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four states. In contrast, no *S. rolfsii* sclerotia survived until June in North Dakota and Iowa, whereas 18.5% survived until August in North Carolina and 10.3% survived in Georgia. To test the hypothesis that sclerotial size influences overwinter survival, we measured diameter of 100 of each of three isolates of *S. rolfsii* var. *delphinii* and *S. rolfsii* that had been grown in moist chambers on cotton wool over moistened sand. Sclerotia of *S. rolfsii* var. *delphinii* were significantly larger, and surface to volume ratio was smaller, than for *S. rolfsii*. A smaller surface to volume ratio may confer a protective effect by shielding the cortex of sclerotia from temperature extremes. This protective effect may help to explain the greater overwinter survival of sclerotia of *S. rolfsii* var. *delphinii* than of *S. rolfsii* in cold-winter regions such as the northern U.S.

Functional analyses of selected parasitism genes of the root-knot nematode *Meloidogyne incognita*

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Proteins encoded by parasitism genes expressed in the esophageal gland cells of root-knot nematodes are secreted into plants through the nematode stylet to promote host plant root infection and the formation of essential feeding sites called giant-cells. Previous analyses of gene expression in *Meloidogyne incognita* esophageal gland cells have identified more than fifty putative parasitism genes, the majority of which are pioneer genes without significant homology to genes currently listed in public databases. Functional analyses of ten of the *M. incognita* pioneer parasitism genes designated 2G10, 4D03, 8D05, 10G02, 16E05, 34F06, 1C05B, 4F05B, 35A02, and 30HO7 are under investigation by overexpression in plant tissue and RNA interference (RNAi) gene knockout assays. The effects of constitutive expression of each *M. incognita* parasitism gene product with and without secretion signal peptide in transformed *Arabidopsis thaliana* plants are analyzed for changes in plant phentoype as one measure of potential parasitism protein function in plant cells. Constitutive expression of double-stranded RNA to each *M. incognita* parasitism gene in transformed *A. thaliana* is also analyzed for potential RNAi effects on root-knot nematode parasitism of host roots. These two strategies are providing evidence of root-knot nematode parasitism gene function and identifying which parasitism gene products are essential to the parasitic interaction.

Pathogenicity and inoculum sources of *Geotrichum candidum* causing sour rot of peaches and nectarines in California

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In the last several years, *Geotrichum candidum*, the main agent causing sour rot, has caused major losses of peaches and nectarines in California. Pathogenicity of 41 isolates of *G. candidum* collected from different peach and nectarine orchards and packinghouses was confirmed by inoculating healthy peaches and nectarines. To determine sources of inoculum in the orchard and contamination of packing house, samples of soil, leaf, and fruit were collected from 41 commercial orchards and the CFU of *G. candidum* were determined using a spiral gradient technique. Rodac plates were used to sample packing lines. *G. candidum* was detected only in 21 out of 41 fields at levels that ranged from 22 to 11,777 CFU/g soil and 5 to 323 CFU per leaf. Fruit collected from the orchards were free of *G. candidum* except for fruit from two orchards, where disease incidences were 0.8% and 1.43%, respectively. Sour rot incidence in cull fruits collected from eight fields ranged from 33 to 100%. *G. candidum* propagules were detected in four areas in four packing lines sampled with the highest numbers recovered from brushes and associated areas. The main source of inoculum is the orchard soil and the major source of contamination of fruit in the packing line occurs in the area of the brushes.

Identification and frequency of *Phytophthora* species causing foliar diseases in California ornamental nurseries

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Attention has traditionally focused on *Phytophthora* species causing root and crown rot diseases, leaving *Phytophthora* species causing foliar infections less well-studied. As part of federally mandated nursery surveys targeting *Phytophthora ramorum*, numerous California ornamental nurseries have been extensively sampled for leaf spot and twig blight. These surveys presented the opportunity to examine the incidence of other foliar-infecting *Phytophthora* species. Diseased tissue collected during the 2005 and 2006 surveys were screened by ELISA and PCR methods to determine if *Phytophthora* species other than *P. ramorum* were present. A total of 375 samples were determined to be *Phytophthora* species other than *P. ramorum*. These isolates were initially identified by matching internal transcriber spacer I sequences with published GenBank sequences. Subsets of these were further verified by morphological characters. Thirteen species of *Phytophthora* were found; *P. syringae* and *P. citricola* were found most frequently making up 31% and 24% of the total number of isolates, respectively. *P.* Pgchlamydo and *P. foliorum*, were also present. To verify pathogenicity, subsets of isolates are currently being inoculated onto common host plants. Knowledge of species causing foliar blights in California nurseries may aide in future management.

Analysis of differentially expressed transcripts of canola (*Brassica napus* L.) in response to infection by the fungal pathogen *Sclerotinia sclerotiorum*

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We profiled the transcriptional changes in canola (*Brassica napus* L.) leaves, in response to infection by the fungal pathogen *Sclerotinia sclerotiorum* using microarrays. Due to a >86% homology between *Arabisopsis thaliana* and *B. napus* and the unavailability of a commercial canola array, we used (70 mers) oligo microarray representing 26,090 *A. thaliana* genes in our studies. Our microarray analysis revealed more than 300 transcripts which exhibited at least a 2-fold significant ($P < 0.05$) increase or decrease in abundance as compared to the uninoculated controls at various time points (12, 24 and 48h) post pathogen-challenge. Included among these were genes involved in jasmonic acid biosynthesis and signaling, reactive oxygen species scavenging, cell wall structure and function, and defense related transcripts that may play important role(s) in mediating plant responses to this pathogen. Furthermore, we selected and validated 15 genes by quantitative RT-PCR (qRT-PCR) and results from these experiments also exhibited a similar trend as those from microarray analysis. Our results will be presented and the roles of selected genes in mediating plant responses to *S. sclerotiorum* will be discussed.

Differential requirements for ribosomal proteins by plant virus

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A recent microarray study by our lab demonstrated that a large group of ribosomal protein (RP) genes (up to 79 genes) were increasingly up-regulated in proportion to *Turnip mosaic virus* (TuMV) accumulation in *Arabidopsis thaliana* leaf tissue. This observation correlates the expression of these essential host genes with viral infection and led us to investigate whether RPs are important host factors for virus amplification. Because loss-of-function of selected RP genes was homozygous lethal in *A. thaliana*, the virus induced gene silencing (VIGS) method was used to silence the expression of RPS6, RPL13 and RPL19 in *Nicothiania benthamiana*. Plants in which the expression of each RP was silenced displayed similar phenotypes characterized by shortened petioles, chlorotic leaves and stunted growth. Leaves showing these phenotypes were inoculated with TuMV or *Tobacco mosaic virus* (TMV) tagged with GFP. The accumulation of TuMV was strongly dependent on expression of each RP, but TMV was much less affected although it replicated somewhat slower in the silenced plants versus the non-silenced plants. TMV could achieve systemic infection in leaves of some of the silenced plants, but systemic movement was never observed for TuMV. These results are particularly interesting in the context of the translation strategies of these two viruses - TuMV is cap-independent and TMV is cap-dependent. Further experiments are underway to understand the differential requirement of RPs in the accumulation of these two viruses.

Genetic diversity of *Mycosphaerella fijiensis* from bananas (*Musa* spp.) in Hawaii

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Black Sigatoka, caused by *Mycosphaerella fijiensis* Morelet (anamorph *Pseudocercospora fijiensis* (Morelet) Deighton), is the most important leaf disease of banana. To evaluate the genetic diversity of the fungal pathogen, a total of 99 *M. fijiensis* isolates collected from three different islands (Maui, Hawaii, and Oahu) of Hawaii were analyzed for DNA polymorphism using amplified fragment length polymorphism (AFLP) markers. Twenty-two *M. fijiensis* isolates from Mexico were also included in the study for comparison. A total of 447 polymorphic AFLP markers were generated and scored using seven *EcoRI-MseI* primer combinations. Cluster analysis showed that the