

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

Denise Weidenbach, Lara Esch, Caroline Höfle², Götz Hensel³, Jochen Kumlehn³, Ralph Hückelhoven², Ulrich Schaffrath

RWTH Aachen University, Department of Plant Physiology, 52056 Aachen, Deutschland

²Technische Universität München, Center of Life and Food Sciences Weihenstephan, 85350 Freising, Deutschland

³Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Plant Reproductive Biology, 06466 Stadt Seeland – Gatersleben, Deutschland

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

Jens Bojahr, Björn Rotter², Nico Krezdorn², Ottilia Nhengiwa³, Bernhard Saal³, Brigitte Ruge-Wehling⁴, Peter Winter², Christine Struck

University of Rostock, Faculty of Agricultural & Environmental Sciences, Group Crop Health, 18059 Rostock Germany

²GenXPro GmbH, Altenhöferallee 3, 60438 Frankfurt, Germany

³Saatzucht Steinach GmbH & Co KG, Wittelsbacherstrasse 15, 94377 Steinach, Germany

⁴Julius-Kühn Institut, Institut für Züchtungsforschung an landwirtschaftlichen Kulturen

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.