have a role in the management of *C. sordidus* on bananas, but lower doses will be required to be economic.

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Thursday, STUDENT POSTER VPS17

Development and use of a DNA diagnostic for ascovirus of *Helicoverpa armigera* in Australia.

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A DNA diagnostic method was developed for the detection of ascovirus in *Helicoverpa armigera* in south-eastern Queensland, Australia. We discuss how the diagnostic method was developed and its potential applications. The diagnostic method uses the Polymerase Chain Reaction (PCR) to amplify a region of the ascovirus polymerase gene (approximately 500 bp). Specific primers were designed for this purpose. This region has been sequenced and will be studied for phylogenetic relationships. Furthermore, virus identification will be undertaken. Ascovirus symptoms were observed in field collected larvae of *Helicoverpa spp.* The diagnostic was developed to study the prevalence of ascovirus in field collected larvae that show typical ascovirus symptoms. Secondly, the diagnostic test will be used to confirm if the parasitoid wasp *Microplitis demolitor* is the primary vector. The diagnostic method will be used to determine if there are other vectors of the ascovirus. Preliminary PCR assays detected ascovirus in the head, abdomen and prolegs of field collected *H. armigera*. The preliminary tests have shown a positive result for the presence of ascovirus in approximately 90% of the larvae diagnosed by visual techniques. The DNA diagnostic will be used to study ascovirus interaction with other biological control agents, such as NPV and parasitoids. This information will be used in developing Integrated Pest Management (IPM) strategies that utilise ascovirus mortality. Further work on the polymerase DNA of this ascovirus will be used for inter and intra-species relationship and phenotype studies, such as differences in virulence between isolates.

Friday, 10:30 SYMPOSIUM

Introduction of *Thelohania solenopsae* as a microbial control agent for the red imported fire ant, *Solenopsis invicta*.

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Thelohania solenopsae is a microsporidium pathogen of imported fire ants. Imported fire ant colonies have been infected with *T. solenopsae* collected from Florida via the introduction of infected brood. Artificial inoculations of laboratory colonies have resulted in infected queens with reduced queen weights and oviposition rates. This has resulted in significantly less brood (88%) and lower queen survivorship than in control colonies. To examine the potential host range of the Florida collected *T. solenopsae*, infected fire ant brood was introduced into laboratory colonies of six species of ants. Infections were detected only in black imported fire ant, *S. richteri*, colonies obtained from Argentina. Examinations of field collected colonies of 7 non-*S. invicta* ant species were also negative for *T. solenopsae* infection.

Field inoculations were initiated in Florida in 1997, and 4 of 5 inoculated colonies became infected. Infections were detected in non-inoculated fire ant nests on subsequent sample dates suggesting that infections had spread. Introductions have also been made in ten states to document the potential impact of *T. solenopsae* on red imported fire ants in different geographic areas of the southern U.S.

Tuesday, 17:15 STUDENT

Partial purification, characterization and molecular cloning of *Bacillus thuringiensis* Cry1A toxin receptor A from *Heliothis virescens*

Daniela I. OLTEAN [1], Sarjeet S. Gill [1,2], Ashok K. Pullikuth [3] and Hyun-Ku Lee[2]

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Although extensively studied, the mechanism of action of insecticidal *Bacillus thuringiensis* Cry toxins remains elusive and requires further elucidation. Toxin receptors in the brush border membrane demand particular attention as they presumably initiate the cascade of events leading to insect mortality after toxin activation. The 170 kDa Cry1Ac toxin binding aminopeptidase from the tobacco budworm, *Heliothis virescens* was partially purified and its corresponding cDNA clone was isolated and sequenced. The cDNA clone identifies a protein with a putative GPI-anchor, and a poly-threonine stretch clustered near the C-terminus with predicted O-glycosylation. Partial purification of the 170 kDa aminopeptidase also resulted in the isolation of a 130 kDa protein that is immunologically identical to the 170 kDa and contains the same N-terminus. Soybean agglutinin lectin blots suggest both proteins are glycosylated. Cry1Ac toxin affinity determinations for the two proteins show that these two proteins have substantially different toxin affinities. These data suggest post-translational modifications can have a significant effect on Cry1A toxin interactions with specific insect midgut proteins.

Tuesday, 14:00

Delaying Resistance Development in Insect Pests Inhabiting Transgenic Corn

ONSTAD, D. W., and C. A. Guse

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We used simulation models to evaluate different strategies for delaying resistance by European corn borer and southwestern corn borer to corn expressing a toxin produced by *Bacillus thuringiensis* . The models included population dynamics, genetics and economics.

Friday, 10:45

Cloning and Sequencing of Molecular Chaperone *p21* Genes from *Bacillus thuringiensis*

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Molecular chaperones can be defined as a class of proteins that interact with non-native states of other proteins. Studying comprehensively molecular chaperones in *Bacillus thuringiensis* is very important and beneficial to develop genetically engineered strains. Previous studies have shown that the 20-kDa protein (P20) from *B. thuringiensis* subsp. *israelensis* (BTI) acts as a molecular chaperone and enhances the net yield of Cry4Aa, Cry11A and Cyt1Aa, but has little influence on the formation of crystals. In order to estimate the distribution of this gene among *B. thuringiensis* strains and to further investigate their potential role in the synthesis, assembly and formation of crystals, PCR primers were designed from the sequence of *p20* gene. PCR analysis was