The rhizosphere-competent entomopathogen *Metarhizium anisopliae* expresses a specific subset of genes in plant root exudate

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*Metarhizium anisopliae* and *Beauveria bassiana* are ubiquitous insect pathogens and possible plant symbionts, as some strains are endophytic or colonize the rhizosphere. We evaluated 11 strains of *M. anisopliae* and *B. bassiana*, and two soil saprophytes (the non-rhizospheric *Aspergillus niger* and the rhizosphere-competent *Trichoderma harzianum*) for their ability to germinate in bean root exudates (REs). Our results showed that some generalist strains of *M. anisopliae* were as good at germinating in RE as *T. harzianum*, although germination rates of the specialized acridid pathogen *Metarhizium acridum* and the *B. bassiana* strains were significantly lower. At RE concentrations of <1 mg ml⁻¹, *M. anisopliae* strain ARSEF 2575 showed higher germination rates than *T. harzianum*. Microarrays showed that strain 2575 upregulated 29 genes over a 12 h period in RE. A similar number of genes (21) were downregulated. Upregulated genes were involved in carbohydrate metabolism, lipid metabolism, cofactors and vitamins, energy metabolism, proteolysis, extracellular matrix/cell wall proteins, transport proteins, DNA synthesis, the sexual cycle and stress response. However, 41.3 % of the upregulated genes were hypothetical or orphan sequences, indicating that many previously uncharacterized genes have functions related to saprophytic survival. Genes upregulated in response to RE included the subtilisin Pr1A, which is also involved in pathogenicity to insects. However, the upregulated *Mad2* adhesin specifically mediates adhesion to plant surfaces, demonstrating that *M. anisopliae* has genes for rhizosphere competence that are induced by RE.

INTRODUCTION

The entomopathogen *Metarhizium anisopliae* is a soil fungus with worldwide distribution (Zimmermann, 2007). Some strains of *M. anisopliae* are rhizosphere-competent (Hu & St. Leger, 2002; St. Leger, 2008), which may explain the persistence of *M. anisopliae* in soils for long periods of time in the absence of an insect host (Bidochka et al., 1998; Quesada-Moraga et al., 2007). It is likely that the distribution of different genotypes of *M. anisopliae* will depend upon environmental factors, such as temperature and humidity, and soil conditions, such as pH and organic matter content (Quesada-Moraga et al., 2007; Zimmermann, 2007). In addition insects, plants and microbial populations will interact at the soil–root interface to affect *Metarhizium* populations (St. Leger, 2008). Similarly, complex interactions occur with the best-known rhizosphere-competent fungus *Trichoderma harzianum*. This fungus is also used as a biocontrol agent because it can parasitize plant fungal pathogens and establishes a symbiotic relationship with the roots of some plants, increasing plant growth and productivity (Harman, 2006). Complex interactions between multiple strains of *Trichoderma*, the roots of plants and other fungal pathogens suggest an established molecular cross-talk between them (Woo et al., 2006). However, the genetic and physiological factors controlling overall, the genetic groups of *M. anisopliae* and their geographical distribution seem shaped by their adaptability to specific soils and habitat types rather than for their pathogenicity to insects (Bidochka et al., 1998; Quesada-Moraga et al., 2007).
rhizosphere competence in fungi, including Trichoderma, are little understood (St. Leger, 2007). In fact, for many economically important pathogens, the least studied aspect of their biology involves the extended periods for which they survive in soil in the absence of a suitable host (Kerry, 2000). Thus, while a lot of research has been performed on the entomopathogenicity of M. anisopliae, its saprophytic lifestyle has received little consideration. Presumably, the same functionally related genes could be adaptive for multiple different environments [insect cuticle, insect blood and root exudates (REs)], but there might also exist different subsets of genes that are adaptive to each environment (Wang et al., 2005).

In this study, we performed a time-course evaluation of gene expression by M. anisopliae growing on plant REs as the first step in elucidating pathways that are used by this fungus for soil survivability and adaptability. We need this knowledge to be able to predict and control outbreaks of plant or animal disease. In addition, lack of knowledge of the fate of fungal genotypes at the population and ecosystem levels creates an inherent uncertainty about the efficacy, survivability and environmental risk posed by any introduced or engineered fungi. A deeper understanding of the mechanistic basis of rhizosphere competency could enable us to identify genes that we could use to develop M. anisopliae as a comprehensive plant symbiont, or at least improve persistence and consequently provide greater long-term protection against insect pests.

**METHODS**

**Bean REs.** In order to simulate rhizospheric conditions in the laboratory, M. anisopliae was grown on bean REs from black pea seeds (Vigna unguiculata subsp. unguiculata). To obtain the RE, bean seeds were disinfected by soaking them for 2 min in 95% ethanol, rinsed in sterile distilled water and transferred to 30% hydrogen peroxide (Fisher Scientific) for 2 weeks at 27°C. Five millilitres of the mycelial suspension was transferred to four 50 ml flasks, each containing sufficient RE to give a final concentration of 5 mg RE ml⁻¹. This relatively high concentration was not limiting to growth during the course of the experiment, thus avoiding changes in gene expression due to nutritional deprivation alone. Samples were incubated at 27°C at 220 r.p.m., and mycelium was collected from individual flasks after 1, 4, 8 and 12 h of incubation. Total RNA was immediately extracted from the samples using the Qiagen RNaseasy Mini kit according to the manufacturer’s instructions, and treated with Qiagen DNase I. Two biological replicates were performed.

**cDNA microarray.** For microarray analysis, we used cDNAs isolated from three libraries that were previously constructed using mycelia of M. anisopliae (ARSEF 2575), grown on insect cuticle (Freimoser et al., 2003), or grown in insect blood or plant REs (Wang et al., 2005). PCR-amplified expressed sequence tags (ESTs) were spotted on aminoethyl II-coated glass slides (Corning, Inc.), following the standard protocol developed at the University of Maryland Biotechnology Institute (http://www.umbi.umd.edu/carb/core-facilities/microarray-services/facility.php). A total set of 1748 unigenes (870 from cuticle, 276 from haemolymph and 602 from the root library) were printed in triplicate per slide. Blanks using water and saline sodium citrate (SSC) buffer were also included as negative controls. The genes were classified in nine groups of functionally related genes, and this classification was also used to initiate comparisons of expressed genes (Wang et al., 2005).

**Microarray design and RNA hybridization.** To analyse expression profiles in RE, we applied a loop design protocol, where every time point was compared with the previous time point. The contrast between adjacent time points provides information about the expression pattern of a gene over time. Total RNA from fungal mycelia grown in SDB (time 0) and RE at each time point (1, 4, 8 and 12 h) was amplified and directly labelled with Cy3 (green) and Cy5 (red) cyanine dyes using the Ovation Aminoallyl system (Nugen). Five slides were hybridized per replicate (time 0 vs 1 h, 1 h vs 4 h, 4 h vs 8 h, 8 h vs 12 h and 12 h vs time 0). Competitive hybridization of the second biological replicate was performed using a reverse dye-assignment to eliminate bias from dye incorporation.

**Microarray data analysis.** Hybridized slides were scanned at the University of Maryland Biotechnology Institute (http://www.umbi.umd.edu/carb/core-facilities/microarray-services/facility.php) using an Axon 4200 microarray scanner (Molecular Devices). To obtain differential signal expression, the TIFF images generated (two image files per hybridized slide) were analysed using the Spotfinder program (http://www.tm4.org/spotfinder.html). Data were then normalized using the LOWESS (Locally WEighted Scatterplot Smoothing) technique with MIDAS software (http://www.tm4.org/midas.html). MIDAS output files included standard deviation regularization, low-intensity filters and in-slide replicate analysis. The percentage spor germination of each fungus was determined after 24 h incubation at 27°C with shaking (250 r.p.m.). In order to detect differences between T. harzianum and M. anisopliae, we also evaluated their germination at concentrations lower than 1 mg ml⁻¹ (0.01, 0.05, 0.1 and 0.5 mg ml⁻¹).
To detect differentially expressed genes in our time-course microarray experiment, the log₂ expression ratios (Cy5/Cy3 for replicate 1 and Cy3/Cy5 for replicate 2) were calculated per gene at each time point in the two replicates. Normalized data were inputted to the Bayesian Analysis of Time Series Microarray Experiments (BATS) software (version 1.0) (http://www.na.iac.cnr.it/bats/) (Angelini et al., 2008). To account for the time instants we chose as parameter of the analysis the maximum expected degree of polynomial equal to 3, the parameter lambda for the truncated Poisson prior probability equal to 4 (corresponding to an expected polynomial degree of about 2), and we accounted for multiple comparisons using the Bayesian Multiple Testing Procedure with the binomial prior. Default values were used for the other parameters.

Validation of differentially expressed genes by RT-PCR. Total RNA extracted for microarray analysis was also used for RT-PCR using the Verso cDNA kit (Thermo Fisher Scientific) and oligo-dT primers according to the manufacturer’s protocol. The cDNA product was subsequently amplified by PCR using gene-specific primers. As a control, RT-PCRs were also performed using the constitutively expressed glyceraldehyde-3-phosphate dehydrogenase (gdpa) gene.

RESULTS

Fungal strains and spore germination on bean REs

All fungal strains showed some germination in RE at 1 mg ml⁻¹. *T. harzianum* and the broad-host-range *M. anisopliae* strain 2105 showed the highest germination rates at the five concentrations of RE (ranging from 1 to 20 mg ml⁻¹) (Fig. 1a). These germination rates ranged from 96.8 to 99.3 %, and did not differ significantly from each other. *M. anisopliae* strains 2575, 549 and 1080 with a broad host range had germination rates ranging from 76.6 to 93.9 % at 1 mg ml⁻¹ of RE, germination rates ranging from 91.6 to 95.2 % at 2.5 mg RE ml⁻¹, and germination rates ranging from 87 to 93 % at 5 mg ml⁻¹. These germination rates were not significantly different from those of the model rhizospheric fungus *T. harzianum* at the same concentrations of RE. However, strain 2575 showed a significantly lower germination rate as compared with *T. harzianum* at concentrations greater than 5 mg RE ml⁻¹ (Fig. 1a).

The specialist *M. acridum* strain 324, specific to locusts and related grasshoppers (Orthoptera: Acrididae), is not rhizosphere-competent (O’Brien, 2008). We also tested other strains of *M. brunneum* with unknown host ranges, including *M. anisopliae* strains 4600 and 4620, which were isolated from the Tasmanian soldier fly (Diptera: Stratiomyidae), and *M. anisopliae* strain 2974, recently reclassified in the Agriculture Research Service Entomopathogenic Fungal Collection (ARSEF) collection as *Metarhizium brunneum*, originally isolated from a mosquito (Diptera: Culicidae) (Supplementary Table S1). These strains have very low rhizosphere competence as determined by microcosm studies (O’Brien, 2008). *M. acridum* 324 showed its highest germination rate (47.3 %) at 1 mg RE ml⁻¹ and its lowest germination rate (24.7 %) at 20 mg RE ml⁻¹. Germination rates of *M. acridum* 324 were significantly different from those of both *T. harzianium* and *A. niger* at each concentration of RE (Fig. 1a). The lowest germination frequencies with 1 mg RE ml⁻¹ were shown by *M. anisopliae* strains 4620 (22.5 %), 2974 (12.5 %) and 4600 (6.5 %), and *A. niger* (19.3 %). However, germination rates of the *M. anisopliae* strains increased at higher concentrations of RE (except at 20 mg ml⁻¹, when strains 4620 and 2974 showed slightly reduced germination rates), while the germination rate of *A. niger* declined with increasing concentrations of RE (germination rates of *A. niger* were 19.3, 14, 13, 2 and 0 % at concentrations of 1, 2.5, 5, 10 and 20 mg RE ml⁻¹, respectively) (Fig. 1a).

*B. bassiana* strains 9205 and 9112 were isolated from Lepidopteran hosts (Supplementary Table S1). *B. bassiana* strain 3113 was isolated from soil but is an endophyte able to colonize corn plants and provide protection against lepidopteran pests (Pingel & Lewis, 1996; Wagner & Lewis, 2000). At 1 mg RE ml⁻¹, germination rates of *B. bassiana* strains 9205, 9112 and 3113 were 73, 50.5 and 64 %, respectively. These germination rates were not significantly different from each other, but they were significantly higher than those of *A. niger* and *Metarhizium* strains 4620, 2974 and 4600 (Fig. 1a). Germination rates of *B. bassiana* strains 9112 and 3113 were significantly lower than those of the *M. anisopliae* generalist strains (2105, 2575, 549 and 1080) and *T. harzianum* strain T22. *B. bassiana* strains 9112 and 9205 showed slightly increased germination at 2.5 and 5 mg RE ml⁻¹, but germination by 9211 decreased significantly at 20 mg RE ml⁻¹. Germination rates of *B. bassiana* strain 3113 gradually declined at concentrations >1 mg ml⁻¹ and had diverged significantly from the other fungal strains at 10 mg RE ml⁻¹ (Fig. 1a).

In order to detect any differences between *T. harzianum* and *M. anisopliae* strains 2105 and 2575 we evaluated concentrations of RE lower than 1 mg ml⁻¹. Fig. 1(b) shows that at concentrations ≤0.5 mg ml⁻¹ the germination rate of *T. harzianum* was significantly lower than that of *M. anisopliae* 2575. The percentage germination of strain 2105 was 1, 12.5 and 42 % with 0.01, 0.05 and 0.1 mg RE ml⁻¹, respectively, whereas germination rates of strain 2575 were 88.6, 98 and 93 % at the same concentrations. This indicates that strain 2575 of *M. anisopliae* is hypersensitive to RE.

Microarray data analysis

Out of 1748 genes included in the cDNA microarrays, we identified 50 genes (2.9 %) that were differentially expressed across the time points evaluated. Differentially expressed genes were automatically detected using BATS and ranked according to their Bayes factors (BF < 0.006). Nucleotide query sequences of these genes were subsequently compared against the already existing sequences in the NCBI non-redundant protein database (BLASTX) (http://blast.ncbi.nlm.nih.gov/) and reorganized into previously classified groups of functionally related genes (Wang et al., 2005) (Fig. 2a). *M. anisopliae* genes that
Fig. 1. Germination of *Metarhizium* (Ma) strains, *B. bassiana* (Bb) strains, *T. harzianum* (rhizospheric) and *A. niger* at different concentrations of REs. (a) Concentrations of RE from 1 to 20 mg ml\(^{-1}\). (b) Concentrations of RE < 1 mg ml\(^{-1}\). Mean values labelled with the same letter are not significantly different (\(P<0.05\)).
Fig. 2. Fifty genes differentially expressed by *M. anisopliae* 2575 during growth in RE. (a) Differentially expressed genes compared with the total number of genes in each functional group. (b) LEM representing the mean of the differentially expressed genes organized according to functional groups. The vertical red bars show functional groups that contain genes that were upregulated at one or more points. The number of upregulated genes/total number of differentially expressed genes per functional group is also shown. (c) Pattern of expression of the differentially expressed genes after 0, 1, 4, 8 and 12 h growth in RE. GenBank accession numbers, the maximum fold values (Max. fold) and the time (h) when the maximum fold value occurred are provided.
were differentially expressed under RE conditions over 12 h included 13 out of 413 arrayed hypotheticals (predicted sequences with homologues in other organisms but no experimental evidence of function) (13/413, 3.1%), an orphan sequence with no homologues in databases (1/236, 0.4%) and genes involved in cell metabolism (7/335, 2.1%), energy metabolism (2/64, 3.1%), protein metabolism (11/172, 6.4%), cell structure and function (10/231, 4.3%), cell cycle, division and growth (3/93, 3.2%), transposable elements (1/13, 7.7%), and stress response and defence (2/107, 1.9%) (Fig. 2a).

Overall, 27 (54%) of these genes were originally isolated from the EST root library, 18 (36%) from the cuticle library and five (10%) from the insect blood library of *M. anisopliae* 2575. Thus, many genes expressed during cuticle degradation and growth in insect blood are also involved in adaptation to RE.

Fig. 2(b) shows the linear expression map (LEM) with the mean of the log2 ratio of differentially expressed genes classified by functional groups at each time point. Of the 50 differentially expressed genes, 29 (58%) were upregulated across all time points when the fungus was transferred from SDB (time 0) to RE. They were involved in carbohydrate metabolism (3/29, 10.4%), lipid metabolism, cofactors and vitamins (2/29, 6.9%), energy metabolism (2/29, 6.9%), proteolysis (1/29, 3.4%), extracellular matrix/cell wall proteins (4/29, 13.9%), transport proteins (2/29, 6.9%), DNA synthesis (1/29, 3.4%), the sexual cycle (1/29, 3.4%), stress response (1/29, 3.4%), hypothetical proteins (11/29, 37.9%) and unknown proteins (1/29, 3.4%) (Fig. 2b).

The level of expression of individual genes, the maximum fold change and the time (h) when the maximum fold change occurred are presented in Fig. 2(c). Of the 29 genes that were upregulated in RE, nine (31%) obtained their maximum fold change after 4 h, 14 (48%) after 8 h and six (21%) after 12 h (Fig. 2c).

Supplementary Table S2 shows the log2 expression ratio through time of the 50 differentially expressed genes. The greatest fold increases were observed in the hypothetical genes. Gene AJ273764 was upregulated 3.7-fold (after 8 h), and genes CN808927 and CN809209 were both upregulated 3.3-fold after 4 and 8 h, respectively. Genes CN808884, CN809514 and AJ274093 were upregulated 3.0-, 2.5- and 2.5-fold, respectively, after 8 h. The expression of the subtilisin-like serine protease (Pr1A) gene (CN808958) increased through time in RE, being upregulated 3.3-fold after 8 h. Genes involved in energy metabolism, dihydrolipoyl dehydrogenase (AJ273762) and oxidoreductase (CN808777), were upregulated 2.9- and 2.0-fold after 8 and 12 h, respectively. A stress response heat-shock protein gene (CN808235) was upregulated 2.9-fold after 4 h in RE. Transport proteins, including an ABC transporter ATP-binding protein (CN809103) and a GABA (γ-aminobutyrate) permease (CN808046) were upregulated 2.4- and 0.8-fold, respectively, after 12 h. Genes required for the metabolism of carbohydrates such as glycosyl hydrolase (CN808813), β-glucosidase (AJ273623) and ferulic acid esterase A (JaeA) (AJ273114) were also upregulated 2.2-fold (after 8 h), 1.9-fold (after 4 h) and 1.3-fold (after 4 h), respectively. RE also increased the expression of genes encoding cell wall proteins and the associated extracellular matrix, including the hydrophobin-like protein precursor (AJ274156) and the predicted cell wall protein AJ273845, which were both upregulated 2.1-fold at 8 and 12 h. Also, the cell wall MAD2 adhesin (CN809626), which is required by *M. anisopliae* to adhere to plant surfaces (Wang & St. Leger, 2007), and a close homologue (CN809322) were upregulated 1.9- and 1.6-fold, respectively, after 4 h. Other genes that are involved in the synthesis of DNA (mediator of replication checkpoint 1, CN809288), lipid metabolism (diacylglycerol O-acyltransferase, DgaT, CN808018), sexual development (EsdC protein, CN809127) and cofactors and vitamins (amidase protein, AJ273042) were also upregulated between 2.0- and 0.8-fold after 4 and 8 h in RE. Although listed as a sex cycle gene, the gene for EsdC is involved in cell wall morphology and is expressed in asexual as well as sexual processes in *Aspergillus* (Han et al., 2008).

Twenty-one differentially expressed genes (42%) were downregulated in RE (Fig. 2c, Supplementary Table S2). Two genes (9.5%) were downregulated ~1.2-fold after 4 h; 5 genes (23.8%) were downregulated 1.0 to 1.6-fold after 8 h and 14 genes (66.7%) were downregulated 0.8 to 2.4-fold after 12 h (Fig. 2c). Downregulated genes included ribosomal proteins, the cold acclamation-induced protein 2-1 (CN808997), the carrier protein ADP/ATP translocase (CN809461) and hypothetical protein AJ272794. Expression of hydrophobin genes (AJ273847 and CN809178) was initially downregulated, but recovered so that by 8 h these genes were upregulated 1.5- and 1.6-fold, respectively. The C-3 sterol dehydrogenase protein AJ274219, the potassium channel protein CN808889 and the hypothetical protein CN808746 were upregulated during the first 4 h of incubation in RE before slowly declining, suggesting a role in the early stages of adaptation to RE.

**RT-PCR verification of differentially expressed genes**

Five genes (predicted protein AJ273764, subtilisin-like serine protease PR1A CN808958, hydrophobin-like protein AJ274156, *Metarhizium* adhesin protein Mad2 CN809626 and a ribosomal protein CN809270) were selected for validation of microarray analysis through RT-PCR. The results indicated that expression patterns of these genes were consistent with the microarray results (Fig. 3).

**DISCUSSION**

Root-mediated rhizosphere interactions are classified as being either positive or negative for the plant (Bais et al.,...
Mycorrhizal associations between fungi and plant roots are clearly positive, being essential for the survival of both partners. While the fungus obtains carbohydrates such as glucose and sucrose (final products of photosynthesis), the plant benefits from the increased uptake of water and nutrients, including nitrogen and phosphorus (Harman & Shores, 2007). REs represent a significant carbon cost to the plant (Bais et al., 2006), but there is clearly coevolutionary potential in favouring populations of mycorrhizal fungi and also, presumably, populations of pathogens of herbivorous insects. It would not therefore be surprising if entomopathogenic fungi benefited from components of REs when adapting to soil environments.

REs are composed of a complex mixture of soluble compounds such as carbohydrates, lipids, amino acids, organic acids, proteins, polysaccharides, nucleotides, flavonoids, growth factors, enzymes, growth inhibitors and repellants (Hale et al., 1978; Rovira, 1965). Our results show that generalist strains of *M. anisopliae* (ARSEF 2105, 2575, 549 and 1080) are as good at germinating in RE as the specialist strains including strain 324 and generalist strains 22. Specialist strains including strain 324 have lost genes related to saprophytic survival. Some of these genes have orthologues in plant pathogens and other soil fungi, so whatever role they play in adapting to soil conditions may be conserved. The presence of at least 10 sugars (including glucose, fructose, sucrose, raffinose, xylose, maltose and rhamnose, among others) has been identified in the RE of a wide variety of plants (Rovira, 1965). *M. anisopliae* genes involved in carbohydrate metabolism (glycosyl hydrolase b-glucosidase AJ273623 and ferulic acid esterase AJ273114) were upregulated during the first 8 h under RE conditions. A formidable array of hydrolytic enzymes is secreted during the pathogenic life cycle of *M. anisopliae*, and these include the subtilisin protease Pr1A (CN808958) (Bagga et al., 2004; Wang et al., 2009). Pr1A was upregulated within 4 h of incubation in RE, and high-level expression was maintained throughout the time-course, demonstrating an important long-term role in proteolysis for Pr1A in the utilization of RE. Cell wall proteins (e.g. adhesin proteins CN809626 and CN809322) were also upregulated in the first 4 h. CN809626 encodes MAD2 (*Metarhizium* adhesin-like protein 2). Its detection in a screen of genes upregulated by RE helps validate the principle of using RE to identify genes involved in rhizosphere interactions. Strains of *Metarhizium* disrupted in Mad2 show a 90% reduction in adherence to plant cells (Wang & St. Leger, 2007). In this study, we found an EST sequence in the root library CN809322, originally designated an unknown protein, but with 98% similarity (E value 2e-136) to the MAD2 transcript (CN809626). Although expressed at lower levels than MAD2, it had an identical pattern of gene expression in RE (Supplementary Table S2).
This suggests that CN809322 is also involved in attachment to plant surfaces, and it is perhaps responsible for the 10% of Mad2 mutant spores that are still adherent. An EST from the root library (CN809103) that was originally designated an unknown protein showed most (46%) similarity to an ABC transporter (ATP-binding protein) from the symbiotic nitrogen-fixing actinobacterium Frankia alni (Supplementary Table S2). ABC transporter proteins are ubiquitous in all organisms and are primarily involved in the active transport of a wide array of different molecules across plasma membranes. Some ABC proteins serve as a cellular toxic defence mechanism by transporting deleterious compounds out of the cell. These may include xenobiotics, anthropogenic contaminants, natural product toxins and endogenous metabolites (Wolfgar et al., 2001). A putative ABC transporter gene (CN809103) of M. anisopliae was upregulated after 1 h under RE conditions with a 2.4-fold increase after 12 h. This indicates that the protein may be required to facilitate the efflux of compounds present in RE that may be toxic to the fungus.

The rhizosphere competence of M. anisopliae and knowledge of the genes involved as it adapts and persists in soil environments is important when considering the potential commercial use of biological control agents against root herbivores and soil-borne plant pathogens. The long-term genetic adaptations and evolution of this fungus in cultivated soils (turf plots) are also being studied in our laboratory (O’Brien, 2008). Comprehensive knowledge of short- and long-term interactions between Metarhizium, insects, plants and microbial soil populations will reveal ecological links that will help us to understand the molecular cross-talk between them, and could ultimately be exploited to benefit plant growth and productivity. Further research is also needed to discern the function of the array of hypothetical/orphan proteins that were differentially expressed in RE in order to elucidate their roles in M. anisopliae, and possibly other fungi. The inability of mutants disrupted in MAD2 to adhere to plant roots provided a clear test of the importance to the fungus of root interactions, and confirms that the most informative approach for analysing the hypothetical proteins will involve comparisons with mutant fungi. Also, comparison of gene expression among rhizosphere-competent and non-rhizosphere-competent strains of Metarhizium would complement studies on the physiology of this fungus.

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REFERENCES


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