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DISTRIBUTION OF A TYMOVIRUS IN TIME AND SPACE IN *ASCLEPIAS VIRIDIS* FROM THE TALLGRASS PRAIRIE PRESERVE OF OKLAHOMA **[1,2]B. E. Min, [3]G. Wiley, [1]T. Feldman, [2]V. Muthukumar, [1]G. Shen, [1]M. Roossinck, [3]B. Roe, [2]M. Palmer, [2]U. Melcher, [2]J. Verchot-Lubicz and [1]R. Nelson** [1]The Samuel Roberts Noble Foundation, Ardmore, OK, 73401, [2]Oklahoma State University, Stillwater, OK, 74078, [3]University of Oklahoma, Norman, OK, 73019

Viruses present in plant extracts from the Tallgrass Prairie preserve (TGP) of Oklahoma were identified through virus-like particle isolation. Sequences similar to members of the *Tymovirus*, *Badnavirus*, *Comovirus* and *Carmovirus* genera and a member of the Flexiviridae were obtained from extracts representing members of the *Ambrosia*, *Asclepias* and *Asplenium* plant genera. Samples from multiple dicotyledonous species, representing the Asclepiadaceae (multiple samples from *Asclepias viridis*) and Apocynaceae, and surprisingly from one monocotyledonous species contained the tymovirus sequence. Extracts from the *A. viridis* samples were infectious to other dicotyledonous species. To further investigate the tymovirus distribution through space (native ecosystem) and time (season) in the TGP, plants in transects adjacent to sampling plots associated with ecological studies were analyzed for the presence of tymovirus sequence by RT-PCR with gene specific primers. Tymovirus sequence was detected from *A. viridis* adjacent to three plots (208, 307 and 343) separated by up to 10 kilometers within the TGP. The percentage of infected plants in plots 343, 307 and 208 were 82%, 64% and 36%, respectively. Samples from *A. viridis* adjacent to these plots the previous two years (single plant sampled per year per plot) were negative for virus (208), positive for virus one of two years (343) and positive for virus both years (307). Additional plants sampled later in the summer from within and far from the original sampling areas contained the tymovirus sequence. These results show that a large population of plants, mostly composed of single plant species, *A. viridis*, covering a large area of the TGP native ecosystem were infected with a tymovirus. Also, the tymovirus was present in *A. viridis* through multiple years. We are studying potential overwintering and vectoring sources for this virus.

LYSINE AS ALTERNATIVE THERAPY IN HERPES SIMPLEX VIRUS INFECTION: A REVIEW OF RESEARCH **E.L. Blewett,** Dept Bioch & Micro, Oklahoma State University – Center for Health Sciences, 1111 W 17 St., Tulsa, OK 74107 (918) 561-8405, **J.L. Kisamore,** Dept of Psych, University of Oklahoma-Tulsa, 4502 E 41st St.-3J06, Tulsa, OK 74135 (918) 660-3603

The public is increasingly turning to alternative medical therapies. There have been a rising number of inquiries in legitimate scientific literature about lysine dietary supplementation in the treatment or prevention of Herpes Simplex Virus (HSV) outbreaks. There is a scientific basis for this therapy, as many *in vitro* studies have shown that arginine is essential for both HSV-1 and HSV-2 virus production. Arginine can be synthesized by humans but addition of lysine reduces the production of arginine. There are at least five essential viral

proteins that are arginine rich. The current poster is a review of research designed to address several questions. Does a reduction of arginine in the diet plus supplementation of lysine reduce the potential for an outbreak of oral or genital lesions? Does this treatment reduce the severity of the outbreak? We will present a review of the scientific literature and a call for a meta-analysis of relevant studies.

FUSION PROTEIN CLEAVAGE IS NOT NECESSARY FOR VIRUS INFECTIVITY OF BOVINE HERPESVIRUS 1 (BHV-1) **E.L. Blewett,** Dept Bioch & Micro, Oklahoma State University – Center for Health Sciences, 1111 W 17 St., Tulsa, OK 74107 (918) 561-8405

The most striking difference between the strongly conserved glycoprotein B (gB) molecules of herpesviruses is that some, such as that of bovine herpesvirus 1 (BHV-1), are cleaved during morphogenesis into fragments of almost equal size, while others, exemplified by the herpes simplex virus (HSV) gB, are not. By altering the cleavage site of BHV gB and reintroducing the gene for the now uncleaved molecule into the viral genome we show that while cleavage is not required for infection or replication within a single host-cell it is needed for efficient cell to cell spread of the virus. Thus, while penetration kinetics and single-step growth curves of BHV-1 with cleaved or uncleaved gB were indistinguishable, the viruses were clearly different when rate of cell to cell spread was measured by comparing plaque size, infectious centre assays and multi-step growth curves.

EXPLORING BIOINFORMATICS IN THE GENETICS LABORATORY **K.A. McDowell,** Natural Sciences, Northeastern State University at Broken Arrow, 3100 East New Orleans Street, Broken Arrow, OK 74014.

This curriculum development project fostered a learning-centered approach to the study of bioinformatics. An undergraduate experience should prepare the student for their chosen profession. Students need firm, solid groundwork in their chosen field if they wish to compete in the job market or go on to professional or graduate school. Biology majors should graduate with a strong background in the basic principles of biology. In today's world students who wish to pursue careers in molecular biology need to be familiar with bioinformatics and the modern way in which genomics is studied. Bioinformatics and genomics are the fastest growing areas of biology. Implementation for the new course curriculum addressed class structure, database exploration, assessment of students, and feedback for improving the course. The databases explored included OMIM, GenBank, BLAST, Spidey, BLink, MMDB, and Primer3. With the use of these databases the students were able to analyze genes responsible for human genetic disorders, design primers for prospective PCR experiments, examine putative proteins for three dimensional structures, explore ramifications shape may have in function, and explore possible affects that mutations may play. In addition, this project enriched the undergraduate experience for these students by providing them with insight into real world applications of genetics. The project described was supported by Grant Number P20RR016478-05 from the National Center for Research Resources (NCRR), a component of the National Institutes of Health (NIH) and "Its contents are solely the responsibility of the authors and do not necessarily represent the official views of NCRR or NIH.

PCR ASSAY TO DETECT CHICKEN FECES Nebojsa Kezunovic, Daniel Owen, Cindy R. Cisar, Department of Natural Sciences, Northeastern State University, Tahlequah, OK 74464.

Fecal pollution is a serious human health problem because of the potential presence of human pathogens in human and other animal feces. Recognizing the source of this contamination is essential for remediation of the problem. Poultry farms are a potentially significant source of fecal contamination in northeastern Oklahoma. Fecal bacteria can be used as indicators of fecal pollution. If the bacteria are specific to a particular host then the source(s) of the fecal contamination can be identified. This approach is known as microbial source tracking. *Bacteroidales* are fecal anaerobic bacteria that are common in warm-blooded animals. Isolates of *Bacteroidales* from different hosts (ruminants, humans, swine, and horses) can be differentiated by amplification of *Bacteroidales* 16S rRNA gene (rDNA) sequences specific to these groups. However, there is no method available to detect *Bacteroidales* from chicken feces. In this study, *Bacteroidales* 16S rDNA sequences from chicken feces were amplified, cloned and sequenced. Phylogenetic analysis was performed and *Bacteroidales* 16S rDNA sequences unique to chicken feces identified. Three sets of primers were designed and tested for specificity. One set of primers specifically amplified chicken fecal DNA, but did not amplify wild turkey, cat, bovine or deer fecal DNAs. The data from these experiments indicates that the PCR assay based on this primer pair is specific for chicken feces.

CREATING A NOVEL ASSAY FOR PEPTIDE PERMEABILITY Matthew C. T. Hartman[a], Department of Chemistry, Virginia Commonwealth University, Richmond, VA 23298, **Ryan T. Morgan and Caroline L. O'Farrell,** Department of Biology, Oral Roberts University, Tulsa, OK 74171

Many successful pharmaceutical drugs like Cyclosporin have been intermediate molecular weight (MW) peptides. Despite the increased potential for intermediate MW peptides to be used medicinally, it is difficult for these peptides to cross cellular membranes. For this reason, a highly sensitive assay for the in vivo measurement of the cell permeability of intermediate MW peptide libraries will be tremendous asset for future drug discovery efforts. Hahn and Muir have developed a technique coined conditional protein splicing (CPS)[1]. In this approach, two constructs are created: an N construct and C construct. The technique uses rapamycin as a chemical inducer of dimerization (CID)[2,3] to cause the heterodimerization of the endo domains FK506 binding protein 12 (FKBP12) and FKBP-rapamycin binding domain (FRB). FKBP and FRB are fused with artificially split intein *Saccharomyces cerevisiae* vacuolar membrane ATPase (VMA) N and C domains respectively, and the heterodimerization of the endo domains causes reconstitution of the intein[1], which leads to luciferase activity and luminescence. Our study will use CPS with a caged version of rapamycin that can distinguish membrane permeable peptides from those that are not. In these preliminary results, the complete DNA sequence of the N and C constructs have been obtained and are ready for protein expression.

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CHARACTERIZATION OF AN OSMOPROTECTIVE LOCUS IN PSEUDOMONAS AERUGINOSA **Arden Aspedon,** School of Allied Health Sciences, Southwestern Oklahoma State University, Weatherford, OK 73096.

Results from DNA microarrays prepared from osmotically-stressed cells showed up-regulation of the alternative sigma factor gene *alg*U, and a putative operon (PA3459-PA3460-PA3461) that is likely to encode enzymes involved in the synthesis of the osmoprotectant N-acetylglutaminylglutamine amide (NAGGN). Growth rate experiments in a minimal medium containing 0.5 M NaCl showed that only two genes in the putative PA3459-61 operon are essential for osmoprotection; mutants harboring an *aac*C1 disruption in either PA3459 or PA3460 were impaired for growth under osmotic stress. However, a mutant carrying a similar disruption in PA3461 grew as well as the wild-type, suggesting that the putative peptidase encoded in PA3461 is involved in the hydrolysis and removal of NAGGN after the osmotic stress has been lifted. A comparison of transcriptional profile data from osmotically-shocked wild-type and *alg*U mutant cells showed that twenty-three osmoadaptive genes, including PA3459-61 and the regulatory genes *alg*B and *alg*R, are positively-regulated by AlgU. Under osmotic stress, an *alg*U mutant showed a growth phenotype similar to that seen with the PA3459 and PA3460 mutants, a result consistent with AlgU being required for expression of the PA3459-61 operon. Results from growth experiments with *alg*B and *alg*R mutants suggest that AlgB and AlgR have very little or no role in regulating osmoprotective gene expression.

PREDOMINANT FUNGAL GENERA FOUND IN HOMES WITH SUSPECTED HEALTH RISK **Charles L. Biles,** Biology Department, East Central University, Ada, Oklahoma 74820.

Indoor air quality has become a major issue in the homes and businesses and is a top priority for the Environmental Protection Agency. A contributing factor to decreased indoor air quality is fungi, commonly referred to as mold, that normally live as saprophytes in soil or plant debris. These organisms have adapted to indoor environments that have moisture problems (e.g. leaks, excess humidity) and trigger respiratory and allergenic symptoms in many individuals. Indoor air quality factors such as mold, is of particular concern to Oklahomans because of the high incidence of asthma (6^{th} in the nation) and other respiratory illnesses. Mold sampling and inspections of over 30 homes or businesses were conducted between 2002 and 2007. Techniques utilized included passive settling plates, vacuum sieve plate, air impaction on an adhesive tape, and tape-lifts for the identification of visible fungi. In the majority of buildings inspected, the outside air contained a much higher level of air than the inside, although many of the occupants complained of respiratory problems. Fungal plate counts varied from 1 to 500 colonies per plate when using the passive plate count technique. When extremely high fungal colony counts were obtained for each technique, visible mold was already apparent. Homes with high counts usually had water damage, old carpets, high humidity, or were left uninhabited without any air conditioning system

operating. The predominant genera observed on building materials were *Stachybotrys, Aspergillus, Penicillium, Cladosporium, Alternaria*, and *Chaetomium*. Sampling techniques need to be improved and baseline levels of mold need to be established to better indicate a health risk caused by indoor mold.

TEACHING TEACHERS TO TEACH SAFETY **K. J. Koll,** Physical Science, Cameron University, 2800 West Gore Blvd., Lawton, OK 73505.

According to the National Science Teachers Association (NSTA) position statement "Inherent in many instructional settings (including science) is the potential for injury and possible litigation. These issues can be avoided or reduced by the proper adherence to and application of a safety plan." NSTA declares that School authorities and teachers must share the responsibility of establishing and maintaining safety standards in the classroom and school campus. Further, NSTA states that all science teachers must be involved in an established and on-going safety training program relative to the established safety procedures. A safety plan is necessary for the health and safety of your students and yourself; as well as, for legal reasons. Future science teachers are prepared by completing a series of science courses and a pedagogical program. How does a candidate for licensure in the teaching of science demonstrate that they have engaged students in science safety? Often teacher preparation require candidates to design a science safety plan which includes a list of safety activities completed with students, a list of safety rules/procedures that ends with a safety contract for the parents and students to sign and date, a safety quiz over rules and procedures, and general safety questions used on science tests during the school year. Candidate safety plans need to communicate the importance of safety and the on-going emphasis on safety throughout the year. How do you develop a functional rubric that demonstrates that a candidate actually does engage classroom students in the practice of good safe science?

INVASIVE HOUSE SPARROWS AS ALTERNATIVE VERTEBRATE HOSTS FOR BUGGY CREEK VIRUS **Valerie A. O'Brien and Charles R. Brown,** Department of Biological Sciences, University of Tulsa, Tulsa, OK, 74104.

Interest in invasive and human commensal species in disease ecology is increasing with continued anthropogenic habitat modification and intentional and inadvertent species introductions. Invasive species can often have a profound effect on disease dynamics as increased contact of native species with human commensals causes changes in the ecology of emerging and endemic diseases. In an arbovirus, if an introduced species is a more effective vertebrate amplifying host than the natural host, formerly enzootic cycles between vectors and their natural hosts can become epizootic. Thus, understanding the effect of an invasive host on virus transmission and persistence can be important in predicting the future spatial and temporal patterns of virus evolution and spread. Buggy Creek virus (BCRV) is an alphavirus which is vectored in the swallow bug (*Oeciacus vicarius*), a parasite of the cliff swallow (*Petrochelidon pyrrhonota*). The relatively recent introduction of the house sparrow (*Passer domesticus*) into the cliff swallow-swallow bug-BCRV system may be serving to provide a continuous and/or optimal amplification cycle for BCRV. In May and June 2006, I blood-sampled 37 nestling house sparrows from a single cliff swallow colony site that contained only nesting house sparrows. Forty-six percent of nestlings were RT-PCR positive for BCRV, with the youngest nestlings most likely to be infected ($\chi^2_1 = 14.8$, $P < 0.001$). In contrast, only 11 of 300 cliff swallow nestlings from all colonies sampled were virus-positive by the same

methods. Young nestling house sparrows may be a highly competent amplifying host for BCRV, and thus have the potential to alter the ecology of this alphavirus.

CARVACROL-INDUCED APOPTOSIS OF HUMAN CARCINOMA CELLS IN VITRO

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Naturally occurring isoprenoids have been shown to have a variety of antiproliferative and anti -tumor effects on malignant cells. Isoprenoid compounds, such as cinnamaldehyde, have been shown to induce apoptotic cell death through the activation of proapoptotic proteins. The ability of these compounds to induce apoptosis in vitro is a new and exciting area of research. Our preliminary data suggests that the terpenoid compound carvacrol is able to induce morphological changes in Huh7 liver carcinoma cells. The focus of this research will be to determine whether carvacrol is able to induce apoptotic cell death in a human liver cancer cell line. Cells undergoing apoptosis will be characterized by a distinctive cellular morphology, alteration in proliferation, and modulation of caspase-3 activity. In addition, we expect cells undergoing carvacrol-induced apoptosis to display altered patterns of expression for genes encoding the anti-apoptotic protein *Survivin*.

CSI TULSA: STATISTICS APPLIED TO FORENSIC PALYNOLOGY REVISITED

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The purpose of this project is to analyze pollen samples in light of Locard's Exchange Principle. A study was done during the 2001-2002 school year. Then a study was done during the 2003-2004 school year. The results from the 2003-2004 study were presented at the Oklahoma Academy of Science in 2005. In 2007, another study was performed in which there were two goals. The first goal was to determine if there was a significant difference between pollen collection by two sided tape and silicon grease. The second goal was to determine if significantly different levels of pollen existed among ten sites in Tulsa, OK. Six slides (two that were control slides) were systematically placed around each of ten sites in Tulsa. Three utilized tape for pollen collection and three utilized grease for pollen collection. The control slides were left out during the placement of the other four slides. One control slide was grease and the other was tape. The control slides indicated no pollen collection at time of placement.

A t-test was performed to determine if there was a significant difference in pollen collection between tape and grease. It was determined that there was insufficient evidence to support any significant difference between the two collection materials. Since no significant difference between the two collection materials existed, the counts from both materials were combined to compare levels of pollen among the ten sites in Tulsa.

The Bartlett and Levene tests indicated that an ANOVA test was appropriate for Ambrosia. However, the Bartlett test indicated that a Kruskal-Wallis test was the test for Poa levels. There was no significant difference in levels of Ambrosia among the ten sites. However, there was sufficient evidence to support the claim that Poa levels differed among the 10 sites at the 0.01 level of significance. The difference can be attributed to site number two in Tulsa. Levels of Poa were significantly higher at site number two.