

From: [Romin, Laura](#)
To: [Larry Crist](#)
Subject: Fwd: Final Notes from 11/18 Genetics Conference Call
Date: Monday, January 05, 2015 2:29:47 PM
Attachments: [2014-11-18_Tavaputs-Anthro Genetics Conference Call Notes.docx](#)

fyi.

Laura Romin, Deputy Field Supervisor
U.S. Fish and Wildlife Service
Utah Ecological Services Field Office
2369 W. Orton Circle
West Valley City, Utah 84119
ph: 801-975-3330, ext. 142
cell: 801-554-7660

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From: **Bahr, Quincy** <qfbahr@blm.gov>
Date: Mon, Jan 5, 2015 at 1:46 PM
Subject: Final Notes from 11/18 Genetics Conference Call
To: Betsy Herrmann <betsy_herrmann@fws.gov>, Jay Martini <jay_martini@fws.gov>, Laura Romin <Laura_Romin@fws.gov>, Renee Chi <rchi@blm.gov>, Karen Mock <karen.mock@usu.edu>

All,

I've had a request for the final notes from the 11/18 genetics conference call for the Anthro area. I've attached the final notes that are in our record. For clarity, all I did with Karen's revisions was to reformat, add the attendees, and move a bit of information from an inserted comment of hers into the body of the notes.

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Quincy Bahr
Project Manager – Greater Sage-Grouse LUP Amendments, Utah Sub-Region
Planning and Environmental Coordinator – BLM, Utah State Office
440 West 200 South, Suite 500
Salt Lake City, UT 84101-1345
801-539-4122 (office)
801-518-1479 (cell)
qfbahr@blm.gov

Greater Sage-grouse Land Use Plan Amendments

Conference Call Summary

PURPOSE: To review the findings of greater sage-grouse genetics literature for the Anthro/Tavaputs areas

DATE AND TIME: November 18, 2014; 1:00 – 2:00 PM (MT)

LOCATION: Conference Call

INVITEES / ATTENDANCE:

- Renee Chi – UT BLM
- Quincy Bahr – UT BLM
- Betsy Herrmann – FWS
- Jay Martini – FWS
- Laura Romin – FWS
- Karen Mock – Utah State University
- Leah Breidinger – Utah State University
- Forest Service (Ron Rodriguez) was invited, but did not attend
- State of Utah (Brian Maxfield, Eric Ellis, Jason Robinson, Brad Crompton, and Dave Dahlgren) was invited, but did not attend

NOTES:

- Breidinger et. al. 2013 is not new information, but is genetic information from the author's 2009 thesis, reformatted for publication.
- On November 18, the FWS hosted a conference call that included background discussion on the scope and nature of genetics research, as well as discussion of what conclusions can and cannot be made from the authors' research:
 - There are two general types of marker systems used to study DNA: mitochondrial DNA sequences ("haplotypes") and nuclear markers. Mitochondrial sequences can be good indicators of deep subdivision between taxa, and are often used to screen for divergent evolutionary lineages, but are limited because they only look at a fragment of the genome contributed by the mother. The more complete method is nuclear, as it studies the genome from both mother and father and generally samples many locations on the genome. Neither of these marker systems is designed to look directly at adaptive genetic variation (i.e. traits). The Breidinger et al. 2013 study used only mitochondrial sequences (also called haplotypes).
 - A previous study by Oyler-McCance (2005) in the journal Molecular Ecology used seven nuclear markers (microsatellites) to characterize populations in the UT/ID/WY region, and also provided mitochondrial sequence data on these populations (used for comparison in Breidinger et al. 2013). The microsatellite data in Oyler-McCance et al. (2005) indicated that the populations in Strawberry Valley and in Wayne County Utah were more closely connected (or related) to each other than to populations in Wyoming and Colorado. Both the Oyler-McCance (2005) and the Breidinger (2013) papers suggested a restriction in gene flow between the populations on either side of the Desolation Canyon area, although neither study used enough sample populations to define this barrier precisely.
 - Mitochondrial research can provide information on maternal evolutionary lineage, but nuclear microsatellite data or next-generation sequencing data are preferred tools for describing small-scale dispersal patterns and connectivity. You can get some information depending on the history of the populations being compared, but a mitochondrial sequence is just a single

location on the genome, is only inherited maternally, and is highly influenced by genetic drift. Because of the drift effect, mitochondrial data can detect recent isolation in some cases, but is more commonly used to identify lineages that are very divergent (e.g., potential ESUs).

- No genetic samples from birds in the West Tavaputs or Emma Park areas were included in this analysis, therefore, no inferences can be made about lineage, dispersal or connectivity between these populations from this study.
- Breidinger et al. (2013) collected genetic samples from Seep Ridge, Deadman's Bench, and Anthro Mountain. Breidinger et al. (2013) also used publicly available data from Oyler-McCance et al. (2005) for comparison. The comparative samples were from Strawberry Valley, Diamond Mountain, Blue Mountain, Cold Springs, Parker Mountain and Seep Ridge.
- Both Breidinger et al. (2013) and Oyler-McCance et al (2005) identified haplotypes (unique genetic signatures) in each population and noted populations where samples shared haplotypes, as well as haplotype frequencies.
- One cannot infer that the absence of shared mitochondrial haplotypes indicates a lack of interaction; two birds from the same population may not share the exact same haplotypes (e.g., two birds that are part of the same population but don't share a common maternal ancestry), mitochondrial haplotypes and haplotype frequency may not represent patterns found in the rest of the genome, and population samples may not include all the haplotypes present in the population.
- This study can only definitively conclude what is seen, not what is absent.
- One cannot definitively infer current connectivity or dispersal from this information, although if connectivity was very high among populations they would be expected to be much more similar in terms of haplotypes and haplotype frequencies. If connectivity is very low or even complete, populations can still seem similar until enough time has gone by that genetic drift and mutation change their haplotype compositions.
- The only definitive finding from Breidinger et al. (2005) is that individuals that were sampled from the Strawberry and Anthro populations share haplotype DR, which is the most common haplotype in both populations and not found elsewhere by either of the 2 studies mentioned.. This finding indicates either recent shared ancestry or gene flow between Strawberry and Anthro populations, but to be definitive, nuclear markers should be employed. Nuclear markers would provide a more sensitive estimate of gene flow between these (and other) populations, and would be more likely to represent processes driving nuclear diversity patterns.