

From: [Grizzle, Betty](#)
To: [John Guinotte](#); [Stephen Torbit](#)
Subject: Excerpts from Zigouris dissertation
Date: Tuesday, May 16, 2017 11:04:29 AM

Hi John and Steve - FYI, I copied in some text that might be of interest to you, though I am still reading through her 2014 dissertation. I wanted you to know that there is inconsistency in suggestions/conclusions from McKelvey et al. 2014 paper, and the complexity of this issue, in general:

Pages 122-123: Interestingly, a very similar phylogeographic study by McKelvey et al. (2014) proposed a southern ice-free refugium in addition to Beringia. While historic samples were also included in McKelvey et al. (2014), they largely represented the southwestern range periphery. These historic samples revealed a localized distribution of the extirpated California haplotypes (Hap21, Hap22), and the basis for a likely southern refugium during the LGM. Historic sampling from Quebec-Labrador in this study identified the presence of Hap21 in northeastern North America, indicating this haplotype was more widely distributed than indicated by McKelvey et al. (2014), **bringing to question the occurrence of a southern refugium. These contradicting results** could reflect the low nucleotide diversity among wolverine sequences, which were unable to provide the resolution needed for making phylogenetic inferences.

Also repeated on pages 232-233: A similar phylogeographic study on wolverines (McKelvey et al. 2014) proposed a southern ice-free refugium in addition to Beringia. Historic samples in McKelvey et al. (2014) were largely from the southwestern range periphery, resulting in the extirpated California haplotype (Cali1) being observed in a localized region. Historic sampling from Quebec-Labrador (Chapter 3) identified the presence of Cali1 in northeastern North America, indicating this haplotype was more widely distributed and a southern refugium may not have occurred. **These contradicting results** could reflect the low nucleotide diversity among wolverine sequences, due to the amplification of a 318 bp fragment of the mtDNA control region, which were unable to provide the resolution needed for making phylogenetic inferences.

From her Synthesis section, page 233: Although phylogeographic analyses revealed a single glacial refugium for wolverines, **contemporary spatial distribution of genetic variability reflects a more complex history of fluctuating population abundance since the last glaciation.** The mismatch distribution (Chapter 3) suggested the occurrence of a historic bottleneck event approximately 400 generations ago (Excoffier and Schneider 1999). Since the cessation of wolf bounties and overall decline in fur harvests (Slough 2007; McKelvey et al. 2011) about eight generations have elapsed, **not enough time for wolverine densities to fully recover.**

Also this discussion in her Synthesis section, which is why I am interested in looking at **road density**, pages 234-235: I investigated the influence of five landscape features (forest age, road density, land cover, spring snow cover mean and variance) on the genetic connectivity of wolverines at the extant periphery of their extant range in North America (Chapter 4). Road density and spring snow cover were associated with wolverine genetic distances (Chapter 4). **Road density effects on the genetic variance of females may have a double effect on wolverine populations, affecting both female survival and reproductive success**

And this:increased genetic distance was correlated to lower mean spring snow cover. (she mentions thermoregulatory advantage, availability of ungulate carcasses, behavioral effects as possibilities).

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