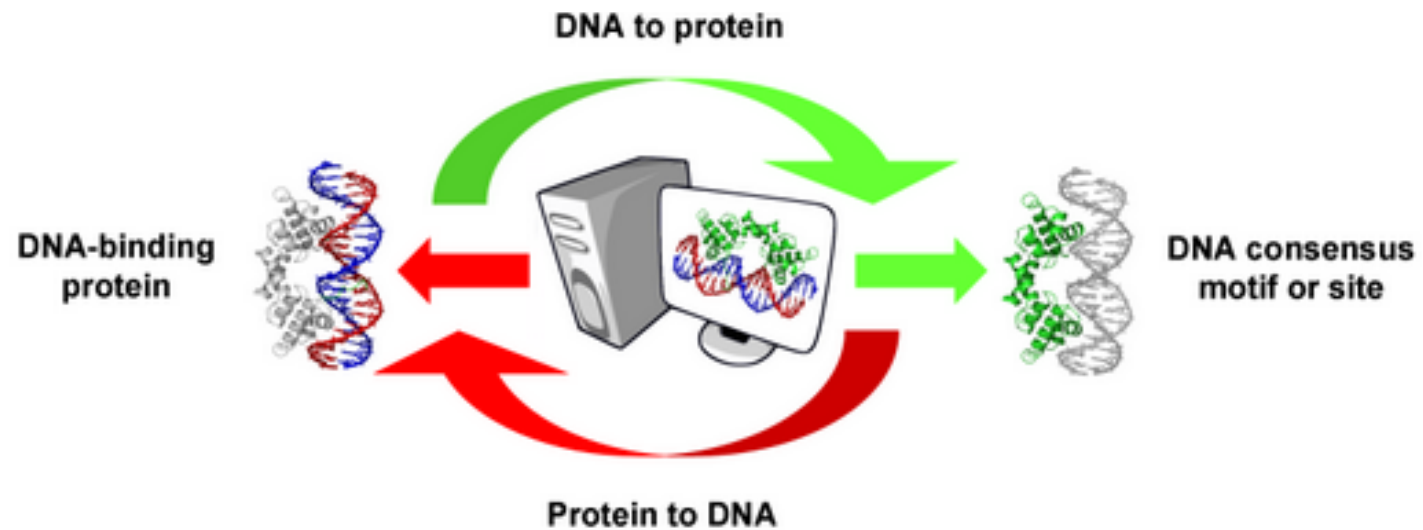
Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity

WT-box	Type	Binding TF
CGACTTTT	I	WRKY70
TGACTTTT	I	WRKY70
GGACTTTT	II	?
GGACTTTG	II	?
GGACTTTC	II	WRKY26



Bioinformatic Prediction of Type II WT-box Interacting Proteins

FootprintDB



[Start Search](#)

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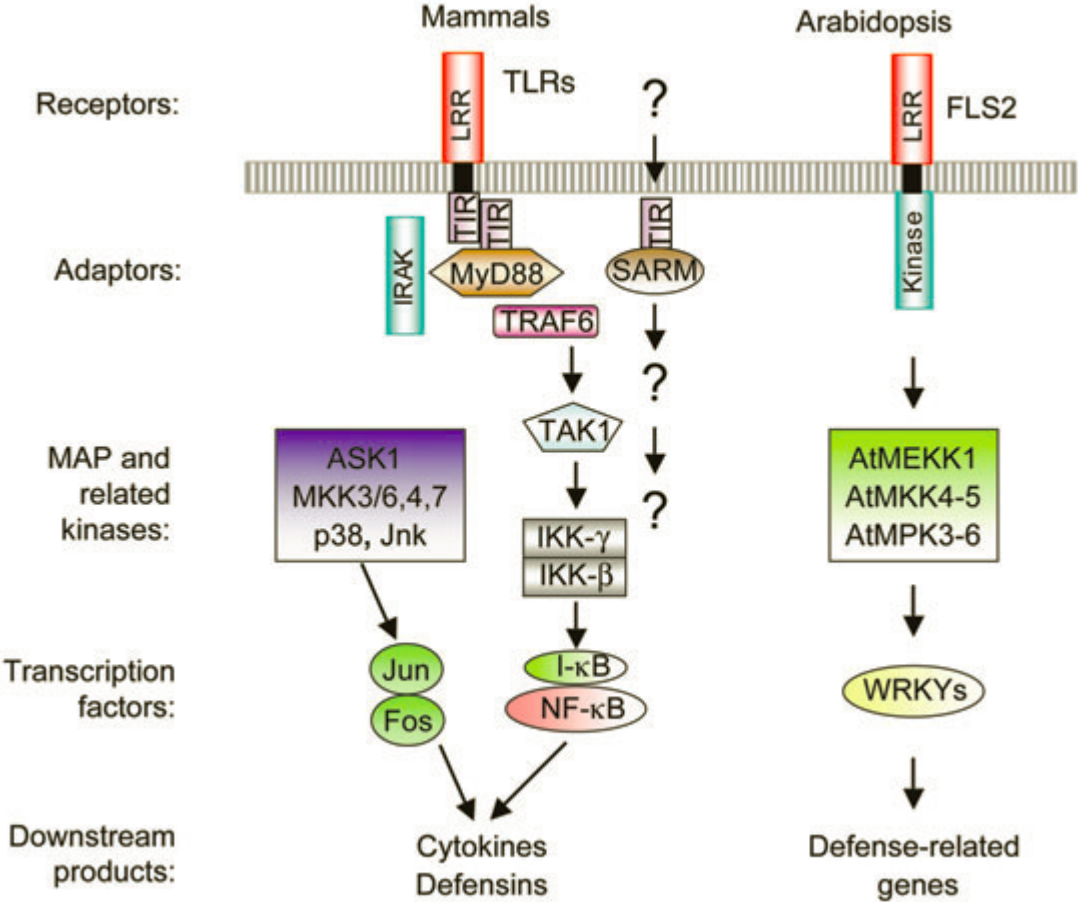


Bioinformatic Prediction of Type II WT-box Interacting Proteins

Query sequence	footprintDB template	Source	Organisms	STAMP e-value	Motif similarity	Query sequence / footprintDB PWM Consensus
GGACTTTC	1le9_AB: NF-κB p65	3D- footprint 20161221	Mus musculus	6.6e-13	8.00 / 8	GGACTTTC-- GGACTtTCct
GGACTTTT	1le9_AB: NF-κB p65	3D- footprint 20161221	Mus musculus	7.9e-09	7.00 / 8	GGACTTTT-- GGACTtTCct
GGACTTTG	1le9_AB: NF-κB p65	3D- footprint 20161221	Mus musculus	7.9e-09	7.00 / 8	GGACTTTG-- GGACTtTCct

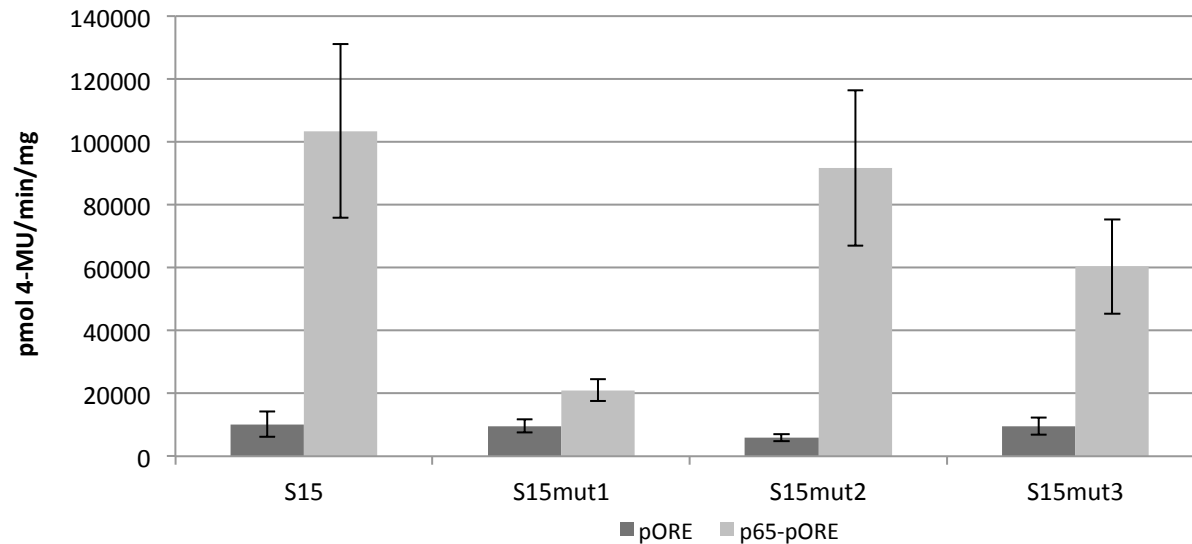


Bioinformatic Prediction of Type II WT-box Interacting Proteins



©Warren Photographic

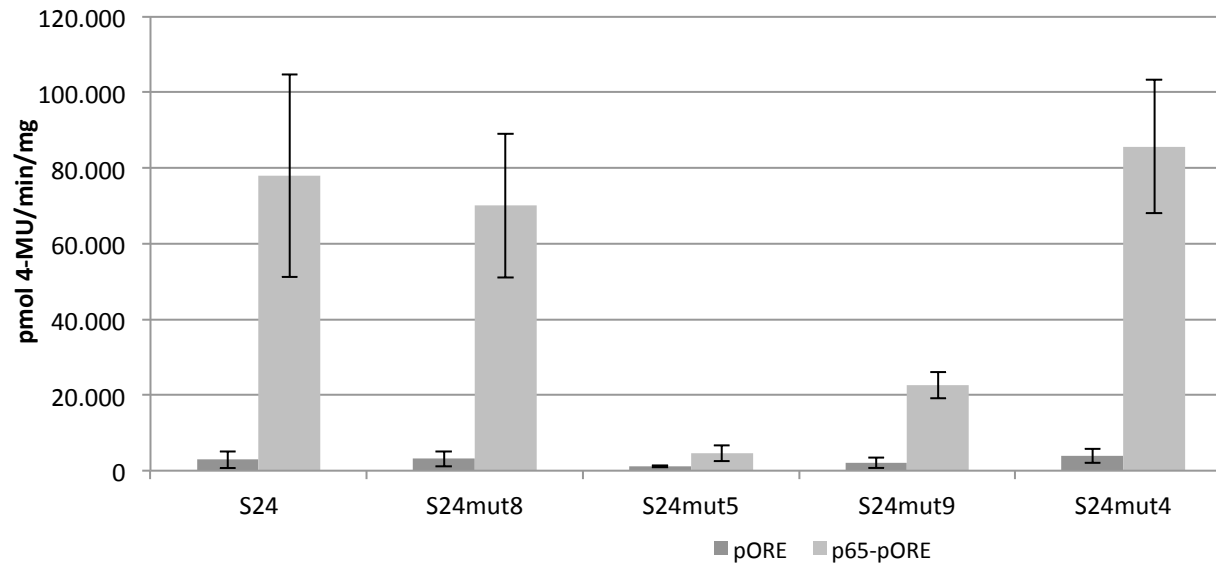
Bioinformatic Prediction of Type II WT-box Interacting Proteins



S15	<u>AGGACTTTTC</u> ACCAGTTGGACTTTGAAGCCACCAA
S15mut1	--AGTCCCC-----
S15mut2	-----TCTTCACCA-----
S15mut3	-----AGTCCCA-----



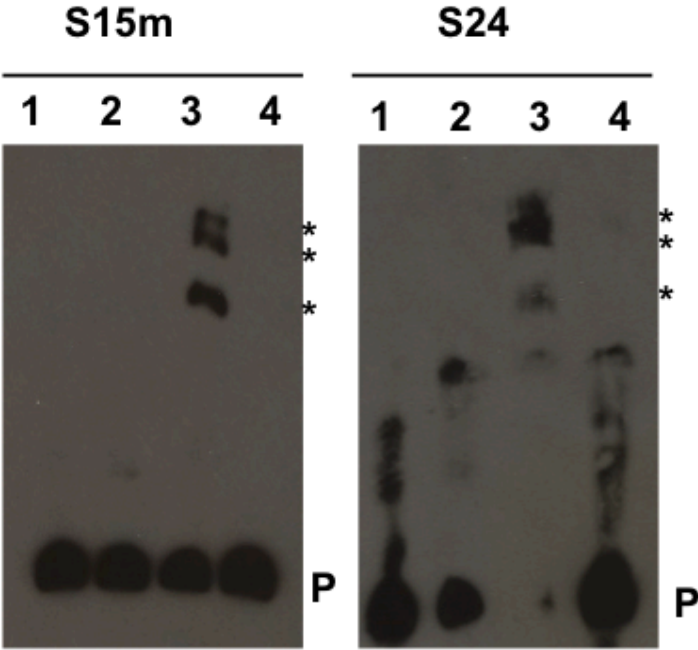
Bioinformatic Prediction of Type II WT-box Interacting Proteins



S24 TGGTCAGCATGTTGGACTTTCCAAATTCATTGACC
 S24mut8 -----ATGCACC-----
 S24mut5 -----AAGTCCCTT-----
 S24mut9 -----GGGCCTG-----
 S24mut4 -----CCAGTT-----



Bioinformatic Prediction of Type II WT-box Interacting Proteins



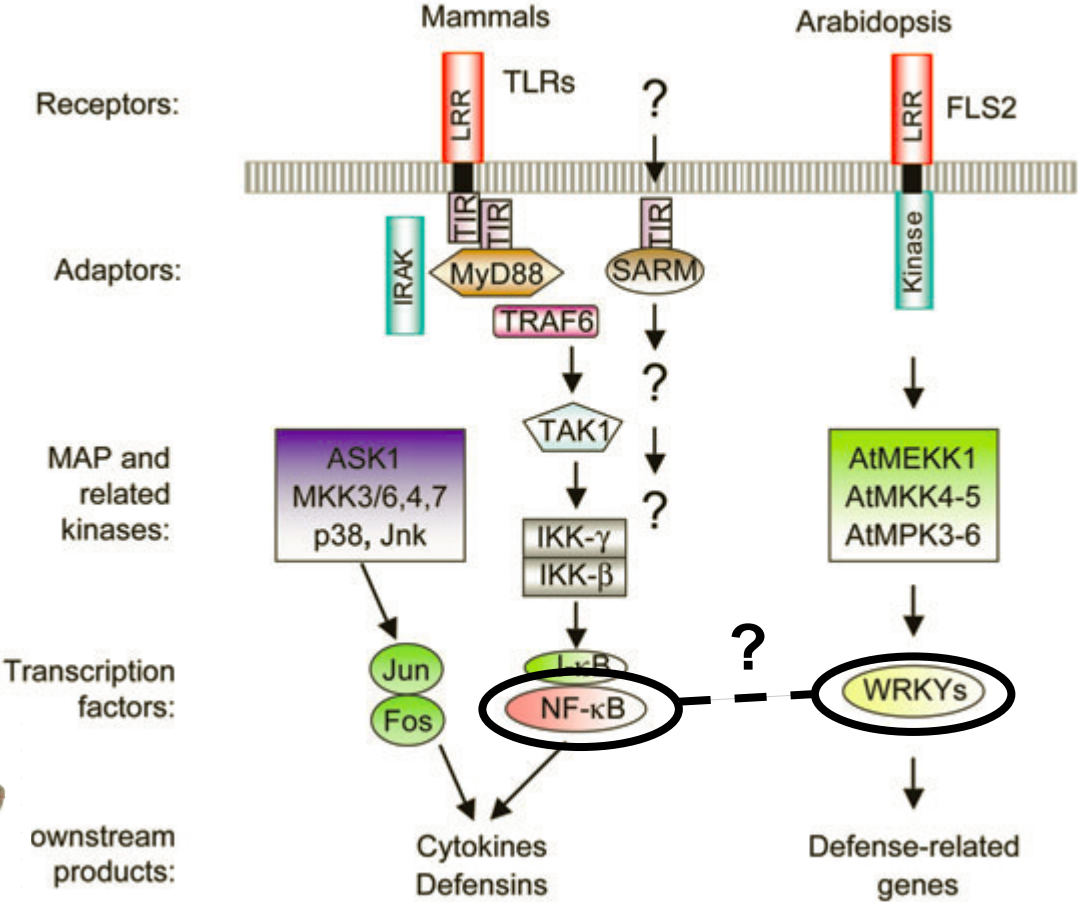
S15m AGGACTTTTCACCAGTTGGACTTTGGGATTGTTGG
 S24 TGGTCAGCATGTTGGACTTTCCAAATTCATTGACC

Identification of Novel *Cis*-Regulatory Sequences Involved in Plant Innate Immunity

WT-box	Type	Binding TF
CGACTTTT	I	WRKY70
TGACTTTT	I	WRKY70
GGACTTTT	II	NF- κ B p65
GGACTTTG	II	?
GGACTTTC	II	WRKY26 NF- κ B p65



Bioinformatic Prediction of Type II WT-box Interacting Proteins



Edgar's Post-Retirement Endeavour in Swakopmund, Namibia



Thank You

