

---

## Poster

### Wirt-Parasit-Beziehungen

---

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

Methoden zur Identifizierung des *Salmonella-Arabidopsis* Interaktoms

**Sylvia Schleker<sup>2</sup>, Judith Klein-Seetharaman**

Metabolic and Vascular Health, Warwick Medical School, University of Warwick, Coventry, UK. <sup>2</sup>Molecular Phytomedicine, Institute of Crop Science and Resource Conservation, University of Bonn, Bonn, Germany

*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

**Vera Schnepf, Ralph Hückelhoven**

Technische Universität München, Lehrstuhl für Phytopathologie, Emil-Ramannstr. 2, 85350 Freising, Deutschland

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-