THE PREVALENCE OF ENTEROBACTERIA AND FUNGI ISOLATED FROM THE CHOANA **AND CLOACA OF WILD YELLOW-NAPED AMAZON CHICKS (AMAZONA AUROPALLIATA).** Christina Sigurdson-Scott Avian Medical Center of Sacramento, 6114 Greenback Lane, Citrus Heights, CA 95621 and Kim L. Joyner, Mariana Aviaries/FUNDAVES, l0a. Avenue, 2-32, Zone 14, Guatemala City, Guatemala.

The incidence of enterobacteria and fungi was determined from choanal and cloacal swabs of twenty-five wild yellow-naped amazon chicks (Amazona auropalliata) at ages 0-2 weeks, 2-4 weeks, and 6-8 weeks of age. The chicks were located within a 33 hectare region in the Pacific lowlands of Guatemala. Gram-negative enteric bacteria were isolated from 20%(12/59) of choanal samples and 47%(28/59) of cloacal samples. Citrobacter spp., Enterobacter spp., and Klebsiella spp. were the most frequently encountered isolates. Fungi were isolated from 6.8%(4/59) of the choanal samples and 27%(16/59) of the cloacal samples. The nest litter was also sampled and determined to have gram-negative enterics in 79%(26/33) of the samples and fungi in 73%(24/33) of the samples.

ASPECTS OF BOVINE TUBERCULOSIS (MYCOBACTERIUM BOVIS) INFECTIONS IN FERAL POPULATIONS OF FERRETS (MUSTELA FURO), STOATS (M. **ERMINEA) AND CATS (FELIS CATUS) IN OTAGO AND SOUTHLAND, NEW ZEALAND.** Justine Ragg. Henrik Moller and Ken Waldrup. AgResearch, Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Mosgiel, New Zealand.

Twenty-one properties around the Otago region of the South Island of New Zealand were surveyed for the presence of lesions due to Mycobacterium bovis infection (Tb) in feral cats, ferrets and stoats during 1993 and 1994. In total, 1286 predators were necropsied for tuberculous lesions and general ecological information. The properties surveyed were chosen based on their status as Tb-endemic or Tb-free. No Tb infected cats, ferrets or stoats were found in Tb-free areas, but prevalence rates in Tb-endemic areas were 0.5% (n=214) for cats, 17.6% (n=544) for ferrets and 4.55%, (n=66) for stoats. More adult (22.4%) ferrets were infected with Tb compared to juvenile (2.5%) ferrets (Chi-square, $p < 0.001$), and a higher proportion of male ferrets (14.8%) were infected with Tb than females (9.5%) (Chi-square, p=0.029). Tb prevalences in adult ferrets increased 32.3% from winter to summer (Multiple regression; p=0.0142). Lymph nodes associated with an oral route of inoculation (submandibular, retropharyngeal,and mesenteric, 64%) contributed to 71.2% of all single site infections. DNA restriction endonuclease analysis of culture isolates showed that 7 of 8 ferrets sampled showed a different biotype of M. bovis than other wildlife (brush-tailed possum and feral pig) or domestic stock (cattle and deer) at the Table Hill study site.

DETECTION AND QUANTIFICATION OF CLOSTRIDIUM BOTULINUM TYPE C TOXIN GENE IN WETLAND SEDIMENTS USING MOLECULAR TECHNIQUES. Judy L. Williamson[1], Tonie E. Rocke[1], and Judd M. Aiken[2]. [1]National Wildlife Health Center, 6006 Schroeder Road, Madison, WI 53711; [2]Department of Animal Health and Biomedical Sciences, University of Wisconsin-Madison, Madison, WI 53706.

Avian botulism, a paralytic disease resulting from the ingestion of a neurotoxin (C_1 toxin) produced by Clostridium botulinum type C, kills thousands of wild waterfowl each year in the United States. Clostridium botulinum is a ubiquitous, spore-forming anaerobe found in the soil and bottom sediments of rivers, lakes, and estuaries. The structural gene for the type C neurotoxin is carried by specific bacteriophages (Tox^+) which must infect C. botulinum for toxin gene expression and protein production. Traditional methods for the isolation and quantification of bacteria in environmental samples have proven unsatisfactory for C. botulinum. In this study, we have modified standard molecular techniques for detection of the C_1 toxin gene in wetland sediments. Polymerase chain reaction (PCR) procedures were developed for detection of the C_1 toxin gene in extracted

DNA and toxin gene expression in extracted RNA. The amplification products from these PCR procedures provide information on the levels of C_1 toxin gene and gene expression in wetland sediments collected from various avian botulism outbreak and non-outbreak sites. This information, when correlated with known environmental conditions, may provide insight into the requirements for type C neurotoxin production and ultimately, a means for evaluating the risk of avian botulism in wetlands.