Wintering Assemblage of Arctic Warblers in the Philippines

Aurora Hoefferle[1], Kyle Campbell[2], Bennett Wong[2], Kevin Winker [2]

[1]Rural Alaska Honors Institute, University of Alaska Fairbanks
[2]University of Alaska Museum, University of Alaska Fairbanks

Introduction

The Arctic Warbler, *Phylloscopus borealis*, is a migratory songbird that breeds in Alaska and is known to overwinter in the Philippines.

We wanted to know whether or not individuals from Alaska overwinter in the Philippines and which other populations of *P. borealis* they may overlap with in their wintering grounds.

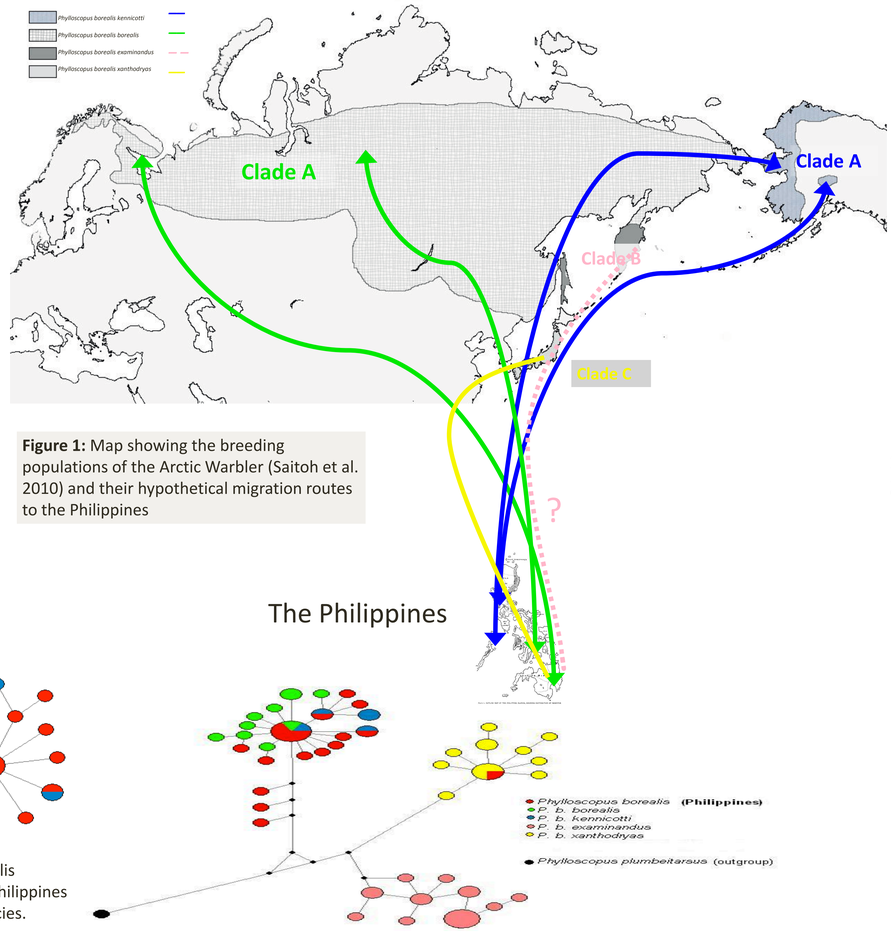

Figure 1: Map showing the breeding populations of the Arctic Warbler (Saitoh et al. 2010) and their hypothetical migration routes to the Philippines

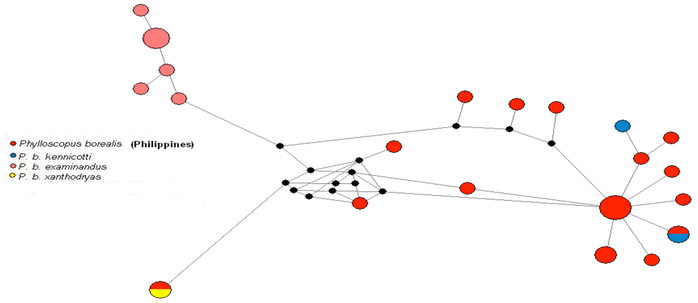

Figure 2: Median-joining network of cyt *b* haplotypes recovered from 29 specimens of P. borealis collected in the Philippines, Alaska, Russia, and Japan. Individual warblers collected from the Philippines are represented in red, and birds collected from their breeding ranges are specified by subspecies.

Figure 3: Median-joining network of cyt *b* haplotypes recovered from the 29 specimens of P. borealis sampled in this study, as well as 41 haplotypes identified from breeding birds by Saitoh et al. (2010). Individual warblers collected from the Philippines are represented in red, and birds collected from their breeding ranges are specified by subspecies.

Methods

We sequenced the mitochondrial gene cyt *b* from 19 Arctic Warblers collected in the Philippines and compared our data against sequences obtained from birds collected from known breeding populations from each of the three clades identified. Phylogenies were inferred with MrBayes 2.2 [2, 3] using a GTR+I model. Haplotype data were combined with data from Saitoh et al. [1] using DNAsP [4] and haplotype trees were created using NETWORK 4.6.1.0 [5, 6].

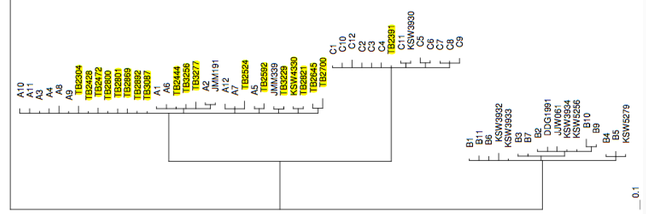

Figure 4: Phylogenetic tree including haplotypes identified by Saitoh et al. (2010) and published on Genbank. Individuals included in this study are identified by ascension number, with birds collected from the Philipippines highlighted in yellow. Haplotypes identified by Saitoh et al. are identified by haplotype number (ie. A1, B1, C1, etc.) We selected *Phylloscopus plumbeitarsus* as our outgroup.

Background

Arctic Warblers breed across much of northern Eurasia and make up several distinct breeding populations. Three main Clades of *P. borealis* have been identified in a recent paper by Saitoh et al. [1]:

Clade A- Eastern Europe to Alaska
Clade B- Kamchatka to Northern Japan.
Clade C- Southern Japan

Results

We found that 18 out of the 19 Arctic Warblers collected in the Philippines that we recovered sequence data from represent Clade A, and we believe both subspecies of Clade A are represented in our sample (*P. b. kennicotti and P. b. borealis)*. One specimen appeared to be representative of Clade C in the Philippines, *P. b. xanthodryas*.
There were no representatives from Clade B, *P. b. examinandus,* in our sample from the Philippines.

Discussion

While our results indicate that Arctic Warblers from Alaska do in fact overwinter in the Philippines with other populations of *P. borealis*, we found it interesting that birds from Clade B were not found in our sample. This could be due to undersampling, however further analyses may reveal that Arctic Warblers from Alaska do not overlap with birds from Kamchatka in the Philippines.

Alaska BioPREP
University of Alaska Fairbanks

UNIVERSITY OF ALASKA MUSEUM

This publication was funded by the National Center for Research Resources and the Division of Program Coordination, Planning, and Strategic Initiatives of the National Institutes of Health through grant number 8R25D011159-5

References:
[1] Saitoh, Takema, Per Alstrom, Isao Nishiumi, Yoshimitsu Shigeta, Dawn Williams, Urban Olsson, and Keisuke Ueda. 2010. Old divergences in a boreal bird support long-term survival through the Ice-Ages. BMC Evolutionary Biology. Volume 10, Issue 35. http://www.biomedcentral.com/1471-2148/10/35
[2] Huelsenbeck, J. P. and F. Ronquist. 2001. MRBAYES: Bayesian inference of phylogeny. Bioinformatics 17:754-755.
[3] Ronquist, F. and J. P. Huelsenbeck. 2003. MRBAYES 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19:1572-1574.
[4] Librado, P. and Rozas, J. 2009. DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. Bioinformatics 25: 1451-1452 | doi: 10.1093/bioinformatics/btp187.
[5] Bandelt H-J, Forster P, Röhl A (1999) Median-joining networks for inferring intraspecific phylogenies. Mol Biol Evol 16:37-48
[6] etwork 4.6.1.0., released 30 December 2011, expiry date 1 January 2013. Network © Copyright Fluxus Technology Ltd 1999-2012 http://www.fluxus-engineering.com/

UAF UNIVERSITY OF ALASKA FAIRBANKS

Alaska INBRE
IDeA Network of Biomedical Research Excellence