

Two positions for PhD students (3 years of guaranteed funding) are available at the Albrecht-von-Haller Institute for Plant Sciences (AG Gatz)

Our laboratory is interested in the signal transduction events that are elicited after attack of higher plants by pathogens. Two competing resistance responses are elicited depending of whether a plant is attacked by a pathogen that kills cells to obtain nutrients or by a pathogen that retrieves nutrients from living cells. Two projects wait to be worked on in our group by highly motivated applicants which have a Master's degree in a topic that has been addressed by molecular methods.

1. Analysis of the function of plant specific CCMC-type glutaredoxins that interact with the bZIP transcription factors of the TGA family

Glutaredoxins (GRXs) are small redox proteins of approximately 12 kDa that are able to catalyze the reduction of disulfides or glutathione (GSH) mixed disulfides. The genome of the model plant *Arabidopsis thaliana* encodes 30 *GRX* genes that have been classified into three major subgroups according to the sequence of the active center. Eight glutaredoxins characterized by a CCMC motif interact with the bZIP transcription factors of the TGA family which are important signalling components of the salicylic acid (SA)-inducible plant defense response "systemic acquired resistance (SAR)". As both, members of the TGA family and NPR1, the central regulator of SAR establishment, are subject to redox changes when plants are treated with SA, a functional role for TGA-interacting glutaredoxins seems likely. Moreover, expression of three of these glutaredoxins is inducible by salicylic acid (SA). We have recently shown that a GRX/TGA complex is involved the negative cross-talk between SA- and jasmonic acid (JA)-induced signalling events. The aim of the project is to elucidate the function of SA-inducible, TGA-interacting members of the glutaredoxin family in SA-mediated responses. This project will unravel an important regulatory principle in plant defense responses that addresses the poorly understood mechanisms of redox modifications of regulatory proteins. The generation of whole genome transcriptome data of mutants with multiple knock-outs in functionally redundant glutaredoxin genes will add an important resource for understanding the network of events that respond to glutaredoxin-mediated redox control mechanisms.

- Ndamukong I, Al Abdallat A, Thurow C, Fode B, Zander M, Weigel R, Gatz C. 2007. SA-inducible *Arabidopsis* glutaredoxin interacts with TGA factors and suppresses JA-responsive *PDF1.2* transcription. *Plant J.* 50(1):128-39

2. Identification of the regulatory principles underlying regulatory mechanisms activated by jasmonic acid, cis-jasmone and coronatine.

Jasmonic acid (JA) is an important plant hormone that orchestrates defense responses after herbivore feeding and attack by pathogens that kill plant cells to obtain nutrients (necrotrophic pathogens). The bacterial toxin coronatine is an efficient JA-mimic that promotes bacterial growth, partially, because JA suppresses defense mechanisms against bacterial pathogens that obtain nutrients from living cells (biotrophic pathogens). A central regulator of jasmonic acid- and coronatine-regulated processes is the F-box protein COI1. However, like *cis*-jasmone, coronatine also elicits COI1-independent processes. We are interested in the mechanisms of *cis*-jasmone- and coronatine-induced effects that are elicited in the absence of COI1. Moreover, we wish to elucidate the function and the mechanism of the antagonistic effects between *cis*-jasmone and jasmonic acid.

