

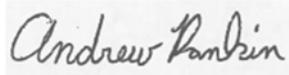
18 June 2015

To Whom It May Concern: We would like to request a destructive sampling loan for 9 yellow-bellied marmot (*Marmota flaviventris*) specimens from the University of Colorado Museum of Natural History (UCM). The specific specimens needed and their UCM catalog numbers are outlined in the following narrative, along with a description of their intended use.

Best regards,



Kurt Galbreath, PhD
Assistant Professor



Andrew Rankin, MS Candidate
Teaching Assistant

Project background. Alpine- and montane-adapted mammals may have evolved in parallel, responding to past climatic events in similar ways (Galbreath et al., 2010). Comparative analyses of alpine/montane mammals have indicated recent range contractions, with some taxa currently experiencing declines in the face of climate change (Lanier et al., 2015). Here, we wish to assess the biogeographic history of yellow-bellied marmot (*Marmota flaviventris*) populations in the Great Basin to test for demographic harmony with other species having similar natural histories.

The yellow-bellied marmot is a large ground squirrel that inhabits rocky meadows of the montane life zone in the Intermountain West (Quinn, 2008). According to fossil evidence, marmots were common in the Great Basin at elevations as low as 1,250 m during the late Pleistocene (Grayson, 1987), despite now being relatively rare below 2,200 m (Floyd, 2004). These upslope shifts in distributions and lowland extinctions were likely caused by climatic warming throughout the Holocene (Brown, 1971). Thus, we propose to use this species as a potential model for elucidating the biogeographic history of small mammals in the Great Basin.

Research objectives. By reconstructing the *M. flaviventris* phylogeny we will be able to address the following research objectives: (1) Describe the phylogeographic structure of Great Basin marmots and infer the ancestral source pool of current Sky Island populations, (2) test for glacial expansion followed by postglacial contraction and (3) determine how Holocene warming and population fragmentation may have influenced genetic diversity.

The results of this work will provide a valuable baseline for future biogeographical studies of montane mammals in the Great Basin and will help to inform conservation efforts focused on Great Basin Sky Islands, the latter of which may be of growing importance due to climate change further increasing isolation and restricting gene flow between ranges (McDonald and Brown, 1992).

Preliminary work and sample requests. During the summers of 1999—2002 and 2013—2014, the researchers performed field work on the island-like mountain ranges of the Great Basin (California, Nevada, and Utah, USA). Tissue samples from 13 mountain ranges were collected and a portion of the cytochrome b gene and part of the D—loop (~700 total base pairs) were subsequently sequenced. This work resulted in 28 sequences from individuals of the Great Basin. In addition to this, 10 sequences from the Rocky Mountains and 5 sequences from the Sierra-Nevada Mountains were added to the data set, totaling 43 sequences in all.

The gene tree constructed from this data set is certainly interesting; however, we require additional data in order to identify interpretable patterns and reach any sound conclusions.

Thus, we would like to inquire if the University of Colorado Museum of Natural History would be willing to assist us in acquiring more data? We queried the Arctos database and came across 9 specimens whose geographic locations are underrepresented in our current dataset (Mamm: 7364, Mamm: 11628, Mamm: 11627, Mamm: 11629, Mamm: 4829, Mamm: 8226, Mamm: 19425, Mamm: 8225, and Mamm: 5372). Acquiring these samples would make a great contribution to our project and we would be greatly appreciative. Further, we would ensure that the University of Colorado Museum of Natural History received due acknowledgment in any poster, presentation or publication resulting from this study. This would be accomplished by properly citing each specimen used by their UCM catalog number.

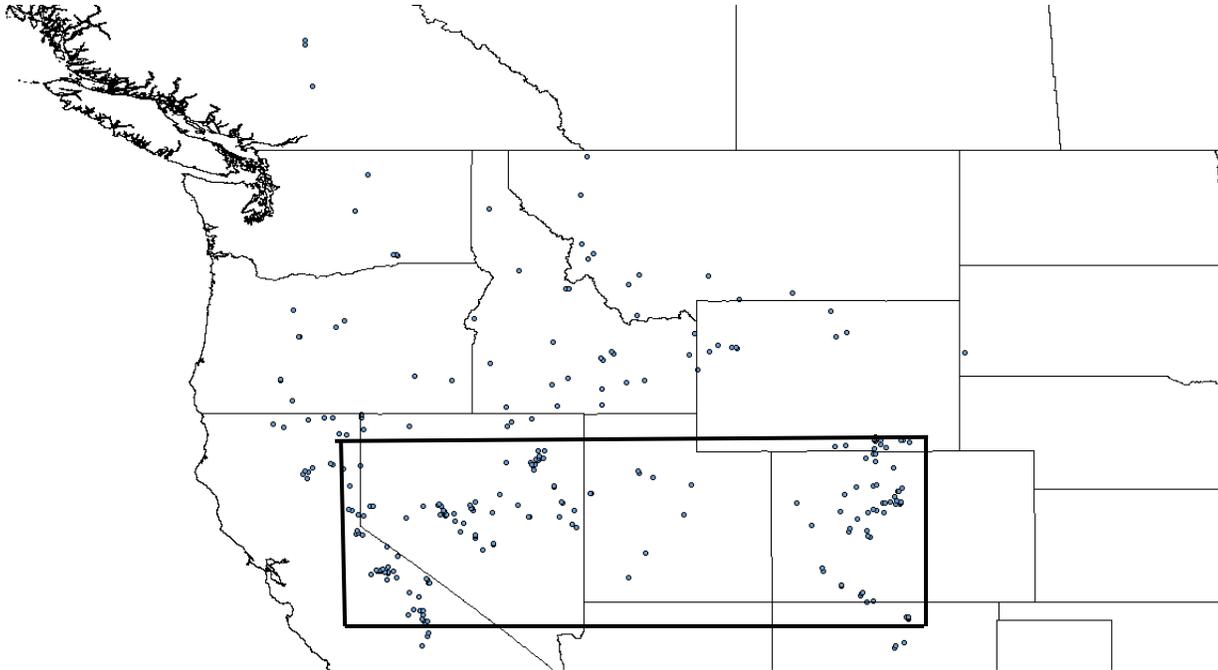


Figure 1 *Marmota flaviventris* range and distribution taken from occurrence records from our surveys of the Great Basin, 48 records from a previously published study (Floyd, 2004), and 417 records of museum specimens from the Arctos database (arctos.database.museum/). Outlined area spans the geographic region represented by our current data set.

Nature of material needed and mode of transport. We would require (if available) approximately 50—100 mg of dried skin or hair from each specimen (Mamm: 7364, Mamm: 11628, Mamm: 11627, Mamm: 11629, Mamm: 4829, Mamm: 8226, Mamm: 19425, Mamm: 8225, and Mamm: 5372).

If approved, samples can be sent to the following address:

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Author qualifications. I am a MS Candidate at Northern Michigan University (NMU) and am currently collaborating on this project with Dr. Kurt Galbreath (NMU) and Dr. Chris Floyd (University of Wisconsin Eau Claire). Since fall of 2014, I have assisted in teaching an upper level course in genetics and have completed course work in both systematics and bioinformatics. In addition, I have obtained experience with DNA and RNA extraction, polymerase chain reaction and gel extraction for my thesis project. I have also secured two external grants, one from the Sigma Xi Research Society and another from the American Society of Mammalogist, to support my research over the summer.

Timeline. The goals in which I have outlined shall encompass 1 summer of data analysis and interpretation. Preparation of the manuscript will begin late summer and continue into the fall. The completed manuscript will then be submitted for publication to The Journal of Biogeography.

Materials and Methods

Description of molecular analyses. Partial sequences of the mitochondrial cytochrome b gene and mitochondrial control region (~700 bp) will be amplified using the primers CB3R and 12SAR (Palumbi, 1996).

Phylogenetic analyses. Sequences obtained from museum specimens will be added to the current data set and multiple alignments will be performed using the MUSCLE (Edgar, 2004) application in the software program MEGA6 (Tamura et al., 2013). The best fit model of nucleotide substitution for the alignment will be identified using jModelTest 2.1.6 (Darriba et al., 2012) using Akaike information criterion (AIC). The data set will then be analyzed using Bayesian inference and Maximum-likelihood. All phylogenies will be rooted with *Marmota himalayana* (Accession # JX069958.1).

Demographic analyses. In order to assess past changes in population size, I will test for demographic expansion. To do this, I will first examine pairwise mismatch distributions (Rogers and Harpending, 1992) using DnaSP v5 for the signature of demographic expansion. In addition, I will use a Bayesian skyline plot as implemented in BEAST v1.7.5 (Drummond et al., 2012) to infer patterns in demographic change.

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