
FRIENDS OF ORNITHOLOGY

Newsletter

Number 12
May 2016



Grus, The Crane (Willughby & Ray 1678)



From the Curator

Kevin Winker

Spring has arrived earlier than usual here in the far north after a record-setting warm winter. As much as we love the spring weather, there is widespread concern over how this unusual weather will affect birds and trees in the short and long term. The other major news in Alaska is our horrible fiscal climate. With oil revenues staying far below levels needed to sustain state government and no new revenues being tapped yet, draconian cuts are being made in Juneau. The university is facing its third straight year of cuts and will come out of this period about one-third smaller. This is causing considerable stress on the system. So far, we are okay (although furloughs are projected), but it is times like these when we profoundly thank you as a member of the Friends of Ornithology for your support.

Sadly, two of our best colleagues (and founding Friends) passed away this past year, Bob Dickerman and Brina Kessel. We miss them.

There is also good news. We have great students and volunteers, we're continuing to experience strong productivity, we hosted a two-week genomics workshop last summer for UA researchers, and a part of our research program is transitioning from genetics to genomics. Basically, we've gone from 1-2 sequences per bird to 9-12 million per bird. This means big changes, especially in software and computation.

We've had a lot of visitors, including such noteworthies as France Córdova, Director of the National Science Foundation, and Gloria Steinem. We're always happy to show people what we do and why it's important, and we're excited about what the coming year will bring in ornithology.

The Department of Ornithology

Although our existence and many of our activities are centered around the Bird Collection, it is the people involved who make it all happen:

Residents

Kevin Winker (Curator)

Jack Withrow (Collections Manager)

Students

Jessica McLaughlin (MS student)

Rebecca Cheek (BA & BS Dec 2015)

Fern Spaulding (BS major undergraduate)

Sonya Edwards (Education major undergrad)

Research Associates

Heinrich Springer

Johannes Erritzoe

Rose A. Z. Meier

Kevin McCracken

Christin Pruett

Daniel Gibson

Kyle Campbell

Volunteers

David Sonneborn

Luke DeCicco

Steven Heintl

Barbara Logan

Bennett Wong

Jayne Williamson

Alex Lewis

Nick Hajdukovich

Mahaut Sorlin

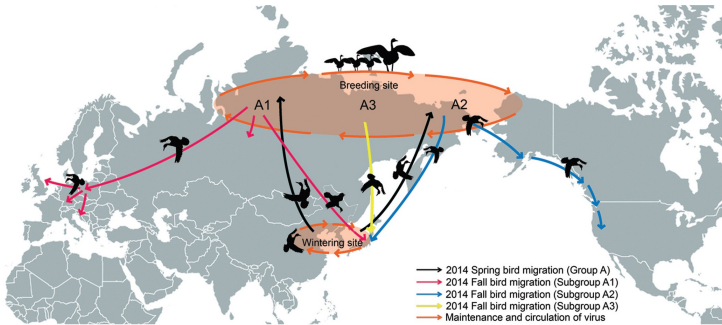
Sarah Miller

Payal Patel

Avian Influenza

Working with collaborators at the U.S. Department of Agriculture (USDA), we've done a fair amount of work on this subject over the past two decades, focusing on the likelihood that migratory birds coming from Asia will transport avian influenza virus

into North America. Well, that prognosis seems to have come true with a bang. As you will see in our publications list this year, we've collaborated again with our USDA colleagues to uncover the route that the highly pathogenic avian influenza (HPAI) took from Asia into North America and then into the poultry industry in the U.S. While surveillance of avian influenza in wild birds in Alaska is low enough to have missed the actual event, it looks like wild birds brought this virus across through Alaska, putting us at ground zero for what eventually turned out to be the worst zoonotic disease to ever hit the U.S. poultry industry.



A reconstruction of avian influenza movements.

FROM STAFF, ETC.

Jack Withrow

Retired collections manager Dan Gibson and I published an updated inventory of the species and subspecies of Alaska birds last year (Gibson and Withrow 2015). Focused as a reference for professional ornithologists, the work is basically a one-stop-shop outlining the status of all avian taxa known from Alaska. It also enumerates the documenting evidence for and nomenclatural nuances associated with Alaska's birds. It is the only source we are aware of that treats every recognized bird taxon in the state, and thus is the single-best work for those interested in avian diversity in Alaska. In this capacity it acts as an element of a larger 'Birds of Alaska' work which has not yet come to fruition.

Also appearing last year was a paper on the results of about a month of field time over seven years

focused on the birds of Chirikof Island (Withrow 2015). Isolated in the western Gulf of Alaska 85 miles southeast of the Alaska Peninsula and 40 miles southwest of the Kodiak archipelago, Chirikof Island had never seen a focused investigation of its birds, unlike nearly every other significant island or island group in the Gulf of Alaska. This work resulted in the refinement of the eastern range limits of three subspecies: Pacific Wren (*Troglodytes pacificus semidiensis*), Song Sparrow (*Melospiza melodia sanaka*), and Gray-crowned Rosy-Finch (*Leucosticte tephrocotis griseonucha*). The work also suggests that the presence of introduced cattle (*Bos taurus*) and foxes (*Vulpes lagopus*) has had significant impacts on the island's bird life. The island is part of the Alaska Maritime National Wildlife Refuge, which is in the process of eradicating the foxes.

Gibson, D. D. and J. J. Withrow. 2015. Second inventory of the species and subspecies of Alaska birds. *Western Birds* 46: 94-185.

Withrow, J. J. 2015. Notes on the birds of Chirikof Island. *Western Birds* 46:28-48.

Rebecca Cheek

My first written contribution to science is approaching the submission phase! For this study, we examined genetic divergence between two coastal subspecies and their mainland populations in Great Blue Heron (*Ardea herodias fannini*) and Sharp-shinned Hawk (*Accipiter striatus perobscurus*). Both these coastal subspecies are examples of regional endemic populations that occur in the Pacific Northwest from southeastern Alaska to Vancouver Island, British Columbia. Both the herons and the hawks are noticeably distinct in appearance compared to their mainland counterparts. Our goal was to determine whether genetic data reflect the observed patterns of phenotypic divergence.

With the aid of funds provided by the



Rebecca Cheek studies hawk specimens

Friends of Ornithology we were able to sequence the mitochondrial gene ND2 from 25 Sharp-shinned Hawks and 36 Great Blue Herons and compare genetic attributes from these two subspecies to the widespread continental populations. Our results revealed a remarkable amount of genetic similarity between the coastal and continental populations in both the Sharp-shinned Hawks and Great Blue Herons. These results suggest that these subspecies may have arisen more recently compared to other regional endemics, or perhaps historically a species-wide selective sweep rendered the ND2 genetic marker less useful for tracking the phenotypic divergence shown in these two subspecies.

I have now graduated (with a B.A. and a B.S.) and have been granted the opportunity to further my career in Ornithology as a PhD student at Colorado State University studying avian evolutionary ecology. So it is almost time for me to conclude my almost four-year career in the UA Museum bird lab. I am grateful for the never faltering support I have received, and am eager to continue my bird-brained pursuits.

From Birds to Bioinformatics Fern Spaulding

Little did I know that when I first began my college career in the fall of 2014 that I would become obsessed with the science of birds.

It all started while frantically skimming through a UAF course catalog trying to find a last-minute class to fit my schedule. I came across a class that seemed too unique to be true, titled the Museum Research Apprenticeship Program (MRAP). Why not? Science is fun, right?

As an MRAP student I worked in the Ornithology Lab. Every Tuesday evening, I would head up to the Museum to skin and prepare bird specimens. This was hands-down the most fascinating class on my agenda. While learning the art of specimen preparation, I also formed a greater appreciation for our feathered friends.

Nearing the end of the fall semester, Kevin Winker came to me and offered me a position in the lab preparing specimens. This was fantastic! I could spend next semester skinning birds, too! Kevin also mentioned that there were funding opportunities the following year for undergraduate research through BLaST (Biomedical Learning and Student Training). He suggested that I apply and assist in researching the magnitude of gene flow between Beringian birds. We would be using bioinformatics, a cutting-edge genomic technique in which biological information is analyzed through the use of a computer. Bioinformatics? How hard could it be?

After writing and submitting a grant proposal to BLaST, I was thrilled when I was funded to conduct genetic research on the amounts of gene flow between Green-winged Teal populations in Beringia, and how this information could be used for avian influenza mitigation policy. Throughout the academic year I worked on my research project, slowly but surely learning the craft and art of bioinformatics. I now have a deeper appreciation for my friends and colleagues that are bioinformaticians.

I can easily say that birds and bioinformatics

are where it is at. I have been funded again to continue research on the magnitude of gene flow between Beringian bird populations. I am truly thankful that the Ornithology Lab is letting me be a part of this new transition into the world of bioinformatics. I find this research exciting and fulfilling. I also enjoy the camaraderie of my fellow lab technicians and mentorship of the those in the Ornithology Lab. I am grateful that the Ornithology Lab and the University of Alaska Fairbanks has given undergraduate students like me the opportunity to participate in real, hands-on, meaningful work.



Fern Spaulding preparing a specimen

Jessica McLaughlin

I am writing this immediately after finishing an email to a fellow graduate student who was asking for insight into a somewhat bizarre and arcane computer issue. If you had asked me a year ago if that was the way I'd be spending a Friday afternoon, I wouldn't have believed you. But my interest in birds, which was unexpected in itself in the beginning, has taken yet another unexpected turn.

I want to understand how populations of birds are connected across a landscape, and particularly in how we can use genetic information to build a picture of how populations have changed over time, how many individuals move between populations, and how these

relate to how the landscape has changed over time. I'm looking specifically at Beringian birds—groups that have a distribution that straddles both sides of the Bering Strait. How many birds from Alaska make it into the gene pool on the Russian side of the strait, and vice versa? How much have these populations diverged from each other? Does it have anything to do with the history of Beringia—the exposure of the land bridge repeatedly throughout the Pleistocene, followed by its being submerged once temperatures warmed?

My tools for answering these questions do not involve being airdropped onto remote Aleutian islands (although that sounds pretty fun); instead, they include large amounts of genomic data and a supercomputer. Together with other members of the lab, I've been working on developing ways to sift through mountains of sequence data. I never expected to spend my days writing Python scripts or learning the finer points of regular expressions. I definitely didn't anticipate that I'd be teaching bioinformatics skills to others. Even if I didn't set out to be to be a "computer person," I'm excited about the questions that I can explore using these tools.

ANNUAL REPORT - ORNITHOLOGY, FY15

This was a huge year for the collection. With an NSF grant, we installed the biggest equipment upgrade the collection has ever had (cabinets and a compactor system). Then we moved the whole collection—parts of it twice, out and back in again. We also added 1,500 new specimens to the collection. Our research associates donated a large number of important specimens. Department staff, students, and research associates produced 7 publications. Fieldwork took staff to Kodiak, Hyder, the Taylor Highway, and parts of Interior Alaska. We also had an excellent group of students and volunteers working with us during the year. As ever, we extend our most sincere thanks to our students, volunteers, and the Friends of Ornithology for their ongoing support.

Volunteer hours	1,498
Acquisitions	1,500

Publications	7
Reports	14
Loans	15
Data requests	198*
Professional visitors	57
Student visitors	46
Public contacts	~100

Students working with collections

PhD	5
MS	3
Undergrad & highschool	2

* Excludes 6,799 electronic database requests.
 ** Excludes Halloween (771), Open House (FY13:556),
 and Military Appreciation (FY13:237) events.



Field work on Mt. Fairplay

FRIENDS OF ORNITHOLOGY

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 David & Alexandra Sonneborn
 Robert W. Dickerman†

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 Carol Juergens & Mark Withrow
 Kodiak Island Medical Associates
 Kevin Winker
 Dorothy Jones (in memory of Bob Jones)

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Gordon Tans
Jeff Walters

If you know of someone who might like to become a member, please pass along a copy of the enclosed membership materials or point them to our web page:

www.universityofalaskamuseumbirds.org

RECENT PUBLICATIONS (ANNOTATED)

(**Bold** denotes our students)

AOU Committee on Classification and Nomenclature (one of 13 members). 2015. Fifty-sixth supplement to the American Ornithologists' Union *Check-list of North American Birds*. Auk 132:748-764.

Lee, D.-H., M. K. Torchetti, K. Winker, H. Ip, Song, C.-S., and D. E. Swayne. 2015. Intercontinental spread of Asian-origin H5N8 to North America through Beringia by migratory birds. *Journal of Virology* 89:6521-6524.
Points to Beringia as being important for the intercontinental spread of highly pathogenic avian influenza (HPAI). The Eurasian H5N8 clade 2.3.4.4 avian influenza virus emerged in China (2013), then spread via migratory birds in early 2014 to South Korea and Japan, and then to Beringia by summer 2014. Three subgroups emerged and spread along different flyways during fall 2014 into Europe, North America, and East Asia. The North American strain provided critical genetic material to the highly pathogenic virus that subsequently infected nearly 50 million poultry in the U.S. in 2014-15. This is the most severe economic impact of a zoonotic disease in the history of the U.S. poultry industry.

Gibson, D. D., and J. J. Withrow. 2015. Second inventory of the species and subspecies of Alaska birds. *Western Birds* 46: 94-185.
The definitive assessment of Alaska avian diversity.

Withrow, J. J. 2015. Notes on the Birds of Chirikof Island. *Western Birds* 46:28-48.

Gibson, D. D., L. H. DeCicco, R. E. Gill, S. C. Heinl, A. J. Lang, T. G. Tobish, Jr., and J. J. Withrow. 2015. Checklist of Alaska birds, 21st edition.

Pranty, B., J. L. Dunn, K. L. Garrett, D. D. Gibson, M. J. Iliff, M. W. Lockwood, R. Pittawy, and D. A. Sibley. 2014. 25th Report of the ABA Checklist Committee, 2014. *Birding* 46:26-36.

Benson, A.-M., and K. Winker. High-latitude passerine migrants overlap energetically demanding events in autumn. *Wilson Journal of Ornithology* 127:601-614.
Time constraints on migratory birds to molt, store fat, and migrate in autumn are probably most severe in populations breeding at high latitudes. We found that time constraints among high-latitude migrants of 17 species at Fairbanks, Alaska are correlated with overlaps of molt and fattening. We found a negative relationship between length of breeding ground occupancy and the amounts of molt-migration overlap and a positive relationship between molt-fat overlap and distance to wintering range. No individual completely overlapped the peak levels of both molt intensity and fat storage observed within a species, but several individuals approached this theoretical maximum in four species. Our results show that high-latitude passerines can overlap energetically demanding events but there is considerable variation among species in how they do this. Many birds appear to push energetic limits by overlapping molt, migration, and fattening to a degree not previously documented.

Ringgenberg, B., and K. Winker. 2015. Indications that the Common Redpoll (*Acanthis flammea*) is double brooded in Alaska. *Western Birds* 46:291-298.

Winker, K., **K. K. Campbell, C. Wong, J. F. Fricilone,** and A. B. Johnson 2015. Phylochronology of an avian migrant during autumn stopover appears to show a time signal in genetic diversity. *Loon* 87:47-52.
A student-led project involving a graduate student, an undergraduate, and a high-school student. Migrant Swainson's Thrushes have a nonrandom distribution of genetic variation through time.

University of Alaska Museum's

Friends of Ornithology

The birds of Alaska have never been in better hands.
