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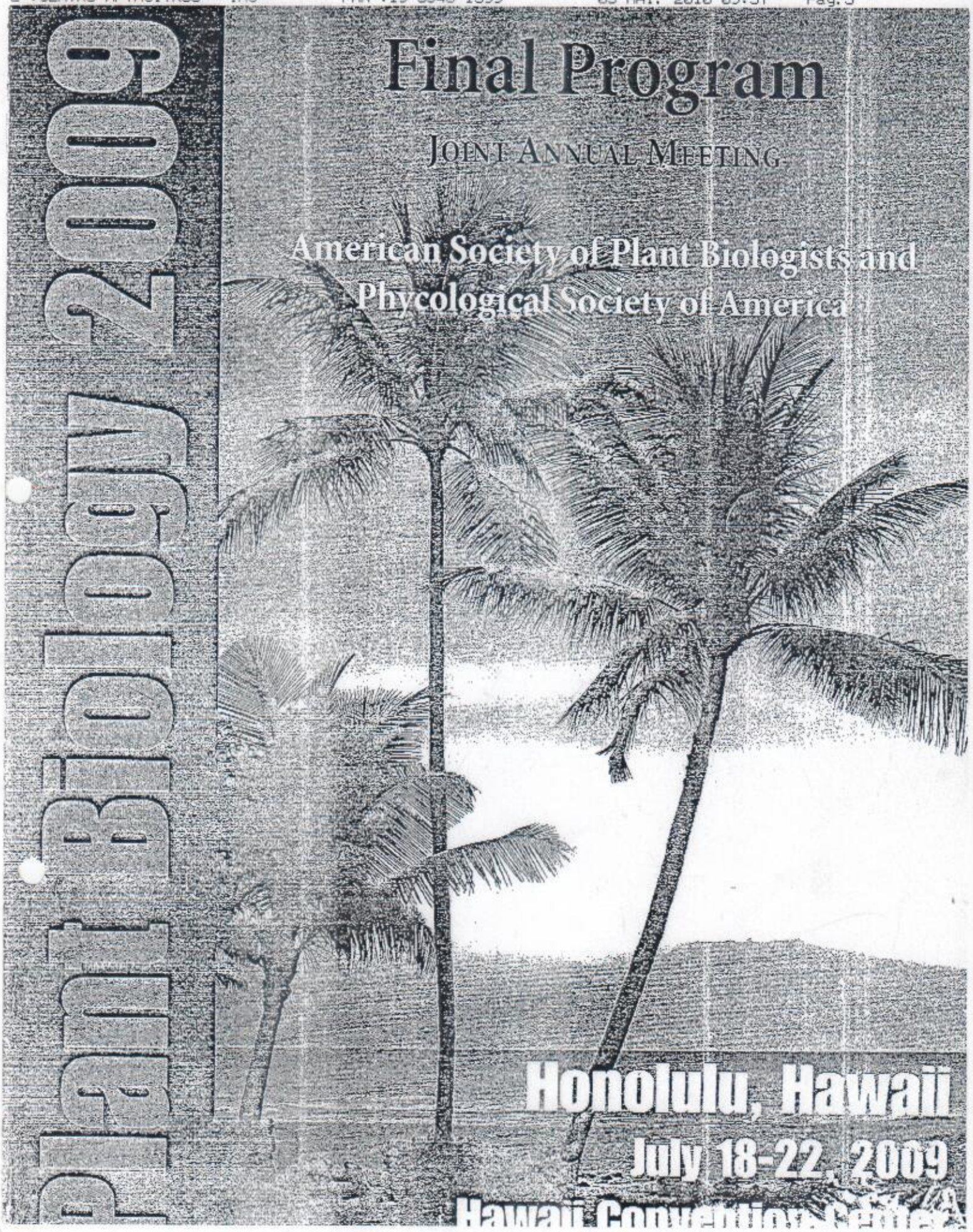

n promoter of one of the Myb transcription factor genes. We have further characterized the response of transgenic maize lines when infected with he fungus that causes southern corn leaf blight. Profiling of several different flavonoid compounds using HPLC and LC-MS has been performed. Results showing induction of specific compounds will be presented."
(a) Pennsylvania State University (b) University of Illinois

P48068 Genetic screening and characterization of *pmr5* suppressors
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" In Arabidopsis, mutation of *PMR5* (*Powdery Mildew Resistant 5*) confers resistance to the powdery mildew species *Golovinomyces cichoracearum* and *G. orontii*. This mutant also displayed a dwarf morphology and had enriched pectin in its cell walls. *PMR5* encodes a novel protein that belongs to a large family of plant-specific proteins of unknown function. Genetic study showed that *pmr5*-mediated resistance does not require signaling through either the salicylic acid or jasmonic acid/ethylene defense pathways. To study the molecular mechanisms of *pmr5*-mediated defense responses, a genetic screen for mutations that restore susceptibility to *G. cichoracearum* was carried out. Twenty *pmr5* suppressors were found that partially or fully suppressed resistance to powdery mildew. Of these, eight suppressor mutants resembled wild type in both morphology and susceptibility to *G. cichoracearum*. Nine kept the *pmr5*-like dwarf phenotype, while three mutants showed a more severe growth defect than the *pmr5* single mutant. Many of the suppressor mutations had pleiotropic effects on plant development including a change of flowering time or root growth. Further characterization and cloning of *pmr5* suppressors will provide knowledge of the molecular mechanisms of *pmr5*-mediated defense responses."
(a) UC Berkeley (b) Agricultural research services, USDA (c) Stanford University

P48069 WRKY53 Transcription Factor Is a Key Component in Flg22 Signaling
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"WRKY proteins, a family of transcription factors consisting of over seventy proteins, are implicated in regulating diverse cellular processes. However, precise functions of most of them are not known. Here, we investigated the role of WRKY53 in flg22 peptide, a Pathogen Associated Molecular Pattern (PAMP), signaling in Arabidopsis. We show that the expression of *WRKY53* is induced by flg22 in an FLS2-dependent manner. Studies with a MAP kinase kinase (MAPKK) inhibitor suggest that the MAP kinase pathway might not be involved in flg22-induced expression of *WRKY53*. The induction of *WRKY53* expression by flg22 is reduced significantly in the presence of an inhibitor of the 26S proteosome, suggesting that proteolysis of a negative regulator might be involved in this activation pathway. In *wrky53-1* mutant plants, promoter activities of *WRKY53* and three other flagellin-induced genes were elevated in the absence of flg22. Furthermore, overexpression of WRKY53 in wild type or *wrky53-1* plants suppressed flg22 activation of its own promoter and three other promoters that are activated by flg22 whereas the activity of one flg22-induced promoter was enhanced. These results suggest that WRKY53 functions as a negative regulator of some and positive regulator of other flg22-induced genes. Infection studies revealed that *wrky53* plants are moderately more susceptible to pathogens and appeared to be compromised in flg22 induced resistance. In contrast, wild type or *wrky53* plants overexpressing WRKY53 showed elevated PR gene expression and reduced disease. GFP-WRKY53 fusion protein, as expected of a transcription factor, localized to the nucleus. Together, our results indicate that WRKY53 plays a key role in flg22 induced defense signaling."
(a) Colorado State University (b) Duke University

P48070 Expression of nbs-LRR gene in Citrus plant infected with Xylella fastidiosa
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"The Brazilian citrus industry is responsible for 85% of the world concentrated orange juice production being the major world exporter for this product. One of the problems affecting the Brazilian citrus orchards is their vulnerability to pests and diseases, mainly due to the low genetic diversity of the commercial varieties used. Citrus Variegated Chlorosis (CVC) caused by Xylella fastidiosa is one of the most important diseases, causing large damages in the production and affecting all commercial sweet orange (Citrus sinensis L. Osb) varieties. However, it has been observed that mandarins (Citrus reticulata) are considered tolerant or resistant to this bacterium. This species is very important for studies on defense mechanisms as source of resistance genes. In silico analysis comparing C. sinensis and C. reticulate EST libraries identified a gene that encodes a NBS-LRR type protein which is possibly involved in the recognition of a molecule from the bacteria or the plant triggering a signaling pathway that induces the e[illegible]ssion of resistance genes. Hereof, the objective of this study was to verify the expression level of the NBS-LRR gene in sweet orange and [illegible]arin plants inoculated with X. fastidiosa 9a5c strain through RT qPCR. As control, plants were inoculated with PBS buffer. After 14 days, PCR analysis with specific CVC primers confirmed X. fastidiosa infection, and RNA was isolated for the expression analysis. The expression level of the NBS-LRR gene did not change in sweet orange infected with X. fastidiosa, however we observed 10 fold increase in mandarin suggesting um possible involvement of the NBS-LRR protein in the defense mechanism of these plants. The copy number of this gene in those species is also under evaluation through Southern blot."
(a) Centro Universitario Hermínio Ometto (b) Centro Apta Citros Sylvio Moreira

ID 36235

P48071 Response of Murcott tangor and Pera sweet orange to Citrus leprosis virus C (CiLV-C) and *Brevipalpus phoenicis* mites analyzed by 2DE
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http://www.centrodecitricultura.br
"Citrus leprosis is transmitted by the tenuipalpidae mite *Brevipalpus phoenicis*, causing chlorotic or necrotic local lesions in leaves, fruits and stems of susceptible hosts. The control of the vector in Brazil costs around US$ 75 million per year. In this work we analysed differentially expressed plant proteins in response to the mite feeding injury and the virus infection 48 hours after inoculation. The experiment consisted of three plants of each Murcott tangor and Pera sweet orange infested with viruliferous mites and three other plants of each genotype inoculated with non-viruliferous mites. The proteins were extracted with phenol from 3g of fresh leaf tissues. Isoelectric focusing was performed using 18cm 3-10pH non-liner immobilized pH gradient strips. Second dimension electrophoresis (SDS-PAGE) was performed according to Laemmli. For image and statistical analysis we used the software Image Master 2D platinum 7 (GE Healthcare). Both genotypes yielded around 15mg of proteins per gram of leaf and exhibited similar pattern in SDS-PAGE for the healthy controls. The 2DE gel analysis showed 712 spots for healthy Murcott tangor and 656 spots for healthy Pera sweet orange. The differentially expressed spots will be further identified by mass spectrometry."
(a) Unicamp (b) Centro APTA Citros "Sylvio Moreira" (c) Embrapa Cassava and Tropical Fruticulture (d) UFRPe