89. Floriculture production with iodomethane, 1,3-dichloropropene and chloropicrin as an alternative to methyl bromide. Gerik, J. S. Phytopathology 97(7)Suppl:S40. 2007.

designed to investigate a highly diverse population. The characterization of ontogenic resistance in this population will be discussed, and significant molecular and biochemical patterns correlating to the gain of resistance will be presented.

Proteomic and metabolic analyses of early berry development in *Vitis* spp. including the period of ontogenic gain of resistance

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Early development of grape berries is marked by several biological changes, including cell division and expansion, as berries initiate double sigmoid growth. In most genotypes, a significant gain of ontogenic resistance (OR) to some pathogens, including powdery mildew (PM) (*Uncinula necator*), also occurs within the first 3-weeks following bloom. The prior identification of a genotype that remains susceptible to PM provided genetic variation for exploring hypotheses for mechanisms of OR while characterizing conserved aspects berry development in diverse Vitis spp. Wax extractions from several time points of 6 genotypes were analyzed using GC-FID. Profile changes related to development were identified, in accordance with previous studies, and are being evaluated for the correlation to OR. Aspects of the physical development of the cuticle were investigated using SEM, but no significant patterns were shown to correlate to OR. Comparative proteomic analysis using computational bulking of samples based on phenotype with DiGE technology was used to compare protein expression of developing berry peels. Identification of the approximately 10% of the total pool of proteins that are differentially expressed in the first weeks of development is being conducted. In this study, genetic diversity is supporting the identification of candidate mechanisms for OR while distinguishing conserved hallmarks of early berry development.

Persistence of metalaxyl insensitivity in *Pseudoperonospora humuli*

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Metalaxyl insensitivity has been reported previously in isolates of *Pseudoperonospora humuli*, causal agent of hop downy mildew, but persistence of metalaxyl insensitivity in this pathogen has not been studied. One hundred fourteen hop shoots systemically infected with *P. humuli* (spikes) were collected from yards in Idaho, Oregon, and Washington and assayed for phenylamide fungicide sensitivity using a leaf disk assay. Metalaxyl and mefenoxam sensitivity was determined from inoculum derived from whole spikes and monosporic isolates in assays of a single discriminatory dose (25 ppm) and dilution series of metalaxyl. Mefenoxam insensitivity was detected in eight of 13 hop yards and 18 of 50 (36%) of spike isolates sampled in 2005. Metalaxyl insensitivity was detected in six of nine (66.7%) yards and 46 of 64 (72%) spike isolates assayed in 2006, including three hop yards in Washington. Among monosporic isolates of *P. humuli* metalaxyl insensitivity was detected in six of 10 hop yards and nine of 35 (27%) of isolates. Preliminary analysis of ED-50 values indicates metalaxyl insensitivity is prevalent among isolates of *P. humuli* in the U.S. and high levels of insensitivity have persisted in the population since the original report of insensitivity in 1992. Further studies to determine quantitative changes in the sensitivity of the population are ongoing.

Floriculture production with iodomethane, 1,3-dichloropropene and chloropicrin as an alternative to methyl bromide

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Cut flower growers in California have routinely used methyl bromide and chloropicrin soil fumigation to control soilborne pathogens and weeds. Because of the ban on methyl bromide production and import, alternative treatments are required. Three field trials were established to test the following treatments: 1) 448 kg ha^{-1} methyl bromide + chloropicrin (50:50); 2) 448 kg ha^{-1} iodomethane + chloropicrin (50:50); 3) 443 kg ha^{-1} 1, 3-dichloropropene + chloropicrin (61:35); and 4) a water control. The fields were tilled and weed free before fumigation. Fumigants and irrigation water were applied through three irrigation tapes. Populations of *Pythium* spp. and *Fusarium oxysporum* were determined from soil samples collected after treatment. Trial 1 was seeded with stock, trial 2 was transplanted with seedlings of snapdragon, and trial 3 was planted with bulbs of Dutch iris. Growth parameters and weed counts were made. The chemical treatments reduced the populations of *Pythium* spp. relative to the control plots. *F. oxysporum* was reduced only in trial 3. Weed control was variable. Stem rot, caused by, *Sclerotinia sclerotiorum*, was not reduced by any treatment. In conclusion, the two alternative treatments performed as well as methyl bromide + chloropicrin, but they are currently not registered for use in flower crops.

Effect of resistance to the soybean cyst nematode on soybean sudden death syndrome development and *Heterodera glycines* reproduction

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Sudden death syndrome (SDS) of soybean, caused by *Fusarium virguliforme*, often occurs and is more severe in the presence of the soybean cyst nematode (SCN), *Heterodera glycines*. These two major soilborne pathogens often occur simultaneously in soybean fields and potentially limit yield in susceptible cultivars. To determine the role of varietal resistance to SCN on SDS development, microplots were infested with *H. glycines*, *F. virguliforme*, both or neither, and planted with four soybean cultivars possessing contrasting resistance and susceptibility to each pathogen. Co-inoculation significantly hastened and increased SDS development and severity, reduced yields and reduced SCN reproduction in the SCN-susceptible but not in the SCN-resistant cultivars. Moreover, yield was negatively correlated to SDS severity levels. In co-inoculated plots nematode reproduction may be reduced due to the direct contact and competition of *H. glycines* and *F. virguliforme* for feeding sites, the presence of a SDS-diseased plant, or both. These results show that the reaction of a cultivar to SDS may be significantly affected by the cultivar's reaction to the population of SCN present in the field. Susceptibility to the predominant population of SCN appears as a key factor in the significant yield reductions observed when SDS was moderate to highly severe.

Multiple gene genealogies and pathogenicity of four *Fusarium* spp. in the *F. solani* complex associated with soybean sudden death syndrome

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Four species in the *Fusarium solani* complex are linked to SDS: *F. virguliforme*, *F. tucumaniae*, *F. brasiliense*, and *F. cuneirostrum*. All species were reported in South America, but only *F. virguliforme* causes SDS in North America. Disease etiology and the ability of some species to cause disease are questioned. We examined the species phylogenetic relatedness using multi-gene genealogy (ITS and 7 protein-coding gene sequences) and compared their ability to cause SDS. A maximum likelihood tree of the combined 2796 bp sequences separated all 4 species into monophyletic clades and was consistent with tree topologies of individual genes. Isolates from each species were used to inoculate susceptible and resistant soybean cultivars in a growth chamber. All isolates produced significant root rot, but only *F. virguliforme* and 2 *F. brasiliense* isolates caused typical foliar SDS symptoms. Foliar symptom severity positively correlated with top and root weight loss, but root rot severity did not. On SDS-resistant cultivars, *F. brasiliense* produced more severe foliar SDS symptoms than *F. virguliforme*. No interactions were observed between cultivar and species. Soybean SDS pathogens likely recently and repeatedly emerged from dry and mung beans in North and South America. This research provides management strategies for SDS and clarifies the evolution of soybean pathogens within the *F. solani* complex.

Molecular analysis of *Nimbya* spp., potential agents for biological control of alligatorweed in Australia, and their relationship to other species in the genus

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Nimbya alternantherae has been identified as a candidate for biological control of alligatorweed (*Alternanthera philoxeroides*) in China, South America and the USA. In Australia, several *Nimbya* spp., including *N. alternantherae*, have been found to cause disease on alligatorweed. One of these species, as yet undescribed, is also found on the Australian native *Alternanthera denticulata*, its probable native host. The others are at present presumed to have entered Australia with alligatorweed or possibly on other