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## Poster

### Wirt-Parasit-Beziehungen

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#### 133 - Approaches to identify the *Salmonella-Arabidopsis* interactome

Methoden zur Identifizierung des *Salmonella-Arabidopsis* Interaktoms

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*Salmonella* bacteria are one of the main causes of foodborne diseases in humans and animals worldwide being transmitted through contaminated vegetables, fruits, plant- and animal-based products. It has been shown that *Salmonella* does not only attach to plant tissue surfaces but is capable of invading and proliferating inside plant cells. This raises the question on how *Salmonella* communicates with and manipulates its plant hosts. During infection of mammalian hosts, *Salmonella* delivers a variety of effector proteins into the host cell which interfere with host cellular processes through protein-protein interactions (PPIs), thereby enabling the pathogen to invade and propagate inside the host cell. We carried out an extensive literature and database survey for the known *Salmonella*-host protein-protein interactome. This resulted in a list of 64 PPIs between *Salmonella* TTSS-1 and -2 effectors and mammalian proteins, but no experimentally identified PPI between *Salmonella* effectors and plant proteins could be retrieved (Schleker et al. 2012b). Thus, we utilized interolog and machine learning computational modeling approaches to predict *Salmonella-Arabidopsis* PPIs based on available knowledge (García-García et al., Schleker et al. 2012a). Pathway mapping of putatively targeted *Arabidopsis* proteins revealed that *Salmonella* may interfere, for instance, with plant defense response signaling pathways, protein catabolic processes and plant metabolism. Comparison with transcriptomic data revealed that genes of the same *Arabidopsis* pathways predicted to be targeted by *Salmonella* effectors are differentially regulated upon infection.

#### References

- GARCÍA-GARCÍA, J., S. SCHLEKER, J. KLEIN-SEETHARAMAN, B. OLIVA, 2012: BIPS: BIANA Interolog Prediction Server. A tool for protein-protein interaction inference. *Nucleic Acids Research*, **40**, W147-51.
- SCHLEKER, S., J. GARCÍA-GARCÍA, J. KLEIN-SEETHARAMAN, B. OLIVA, 2012a: Prediction and comparison of *Salmonella*-human and *Salmonella-Arabidopsis* interactomes. *Chemistry and Biodiversity*, **9** (5), 991-1018.
- SCHLEKER, S., J. SUN, B. RAGHAVAN, M. SRNEC, N. MÜLLER, M. KOEPFINGER, L. MURTHY, Z. ZHAO, J. KLEIN-SEETHARAMAN, 2012b: The current *Salmonella*-host interactome. *Proteomics Clinical Applications*, **6**: 117-133.

#### 134 - Untersuchungen zur Rolle der transkriptionellen Umprogrammierung der Gerste in der Interaktion mit dem Echten Mehltaupilz

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RACB ist eine kleine GTPase in Gerste, die zur Familie "Rho of Plants" (ROPs) gehört und als molekularer Schalter zwischen einem inaktiven und aktiven Status agiert (Berken et al. 2006). Dabei werden verschiedenste Prozesse innerhalb der Zelle angesprochen wie z.B. Zytoskelettveränderungen, Zellpolarität und Pathogenabwehr. Fehlendes oder vorhandenes RACB beeinflusst stark die Anfälligkeit von Gerste gegenüber seinem Mehltaupilz *Blumeria graminis f. sp. hordei* (Bgh) (Schultheiss et al. 2003, Hoefle et al. 2011). Wir fokussieren auf die Unter-

suchung von transkriptionellen Veränderungen, die durch RACB während einer Mehltauinfektion hervorgerufen werden. Dazu wurden 44k Mikroarrays mit drei verschiedenen Pflanzenlinien mit unterschiedlichem RACB Expressionsmuster (Wildtyp, konstitutiv aktives überexprimiertes RACB und ausgeschaltetes RACB) durchgeführt. Wir konnten eine Vielzahl von Genen identifizieren, die durch *Bgh* im Wildtyp und konstitutiv aktiv in den super anfälligen Überexprimierern hochreguliert sind. Es konnten vor allem Kandidatengene aus dem Bereich des „Signallings“ herausgefiltert werden, die als potentielle Zielgene von RACB agieren könnten. Daher werden diese RACB- und *Bgh*- abhängig exprimierten Gene momentan funktionell charakterisiert, um das Resultat in der Mehltau-Gersteninteraktion näher zu verstehen.

#### Literatur

- BERKEN, A. (2006). ROPs in the spotlight of plant signal transduction. *Cellular and Molecular Life Science* **63** (21): 2446–2459.
- HOEFLE, C., HUESMANN, C., SCHULTHEISS, H., BÖRNKE, F., HENSEL, G., KUMLEHN, J., HÜCKELHOVEN, R. (2011). A barley ROP GTPase ACTIVATING PROTEIN associates with microtubules and regulates entry of the barley powdery mildew fungus into leaf epidermal cells. *The Plant Cell* **23**: 2422–2439.
- SCHULTHEISS, H., DECHERT, C., KOGEL, K.-H., AND HÜCKELHOVEN, R. (2003). Functional analysis of barley RACROP Gprotein family members in susceptibility to the powdery mildew fungus. *The Plant Journal*: 589–601.

### **135 - Molecular identification and pathogenicity of *Colletotrichum* isolates from infected apple leaves in southern Brazil**

*Molekulare Identifizierung und Pathogenität von Colletotrichum-Isolaten aus infizierten Apfelblättern im Süden Brasiliens*

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The Glomerella leaf spot (GLS) is nowadays one of the most important diseases affecting apple trees (*Malus domestica* Borkh.) in subtropical regions, such as, Southern Brazil. Symptoms begin with reddish-purple spots that evolve to irregular necrotic lesions between 7 and 10 days after infection, when leaves often turn yellow and fall off. Apple cultivars descending from 'Golden delicious' group are highly susceptible to GLS, whereas those from 'Delicious' group have complete resistance to disease. *Colletotrichum gloeosporioides* and *Colletotrichum acutatum* have been frequently associated to this leaf disease. Furthermore, *Colletotrichum* spp. are also known to cause apple bitter rot, but the relationship between isolates from leaves and fruits is not yet completely understood.

The aim of this work was to identify *Colletotrichum* isolates causing GLS and to test their ability to infect leaves and fruits. Pure cultures were obtained by monosporic isolation and grown on PDA at 25°C and 12h photoperiod under fluorescent light. Sequencing of the ITS-rDNA region using ITS1/IT4 primers and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) using GDF/GDR primers allowed the identification of *Colletotrichum fructicola* and *Colletotrichum karstii* (Fig 1), belonging to *C. gloeosporioides* and *Colletotrichum boninense* species complexes, respectively.