Phytophthora cinnamomi is a devastating pathogen that can infect over 900 hosts. It is the most common species of *Phytophthora* isolated from woody ornamental crops in South Carolina but little is known about variability among isolates of *P. cinnamomi* that attack these plants. Therefore, 142 isolates of *P. cinnamomi* recovered from diseased plant samples submitted to the Clemson University Plant Problem Clinic between 1996 and 2011 were characterized for growth rate, mycelium growth habit, mefenoxam sensitivity, and mating type. Average growth on PARPH-V8 selective medium was 60 mm in 72 h at 25°C in the dark. Mycelium growth habit on PARPH-V8 was classified as aerial, sparse, dwarf, or appressed, and 85% of isolates had aerial mycelium. All isolates were sensitive to the fungicide mefenoxam at 100 ppm. The population was composed of 129 A2 and 13 A1 isolates with six A1 isolates recovered from camellia. The ITS 1 and 2 loci were sequenced, and this region had low diversity with only two genotypes that were different from the majority of the population. One of these genotypes consisted of an isolate matching *P. cinnamomi* var. *parvispora*, and the other genotype included four morphologically diverse isolates. Consequently, there was a high degree of genetic uniformity in the ITS region among these 142 isolates. Host-pathogen relationships for this population were compared to reports in the literature, and 33 new associations were found.

The detection of '*Candidatus* Liberibacter asiaticus' in worldwide populations of *Diaphorina citri*

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Key to controlling the spread of the destructive citrus disease Huanglongbing is controlling the spread of the vector. One part of understanding the spread is to know what percentage of the vectors are carriers of the pathogen. Previous studies resulted in rates from 20% to 60%. These differences could be due to the small sample size, difference population sampled and molecular detection methods. For this study, a worldwide sampling of over 2000 *Diaphorina citri* was collected by collaborators. The extracted DNA from single psyllids were amplified using whole genome amplification using Repli-g kits (Qiagen). This process amplifies all DNA in the sample including insect and all bacteria. Two genetic loci were amplified with classical PCR and sequenced when bands were detected with gel electrophoresis. The 'Liberibacter' specific 16s rRNA primers were used. While the standard for identification, the 'Liberibacter asiaticus' metagenome indicates that as many as 3 copies may be present increasing sequencing difficulty. The second loci, the single-copy gene zinc metalloprotease A (*zmpA*), was also sequenced. *ZmpA* is known to play a role in pathogenicity in *Burkholderia* species. Sequencing data from a subset of psyllids from Texas and Pakistan repeated the pattern of variable carrier rates. A larger sampling is still needed to understand how disparate the carrier rates are from different regions.

Steaming is a sustainable method to eradicate the quarantine pathogen *Phytophthora ramorum* from infested nursery soil

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The long-distance spread of *Phytophthora ramorum*, causal agent of Sudden Oak Death, through infected nursery plants is a serious thread for environments not yet affected by the pathogen. Nurseries tested positive for the presence of *P. ramorum* are required by federal and state regulations to eradicate infested plants and to disinfest soil and water. At NORS-DUC we study environmental friendly methods to eradicate *P. ramorum* from infested soils, among them biological control, solarization and steaming. Research beds (surface 9.1 x 3.7 m, depth 30 cm) filled with high clay content soils were treated with hot steam at a target temperature of 50°C for 30 minutes. As controls, teabag sachets containing Rhododendron leaf disks colonized by *P. ramorum* were buried at various depths in the soil. Leaf disks collected before and after steaming were assessed for *P. ramorum* by plating on PARPH-V8 medium. All leaf disks were *P. ramorum*-positive pre-steam and negative post-steam. Seasonal effects of environmental temperature on the steaming process and temperature gradient were measured by steaming at different times of the year. Additionally, soil at a commercial nursery tested positive for *P. ramorum* was steam-treated and -after eradication of the pathogen- released from quarantine. Soil texture and water content play an important role for the dynamics of the steaming process. Our results confirm that steaming can be used to eradicate quarantine pathogens from nursery soils.

Host-derived RNA interference targeted to the root-knot nematode parasitism gene 16D10 in tobacco

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The four major species of root-knot nematode (RKN), *Meloidogyne incognita*, *Meloidogyne arenaria*, *Meloidogyne javanica*, and *Meloidogyne hapla* have many host plant species, including tobacco, and are a global menace in agriculture. RKNs are sedentary endoparasites that transform plant cells into complex feeding sites called giant-cells via effector proteins secreted by the nematode through the stylet. Huang et al demonstrated that one secreted effector called 16D10 interacts with a SCARECROW-like transcription factor and that *M. incognita* grown on transgenic *Arabidopsis* engineered to produce 16D10RNAi produced 69-93% less eggs than controls. In this study 2 cultivars of tobacco (TN90 and Hicks) were transformed with Huang's 16D10RNAi constructs. Infection assays of the transformants with *M. arenaria*, for which there is no resistance in tobacco, showed reductions in egg counts for 3 out of the 4 lines of TN90 and 2 out of the 4 lines of Hicks tested. One of these lines, TN90 I-8, showed a 56% reduction in egg counts and was tested further with all 4 major species. TN90 I-8 was found to reduce the egg production of 3 of the 4 major species; *M. incognita* was reduced by 42%, *M. javanica* by 56%, and *M. arenaria* by 49%. To correlate the resistance with the siRNA levels, siRNA sequencing of infection assay root tissue is underway. New RNAi constructs created to improve the siRNA production are currently being transformed into both *Arabidopsis* and tobacco.

Evaluating human exposure to aflatoxins: A case study on aflatoxin-albumin adduct levels in end stage liver disease patients in India

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Aflatoxin B1, a secondary metabolite of *Aspergillus flavus* and *A. parasiticus*, is a frequent contaminant of several food crops. The main objective of this study was to know the effect of post exposure of aflatoxin in humans through consumption of contaminated foods. The aflatoxin-albumin level of selected human populations in India were analysed. A total of 673 blood samples were further analyzed by Indirect competitive Enzyme linked immunosorbent assay (IC-ELISA) method. The samples were collected along with clinical profile, demographic and food consumption data from the individuals with different stages of liver disease. The severity of the liver disease was calculated based on the "Model for End stage Liver Disesae" (MELD) score. The results indicated 86 of 673 samples have concentration of aflatoxin-albumin adduct ranged between 2.5 to 677 pg mg^{-1} of albumin with mean adduct level 181.9 ±5 and SD 1.49 ± 7. At 5% level of significance pb value 0.039 (<0.05) indicates presence of aflatoxin B1-lysine adducts and hepatitis B has synergistic effect on liver damage especially in end stage liver disease based on model for end stage liver disease (MELD). This shows that there is considerable intake of aflatoxin through contaminated food. Interestingly the concentration of aflatoxin-albumin was high and this along with the HBV positivity was found to be contributing to the severity of liver disease and lead to decompensated liver disease.

Late blight resistance in heirloom and hybrid tomato cultivars against the US-22, US-23, and US-24 clonal lineages of *Phytophthora infestans*

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Phytophthora infestans causes late blight, an important disease of tomato worldwide. Resistance genes are known, but few cultivars with effective resistance are commercially available. Using detached leaves, we tested 11 tomato cultivars for resistance to 3 current clonal lineages, US-22, US-23, and US-24. Lesion length and percent mycelial cover were plotted separately against days post inoculation and area under each curve was analyzed. Pooling the lineages, 3 heirloom cultivars with no known resistance genes, Matt's Wild Cherry, Wapsipinicon Peach, and Pruden's Purple exhibited lesion lengths not significantly different (NSD) than Mountain Magic (contains *Ph-2* and *Ph-3* resistance genes). Analysis of mycelial cover gave similar results and indicates the utility of these cultivars for mitigating disease impact and secondary inoculum production. 'Plum Regal' (*Ph-3*) had lesion lengths NSD than 'Mountain Magic' when inoculated with US-23, but lesion lengths NSD than the most susceptible cultivar when inoculated with US-22 and US-24.