



# Genetic restoration of a threatened population of greater prairie-chickens



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## ARTICLE INFO

### Article history:

Received 26 November 2013

Received in revised form 22 February 2014

Accepted 14 March 2014

Available online 16 April 2014

### Keywords:

Bottleneck

Conservation genetics

MHC

Neutral genetic diversity

Prairie grouse

Supplemental translocations

## ABSTRACT

Supplemental translocations to small, isolated populations can be a valuable strategy to counteract the effects of genetic drift by increasing genetic diversity. We studied the genetic consequences of a translocation of greater prairie-chickens (*Tympanuchus cupido pinnatus*) to Wisconsin, which has a small population (<550 birds) with low genetic diversity. During 2006–2009, 110 females were translocated to Wisconsin from Minnesota, which has greater genetic diversity. Two years after the final translocation, we detected introgression of unique Minnesota alleles. Although there was an increase in mtDNA diversity to near historic levels, there was no change in diversity at microsatellites or the major histocompatibility complex (MHC). Computer simulations of drift predicted that microsatellite diversity would have been lower in the absence of the translocation, and, thus, the translocation was a success in temporarily stemming the ongoing erosion of genetic variation through drift. Overall, our results caution that introgression of new alleles varies for genetic markers that differ in selection and inheritance, and, thus, the success of genetic restoration projects may depend on how the goals are defined.

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## 1. Introduction

Many species that once inhabited large continuous landscapes are now forced to exist in small isolated populations whose long-term persistence is uncertain. Supplemental translocation or restocking is being used increasingly to reduce the risk of extinction from both demographic and genetic stochasticity (reviewed by [Champagnon et al., 2012](#); [Perez et al., 2012](#)). Some supplemental translocations have resulted in greater reproductive success or population growth following translocation, but claims for genetic “rescue” or “restoration” are often controversial, because it is not always clear if the population response was due to genetic or environmental changes ([Adams et al., 2011](#)). Genetic analysis of translocated individuals is important in this respect ([Table 1](#)), because it allows researchers to ascribe population responses directly to changes in genetic diversity from the translocation, rather than natural processes such as mutation or immigration.

Another issue with genetic studies of translocations is that they often estimate levels of variation using adaptively neutral markers, which may not reflect variation at functional genes that are

important to population fitness. In particular, variation at immunity genes is of increasing concern as previously unknown diseases in wildlife, such as amphibian chytridiomycosis and Tasmanian devil facial tumor disease, have emerged as serious threats to populations. In these cases ([Siddle et al., 2007](#); [Savage and Zamudio, 2011](#)) and others, resistance to disease has been linked to genes of the major histocompatibility complex (MHC), which code for molecules that recognize pathogens and initiate the adaptive immune response. Similar to neutral diversity, MHC diversity in small isolated populations is typically low, but the impact on population viability is not well understood ([Radwan et al., 2010](#)). To date, only one study of snakes has documented the effect of supplemental translocations on MHC genetic diversity ([Madsen et al., 1999](#)).

Here, we assess the consequences of a supplemental translocation on both neutral and MHC genetic variation in a bottlenecked population of greater prairie-chickens (*Tympanuchus cupido pinnatus*) in Wisconsin (WI). Early in the 1900s, there were >50,000 prairie-chickens in WI and they occupied nearly every county in the state ([Grange, 1948](#)). However, during the 1950s the population declined to 1500 birds, and the range contracted to 344 km<sup>2</sup> in central WI ([Fig. 1](#)). Today, the population has declined to 256 displaying males, most of which (122) are in the Buena Vista management area (Wisconsin Department of Natural Resources,

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WDNR, unpubl. data). The population continues to be isolated as the nearest contemporary populations are over 590 km away in MN and IL. Comparisons of genetic variation before the bottleneck in the 1950s and afterwards (1996–1999) showed that the population has lost genetic variation. Surprisingly, more variation has been lost at functional (44%, MHC) than neutral (8%, microsatellites) markers in the Buena Vista population (Bellinger et al., 2003; Johnson et al., 2004; Eimes et al., 2011).

Based on the isolation and loss of genetic diversity of the WI prairie-chicken population, the WDNR decided to translocate birds from Minnesota (MN) to increase genetic diversity. The population in western MN was chosen as the source of translocated birds, because it had greater genetic diversity than the WI population, similar to larger populations in Kansas and Nebraska (Fig. 1; Johnson et al., 2003), and it was at a similar latitude, so birds would be acclimated to a more northern environment. The Buena Vista management area was chosen to receive all of the MN birds because it had the most grassland habitat (5140 h) and was intensively managed for prairie-chickens.

In this study, we evaluated whether these translocations from MN were successful at increasing genetic diversity of prairie-chickens on the Buena Vista management area, hereafter referred to as the WI population. We also examined the potential and actual genetic contributions of translocated females from MN, and, thus, the efficiency of introgression at both neutral (microsatellite, mitochondrial DNA) and functional (MHC) genetic markers. Overall, our results caution that introgression of new alleles

varies for genetic markers that differ in selection and inheritance, and, thus, interpreting the success of genetic restoration projects may depend on how the goals are defined. Although many studies claim that translocations are successful in restoring genetic variation, at least in the short term (Table 1), our study also revealed that drift continues to erode genetic variation, and, thus, translocations may only be a temporary solution for small, isolated populations.

## 2. Methods

### 2.1. Pre- and post-translocation Wisconsin sample collection

For the pre- and post-translocation samples, we collected blood and feathers, respectively, for genetic analysis from greater prairie-chickens at the Buena Vista management area, Portage County, WI (44°20'15", 89°38'49"; Fig. 1). The WI pre-translocation blood samples ( $n = 41$ ) were from males captured between 1996 and 1999 that were previously studied by Bellinger et al. (2003) and Johnson et al. (2003, 2004). The WI post-translocation samples consisted of feathers collected by the WDNR at 12 leks located throughout the Buena Vista management area during the March–May 2011 breeding season. These post-translocation samples covered the same geographic area as the pre-translocation samples. To extract DNA from the post-translocation WI feathers, we followed the molted feather protocol of Bush et al. (2005) using a Qiagen DNeasy® Tissue Kit (Valencia, California, USA).

**Table 1**

Comparison of supplemental translocation studies that included genetic analyses. Studies are based on human-facilitated translocations of free-ranging animals to threatened populations. Included are estimated population sizes before translocation (note that some studies examined two populations indicated by letters), number and sex of individuals translocated ( $n$  translocated), the number of individuals sampled pre- and post-translocation for genetic analyses, and whether genetic samples were analyzed of the translocated individuals (yes/no). For studies that used microsatellites (Msats), allelic richness ( $A_r$ ) and expected heterozygosity ( $H_e$ ) are presented.

Genetic sampling							
Species	Population size pre-translocation	$n$ translocated (sex)	$n$ sampled Pre, Post	Translocated individuals	Markers	Conclusions	Reference
Greater prairie-chicken ( <i>Tympanuchus cupido pinnatus</i> )	550	110 (F)	41, 81	Yes	Msats, mtDNA, MHC	Significant increase of mtDNA diversity but no change of Msats and MHC diversity in post-translocation population	This study
White-spotted charr <sup>a</sup> ( <i>Salvelinus leucomaenis</i> )	?	K: 20 (F) H: 20 (F)	50, 48 52, 46	Yes	Msats	Increased $H_e$ and $A_r$ diversity of post-translocation populations to levels of the source populations	Yamamoto et al. (2006)
California bighorn sheep <sup>b</sup> ( <i>Ovis canadensis californiana</i> )	S: 185 L: 125	S: 15 (F) L: 16 (F)	19, 48 23, 50	Yes	Msats, mtDNA	Increased mtDNA diversity (S & L) and significant increase of Msats $H_e$ (L only) and $A_r$ (S and L) in post-translocation populations following one generation	Whittaker et al. (2004) and Olson et al. (2012)
Bighorn sheep ( <i>Ovis canadensis</i> )	42	15 (8 M, 7F)	20 <sup>c</sup> , 115	No?	Msats	Increased $H_e$ , $A_r$ and fitness in post-translocation population.	Hogg et al. (2006)
Florida panther ( <i>Puma concolor coryi</i> )	25	8 (F)	62, 67	Yes	Msats	Increased $H_e$ and $A_r$ in post-translocation population. Decreased frequency of kinked tails and undescended testicles	Johnson et al. (2010), Table S3A
Greater prairie-chicken	50	518 (M, F)	32, 18	No	Msats, mtDNA	Increased mtDNA diversity and increased Msat $H_e$ and $A_r$ in post-translocation population.	Bouzat et al. (2009)
European adder ( <i>Vipera berus</i> )	30	20 (M)	7, 7	No	MHC	Increased MHC diversity, number of recruiting males and population size	Madsen et al. (1999)
South Island robin <sup>d</sup> ( <i>Petroica australis</i> )	A: 60 M: 300	A: 13 (F) M: 18 (F)	45, 50 82, 122	No	Msats	Significant increase of $A_r$ and $H_e$ in post-translocation populations. Increased juvenile survival and recruitment, sperm quality and immune response	Heber et al. (2013)
Anacapa deer mouse ( <i>Peromyscus maniculatus anacapa</i> )	173	1023 (M,F)	185, 60	No	Msats	Significant increases of $H_e$ and $A_r$ two years after translocations.	Ozer et al. (2011)
Eurasian otter ( <i>Lutra lutra</i> )	?	54 (M, F)	15, 20	No	Msats, mtDNA	Increase of mtDNA diversity. Decrease in Msat diversity	Arrendal et al. (2004)

<sup>a</sup> Studied the effects of translocations upstream of dams in two populations: Kame River (K) and Hitozuminai River (H), Hokkaido Island, Japan.

<sup>b</sup> Experimental translocations into two populations: Steens Mountain (S) and Leslie Gulch (L), Oregon, USA.

<sup>c</sup> sampled 20 descendants of original population in 1985 before translocations.

<sup>d</sup> Reciprocal translocations between two populations: Allports Island (A) and Motuara Island (M), Marlborough Sounds, New Zealand.

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