

SUPPLEMENTARY MATERIALS

Comparison of Patterns of Genetic Variation and Demographic History in the Greater Sage-Grouse (*Centrocercus urophasianus*): Relevance for Conservation

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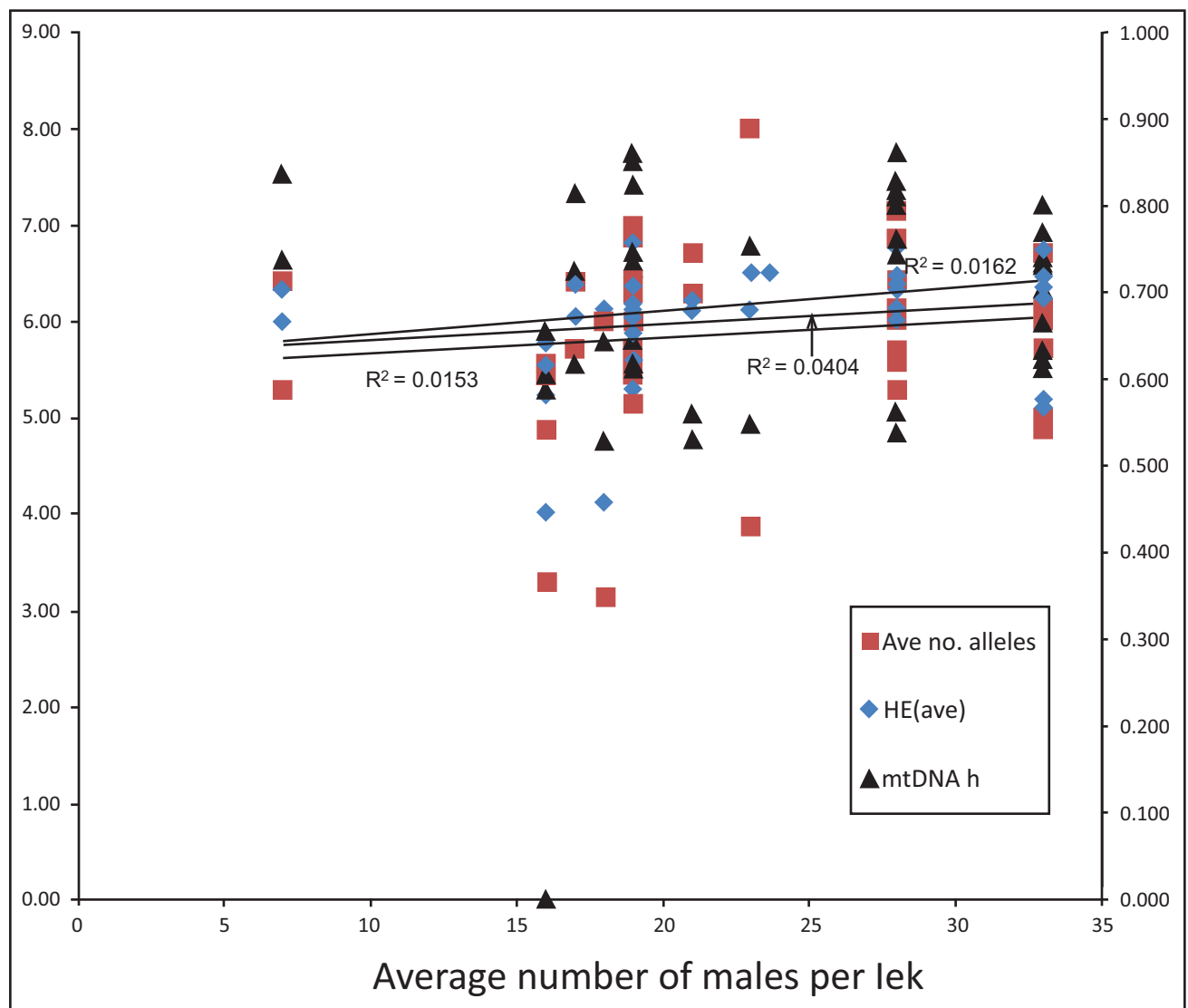
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Fig. (S1). Plot of average number of alleles, average heterozygosity and mtDNA haplotype diversity for 45 populations [1] of greater sage-grouse, and associated R² values from regression on average number of males per lek. MtDNA nucleotide diversity not plotted because R² = 0.0011.

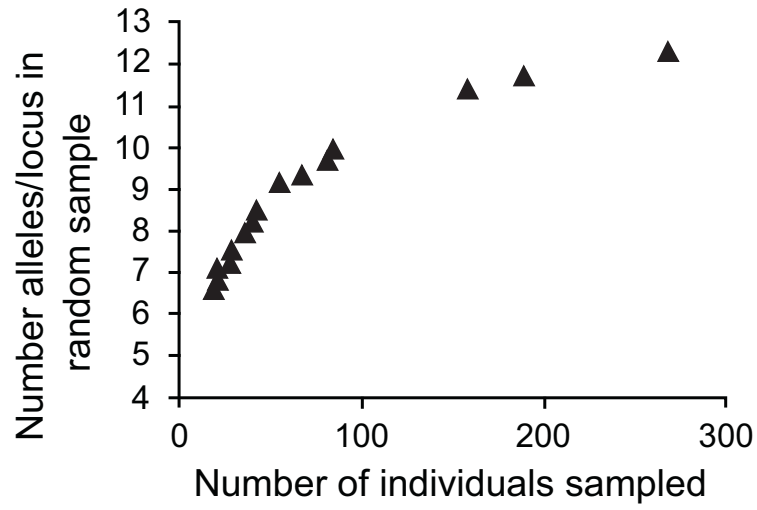


Fig. (S2). Relationship between number of individuals of greater sage-grouse sampled randomly from the total ($n = 1181$) number of greater sage-grouse and average number of microsatellite alleles/locus ($n = 7$). Sample sizes represent actual sample sizes/locality in [1]. Each triangle represents average of 10 random replicates. As expected, small samples show reduced genetic variability.