

## **Function and transcriptional regulation of a plant detoxification program**

Plants are challenged by toxic chemicals that are either released by man, neighboring plants or pathogenic microbes. Moreover, endogenous reactive molecules accumulate under conditions of oxidative stress generated under adverse abiotic conditions or pathogen attack. Inactivation and elimination of harmful xenobiotic or endogenous substances is facilitated by an inducible set of detoxifying enzymes and transporters. Activation of at least part of this detoxification program can be triggered by xenobiotics like INA (2,6-dichloroisonicotinic acid), 2,4-D (2,4-dichlorophenoxy- acetic acid) and TIBA (2,4,6-triiodobenzoic acid), as well as by high levels of salicylic acid. We have shown that the TGA family of bZIP transcription factors and the interacting GRAS protein SCL14 are important for this activation (Fode et al., 2008). We aim to obtain further insight into SCL14/TGA-dependent transcriptional control mechanisms in chemically stressed plants. Experimental approaches include the identification of proteins interacting with SCL14 using yeast screens, analysis of post-translational modifications, and functional analysis of SCL14-related genes.

**Fode, B., Siensen, T., Thurow, C., Weigel, R., and Gatz, C. (2008).** The Arabidopsis GRAS protein SCL14 interacts with class II TGA transcription factors and is essential for the activation of stress-inducible promoters. *Plant Cell* **20**, 3122-3135.