

A proteomics approach to dissect *Stagonospora nodorum* effector mode-of-action in wheat

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Introduction

ToxA, the first effector identified in a necrotrophic fungus (*Pyrenophora tritici-repentis*)

1989

1990

1995

1997

1998

2000

2002

2004

2005

2007

2008

2009

2010

ptr necrosis toxin isolated in *P. tritici-repentis* (Ballance et al. 1989; Tomas et al. 1990).

Ptr ToxA = 13.2 kD secreted protein triggering necrosis at 60mM (Tuori et al. 1995)

Ptr ToxA gene cloned (Ciuffetti et al. 1997)

activity requires host metabolism (Kwon et al. 1998).

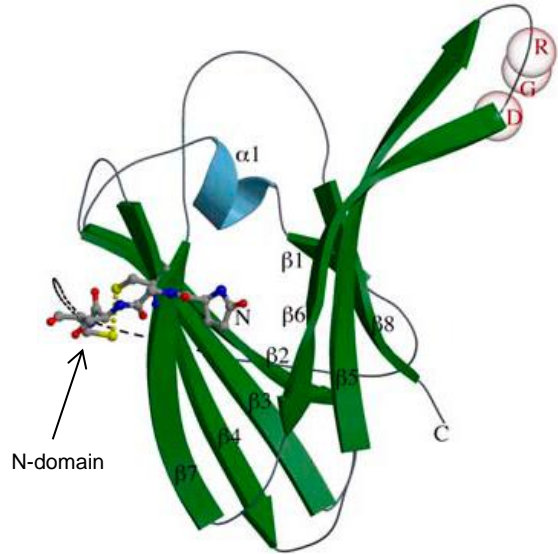
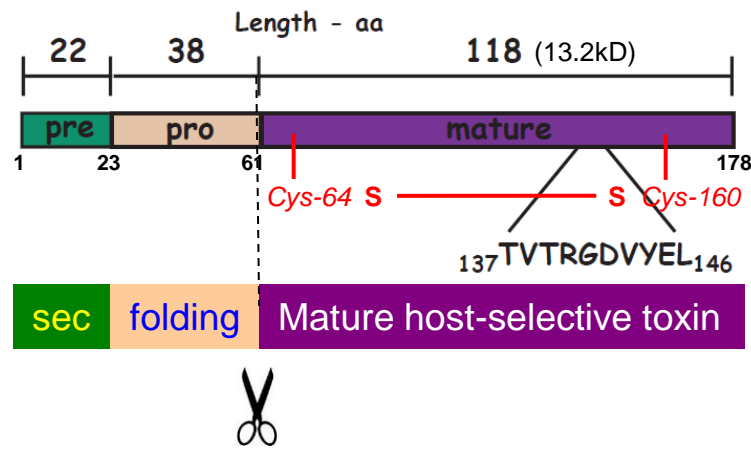
Cys64-Cys160 (Tuori et al. 2000)
RGD (Meinhardt et al. 2002)
CK2-like & vitronectin-like (Manning et al. 2004).

crystallography structure (Sarma et al. 2005).
internalised by sensitive wheat cells only (Manning et al. 2005).

internalisation through RGD motif (Manning et al. 2008). Targets chloroplast, binds to ToxABP1 (Manning et al. 2007) and PC (Tai et al. 2007).

ROS accumulation and PS alteration (Manning et al. 2009)

ToxA alters ToxABP1 function (Manning et al. 2010).



Tsn1-mediated host responses to ToxA from *Pyrenophora tritici-repentis*.

Adhikari TB, Bai J, Meinhardt SW, Gurung S, Myrfield M, Patel J, Ali S, Gudmestad NC, Rasmussen JB

MPMI 2009, 22 (9): 1056-68

Time course: 0, 0.5, 4, 12, 24, 48 hpi

Affymetrix GeneChip
Wheat Genome Array

Induction of signalling events and lignification, and production of reactive oxygen species

Analysis of transcriptome changes induced by Ptr ToxA in wheat provides insights into the mechanisms of plant susceptibility.

Pandelova I, Betts MF, Manning VA, Wilhelm LJ, Mockler TC, Ciuffetti LM

Molecular Plant 2009, 2 (5): 1067-83

Time course: 0, 3, 9, 14 hpi

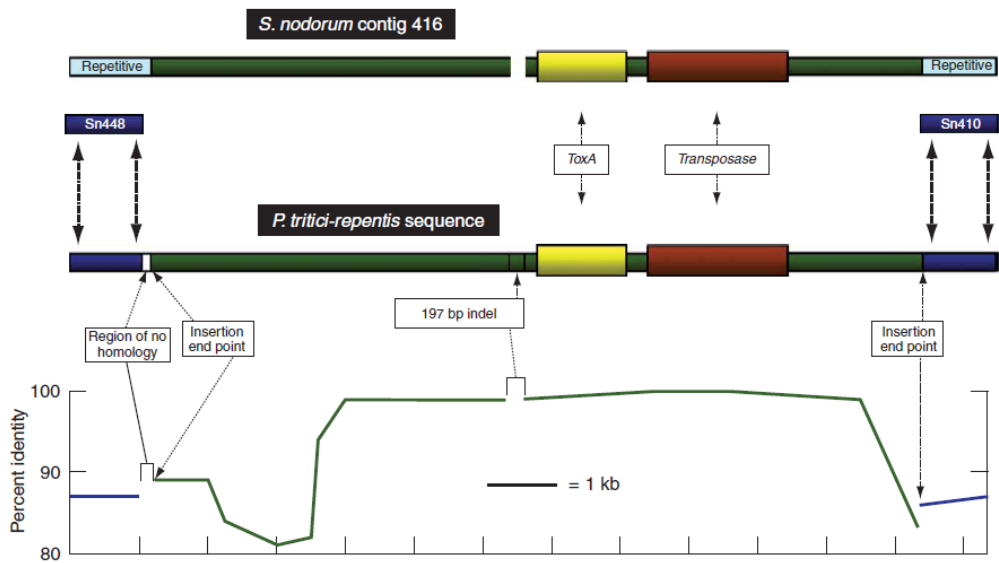
Affymetrix GeneChip
Wheat Genome Array

Impairment of the photosynthetic machinery and accumulation of reactive oxygen species

SnToxA/Tsn1: the wheat susceptibility gene

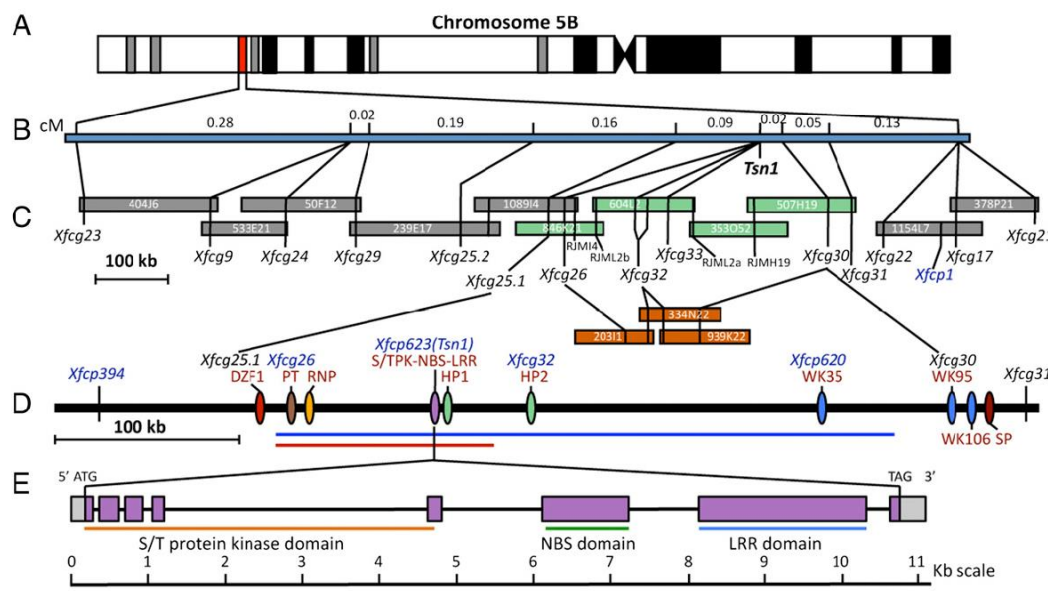
2006

Stagonospora nodorum closely related to *P. tritici-repentis*.
ToxA exists in *S. nodorum* (SnToxA) and is 99.7% similar to Ptr ToxA.
Ptr ToxA was acquired from SnToxA through HGT (Friesen et al. 2006).

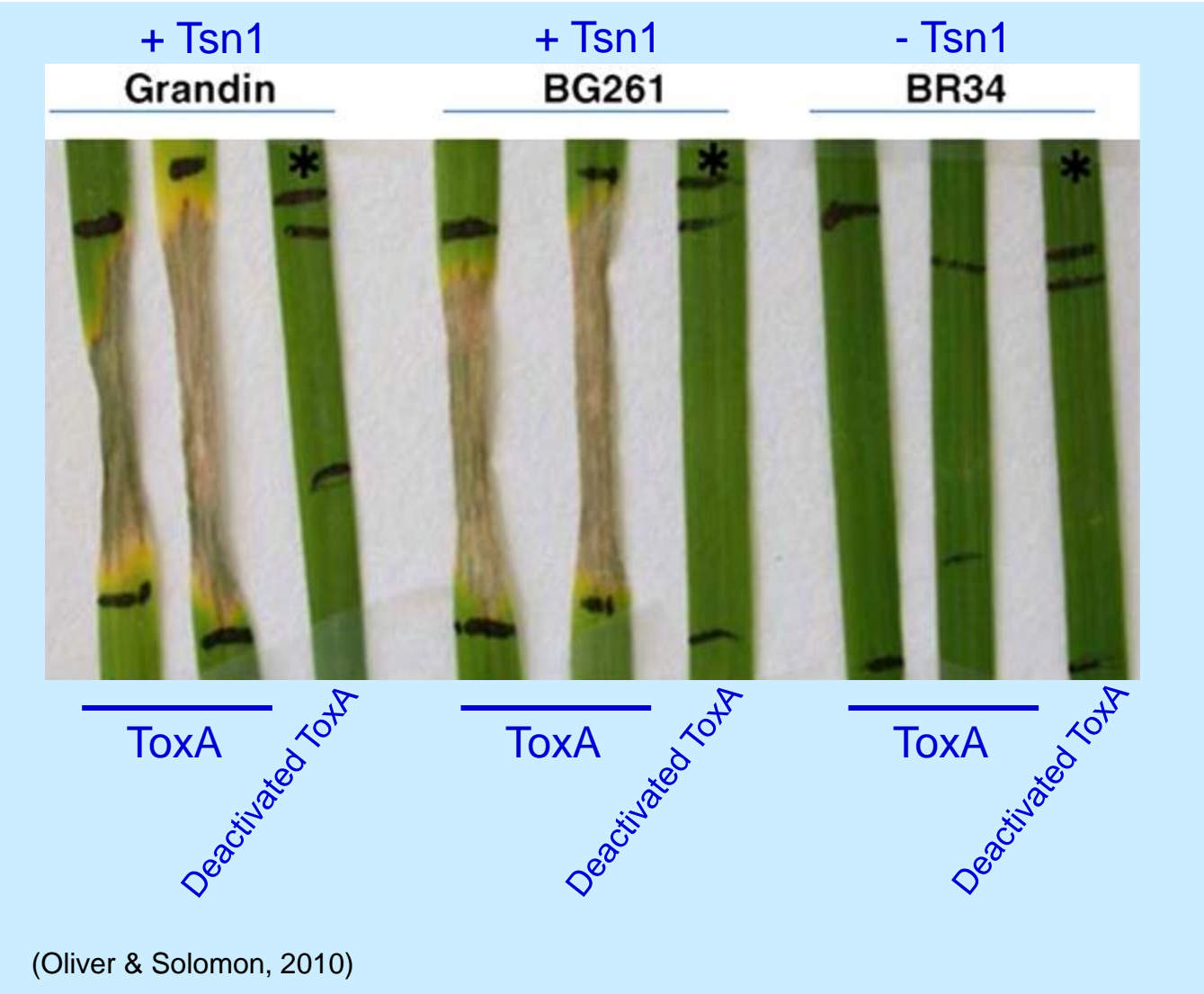


2010

Tsn1 gene cloned (Faris et al. 2010).
-located on chromosome 5BL
-features of a R gene
-not a receptor of ToxA



ToxA/Tsn1: inverse gene-for-gene system, *i.e.* Effector Triggered Susceptibility (ETS)



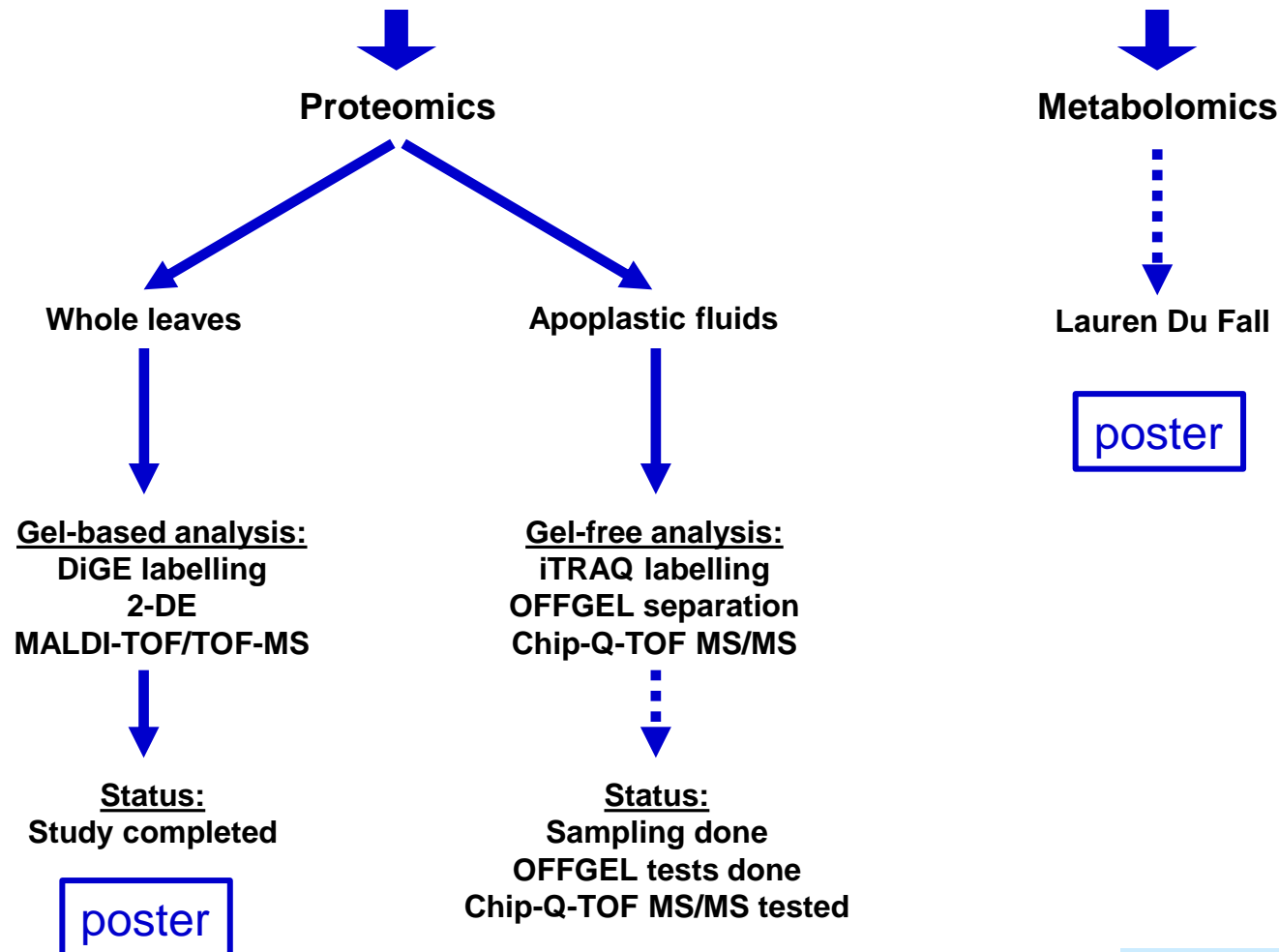


Strategy

Hypothesis: SnToxA infiltration triggers defence responses in wheat leaves.



Strategy: Post-genomics to unravel the post-transcriptional regulations

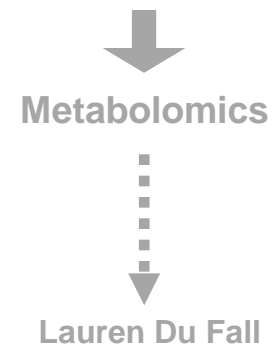
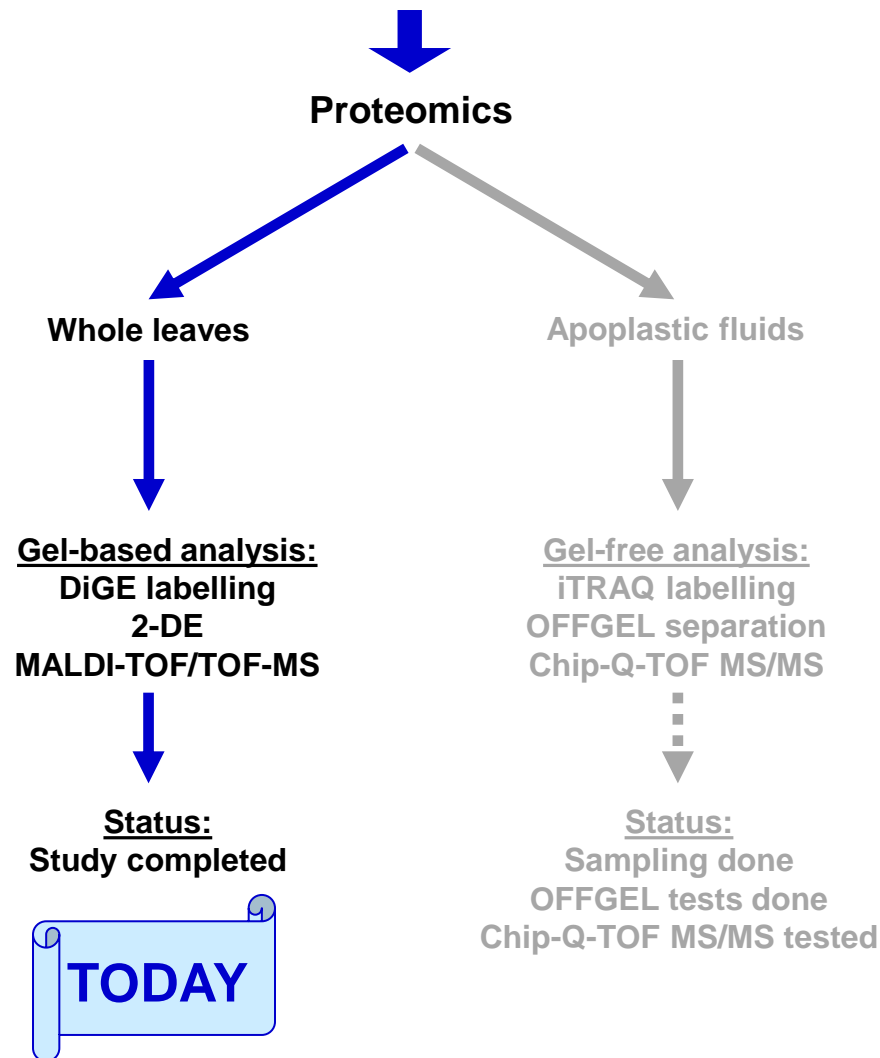


Proteome=set of all proteins
Metabolome=set of all metabolites

Hypothesis: SnToxA infiltration triggers defence responses in wheat leaves.



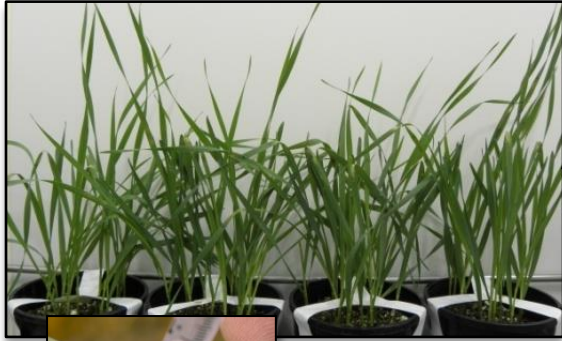
Strategy: Post-genomics to unravel the post-transcriptional regulations





Materials

Flowchart of the experimental design for gel-based proteomics



Plant culture (*T. aestivum* cv. BG261) & leaf infiltration in growth room



Post-infiltration leaf sampling over time course:

2 treatments (H_2O , ToxA)



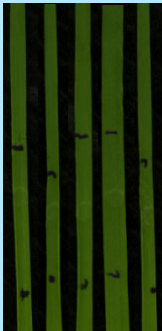
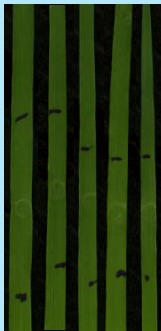





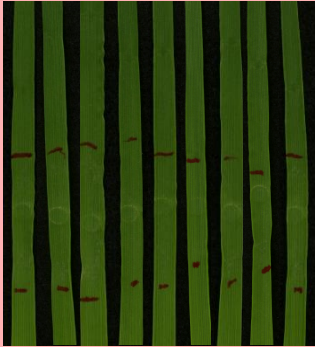
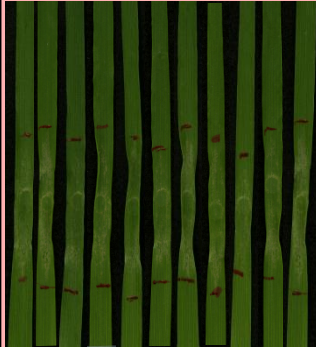
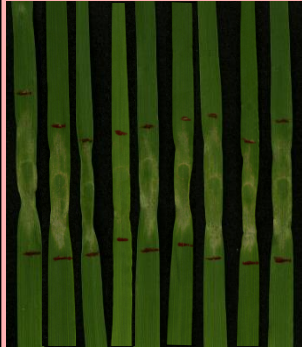
6 time points (0, ½, 4, 12, 24, and 48h) (Adhikari et al. 2009)

3 biological replicates (1BL=pool of 10 leaves)

→ 36 samples



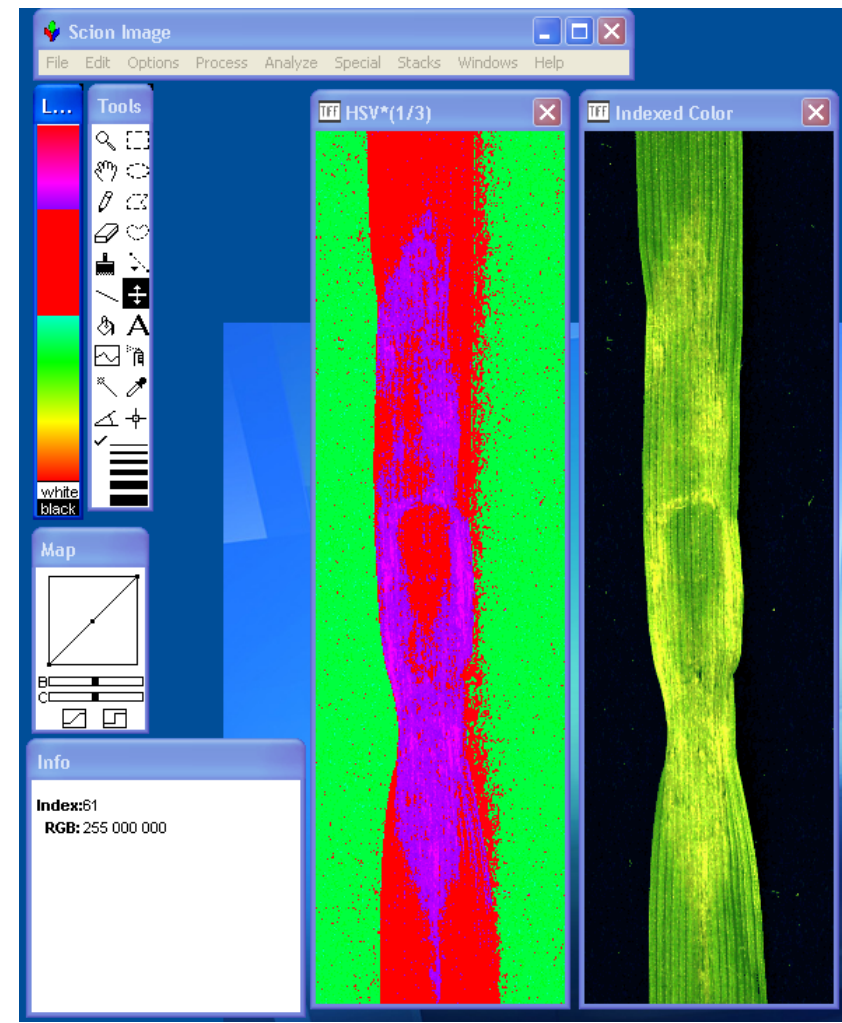
Quantitation of ToxA symptoms

| 0.5h | 4h | 12h | 24h | 48h | 72h |
|--|---|---|---|---|---|
| <div>H2O</div>  |  |  |  |  |  |
| <div>ToxA</div>  |  |  |  |  |  |

Gradual appearance of the symptoms.
Obvious yet subtle chlorosis/necrosis after 48h.
Tissues not too damaged for protein extraction.

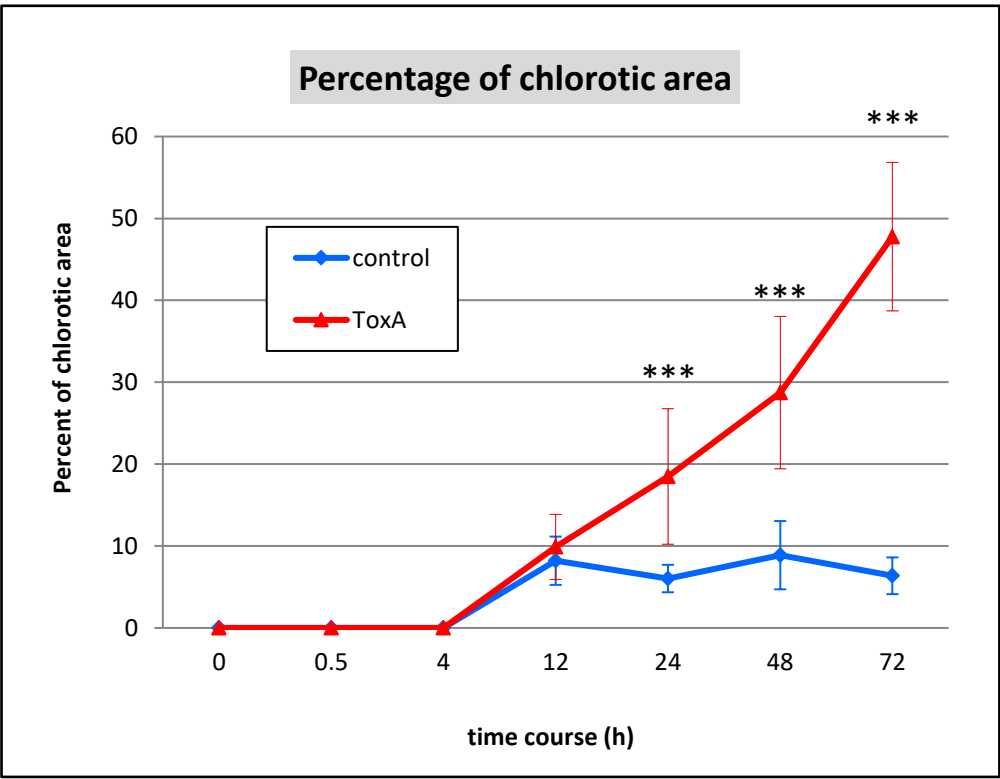


Quantitation of ToxA symptoms



Quantifying fungal infection of plant leaves by digital image analysis using Scion image software.

Wijekoon CP, Goodwin PH, Hsiang T.
J Microbiol Meth 2008, 74:94-101



Accurate quantitation of symptoms.
Infiltration damage starts to be visible after 12h and is stable over time (blue curve).
ToxA symptoms become noticeable after 24h and steadily worsen (red curve).



Methods

Flowchart of the experimental design for gel-based proteomics



Plant culture (*T. aestivum* cv. BG261) & leaf infiltration in growth room



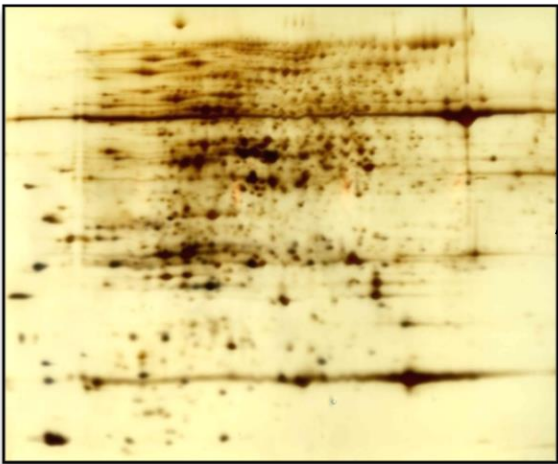
Post-infiltration leaf sampling over time course:
2 treatments (H₂O, ToxA)
6 time points (0, ½, 4, 12, 24, and 48h) (Adhikari et al. 2009)
3 biological replicates (1BL=pool of 10 leaves)
→ 36 samples



Extraction of soluble proteins



Protein abundances determined using 2-DE



| | Acidic proteins | Basic proteins |
|--------------|------------------|----------------|
| Samples | 36 | 12 (24/48h) |
| Protein load | 0.1 mg | 0.5 mg |
| pH range | 4-7 | 7-10 |
| Labelling | DiGE minimal kit | none |



Differentially-regulated proteins analysed using statistical analyses

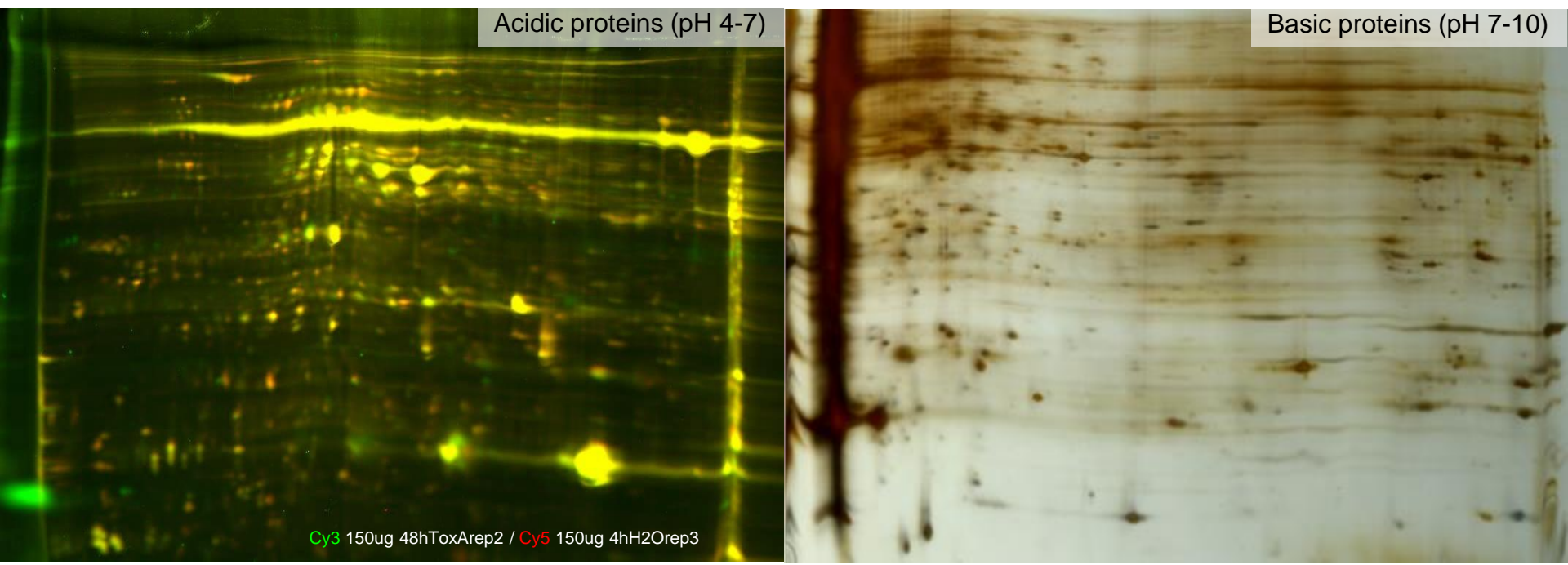


Identification of significant spots by mass spectrometry (MS)



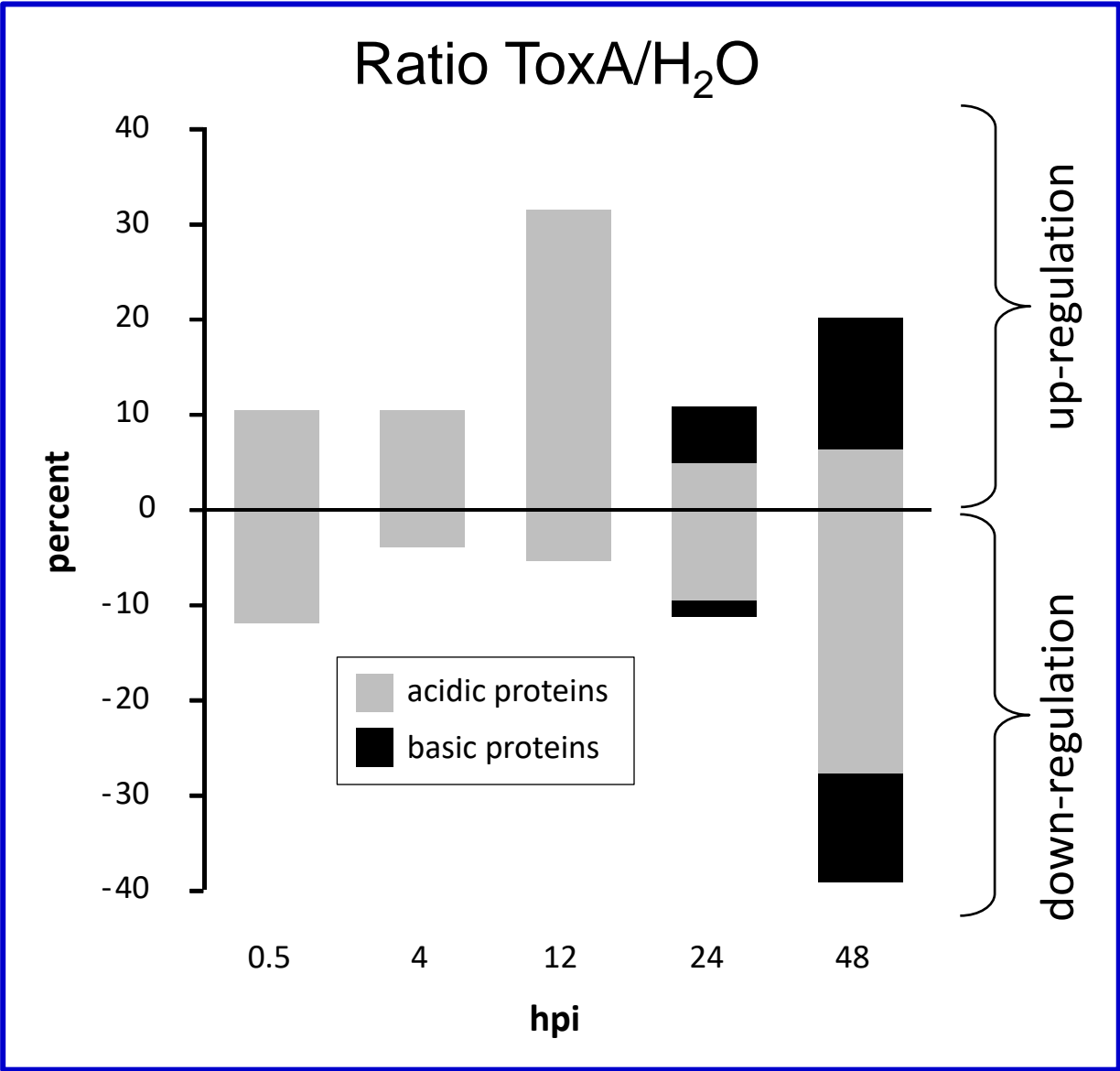
Results

Proteomic analysis using two-dimensional electrophoresis



| | Acidic range | Basic range | TOTAL |
|-------------------------------------|--------------|-------------|---------------|
| Detected spots | 1070 | 530 | 1600 |
| Significant spots (2-way ANOVA) | 294 | 72 | 366 |
| Identified spots (MS/MS) | 70/76 | 40/54 | 110/130 |
| Unique description | 46 | 38 | 81 (3 shared) |
| Unknown | 10 | 6 | 16 |
| Chloroplastic (ChloroP, literature) | 57 | 18 | 75 |

Protein expression profiling



Most of the differences occur at 48 hpi.

Main trend:
- induction at 12 hpi
- repression at 48 hpi

Comparison with other pathosystems

► wheat leaves infected with *Puccinia triticina* (Rampitsch et al., 2006):

14-3-3 proteins,
peptidyl-prolyl cis-trans isomerases,
elongation factors 1b,
70 kD heat shock proteins,
Cp31BHv nucleic acid-binding proteins,
cytosolic triosephosphate isomerase.

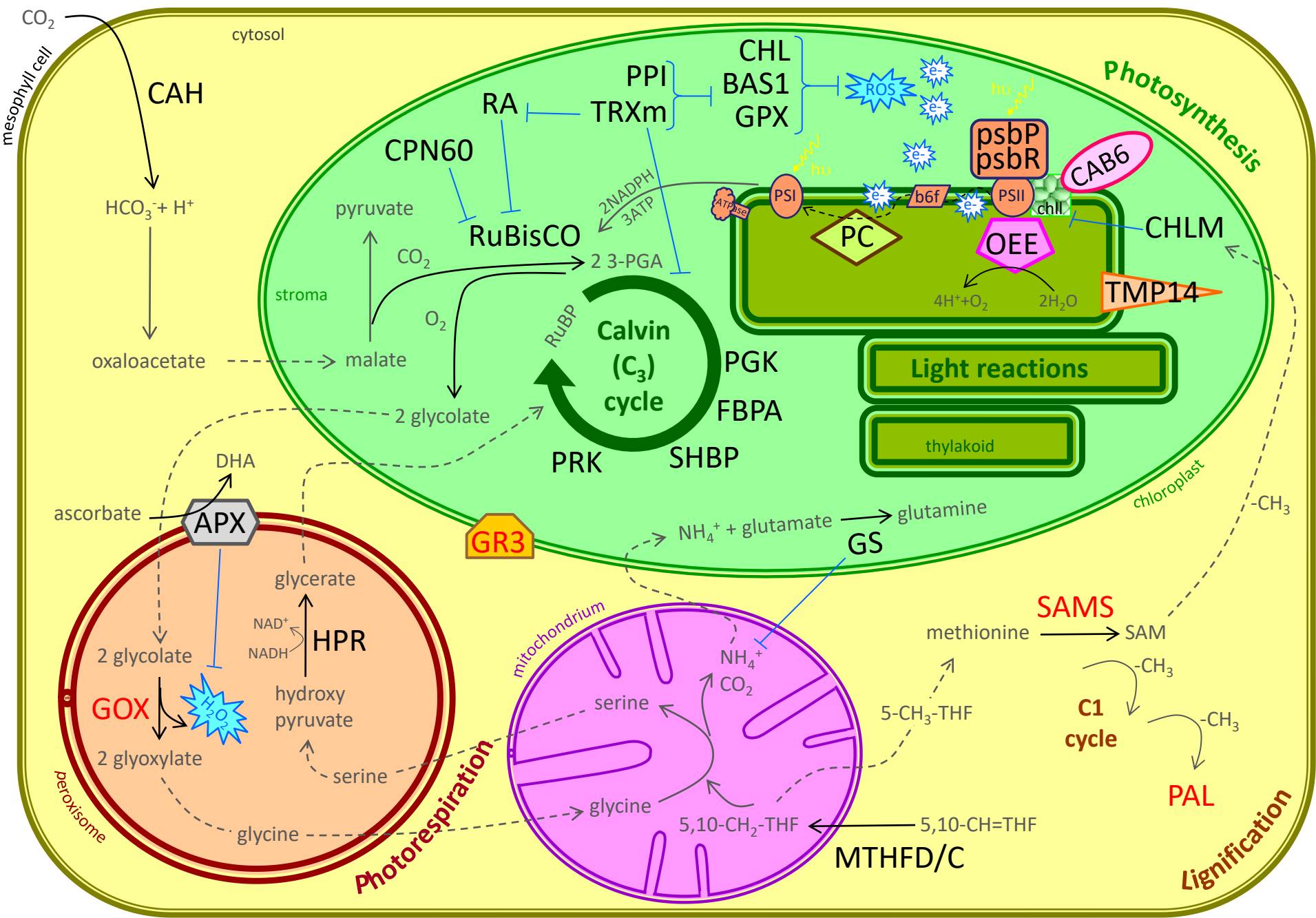
► wheat spikes infected with *Fusarium graminearum* (Wang et al., 2005; Zhou et al., 2006; Dornez et al., 2010):

90 kD heat shock proteins,
thioredoxin m,
ascorbate peroxidase,
RuBisCO,
RuBisCO activase,
fructose-bisphosphate aldolase

The induction of host proteins interacting with fungal components in our system which lacks the pathogen highlights the ability of SnToxA to tricking the host in believing in a pathogen attack and initiating a hypersensitive response (HR) leading to cell death.

HR would be mediated by an early antioxidant mechanism (within 24h) and a late PR-protein induction as well as photosynthesis and photorespiration collapse (at 48 hpi).

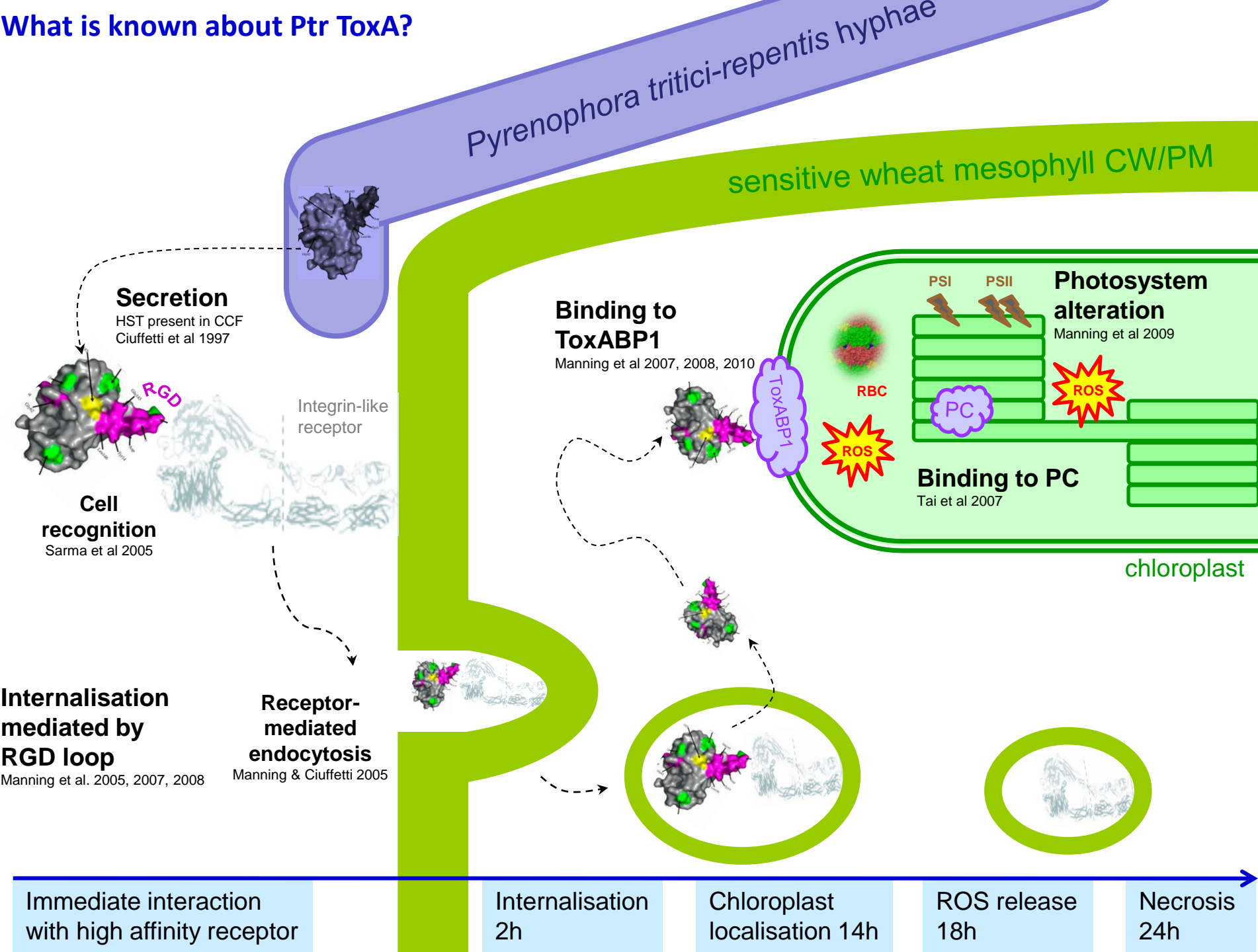
Putative roles of ToxA-responsive proteins in wheat mesophyll cells



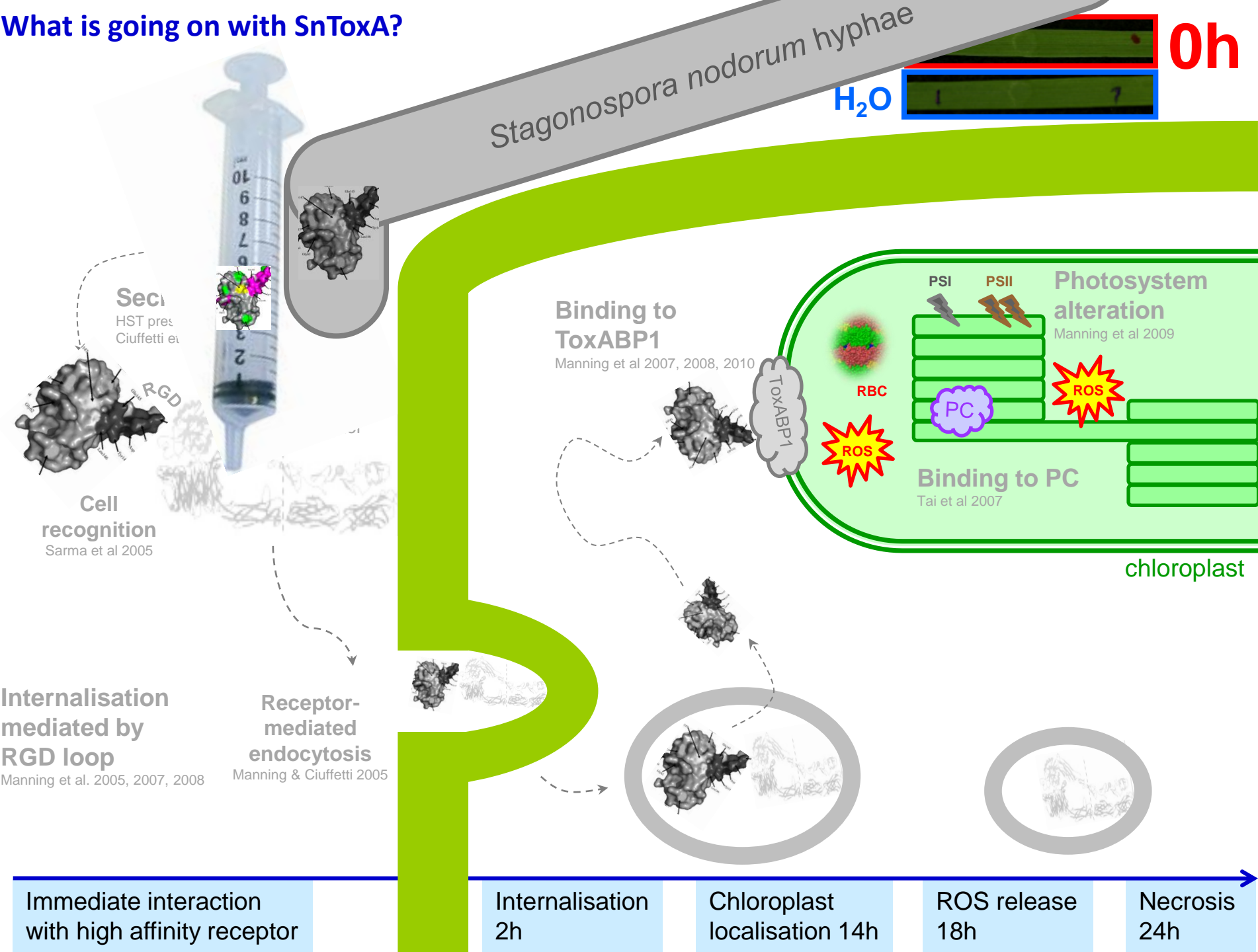


Working model

What is known about Ptr ToxA?

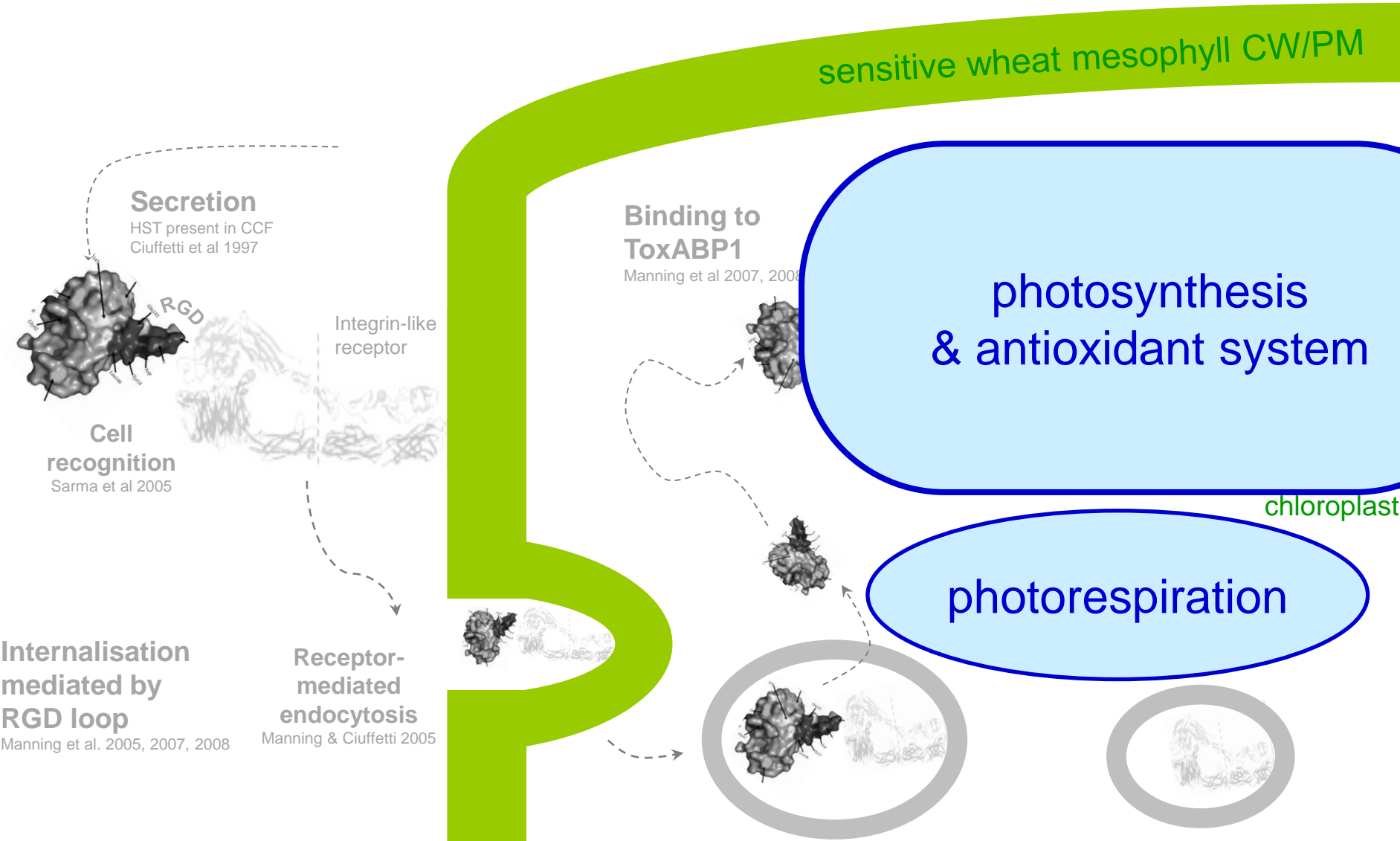


What is going on with SnToxA?



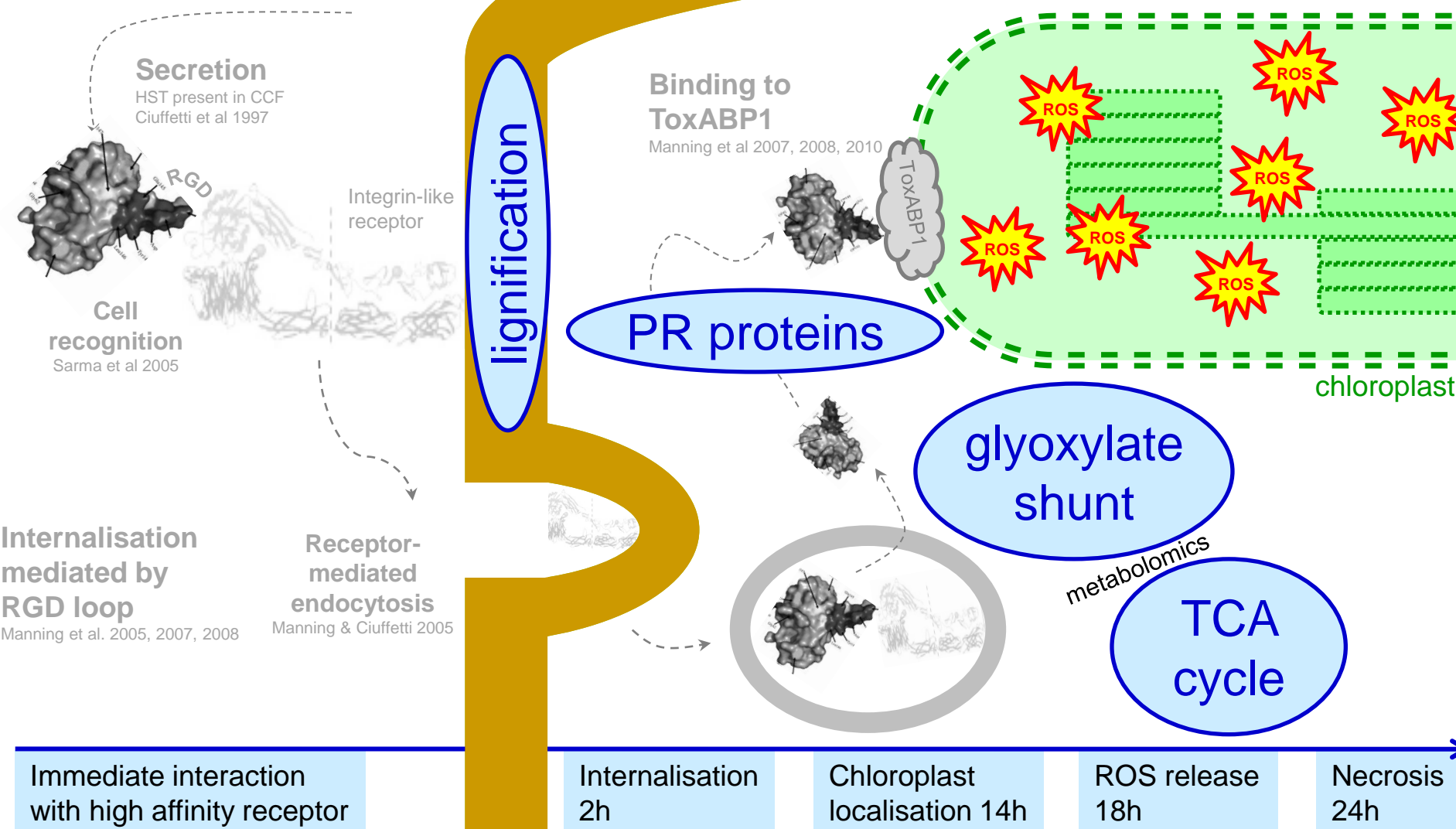
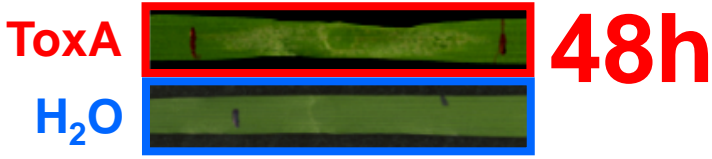
What is going on with SnToxA?

ToxA  **12h**
H₂O 



| Immediate interaction with high affinity receptor | Internalisation 2h | Chloroplast localisation 14h | ROS release 18h | Necrosis 24h |
|--|-----------------------|---------------------------------|--------------------|-----------------|
|--|-----------------------|---------------------------------|--------------------|-----------------|

What is going on with SnToxA?





Conclusions

Future directions



Proteomics + metabolomics (complementary techniques) complete the mode-of-action picture drawn from transcriptomics.

Another finding is that the drop in carbohydrate and ATP supplies due to photosynthesis collapse (proteomics) seems to be salvaged, to a limited extent, by enhanced TCA cycle and glyoxylate shunt (metabolomics).

This proof-of-concept study helped us establishing post-genomics techniques never used before in this system.

The same strategy will be applied to study the mode-of-actions of Tox3 and Tox1, other effectors of *S. nodorum*.



Australian
National
University

Thank you!

