

isolates that were highly variable for temperature tolerance and identified as tolerant, sensitive or intermediate in tolerance of exposure to -5°C for 5 days. Single oospore isolates of *P. infestans* produced *in vitro* from the selected nine crosses between different temperature tolerance were exposed to several other phenotypic characteristics and their survival was assessed. In this project mating type is used as a biological tool for enhancing the mutation in the pathogen. To determine if temperature tolerance is a genetically inherited trait or occurs as a result of physiological adaptation, the progeny isolates of *P. infestans* from these crosses were assessed by using the phenotypic and genotypic characteristics of progeny such as mating type, isozyme analysis, Simple Sequence Repeats, metalaxyl sensitivity, virulence and pathogenicity tests. Additionally, DNA content of nuclei and nuclear condition of a few isolates was examined with laser flow cytometry to clarify interpretation of inheritance patterns. These data illustrated the variation in different characteristics of the pathogen after recombination or mutation has occurred. Oospores formed at the beginning of epidemics could therefore contribute to the emergence of novel phenotypes within a growing season as well as between seasons.

Epidemiological analysis of multi-virus infections of watermelon in experimental fields in Southwest Florida

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Whitefly-transmitted Squash vein yellowing virus (SqVYV) and *Cucurbit leaf crumple virus* (CuLCrV) have seriously impacted watermelon production in west-central and southwest Florida in recent years. We monitored the progress of SqVYV and CuLCrV and whitefly density in 2.5 acre experimental fields of 'Fiesta' located in Immokalee, FL over the course of 3 growing seasons. Symptoms of CuLCrV were always found before SqVYV and were present as soon as 5 weeks after planting. Symptoms of SqVYV consistently appeared 7 weeks after planting and in 2 of 3 seasons the planting fully collapsed from disease by week 12. The largest number of whiteflies was typically found in the weeks preceding rapid collapse of plants. Preliminary analyses indicated that the degree of association between the two diseases was not greater than would be expected from random arrangement of the two viruses, and that SqVYV was distributed randomly at low incidences, but became more aggregated as disease incidence increased. These results are an indication that the viruses are being introduced independently by whiteflies, although the whiteflies may be emigrating from the same source, with secondary spread being dominated by within-field populations of whiteflies. This is conceivable based on results in which it was discovered that the distribution of the two viruses in individual watermelon plants was somewhat spatially separated. Additional field surveys are in progress to verify and extend these findings.

Response of processing tomato varieties to TSWV under Fresno County, California conditions

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Tomato spotted wilt virus has caused substantial losses in California processing tomatoes. Use of available TSWV-resistant varieties is limited because few have yield or quality comparable to commercial standards. The objective of this study was to compare susceptibility of processing tomato varieties to this virus. In three 4 replication randomized complete block trials, 13 mid-maturity processing tomato varieties were evaluated at the University of California West Side Research Center in Fresno County in 2008. Entries included AB 2, AB 8058, H 2005, H 2601, H 4007, H 8004, H 9780, HM 6898, NDM 5578, NUN 672, PX 1723, SUN 6368 and UG 4305. Trials were transplanted on 16 Apr and 13 May and one was direct seeded on 13 May. The number of plants expressing TSW-symptoms was recorded one to three days before harvest in each one bed by 21.3 meter long plot. Representative samples were tested with TSWV immunostrips. Highest percentage of TSW-symptomatic plants was 20, 16 and 11 in 16 Apr and 13 May transplant, and 13 May direct seeded trial, respectively. Variety AB 8058 has genetic resistance to the virus (SW5 gene) and incidence was very low. Incidence in Sun 6368, without SW5 gene, was similar to AB 8058. Other entries with consistently low incidence included H 2005, H 4007 and UG 4305. Knowledge of relative susceptibility of processing tomato varieties is important for those making management decisions regarding TSWV in this production area.

The transmission and management of Tobacco mosaic virus in a greenhouse environment

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Tobacco Mosaic Virus (TMV) is a troublesome virus in greenhouse production. Experiments were carried out to investigate the ease with which the virus spreads from infected greenhouse plants to non-infected plants through workers clothing, cutting tools, and contaminated greenhouse benches. Two tobacco cultivars (*Nicotiana tabacum* cvs White Burley and Samsun NN) were used as indicator plants. Two commonly used clothing materials (Cotton and Polyethylene fibre, Tyvek) for greenhouse dustcoats and latex for gloves were tested as vehicles for transmission of the virus. Workers contact on plants were simulated by applying various contact grades on infected and then healthy plants. The slightest brushing of the materials against infected plants and to healthy ones caused a disease incidence of $>70\%$ for cotton, 60% for Latex, and 30% for Tyvek. However, cleaning of these materials using various cleaning agents in a simulated laundry condition eliminated the virus. The efficacy of various disinfectants used in cleaning greenhouse cutting tools depended on the concentration and time of exposure. A simple dip into a 2% dry milk solution, 3% Menno-Florades (MF) or 14.6 g/liter of trisodium phosphate (TSP) eliminated the virus. The potential of these disinfectants to clean contaminated workers clothing, cutting tools and benches may allow reuse of these resources hence cutting down on production costs.

Soybean vein necrosis virus: A new threat to soybean production in Southeastern United States?

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A new soybean disease was identified in 2008 in Tennessee. Symptomatic soybeans were exhibiting vein clearing along the main veins that turned necrotic as leaves matured. Eventually, large portions of the leaves became necrotic. The symptomatic tissues were probed with antisera against 16 known soybean viruses, but none was found associated with the observed symptoms. Double-stranded RNA was extracted from infected plants and used as template for shotgun cloning. The majority of the clones corresponded to a new tospovirus that was given the provisional name of soybean vein necrosis virus (SVNV). Many tospoviruses cross-react in immunological tests, but SVNV did not react with antibodies against impatiens necrotic spot virus or tomato spotted wilt virus. These observations prompted us to further characterize the virus. SVNV shows minimal similarity to characterized members of the genus *Tospovirus* as it shares about 50% amino acid identities in the polymerase of L RNA and about 45% and 40% in the proteins of the M and S RNAs, respectively. Although a molecular detection test is currently available, however, we are working towards the development of an immunological-base assay that allows us to extend screening of soybean fields in Tennessee and the surrounding states for the presence and prevalence of SVNV in the Southeastern United States.

New viruses found in fig exhibiting mosaic symptoms

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It has been established that fig mosaic (FM) is caused by one or more viruses. The hypothesis that more than one virus can cause FM is due to the different intensity and symptom patterns that is often observed on infected plants. There has been limited information on the identity of the causal agent(s), a knowledge gap we aim to close. We have identified at least four new viruses in FM trees (FM virus 1-4). Sequence information of the polymerase region of FMV-1 indicates that is related to European mountain ash ringspot-associated virus and is probably the same virus identified recently and given the name Fig mosaic associated virus. FMV-2 is a typical badnavirus, closely related to *Citrus yellow mosaic virus*. FMV-3 and -4 belong to the genus *Clusterovirus* in the family *Clusteroviridae* and are different from the recently identified Fig leaf mottle associated virus-1. Detection protocols have been developed for these four viruses. A survey of FM trees showed that FMV-1 is present in all samples whereas FMV-2, -3, -4 were found in subsets of the samples. Transmission trials are under way for the latter three new viruses to identify vectors and better understand their involvement in disease development and severity. Mechanical inoculations onto herbaceous hosts resulted in several plants that developed severe virus-like symptoms but were not infected with FMV-1, -2, -3, -4, indicating that the number of viruses found in FM plants will continue to increase.