

conventional fungicides becoming an increasing problem, alternative solutions are required. Primary stages of infection occur in the extracellular spaces of the wheat leaf, where bacteria such as *Pseudomonas fluorescens* can also be found. In our first experiment a *Pseudomonad* library was screened for direct inhibition of *Z. tritici* on agar plates, to determine if any exhibit antifungal activity. Using a high-throughput screening methodology developed in this project which tested 460 bacterial endophytes and rhizosphere associated *Pseudomonads*, 40 isolates showed an ability to directly inhibit the growth of *Z. tritici*. Our results raise the possibility that bacteria present on wheat leaves may affect the incidence and/or severity of STB via direct inhibition of fungal growth, through secreted fungal inhibitors. In a second experiment, we plan to grow surface sterilised wheat seeds in sterile growth medium amended with synthetic microbial communities before infecting the plants with *Z. tritici*. This will allow us to monitor the impact of the below ground microbiome on the plant's response to foliar disease, through priming or other mechanisms. These combined approaches may lead to novel mechanisms, which could be exploited for chemical and/or biological control of *Z. tritici*.

Exploring NGS, HIGS and si-RNA technologies for the control of *Fusarium* ear blight in wheat

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Fusarium ear blight (FEB) is a major problem in most small-grain cereal growing regions and now threatens global food security. Currently strategies to control FEB are not very effective, fungicides give partial protection and development of genetic-based resistant

transformed into a commercial moderately-FEB resistant Brazilian wheat in preparation for field testing in southern Brazil during 2018 and 2019. By taking a Fusarium genome/ reverse genetics guided approach, this is enabling the development of flexible new ways to control FEB disease in wheat crops grown in Brazil. The main prerequisites needed to apply this approach in other wheat growing regions will be addressed, as well as additional scientific, societal and industry benefits that could potentially emerge when using HIGS technologies for plant disease control.

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Heterologous expression of feruloyl esterase of *Aspergillus terreus*

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In the cell walls of gramineous plants, hemicelluloses are crosslinked to the aromatic lignin polymer via hydroxycinnamic acids (ferulic acid and p-coumaric acid). Feruloyl esterases (ferulic acid esterases, EC3.1.1.73), present in CAZy family CE1 (www.cazy.org), are enzymes that catalyse the cleavage of covalent ester bonds between carbohydrate and lignin moieties in plant cell walls. Due to the ability to specifically cleave ester linkages, feruloyl esterases are promising biocatalysts for a broad range of biotechnological applications. These include e.g. pharmaceutical, agricultural and food industries, as well as the production of biofuel.

Analysis of the CAZomes of eight *Aspergillus* species revealed a high variability in the gene sets related to plant biomass degradation (1). One of these variations was in the putative FAEs of CAZy family CE1, where all species contain one conserved fae gene, but some species possess additional candidate genes for this activity. *Aspergillus terreus* contains two additional putative FAE encoding genes, one of which has orthologs in *Aspergillus oryzae* and *Aspergillus flavus*, but not in any of the other tested species (*Aspergillus niger*, *Aspergillus nidulans*, *Aspergillus clavatus*, *Aspergillus fumigatus* and *Aspergillus fisheri*). One of these putative *A. terreus* FAE encoding genes was chosen to