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Subject: Wolverine - Revised Genetics Option Paper
Date: Thursday, June 15, 2017 9:34:30 AM
Attachments: [Talking Points for Wolverine Genetic Options Discussion_06152017.docx](#)

Mike and Marj,

Attached is a revised genetics option paper.

Copies will be available for today's discussion w/ Noreen.

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Talking Points – Funding Request for Wolverine Genetic Analyses

Background

In the U.S. District Court decision (April 4, 2016), the court vacated our withdrawal of the wolverine proposed rule for further consideration based on two primary issues: 1) ignoring best available science in dismissing the threat to wolverine from climate change and 2) ignoring best available science by dismissing the **threat to wolverine from genetic isolation and small population size**. Specifically, the court said that, in our 2014 withdrawal, we failed to articulate how our statements regarding the following did not constitute adverse effects to wolverine:

- Apparent loss of connectivity between Rocky Mountains and Canada prevented influx of genetic material needed to maintain or increase the genetic diversity in contiguous U.S.
- Effective population size is too low to support the subpopulations in contiguous U.S.
- Genetic drift has already occurred in subpopulations in contiguous U.S. as compared to Canada, and a continued loss of genetic diversity may lead to inbreeding depression and inability of wolverines in contiguous U.S. to persist

Thus, we need to evaluate our statements that there is “good evidence” that genetic diversity is lower in wolverines in the contiguous U.S. as compared to Canada and Alaska. We also need to determine whether there is a threat for inbreeding depression based on small population size. The following talking points provide potential pathways for addressing the court’s remand.

Microsatellite analysis options

- Option 1 - Provide funding to USFS genomics lab (Missoula) to prepare mitochondrial DNA and microsatellite loci analyses using existing samples provided to this lab (by western States) to examine current genetic structure of wolverines in contiguous U.S. Costs are estimated at \$60,000 based approximately 300 samples collected already submitted, at \$200/sample. If only microsatellite loci analyses is conducted, which is the approach needed to evaluate population genetics, the total cost will only be reduced by about \$500.
- Option 2 - Provide funding to an independent lab (e.g., Wildlife Genetics International (WGI), British Columbia) for this analysis. This will require that the USFS lab release the collected samples. WGI has previously run genetic analyses for wolverines. However, because the USFS has already processed these samples, the quality of the DNA for a secondary extraction will likely be degraded and therefore may not provide useful results.
- Option 3 - Provide funding to FWS Conservation Genetics Laboratory in Alaska. This would also require that samples be retrieved from USFS lab. Cost estimated at \$100/sample and several months (estimate) to complete. However, the costs may, in the long run, be similar to USFS as they have not previously run any genetic testing for wolverine and therefore would require several weeks of lead time and acquisition of materials.
- Option 4 - Provide funding to an independent genetics group, assess current wolverine genetic data and publications and provide FWS with an overview of the state of knowledge and a critical assessment of wolverine genetics. No outreach has occurred for this option, therefore no cost estimate can be provided at this time. We are still assessing potential reviewers for this option.

If the microsatellite analysis is funded, options to conduct independent review of USFS results

- Option 1 - Provide funding to FWS Alaska lab to obtain from the USFS lab approximately 20 samples and analyze this subsample to verify USFS lab results. Cost likely to be \$100/sample.
- Option 2 - Provide funding to independent lab (e.g., WGI, who have analyzed 1000s of wolverine samples) to prepare a review and interpretation of the results of the USFS analysis to assess current genetic structure of populations of wolverines across North America (not just the contiguous U.S.) using results from other studies, including data obtained from wolverine specimens in Alaska and Canada.

Effective population size analysis (if funds available)

- Provide funding for independent assessment of minimum viable population size following methods from Koskela (Finland) using results from USFS lab.

DPS

We previously argued for discreteness of the contiguous United States wolverine population based on the international border and differences in conservation status in Canada and the United States. The following is from our analysis of discreteness under our DPS policy in the 2010 12-month finding, also relied upon in the 2013 proposed rule: “The international boundary between Canada and the United States currently leads to division of the control of exploitation and conservation status of the wolverine. This division is significant because it allows for potential extirpation of the species within the contiguous United States through loss of small populations and lack of demographic and genetic connectivity of the two populations.” We did not rely on marked genetic differences in our determination of significance for the DPS in the 2010 finding and 2013 proposed rule; significance of the wolverine in the contiguous United States was based on a significant gap in the range argument.

Preliminary interpretation by the FWS Alaska lab of recent genetic studies indicate that wolverines in the contiguous U.S. are likely decedents of wolverines that migrated from Canada years ago to repopulate the area after persecution of predators ceased. As such, wolverine populations in the contiguous U.S. may not represent a distinct genetic structure (no unique alleles) as it may apply to discreteness in our DPS policy. Additional knowledge gained through a more thorough and complete comparison of the genetic structure of wolverine population in the contiguous U.S. as well as Alaska and Canada would provide a more legally and scientifically robust basis on which to base our DPS determination.