

Das Genom von *C. graminicola* enthält etwa 40 Gene, die für Polyketidsynthasen (PKS) kodieren. Mittels RNA-Seq wurden die Transkriptprofile dieser Gene während der Maisinfektion analysiert. Zahlreiche PKS wiesen ein Maximum transkriptioneller Aktivität zu bestimmten Phasen der Infektion auf, z. B. während der Penetration oder des Übergangs von der biotrophen zur nekrotrophen Lebensweise. Um die Bedeutung einzelner PKS für den Infektionserfolg zu ermitteln, wurden bisher etwa 30 PKS-Gene deletiert. Für zwei unterschiedliche PKS-Deletionsstämme konnte dabei ein vollständiger Verlust der Penetrationskompetenz nachgewiesen werden.

### **39-6 - The function of a fusion protein with lectin and dirigent domain in pathogen resistance of crop plants**

*Die Funktion eines Fusionsproteins mit Jacalin- und Dirigent-Domäne in der Pathogenresistenz von Getreidepflanzen*

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Lectins and dirigent proteins are both thought to be involved in plant defense; lectins due to their ability to recognize cell surface carbohydrates highly specifically, and dirigent proteins because of their crucial role in controlling free radical coupling of monolignols to yield lignans and lignins. We identified a rice gene (*OsJAC1*) encoding for a protein with a lectin and dirigent domain which conferred broad-spectrum disease resistance in transgenic rice plants overexpressing the gene. This type of modular protein has exclusively developed within the *Poaceae* family. FRET analysis revealed that both domains physically interact with each other and transient overexpression showed that both domains are required for full pathogen resistance.

### **39-9 - Gene expression analyses and histological characterization of crown rust inoculated *Lolium perenne* genotypes**

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Perennial ryegrass (*Lolium perenne*) is one of the most widely cultivated cool-season grass species of the world and used in forage production and as turfgrass (Pfender et al. 2011). Ryegrass is susceptible to several diseases especially rusts of the genus *Puccinia*. Crown rust of the perennial ryegrass, caused by the obligate biotroph pathogen *Puccinia coronata* f. sp. *loli* is the most widespread and damaging disease in forage-grass, which is associated with a decrease in dry matter production and its digestibility by the grazing animal (Schejbel et al. 2007). The development of cultivars with resistance to crown rust is the most economically and environmental efficient solution for disease control.

We have examined an inbred full-sibling population of perennial ryegrass genotypes (Beckmann et al. 2010) using crown rust field isolates collected in 2012 and 2013 from three locations in Germany (Steinach, Bavaria; Bornhof and Rostock, Mecklenburg-Western Pomerania). Differences in virulence were observed among the field isolates in severity of disease symptoms and the ability to sporulate. The population showed different levels of resistance: most of the individuals were fully resistant, some were moderate resistant and very few were highly susceptible to *P. coronata*. Histological analyses and gene expression analysis by Massive Analysis of cDNA Ends (MACE) were conducted to characterize fungal development and resistance reactions.

Microscopical analyses of calcofluor stained leaf segments revealed: a late resistance response of the fully resistant and a delayed fungal development in the moderate resistant genotype.

Gene expression analyses revealed that after rust inoculation numerous genes involved in plant defense response including R-genes and pathogenesis related genes are upregulated. Compared to the susceptible *Lolium* genotype in the moderate resistant genotype expression of up to 415 genes and in the fully resistant genotype expression of up to 470 genes are differentially expressed. Some genes involved in plant defense response were exclusively expressed in the fully resistant genotype.

#### Literatur

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