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A SHORT NUR77-DERIVED PEPTIDE CONVERTS BCL-2 FROM A PROTECTOR TO A KILLER – THE MECHANISM SUPPORTED BY LIPOSOME BASED BIOPHYSICAL STUDIES. ¹Xuefei Tian, ¹Feng He, ^{2,3}Siva Kumar Kolluri, ²Xiuwen Zhu, ²Xin Zhou, ²Bingzhen Lin, ²Ya Chen, ²Kai Sun, ²James Town, ²Xihua Cao, ²Feng Lin, ²Dayong Zhai, ²Shinichi Kitada, ²Frederick Luciano, ³Edmond O'Donnell, ²Yu Cao, ²John C. Reed, ²Arnold C. Satterthwait, ²Xiao-kun Zhang, and ¹Jialing Lin, ¹Department of Biochemistry and Molecular Biology, University of Oklahoma Health Sciences Center, Oklahoma City, OK 73336, USA, ²Cancer Center, Burnham Institute for Medical Research, La Jolla, CA 93037, USA, ³Cancer Biology Laboratory, Department of Environmental and Molecular Toxicology, Oregon State University, Corvallis, OR 97333, USA.

Bcl-2 can be converted into a proapoptotic molecule by nuclear receptor Nur77. However, the development of Bcl-2 converters as anticancer therapeutics has not been explored. Here we report the identification of a Nur77-derived Bcl-2-converting peptide with 9 amino acids (NuBCP-9) and its enantiomer, which induce apoptosis of cancer cells in vitro and in animals. The apoptotic effect of NuBCPs and their activation of Bax are not inhibited but rather potentiated by Bcl-2. NuBCP-9 and its enantiomer bind to the unstructured loop of Bcl-2, acting as molecular switches to dislodge the Bcl-2 BH4 domain and expose its BH3 domain. This NuBCP-9 induced Bcl-2 conformational change not only blocks the anti-apoptotic activity, but also converts Bcl-2 to a BH-3 only protein that inhibits the anti-apoptotic activity of Bcl-XL. Therefore, NuBCP-9s represent a novel anti-Bcl-2 mechanism that can be explored in developing future anti-cancer therapeutics. (This work was supported in part by grants to J.L., X-k.Z., J.C.R., and A.C.S. from the National Institutes of Health, CA109345, CA119785, GM060554 and GM062964)

THE UL82 GENE FAMILIES IN CYTOMEGALOVIRUSES. E. I. Blewett, Biochemistry and Microbiology, OSU-CHS 1111 W 17 St. Tulsa, OK 74107.

The baboon and rhesus CMV (BaCMV and RhCMV) homologs of the UL82 gene family were cloned and sequenced revealing strong homology to each other and to HCMV AD169. The simian virus genomes contained genes collinear with HCMV but had an additional open reading frame (orf) between the homologs to HCMV UL82 and UL83 that was very similar to UL83 and has been named B83a (BaCMV) or R83a (RhCMV). PCR analysis showed that neither HCMV strains Towne or Toledo contained this extra gene.

IMPACT OF WASTEWATER TREATMENT EFFLUENT ON ANTIBIOTIC RESISTANCE IN AEROMONADS. C.R. Cisar, Department of Natural Sciences, Northeastern State University, Tahlequah, OK 74464.

Aeromonads, gram-negative bacteria belonging to the genus *Aeromonas*, are ubiquitous in freshwater ecosystems. They cause disease in aquatic organisms (fish, frogs, etc.) and are

opportunistic pathogens in humans. Recent evidence suggests that aeromonads may be an important group of emerging human pathogens. Our objective in this study was to determine whether wastewater treatment plant (WWTP) effluent contributes to antibiotic resistance in aeromonads. In November 2007 bacteria were isolated from Tahlequah Creek sediment samples taken upstream and downstream of the Tahlequah WWTP. Aeromonad strains were identified by sequencing their 16S rRNA genes. Forty-five aeromonad strains were isolated from sediment samples taken upstream of the WWTP and 28 aeromonad strains were isolated from sediment samples taken downstream of the WWTP. Each strain was tested for susceptibility to the antibiotics tetracycline, trimethoprim, and ofloxacin. Seven strains were resistant to trimethoprim (1 from upstream of the WWTP, 6 from downstream of the WWTP), 6 strains were resistant to tetracycline (2 from upstream of the WWTP, 4 from downstream of the WWTP) and 4 strains were resistant to ofloxacin (all from downstream of the WWTP). In addition, none of the upstream aeromonads exhibited multidrug resistance, but four of the downstream strains were resistant to more than one antibiotic. Although the sample size is small, the data indicates a statistically significant increase in the incidence of antibiotic resistance in aeromonads exposed to effluent from the WWTP. Furthermore, we believe that this is the first report of fluoroquinolone (ofloxacin) resistance in aeromonads in the United States.

EFFECT OF MUTATIONS IN ANTIGENIC SITE B IN HEMAGGLUTININ OF INFLUENZA VIRUS A/OKLAHOMA/309/2006. Lyubov Popova¹ and Jing Qi Feng, Gillian Air, Department of Biochemistry & Molecular Biology, University of Oklahoma Health Science Center, Oklahoma City, Oklahoma 73104.

Influenza viruses cause serious problems to human health, with 36,000 deaths and ~200,000 hospitalizations estimated in the USA each winter. The surface glycoprotein hemagglutinin (HA) is believed to be the most important antigen of influenza virus. Antigenic drift of HA is the reason the vaccine has to be updated every year, and subtype H3 HA has accumulated ~20% amino acid sequence changes in the 40 years since it appeared in humans in 1968. Five antigenic sites have been mapped on the surface of HA by competition assays of mAbs against early H3 HA. The goal of our research is to determine if immunodominance of particular antigenic sites changes as the antigen accumulates sequence changes. We made 4 mutations in antigenic site B: HL156-157KS, KFK158-160GST, NGQI189-192QEQT, A196V. None of the mutations affected the binding to a site A mAb (EO5), but HL156-157KS dramatically decreased the binding to mAb 1CO2, indicating it is directed to site B.

GROWTH AND REPRODUCTION OF A PATHOGENIC MOLD, *CHAETOMIUM GLOBOSUM*, IN CHEMICAL AMENDED MEDIA. Marianni Fuego, Rachael Pattison, and Charles Biles, Biology Department, East Central University, Ada, Oklahoma 74820.

Chaetomium globosum is a fungus commonly found on water-damaged building materials. It has been implicated as an allergen and can cause severe human diseases, especially in an immune-compromised individual. The spores of this fungus are highly resistant to any known method of control or treatment. The fungus was grown on salts at different concentrations in order to determine chemical regulators for perithecia and hyphal growth. Four isolates of *C. globosum* (NMSU, mtNM, Carolina, and PC 932) were placed on 7 salts each with 1 mM, 10 mM, and 100 mM concentrations and then incubated in the dark at 25°C.

The hyphal growth and production of perithecia were measured on days 4, 7, 14, 21. For most isolates tested, salts such as KCl and CaCl₂ appear to stimulate perithecia production, whereas, KClO₃ and NH₄Cl inhibit hyphae and perithecia production. Seven days after plate inoculation, perithecia formation was observed on 1 mM NaCl, 10 mM NaCl and KCl, and 100 mM KCl, NaCl, and CaCl₂. Perithecia were observed on non-amended media after 21 days. KClO₃ did not inhibit hyphal growth of the Carolina isolate at low concentrations (1 mM), however perithecia production was inhibited at all concentrations (1-100 mM) tested. Inhibition of hyphal growth was concentration dependent and varied among the salts and isolates. These experiments showed that low concentrations of various chemicals can inhibit fungal growth and reproduction. Use of these chemicals in building materials may be helpful in deterring building degradation and airborne allergens. Further research is needed to understand the genes affected by the chemicals that regulate growth of this pathogen.

GROWTH AND REPRODUCTION OF *CHAETOMIUM GLOBOSUM* ON VARIOUS CARBON SOURCES EXPOSED TO DIFFERENT LIGHT REGIMES. Jennnifer Young, Marianni Fuego, Rachel Pattison, and Charlie L. Biles, Biology Department, East Central University, Ada, Oklahoma 74820.

Indoor mold is a major health concern especially in homes that have experienced water damage. *Chaetomium globosum* is in the Kingdom Fungi, Phylum Ascomycota and forms perithecia containing light brown to olive subglobose ascospores. *C. globosum* grows well on building materials and the spores, hyphae, and mycotoxins can cause human health disorders. Experiments were conducted to investigate the growth and reproductive ability of 4 different *C. globosum* isolates on 10 different media. In addition, each set of media was placed in 3 different light regimes. Fungal hyphal growth was fastest on oat, rice (RM), and V-8 agars. After 8 days of growth, perithecia were most numerous on oat, RM, V-8 and SNA, respectively. Perithecia were not observed on Czapeks, Corn Meal, or ¼ Potato Dextrose agars (PDA), until several days later. After 21 days in culture, ascospores were removed from the Petri dishes by adding sterile water to the media surface and dislodging the spores with a sterile slide. A hemocytometer was used to quantify ascospore production. Ascospore production was highest on oat, RM, V-8, and PDA. *C. globosum* growth when exposed to the different light regimes varied in regard to media and isolate. When dark, 12, and 24 hr treatments were combined and analyzed based on light regime only, there were no significant differences (P<0.05). In previous experiments, *C. globosum* was inhibited when grown on sheetrock exposed to continuous light. Nutrient requirements are often used to categorize organisms and understand genetic regulation. By studying the nutrients and light regimes that stimulate or inhibit *C. globosum* possible control mechanisms may be developed.

FUNGAL PATHOGENS OF GREENBRIERS (*SMILAX SP.*): POSSIBLE BIOCONTROL AGENTS OR INTERESTING ENDOPHYTES? Charles Biles, Terry Cluck, and Mason Groves, East Central University, Ada, Oklahoma 74820.

Greenbrier (*Smilax* sp.) also known as Cat brier, is a major weed problem in home landscaping and agricultural environments. *Smilax* sp. is native to much of the southeastern third of the U.S. and northeastern Mexico. Although chemical control has shown limited

success, alternative methods, such as biological controls are becoming more desirable as homeowners become more conscious of the environment and the possible hazards of excessive chemical use. In the summer of 2008, 51 Greenbrier plants were collected from 7 locations. Sections were taken from symptomatic regions of the plants, surface sterilized, and placed on potato dextrose agar (PDA). After 3-5 days, subcultures were placed on ¼ PDA and incubated. A total of 123 subcultures were examined microscopically. Eighteen different genera were identified from the 7 locations. The most common fungi isolated were *Alternaria* (6 out of 7 sites), *Fusarium oxysporum* (5 out of 7 sites), and *Pestalotia* sp. (4 out of 7 sites). Other species commonly observed were *Nigrospora*, *Chaetomium*, *Phomopsis*, *Trichoderma*, and *Geotrichum*. Some of these genera are known pathogens of *Smilax* sp.; however, many are common endophytes in several plant species. Endophytes are usually ascomycetes that live asymptotically in the tissue of plants, beneath the epidermal cell layer. Reports have found that fungal endophytes inhibit herbivore grazing and impart disease and insect resistance to the symbiotic plant partner. *Smilax* sp. is a very hardy plant and we hypothesize that the endophytes found in this study contribute to their hardiness. Further investigations will test the bioherbicide potential of these fungal isolates and also consider the prevalence of certain endophytes of *Smilax* sp.

RETHINKING CAREER PERCEPTIONS AND PATHS: A REVIEW OF AND RECOMMENDATIONS FOR CAREER MANAGEMENT RESEARCH. L. Cline¹ and J. L. Kisamore, Department of Psychology, University of Oklahoma-Tulsa, 4502 East 41st Street, Schusterman Center-3J06, Tulsa, OK 74135.

A number of trends and events over the past several decades have led to substantial workforce and organizational changes. These changes have redefined the notion of 'career' and forever changed the way careers are managed. This poster highlights the mutual responsibilities of organizations and individuals in the management of careers. Additionally, specific suggestions are provided regarding tools employees and organizations can use in the process of career management. The poster concludes with suggested directions for future career management research.

¹ L. Cline is now with Arvest Bank, 502 South Main Street, Tulsa, OK 74103, (918) 382-4097

EXPLORING THE FAUNAL CONNECTION BETWEEN THE OZARK PLATEAU AND THE APPALACHIAN MOUNTAINS: A PHYLOGEOGRAPHIC STUDY OF THE LONG-TAILED SALAMANDERS OF THE *Eurycea longicauda* COMPLEX, Elizabeth K. Timpe, Department of Biological Sciences – Oliphant Hall, 800 S. Tucker Dr., University of Tulsa, Tulsa, OK 74104.

The Ozark Plateau is a major geographic feature in eastern North America that harbors a wide diversity of endemic plants and animals. The colonization of this region is believed to have occurred from numerous independent invasions from adjacent areas, including the Appalachian Mountains and the Coastal Plain. Although in recent years there have been several detailed phylogeographic studies of eastern North American, few examine species groups that are distributed across the Ozarks and surrounding areas in order to test the origin and dispersal of fauna of this region. Long-tailed salamanders are relatively

abundant and widely distributed throughout eastern North America, providing an ideal model system to investigate the faunal connections between these regions. Using a phylogeny based on mitochondrial (cyt *b*, *ND2*, *16S*) and nuclear (*Rag1*) DNA sequences, we test the patterns and timing of dispersal of the *Eurycea longicauda* complex, to make inferences about the historical biogeography of the Ozark Plateau and the Appalachian Mountains. All phylogenetic analyses recover four major well-supported lineages, that represent each of the nominate taxa of long-tailed salamanders (*E. l. longicauda*, *E. l. melanopleura*, *E. guttolineata*, and *E. lucifuga*). Ozark long-tailed salamanders (*E. l. melanopleura* and some populations of *E. lucifuga*) are phylogenetically nested among Appalachian lineages indicating multiple colonization events from the Appalachian Highlands onto the Ozark Plateau. Divergence time estimates indicate that the *E. l. melanopleura* lineage has been in the Ozarks since the Miocene, whereas, Ozark populations of *E. lucifuga* appear to be the result of recent Pleistocene colonization.

TEACHING ¹³C NMR IN ORGANIC I. Daniel M. McInnes, East Central University, Ada, OK 74820.

Students often find it overwhelming to learn both ¹H and ¹³C NMR in the second semester of sophomore organic chemistry. We've begun teaching ¹³C NMR in Organic I with the intention of making it less difficult for students to grasp the more advanced concepts presented in Organic II. Starting the first week of the semester topics relevant to interpreting NMR spectra are presented one week at a time, leading up to the students being able to determine structure by mid-semester. After several weeks of examining sample ¹³C NMR spectra, students become familiar with how to identify various functional groups based on chemical shifts. Finally, there is an NMR dry lab that requires students to determine structures based on ¹³C NMR spectra and molecular formulas. It is our hope that having learned ¹³C NMR thoroughly in Organic I, students will find it less problematic to master ¹H NMR and other advanced NMR techniques that are covered in Organic II.

EFFECTS OF ABIOTIC FACTORS AND CATTLE GRAZING ON GYPSUM OUTCROP PLANT COMMUNITIES IN THE CIMARRON GYPSUM HILLS, NORTHWESTERN OKLAHOMA. Kristi Rice and Gloria Caddell, Department of Biology, University of Central Oklahoma, Edmond, OK 73034.

Patterns of vascular plant species composition in relationship to abiotic factors and cattle grazing history were quantified for gypsum outcrop communities of the Cimarron Gypsum Hills of northwestern Oklahoma. We sampled thirty-nine 10 x 10m quadrats at 13 sites during summer and fall of 2006, and spring and summer of 2007. One hundred and fifty-five species were identified, of which only 7 were introduced. The dominant species were native perennial herbs, and the outcrops appear to be "islands" of predominantly native vegetation. Although there were differences in species composition among sites, plant assemblages were similar enough to be considered the same community, and richness and diversity differed little among sites. Detrended Correspondence Analysis showed that differences in species composition along Axis 1 were significantly correlated with changes in average annual precipitation, average annual temperature, longitude, and elevation, with a weak grazing history gradient shown along Axis 2. Indicator Species Analysis identified few significant indicators for a particular grazing history. The native plant community

persists in spite of grazing; however, plant cover was higher on long-ungrazed than on currently-grazed outcrops.