



## Analysis of genetic diversity of bighorn sheep (*Ovis canadensis*) from Mexican populations

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The current distribution of the bighorn sheep in Mexico represents a reduced proportion of its original area. Previous population genetics studies conducted in Mexico have only included data from Tiburon Island in the Gulf of California and few individuals from the continent. The aim of this article was to describe aspects of the population genetics of Mexican bighorn sheep in order to aid in the management and conservation of the species. We analyzed 117 samples from the states of Sonora and Baja California Sur using 91 intersimple sequence repeat loci. Our results indicated that the Mexican samples of bighorn sheep have relatively low levels of genetic diversity ( $H \approx 0.26$ ) and low genetic differentiation ( $\theta \approx 0.07$ ) that may be the result of the recent colonization and origin of the populations in Mexico. The individuals from Southern Baja California are genetically different from the Sonoran sample, but this genetic differentiation is low, perhaps due to the low levels of genetic variation of the Mexican populations. The results obtained in this study are relevant for population management of the bighorn sheep in Mexico in order to design translocation plans and management strategies to maintain genetic diversity and, in consequence, the health and future survival of the populations.

Key words: bighorn sheep, conservation genetics, genetic differentiation, genetic diversity, ISSR, Mexico

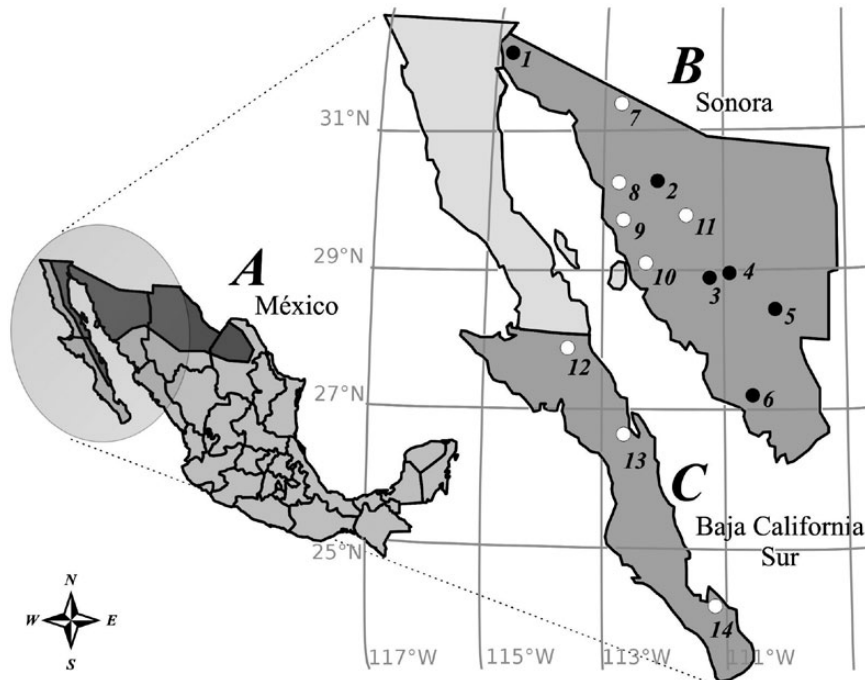
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The current total population of bighorn sheep (*Ovis canadensis* Shaw 1804, Bovidae; [Shackleton 1985](#)) is approximately 33,000 individuals distributed across North American mountain ranges, from southwestern Canada to northern Mexico ([Buechner 1960](#); [Sandoval 1985](#); [Smith and Krausman 1988](#); [Lee 1989](#); [Festa-Bianchet 1999, 2008](#); [Valdez and Krausman 1999](#)). Nevertheless, the current populations represent only approximately 4% of the original distribution of the species ([Buechner 1960](#); [Ceballos and Oliva 2005](#)). This reduction is attributed to habitat destruction and modification resulting from urban growth, the development of highways, increased competition for resources with humans and livestock, and diseases propagated from domestic sheep, goats, and cattle ([Buechner 1960](#); [Smith and Krausman 1988](#); [Monson and Lowell 1990](#)).

In particular, the historical distribution of the bighorn sheep in Mexico comprised 3 main areas, the Vizcaíno Desert on the Baja California peninsula, northern Sonora and Baja California, and from northern Chihuahua to Coahuila ([Sandoval 1985](#); [Ceballos and Oliva 2005](#); [Medellín et al. 2005](#); [Fig. 1A](#)). However, the bighorn sheep populations from the Mexican states of Chihuahua, Coahuila, and Nuevo Leon were eradicated in the last century, and the remaining

populations in other areas of Mexico are highly fragmented and have low population numbers ([Sandoval 1985](#); [Smith and Krausman 1988](#); [Ceballos and Oliva 2005](#)), although currently the Sonora and El Vizcaíno populations are reported to be stable ([Lee 1997, 2003](#)).

Recently, a number of ranches called UMAs (*Unidad de Manejo para la Conservación de la Vida Silvestre*, for sustainable management and conservation) and PIMVS (*Predios o Instalaciones que Manejan Vida Silvestre*, only handling animals in captivity without reintroduction of individuals to wildlife), designated by Mexican law, have increased the total number of individuals of the species ([Secretaría de Medio Ambiente Recursos Naturales y Pesca \[SEMARNAP\]/Instituto Nacional de Ecología \[INE\] 2000](#); [Secretaría de Medio Ambiente Naturales \[SEMARNAT\] 2013](#)). Nowadays, the legal hunting activities in Mexico are primarily conducted in the states of Baja California Sur and Sonora, while in the state of Baja California Norte, hunting has been banned intermittently since 1917 until the early 1990s, when it was definitively banned ([Mellink 1993](#); [SEMARNAP/INE 2000](#); [Medellín et al. 2005](#)). However, poaching has overwhelmed the law enforcement capabilities of Mexican federal and state conservation



**Fig. 1.**—Bighorn sheep (*Ovis canadensis*) in Mexico. A) Distribution of bighorn sheep in Mexico. B) Samples from Sonora; black circles represent the captive group (CS;  $n = 49$ . 1: La Esperanza, 2: Gran Chaparral, 3: El Churi, 4: Los Chinos, 5: Las Animas, and 6: Agua Blanca) and white circles represent the wild group (WS;  $n = 29$ . 7: El Cubabí, 8: La Candelaria, 9: La Tordilla, 10: Santa Maria, and 11: Noche Buena). C) Samples from Baja California Sur; white circles represent the wild group (WBCS;  $n = 39$ . 12: El Vizcaino, 13: San Javier, and 14: La Noria).

agencies, thereby representing an additional threat to bighorn sheep populations (Franklin 1980; Medellín et al. 2005).

The population and conservation genetics (Frankel and Soule 1981; Nei 1987; Frankham et al. 2010) of bighorn sheep have been described in different studies (Gutiérrez-Espeleta et al. 2000, 2001; Whittaker et al. 2004; Epps et al. 2005). Some studies have included samples from the Tiburón Island in the Gulf of California, in Mexico, and a few individuals from the mainland (i.e., Montoya and Gates 1975; Ramey 1995; Hedrick et al. 2001; Abad-Zavaleta et al. 2011; Gasca-Pineda et al. 2013). The aim of this article is to describe aspects of the population genetics of Mexican bighorn sheep. This information is relevant for the management and conservation of the species, since it is important to integrate the genetic population data into programs in sustainable management and conservation in order to make more effective decisions on the long-term conservation of gene pools of organisms (Franklin 1980; Frankham et al. 2010). We analyze samples from the states of Sonora and Baja California Sur, Mexico, using intersimple sequence repeats (ISSRs) as molecular markers (Zietkiewics et al. 1994; Tsumura and Strauss 1996; Nagaoka and Ogihara 1997; Wolfe et al. 1998; Wolfe and Liston 1998; Bornet and Branchard 2001). ISSRs have been used recently in several studies of genetic diversity and structure in different artiodactyls and other mammals (Kol and Lazebny 2006; Machkour-M'Rabet et al. 2009; Pashaei et al. 2009; Antunes et al. 2010; Aytekin et al. 2010; Al-Otaibi and Fahmi 2011; Askari et al. 2011; Zamani et al. 2011). Our results indicate that natural populations of bighorn sheep in Mexico exhibit relatively low levels of genetic diversity and low genetic differentiation, patterns that can be the result of the relatively recent colonization and origin of the populations.

## MATERIALS AND METHODS

*Description of sampling site.*—Samples were collected from both wild and captive populations in the states of Baja California Sur and Sonora (UMAs or PIMVS; Figs. 1B and 1C) as part of the Recuperation Program of Mexican species (SEMARNAP/INE 2000) and hunting activities. In total, we obtained 117 samples from muscle, liver, and hair. The samples were originally labeled according to their geographic origin and whether they came from wild or captive populations. The 117 individuals were thus divided into the following groups: Captive Sonora (CS;  $n = 49$ ), Wild Sonora (WS;  $n = 29$ ), and Wild Baja California Sur (WBCS;  $n = 39$ ; no captive populations from Baja California Sur were analyzed). The founder individuals of the captive populations were all obtained from adjacent wild populations in the same area. There are no records of translocation of founding individuals from geographically distant populations (Florentino Chillopa, Dirección General de Vida Silvestre-SEMARNAT, pers. comm. August 2014).

Muscle samples were retrieved from 77 mandibles following the hunting seasons of 1998–1999 and 2007–2008 (29 for the 1998–1999 and 88 for the 2007–2008 season), collected by the Federal Delegation of SEMARNAT in Sonora and Baja California Sur. Jaws were separated by removing individual antlers, dried in the sun, and stored in paper bags to keep them dry and prevent contamination. The procedure was the same for both seasons. The mandibles were collected in individual plastic bags and sent to our laboratory for further processing. The liver samples ( $n = 14$ ) were obtained by the Dirección General de Vida Silvestre (SEMARNAT) during the 2007–2008 hunting

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