Rust Fungal Effectors

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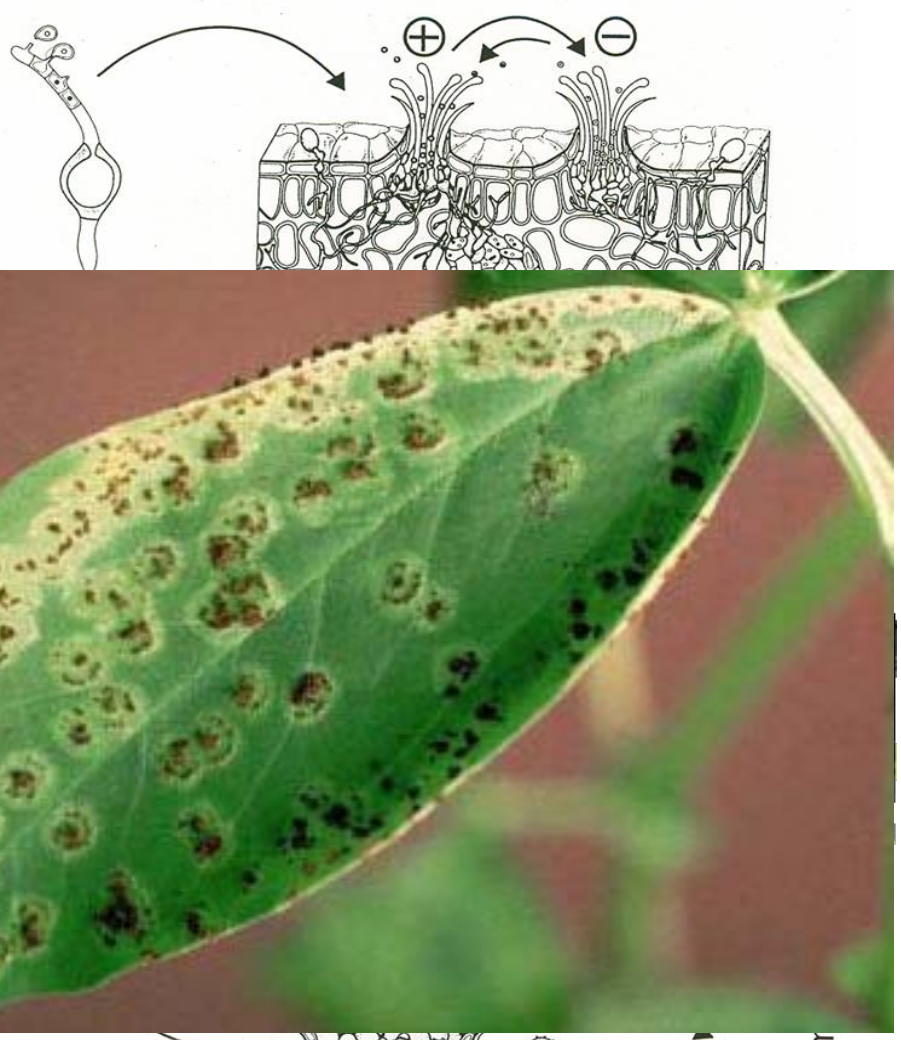
Rust fungi

- Biotrophic fungi
- Order Pucciniales:
  7.000 species
  - Genus *Puccinia* 4.000
  - Genus *Uromyces* 600
- Complex life cycle
- Mass propagation in uredial stage
  - Most investigated



Voegele (2006) FEMS-ML 259

Mendgen (1997) The Mycota V, Springer

Legume rusts studied

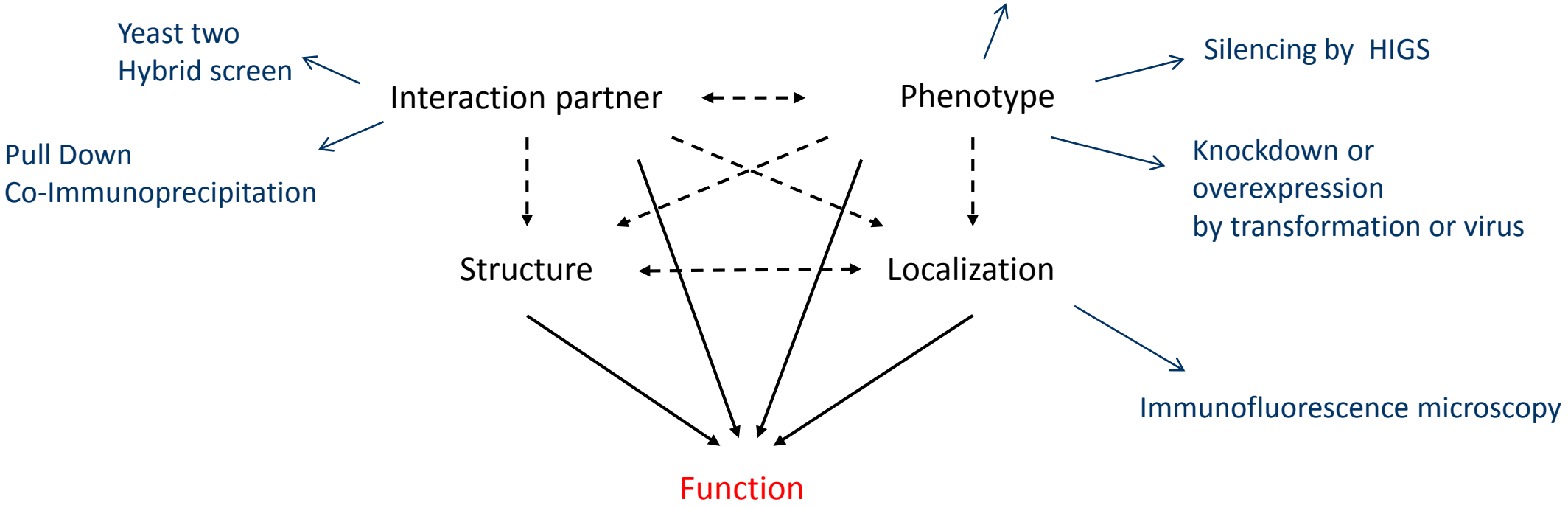
- *Phakopsora pachyrhizi*
  - Soybean rust, causing huge damages
  - Specialties: direct penetration of structures originating from urediospore, only urediospore stage known
  - Collaborations with USA and BCS
- *Uromyces appendiculatus*
  - Collaboration with USA
- *Uromyces fabae*
  - model species: nutrient uptake, carbohydrate metabolism, RTP

Others:

Puccinia striiformis, *Hemileia vastatrix*, …

Effectors

Precondition: Effector candidates are secreted proteins that are (or belong to gene families) specific to the rust lineage or a lower phylogenetic level.



Families of secreted proteins

- Collection of secreted proteins from *U. fabae*, *U. appendiculatus*, *P. pachyhizi*, and *Hemileia vastatrix*
- BLAST against respective protein collections
- BLAST against predicted proteins from genomes of *Puccinia graminis*, *P. striiformis*, *Melampsora larici-populina*, *M. lini*

➢ Collection of 17,272 proteins

- Clustering

➢ 694 clusters with 16,973 proteins

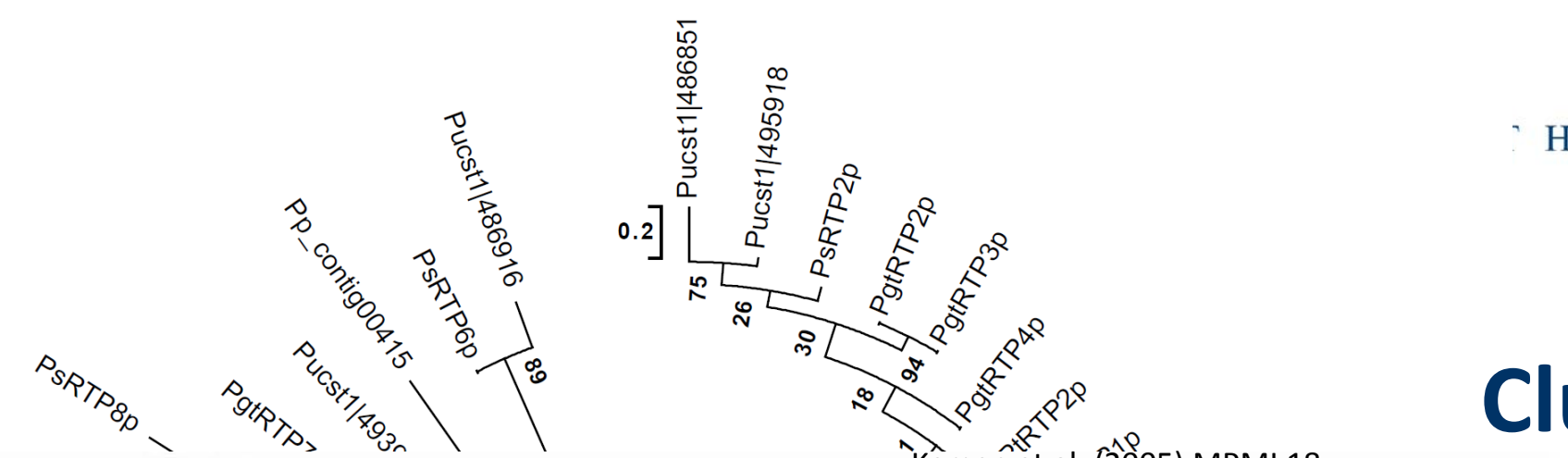
- BLAST against other basidiomycete species

➢ 230 clusters specific for rust fungi

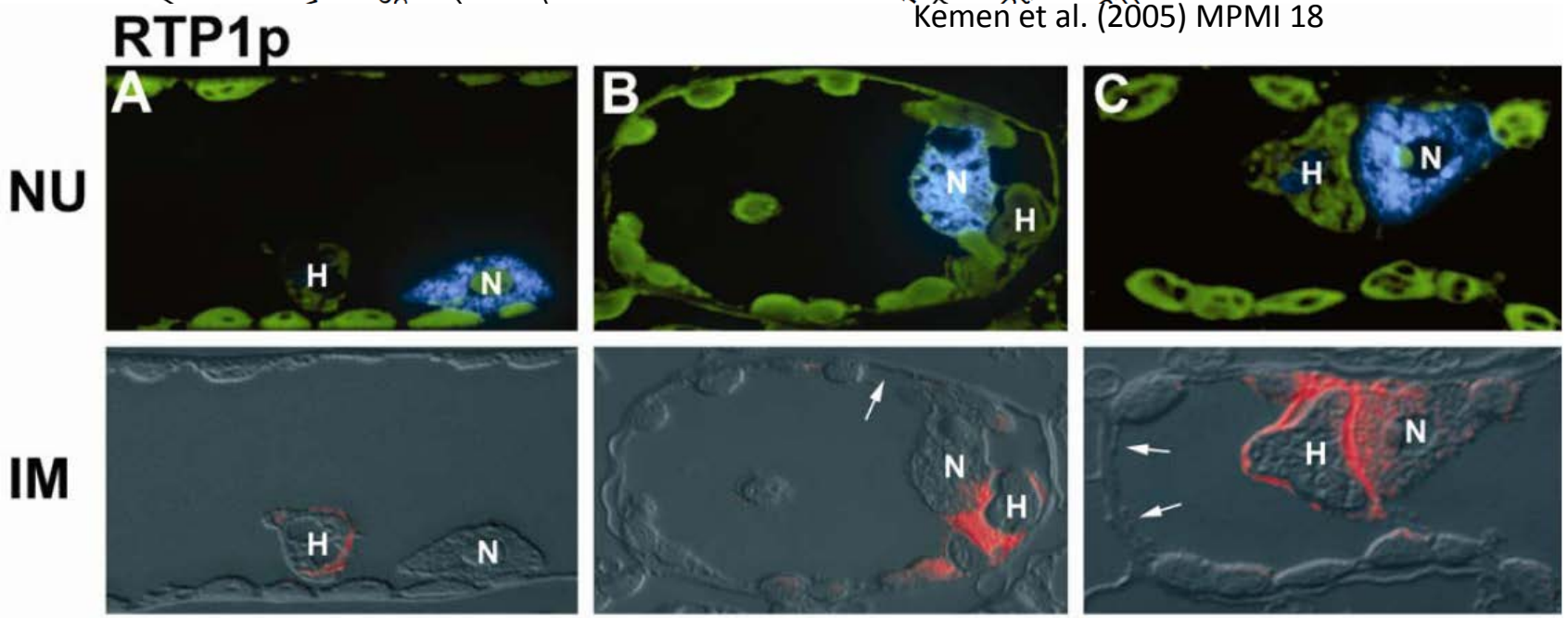
Cluster 99

-

RTP



Kemen et al. (2005) MPMI 18



nosporangium sabinae
ileia vastatrix
ampsora lini
ampsora larici-populina
ampsora medusae f. sp. *deltoides*
ampsora medusae f. sp. *tremuloides*
ampsora occidentalis
Puccinia coronata
Pgt: *Puccinia graminis* f. sp. *tritici*
Pp: *Phakopsora pachyrhizi*
Ps/Pst: *Puccinia striiformis*
Pt: *Puccinia triticina*
Ua: *Uromyces appendiculatus*
Uf: *Uromyces fabae*

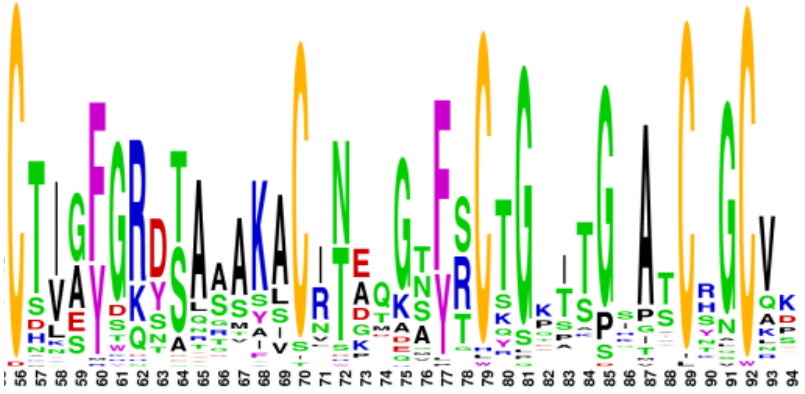
RTP1p forms aggregates *in vitro* and fibrils *in situ*

RTP1p has proteinase inhibitor function

Cluster 53 / 112

mostly short secreted proteins with a pattern of 10 conserved cysteines

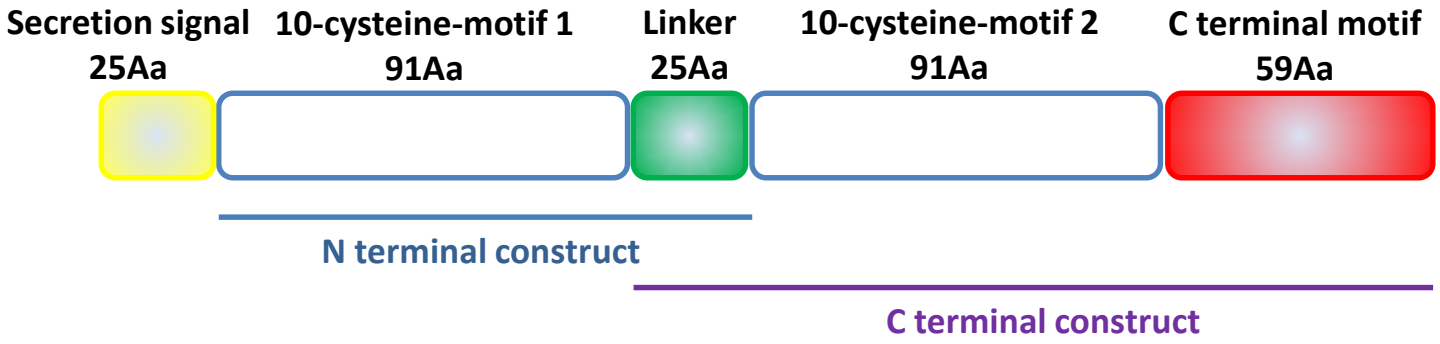
Hv:	*Hemileia vastatrix*
Melli:	*Melampsora lini*
Mellp:	*Melampsora larici-populina*
Pgt:	*Puccinia graminis* f. sp. *tritici*
Pp:	*Phakopsora pachyrhizi*
Pucst:	*Puccinia striiformis*
Ua:	*Uromyces appendiculatus*
Uf:	*Uromyces fabae*



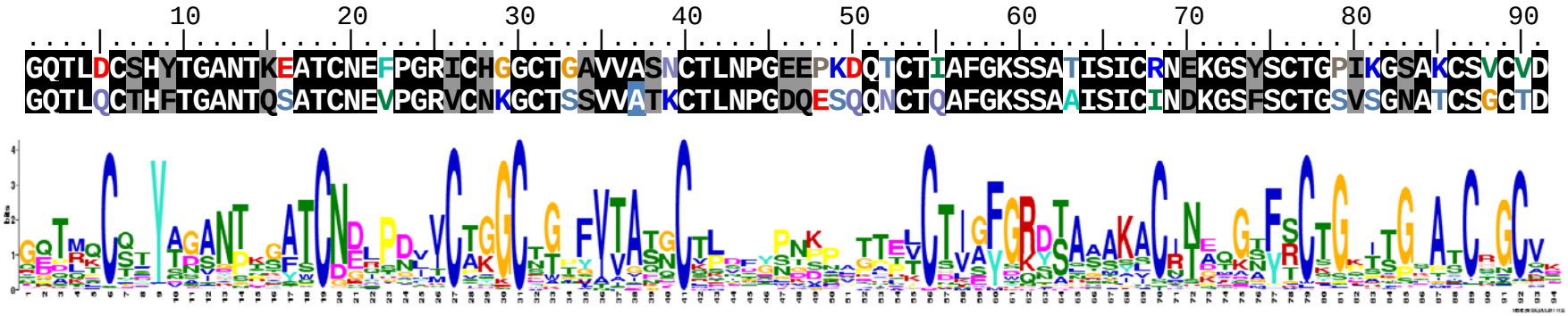
C

weblogo.berkeley.edu

PpEC23



10-cysteine-motif

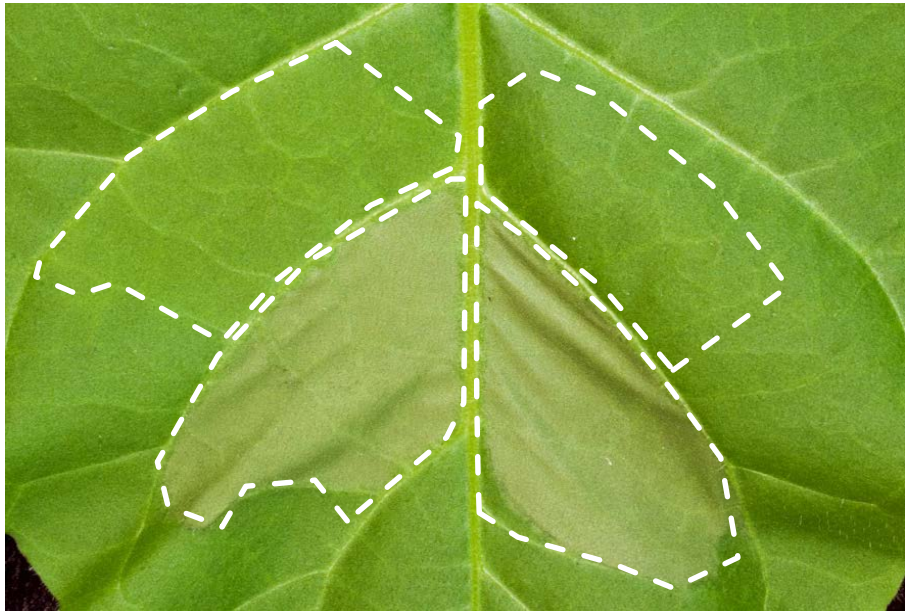


C terminal motif

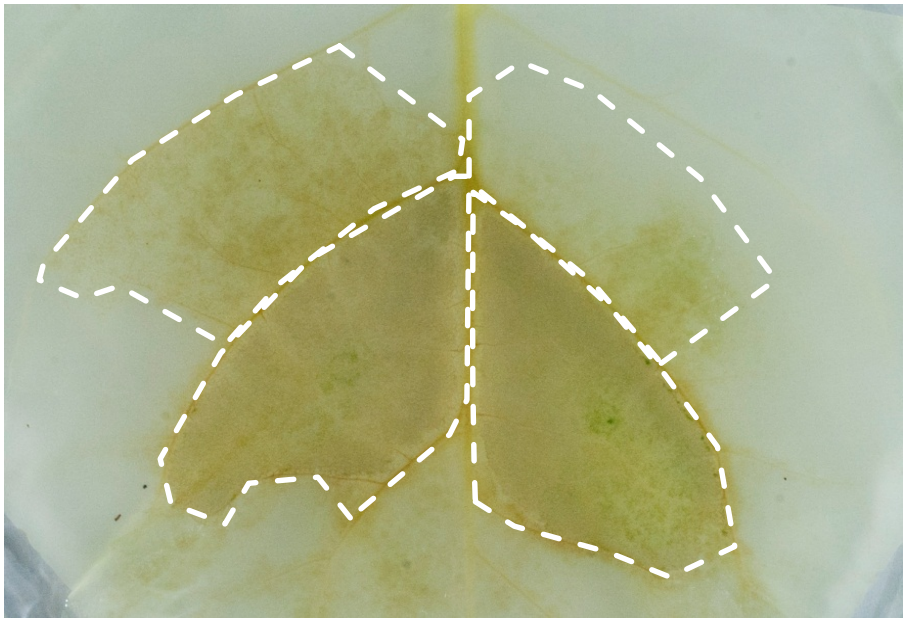
TCSGCTDQSSSGSSEYPGSSGTTKPPTDPTGGENKDQDKKAEATSLQFAMSSFCLALSLMIGVAVL

Low complexity segment: 8 serine, 6 threonine, 6 glycine out of 32 Aa

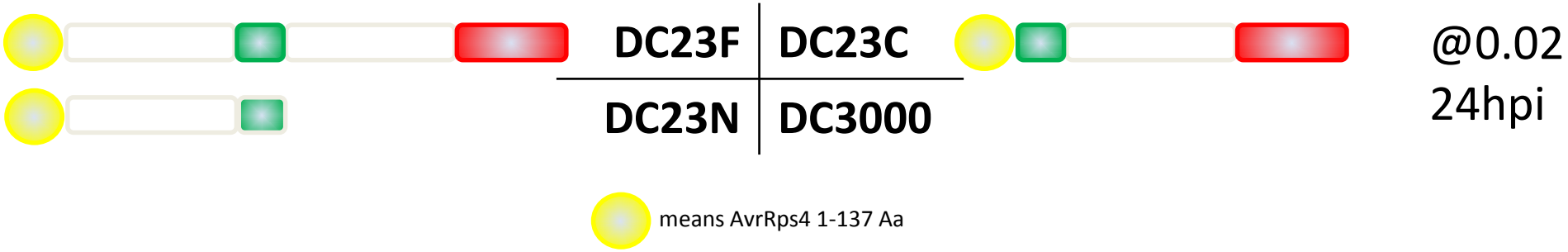
PpEC23



Native leaf



Leaf cleared with ethanol



@0.02
24hpi

means AvrRps4 1-137 Aa

Effector Targets

- *Pp*EC23: SPL
  - Squamosa promotor binding-like protein
  - regulatory function
  - down regulation of defense responses
- Effectors with similar targets in *Acidovorax citrulli*?
- Effectors with similar targets in other plant pathogenic bacteria?

Effector Transfer

- Use of *Pseudomonas syringae* DC3000 as delivery system for rust effectors
- Use of *Acidovorax citrulli* as delivery system for rust effectors?

- Transfer of rust effectors to host cytoplasm is still unexplained. Similarities to bacteria?

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Acknowledgements

Ralf Vögele
Christian Seibel

Matthias Kohlndorfer
Daniela Schmidt
Benjamin Mülleder
Sandra Rollar
Iris Häusermann

Pedro Talhinhas
Sílvia Tavares

Steve Whitham
Qi Mingsheng
Thomas Baum