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Highlights of Tick-borne Disease Research at Mississippi State University

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ABSTRACT

Ticks are important public health pests in Mississippi, being carriers of numerous disease agents, including the agents of Rocky Mountain spotted fever (and related “spotted fever” illnesses), Lyme disease, ehrlichiosis, anaplasmosis, and tularemia. A seven-member team at Mississippi State University is currently investigating the ecology, prevalence, and natural history of these tick-borne diseases in the state. Preliminary data indicate the presence of a Lyme-like disease organism, *Borrelia lonestari*, as well as *Ehrlichia chaffeensis*, *Anaplasma phagocytophilum*, and several spotted fever group rickettsial organisms in Mississippi ticks and wildlife, including the newly emerging human pathogen, *Rickettsia parkeri*. In addition to an overview of tick biology, the significance of these research findings are presented and discussed, along with an outlook for future research.

INTRODUCTION AND MEDICAL SIGNIFICANCE

Ticks are second only to mosquitoes as vectors of human disease agents, being responsible for thousands of cases of human illness worldwide annually. In fact, they transmit more cases of human disease than any other arthropod in Europe and North America. Lyme disease alone is considered responsible for perhaps as many as several hundred thousand clinical cases each year in Europe (Ginsberg and Faulde 2008). There are at least 20,000 cases of the illness reported in the U.S. annually, with over 27,000 reported in 2007 (CDC 2008). In addition, many tick-borne diseases are quite severe clinically, with sudden onset of high fever, headache, and myalgias, often accompanied by nausea and other symptoms. Rocky Mountain spotted fever is fatal in as many as 5% of cases, even with treatment, while Crimean-Congo hemorrhagic fever, caused by a virus, is the most severe tick-borne disease in Europe with a fatality rate of about 10% (Ginsberg and Faulde 2008).

The ecology of infectious diseases, and especially that of emerging tick-borne diseases, is a crucial component of public health and safety in the 21st century. Many tick-borne human diseases, especially those that are zoonotic, have complex life cycles wherein different stages of the tick feed on different hosts, become infected, and (later) infect humans or other animals. One flaw of modern medicine is to depend too heavily

on pharmacologic agents for disease prevention and control without understanding the natural life cycles of the causative agents and using this knowledge to intervene and mitigate those negative health effects. The relationship of diseases to the environment has been neglected in recent decades, making us vulnerable to widespread and potentially devastating outbreaks. This paper highlights past and current research at Mississippi State University concerning ticks, their relationship to the environment, tick ecology, tick-borne disease transmission, and the factors affecting that transmission.

TICK BIOLOGY AND ECOLOGY

Basic Tick Biology. Ticks are arachnids in the Phylum Arthropoda. Within this phylum, three families of ticks are currently recognized in the world: 1) Ixodidae (hard ticks), 2) Argasidae (soft ticks), and 3) Nuttalliellidae (a small, curious, little-known group with some characteristics of both hard and soft ticks). The terms hard and soft refer to the presence of a dorsal shield or scutum in the Ixodidae, which is absent in the Argasidae (Figure 1). Hard ticks display sexual dimorphism, whereby males and females look obviously different, and the blood-fed females are capable of enormous expansion. In some species of hard ticks the males do not feed; others imbibe only small quantities. Hard tick mouthparts are anteriorly attached and visible from dorsal view (Figure 1A). If

eyes are present, they are located dorsally on the sides of the scutum (Figure 2). Soft ticks are leathery and nonscutate (no shield), without sexual dimorphism (Figure 1B). Their mouthparts are subterminally attached in adult and nymphal stages and not visible

from dorsal view. Eyes, if present, are located laterally in folds above the legs.

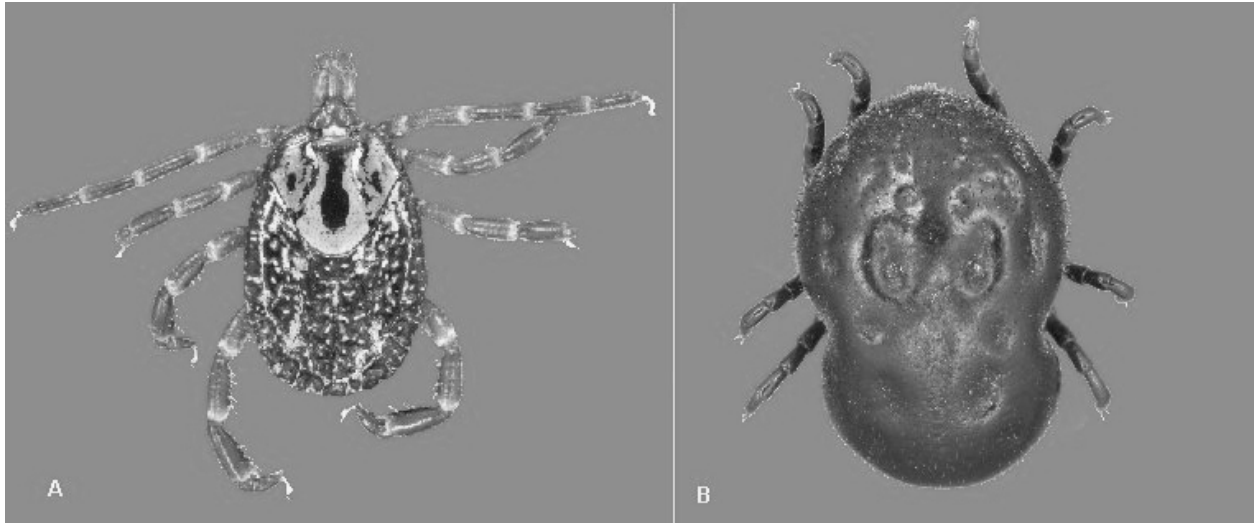


Figure 1. Examples of a hard tick (A) and soft tick (B) (Photos courtesy Blake Layton, Mississippi State University).

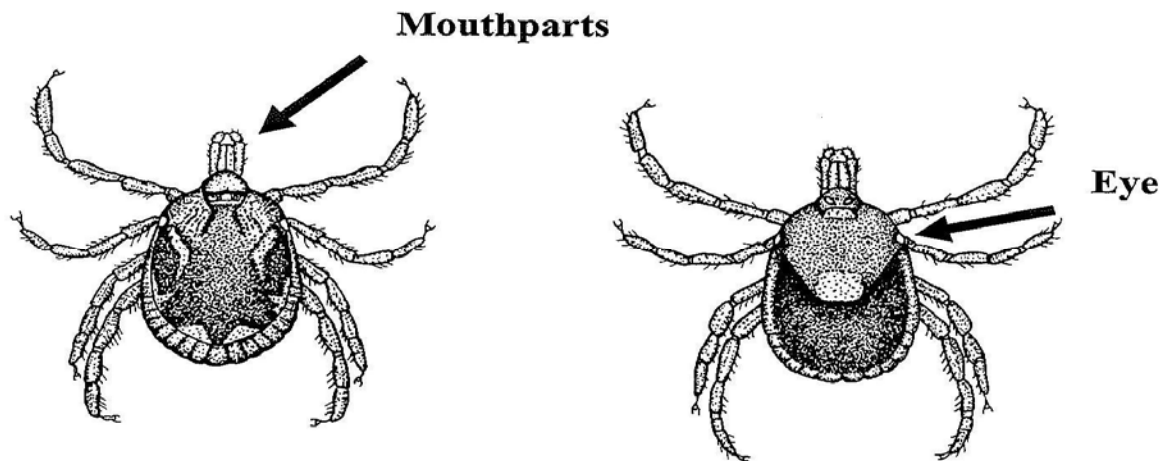


Figure 2. Lone star tick, showing locations of mouthparts and eyes.

Hard ticks have three feeding stages in their life cycle (larvae, nymphs, and adults) which normally utilize a different host animal during each stage (Figure 3). An example of such a “three-host” tick is the lone star tick, *Amblyomma americanum* (Figure 2).

Modifications of this feeding pattern occur. For example, *Rhipicephalus evertsi* (not a North American species) uses only two hosts, and the cattle tick, *Rhipicephalus (Boophilus) annulatus* (essentially eradicated from the United States in the 1940s),

parasitizes only one. In the former case, the larvae and nymphs feed on the same animal, and in the latter case, all three stages feed on the same animal. Except for some *Ixodes* spp., hard tick adults mate on a host and, after the fully fed female drops from the host animal to the ground, she lays from 2000 to 18,000 eggs and subsequently dies. Many hard tick species “quest” for hosts, by climbing vegetation and remaining attached, forelegs outstretched, awaiting a passing host. They may travel up a blade of grass (to quest) and back down to the leaf litter where humidity is high (to rehydrate) several times a day. This useful physiological adaptation allows them to recover moisture from the air. Also, some hard ticks are considered “hunters,” traveling a short distance toward host cues, such as a CO₂ source. Adult ticks are more

adept at traveling through vegetation than the minute larvae.

Ticks feed exclusively on blood, and begin the process by cutting a small hole into the host epidermis with their chelicerae and inserting the central hypostome into the cut, thereby attaching to the host. Blood flow is presumably maintained with the aid of anticoagulants from the salivary glands. Some hard ticks secure their attachment to the host by forming a cement cone around the mouthparts and surrounding skin. Two phases are recognized in the feeding of nymphal and female hard ticks: 1) a growth feeding stage characterized by slow continuous blood uptake and 2) a rapid engorgement phase occurring during the last 24 h or so of attachment.

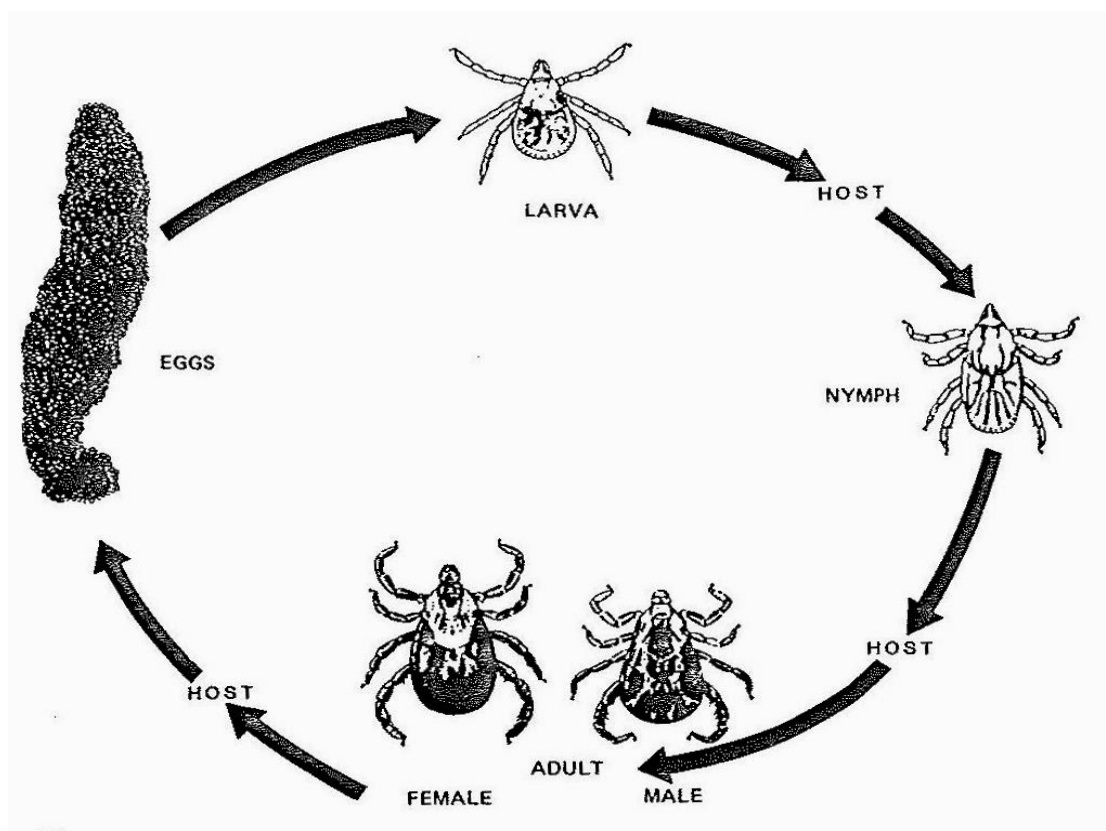


Figure 3. Hard tick life cycle (U.S. Tennessee Valley Authority drawing)

Ecology of ticks. Hard ticks and soft ticks occur in different habitats. In general, most hard ticks are non-nidicolous, occurring in brushy, wooded, or weedy areas containing numerous deer, cattle, dogs, small mammals, or other hosts. Soft ticks are generally nidicolous, being found in animal burrows or dens, bird nests, bat caves, dilapidated or poor-quality human dwellings (huts, cabins, and so forth), or animal rearing shelters. Many soft tick species thrive in hot and dry conditions, whereas ixodids which are more sensitive to desiccation are usually found in areas providing protection from high temperatures, low humidities, and constant breezes.

Being sensitive to desiccation, most hard ticks must practice water conservation and uptake. Their epicuticle contains a wax layer, which prevents water movement through the cuticle. Water can be lost through the spiracles; therefore, resting ticks keep their spiracles closed most of the time, opening them only one or two times an hour. Tick movement and its resultant rise in CO₂ production cause the spiracles to open about 15 times an hour with a corresponding water loss.

Development, activity, and survival of hard ticks are influenced greatly by temperature, humidity, and host availability within the tick microhabitat. Because of their temperature and high humidity requirements, as well as host availability, most hard ticks tend to congregate in areas providing those factors. Ecotonal areas (interface areas between major habitat types) are excellent habitats for hard ticks. For example, open meadows/prairies, along with climax forest areas, support the fewest lone star ticks, but ecotone areas and small openings in the woods are usually heavily infested. Deer and small mammals thrive in ecotonal areas, thus providing blood meals for ticks. In fact, deer are often heavily infested with hard ticks in the spring and summer months. The optimal habitat of white-tailed deer has been reported to be the forest ecotone, since the area supplies a wide variety of browse and frequently offers the greatest protection from their natural enemies. Many favorite deer foods are also found in the low trees of an ecotone, including greenbrier, sassafras, grape, oaks, and winged sumac. On the other hand, some ticks, such as the American dog tick, *Dermacentor variabilis*, concentrate along paths and roads, presumably because their hosts spend more time along roads than along any single comparable line in the surrounding fields. This concentration is believed to be a result of movements of ticks from adjacent fields to the roads, where they remain.

CURRENT RESEARCH ON TICKS IN MISSISSIPPI

A seven-member team is currently investigating tick-borne diseases at Mississippi State University (Figure 4). Prior to joining the faculty of the College of Veterinary Medicine at Mississippi State University, Dr. Andrea Varela-Stokes concentrated mainly on *Ehrlichia chaffeensis*, the agent of human monocytic ehrlichiosis (HME), and *Borrelia lonestari* (Figure 5), putative agent of “southern tick-associated rash illness” (STARI) in her PhD and post-doctoral work. However, since her arrival in summer of 2007 and her collaborations with Dr. Jerome Goddard, the laboratory has explored various aspects of tick-borne disease, including, but not limited to, the above agents.

One of the initial objectives of the lab was to begin to evaluate the presence of tick-borne agents in the lone star tick, *Amblyomma americanum*, and selected wildlife in Mississippi. As it is the most common tick in the state and in the Southeast, determining the prevalence of disease agents in the lone star tick will help us understand the importance of tick-borne diseases here and potential risk of human exposure. In addition, our objective in monitoring tick-borne disease exposure and infection in wildlife is to begin to understand the maintenance of these organisms in nature.

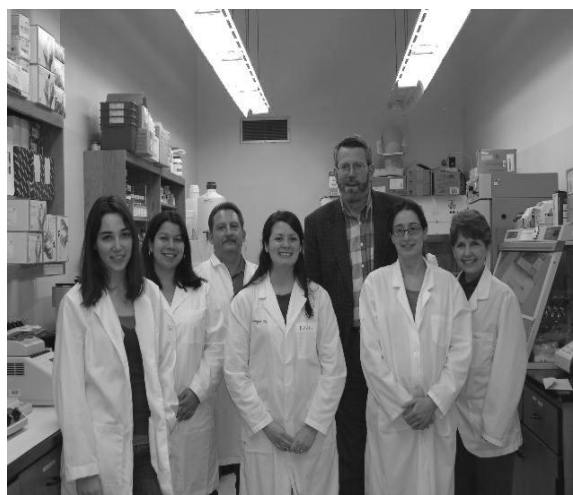


Figure 4. Mississippi State University tick research team, L-R, Gail Moraru, Flavia Girao, Erle Chenney, Ashley Harris, Jerome Goddard, Andrea Varela-Stokes, and Kristine T. Edwards.

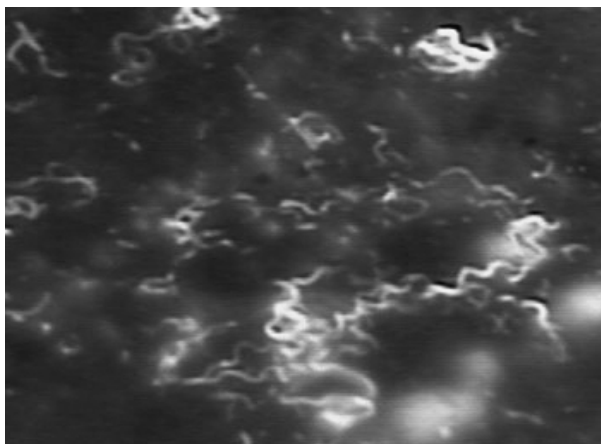


Figure 5. *Borrelia lonestari* stained by fluorescent antibody method (FA) (Photo courtesy Andrea Varela-Stokes, Mississippi State University).

Ashley Harris is currently working towards an MS degree in Veterinary Science and is testing ticks and wildlife collected from several places around Mississippi. With the help of a summer vet student worker, Jamesia Showers, a survey of Mississippi lone star ticks was conducted last summer. A total of 192 adult ticks were collected by drag cloth or dry ice traps from four regions of Mississippi: East (Noxubee National Wildlife Refuge and Lowndes County, MS), Northwest (Wall Doxey State Park), Northeast (Tishomingo State Park), and Southeast (Natchez State Park). In addition, 42 pools of larval ticks were collected from Southwest Mississippi (Copiah Co.). DNA from adult ticks and larval pools were tested for *E. chaffeensis*, *Borrelia* spp., *Francisella tularensis*, and *Rickettsia* spp., as well as for the presence of tick-specific DNA. All ticks tested were positive for tick-specific DNA, demonstrating that DNA was successfully extracted from the tick tissues. Thus far, *Borrelia* sp. DNA was amplified from 5/192 (2.6%) of adult ticks tested, 7/192 (3.7%) had evidence of *E. chaffeensis*, and 34/192 (17.7%) were positive for a *Rickettsia* species. Nine of forty-two (21.4%) of the pools of larval ticks were positive for a *Rickettsia* species. No ticks have been found co-infected with any of these organisms. The region with the highest prevalence of ticks infected with *E. chaffeensis* was the Northeast (Tishomingo SP), however because the sample size at that location was very small, this prevalence may not reflect true prevalence in nature. The Northwest (Wall Doxey SP) had the highest prevalence of *Borrelia* and *Rickettsia* sp. infections.

We are currently in the process of sequencing these products to determine the *Borrelia* species as well as the *Rickettsia* species involved. The sequence of one of the *E. chaffeensis* amplicons was identical to that of *E. chaffeensis*. In addition to the PCR assays of ticks, 2 pools of ten ticks were dissected and cultured in an attempt to cultivate rickettsial or *Borrelia* species. Organisms resembling *Rickettsia* spp. were visualized in stained slides from two flasks of the same set of cultivated ticks (Figure 6). PCR for *Rickettsia* spp. revealed two amplicons of appropriate sizes. We are currently working to sequence these amplicons.

The prevalence of known and putative zoonotic, tick-borne agents is also being assessed in white-tailed deer (*Odocoileus virginianus*), feral swine (*Sus scrofa*), raccoons (*Procyon lotor*) and opossums (*Didelphis virginiana*) in the state of Mississippi. Animals are being tested for exposure to or infection with six tick-borne agents: *Borrelia* spp., *E. chaffeensis*, *E. ewingii*, *Anaplasma phagocytophilum*, *Francisella tularensis*, and *Rickettsia* species. Both whole blood and serum from white-tailed deer and feral swine are being tested, while only serum is being tested from raccoons and opossums. DNA from these samples is being tested by single or nested PCR for the above-mentioned organisms. An indirect immunofluorescent antibody assay (IFA) using antigen from *E. chaffeensis*, *B. lonestari*, and *Rickettsia parkeri* is being used to test for antibodies against these organisms. Thus far, molecular evidence of infection to *B. lonestari*, *E. chaffeensis*, and *A. phagocytophilum* has been detected only in deer; all swine have been negative. In general, deer have had the greatest evidence of exposure to *E. chaffeensis* and *B. lonestari*, which supports previous work suggesting that deer are primary reservoirs for these two agents (Dawson et al. 1994, Lockhart et al. 1997, Moore et al. 2003, Moyer et al. 2006). However, interestingly, the other animal species also showed evidence of exposure to most agents. These results demonstrate that wildlife in Mississippi are exposed to tick-borne diseases, suggesting that ticks carry and have the potential to transmit these agents to humans in Mississippi as well.

In addition to the tick-borne diseases mentioned above, we have recently become interested in the newly emerged pathogen, *R. parkeri*. Dr. Kristine Edwards is a DVM, MPH, who is currently working on her PhD in medical entomology in our laboratory. She is testing the hypothesis that cattle play a central role in the maintenance of *R. parkeri* as a host for the Gulf Coast tick (*Amblyomma maculatum*).

An experiment was designed using healthy Holstein bull calves from the Mississippi State University. One group comprised calves injected with *R. parkeri* organism cultured in Vero cells and one negative control calf injected with Vero cells containing no organism. Another group comprised calves infested with adult *A. maculatum* ticks injected with cultured *R. parkeri* placed on each right ear and one negative control calf with adult *A. maculatum* ticks injected with phosphate-buffered saline (PBS) placed on the right ear. Ticks were confined to the feeding site by a sock fitted over the calf's ear (Figure 7). Dr. Edwards found that in addition to successful tick feeding on the calves, a transient rickettsemia was demonstrated by PCR in some exposed calves and evidence of organisms in biopsies was demonstrated by immunohistochemistry. Also, the calves produced antibodies to *R. parkeri* as revealed by IFA. Hematologic changes were not conclusive and the calves were not clinically ill for the duration of the study. However, a condition known as "gotch" ear was manifest in all the tick-infested calves wherein the ears became edematous and erythemic near sites of tick attachment.

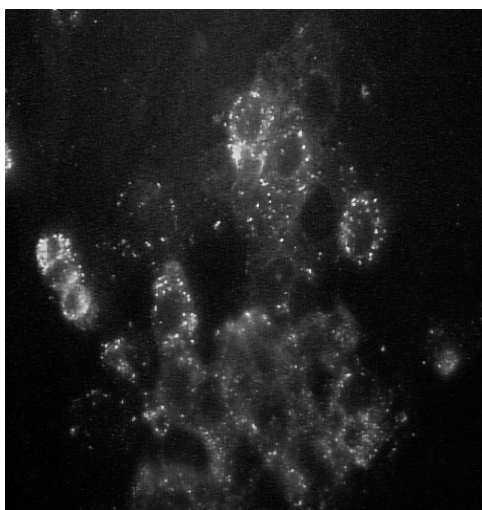


Figure 6. Rickettsial organisms in cell culture stained by FA (Photo courtesy Andrea Varela-Stokes, Mississippi State University).



Figure 7. Calf with sock on ear for tick feeding (Photo courtesy Dr. Kristine Edwards, Mississippi State University)

Dr. Edwards has also been investigating *R. parkeri* in cattle naturally infested with Gulf Coast ticks in Mississippi. Beginning in July 2008, blood and ticks were collected from cattle from sale barns in Tupelo, West Point, Macon, Tylertown, Natchez, and Meridian. Cattle were bled either from the tail vein or by jugular venipuncture and samples for PCR and serology were obtained. Animals were examined rapidly for ticks as they were held in the chute. Blood was obtained from all cattle regardless of whether ticks were present. Sites of tick attachment were biopsied whenever possible. Blood samples, biopsy samples, and tick specimens were all designated with a unique identifier associated with the animal and recorded on each individual animal's chart as well as the animal's signalment (age, gender, breed, use, approximate weight). Hemolymph tests and IFA tests are currently being performed on these samples (Figures 8). DNA extracts are being evaluated using nested PCR assays. Preliminary results of cattle from sale barns in Mississippi naturally infested with *A. maculatum* ticks revealed Spotted Fever Group (SFG) rickettsiae in some of the ticks as demonstrated by hemolymph tests. Further PCR and IFA analyses are currently underway to confirm these findings.

We have recently expanded our studies of *R. parkeri* with the addition of two other graduate students to the lab. Gail Moraru is a student working on both her PhD and DVM, while Flavia Girao is working on her MS degree in Veterinary Science.

Gail's project will concentrate on the ecological aspects of the natural history of *R. parkeri*. Because *R. parkeri* is carried by a vector to its host, the vector largely determines in which host the bacterium ends up. Therefore, it is important to know what animal hosts the Gulf Coast tick prefers. One objective of her proposal is to learn which host(s) the larvae and nymphs prefer to feed on, feeding success on available host(s), and potentially which host(s) the bacterium grows best in. In one experiment, a "choice" of host will be offered to ticks to determine host preference, while in another experiment, feeding success will be determined by placing the ticks directly on several different hosts. In addition, infection with *R. parkeri* might be performed on the various animal hosts if time allows. Further, field work will be necessary to help put the pieces together of where both the ticks and the rickettsiae are found. Both animals and ticks will be collected from at least two sites in Mississippi and blood samples will be taken from the animals and used in serologic (IFA) and PCR assays. DNA from ticks will be tested for *Rickettsia parkeri* by PCR and sequencing of a key gene. The information gathered from this study should help uncover missing information about the natural history of *R. parkeri* and *A. maculatum*. Ideally, information pertaining to potential reservoir host(s) might be obtained; however, this will have to be determined by combining results from several different components of her study. Through Gail's work, we anticipate gaining better understanding of the natural history of *R. parkeri* as it involves potential wild reservoirs.

Flavia's project is currently investigating *R. parkeri* and *A. maculatum* populations as a model for the movement of the foreign animal disease, heartwater, in the event of an accidental or intentional introduction to the United States. Approximately 700-1000 ticks will be collected from ten sites within Mississippi and DNA from these samples will be tested by PCR targeting the tick mitochondrial 16S rRNA gene (Qiu et al. 2002) and the Rickettsial ompA gene as described by Paddock (Paddock et al. 2004) to generate specific sequence products for single stranded conformational polymorphism (SSCP) analysis. We intend to use SSCP data to estimate gene frequencies of individual alleles in the *R. parkeri* and *A. maculatum* populations. The comparison of these frequencies will provide information regarding variation within and among geographically distinct populations and determine the amount of movement and interbreeding in the tick populations while also relating this to *R.*

parkeri populations. This project will provide the basis for further studies of population structures over time.

Our fifth lab member, Erle Chenney, plays the invaluable role of technician. In addition to maintaining day to day operations of the lab, Erle has also been invaluable in data collection for the tick and wildlife surveys. He handles the task of ordering supplies, equipment, and reagents for use in the lab and makes various media for use in several types of cell culture, which he also maintains. Erle is familiar with all the research projects of the graduate students as well as other projects ongoing in the lab. His work is essential to the survival of the laboratory.

Dr. Jerome Goddard has been conducting ecological studies of ticks in Mississippi for twenty years. Ticks are not evenly distributed in the wild; but instead, they are localized in areas providing their necessary temperature, humidity, and host requirements. Earlier ecological studies performed by Dr. Goddard included studying the effect of weather on questing populations of hard ticks (Goddard 1992, 2001) as well as mark-release-recapture experiments which estimated tick populations in Mississippi forests (Goddard 1993, Goddard and Goddard 2008). Studies on the spatial and geographic distribution of the tick, *A. americanum*, revealed that they "cluster" in spots in the woods, and are not evenly distributed (Goddard 1997). For example, in one study, the majority of adult and nymphal ticks were collected by drag cloth in only 17.7% and 9.7% of the field plots, respectively (Figure 9) (Table 1) (Goddard 1997). In addition, ticks, being subject to desiccation, are found in predominantly shady spots. In field plots with the amount of shade ranging widely from 0 to 90 percent, we have found 21/31 (68%) of adult ticks and 24/33 (73%) of nymphs were collected in areas of 71% and 65% shade, respectively (Table 2) (Goddard, 1997).

Oddly, current preliminary data with the Gulf coast tick, *A. maculatum*, reveals just the opposite behavior. Careful collections of this tick along the Mississippi Gulf Coast have shown that adults of this tick are found in grasslands in open sunshine, with little relation to shade or soil moisture. One 0.5 ha collection site in open sunshine within the Grand Bay National Wildlife Refuge yielded over 100 adult *A. maculatum*. Also, systematic drag cloth collections within the Sandhill Crane National Refuge revealed that most *A. maculatum* were found along the road, in bright sunshine, as opposed to wooded areas.

Further ecological research is needed to determine the variables predicting *A. maculatum*

questing and host-finding activity, especially in relation to the changing climate and habitat transformation. Knowledge of these variables could

theoretically lead to precision-targeting of pesticides or other pest control interventions to lower human exposure to the disease-bearing ticks.



Figure 8. Hemolymph staining for rickettsial organisms



Figure 9. Collecting ticks by drag cloth

Table 1. Clustering of lone star ticks in study sites in central Mississippi.

| Site | Tick stage | Percent of area where majority ticks found |
|------|------------|--|
| 1 | Adult | 17.7 |
| 1 | Nymph | 9.7 |
| 2 | Adult | 14.5 |
| 2 | Nymph | 25.8 |

Table 2. Percent shade in study sites in central Mississippi where majority of lone star ticks were collected.

| Site | Tick stage | Number of LSTs collected | Percent Shade |
|------|------------|--------------------------|---------------|
| 1 | Adult | 21/31 (68%) | 71 |
| 1 | Nymph | 24/33 (73%) | 65 |
| 2 | Adult | 31/44 (70%) | 45 |
| 2 | Nymph | 81/113 (72%) | 71 |

THE FUTURE

Tick-borne diseases continue to emerge. Therefore, ticks will remain an important threat to human health for the foreseeable future. For example, in the 1970's, Lyme disease was virtually unknown; now it is the most important tick-borne disease in the United States, if not the world (Bonnefoy et al. 2008). Other such disease entities likely occur but have yet to be recognized. For example, a brand new tick-borne agent called the Panola Mountain ehrlichia was recently found to infect humans (Loftis et al. 2008, Reeves et al. 2008). Changes in pathogens, increased human populations, environmental and ecological changes, and other such factors are contributing to the emergence of these and other vector-borne diseases. University researchers, public health officials, and clinicians all play important roles in the control of tick-borne diseases and must work together to find, treat, manage, and/or prevent such diseases in the future. We are hopeful that the contributions of Drs. Goddard and Varela-Stokes to the field of tick-borne research will serve to heighten our understanding of the natural history of tick-borne disease in such a way as to help prevent further transmission.

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Modeling Intraspecific Competition and Temporal Variation in the Distribution of Juvenile Body Sizes of a Wolf Spider

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Abstract

We assayed rates of cannibalism, the strength of size-dependent competition for food resources, and a number of other biological factors associated with variation among individuals in their growth rates, in natural populations of the wolf spider *Rabidosa rabida* (Walckenaer 1837). Two of our more important findings are that: (1) large spiders have a significant advantage in the amount of prey captured when compared to smaller spiders and (2) approximately 15% of all mortality in *R. rabida* is due to cannibalism. Using data from natural populations, we built a stochastic computer simulation to model the growth rates of individuals within populations of *R. rabida*. The results of the model were then compared to the observed shape of the distribution of body sizes and the observed temporal changes in that distribution. The results of the simulation resemble the distribution of body weights for juvenile wolf spiders found in natural populations, despite the fact that most of the mortality within the population remains unaccounted for. This suggests that other forms of mortality, when considered together, may be relatively size-independent. The distribution of body weights within a population changes from approximately normally distributed to bimodal to strongly positively skewed through time. We suggest that these changes are due primarily to the effects of cannibalism and asymmetrical competition amongst spiders of different sizes. The levels of cannibalism and asymmetrical competition estimated in this species lead to evolutionary questions about selection on the timing of reproduction.

INTRODUCTION AND BACKGROUND

The distribution of body sizes within a given cohort of a plant or animal population, and how that distribution changes through time, has been of longstanding interest to biologists. This interest stems from the importance of size structure within a population for life history evolution and population dynamics (Peacor et al., 2007a). The interest often also relates to a hope that the causal mechanisms involved in creating the distribution can be inferred *a posteriori* from the shape of the distribution itself. However, inferring such mechanisms from known size distributions can be difficult or impossible, since different interacting combinations of the factors affecting growth and mortality rates can produce similar distributions of body size (Huston and DeAngelis, 1987; Schwimming and Weiner,

1998). Analytical and computer models, while having limitations of their own, are often used to help sort out likely mechanisms and their consequences for populations.

Huston and DeAngelis (1987) describe the primary factors that determine the distribution of body sizes within a cohort. We have modified these factors slightly as follows: (1) the distribution of initial body sizes; (2) the distribution of growth rates among individuals due to genetic or microhabitat differences; and (3) size-specific mortality rates. Peacor et al. (2007b) approach variation in cohort size in a different way, dividing the factors into two broad categories: size-dependent factors and size-independent factors (e.g., morphology, behavior). Examples of specific biological mechanisms that can impact the distribution of body sizes include: asymmetrical competition amongst individuals,

cannibalism, density-dependent and density-independent sources of mortality, and lethal and nonlethal effects of predators (Peacor et al., 2007a,b). In order for these mechanisms to change the initial distribution of body sizes, the values for these biological parameters must be size-dependent. Genetic variation among individuals for rates of growth due to, for example, more efficient metabolism or greater prey capture rates under the same prey densities also contribute to the changes in the distribution of body sizes within a cohort.

In this study we focus on the distribution of body sizes within a cohort of the wolf spider *Rabidosa rabida* (Walckenaer)(Araneae:Lycosidae), a species common in the southeast region of the USA. Though much is known about the behavior of this species (e.g., Stratton and Uetz, 1981), very little is known about its ecology and life history (but see Reed and Nicholas 2008). *Rabidosa rabida* matures in late June to early August in north Mississippi. When mature, *R. rabida* is one of the largest spiders found in meadows and fields, with adult females weighing about 600 mg. *Rabidosa rabida* is a semelparous species that produces approximately 350 offspring during the female's single reproductive event (Reed and Nicholas 2008).

In this paper we: (1) present data on the distribution of juvenile body weights for *R. rabida*, through time; (2) show that larger individuals are at a competitive advantage and consume more prey; (3) estimate rates of cannibalism, as well as other important parameters associated with variation among individuals in growth and mortality rates; and (4) present the results of a stochastic simulation model of spider growth rates, parameterized from data gathered during our study. We then compare the simulation results to the actual observed distribution of body weights and suggest reasons for departures from the model predictions.

MATERIAL AND METHODS

A population of *Rabidosa rabida* was sampled four times, approximately every two weeks, during May and June of 2005 (~ 325 individuals per sample). The sampling site was a field dominated by broom sedge, in the Oxford area of north Mississippi (USA). Data gathered from the sampled individuals include the mass of the individual to the nearest milligram, presence or absence of a prey item (i.e.,

whether the individual was feeding at the time of capture), and rates of cannibalism (that is, if prey was a conspecific). Immediately after all assays the animals were returned to their site of origin. To obtain initial body size distributions, female *R. rabida* with an egg sac were captured and their emerging offspring were weighed. Estimates of the variance among individual growth rates were acquired through repeated measures of 60 juvenile individuals under field (i.e., natural) conditions.

Statistics and Comparisons. Weights of individuals with prey versus those without prey, during a given sampling period, were compared using a randomized block design ANOVA.

Comparison of the observed distribution of body sizes at a given time with the predicted distribution of body sizes was made using measures of kurtosis, skewness, and the coefficient of variation, as well as visual inspection. Statistical tests of significance levels for kurtosis and skewness are useless as the simulated number of individuals can be made arbitrarily large and, therefore, the standard errors arbitrarily small. Distributions are usually considered not to differ (or to differ trivially) from a normal Gaussian distribution if the moments of kurtosis and skewness are within ± 0.5 units. Differences from ± 0.5 -1.0 units can be considered as moderate deviations from a normal distribution, and differences of > 1.0 units are considered large deviations from a normal distribution.

Estimates of the mean, and confidence intervals for the, coefficient of variation of body mass at the different time points were bootstrapped by sampling 200 individuals and the coefficient of variation calculated from the sampled data. This was repeated 2,000 times for the observed and predicted data at each time point. From these 2,000 estimates of the coefficient of variation, 95% confidence intervals determined.

The Model. A stochastic computer simulation was built using MATLAB, to model growth rates of individual *Rabidosa rabida*. Two thousand spiders were initially generated by the computer, with the parameters concerning growth and mortality rates modeled as follows:

Distribution of Offspring Size at Birth: We collected data on offspring size from 275 adult female *R. rabida*. Mean offspring size, using the mean offspring size of each female as the unit of measure, is 1.055 mg with a standard deviation of

0.144 mg. Offspring size is approximately normally distributed.

Timing of Birth: Offspring cohorts were modeled as being born in pulses once every fourteen days during a period of 42 days: 300 individuals on day zero, 600 on day 14, 700 on day 28, and 400 on day 42. Reproduction is mildly synchronized in *R. rabida* and the proportion of the total number of individuals eventually being born in a given 14 day interval was estimated from field data (Nicholas 2007). However, births in a natural population are a continuous process which we have made discrete in order to simplify the modeling process.

Mean Growth Rate: The growth rate of individuals can be modeled in the same fashion as population growth rates:

$$M_t = M_0 e^{rt}$$

Where M_t is the mass at time t , M_0 is the initial mass, t is time in days, and r is the instantaneous growth rate. Measurements from this population suggest that r is approximately 0.0388.

Variance among Individuals in Growth Rate: The variation among individual growth rates was estimated from repeated measures on 60 individuals under field conditions. The variance in individual growth rates was then apportioned among three causes: (1) A fixed genetic component (V_G) that reflects differences among individuals in their relative ability to capture and metabolize food resources regardless of the absolute level of prey available. This was considered fixed throughout the spider's life and was not subject to genotype-environment interactions. The model was parameterized using information from broad-sense heritabilities for growth rate estimated from the laboratory (Reed et al., 2007a). The broad-sense heritability for growth rate was estimated at 29% ($H^2 = 0.29$). (2) A variance component based on the size of the individual relative to other individuals with which it is currently competing. This estimate was obtained from data on prey capture rates for spiders of different sizes competing in natural populations (Table 1). (3) A completely random component representing stochastic changes in the microenvironment.

The formula is as follows:

$$r_t = 0.0388 + [((0.29) Z_{\text{Genetic}} (0.0222)) + ((0.32)$$

$$Z_{\text{Size}} (0.0222)) + ((0.39) Z_{\text{Rand}} (0.0222))]$$

where r_t is the individual's growth rate for the specified 14 day period, Z_{Genetic} comprises a Z-score drawn from a standard normal distribution representing the genetic component of the individual's growth rate that is permanent throughout its lifetime, Z_{Size} is the individual's Z-score in a standard normal distribution of current body sizes (larger individuals have an advantage in capturing prey), and Z_{Random} represents a random draw from a normal distribution reflecting the quality of an individual's microhabitat during the two week period. The number 0.0222 was derived from repeated runs of the model and is the variance for each individual parameter that produces a total variance among individuals in growth rate equal to that derived from the field study.

Density-Dependent Mortality: Truncation selection was used against the 1.0% of the population with the lowest growth rate during each 14 day interval. These individuals are assumed to die of starvation or malnutrition. Strong evidence for density-dependent mortality exists in this species of wolf spider (Reed et al., 2007b), though the form and intensity of selection against individuals with slower growth rates is unknown.

Cannibalism: The cannibalism rate of 1.5% over a two week period is extrapolated from cannibalism rates observed in the field. At each sampling period the total number of *Rabidosa rabida* captured is known and the proportion of the captured individuals that is a victim of cannibalism is also known. This gives us multiple estimates of the proportion of spiders cannibalized per day, which can then easily be turned into an estimate of the proportion of the population cannibalized per two week period (1.5%) and over the entire season (nearly 15%).

Of nearly 300 *R. rabida* captured with identifiable prey items (~ 4,500 captured spiders), 5.7% \pm 1.3% of the prey items were smaller *R. rabida*. This is in reasonable agreement with estimates from other studies. Cannibalism accounts for approximately 5% of the prey items in the diet of fishing spiders (Zimmerman and Spence 1989) and cannibalism has been estimated at 10%-20% for other wolf spider species (Edgar, 1969; Hallander, 1970; Yeargan, 1975).

For the computer simulation, individuals from the population were randomly chosen and paired. If the larger individual was at least twice as large (heavy) as the smaller individual, the larger individual was assumed to eat the smaller individual and remove it from the population. This is continued until 1.5% of the population is removed this way during each 14 day time step in the model. The estimates of the size differential necessary for cannibalism to occur are from laboratory trials on about 90 pairings (Reed, unpublished data).

Finite Growth: Once individuals become ≥ 310 mg in weight, they were checked for adult status. For every 6 mg that an individual weighs > 300 mg, it has a 1% chance of having reached maturity and being incapable of undergoing further growth. For example, if on day 126 the body mass for a given spider is calculated to be 468 mg, then the individual has a 28% chance of undergoing its final molt. The computer randomly generates a whole number between 1 and a 100, and that number is checked against the percent chance of maturity. If the number is equal to or less than that percent, the spider is considered mature and does not undergo further growth. If the randomly drawn number is larger, the spider is not mature and continues to grow. Fourteen days later the same spider might weigh 804 mg and will have an 84% chance of being considered mature. These estimates come from the distribution of adult sizes for this species (Reed et al., 2007b). Though males and females mature at considerably different mean sizes, only a small number of individuals will reach maturity during the time frame modeled and sexual dimorphism is expected to bias the results only slightly.

The general structure of the model is: (1) Newborn individuals are created and added to the population, but only during the first 42 days (four time steps). (2) Initial body mass is determined by a random draw from a normal distribution with a mean and standard deviation estimated from a large data set. (3) Individual growth rates are determined. Variation in an individual's growth rate consists of: (i) A genetic component (29% of the variation) that varies among individuals due to their genetic quality,

but does not vary temporally. (ii) A size component (32% of the variation) that reflects the size of the individual compared to other individuals in the population at that time. Depending on time of birth and growth rate, this component of an individual's growth rate will vary temporally. Larger individuals are assumed to have a competitive advantage and faster mean growth rates. (iii) A microhabitat component (39% of the variation). The quality of the microhabitat is determined by a random draw from a normal distribution. (4) The new distribution of body weights fourteen days later is determined. (5) The 1.0% of individuals with the lowest growth rates during the proceeding 14 days is removed from the population by truncation selection (starvation). (6) Individuals from the population are chosen randomly and paired. The larger of the two individuals is assumed to eat the smaller of the two, and the smaller individual is removed via cannibalism (1.5% reduction in population size). (7) Surviving individuals are checked to see if they have reached maturity. (8) Steps one through seven are repeated until 140 days (10 time steps) have passed.

RESULTS

At all four sampling intervals, the mean weight of individuals captured with prey was significantly larger than the mean weight of individuals without prey (Table 1). We estimate that the mean weight of individuals captured with prey is approximately 50% greater than that of individuals captured without prey. Because in a large random sample of spiders larger spiders are more likely to be found consuming prey, we conclude that larger wolf spiders are at a competitive advantage and consume more food than do smaller spiders. This conclusion assumes that there is a linear relationship between the size of the prey eaten and its handling time (larger spiders eat larger prey). If this assumption does not hold and larger prey have disproportionately larger handling times than smaller prey items, then our conclusions could be wrong or at least the magnitude of the difference exaggerated.

Table 1. The mean body weights (in mg) of randomly sampled juvenile *R. rabida* with and without prey at the time of capture. N_1 equals the total number of spiders caught in the sample and N_2 the number caught with prey. A randomized block design ANOVA shows that individuals with prey are consistently and significantly larger than individuals without prey ($p < 0.001$) at all time points.

| <u>Without</u> | <u>With</u> | <u>N_1</u> | <u>N_2</u> |
|----------------|-------------|-------------------------|-------------------------|
| 53.7 | 95.1 | 228 | 20 |
| 126.6 | 181.9 | 446 | 44 |
| 204.2 | 271.1 | 354 | 28 |
| 267.2 | 385.7 | 261 | 23 |

The observed and simulated distribution of body weights at 98, 112, 126, and 140 days after birth (time points one through four, respectively) are presented in Figure 1 (panels a-d). Measures of kurtosis and skewness are presented in Table 2. Confidence intervals (95% CI) for estimates of the coefficient of variation are contained in Table 3.

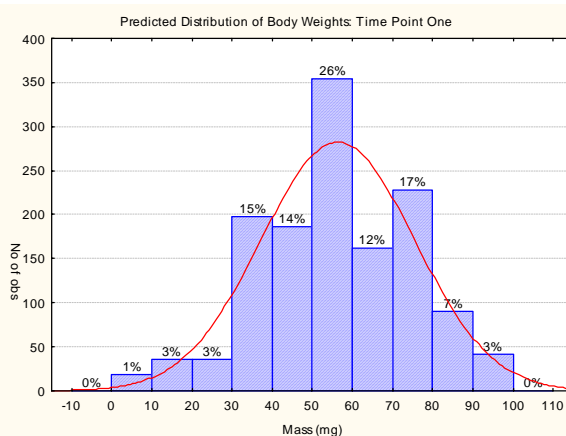
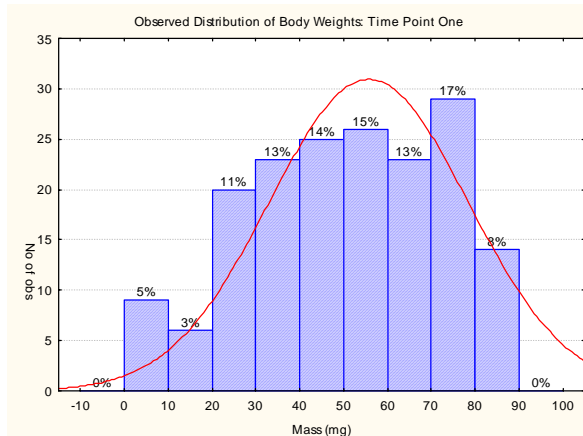
At time point one the predicted distribution of body weights is approximately normal, with very little kurtosis or skewness. The observed distribution of body weights from the natural populations is also close to normally distributed, but is slightly platykurtic compared to the distribution predicted from the model.

At time point two, the observed and predicted distributions are nearly identical. Both have very little skewness, but are mildly platykurtic. A platykurtic distribution is often the result of two normal distributions with similar variances but different means, as often occurs with a bimodal

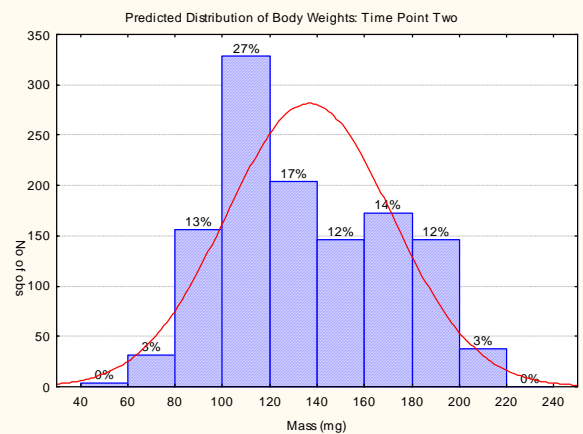
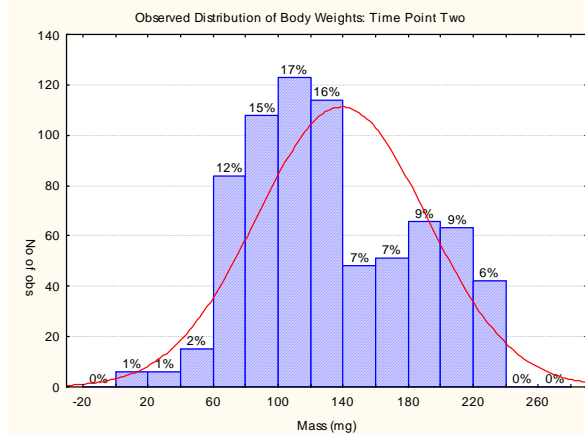
distribution. Visual inspection of both the observed and predicted distributions suggests a bimodal distribution.

At time point three both distributions are beginning to become positively skewed, with the skew being a bit stronger in the observed population than in the simulated population. The modeled population is also still slightly platykurtic while the observed population is moving towards a leptokurtic distribution.

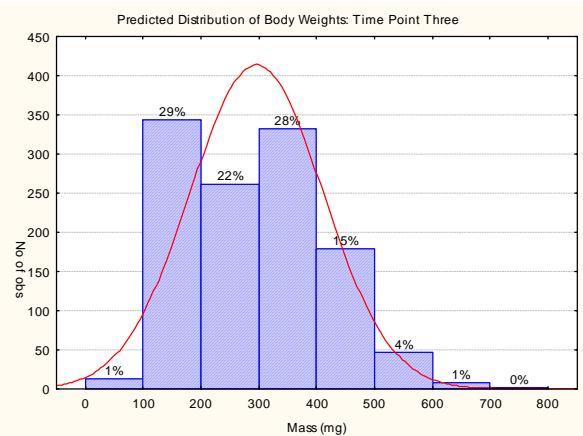
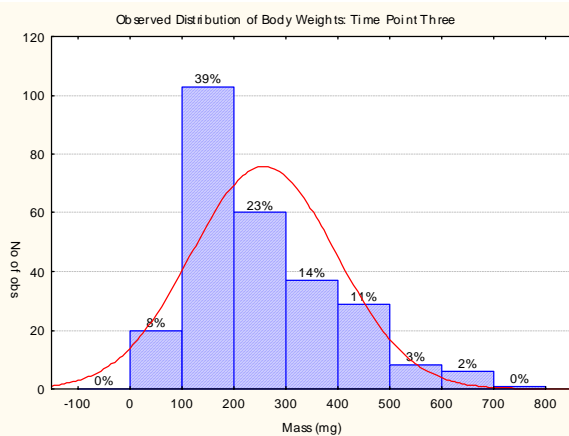
At time point four, both observed and predicted distributions have become strongly and positively skewed. The observed and predicted distributions look almost identical upon visual inspection. However, the observed data is very strongly leptokurtic, while the predicted distribution is only slightly so.



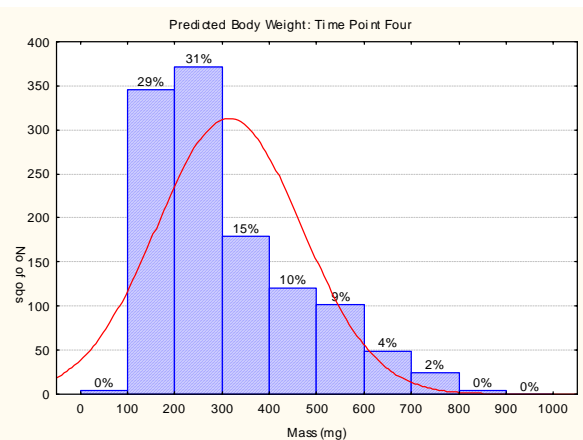
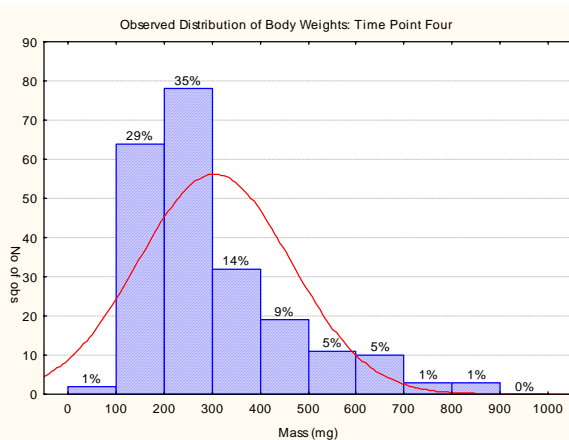
A



B



C



D

Figure 1 (a-d). Observed distribution of body mass and distribution of body mass predicted from the stochastic simulation for *Rabidosa rabida* through time. Time point one is after 98 days, time point two after 112 days, time point three at 126 days, and time point four at 140 days. The curve in each panel represents the expectation under a normal distribution with observed mean and standard deviation.

Table 2. Comparison of kurtosis and skewness measures in the distribution of body weights predicted from the model and those observed from field collections. The number in parentheses refers to the collection period.

| | <u>Model</u> | <u>Observed</u> |
|--------------|--------------|-----------------|
| Kurtosis (1) | -0.07 | -0.60 |
| Skewness (1) | -0.17 | -0.36 |
| Kurtosis (2) | -0.91 | -0.75 |
| Skewness (2) | 0.38 | 0.30 |
| Kurtosis (3) | -0.55 | 0.39 |
| Skewness (3) | 0.49 | 0.96 |
| Kurtosis (4) | 0.47 | 1.63 |
| Skewness (4) | 1.12 | 1.43 |

Table 3. Comparison of coefficient of variation measures for the distribution of body weights predicted from the model and those observed from field collections. The collected samples and simulation results were bootstrap sampled and their 95% confidence intervals estimated (shown below).

| | <u>Model</u> | <u>Observed</u> |
|--------------|---------------|-----------------|
| Time Point 1 | 30.9% - 38.7% | 36.7% -45.5% |
| Time Point 2 | 33.0% - 38.3% | 34.1% - 42.0% |
| Time Point 3 | 43.5% - 54.0% | 49.0% - 60.8% |
| Time Point 4 | 44.9% - 55.5% | 45.5% - 58.1% |

Overall, the predictions from the final model match the observed data surprisingly well. In particular, both distributions go from being normally distributed to highly skewed to the right through time. However, the modeled population is never very platykurtic or leptokurtic and changes little through time in this regard. The observed distribution, on the other hand, becomes increasingly leptokurtic through time. Coefficients of variation for the observed and predicted data are never significantly different from each other. However, there is a trend for the observed population to have a larger coefficient of variation at all time points. This appears to be due to the presence of larger proportion of individuals of the smallest weight class being present in the natural population than the model predicts.

DISCUSSION

Asymmetric Competition. Few studies have provided evidence for intraspecific competition

in spiders (but see Wise, 1983; Wagner and Wise, 1996; Chen and Wise, 1999; Miyashita, 2001; Reed et al., 2007b). Increasing the strength of intraspecific competition leads to increasing variation among individual growth rates. This has been predicted to skew the distribution of body sizes toward the right. Such positive skewness has been considered evidence for asymmetrical competition in which larger individuals are at an advantage compared to smaller individuals (Harper, 1967). In the wolf spider, *Rabidosa rabida*, we have demonstrated that larger individuals are found with prey more often than smaller individuals. We have shown that the observed distribution of body sizes in this species becomes positively skewed through time. We have also shown that a stochastic model of individual growth rates that includes asymmetric competition amongst individuals of different sizes mimics the increasing positive skewness found in the observed distribution of body sizes quite accurately. Further, increasing the proportion of the variation in

individual growth rates that is due to differences in body size (i.e., increasing the asymmetry in competition), in the model, increases the eventual amount of skewness in the distribution of body sizes and how early in the growing season one can detect it.

Cannibalism. Larger spiders experience another competitive advantage in natural populations and the simulation model, the ability to cannibalize smaller individuals. Cannibalism is a common ecological interaction in the animal kingdom and may be particularly important in wolf spiders (Edgar, 1969; Hallander, 1970; Yeargan, 1975; Polis, 1981; Wagner and Wise, 1996; Samu et al., 1999; Moya-Laraño and Cabeza, 2003; Anthony, 2003; Buddle et al., 2003; Iida, 2003; Roberts et al., 2003). Not surprisingly, larger individuals eat smaller individuals (Polis et al., 1989; Samu et al., 1999; Anthony, 2003; Buddle et al., 2003). We observed larger juvenile *R. rabida* frequently consuming smaller juveniles in our field studies.

There are two important benefits to the cannibal of conspecific predation: (1) cannibalism provides high-quality calories and nutrients through the consumption of the individual, and (2) it removes a potential exploitive competitor (Polis, 1981; Wagner and Wise, 1997; Claessen et al., 2004). There are also potential costs to cannibalism, most notably the possibility of injury or death (Wise 2006).

The effect of cannibalism on the distribution of body sizes has received much less attention than its effects on population stability (Claessen et al. 2004). Three studies (Cooper 1936; DeAngelis and Cox 1979; Fagan and Odell 1996) have demonstrated that cannibalism promotes size bimodality in populations and that prolonged cannibalism will completely remove the smaller size class. In both natural and simulated *R. rabida* populations, the distribution of body sizes appears to become briefly bimodal. Removing cannibalism from the model creates far more leptokurtic distributions without passing through the bimodal phase. We suggest that cannibalism is an important force determining the distribution of body sizes in these populations. This appears to be especially true during the early stages of development. Sample sizes are not large enough to quantify this generalization, but observation suggests that cannibalism is strongest early in the season when there is little else

of the appropriate size to eat. Samu et al. (1999) suggest that the smallest spider instars might be more prone to cannibalism and more likely to tackle similar-sized spiderlings, due to their low energy reserves. Field observations of cannibalism in spiders most often involves juveniles feeding on juveniles (Wise 2006). Fagan and Odell (1996) found that early hatching preying mantids also faced starvation due to insufficient alternative prey and were avid cannibals.

Sensitivity Analysis. All models are wrong to some extent, but they often have heuristic value regardless. In this paper we use a stochastic computer simulation to test if limited data gathered under noisy field conditions can be used to produce similar outcomes to those observed in a natural population with respect to the temporal changes in the distribution of body sizes for a wolf spider; and to test which inputs the model outputs are most sensitive to. We do not hold our model to be an accurate description of what is happening in natural populations, because all models are simplifications of reality and we have far from perfect knowledge of the factors impacting individual growth rates.

Sensitivity analysis can be defined as an investigation into how a projected outcome varies along with a change in a single assumption (while all other assumptions are held constant) upon which the projection is based. We performed a limited type of sensitivity analysis by altering inputs to test in a very general way the model's sensitivity to changes in a small number of parameters. The model was most sensitive to changes in the asymmetry of competition between individuals of different sizes. Increasing the variance in growth rates among individuals of different sizes rapidly leads to highly skewed distributions. The model was moderately sensitive to changes in the cannibalism rate. If the proportion of individuals cannibalized during a given time period is increased, the bimodality of the data is made more prominent and it persists longer. Reducing it sufficiently eliminates the bimodality altogether. The model was very insensitive to changes in the timing of offspring births, and this did not seem to contribute very much to variation among body sizes at the time points where sampling occurred. Trait heritabilities are often slightly inflated in laboratory experiments versus natural conditions (Roff, 2002), though our heritabilities are within the normal range for heritabilities reported for

growth rates in other organisms (Mousseau and Roff, 1987). Thus, we decided to lower the proportion of the variance in individual growth rates attributable to genetic differences (adding them to the random microhabitat component). The model was only slightly or moderately sensitive to such changes. The major effect of lowering heritability was to increase the coefficient of variation for body size and to increase the benefit of reproducing earlier.

Insights from the Model. A stochastic simulation model of individual growth rates in the wolf spider (*R. rabida*) that includes cannibalism, asymmetric competition amongst individuals of different sizes, variation in size at birth and the timing of birth, a constant genetic component to growth, truncation selection against slow-growing individuals, the cessation of growth upon reaching a certain variable size, and random fluctuations in the quality (food supply) of the microhabitat was able to reproduce the distributions of actual body weights assayed from natural populations accurately. Despite the success of the model, it cannot be stressed strongly enough that models can have any number of erroneous assumptions and still produce correct 'answers'. The only sources of mortality in our models were cannibalism and starvation. The mortality imposed in the model from cannibalism and starvation probably accounts for < 25% of the actual mortality over the course of a cohort's growing season. Sources of mortality not modeled, but witnessed by us, are predation by other wolf spiders (especially the sympatric *Rabidosa punctulata*, Hentz 1844) and praying mantids. Other sources of mortality almost certainly include predation by numerous wasp species that specialize on spiders, birds, small terrestrial mammals, and other species of spiders. In addition, wolf spiders suffer mortality from desiccation, problems during molting, infestation from parasitic nematodes, and freezing during unusually cold weather. At this point we cannot assess the magnitude of these effects or whether mortality is size-dependent in these instances. However, the ability of the model to give size distributions that strongly resemble those seen in natural populations suggests that the sum of all other sources of mortality is not strongly size-dependent. The only estimation of mortality rates that we are aware of, due to the suggested causes

above, is one for overwinter survival in relation to body mass in the wolf spider, *Hygrolycosa rubrofasciata* (Kotiaho et al., 1999). Kotiaho et al. (1999) found no difference in initial body sizes between individuals that survived and those that did not survive winter torpor.

Most significantly, our field observations on the extent of asymmetrical competition between spiders of different sizes may provide an exaggerated estimate of the true level of competitive asymmetry. This could be due to numerous factors: higher metabolic costs for larger spiders means that the absolute level of increased food consumption may not translate entirely into faster growth rates, differences in handling times for prey items of different sizes may have skewed the results, or the fact that some spiders had partially consumed the prey before capture might have exaggerated the differences in weight between those with and without prey.

Cannibalism as modeled (random meetings between spiders with the larger individual consuming the smaller) probably does not represent accurately what occurs in natural populations. There is usually an upper limit to victim size in cannibalism (Amundsen, 1994; Lovrich and Sainte-Marie, 1997; Mittelbach and Persson, 1998; Persson et al., 2000; Juanes, 2003). We allowed one individual to consume another if it was twice as heavy as its victim. This is in line with other studies and our unpublished data, though some studies imposed even larger size difference limitations (Buddle et al., 2003). Observations from the laboratory suggest that the size differential needed to spur cannibalism in *R. rabida* may be slightly smaller than in other wolf spiders that have been studied.

Our observations of cannibalism from natural populations of *R. rabida* suggest that the predator normally has a substantial size advantage over its prey. However, studies provide evidence that there is also a lower limit to the victim sizes that cannibals will take. This can be explained in terms of difficulties in the detection and retention of very small prey (Lundvall et al., 1999) or because it is not worth foraging on prey below a certain size (Amundsen, 1994; Lovrich and Saint-Marie, 1997; Lundvall et al., 1999).

We suspect that the relative size of cannibals

and their prey might be at least partly due to size-dependent microhabitat use. Though we have not quantified it, our observations are that the spiders segregate themselves loosely by body size. This type of microhabitat selection is known in wolf spiders (e.g., Hallander, 1970). This segregation also provides larger spiders a two-fold advantage in obtaining food: (1) their larger size allows them to choose from a far larger selection of potential prey items and (2) they are able to commandeer the best microhabitat areas (higher densities of food items). Of course, the segregation could be related to reasons other than cannibalism and prey capture. For example, smaller spiders maintain higher activity levels and faster movement rates during cold nights than do larger spiders (personal observation).

Finally, the results of the simulation present some interesting evolutionary questions. The structure of the model introduces moderately strong selection favoring individuals born earlier in the breeding season because of their head start in the growth trajectory. However, in natural populations, reproduction is only weakly synchronized (Nicholas, 2007). Thus, there must be counter-selection maintaining phenotypic variation in the timing of births. An obvious trade-off is that females that wait to reproduce can grow to larger size and therefore produce more offspring. Thus, larger females might be hypothesized to produce offspring earlier in the season than smaller females. However, if one regresses time of birth onto female mass there is only a very weak, albeit significant, trend in this direction ($r^2 = 0.088$, $n = 275$). There is no evidence that spiders reproducing late in the season adjust by producing larger offspring than spiders reproducing early in the season ($r^2 = 0.004$, $n = 275$). Thus, there must be other selection pressures determining the timing of reproduction. Good candidates include decreased mortality rates for late hatching offspring due to favorable temporal changes in the density of other potential predators, especially other spiders, and in the availability of suitably sized prey items. Fagan and Odell (1996) faced the same quandary in their deterministic analytical model (using a nonlinear partial differential equation) of growth rates of praying mantids, where selection pressure under the model structure should lead to relentless selection for earlier hatching each season. They suggest that counter-selection is in the form of late frosts and insufficient prey.

CONCLUSIONS

Observations from the field and laboratory, combined with a stochastic computer simulation identified a mix of potential deterministic and stochastic factors involved in determining the temporal changes in the distribution of body weights for a population of the wolf spider, *Rabidosa rabida*. Most important among the factors are asymmetric competition among spiders of different sizes, cannibalism, and genetic variation for individual growth rates. The observed distribution changes from a normal distribution, to a slightly bimodal distribution, to a strongly positively skewed distribution throughout the growing season in both the natural population and the refined model.

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Lice (*Haematopinus suis* (L.) (Anoplura: Haematopinidae) Infestation of Swine From Southwestern Mississippi

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ABSTRACT

The prevalence of lice in swine from Southwestern Mississippi was investigated to document the extent to which lice infestation poses a problem for swine farmers. During the period from December 1996 to December, 1997 lice were collected from pigs' bodies by brushing, searching, and picking them with forceps and then placed in vials containing 70% alcohol. The specimens were mounted in CMC-10 medium and identified. A total of 407 pigs from 22 farms in 14 countries were investigated, and of the 407 pigs, 129 (31.7%) were infested with the hog louse (*Haematopinus suis* (L.) (Anoplura)). One hundred and twenty (32.6%) of 368 sows and 9 (23.1%) of 39 boars were infested. Heavy infestations were observed where pigs were kept in poor husbandry conditions and left unsprayed with insecticide for a long time. This is the first significant report on lice infestation in swine covering the southwestern region of Mississippi. Hog lice appear to be of common occurrence on swine in Mississippi and need to be kept under surveillance, and controlled by swine famers.

INTRODUCTION

Lice are a group of common ectoparasites of swine that are of concern to pig farmers. Hall (1993) reported that the major external parasite attacking hogs in Missouri was the hog louse; *Haematopinus suis* (L.) (Anoplura: Haematopinidae).

Lice of domestic animals are largely host specific, hence, *Haematopinus suis* is specially recognized as a hog louse. In the U.S. it is the largest louse found in domestic animals (Figure 1) It cannot live long away from the host. The entire life cycle is spent on the host.



Figure 1. Representative photograph of *Haematopinus suis* collected from the hogs.

They are incriminated in the transmission of the virus of swine pox that often accompanies skin lesions (papules, pustules, scabs) (Dobson, 1986) and *Staphylococcus* infection. They are potential vectors of hog cholera and eperythrozoonosis, a reckettsial disease caused by *Eperythrozoon suis* which causes anemia and icterus (yellow discoloration of mucus membranes, sclera and inner ears). This disease may lead to death. The main economic of hog lice are due to their irritation to the pigs making them restive, and retarding their growth. The irritation and itching caused by lice puncturing the skin, causes the pigs to rub against any convenient object. They may rub so hard as to cause their hair to fall off in patches and even cause bleeding (Nickel and Danner, 1979; Hall, 1993; Franc, 1994). High infestation may cause a skin condition that makes hair removal difficult at slaughter. Hogs that are infested may take a longer time to gain weight or may suffer from weight loss. The lice are a stress for the swine and increase their susceptibility to disease. Heavy infestations may cause anemia in young pigs, especially since each time the lice feed, they puncture the skin at a different place and draw blood and lymph (Hall 1993). They readily feed on man (James and Harwood, 1969). This may thus cause hazardous conditions for those who handle the hogs. The U.S. Department of Agriculture estimated that hog lice

caused a 2-6% loss in market value of infested swine. Farmers spend a lot of money to control the infestation.

The present study was conducted to gain an insight into the extent to which lice infestation is a problem to swine in the state of Mississippi, and to contribute more knowledge on its prevalence in the state.

MATERIAL AND METHODS

During the period from December 1996 to December 1997, lice (adults and nymphs) were collected from hogs from 22 swine farms in 14 counties (Figure 2) by parting their body hair, brushing, searching, and picking them with forceps. They were placed in vials containing 70% alcohol and transported to the laboratory. The specimens were next mounted in CMC-10 medium and identified

RESULTS

A Total of 407 pigs were examined from 22 farms located in 14 counties from December 1996 through December 1997. Hog lice were found in 129(31.7%). A sample of 368 sows were investigated and 120(32.6%) showed signs of infestation, while of the 39 boars examined, 9(23.1%) were infested (Table 1 and Figure 3)

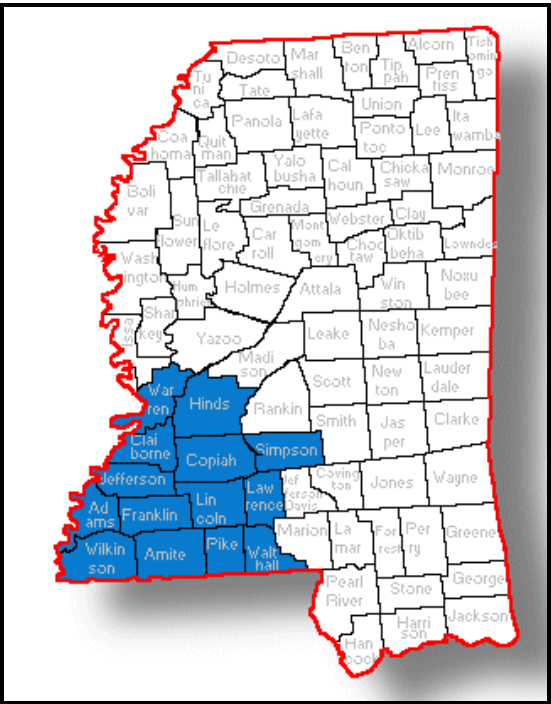


Figure 2. Map of Mississippi showing south-western counties

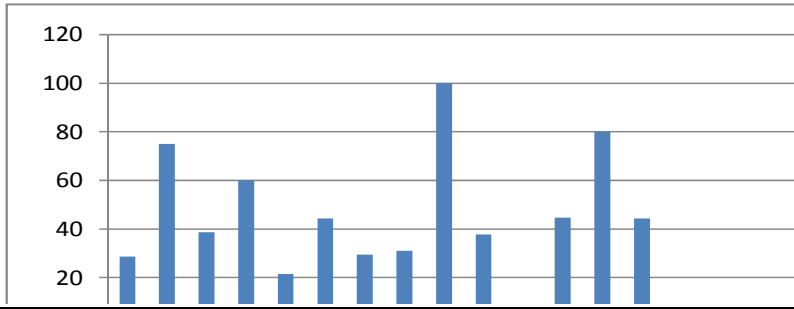


Figure 3 Prevalence of Lice Infestation on Swine in 14 counties

TABLE 1. PREVALENCE OF LICE INFESTATION ON SWINE FROM 14 COUNTIES IN SOUTHWESTERN MISSISSIPPI.

| Counties | Number of Sows Examined | Number of Boars Examined | Total number of Pigs Examined | Sows Infested #(%) | Boars Infested #(%) | Total Pigs Infested #(%) |
|--------------|-------------------------|--------------------------|-------------------------------|---------------------|----------------------|---------------------------|
| Adams | 7 | 00 | 7 | 2 (28.6) | 0 (0) | 2 (28.6) |
| Amite | 11 | 1 | 12 | 9 (82.0) | 0 (0) | 9 (75.0) |
| Claiborne | 57 | 5 | 62 | 24 (42.1) | 0 (0) | 24 (38.7) |
| Copiah | 8 | 2 | 10 | 6 (33.3) | 0 (0) | 6 960.0) |
| Franklin | 13 | 1 | 14 | 3 (23.1) | 0 (0) | 3 921.4) |
| Hinds | 8 | 1 | 9 | 3 (37.5) | 1 (100) | 4 (44.4) |
| Jackson | 14 | 3 | 17 | 5 (35.7) | 0 (0) | 5 (29.4) |
| Lawrence | 55 | 3 | 58 | 15 (27.0) | 3 (100) | 18 (31.0) |
| Lincoln | 5 | 1 | 6 | 5 (100) | 1 (100) | 6 (100) |
| Pike | 65 | 4 | 69 | 23 (35.4) | 3 (75) | 26 (37.7) |
| Simpson | 75 | 6 | 81 | 0 (0.0) | 0 (0) | 0 (0.0) |
| Wathall | 21 | 3 | 24 | 10 (47.6) | 0 (0) | 10 (44.7) |
| Warren | 4 | 1 | 5 | 3 (75.0) | 1(100) | 4 (80) |
| Wilkinson | 25 | 4 | 29 | 12 (48.0) | 0 (0) | 12 (44.4) |
| Total | 368 | 39 | 407 | 120 (38.6) | 9 (23) | 129 (31.7) |

DISCUSSION AND CONCLUSIONS

This study shows that hog lice are of fairly common occurrence in Southwestern Mississippi with 31.7% of 407 hogs infested and widely distributed. Infestation was recorded from all but one (Simpson) of the 14 counties surveyed (93.0%). This is in contrast with Danish organic swine herds where no pig showed any signs of infestation with lice (Carstensea et al. 2002). The highest infestation was recorded in Lincoln County (5 of 5; (100%) although the sample size was not much followed by Warren County 4 of 5(80%) and Amite with 9 of 12 (75.0%) infested. The boars were much less in number and generally less infested (23% and 38.6% respectively). The boars lower numbers is to be expected as this is usually the case in swine farms.

Heavy infestations were observed where hogs were kept in poor husbandry conditions and left unsprayed with insecticide for a long time. It is interesting to note that not a single hog out of 81 had lice infection in Simpson County- evidence of good control. Normally, healthy mammals and birds usually apply some natural louse control by grooming and preening themselves. Poorly nourished or sick animals

that do not exhibit normal grooming behavior often are heavily infested with lice (Roberts and Janovy, Jr. 2000). This study precludes seasonal patterns of lice infestation such as the one conducted by Foata et al (2006). They reported on the influence of season and host age on wild boar parasites in Corsica. It is recommended that a study on seasonal pattern of lice infestation in hogs be conducted by subsequent investigators. But analysis of our data shows that infestation was greatest during the winter when it was cold and early spring. This is in consonance with the report of Wooten-Saadi et al. (1987). The hogs in the Alcorn State University piggery farm (in Claiborne County) were treated in January 1997. In February 1997, they were infested again. All the hogs except the sows with gilts (piglets) were treated. They were placed within the furrowing house. Their body weights were low; they lost hair and their piglets were infested with lice. The animals that were not infested were placed in the pasture.

It is believed that the best control measure for hog lice is to spray the hogs with insecticide twice a month in the winter and once a month in the summer Gipson et al. (1999) recommended that hogs be examined periodically to monitor their health status

since new animals may enter populations through deliberate translocation. However, lice infestations can hardly be stopped but they can be controlled.

To our knowledge this is the first significant report on lice infestation in hogs covering the southwestern region of Mississippi. Hog lice appear to be fairly highly prevalent in Mississippi, and require control. Swine farmers should be on the lookout for them and guard their swine against infestation.

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Description of an Upland Oak-Hickory Forest in the Black Belt from Osborn Prairie, Oktibbeha County, Mississippi.

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ABSTRACT

Plant composition, trees per hectare, basal area, soil information, and approximate forest age are provided for a one hectare forest located at Osborn Prairie (Sixteenth Section Prairie), in the Black Belt Prairie region of Oktibbeha County, Mississippi. Thirty-six species were documented from this forest, which was dominated by post oak, *Quercus stellata* and eastern red cedar, *Juniperus virginiana*. The name of “upland oak-hickory forest” is proposed for this forest assemblage in the Black Belt.

INTRODUCTION

The Black Belt Prairie physiographic region extends from McNairy County, Tennessee in an arc south through eastern Mississippi to Russell County, Alabama (Figure 1). This region is primarily characterized by the Selma chalk that forms much of the soil in the area. This chalk was formed from marine sediments that were deposited when the Mississippi embayment occupied the region during the Cretaceous period (Logan, 1904; Kaye, 1955 and 1974). Over time it weathers into a fertile, heavy and tenacious, calcareous, loamy clay soil (Lowe, 1921; Schauwecker, 1996). The secondary edaphic feature of interest in this region is that in some areas, a red acidic soil of the Oktibbeha Series, called “Post Oak Soils” is situated atop the Selma Chalk. This soil is formed from a bed of heavy clay that overlays the Selma Chalk, does not retain and supply sufficient moisture to plants in dry

weather and is rather low in plant nutrients (Scott 1939).

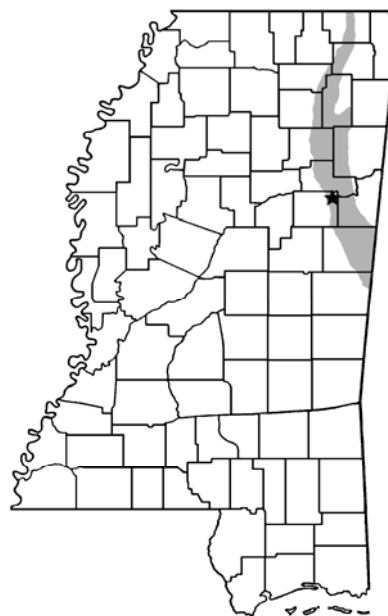


Figure 1. Map of Mississippi showing the Black Belt (shaded) and Osborn Prairie (H).

The soil formed from Selma Chalk generally supports grasslands, while the acidic soil typically supports a post oak (*Quercus stellata* Wang., Fagaceae) forest (Lowe, 1921 and Kaye, 1955). This dichotomous feature of the landscape has been reported since European settlers first arrived in the region (Barone, 2005). These observations are further substantiated by studies using historic documents, soil maps, and General Land Office (GLO) surveyor's notes from Montgomery (Rankin and Davis, 1971) and Sumter (Jones and Patton, 1966) Counties in the Black Belt of Alabama to locate areas of forest and prairie. These studies found a high correlation between alkaline soils and open prairies (low tree density), and acidic soils and forest (high tree density).

However, descriptive studies of the forests that occur on these acidic soils are generally lacking, as the most recent research on the native flora in the Black Belt region of Mississippi has focused on the open prairie remnants (Schuster and McDaniel, 1973; Schauwecker, 1996 and 2001; Leidolf and McDaniel, 1998; Forbes, 1999; Peacock and Schauwecker, 2003; Hill, 2004; Barone, 2005; Barone and Hill 2007, and Hill and Seltzer, 2007). Works on the forest vegetation of the Black Belt region have been limited, and consist mostly of a list of the characteristic species (Lowe, 1913; 1921; Rankin and Davis, 1971, Leidolf et al. 2002).

In this study we describe the flora (presence/abundance) of a one ha xeric forest located at Osborn Prairie, also known as Sixteenth Section Prairie, Oktibbeha, County, Mississippi. Osborn Prairie is one of the larger intact examples of Black Belt Prairie biota remaining in Mississippi. This tract of land is permanently owned by the Oktibbeha County School Board, and as mandated by the state constitution, is leased at a percentage of its assessed value to generate funds for the school district. In 2002 a group of concerned citizens organized a group "Friends of the Black Belt"

and entered into a 40-year lease covering approximately 24 ha, which in 2005 was expanded to encompass approximately 57 ha. that is frequently used as a study site for researchers "outside laboratory" for teachers at Mississippi State University. Leidolf and McDaniel (1998) described three plant communities (open prairie, prairie-cedar woodland, and chalk outcrops) from 16 hectares along a power line right-of-way at the site. This study provides more detailed information on the flora of a forest in the Black Belt than was previously available and also should be useful to researchers working at Osborn Prairie, as we describe an additional vegetation type that occurs on the newly leased acreage

MATERIALS AND METHODS

Study site: In 2003, a 1 ha forest at Sixteenth Section (33°30'51"N 88°43'52"W) was surveyed for herbaceous and woody plant species composition, basal area, and trees per hectare (Table 1). This forest is situated on an elevated area of reddish soil belonging to the Kipling-Savannah-Oktibbeha association, and is bordered on the east and south sides by prairie and on the west by a chalk outcrop. The north side slopes downward, eventually turning into a bottomland hardwood forest.

The climate of Oktibbeha County is humid and warm and is influenced by its subtropical latitude, the extensive landmass to the north, and the warm temperatures of the Gulf of Mexico (Brent 1973). The mean annual temperature is approximately 17° C, and precipitation is relatively evenly distributed throughout the year with an average high in March of 15.42 cm and an average low in October of 8.51 (Office of Climate Divisions of Mississippi, 2005). There is an annual average of 226 frost-free days (above 0° C) (Brent 1973).

The forest inventory was conducted by performing a 24 % cruise, consisting of six, 400 m² round plots with a radius of 11.28 m.

Diameter at breast height (dbh), measured at 1.4 meters above the ground, was recorded for all living trees whose diameter was ≥ 1 cm. For analysis, the trees were placed into diameter classes based on 2.5 cm intervals. Basal area and trees per hectare were calculated following Wenger (1984). A general survey of other woody and herbaceous vegetation occurring in this forest was also conducted. Voucher specimens have been deposited in the Mississippi State University Herbarium (MISSA) and the Cobb Institute of Archeology comparative collection. Specimens were identified using Radford et al. (1968) and Smith (1994), and nomenclature follows Kartesz (1994). Three soil samples were taken from the site and analyzed by the Mississippi State Soil Testing Laboratory. Seven of the mature pines were cored with a Suunto® (Vantaa, Finland) increment borer to determine the approximate age of the forest.

RESULTS AND DISCUSSION

The general survey of the site revealed a total of 36 taxa, with 23 being woody and 13 being herbaceous (Table 1). The most diverse genus in this forest was *Quercus* (Fagaceae) represented by 7 species. Ground cover was almost non-existent, however when present it was typically represented by a few scattered individuals of the shrub or herbaceous species listed in Table 1.

The inventory of the forest resulted in a total of 405 trees from 17 species being measured within the six, 400 m² plots. Total basal area measured 24.44 m²/ha with 1470 trees per ha. Numerically this forest was dominated by small eastern red cedars (*Juniperus virginiana* L., Cupressaceae), post oak (*Quercus stellata*), and blackjack oak (*Q. marilandica* Muenchh.), respectively. However, basal area was dominated by *Q. stellata*, *J. virginiana*, and *Q. marilandica*, respectively (Table 2).

While eastern red cedar and post oak were the most abundant tree species in this forest, many of the eastern red cedars were small (≈ 1 cm dbh) and contributed significantly less to the total basal area of the forest (Table 2). These cedars are likely remnants of an early successional stage that occurred after the forest was cut approximately 50 years ago based on the age of the cored pines. The majorities of these cedars lacked the typical conical shape of a cedar, and instead have trunks with branches only occurring near the top of the tree, which is probably a result of shading.

Table 1. List of plants found in a xeric oak-hickory forest at Osborn Prairie, Oktibbeha County, Mississippi.

PTERIDOPHYTA

POLYPODIACEAE

Pleopeltis polypodioides (L.) Andrews and Windham

CONIFEROPHYTA

CUPRESSACEAE

Juniperus virginiana L.

PINACEAE

Pinus echinata Miller

Pinus taeda L.

MAGNOLIOPHYTA

MAGNOLIOPSIDA

ANACARDIACEAE

Toxicodendron radicans (L.) Kuntze

AQUIFOLIACEAE

Ilex decidua Walt.

BERBERIDACEAE

Podophyllum peltatum L.

CAPRIFOLIACEAE

Lonicera japonica Thunb.

Symphoricarpos orbiculatus Moench.

ERICACEAE

Vaccinium arboreum Marsh.

FABACEAE

Cercis canadensis L.*Clitoria mariana* L.*Lespedeza cuneata* (Dumont) G. Don

FAGACEAE

Quercus alba L.*Quercus durandii* Buckley*Quercus falcata* Michx.*Quercus marilandica* Muenchh.*Quercus muehlenbergii* Engelm*Quercus stellata* Wang.*Quercus velutina* Lam.

JUGLANDACEAE

Carya myristiciformis (Michx. f.) Nutt.*Carya ovata* (Mill.) K.Koch*Carya tomentosa* (Poir.) Nutt.

LAURACEAE

Sassafras albidum (Nutt.) Nees

MENISPERMACEAE

Cocculus caroliniana (L.) D. C.

OLEACEAE

Fraxinus americana L.

OXALIDACEAE

Oxalis violacea L.

PASSIFLORACEAE

Passiflora lutea L.

RHAMNACEAE

Berchemia scandens (Hill) K. Koch

ROSACEAE

Prunus serotina Ehrh.

ULMACEAE

Ulmus alata Michx.

VERBENACEAE

Callicarpa americana L.

VITACEAE

Vitis sp.**LILIOPSIDA**

CYPERACEAE

Carex cherokeensis Schwein

POACEAE

Panicum dichotomum L.

PYROLACEAE

Montropa sp.

SMILACACEAE

Smilax bona-nox L.

Table 2. Basal area and trees per hectare in a Mississippi Black Belt Prairie xeric oak-hickory forest.

| Species | Basal Area (m ² /ha) | Trees per ha |
|--|---------------------------------------|-----------------|
| Post oak, <i>Quercus stellata</i> Wang. | 11.507 | 514.08 |
| Cedar, <i>Juniperus virginiana</i> L. | 3.73 | 552.45 |
| Blackjack Oak, <i>Quercus marilandica</i> Muenchh. | 3.60 | 112.24 |
| Durand Oak, <i>Quercus durandii</i> Buckley | 1.725 | 32.13 |
| Loblolly pine, <i>Pinus taeda</i> L. | 1.134 | 82.11 |
| Southern Red Oak, <i>Quercus falcata</i> Michx. | 1.029 | 21.42 |
| Shagbark Hick, <i>Carya ovata</i> (Mill.) K.Koch | 0.900 | 42.84 |
| Black oak, <i>Quercus velutina</i> Lam. | 0.401 | 14.28 |

| | | |
|--|--------|---------|
| Ash, <i>Fraxinus americana</i> L. | 0.125 | 28.06 |
| White Oak, <i>Quercus alba</i> L. | 0.124 | 3.75 |
| Nutmeg Hickory, <i>Carya myristiciformis</i> (Michx. f.) Nutt. | 0.114 | 7.14 |
| Mockernut Hickory, <i>Carya tomentosa</i> (Poir.) Nutt. | 0.027 | 21.42 |
| Winged Elm, <i>Ulmus alata</i> Michx. | 0.016 | 21.42 |
| Sassafras, <i>Sassafras albidum</i> (Nutt.) Nees | 0.004 | 3.57 |
| Deciduous Holly, <i>Ilex decidua</i> Walt. | 0.003 | 7.14 |
| Black Cherry, <i>Prunus serotina</i> Ehrh. | 0.003 | 3.57 |
| Red Bud, <i>Cercis canadensis</i> L. | 0.001 | 3.57 |
| Totals | 24.443 | 1471.19 |

Other authors have noted the abundance of eastern red cedar in the Black Belt, and have suggested that an increase in abundance of this tree happened within the last century. Based upon General Land Office surveyors notes dating to the early 1830's, Peacock and Miller (1990) provide the following account of eastern red cedar in the Black Belt prior to European settlement "the data speaks clearly: out of 2,304 witness trees recorded in the early survey reports from the Black Prairie in Mississippi, only one cedar tree was noted". By the early 1900's eastern red cedar is mentioned by Lowe (1913 and 1921) as occurring on ledges where the limestone comes to the surface or as scattered clumps in low or wet areas. Leidolf and McDaniel (1998) describe cedar woodlands as a community type that is characterized by almost pure stands of cedar. However, a plant community resembling a cedar woodland was not mentioned by Lowe (1921) or in any other early descriptions of the region. This implies that the profusion of cedar as well as the emergence of cedar woodlands are of recent origin, likely resulting from human impact.

The Black Belt was once the major agricultural center of Mississippi and Alabama, but large tracts of land formerly in production are now severely eroded with exposed chalk, or sit vacant (Harper, 1857; Lowe, 1913; Wilson, 1981, Webster and Sampson, 1991). Once abandoned, these disturbed areas subsequently grow up in cedar (J.G. Hill pers. obs.). These

factors point to human disturbance of the soil as well as a lack of fire as the possible reason for the increasing abundance of cedar since pre-European settlement times. In addition, prehistoric evidence of cedar has been found at Lyon's Bluff, which is located approximately 6.44 km north of Osborn Prairie (Seltzer, 2007). Lyon's Bluff is situated along Line Creek and was an area with significant amounts of prehistoric human impact, both of which factors influenced the likelihood of cedar's presence.

Eastern red cedar is a fire intolerant species and prescribed burns are a typical method of removal from a site (Solecki, 1997). Lowe (1913) called for action to prevent the severely damaging fires that were frequent in the Black Belt during periods of drought. His rationale was that fires damaged trees making them unusable for building material and firewood, and the removal of leaf litter by fire resulted in runoff of the less fertile forest soil onto the surrounding rich prairie soil.

The results of the soil samples revealed an acidic soil with a mean pH of 5.2. In moderately acidic soils (pH 4-5.5) some nutrients and solutes, such as Al, may be present in toxic levels, which can limit plant growth. The mean age of the pine corings suggested that this forest was approximately 46 years old \pm 11.9 years. If this approximate age can also be applied to the deciduous species, then the low availability of nutrients, due to soil acidity, coupled with the xerophytic nature of the soil are

probably the main factors influencing the poor growth of trees in these habitats, as Lowe (1913 and 1921) indicated by calling them “dwarfed forests”. A reason for the low diversity of the flora of this forest may be that the acidic soils limit the types of plants that can grow in the area.

With exception of the presence of cedar, the trees found in the forest surveyed correspond in composition with the “dwarfed forests” that Lowe (1913 and 1921) described as typically “occurring on higher reddish soil” (Table 3). Based on the similarities with Küchler’s (1964) and Bryant et al.’s (1993) description of oak-hickory forests in the southeastern United States and the apparent lumping of several kinds of forests within Küchler’s “Black Belt forest” type, the name of “upland oak-hickory forest” is proposed for this forest assemblage in the Black Belt. Future monitoring and observations should be made in this forest to examine any changes in abundance of cedar or other tree species that may take place, in order to better understand the role of eastern red cedar in the landscape of Black Belt.

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***Panicum repens* (Torpedo Grass) in Mississippi**

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ABSTRACT

Panicum repens is a perennial grass commonly found in the southeastern United States. It is considered to be introduced and often reported as being highly invasive. It has been recorded in Mississippi since the late 1800s but has not been considered to be a major problem. Recent collections suggest that this species may be increasing its range in the state, at least through anthropogenic disturbance. Species circumscription, current distribution and invasive potential in Mississippi and elsewhere, as well as cytological information are discussed.

TAXON CHARACTERISTICS AND CIRCUMSCRIPTION

Panicum repens L. (Torpedo Grass) is a highly rhizomatous, perennial grass that forms dense mats (Fig. 1a) mostly through vegetative reproduction, via deep penetrating rhizomes (Fig. 1c). According to some researchers, this species never produces viable seed and the main mode of reproduction of the species is asexual by rhizomes (Wilcut et al. 1988). However, Martínez et al. (1992) found that fluctuating temperatures and salinity strongly encourage the germination of *P. repens*. They also found that varying depths of seed burial had no major effect on germination rates, which may be important for a species commonly found in coastal areas frequently disturbed by meteorological events. Tarver (1979) states that torpedo grass was planted by the USDA via seeds, so obviously at least some seeds of this species are viable (see below, polyploidy).

Leaves of *P. repens* are dark green to greenish-grey (sometimes almost glaucous), which often make colonies of the species very conspicuous growing among associate vegetation. The leaves typically are distichous and may be 3-25 cm long and 2-8 mm wide with a basally pilose adaxial surface and a glabrous to pubescent abaxial surface (Freckmann & Lelong 2003). The upper sheathing

leaf bases usually are densely hirsute or pilose (Fig. 1b). Culms are erect to geniculate and range from 20-90 cm tall (Freckmann & Lelong 2003).

Inflorescences of *P. repens* are diffuse panicles from 3-24 cm long with spikelets ranging from 2.2-2.8 mm long (Freckmann & Lelong 2003) and often may be nearly glaucous in some specimens, or purplish in those specimens which have been referred to as *P. gouinii* E. Fourn. (Freckmann & Lelong 2003).

Panicum repens was formerly placed in the large (~ 450-500 spp.), and highly polyphyletic genus *Panicum* (*sensu lato*) and included in the subgenus *Panicum* (Zuloaga et al. 1993, Aliscioni et al. 2003) of the subfamily Panicoideae in the family Poaceae. It currently is included within the section *Dichotomisflora* in the monophyletically circumscribed genus *Panicum* (*sensu stricto*), which contains around 100 species. Species in this genus are characterized by the C4 photosynthetic pathway and having a base chromosome number of $x = 9$ (Aliscioni et al. 2003). *Panicum repens* has been reported as diploid (Ashan et al. 1994) and also as forming a polyploid complex having tetraploid, hexaploid, and aneuploid cytotypes (Freckmann & Lelong 2003). Freckmann & Lelong (2003) report that another taxon, *P. gouinii*, is not recognizable on the basis of morphology and that intermediates are

often found between the two species. They consider *P. gouinii* to be conspecific with *P. repens*. However, on the basis of the chloroplast gene *ndhF*, Aliscioni et al. (2003) found that the two taxa were molecularly divergent, although there was little support for this separation (e.g., Fig. 2). Some specimens from Mississippi have been identified as *P. gouinii*, but more work would be necessary to determine whether or not the taxon should actually be recognized as a good species.

ORIGIN AND DISTRIBUTION

Panicum repens is a cosmopolitan species found in many countries throughout the world (Freckmann & Lelong 2003). It has been reported as native to the Americas (Liu et al. 2006), although there is some debate over its place of origin. Freckmann and Lelong (2003) suggest that it may have been introduced into the Americas. Guglieri et al. (2004) consider the species native to the United States, Argentina, Belize, the Caribbean, and throughout Brazil, although they consider it as an invasive species of gardens and other cultivated areas. Schmitz et al. (1988) report that *P. repens* is a native of Europe. So obviously there is some confusion over the true origin of the species. Waterhouse (1994) reports the species from North Africa and the Mediterranean region and Hoyer et al. (1996) report it from Australia. It is a common weed in parts of Asia as well (Hossain et al. 2001, Liu et al. 2006).

Panicum repens can withstand relatively dry, sandy soils or “mucky” soils under flooded conditions (Sutton 1996). It is quite common in the southeastern United States being found from North Carolina to Texas (USDA, NRCS 2009) in a variety of habitat types but most frequently in coastal areas (Freckmann & Lelong 2003, Majure pers. observ.). Torpedo grass was planted throughout the southern states in the 1920s by the United States Department of Agriculture for use as a forage grass (Schmitz et al. 1988). It also is found in California, Utah (Freckmann & Lelong 2003) and Hawaii according to The Plants Database (USDA, NRCS 2009).

This species has been collected in Mississippi

for quite some time. Records for this species exist at the Mississippi State University Herbarium (MISSA) from Deer Island, one of the barrier islands off of the Mississippi coast, from as early as 1891 collected by A. B. Seymour and 1894 by S. M. Tracy. Lloyd and Tracy (1901) recorded this species as a main component of the sand plain formation of the insular flora of Mississippi and Louisiana. Penfound and O’Neill (1934) and Pessin and Burleigh (1941) recorded *Panicum repens* from the Mississippi gulf islands Cat and Horn, respectively, also as a main component of the island vegetation.

Until recently torpedo grass was considered to be mostly restricted to coastal areas within the state of Mississippi. *Panicum repens* previously was only known from five southern counties (Forrest, Hancock, Harrison, Jackson, and Lamar; Freckmann & Lelong 2003), including records from state herbaria (MISS, MISSA, MMNS, USMS). However, more recent collections of this species from Lauderdale and Newton counties have increased its distribution to east-central Mississippi. *Panicum repens* found in Lauderdale County apparently originated from sod brought in from south Alabama (C.T. Bryson pers. comm.). It also was collected from Pearl River, Perry, Greene, and George counties, where it had not been recorded in recent treatments (Appendix 1). *Panicum repens* has been observed or suspected, but not collected, in other counties (Jeff Davis Co., Simpson Co.; H. Sullivan, Mississippi Museum of Natural Science, pers. comm.; Covington Co., Jones Co., Lee Co., Madison Co., Stone Co., C.T. Bryson, USDA-ARS, Southern Weed Science Laboratory, pers. comm.; Clarke Co., Wayne Co., V. Maddox, Mississippi State University, pers. comm.; Hinds Co., Rankin Co., W. Wells, Mississippi State University, pers. comm.) (Fig. 3). Considering the current distribution in the state, this species should also be found in several of the southwestern and south-central Mississippi counties that border southeastern Louisiana counties where the species has been recorded (Freckmann & Lelong (2003).



Figure 1. *Panicum repens* in Jackson Co., MS. 1a) large monotypic colony of *P. repens* adjacent to salt marsh, 1b) culm showing hirsute leaf sheaths and pubescent leaves, 1c) characteristic rhizome of the species.

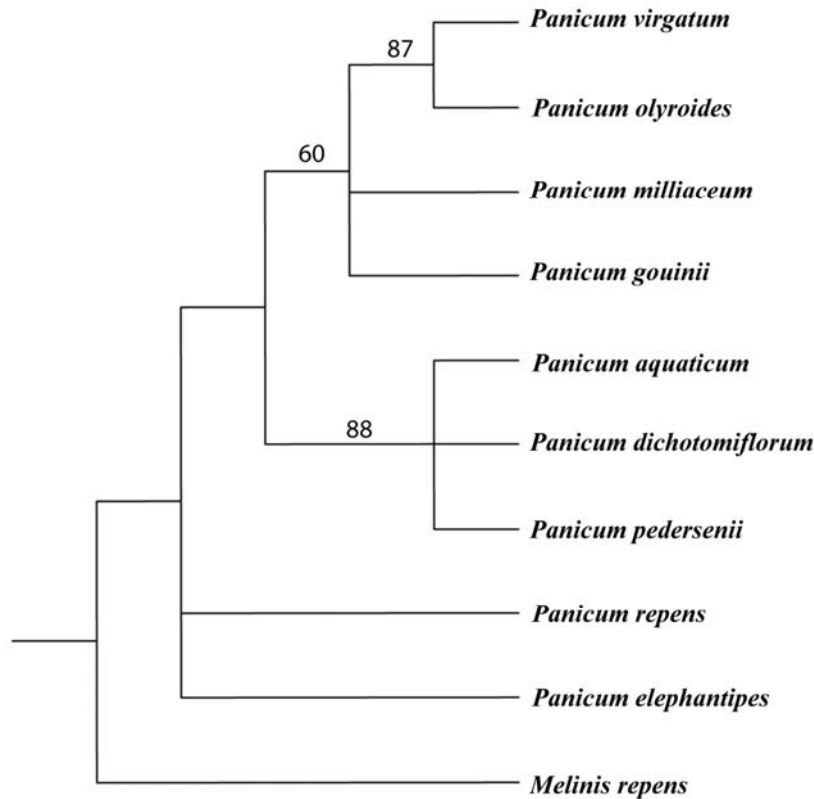


Figure 2. Maximum Likelihood (ML) tree of most members of sect. *Dichotomiflora* of the genus *Panicum* (sensu Alicioni et al. 2003) created from accessions downloaded from Genbank (NCBI 2008) using PAUP 4.0 (Swofford 2002) based on the TrN+G model under AIC using Modeltest 3.06 (Posada & Crandall 1998). *Melinis repens* is used as the outgroup to polarize the tree. This tree shows that *P. repens* and *P. gouinii* are not necessarily most closely related and could lend support for the separation of the two taxa, however, bootstrap support is really low for subclades, and there is little resolution in the phylogenetic reconstruction (i.e., represented by polytomies). This tree was generated from the maternally inherited chloroplast gene *ndhF*, so a potential hybridization event resulting in the discontinuity of two morphologically similar taxa (i.e., chloroplast capture by a taxon other than *P. repens*) would not be detected unless, for example, a biparentally inherited nuclear gene were also used for phylogeny reconstruction. On the contrary these two entities, *P. gouinii* and *P. repens*, may truly represent divergent lineages that have a strongly homoplasious (convergent) morphology.

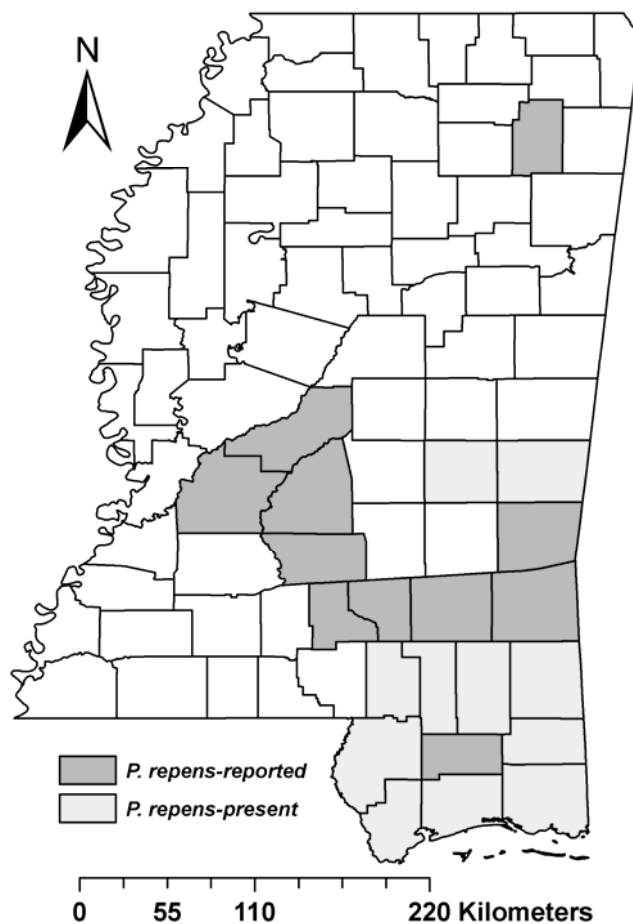


Figure 3. The present distribution of *P. repens* in Mississippi for which herbarium records exist are represented in light grey, and other counties from which *P. repens* has been reported or suspected (e.g., Madison Co.) are highlighted in dark grey

POLYPLOIDY AND INVASIVE POTENTIAL

It is widely accepted that polyploidy (genome duplication) in plants is a major evolutionary force (Tate et al. 2005, and refs. therein). Polyploidy has had an enormous influence on the evolution of grasses, and it is estimated that all grasses are polyploids (paleo or neopolyploids; Levy & Feldman 2002). Polyploidy via hybridization (allopolyploidy) is often associated with the incurrence of an increased adaptive ability in progeny (i.e., hybrid vigor). Stebbins (1940) related this to the inclusion of the combined physiological traits of the putative parental taxa within the subsequent allopolyploid. A great example of this is the relatively recent speciation of the Chloridoid

grass *Spartina anglica* C.E. Hubb., an allopolyploid derivative of the two hexaploid parental taxa (reviewed in Ainouche et al. 2003), the introduced *S. alterniflora* Loiseleur from the eastern United States and the European native, *S. maritima* (Curtis) Fernald (Ayres & Strong 2001). This species has become highly invasive in coastal marshes that it inhabits, subsequently occupying a larger geographical area than its parental progenitors (Baumel et al. 2002, Ainouche et al. 2003).

Polyploidy via genome duplication within one species (autopolyploidy) has typically been considered of little importance evolutionarily, although recent work suggests that plant systematists may be overlooking many species which have arisen through this process (Judd et al. 2007, Soltis et al. 2007). Polyploids in general can be considered to

have an advantage over their diploid progenitors for several reasons. Polyploidy can lead to asexual reproduction and self-compatibility, so newly formed polyploids may be able to maintain viable populations without having a large group of mates to choose from. Polyploidy via hybridization can lead to heterosis, or hybrid vigor as mentioned above. Also the result of having more than one copy of most genes within a polyploid, or gene redundancy, provides a buffer system against deleterious gene mutations (Comai 2005). Being a polyploid species in some instances, *Panicum repens* may be more adaptable than taxa with which it is in direct competition. In this manner polyploidy may confer a higher degree of “weediness” in torpedo grass than for other species. As well though, some aneuploid cytotypes of *P. repens* may be sterile, and so accounts of nearly complete asexual reproduction of the species and non-viable seeds may thus be explained. Hence, polyploidy is not necessarily always advantageous.

Panicum repens (and *P. gouinii*) is listed on the website, A Global Compendium of Weeds (2009), so is considered by some authors to be a weedy species. Tarver (1979) considered this species a serious weed. In fact, control of this species has been tested using different herbicides in turf management (Brecke et al. 2001) and in natural areas, such as Lake Okeechobee, FL, where *P. repens* has invaded thousands of hectares of lakeshore and adjacent areas (Hanlon & Langeland 2000). Hanlon and Langeland (2000) also state that the invasion by *P. repens* has had deleterious effect on the sports fish habitat by reducing inhabitable space and dissolved oxygen for those species. Gordon (1998) lists this species as a Category 1 (on the most invasive plant species list) in Florida. Schmitz et al. (1988) state that torpedo grass is especially problematic in flood control canals. It has also been reported as impeding radio-telemetry work for tracking fish in southern Mississippi (M. Dugo pers. comm.), where *P. repens* forms large mats extending into the water. So there are obvious economic repercussions to large invasions by torpedo grass. Cuda et al. (2007) consider economic losses to be very large. The estimated cost of control annually in Florida in 1990 was \$2 million (Schardt & Schmitz 1991). On the contrary, torpedo grass was found by Cuda et al. (2007) to contain a large number of associate insects

(e.g., 12 orders, 37 families, and 54 genera) at Lake Okeechobee, although some of these insects are considered pests (e.g., *Blissus insularis* Barber). *Panicum repens* is also known for stabilizing edges of water bodies, which could either alter natural hydrological features of an area (Smith et al. 1992) or help prevent erosion.

DISCUSSION

It would be interesting to know whether or not polyploid cytotypes of *P. repens* represent auto or allopolyploids. If allopolyploidy were found, then the putative parental taxa could be determined and the evolutionary origin of polyploid *P. repens* could be established. Considering hybridization could be a factor and the fact that in phylogenetic analyses the morphologically similar *P. gouinii* and *P. repens* are not resolved as sister taxa (Alisconi et al. 2003; e.g., Fig. 2), this may actually be evidence for a hybrid origin for either *P. repens* or *P. gouinii*. Testing this hypothesis would require a biparentally inherited marker, such as from the nuclear genome (see Fig. 2). In any case, a close inspection of life history traits and ploidy in *P. repens* over a wide geographical range could reveal correlations among cytotypes and self compatibility, vegetative reproduction, and morphological features.

Considering the invasive potential of torpedo grass (Bodle & Hanlon 2001) and its status as a worldwide weed (Holm et al. 1977), this species probably should be considered as a weed to watch in MS. C.T. Bryson (pers. comm.) also considers this species as one that may need to be tracked as a potential weed in the state. It apparently is being spread by contaminated sod and is frequently found in disturbed areas (e.g., road construction, building construction areas, etc.), so anthropogenic actions are most likely the main cause for the increasing distribution of the species within the interior of the state. However, considering that sexual reproduction has been documented in *P. repens* (Martínez et al. 1992), seeds could be spread by any of numerous ways (e.g., hydrochory, zoochory, etc.) further increasing the distribution of the species in Mississippi.

APPENDIX 1. New records of *P. repens* in Mississippi.

***Panicum repens* L. George Co.** in front of Salem Volunteer Fire Department, off of Hwy. 57 S, S of Benndale; common in lawn and ditch; L.C. Majure 2598 w/ T. Majure (MISSA, MMNS); **Greene Co.** off of Hwy. 57 S along small creek near junction with Thelma Road, just south of McLain past railroad tracks; 31.08494 °N, 88.81259 °W; L.C. Majure 2597 w/ T. Majure (MISSA, MMNS); **Lauderdale Co.** Meridian, Bonita Lakes Recreation Area off of Hwy. 19 S of I-20; 32.35934°N, 88.65360°W; common along roadside and bank of Bonita Lake; L.C. Majure 1200 (MISSA, MMNS). **Newton Co.** off of Hwy. 80 W; ca. 2 km W of the town of Chunky; 32.32627 °N, 88.93763 °W abundant along roadside in ditch and adjacent areas; L.C. Majure 2474 (MISSA, MMNS). **Perry Co.** off of Hwy. 15 S, ca. 0.5 km north of the town of Richton; 31.36247°N, 88.93543 °W; abundant adjacent to small stream. L. C. Majure 2596 w/ T. Majure (MISSA, MMNS). **Pearl River Co.** Picayune, 0.1 mi. W jct. of Hwy I-59 and MS 43 (N jct.), N of Hwy MS 43 between I-59 and Cooper Street, open area on sandy to silty loam soil, 16 Aug 1994, C.T. Bryson 14249 (SWSL).

ACKNOWLEDGMENTS

I wish to thank M. Alford, C.T. Bryson, V. Maddox, H. Sullivan, and W. Wells for information regarding herbarium collections and observations of *P. repens* in MS.

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***Tapinoma melanocephalum* (Hymenoptera: Formicidae), a new exotic ant in Mississippi**

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Corresponding Author: Joe MacGown

Tapinoma melanocephalum (Fabricius) (Hymenoptera: Formicidae), commonly called the ghost ant, is an exotic tramp species thought to have originated from tropical regions of Africa or Asia (Smith, 1965). Due to its spread by commerce, it is now widespread in subtropical and tropical regions around the globe. However, it also has become established in greenhouses and other buildings in temperate regions (Nickerson and Bloomcamp, 2006). In the United States, the ghost ant is well established in Florida, where it is ranked as one of the top three urban pest ants in the state along with the red imported fire ant, *Solenopsis invicta* Buren, and the crazy ant, *Paratrechina longicornis* (Latreille) (Klotz et al., 1995), and it is also considered to be a significant pest in Hawaii (Nickerson and Bloomcamp, 2006). This species was discovered in Texas in the mid 1990's, when it was thought to have been accidentally introduced with plants shipped from Florida (Chenault, 1997). Although this species has been found in some northern states in the United States and even in Winnipeg, Manitoba, Canada, these occurrences were in greenhouses or in other heated structures (Nickerson and Bloomcamp, 2006).

Here, we report the first record of *T. melanocephalum* in Mississippi. Specimens were collected by Hill and MacGown on 30 April 2008 at an outdoor nursery specializing in palm trees (Arecaceae) in Bay St. Louis, Hancock County, Mississippi. This particular nursery was known to import plants from Florida, and our investigation of this nursery (and others in the region) was based on the idea that it had a higher probability of harboring exotic species from Florida, the state with the highest number of exotic ants (Deyrup et al., 2000). Therefore, it is likely that this species was accidentally introduced to the nursery with the plant material from Florida, as this species is known to

nest in bases of palm fronds (Harris, 2005). Many of the palm trees at the nursery were planted directly in the sandy soil on the property, which was open and adjacent to both natural and urban areas. *Tapinoma melanocephalum* workers were first observed as they foraged on the ground within two meters of the base of a large palm tree that was planted in the soil and on the tree itself. Workers were abundant and a series of specimens was collected, stored in 95% ethanol, and deposited in the Mississippi Entomological Museum. Scattered foraging workers were also found in several other areas of the nursery. It is not known whether this species is established in the region, but based on its relative abundance at this site, and the generally subtropical climate of the Gulf Coast counties, it is possible that this species could become established in the area.

In addition to the ghost ants, several other species of ants, all of which were exotic, were collected at the site, including *Brachymyrmex patagonicus* Mayr (the dark rover ant), *Paratrechina longicornis*, *Hypoponera opaciceps* (Mayr), *Solenopsis invicta*, and *Pheidole moerens* Wheeler. With the exception of *P. longicornis*, these introduced species are known to be well established in southern Mississippi. *Paratrechina longicornis*, however, is much less frequently found in this area, and it is possible that this population was also accidentally introduced with plant material from Florida.

Ghost ants are known to nest both indoors and in disturbed areas outdoors. They have polygyne, unicolonial colonies that vary from having only a few workers to thousands per nest. They are opportunistic colonizers, and queens from one colony may be dispersed in smaller subcolonies, with workers freely being exchanged between different nests (Harris, 2005). They nest in a variety

of places outdoors, some of which are temporary, including plant stems, dried grass clumps, debris, dead tree limbs, in plant pots, under objects on the ground, under bark, at bases of palm fronds, or other similar situations, and indoors they nest in wall voids or potted plants (Harris, 2005; Nickerson and Bloomcamp, 2006). This species does not sting or bite, but is considered a nuisance pest in houses and businesses because it invades food stores, especially sweet substances such as sugar and syrup (Smith, 1965).

Tapinoma melanocephalum workers (Figure 1) can be easily identified by their extremely small size and distinctive coloration. Workers are

monomorphic and are only 1.3 to 1.5 mm in total length. They are bicolored with the head and mesosoma being dark brown to blackish brown and appendages, petiole, and gaster being milky white. Additional characteristics include their having 12-segmented antennae, lack of spines, lack of a stinger, lack of large erect hairs on the body, and the lack of a protruding node on the petiole. The petiole is often hidden by the gaster, which often overlaps it. These minute ants are difficult to detect because of their diminutive size and partially light coloration

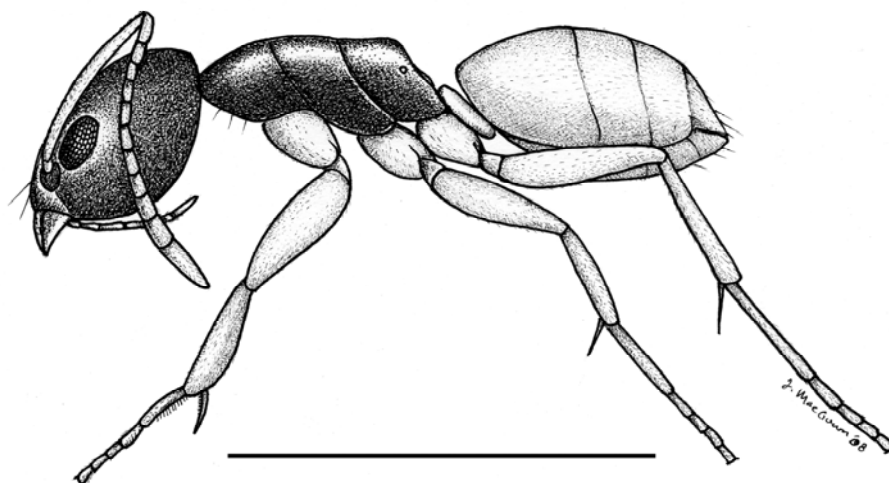


Figure 1. Profile view of a *Tapinoma melanocephalum* worker. Scale bar equals 1.0 mm.

ACKNOWLEDGEMENTS

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MISSISSIPPI ACADEMY OF SCIENCES
Seventy-Third Annual Meeting – Program
Corrections

**Cellular, Molecular, and Developmental
Biology**

Add 3 Oral Presentations

Thursday afternoon:

3:30p

**O2.16 EXPRESSION ANALYSIS OF *CDO1*, *GSH1*,
AND *GSH2* GENES IN THE DIMORPHIC FUNGUS
*HISTOPLASMA CAPSULATUM***

Melissa Adams, Glen Shearer, *University of Southern
Mississippi*

The dimorphic fungus, *Histoplasma capsulatum* (Hc) can be found in the soil as a saprophytic multicellular mold. In the lungs of an infected host, a shift to the unicellular parasitic yeast occurs. The mold to yeast shift is required for the progression of the disease. Sulfur metabolism plays a critical role in the dimorphic process. Sulfhydryl groups, especially cysteine, are a necessary nutrient for the transition to the yeast state. Enzymes involved in the cysteine metabolism pathway are being studied in order to evaluate their role in the dimorphism. Cystiene dioxygenase (*CDO1*), Gamma-glutamyl cysteine synthetase (*GSH1*), and Glutathione synthetase (*GSH2*) are involved in the cysteine metabolic pathway. The isolation of the cDNA of these three genes was accomplished by RACE PCR. The expression level of each gene in both the yeast and mold morphotypes of four Hc strains was examined by northern blotting and real-time PCR. *CDO1*, which was previously isolated in our lab, is expressed in both the mold and yeast phases of the organism while *GSH1* and *GSH2* appear to be expressed in only the yeast phase. Experiments are underway to see if the enzyme levels correlate with transcription levels.

3:50p

**O2.17 TRANSCRIPTION REGULATION OF THE
MOLD SPECIFIC GENE *M46*, IN THE
PATHOGENIC DIMORPHIC FUNGUS
*HISTOPLASMA CAPSULATUM***

Davida Crossley, Glen Shearer, *The University of
Southern Mississippi, Hattiesburg, MS*,

Histoplasma capsulatum is the causative agent for the respiratory disease histoplasmosis which infects an estimated 500,000 Americans each year. The dimorphic fungus grows in the soil as a multi-cellular mold. Once

the soil is disturbed, spores are released and are inhaled into the lungs. In the lungs, the fungus converts to a unicellular yeast. The mold-to-yeast conversion is a requirement for pathogenesis. Therefore, to understand the molecular basis of dimorphism, we have isolated several mold-specific and yeast-specific genes. The subject of this study is the mold-specific *M46* gene. Northern blot analysis has shown that *M46* is expressed in G186AS and Downs strains, but is transcriptionally silent in G184AS and G217B strains. The reason for lack of transcription in the latter strains is currently being studied. The putative protein sequences of all four strains is highly conserved. Fusion of the reporter gene, *GFP* to each of the four *Hc* promoters has shown that all four strains have a functional *M46* promoter. We now hypothesize that the reason for lack of expression of *M46* in strains G184AS and G217B may be due to a missing or non-functional trans-regulating factor(s). In order to characterize the presence of the trans-regulating factors, gel shift analysis is underway. Comparison of electrophoretic mobility shifts of the DNA-protein complexes from the expressing *M46* stains and non-expressing *M46* stains may give insight on the reason for lack of expression from stains G184AS and G217B.

4:10p

**O2.18 IMMUNOISOLATION OF CFTR-
ENRICHED ENDOCYTIC VESICLES,
Ghanshyam Heda¹, Christopher Marino², ¹*Mississippi
University for Women, Columbus, MS*, ²*V.A. Medical
Center, Memphis, TN*, ³*The University of Tennessee
Health Sciences Center, Memphis, TN***

Cystic fibrosis (CF) is caused by mutations that affect the cellular processing of CFTR protein. Half-life of $\Delta F508$, the most common CFTR mutation, at the plasma membrane is shorter (~4 h) than that of wild-type CFTR (>48 h). Effective correction of the CF defect, however, requires stable expression of $\Delta F508$ -CFTR at the plasma membrane. We hypothesize that surface instability of $\Delta F508$ -CFTR may result from its selective targeting to cellular sites different than that of wild-type CFTR, and is controlled by certain regulatory proteins. OBJECTIVES: To identify regulatory proteins by comparing the proteome of $\Delta F508$ or wild-type CFTR-enriched endosomal vesicles. METHODS: LL-CPK₁ cells transfected with $\Delta F508$ or wild-type CFTR were treated with 5 mM sodium butyrate at 27°C to upregulate plasma membrane CFTR levels. Endosomal vesicle fraction was obtained by continuous (12-48%) iodixanol density gradient centrifugation. CFTR-enriched endosomes were visualized by immuno-EM, affinity purified by AminoLink® gel, and analyzed by 2D-PAGE. RESULTS: Immunoblotting showed that endosomal fraction was enriched with Rab5 (96.23±2.38%, n=6) and

Rab11 (95.01±3.96%, n=6), markers of early and recycling endosomes respectively. CFTR enriched endosomes eluted from anti-CFTR linked AminoLink® gel retained ~30% of total endosomal proteins in 2-D gels, suggesting their specificity to CFTR-enriched endosomes. Further, CFTR-enriched endosomes contained 3 proteins (~45-50 kDa, pI ~5.5-6.5) that were significantly enriched and remains to be identified. CONCLUSION: Regulatory proteins may be differentially associated with CFTR-enriched endosomes in cells expressing ΔF508 or wild-type CFTR. Their identification may help us understand the mechanisms that regulate endocytic trafficking and plasma membrane CFTR expression.

Add 1 Poster Presentation
P2.21

DETERMINE THE LOCATION OF THE MOLD SPECIFIC *M46* PROTEIN IN THE DIMORPHIC FUNGUS *HISTOPLASMA CAPSULATUM*.

Rupesh Patel, Davida Crossley, GLen Shearer
The University of Southern Mississippi, Hattiesburg, MS,

Histoplasma capsulatum is a dimorphic fungus that causes histoplasmosis, a respiratory disease. The fungus grows as a multicellular saprophytic mold in soils with bird and bat excreta, at 25 °C. Conversion to unicellular parasitic yeast takes place in the lungs, at 37 °C. The yeast causes histoplasmosis; hence, the mold-to-yeast transition is required for the development of the disease. The *M46* gene was studied in this project to help determine the mechanism of this conversion. Though the function of *M46* is unknown, recent data states that *M46* is only expressed in the mold form. Therefore in aid to determine the function of *M46*, the location of *M46* in the cell will be determined. GFP (Green Fluorescent Protein) was fused to the c-terminus of *M46* from strains WU24 and G186AS. Calcofluor white was used as a control to stain the cell wall. The distribution of GFP as determined by fluorescence microscopy, throughout the hyphae indicates that *M46* localizes in the cytoplasm. We hypothesized that the *M46* protein is located in the cytoplasm. Cytoplasmic proteins generally function as signaling proteins, metabolic regulators, etc. To help determine the function of *M46*, future work includes the n-terminus construct and creation of a knockout.

2009 MAS DIVISIONAL REPORTS

DIVISION OF MATHEMATICS, COMPUTER SCIENCES, AND STATISTICS

A total of 17 oral presentations and 5 Posters were submitted for presentation at the annual Meeting. 10 presentations were made on Thursday and five on Friday. Two of the presenters did not show up. Poster session conducted Thursday evening.

The Division Received \$ 200.00 donations form Mississippi Super Computing (\$100.00) and from Dr. Elgenaid Hamadain (\$100.00). Donations were used for students Awards. Four Awards of \$50.00 each including a certificate went to the following students:

1. University of Mississippi's Deepak Mantena won the Best Undergraduate Oral Presentation Award for his talk: "Writing People Friendly Software"
2. University of Mississippi's graduate student James Church. won the Best Graduate Student Oral Presentation award for his talk: "Approximation Algorithm for generating Neighborhood Graphs"
3. University of Mississippi's graduate student Carl Jensen won the Best High Performance Computing Award for his presentation on "Simulating Acoustics in 3-Dimensional Porous Materials"
4. Mississippi Valley State University undergraduate student Gabrielle Meeks won the Best Poster Award on her poster: "Technical Library Database Update"

The Business Meeting conducted at the end of the oral presentations on Friday. The following were elected to serve the Division for the next year:

1. Dr. Paul Ruth, Assistant Professor of Computer and Information Science at the University of Mississippi, elected as the Chair of the Division
2. Dr. Elgenaid Hamadain, Associate Professor, Department of Diagnostic and Clinical Health Sciences, UMC elected as the Vice- Chair of the Division

Link for pictures inclusion in the report if appropriate

<http://picasaweb.google.com/gotazero/MAS2009?feat=directlink>

Physics and Engineering Highlights

Physics and Engineering Division had 20 oral presentations and 5 posters.

Steven K. Fortenberry of University of Southern Mississippi received the “Best Undergraduate Presentation” Award.

Jutima Simsiriwong of Mississippi State University received the “Best Graduate Presentation” Award.

Report on Division of Marine and Atmospheric Sciences 2009

Chair: Hyun Jung Cho, Jackson State University

Vice Chair: David Rosenfield, University of Southern Mississippi

Division of Marine and Atmospheric Sciences met on Friday February 27th, 2009 during the Annual Conference of Mississippi Academy of Sciences (MAS) at Whispering Woods Hotel and Conference Center, Olive Branch, Mississippi. The total number of participants in the division was not large compared to some other divisions, but the topics of the oral and poster presentations given this year were broad including, but not limited to, coastal/marine biology, remote sensing, marine education, fresh and salt water mixing, ocean currents and transportation, land & sea surface energy fluxes and balance, and marine pathology. The student participation and attendance were especially active and demonstrated good quality in both science and presentation; they were also very attentive to the audience and other presenters. There were several oral presentations and seven poster presentations by student participants from Jackson State University (Departments of Biology, Mathematics, Physics, and the Environmental Science Program) and the University of Southern Mississippi (Departments of Marine Science and Coastal Sciences).

The student presentations were judged based on criteria for scientific merit, knowledge and independence, clarity, and organization/aesthetics. The MAS and the division awarded certificates and cash prizes to four student presenters. The first place prizes for the best oral and poster presentations, sponsored by MS-AL Sea Grant Consortium (MASGC), went to Philemon Kirui (Ph.D. student, JSU) and William Thompson (Undergrad. Honor's Research, USM). The second place prizes, sponsored by Korean-American Engineers and Scientist Association (KSEA)-MS Chapter and Navigation Electronics, Inc., went to Virgilio Maisonet (MS student, USM) and Chudong Pan (Ph.D. student, USM).

• First Place Oral Presentation Awardee

- Philemon Kirui: Classification of Airborne Hyperspectral Data for Shallow Estuarine Seagrass Beds

• First Place Poster Presentation Awardee

- William Thompson: Experimental Infection of *Litopenaeus vannamei*, *Palaemonetes pugio*, and *Farfantepenaeus aztecus* with Necrotizing Hepatopancreatitis Bacterium (NHPB) by Per Os Exposure

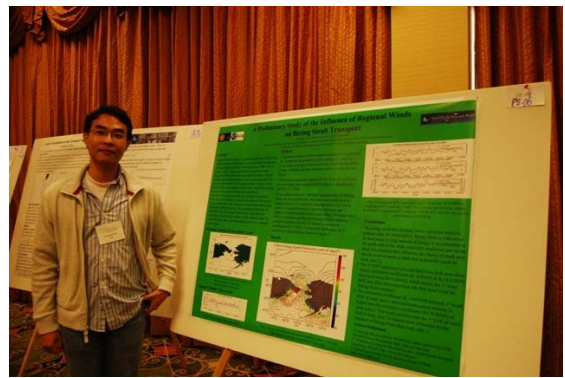
- **Second Place Oral Presentation Awardee**

- Virgilio Maisonet: Using Ocean Color to Measure Coastal Sea-Surface Salinity of the Louisiana Shelf

- **Second Place Poster Presentation Awardee**

- Chudong Pan: A Preliminary Study of the Influence of Regional Winds on Bering Strait Transport

Due to the low participation by faculty and senior scientists, the division chose to postpone the election of the next division vice chair, however, it tentatively nominated David Rosenfield for the next division Chair. Thus far, Dr. Kevin Yeager of Department of Marine Science at USM has been nominated for the next division vice chair. This year's participants greatly appreciate the hard work of the MAS board members. Our sincere thanks go to Ms. Cynthia Huff at MAS, Dr. Ladon Swann and Ms. Devaney Cheramie at MASGC, Dr. Hyung Lae Park at JSU, and Mr. Chad Hicks and Mr. Eric Bock at Navigation Electronics, Inc. for their support and sponsorships.





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Mississippi Academy of Sciences 2010

Hattiesburg, MS Convention Center

More Information will be available in the July issue

CALL FOR ABSTRACTS

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ABSTRACT INFORMATION

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Name of Presenting Author(s): _____

(Presenter must be current (i.e., 2007 membership dues must be paid), student member, regular member or life member of the MAS)

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Check the division in which you are presenting

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| <input type="checkbox"/> Cellular, Molecular, and Dev. Biol | <input type="checkbox"/> History and Philosophy of Sciences | <input type="checkbox"/> Psychology and Social Sciences |
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| <input type="checkbox"/> Ecology and Evolutionary Biology | <input type="checkbox"/> Marine and Atmospheric Sciences | <input type="checkbox"/> Zoology and Entomology |
| <input type="checkbox"/> Geology and Geography | | |

Type of presentation

☐ **Poster presentation** ☐ **Workshop** ☐ **Lecture presentation** ☐ **Invited Symposium**

If the presenting author for this paper will also present in another division, please list the other division _____

Audiovisual Equipment needs:

☐ 2" X 2" slide projector ☐ Powerpoint ☐ Overhead projector

MEMBERSHIP INFORMATION

New _____ **Renewal** _____

Mr. Ms. Dr. _____

Address _____

City, State, Zip _____

School or Firm _____

Telephone _____ **Email** _____

PLEASE INDICATE DIVISION YOU WISH TO BE AFFILIATED _____

Regular Member \$25

Student Member \$5

Life Member \$250

Educational Member \$150

Corporate Patron \$1000

Corporate Donor \$500

CHECKLIST

Please complete the following:

- ☐ Enclose copy of abstract (even if abstract has been submitted electronically)
- ☐ Complete and enclose abstract/membership form (this form)
- ☐ Enclose the following payments (Make checks payable to Mississippi Academy of Sciences)
 - ☐ \$25 per abstract
 - ☐ \$25 regular membership fee OR \$5 student membership fee (2007 membership must be paid for abstract to be accepted)
- ☐ You must supply a check # _____ or P.O. # _____ (credit cards are not accepted)

In addition, you MAY preregister at this time to take advantage of the saving

- ☐ Enclose the following payments:

| | |
|---|--|
| <input type="checkbox"/> \$80 regular member (after 23 Jan) | <input type="checkbox"/> \$55 regular member (Preregistration before Jan 23) |
| <input type="checkbox"/> \$40 student member (after 23 Jan) | <input type="checkbox"/> \$25 student member (Preregistration before Jan 23) |
| <input type="checkbox"/> \$105 nonmember (after 23 Jan) | <input type="checkbox"/> \$85 nonmember (Preregistration before Jan 23) |

Note: Abstracts that are resubmitted for changes will incur a \$10 resubmission fee. Late abstracts will be accepted with a \$10 late fee during November increased to \$25 after that. Late abstracts will be accepted only if there is room in the appropriate division. They will be published in the April issue of the MAS JOURNAL.

MISSISSIPPI ACADEMY OF SCIENCES—ABSTRACT INSTRUCTIONS
PLEASE READ ALL INSTRUCTIONS BEFORE YOU SUBMIT YOUR ABSTRACT ON-LINE

- Your paper may be presented orally or as a poster. Oral presentations are generally 15 minutes. The speaker should limit the presentation to 10-12 minutes to allow time for discussion; longer presentations should be limited accordingly. Instructions for [poster presentations](#) are linked here.
- Enclose a personal check, money order, institutional check, or purchase order for \$25 publication charge for each abstract to be published, payable to the Mississippi Academy of Sciences. The publication charge will be refunded if the abstract is not accepted.
- The presenting author must be a member of the Academy at the time the paper/poster is presented. Payment for membership of one author must be sent for the abstract to be accepted.
- Attendance and participation at all sessions requires payment of registration.
- Note that three separate fees are associated with submitting and presenting a paper at the annual meeting of the Mississippi Academy of Sciences.
 1. An abstract fee is assessed to defray the cost of publishing abstracts and
 2. a membership fee is assessed to defray the costs of running the Academy.
 3. Preregistration payment (\$20 regular; \$10 student) may accompany the abstract, or you may elect to pay this fee before February 1, or pay full registration fees at the meeting.
- Abstracts may **only** be submitted on line via a link through the MAS website. The URL is <http://www.msacad.org/index.html> (case sensitive). The appropriate abstract fees can be paid via Paypal or sent via mail to Cynthia Huff at the Academy address .
- **Abstracts that are resubmitted for changes will incur a \$10 resubmission fee.**
- **Late abstracts will be accepted with a \$10 late fee during November increased to \$25 after that. Late abstracts will be accepted only if there is room in the appropriate division. They will be published in the April issue of the MAS JOURNAL.**
- Submit your appropriate fees t **NO LATER THAN NOVEMBER 1, 2008.**

Ms. Cynthia Huff
Mississippi Academy of Sciences
Post Office Box 55907
Jackson, MS 39296-5907

msacad@bellsouth.net

GUIDELINES FOR POSTER PRESENTATIONS

- The Academy provides poster backboards. Each backboard is 34" high by 5' wide. Mount the poster on the board assigned to you by your Division Chairperson. Please do not draw, write, or use adhesive material on the boards. You must provide your own thumb tacks.
- Lettering for your poster title should be at least 1" high and follow the format for your abstract. Lettering for your poster text should be at least 3/8" high.
- Posters should be on display during the entire day during which their divisional poster session is scheduled. They must be removed at the end of that day.
- Authors must be present with their poster to discuss their work at the time indicated in the program.