tillering phase. A qualitative and quantitative diagnostic assay was evaluated using a crude extract and a purified DNA, respectively, from a 0.5-1 cm of the basal shoots (30, 49 and 79 dfs) and from first and second leaves (102 dfs) of naturally infected wheat plants. A TaqMan Real Time PCR assay with species-specific primers and probe was used. The amplification standard curves for both the extracts showed an efficiency >90% and <100%, with a high coefficient of determination (R2 > 0.99) and a high sensitivity (10 fg). The percentages of molecular detection were 83% at 30 dfs, 57% at 49 dfs and 100% at 79 dfs for shoots; 83% and 50% at 102 dfs for first and second leaves of the same plant respectively. Symptom assessment, at maturity stage, will need to confirm the accuracy of the molecular predictions.

Regulation of griseofulvin biosynthesis and role on growth and virulence of *Penicillium griseofulvum*, causal agent of apple blue mold

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Many *Penicillium* spp. can cause apple blue mold, an important post-harvest disease of apple fruits. These species are able to produce many secondary metabolites including mycotoxins on infected fruits, such as patulin and cyclopiazonic acid. Among the casual agents of apple blue mold, *P. griseofulvum* produces huge amount of patulin and a characteristic antifungal compound called griseofulvin. In order to study the role of griseofulvin for the growth and pathogenicity of *P. griseofulvum*, the regulation of its biosynthesis was investigated. Two approaches were followed: generation of deletion mutants for the putative genes encoding transcription factors in griseofulvin gene cluster and promoter analysis to study the involvement of global regulators. The analyses revealed that *gfR1* encodes a negative transcription factor of the cluster, which could be involved in the regulation of other genes, such as other secondary metabolites biosynthetic genes and genes involved in the asexual development and virulence of the pathogen. Many stimuli are also important to activate griseofulvin biosynthesis, such as carbon and nitrogen available in the environment, stress response and sporulation. This study reveals that the regulation of griseofulvin involves both a pathway-specific transcription factor and global regulators of gene clusters. Furthermore, the analysis highlights a deep interconnection between secondary metabolism and fungal development.

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Terpene synthases in *Trichoderma gamsii* T6085

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Secondary metabolites (SM) play an important role in the interaction between fungi and the environment. The isolate T6085 of *Trichoderma gamsii* is a promising biocontrol agent, with demonstrated activity against *Fusarium graminearum*, one of the most aggressive causal agents of Fusarium Head Blight on wheat. The complete genome sequence of *T. gamsii* T6085 was screened by antiSMASH 5.0 for the identification of the gene clusters putatively involved in SM biosynthesis. The availability of genomic sequences of a large number of *Trichoderma* species enabled to compare the core-gene content involved in SM biosynthesis among them. Genes encoding terpene synthases (TS) are widely represented in this genus, suggesting an important role in the ecology of *Trichoderma*. A comparative genomic approach has been carried out in order to characterize TS genes within *Trichoderma* genus. The genome of *T. gamsii* T6085 harbours eleven putative terpene synthase-encoding genes, seven of which have been predicted to belong to SM clusters. Interestingly, one of these was predicted to encode a trichodiene synthase (TRI5), which has only been described in the trichothecene-producer *Trichoderma* species belonging to the *Brevicompactum* clade. Aimed to decipher the putative function of these genes and to infer their possible role in the interactions of our isolate with the environment, expression patterns of TS genes have been assessed in several induction media and during *T. gamsii* T6085-wheat and *T. gamsii* T6085-*F. graminearum*-wheat interactions. In addition, a preliminary metabolic profile has been determined by HPLC-RMN in 12-day PDB cultures of this *Trichoderma* strain.

Insight into the citrus Huanglongbing pathosystem and disease control

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Citrus is one of the most important fruit crops worldwide. However, citrus production is facing an unprecedented challenge due to Huanglongbing (HLB, also known as greening). HLB is the most destructive disease of citrus and causes tremendous damage to citrus industry in the world. HLB, caused by the Gram-negative bacterium *Candidatus* Liberibacter, is widely distributed in the citrus producing regions in Asia, Africa, and Americas. *Ca*. Liberibacter resides inside the phloem and is vectored by psyllids. All commercial citrus varieties are susceptible to HLB. The understanding of the biology and virulence mechanism of the pathogen remains limited due to the inability to culture the bacteria. Here I will present our current progress in understanding the biology and virulence mechanism of Las, as well as their implications in HLB/ACP management. I will talk about HLB/ACP control strategies based on the epidemiological stages of HLB pathosystem.

Walnut blight causing by endophytic fungi during different phenological phases of the host

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