

Texas A&M University Department of Entomology

Sixth Annual Graduate Student Forum



Suraj Saksena

Major Professor: Dr. Max Summers
Ph.D. Candidate

“Molecular Mechanism of Targeting and Integration of AcMNPV-ODV E66.”

During baculovirus infection, integral membrane proteins destined to become envelope proteins of the occlusion-derived virus (ODV) are synthesized and trafficked to viral-induced intranuclear microvesicles and the ODV envelope. This laboratory is using several of the ODV envelope proteins as markers to investigate the molecular basis of trafficking and ODV envelopment. In this study focus was placed upon the first event in the trafficking pathway, primary integration in the ER membrane, and interaction with the translocon components during the process of integration. The data show that ODV-E66 targets to the ER membrane in a SRP (Signal Recognition Particle)-dependent manner, specifically associates with the translocon of the ER, and integrates into the ER membrane through the translocon. Membrane integration of signal anchor transmembrane segments is believed to be driven by hydrophobicity; however, we demonstrate that two translocon proteins, Sec61 α and TRAM, associate with the transmembrane segment of ODV-E66. Similar interactions with Sec61 α and TRAM were observed with the first transmembrane segment of an inner nuclear membrane protein, LBR (Lamin B Receptor). Thus, at the time of primary insertion and integration into the ER membrane, the viral protein ODV-E66 is using the cellular pathway used by a well-characterized host inner nuclear membrane protein.



Lucille Benavides

Major Professor: Drs. Craig Coates and Patricia Pietrantonio
M.S. Candidate

“RNA Interference of the 5HT₇-like Serotonin Receptor of the Mosquito *Aedes aegypti*, a Vector of Dengue and Yellow Fever.”

Aedes aegypti is the major vector of viruses that cause dengue and yellow fever. Little is understood about how diuresis is controlled and regulated in *Ae. aegypti*, a highly important function due to the haematophagic nature of this insect. It has been hypothesized that a G-protein coupled receptor, 5HT₇-like serotonin receptor, cloned from *Ae. aegypti* and localized to the tracheolar cells associated with the Malpighian tubule, may be important in the regulation of tracheolar ventilation in the adult female mosquito. However, the involvement of this receptor in this function has not yet been demonstrated *in vivo*. In order to determine the function of this receptor in *Ae. Aegypti*, we propose to silence gene expression of the 5HT₇-like serotonin receptor gene through the use of RNA interference. RNA interference involves the homology-dependent degradation of specific mRNAs that code for a gene of interest in response to the presence of double-stranded RNA molecules specific to the target gene. Using the HiScribe RNAi Transcription Kit (New England Laboratories Inc.), dsRNA homologous to three specific regions of the receptor cDNA will be generated. *In vitro*, we will introduce the dsRNA through electroporation into mammalian cells that express the receptor in order to determine receptor sensitivity to RNA interference. *In vivo*, dsRNA will also be introduced into the pupae and adult life stages using microinjection. The hypothesis is that silencing of receptor gene expression will result in an absence of serotonin receptors needed for binding of serotonin and that this will result in failures in respiration/ventilation in the Malpighian tubule that may influence other physiological processes such as post-emergence and post-feeding diuresis. In addition, the reduced ability of the insect to signal through the serotonin receptor may result in reduced fitness, altered diuresis, altered ability to fly, or alteration of other, yet unforeseen, physiological processes.

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Joe Gillespie

Major Professor: Dr. Anthony Cognato
Ph.D. Candidate

“A Predicted Structure for the Expansion Segments D2 & D3 of the LSU 28S rRNA from Chrysomelid Beetles: Applications for Homology Assignment and Maximum Likelihood Modeling of rRNA Molecules.”

Standard models of DNA substitution are not appropriate for the phylogenetic analysis of ribosomal-encoding DNA (rDNA) sequences because of the non-independence of pairing-nucleotides maintaining higher order structure in these molecules. Several models of rDNA evolution (that are dependent on predicted secondary structure) have recently been proposed, and 2 programs now exist to simultaneously combine pairing and non-pairing regions using more appropriate likelihood models for phylogenetic analysis. Specifically, I present an approach that incorporates both a standard 4x4 substitution model for non-pairing regions and a more complex rRNA model that treats pairing-regions as linked characters in the substitution matrix. I explore a wide range of existing rRNA models and report on the efficiency of each model as it pertains to the helical regions of the nuclear 28S expansion segments D2 and D3 in 230 rootworm beetles (Coleoptera: Chrysomelidae). The results of these rRNA-specific models are compared to standard methods of phylogeny reconstruction. In general, phylogenetic methods that do not account for the dependence of pairing-nucleotides in rRNA data yield trees with inflated resolution and branch support measures (bootstrap, Bremer support, posterior probabilities). Thus, the accommodation of character non-independence is more suitable for the phylogenetic analysis of rRNA data than standard methods (i.e., parsimony, weighting, DNA likelihood models) that ignore the coevolution (hence dependence) of pairing-nucleotides.



Mei-Er Chen

Major Professor: Dr. Larry Keeley and Dr. Patricia Pietrantonio
Ph.D. Candidate

“cDNA Cloning and Transcriptional Regulation of the Vitellogenin Receptor from the Imported Fire Ant, *Solenopsis invicta* Buren (Hymenoptera: Formicidae).”

The fire ant, *Solenopsis invicta*, is an urban, agricultural, and medical problem in the United States. Fire ant polygyne colonies contain multiple inseminated queens. Its high reproductive capacity makes *S. invicta* difficult to control. One polygyne colony can produce 700 eggs within 5 hours. Thus, inhibiting egg maturation is a promising strategy for fire ant control.

Receptors that transport vitellogenin into oocytes are of vital importance to egg-laying species because they promote oocyte development. In this study, we describe the cloning of the first hymenopteran vitellogenin receptor (VgR) cDNA. Using reverse transcription polymerase chain reaction (RT-PCR) and 5', 3' rapid amplification of cDNA ends (RACE), fragments encompassing the entire coding region of a putative VgR were cloned and sequenced. The complete cDNA has a length of 5764bp, coding for a 1982-residue protein with a predicted molecular mass of ~201 kDa (=SVgR). Northern blot analysis demonstrated that the 7.4-kb SVgR transcript was present only in ovaries of reproductive females – both alates (virgins) and queens (mated). The transcript was more abundant in alates prior to the onset of oocyte maturation. The developmental profile of transcriptional expression was determined by semi-quantitative RT-PCR and showed that SVgR transcriptional expression increased with age in alate females. *In vitro* treatment of ovaries with methoprene, a juvenile hormone (JH) analog, showed a 2-fold increase in SVgR transcript. This suggests that the SVgR gene is regulated by JH. Future studies will determine the SVgR protein levels by western blot analysis.

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Jeremiah Dye

Major Professor: Dr. Kevin Heinz
M.S. Candidate

“Implications of Natural Enemy Strain Differences for Biological Control of Aquatic Weeds (*Salvinia* spp.)”

Giant salvinia, *Salvinia molesta* Mitchell, and common salvinia, *Salvinia minima* Baker, are free floating aquatic ferns native to South America that can grow rapidly to cover the surface of lakes and streams. Giant salvinia has caused severe problems in the waterways of 13 countries (including the U.S.) on three continents, while common salvinia can be problematic in areas of the southeastern United States. Giant salvinia has been controlled successfully in Australia and also in many other countries through releases of the weevil, *Cyrtobagous salviniae* Calder and Sands. In Florida, a genetically distinct strain of *C. salviniae* appears to reduce the severity of *S. minima* infestations. To date, there has been no published comparison of the relative efficacy of different strains weevil in controlling each salvinia species; and the effect of temperature has only been studied for the strain used in Australia. In a factorial experiment with weevil strain, plant species and temperature profile as factors, we examined differences in population growth rates of both weevil strains on both host plants. We also examined the effects of adult and larval feeding in these treatments on the change in biomass of the plants. This information allows us to make recommendations about conditions in which it is appropriate to release each weevil strain against salvinia infestations.



Jared Burks

Major Professor: Dr. Max Summers
Ph.D. Candidate

“BV/ODV E26 localization in *Spodoptera frugiperda* Cells Suggests Two Models for Protein Trafficking.”

Autographa californica nuclear polyhedrosis virus (AcNPV) has two viral forms, budded virus (BV) and occlusion derived virus (ODV). AcNPV encodes a 26-kDa protein named BV/ODV E26, an envelope protein of both viral forms. Viral maturation processes for these two viral forms allow for different sources of viral envelopes. BV is enveloped by budding through the plasma membrane and ODV is enveloped in the nucleus. E26 is an envelope protein of both viral forms and localizes to the plasma membrane and nucleus resulting in bi-directional trafficking. Currently, the data supports two methods for trafficking E26 to these locations. Model I, membrane-mediated trafficking requires an interaction between E26 and the endoplasmic reticulum. Early events in model I would localize E26 to the cell surface, with later events redirecting it to the nucleus. Model II, nuclear localization signal mediated trafficking, requires an interaction with the cellular Importin proteins, allowing import through the nuclear pore complex. Once in the nucleus, maturation events or nuclear proteins function to relocate E26 to the cell surface; and with infection progressing, these events diminish allowing nuclear accumulation of E26. The focus of my Ph.D. project is to identify domains in E26 and/or proteins responsible for trafficking E26 to membranes located in the nucleus. Experiments will be conducted in three basic areas: determination of the basis of the E26 intracellular membrane interaction; identification of putative E26 nuclear trafficking domains; and identification of protein-protein interactions, if present, that are specific to directing E26 to the nucleus.

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Darren Hagen

Major Professor: Dr. Craig Coates
Ph.D. Candidate

“Assessment of the Use of Endogenous and Exogenous Germline Tissue-specific Promoters within the Mosquitoes, *Anopheles gambiae* and *Aedes aegypti*.”

Aedes aegypti and *Anopheles gambiae* are vectors for pathogens that have a dramatic effect on world health. Currently, methods of transformation are being developed for these species in order to create stable transgenic lines incapable of transmitting disease-causing pathogens. The creation of genetic transformants relies on the expression of a transposase protein in the germline cells to promote the integration of transgenes into the insect chromosomes. Spatial restriction of gene expression is a powerful tool for transposon-mediated transgenesis. By confining transposable element mobility to the germline, the number of double strand breaks occurring in somatic cells will be reduced and will potentially increase the number of transgenic offspring produced, by concentrating transposition events in the germline cells. My work is directed towards the identification of genes expressed strictly within the cells of the germline. By identifying these genes, the promoters can then be cloned and used to drive transposase expression. The identification of endogenous germline tissue-specific promoters within *Ae. aegypti* and *An. gambiae* will allow for increased rates of transcription as well as ensuring germline specificity of the transposase. It is hypothesized that the use of endogenous tissue-specific promoters will allow for the creation of stable lines of transgenic insects. Additionally, function will be tested across species to assess the promoter's ability to retain tissue specificity.



Matt Yoder

Major Professor: Dr. Robert Wharton
Ph.D. Candidate

“The Role of Diapriid (Hymenoptera: Diapriidae) Phylogenetics in Hymenopteran Systematics”

Hymenopteran (bees, wasps, and ants) systematics has been in vogue in recent years. This is due in part to a desire to re-analyze past hypotheses of evolutionary relationship (synapomorphy) in a quantitative manner. Some of these larger scale analyses have been hindered by a lack of knowledge regarding obscure or relatively-poorly known hymenopteran families. Here I outline some of the problems that have arisen both in extrafamilial hymenopteran phylogenetic analyses and in intrafamilial diapriid taxonomy due to gaps in our knowledge of diapriid phylogenetics.

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Amy Bader

Major Professor: Drs. Kevin Heinz and Robert Wharton
M.S. Candidate

“Parasitoid Invasive Ability: Its Importance to Leafminer Biological Control in Chrysanthemum.”

Liriomyza huidobrensis (Blanchard) (Diptera: Agromyzidae), the pea leaf-miner, is a highly polyphagous and economically important pest of many vegetables and ornamentals worldwide. Biological control of this pest is becoming increasingly popular in protected culture in North and South America, Europe, and Japan. Currently the only two natural enemies of *Liriomyza* species being commercially reared are *Diglyphus isaea* (Walker) (Hymenoptera: Eulophidae), and *Dacnusa sibirica* Telenga (Hymenoptera: Braconidae). Although they are currently available to be released alone or in tandem, their invasive abilities have not been closely investigated. I am testing the competitive interactions and invasive abilities of the commercially available natural enemies and determining the feasibility of producing a marketable crop using these parasitoids either alone or in tandem.



Shawn Williamson

Major Professor: Dr. Max Summers
Ph.D. Candidate

“AcMNPV ODV-E66 Encodes a Nuclear Targeting Sequence That Is Sufficient for Nuclear Envelope and Microvesicle Localization of Integral Membrane Proteins.”

Infection by baculoviruses induces the production of intranuclear unit membrane structures termed microvesicles (MV). Proteins destined for the ODV envelope localize to these structures, and viral nucleocapsids have been visualized interacting with MV, providing evidence that MV are likely the source of the ODV envelope. ODV envelope proteins also localize to the inner nuclear membrane (INM), the outer nuclear membrane and cytoplasmic membranes in close proximity to the nuclear envelope (NE). Previous work in the Summers' Laboratory identified a domain within one of these proteins, ODV-E66 (E66), as sufficient to localize proteins to ODV envelopes, MV, and NE. Comparison of the amino acid sequence of this domain with cellular INM proteins finds an overall similarity between the E66 domain and domains within cellular INM proteins. The goal of this study is to determine the specific character of the nuclear envelope targeting domain of E66. Site-directed mutational analysis will be utilized to remove or modify regions within this E66 domain. Additionally, an INM protein, lamin B receptor (LBR), will undergo similar analysis. Furthermore, we hope to provide insights into the mechanism of localization to the inner nuclear membrane using both LBR and E66.

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Lara Lewey

Major Professor: Dr. Craig Coates

Ph.D. Candidate

“Identifying the Genetic Basis for Varroa mite Resistance in the Honey Bee, *Apis mellifera*.”

The European honey bee, *Apis mellifera*, has been manipulated by man for thousands of years and is very valuable to the agriculture industry. The honey bee is depended upon by apiculturists who take advantage of their honey-making ability and by farmers as a pollination agent to increase the yield of their crops. *Apis mellifera* is plagued by many pathogens, the most significant of which is the Varroa mite, *Varroa destructor*, which feeds on the hemolymph of honey bee pupae. This affects the hive by weakening the young bees; and when heavily concentrated, the mites can kill the entire hive within a matter of years. There is no preventative measure for Varroa infestation; and as such, the only way to combat the mites is to treat the entire hive with a miticide every year. If the treatment is not administered, the hive will eventually die as a result of mite invasion. However, these treatments can become costly and time consuming to the beekeeper. Feral honey bee colonies, which some farmers rely on, are typically not treated, and an infestation results in the loss of the hive.

A particular strain of honey bee has been developed through selective breeding, which shows a natural resistance to the Varroa mite. This strain is referred to as SMaRt, for Suppression of Mite Reproduction. The resistance trait is inherited from parent to offspring as an additive trait. We feel that resistance to the Varroa mite is due to a genetic component possessed by the SMaRt bee but not by the susceptible bee.

Our goal is to identify the honey bee gene(s) responsible for conveying resistance to the Varroa mite. To evaluate the genetic basis underlying this resistance we propose to use Suppressive Subtractive Hybridization (SSH) to investigate differences in gene expression between lines and infection states. Many cDNAs are expected to be revealed through the SSH procedure and to eliminate some of the background, a differential screening procedure will be performed. All positive results obtained through differential screening will be confirmed by Northern blot and RT-PCR analysis. Isolation of the particular gene(s) which confer resistance to the mites will be beneficial, allowing an assay to be developed to detect the presence of the resistance trait in a particular hive. The ability to genetically select for this trait will benefit beekeepers and farmers, reducing the necessity of miticide treatments.



Christine E. Gray

Major Professor: Dr. Craig Coates

Ph.D. Candidate

“Cloning of Mosquito CTCFs and PCR-assisted *in-vitro* Identification of Their DNA Binding Sites.”

CTCCC-binding factor (CTCF) has been well-characterized in vertebrates as a multivalent transcription factor and a key component of all known vertebrate insulators. It has been implicated in the maintenance of imprinted loci, X-chromosome inactivation and genome-wide de-methylation during male germ-line development. CTCF was long-thought to be limited to vertebrates, but it appears to have more ancient origins. A single database entry describes a putative homologue cloned from *Drosophila melanogaster*. Additional *in-silico* analysis reveals significant sequence homologies in both *Anopheles gambiae* and *Apis mellifera*. Of particular interest in this study is the central role CTCF plays in insulator function. Insulators are wide-spread among eukaryotic organisms and function in maintenance of divergent gene expression profiles and genome organization. Transformation of medically-important insect species remains labor-intensive and generally inefficient, with variable expression both within and between families. The cDNAs of CTCF homologues from *Aedes aegypti* and *An. gambiae* will be cloned, expressed and used in PCR-assisted binding site selection to identify putative endogenous insulators. Once characterized, these insulators could be used to protect transgenes from silencing the effects of neighboring regulatory elements.

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Jessica Usener

Major Professor: Dr. Anthony Cognato
M.S. Candidate

“Phylogenetic Revision of Desert Fireflies (Coleoptera: Lampyridae: *Microphotus*).”

Microphotus species occur in the southwestern United States and adjacent parts of Mexico. These glowworm fireflies do not flash in sexual communication, rather the apterous females glow to attract males (Green 1959). Males are fully winged and weakly bioluminescent. Seven species are currently recognized, primarily by male genitalia and secondarily by elytral length, color, and number of antennomeres. However, color and number of antennomeres are polymorphic within some species. The dearth of diagnostic characters and the sympatric range of most species confounds the identification and delimitation of species.

A phylogeny based on morphological and molecular data will help determine species boundaries and address patterns of speciation in *Microphotus*. Specimens used in J. W. Green's 1959 revision have been borrowed from institutional collections. A number of these will be dissected and explored for taxonomically informative morphological characters. DNA for molecular analysis will be extracted from fresh specimens and sequenced. Polymerase chain reaction will amplify a portion of DNA coding for a mitochondrial gene (cytochrome oxidase I), a nuclear gene (luciferase), and a ribosomal gene (28S). The morphological and molecular data matrices will be combined for parsimony analysis. Monophyletic groups that are morphologically or ecologically distinct will be considered valid species and described.



Brandon Ripple

Major Professor: Dr. Marvin Harris
M.S. Candidate

“Screening for Resistance to Whiteflies in Cotton Race Stocks.”

Whiteflies (*Bemisia tabaci*, *Biotype B*, Homoptera: Aleyodidae) have increased in importance to cotton farmers in the United States. In 2002, whiteflies caused losses of 23,169 bales of cotton and infested over 1 million acres, mostly in California, Texas, and Arizona. Whiteflies feed on the leaves of cotton plants and produce “honeydew”, a sticky liquid secretion. Honeydew sticks to the lint and causes difficulties during cotton processing. High densities of whiteflies can also cause direct damage to the cotton plant by stripping it of vital nutrients, thus decreasing the productivity and health of the plant.

This research evaluates 116 cotton race stocks and two commercial controls (PSC 355 and Delta Pearl) for resistance to whiteflies. Screening is performed using an excised leaf technique with a cohort population of immature whiteflies. Cotton is grown in a greenhouse to about 8-10 true leaf stage. Four upper leaves are then cut from the plant and the petioles are placed in test tubes containing ¼ strength Hoagland's solution. Ten whiteflies are placed on each leaf and allowed to oviposit for 24 hours. Adults are subsequently removed leaving the cohort population of eggs. Periodic measurements are taken on the whitefly number and the life stage. These observations are continued until all of the cohort has reached adulthood or is considered dead some 30-40 days later. Data are then analyzed to compare mortality rates and time to adulthood of the different cotton race stocks with the controls.

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Johnny Chen

Major Professor: Dr. Brad Vinson

Ph.D. Candidate

“Effects of *Thelohania solenopsae* (Microspora: Thelohaniidae) on Profiles of Hemolymph Proteins of Queens in Red Imported Fire Ants, *Solenopsis invicta* (Hymenoptera: Formicidae).”

Because insect fat bodies are known to contribute most of the hemolymph proteins, the effects of fat body intracellular parasitism by the microsporidia, *Thelohania solenopsae*, on fire ant hemolymph proteins were investigated. Protein profiles were compared between infected and uninfected fire ant alates and dealates (both inseminated and uninseminated) using sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS–PAGE) and silver staining detection. Uninfected dealated (both inseminated and uninseminated) queens from infected colonies were also analyzed. In the case of inseminated, dealated queens, several protein bands were found to be down-regulated in the infected queens; while other protein bands were found to be up-regulated in the control queens from uninfected colonies. In the case of uninseminated dealates, protein bands were also observed to be down-regulated in infected queens. In the case of alated queens, several protein bands are also found to be down-regulated in infected queens. These results suggest that, by infecting the fat body tissues, *T. solenopsae* may cause the down-regulation of several proteins and peptides in the hemolymph of fire ant alates and dealates.



Paul D. Barron

Major Professor: Dr. Craig Coates

Ph.D. Candidate

“Differential Gene Expression Among *Amblyomma americanum* Nymphs in Response to Feeding.”

Ticks are obligate ecto-parasitic hematophagous Arthropods. Sclerotization of the exoskeleton is the key character for dividing ticks into two primary families. Those ticks with a sclerotized exoskeleton are referred to as hard ticks and are placed in the family Ixodidae. Ixodid ticks transmit a variety of disease pathogens including those that cause Lyme disease, Ehrlichioses, Heart Water, Texas Cattle Fever and many others. Lone star ticks, *Amblyomma americanum*, are the vectors of Human Monocytic Ehrlichiosis, Tularemia, and clinical evidence suggests the transmission of a “Lyme-like” borreliosis. Typically, Ixodid ticks feed on several hosts, although there are exceptions. When a tick feeds on paratransmitting host, that tick has the potential to become infected and transmit the disease to other hosts. The tick becomes a vector of these diseases perpetuating complex zoonotic cycles. Feeding behavior is central to these zoonotic cycles. Additionally, feeding is known to induce the production of a variety of pharmacologically active substances by the salivary glands among Ixodid ticks. Histological examination during feeding reveals a dramatic increase in the production RNA in all tissues examined. Theoretically, feeding induces *de novo* synthesis of RNA, including mRNA. Thus, feeding induces gene expression. Subtractive Suppression Hybridization (SSH) was employed to examine gene expression during feeding at the transcriptional level. Subsequent cloning, isolation, and sequence analysis of these differentially-expressed genes in response to feeding will be discussed.

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Andrea Julian

Major Professor: Dr. Craig Coates
M.S. Candidate

“Use of Bioinformatics to Investigate and Analyze Transposable Element Insertions in the Genomes of *Caenorhabditis elegans* and *Drosophila melanogaster*, and Into the Target Plasmid pGDV1.”

Most transposons do not insert completely randomly into their host genome, with class II transposable elements (TEs) utilizing target sequences of between 2 – 8 bp in length, which are duplicated upon insertion. Furthermore, amongst insertion sites, certain sites are preferred for insertion and hence are classified as “hot spots,” while others not targeted by TEs are referred to as “cold spots”. The hypothesis tested in this analysis is that, in addition to the primary consensus sequence, secondary and tertiary DNA structures have a significant influence on TE target site preference. Bioinformatics was used to predict and analyze the structure of the flanking DNA around known insertion sites and cold spots for various TEs, to understand why insertion sites are used preferentially to cold spots for element integration. Hidden Markov Models were modeled and trained to analyze datasets of insertions of the *P* element in the *Drosophila melanogaster* genome, the *Tc1* element in the *Caenorhabditis elegans* genome, and insertions of the *Mos1*, *piggyBac* and *Hermes* transposons into the target plasmid pGDV1. Analysis of the DNA structural profiles of the insertion sites for the *P* element and *Hermes* transposons revealed that both transposons targeted regions of DNA with a relatively high degree of bendability/flexibility at the insertion site. However, similar trends were not observed for the *Tc1*, *Mos1* or *piggyBac* transposons. Hence, we believe that the secondary structural features of DNA can contribute to target site preference for some, but not all transposable elements.



Ryan Caesar

Major Professor: Dr. Anthony Cognato
M.S. Candidate

“Population Structure of Featherwing Beetles (Coleoptera: Ptiliidae) in the Klamath Ecoregion of Northern California: Implications for Conservation Practices.”

The Klamath Ecoregion of Northern California is one of the most unique temperate conifer forest ecosystems in the world, yet land management and conservation in the Klamath concentrates on a myopic “umbrella species” approach. Late Successional Reserves (LSR’s) have been established throughout the region, however no consideration has been given to the ecology, biogeography, or biodiversity of sympatric organisms. Phylogeographic structure of populations, as revealed by phylogenetic analysis of DNA sequences, allows investigators to make inferences about evolutionary processes such as current and historical gene flow and historical biogeography. This information is valuable for the improvement of conservation decision-making processes. Examination of intraspecific phylogeography of edaphic macroarthropods can reveal patterns of genetic diversity, which may allow for an improved regional conservation plan. In this study, a portion of the mitochondrial DNA cytochrome oxidase I (mtDNA COI) gene is used to infer intraspecific phylogenetic structure among populations of the featherwing beetle genera *Acrotrichus* and *Ptiliolum* (Coleoptera: Ptiliidae). The implications of phylogeographic patterns in edaphic insects and the processes that shape them for conservation biology in the Klamath are discussed.

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Michael (Walker) Hale

Major Professor: Dr. Brad Vinson
MS.Candidate

“Host/parasite Relationship Between Microsporidia, *Thelohania solenopsae* and Host, *Solenopsis invicta*.”

Thelohania solenopsae Knell, Allen and Hazard, an obligate intracellular parasite of *Solenopsis invicta* Buren, has been examined as a potential biological control agent for the imported fire ant. This study was conducted in 2002 and 2003 to assess the effects of the entomopathogen, *T. solenopsae*, on polygynous, red imported fire ant colonies. Field colonies were excavated from College Station, TX (n=29). Brood masses of 13 colonies were measured and total number of queens per colony counted. All queens (n=263) were dissected to determine insemination status, then were macerated and screened for *Thelohania* using phase-contrast microscopy at 400X. Alates were counted and total wings per individual were assessed. There was a significant positive correlation of total queens to brood mass ($p=.05$ Spearman's rho). Total queen numbers were greater in infected colonies when compared to non-infected colonies ($p<.001$ Mann-Whitney U). An average of 67% of all queens sampled in infected mounds showed no indication of microsporidian infection and a mean of 79% of all infected queens sampled were also inseminated. These data suggest increased acceptance of queens in an infected colony, a slow infection transfer rate within an infected mound, and behavior to transfer the intracellular parasite to inseminated queens over un-inseminated queens within an infected colony.



Brian K. Urbain

Major Professor: Dr. Robert Wharton and Dr. Jim Woolley
Ph.D. Candidate

“A Comparison of Ichneumon Wasp (Hymenoptera: Ichneumonidae), Species Diversity Between Two Habitats in Western Washington: The Latitude Issue, or Lack of, Revisited.”

Ichneumon wasps comprise the largest family (Ichneumonidae) in the order Hymenoptera (bees, wasps, ants, etc.), with an estimated 60,000 species worldwide and a cosmopolitan distribution. The vast majority are parasitoids of other arthropods, mainly insects, potentially playing an important role in the population dynamics of their hosts. Several studies have suggested that ichneumonid species diversity is greater at higher latitudes than lower ones, a trend contrary to that found in most groups of organisms. Some authors have indicated that peak diversity within North America occurs at mid-latitudes. Little attention, however, has focused on variation in diversity between different habitats of similar latitude and how such variance may skew diversity estimates made from comparisons of single localities, irrespective of habitat, along a latitudinal gradient. This study compares ichneumonid species diversity between two habitats of similar latitude in western Washington based on simultaneous collections from single Malaise traps at each site over a period of two consecutive years (1999-2000). Data from an additional year of collecting (1998) at one site are also presented to further examine species accumulation over time.

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