

THURSDAY, 4 FEBRUARY 2016		
<i>Caucus</i>		
<b>15:40 - 17:40</b>	<b>L.4: Contaminants, Disease, and Genetics (Chair: )</b>	
15:40	<b>L.4.1: Latty<sup>^</sup></b>	<b>Prevalence and Potential Sources of Elevated Strontium in Waterfowl Eggs in Interior Alaska</b> (Christopher J. Latty*, Angela C. Matz, Keith A. Hobson, Tuula E. Hollmen)
16:00	<b>L.4.2: Miller<sup>^</sup></b>	<b>Trace Elements in Eiders and Long-tailed Ducks of the Alaskan Arctic</b> (Micah W. C. Miller*, James R. Lovvorn, Angela C. Matz, Robert J. Taylor, Christopher J. Latty, David E. Safine)
16:20	<b>L.4.3: England<sup>^</sup></b>	<b>Helminths and Health of Spring-Migrating Lesser Scaup in the Upper Midwest</b> (J. Conner England1*, Jeffrey M. Levensgood, Heath M. Hagy, Rebecca A. Cole, John M. Kinsella)
16:40	<b>L.4.4: Spivey<sup>^</sup></b>	<b>Influenza A Virus Dynamics in High-Latitude Wintering Populations of Mallards</b> (Timothy J. Spivey*, Mark S. Lindberg, Brandt W. Meixell, Kyle R. Smith, Jonathan A. Runstadler, David E. Stallknecht, Andrew M. Ramey)
17:00	<b>L.4.5: Meixell<sup>^</sup></b>	<b>Seasonal Prevalence of Influenza in a Reservoir Host: Waterfowl Life History and the Dynamics of Viral Flow</b> (Brandt W. Meixell*, Nichola J. Hill, Eric J. Ma, Mark S. Lindberg, Todd W. Arnold, and Jonathan A. Runstadler)
17:20	<b>L.4.6: Lavretsky</b>	<b>Population Genomics and Hybridization between Lesser and Greater Scaup</b> (Philip Lavretsky*, Jeffrey L. Peters, Kevin G. McCracken)

**L.4: Contaminants, Disease, and Genetics (Chair: )**

L.4.1: Latty^

**Prevalence and Potential Sources of Elevated Strontium in Waterfowl Eggs in Interior Alaska**Christopher J. Latty<sup>1,2\*^</sup>, Angela C. Matz<sup>1,2</sup>, Keith A. Hobson<sup>3</sup>, Tuula E. Hollmen<sup>2,4</sup><sup>1</sup> U.S. Fish and Wildlife Service, Fairbanks, Alaska, USA, [christopher\\_latty@fws.gov](mailto:christopher_latty@fws.gov)<sup>2</sup> University of Alaska Fairbanks, School of Fisheries and Ocean Sciences, Fairbanks, Alaska, USA<sup>3</sup> Environment Canada, Saskatoon, Saskatchewan, Canada<sup>4</sup> Alaska SeaLife Center, Seward, Alaska, USA

Studies have implicated strontium (Sr) as a contaminant of concern in avian population declines. Previous work on contaminants in eggs of waterfowl breeding in Interior Alaska found an inverse relationship between egg Sr concentrations and eggshell thickness and measurable levels of radioactive Sr in egg contents and shell. Strontium is a naturally occurring alkaline earth metal with no known biological function in birds. It is chemically similar to calcium, which can lead to substitution for calcium in tissues, affecting physiological processes and mechanical characteristics. We measured Sr concentrations in the eggs of five species of waterfowl in Interior Alaska at three locations. To determine potential sources, we compared eggshell chemistry with food and water chemistry at breeding sites. We also examined eggshell d13C and d15N to assess if trophic level and/or nutrient allocation strategy affected eggshell Sr concentrations. Preliminary data suggests eggshell Sr varied by species, site, and year and was related to local water chemistry and the nutritional strategy of the hen during egg production.

L.4.2: Miller, M^

**Trace Elements in Eiders and Long-tailed Ducks of the Alaskan Arctic**Micah W. C. Miller<sup>1,2\*^</sup>, James R. Lovvorn<sup>1</sup>, Angela C. Matz<sup>2</sup>, Robert J. Taylor<sup>3</sup>, Christopher J. Latty<sup>4</sup>, David E. Safine<sup>2</sup><sup>1</sup> Department of Zoology and Center for Ecology, 1125 Lincoln Drive, Southern Illinois University, Carbondale, IL 62901, USA, [mwcmiller@siu.edu](mailto:mwcmiller@siu.edu)<sup>2</sup> U.S. Fish and Wildlife Service, Fairbanks Fish and Wildlife Field Office, Fairbanks, AK 99701, USA<sup>3</sup> Trace Elements Research Laboratory, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX 77843, USA<sup>4</sup> U.S. Fish and Wildlife Service, Arctic National Wildlife Refuge, Fairbanks, AK 99701, USA

Increasing industrialization in the Arctic calls for collection of reference data for assessing changes in contaminant levels. For migratory birds, identifying and interpreting changes in trace element burdens on Arctic breeding areas requires insights into factors such as gender, body size, or wintering area that may modify patterns independently of local exposure. In the Alaskan Arctic, we determined levels of trace elements in liver and kidney of Pacific common eiders *Somateria mollissima v-nigrum* and long-tailed ducks *Clangula hyemalis* from the Prudhoe Bay oil field, and of king eiders *S. spectabilis*, spectacled eiders *S. fischeri*, and Steller's eiders *Polystica stelleri* from near the town of Barrow. Small-bodied Steller's eiders and long-tailed ducks from the different sites had similarly low levels of Se, Cd, Cu, and Pb, perhaps reflecting high rates of metabolic depuration during long spring migrations through areas of low exposure. Adult male spectacled eiders had

much higher levels of Se, Cd, and Cu than did male king eiders of similar body size; however, these differences were not apparent in adult females, possibly because depuration into eggs and longer occupancy of non-marine habitats by females offset differing exposure at quite different wintering sites. Female common eiders at Prudhoe Bay had very high levels of Pb not seen in other species, likely resulting from local exposure. Reasons for substantial variations in Hg levels were not apparent. Future research should further explore reasons for variation among species and sexes to identify exposure routes leading to future changes.

L.4.3: England<sup>^</sup>

### Helminths and Health of Spring-Migrating Lesser Scaup in the Upper Midwest

J. Conner England<sup>1\*^</sup>, Jeffrey M. Levensgood<sup>1</sup>, Heath M. Hagy<sup>1</sup>, Rebecca A. Cole<sup>2</sup>, John M. Kinsella<sup>3</sup>

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The continental lesser scaup (*Aythya affinis*) population has declined for more than 40 years, and the breeding population has remained well below the goal of 6.3 million set by the North American Waterfowl Management Plan. Although many mechanisms have been proposed as factors in the decline of scaup (e.g., habitat degradation and loss, pollution, climate change), research indicates that females reach the breeding grounds in poor body condition due to the lack of adequate forage along spring migration corridors, particularly in the upper Midwest. Additionally, infection with exotic trematodes mediated by the invasive faucet snail (*Bithynia tentaculata*) may lead to further declines in body condition and the consequential deaths of thousands of lesser scaup annually. Remarkably, few researchers have examined the associations of intestinal helminths and health parameters in migrating lesser scaup. To date, most parasite assessment has been performed on birds that were found dead. For this study, the collection of random individuals across a continuum of body condition and parasite loads allowed us to examine sub-lethal effects of helminthiasis. Our objectives were to 1) quantify and compare intestinal helminth infections; 2) examine body composition (i.e., protein and lipid content of carcasses) and blood parameters (i.e., plasma metabolites, packed cell volume, white blood cell differentials); and 3) compare these parameters with other metrics of waterfowl health and wetland condition for spring-migrating female lesser scaup. During the spring migrations of 2014 and 2015, we experimentally collected 130 foraging female lesser scaup, obtained blood and tissue samples, removed and preserved intestines, determined total lipids and protein from carcasses, and enumerated and identified all helminths in a 10% aliquot of intestinal ingesta. Preliminary analyses indicated that % carcass lipids ( $F_{2,56}=4.87$ ,  $P=0.01$ ) and packed cell volume ( $F_{2,57}=10.78$ ,  $P<0.001$ ) generally decreased with collection latitude. Plasma metabolites differed across regions in both years of the study, with the northernmost region having the lowest quality scores (2014 -  $F_{14,88}=3.70$ ,  $P<0.001$ ; 2015 -  $F_{21,161.35}=1.71$ ,  $P=0.035$ ). Further analyses suggest that intestinal helminth loads are indeed negatively impacting the health of lesser scaup in the upper pools of the Mississippi River where faucet snails are present. Most scaup collected from northerly pools of the Mississippi River were infected with the invasive trematode species *Cyathocotyle bushiensis* and *Sphaeridiotrema pseudoglobulus* and were typically in poorer condition than scaup without infections. Due to the complexity of host-parasite interactions, parasitism is often misunderstood and therefore overlooked as an influential regulator of wildlife populations. However, when parasitic infections result in the reduction of host survival and/or fecundity in a density dependent manner, the idea becomes plausible. To understand the effect of a parasite on a host population, one needs to understand the effect of a parasite on the individual host, the prevalence

and intensity in the host population, and the context within which the interaction is occurring. These findings emphasize the need for continued investigations of the effects of parasites on waterfowl populations during critical periods of their annual cycle.

L.4.4: Spivey<sup>^</sup>

### **Influenza A Virus Dynamics in High-Latitude Wintering Populations of Mallards**

Timothy J. Spivey<sup>1,2\*^</sup>, Mark S. Lindberg<sup>2</sup>, Brandt W. Meixell<sup>1</sup>, Kyle R. Smith<sup>3</sup>, Jonathan A. Runstadler<sup>4</sup>, David E. Stallknecht<sup>5</sup>, Andrew M. Ramey<sup>1</sup>

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Mallards (*Anas platyrhynchos*) wintering in urban areas of Alaska provide a unique opportunity to study infection dynamics of influenza A viruses (IAVs) in a natural reservoir host. While previous studies support high infection rates of waterfowl in Alaska during autumn, infection dynamics throughout winter are unknown, and can be investigated due to the non-migratory nature of these populations. We screened Mallards captured in both Fairbanks and Anchorage, Alaska for active infections and previous exposure to IAVs, using molecular methods and a standard serologic assay. Additionally, we used a virus neutralization procedure to characterize the immune response of mallards found to be seropositive upon multiple capture occasions. A total of 500 birds were captured in Fairbanks during the fall/winter of 2012-2013 and 2013-2014, and a total of 699 birds were captured in Anchorage during the fall/winter of 2014-2015. Results from the winter of 2012-2013 in Fairbanks indicate rates (> 10%) of active IAV infection during the months of September, December, and April, highlighting the potential for circulation of IAVs during this time. Antibodies were detected throughout the August to April sampling period in both populations during all three years of the study. In both wintering populations of mallards, sero-prevalence increased from the first sampling period in August-September to subsequent sampling periods in fall/winter. The individual immune response of mallards, as characterized via virus neutralization, revealed instances of both sero-conversion and sero-reversion. Our results establish baseline information regarding influenza A dynamics during the wintering period in two understudied populations of mallards in Alaska.

L.4.5: Meixell<sup>^</sup>

### **Seasonal Prevalence of Influenza in a Reservoir Host: Waterfowl Life History and the Dynamics of Viral Flow**

Brandt W. Meixell<sup>1,2\*^</sup>, Nichola J. Hill<sup>3</sup>, Eric J. Ma<sup>3</sup>, Mark S. Lindberg<sup>4</sup>, Todd W. Arnold<sup>2</sup>, Jonathan A. Runstadler<sup>3</sup>

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Many pathogens show temporal patterns in transmission that are synchronous with the life cycle of their hosts. For example, avian influenza in migratory ducks is characterized by low levels of infection during winter and spring followed by a sharp rise in prevalence that peaks during late summer in correspondence with completion of the breeding season. To better understand the processes regulating viral flow across the seasonal rise and fall of influenza prevalence, we coupled results from intensive field surveillance at a high density waterfowl breeding area with phylogenetic network analysis of virus sequences. During 2008-2010, we captured and sampled approximately 20,000 ducks of 15 species throughout the ice-free season at a study site in Interior Alaska. We modeled variation of influenza prevalence relative to season date and a suite of host traits including species, age (duckling/juvenile/adult), and foraging behavior (dabbling/diving) to identify factors explaining variation in influenza infection. Using a subset of influenza-positive samples that yielded full genome sequences (n = 545), we characterized viral flow among hosts relative to sources of variation in prevalence. Prevalence was lowest in May and June during pre-nesting and nesting (<1%), moderate in July (4-8%) when ducklings accounted for the majority of infections, and highest for flighted juveniles (10-14%) and adults (6-10%) during autumn staging in August and September. Network analysis revealed that viral flow occurred primarily within species and age classes (i.e., duckling to duckling) during July, but as mobility of ducks increased later in the breeding season, viruses were increasingly connected across species and ages. Our results demonstrate a strong relationship between dynamics of viral flow and seasonal changes in waterfowl behavior, highlighting the role of young in virus transmission, and suggesting that virus dispersal is limited by host-host interaction during periods of reduced host mobility.

L.4.6: Lavretsky

### **Population Genomics and Hybridization between Lesser and Greater Scaup**

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Estimating the frequency of hybridization is important when attempting to incorporate such interactions into conservation efforts. Along with the mitochondrial DNA (mtDNA) control region, 3,589 nuclear markers across the Z-chromosome (N = 140) and autosomes (N = 3,448) were isolated using ddRAD-seq methods to estimate the extent of hybridization between lesser (*Aythya*

*affinis*) and greater (*A. marila*) scaup. Overall marker divergence was consistent with a scenario of genetic drift acting on markers with different effective population sizes. Population structure recovered across marker types followed current taxonomy, which included significant structure between lesser and greater scaup, no structure within lesser scaup, but differentiation between Eurasian and North American greater scaup subspecies. Estimated gene flow rates using autosomal markers suggested asymmetrical gene flow from lesser into greater scaup, which corresponded with mtDNA results in which four greater and one lesser scaup were found with introgressed mtDNA. Finally, methods were developed to mimic a breeding experiment in which empirical data was used to simulate a hybridization event (F1) and nine generations (F2-F10) of backcrossing to determine whether assignment probabilities of <99% were indicative of hybrid ancestry. In short, a total of four hybrid classes (i.e., F1, F2, F3/F4, and F5/F6) were distinguishable, with admixed histories effectively lost within the sixth generations of backcrossing. We concluded that the low interspecific assignment probabilities (range = 0.011 – 0.043) recovered for two lesser and nineteen greater scaup were consistent with the F4/F5 generation, which further supported asymmetric gene flow. These results suggest that although the two species are known to hybridize in captivity, the propensity to do so in the wild appears to be relatively low. In general, conservation efforts can benefit from these methods, which provide power for classifying hybrids and estimating the time until admixed histories are effectively lost, and thus “purity” restored.