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Genetic population structure of Peninsular bighorn sheep (*Ovis canadensis nelsoni*) indicates substantial gene flow across US–Mexico border

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ABSTRACT

Within the United States (US), Peninsular bighorn sheep (*Ovis canadensis nelsoni*, PBS) are listed as federally endangered. Despite known metapopulation structure, little is known regarding functional connectivity across the international border with Mexico. Increasing threats to connectivity associated with highway expansion, renewable energy development, and completion of the US–Mexico border fence, led us to conduct a study of genetic variation and spatial structure. Blood and fecal samples were collected ($n = 224$) on both sides of the border from 1992 to 2013. Genetic data was obtained for 25 microsatellite loci and 515 base pairs of the mitochondrial DNA control region. Microsatellite diversity (observed heterozygosity = 0.56; allelic richness = 4.1; inbreeding coefficient = 0.01) was substantial despite past demographic declines. STRUCTURE analysis indicated the presence of three genetic populations, one of which spanned the international border. This pattern of genetic structure was supported by analysis of molecular variance for both microsatellites and mitochondrial DNA ($P < 0.01$), and low-moderate pairwise fixation indices ($F_{ST} = 0.09–0.15$; $\Phi_{ST} = 0.18–0.27$) indicated substantial gene flow among populations. Migrant detection tests indicated natal dispersal occurred within both sexes, with no evidence of sex bias. Despite the severe reductions in population abundance which led to federal listing in the US, these data suggest PBS have retained substantial genetic variation and show little evidence of a recent genetic bottleneck. Patterns of genetic spatial structure indicate gene flow throughout the ranges is common, and construction of a US–Mexico border fence or wind energy infrastructure would disrupt connectivity of the metapopulation. Future conservation efforts should focus on identifying dispersal corridors and maintaining functional connectivity to facilitate recolonization of unoccupied habitat.

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1. Introduction

Functional connectivity across a landscape is important for the persistence of populations, facilitating gene flow (Fischer and Lindenmayer, 2007) and recolonization of unoccupied habitats (Epps et al., 2010). Loss of connectivity is often deleterious, as fragmented populations can suffer from rapid reduction in genetic diversity and increased extinction risk (Epps et al., 2005; Keller and Largiader, 2003; Purvis et al., 2000). Characterizing the genetic spatial structure of a population has applied conservation value, including quantifying standing levels of genetic diversity, identifying dispersal corridors/barriers, and predicting the effects of proposed management actions on population connectivity (Segelbacher et al., 2010; Storfer et al., 2007). This level of understanding is essential for effective management of endangered species, which often exist in small populations occupying naturally patchy habitat. Desert bighorn sheep (*Ovis canadensis nelsoni*) within the Peninsular Ranges of southern California, United States (US) and Baja California, Mexico represent such a group.

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Human-altered landscapes are known to negatively impact bighorn sheep populations in the desert regions of North America (Bleich et al., 1996; Epps et al., 2005; Krausman et al., 1999). Recently, efforts to construct a US–Mexico border fence preventing human immigration (US Public Law 109-367) have resulted in elevated concern regarding impacts to wildlife (Cohn, 2007; Sayre and Knight, 2010), including bighorn sheep (Flesch et al., 2010). In addition, renewable energy development within this region is rapidly increasing because of high wind and solar potential (Lovich and Ennen, 2011). Large energy projects create potential threats to wildlife through habitat loss (Lovich and Bainbridge, 1999) and fragmentation from road construction (Gerlach and Musolf, 2000; Lodé, 2000; Saunders et al., 2002). Potential border fence completion, and wind energy development within bighorn sheep habitat on both sides of the border (Fig. 1), represent threats to habitat quality and population connectivity.

Desert bighorn sheep (*O. c. nelsoni*) populations in the southwestern US and Mexico have significantly declined over the past two centuries (Buechner, 1960; Krausman et al., 1999). Declines have been attributed to overhunting, disease, negative interactions with domestic livestock, and habitat loss (Valdez and Krausman, 1999). Peninsular desert bighorn sheep (hereafter PBS) occupy the Peninsular Ranges, extending from southern California southward into the Baja Peninsula. Suitable habitat for this taxon consists of a narrow band of mid-elevation, east facing slopes (Rubin et al., 2009) that are highly vulnerable to fragmentation (Fig. 1). Catastrophic declines (~276 animals remaining) coincident with land use changes and other threats were documented within the US (Rubin et al., 1998; Torres et al., 1994), and PBS were listed as a federally endangered population segment in 1998 (63 FR 13134). The US population is currently managed in a series of nine recovery regions (Fig. 1), each

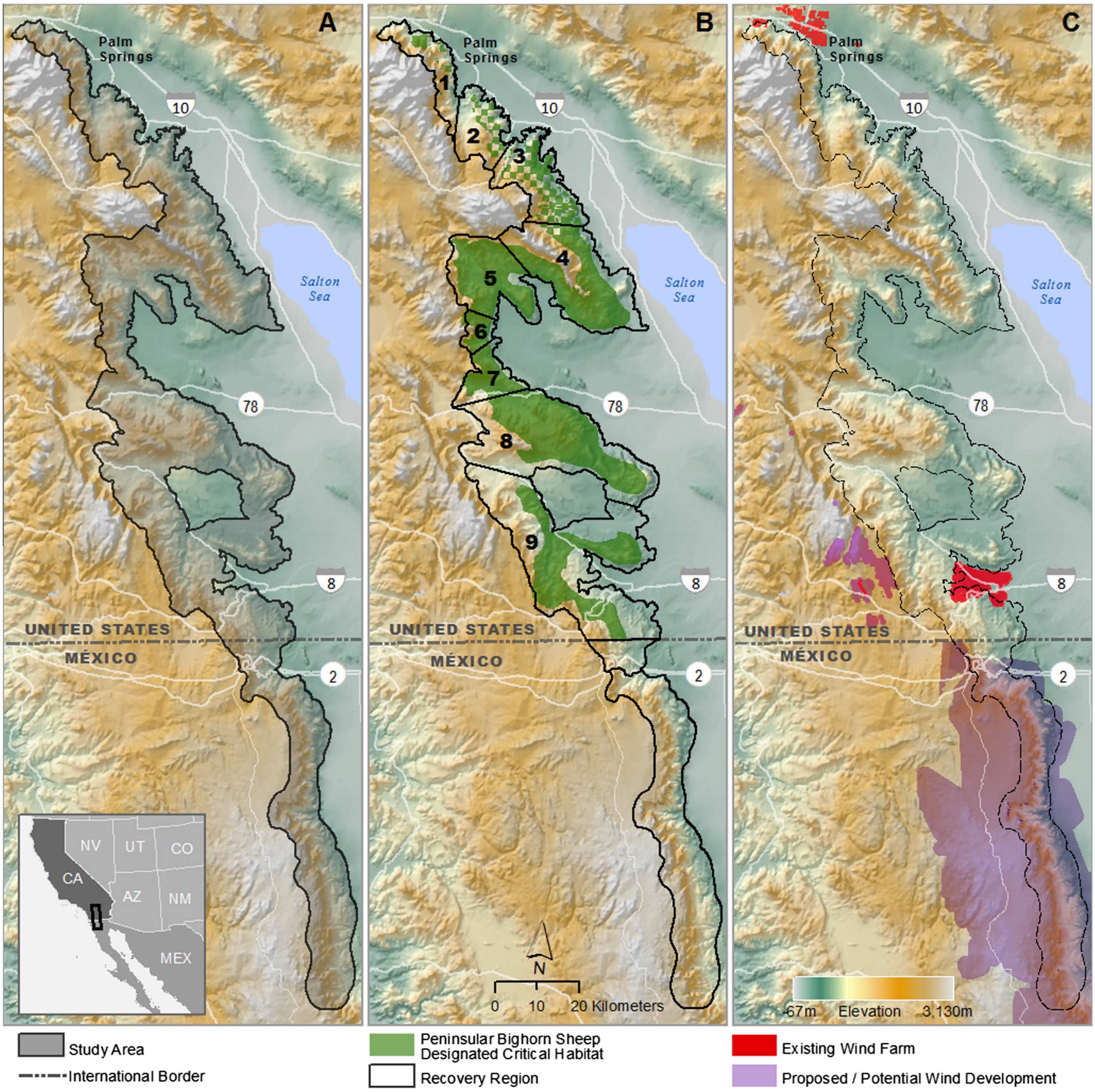

Fig. 1. Site map. (A) Study area for Peninsular bighorn sheep (*Ovis canadensis nelsoni*) in southern California and northern Baja California, including the US–Mexico border. (B) Location of designated Critical Habitat, numbers indicate USFWS recovery regions: (1) San Jacinto, (2) North Santa Rosa, (3) Central Santa Rosa, (4) South Santa Rosa, (5) Coyote Canyon, (6) North San Ysidro, (7) South San Ysidro, (8) Vallecito, (9) Carrizo Canyon. (C) Position of major highways and areas of wind energy development.

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