

CANDIDATE GENE MICROSATELLITE VARIATION IS ASSOCIATED WITH PARASITISM IN WILD BIGHORN SHEEP

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The loss of genetic variation in host populations is thought to increase host susceptibility to parasites. However, few data exist to test this hypothesis in natural populations. Bighorn sheep (*Ovis canadensis canadensis*) populations occasionally suffer disease-induced population declines, allowing us to test for associations between reduced genetic variation and parasitism in this species. Here we show that individual mean heterozygosity for 15 microsatellite loci is associated with lungworm abundance (*Protostrongylus* spp.) in a small, recently bottlenecked population of bighorn sheep (linear regression, $R^2 = 0.339$, $P = 0.007$). This association remains significant for seven microsatellites located in genes ($P = 0.010$), but not for eight neutral microsatellites ($P = 0.306$). Furthermore, heterozygotes at three of four microsatellites located within disease-related genes had lower lungworm burdens. This study corroborates theoretical findings that increased parasitism and disease may be a consequence of reduced heterozygosity in wild populations, and that certain individual loci influence

parasite resistance. The results illustrate the usefulness of using genomic information, strong candidate genes, and noninvasive sampling for monitoring both genetic variation and fitness-related traits, such as parasite resistance, in natural populations.