

Longitudinal monitoring of water quality parameters in commercial catfish ponds. CL Huston¹*, T Leard², K Camp², SW Jack¹, L Khoo², AC Camus², P Gaunt². ¹Dept. of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Mississippi State, MS. ²Delta Research and Extension Center, MSU College of Veterinary Medicine, Stoneville, MS.

Mississippi is the largest producer of farm-raised catfish in the US, accounting for over 70% of the total catfish production. Producers have intensified production practices in an attempt to increase yields and decrease production costs, resulting in apparent water quality changes and increased incidences of disease. The objective of this study was to investigate interactions of water quality and disease occurrence in commercial catfish ponds. Water quality parameters (temperature, dissolved oxygen, total ammonia, nitrite, pH, chloride, total alkalinity, and hardness) were monitored from thirty-five ponds from four commercial catfish operations. Water samples were taken twice a week for 6 years, resulting in 20,911 pond observations. Mortality estimates were obtained at the time of each visit. Overall, 807 cases of disease were reported over the 6-year monitoring period. Unknown causes accounted for the majority of losses (29.4%), followed by winter fungus (28.6%), enteric septicemia of catfish (15.7%), columnaris (5.6%), and proliferative gill disease (4.2%). No significant associations were detected between water quality parameters and mortality numbers or mortality type using multiple logistic regression and ANOVA. Several areas for consideration in the monitoring and surveillance of pond health and management were identified. This study further emphasizes the need for the continued incorporation of epidemiologic methods in the field of aquaculture.

17P

Assessment of Dog Adopter Preparations and Expectations: Adoption through the First Several Weeks. Holly J. Monke*, Thomas E. Wittum. Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH

Characterization of dog adopters' expectations and preparedness for daily ownership challenges might be useful for predicting the success of integrating a dog into the home. Individuals who adopted dogs from either of two animal care and control agencies in central Ohio during a two-month time interval were asked to voluntarily complete a written questionnaire prior to leaving the shelters with their newly adopted dog. Questions targeted the adopters' animal care history, pre-adoption preparation, assessment of their selected dog while at the shelter, and expectations of the dog. A follow-up mail survey was conducted 3 weeks post-adoption, followed by reminders to maximize response.

A total of 175 adopters completed the initial survey, 20% from shelter A and 80% from shelter B. Over 80% of adopters reported wanting to adopt a dog for more than a month and 60% sought information regarding dog ownership prior to the adoption, primarily from printed sources. Dog behavior was reported as the most important selection criteria. Over 90% of adopters reported anticipation and familiarity with addressing many common behaviors; 40% planned to attend obedience training classes.

Fifty percent of the adopters responded to the 3-week follow-up survey (adjusted for loss associated with follow-up). Ninety-five percent of these individuals retained the dog in the home. Fifty-five percent of adopters reported the dog exhibited at least 2 undesirable behaviors that needed resolution, most commonly jumping and pulling. However, only 40% of adopters planned to attend obedience training classes. When considering all factors of dog ownership, 95% of the adopters were satisfied with the dog 3 weeks following adoption.

18P

Effectiveness of methods for tracking a large cohort of pet adopters. C. Victor Spain¹*, Janet M. Scarlett¹, ¹Cornell University College of Veterinary Medicine, Department of Population Medicine and Diagnostic Science, Section of Epidemiology, Ithaca, NY.

In a large retrospective cohort study of pet adopters, several methods for tracking and contacting pet adopters were evaluated. The adopters' addresses and telephone numbers at the time of adoption were obtained from SPCA adoption records. All addresses were processed through a National Change of Address (NCOA) service provider to see if the person had registered a forwarding order within the previous 3 years. If mail to an adopter was returned undeliverable by the postal service, then a search was conducted using internet databases to locate a current address or phone number. For adopters for whom we believed we had correct contact information but who did not respond to the initial mailing, half were randomly assigned to receive a second mailing with first class mail, and the other half received the second mailing sent via priority mail with delivery confirmation. All adopters who did not respond to mail delivery were also contacted by telephone. Data will be presented on the effectiveness of the NCOA system and internet databases in identifying correct contact information for pet adopters. In addition, overall response rates to mail and telephone contact will be presented along with data on the increase in response provided by priority-mail delivery.

19P

Efficacy of decoquinate fed in milk replacer to experimentally-challenged calves 2 to 28 days of age on clinical symptoms and oocysts shedding of *Cryptosporidium parvum*. D.A. Moore, E.R. Atwill, J. Kirk, D. Brahmabatt, L.A. Herrera, L. Hou, E. Ward, T. Miller, M.D. Singer*. VMTRC, University of Calif, Tulare CA 93274

Cryptosporidium parvum is one of the most common causes for diarrhea and one of the largest threats for mortality due to the presence of concurrent infections in neonatal calves. There is no labeled, cost-effective treatment for *Cryptosporidium parvum* infections other than supportive therapy. Currently decoquinate is being used in high doses as an extra label prophylactic measure for the control of *Cryptosporidium parvum* infections in calves for the first four 4 weeks of life by dairy producers and veterinarians. The purpose of this study was to test the efficacy of decoquinate in milk replacer against *Cryptosporidium parvum* infections in 2-28 day old calves with respect to shedding pattern (onset, duration, and intensity of shedding) and the clinical course of cryptosporidiosis. This study consisted of 75 Jersey bull calves taken from a farm in the Central Valley of California. Each of the calves was randomly assigned to one of 10 challenge/ treatment groups. The treatment groups consisted of either a decoquinate dose of 2mg/Kg BW/d for 28 days, or no treatment for 28 days. Each treatment group was challenged orally once with a suspension of 0, 50, 100, 1000, or 10,000 *Cryptosporidium parvum* oocysts. The oocysts used for the challenge were collected from bovine isolates at a local dairy. Fecal samples were given a score based on viscosity and were later used to determine oocyst concentrations of shedding. All data were analyzed using multiple regression techniques. Higher challenge doses revealed a longer shedding duration however the use of decoquinate had no effect on any aspect of the shedding pattern or clinical course.

20P

Economic implications of bovine leukemia virus infection in dairy cattle. J. K. Rhodes¹*, K. D. Pelzer², Y. J. Johnson³. ¹Virginia-Maryland Regional College of Veterinary Medicine (VMRCVM), College Park, MD. ²VMRCVM, Blacksburg, VA. ³VMRCVM, Salisbury, MD.

Bovine leukemia virus (BLV) is the primary cause of lymphosarcoma in dairy cattle and subclinical infection has been implicated in reduced milk production and premature culling. A stochastic spreadsheet model was developed to estimate the relative cost of BLV infection versus on-farm control measures on dairies in the Mid-Atlantic region. Cost of infection in the model included both the cost of clinical disease (lymphosarcoma) and the cost of subclinical infection. Model input values and distributions were obtained from regional estimates and analysis of the available literature. The estimated cost per case of lymphosarcoma remained relatively constant at approximately \$1720. In contrast, the estimated annual cost of infection varied with the prevalence of infection. At 50% prevalence, the hypothetical model herd of 100 milking cows experienced approximately 2 cases of lymphosarcoma in 3 years. The predicted annual cost of a test-and-manage type control program was approximately \$1860. Despite considerable uncertainty associated with certain model input variables, the results of this analysis suggest that a basic BLV control program may be economically beneficial in herds where the prevalence of infection is greater than 7.5%.

21P

Newly characterized hantavirus isolated from *Peromyscus maniculatus* (deer mouse) in East Tennessee and the phylogenetic relationship with other pathogenic hantaviruses. S.L. Lewis*, S.A. Kania, M. Woldemeskel, J.C. New Jr.. Dept. of Comparative Medicine, College of Veterinary Medicine, University of Tennessee, Knoxville, TN.

The genus *Hantavirus*, in the family *Bunyaviridae*, is the etiologic agent responsible for hantavirus pulmonary syndrome (HPS) in North America. HPS has a high mortality rate with most reported cases occurring in the southwest U.S. The primary reservoir host is the deer mouse, however viral strains are associated with a single sigmodontine rodent host within specific geographical foci. MRNA was extracted from tissue taken from a deer mouse captured in the Great Smoky Mountains National Park in 2000. We molecularly cloned and sequenced amplicons of the G1 and G2 envelope glycoproteins, 290 and 201 nucleotides (nt) respectively, from the M segment and a 947 nt amplicon of the Nucleocapsid region of the S segment. Comparisons of the nucleotide and deduced amino acid (aa) sequences were made. The G1 amplicon had an 83% identity at the nt level and a 96% identity at the aa level to New York virus and the G2 amplicon had an 85% identity at the nt level and a 100% identity at the aa level also to New York virus. The N amplicon had an 86% identity at the nt level and a 97% identity at the aa level to Monongahela virus. Phylogenetic analysis of the nt differences between different hantaviral strains were performed using CLUSTAL® alignment software and the distance-based neighbor-joining method. The analysis of the 947 nt N amplicon demonstrated robust bootstrap values indicating a probable evolutionary relationship to both Monongahela and New York viruses. The bootstrap values for both G1 and G2 amplicons were inconclusive but suggest a relationship to New York virus. The phylogenetic tree suggests an evolutionary relationship between our isolate, designated Newfound Gap virus and highly pathogenic strains, all of which have been implicated in fatal hantavirus cases. We have identified 2.1% of *P. leucopus* and 7.3% of *P. maniculatus* (n=96) that were serologically positive (ELISA) for hantavirus which will be the focus of future characterizations and comparisons. This first isolate represents the discovery of a unique viral strain and a potentially pathogenic hantavirus in a previously unknown area.