



Increasing distribution of non-native red fox genes within the range of the native Sacramento Valley red fox (*V.v. patwin*)?

Sophie Preckler-Quisquater^{1, 2}, Tom Batter^{1, 2}, Stacy Anderson², and Ben Sacks^{1,3}

(1) Mammalian Ecology and Conservation Unit, Veterinary Genetics Laboratory, School of Veterinary Medicine, University of California, Davis, Davis, CA; (2) California Department of Fish and Wildlife, Rancho Cordova, CA; (3) Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, Davis, CA.

Introduction

The Sacramento Valley red fox (*Vulpes vulpes patwin*) is a subspecies native to the northern area of California's Central Valley¹. This subspecies is genetically distinct from the nonnative red fox currently occupying areas adjacent to the native range. Hybridization between native and non-native red foxes was previously determined to occur within a restricted contact zone². Hybridization is a potential threat to the genetic integrity of this unique endemic subspecies. Our research aimed to determine if this hybrid zone has shifted since sampling last occurred in 2009.

Methods

- 2007-2009: Opportunistically collected scat and tissue samples during investigations of sightings reported via our project website²
- 2013-present: Deployed and baited camera stations to detect red fox presence according to a stratified random design based on a range-wide habitat suitability model³
- Processed samples to extract and amplify DNA at the cytochrome-b gene in order to determine species
- Used 33 microsatellites to genotype a subset of confirmed red fox samples to determine nuclear ancestry in the program *Structure*

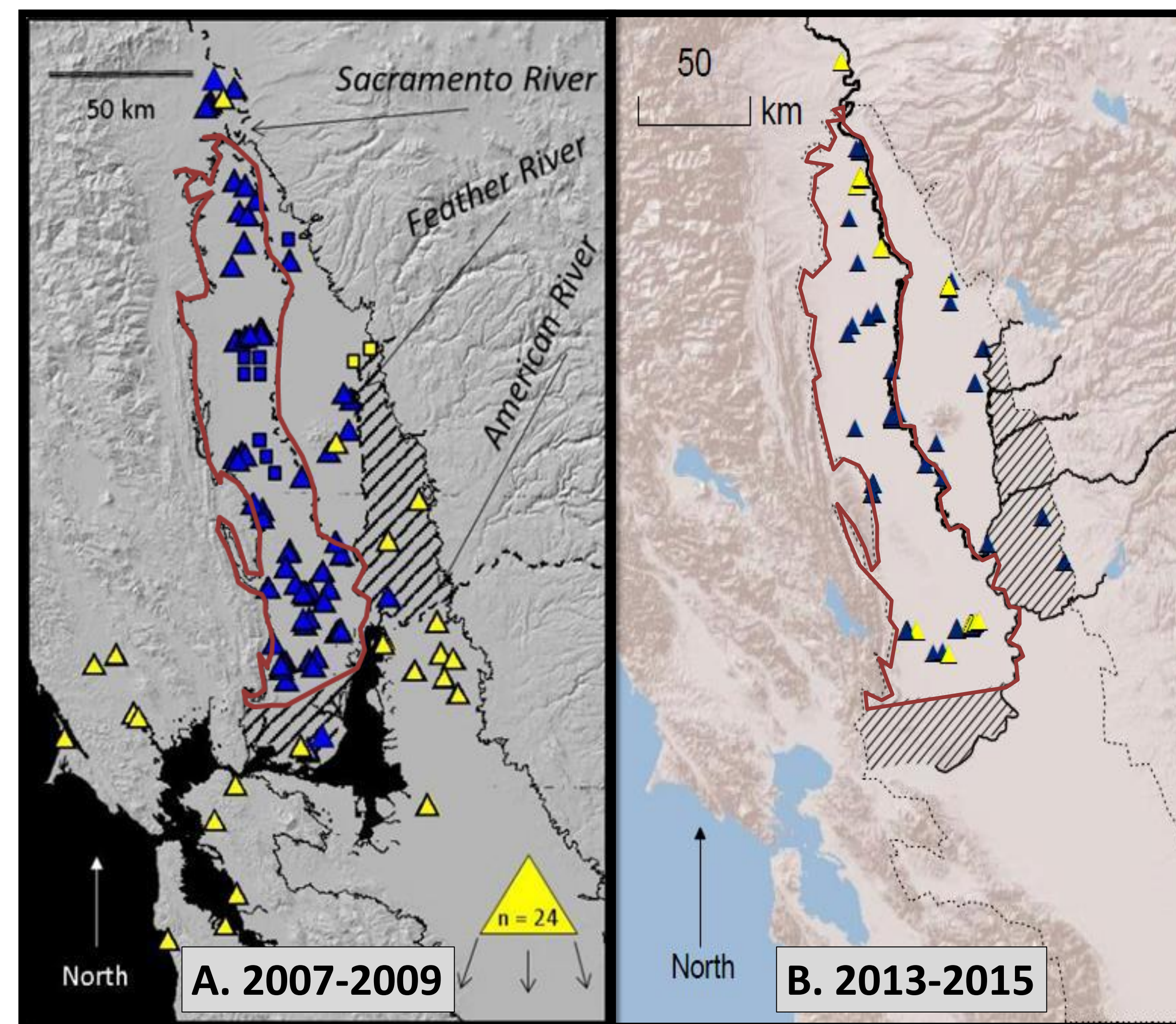
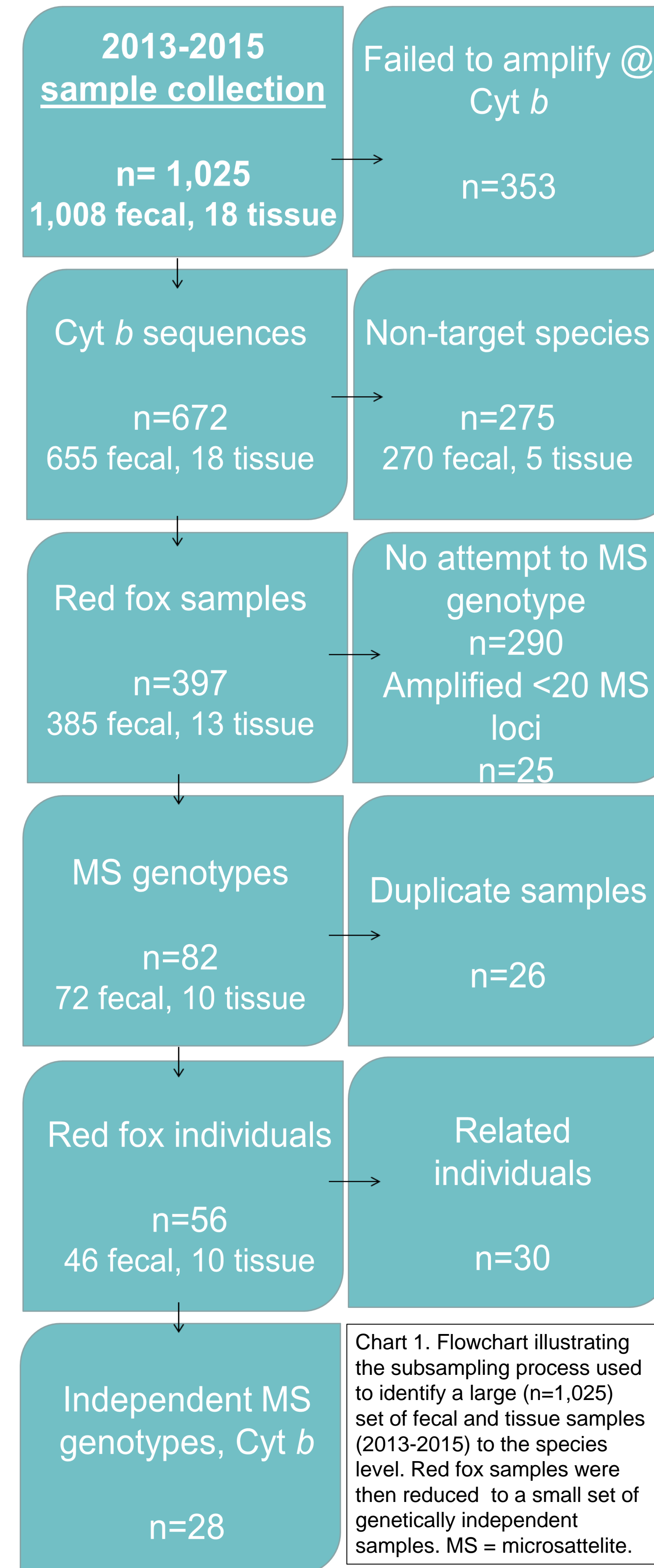


Figure 1. Distribution of native haplotypes (blue triangles/squares) and nonnative haplotypes (yellow triangles/squares) in (A) 2007-2009⁴ [Note: squares represent samples from museum specimens] and (B) 2013-2015. In both panels, the 2 cross-hatched zones in the east/southeast and southwest Sacramento Valley were previously identified as hybrid zones⁴. The red line in both panels was added to illustrate the core of the native population as identified in Sacks et al. 2011 and to emphasize the encroachment by nonnative haplotypes. In 2007-2009, 0% of haplotypes sampled in the core area were nonnative vs. 31% during 2013-2015 (based upon detections at "unique sites" across the SV).

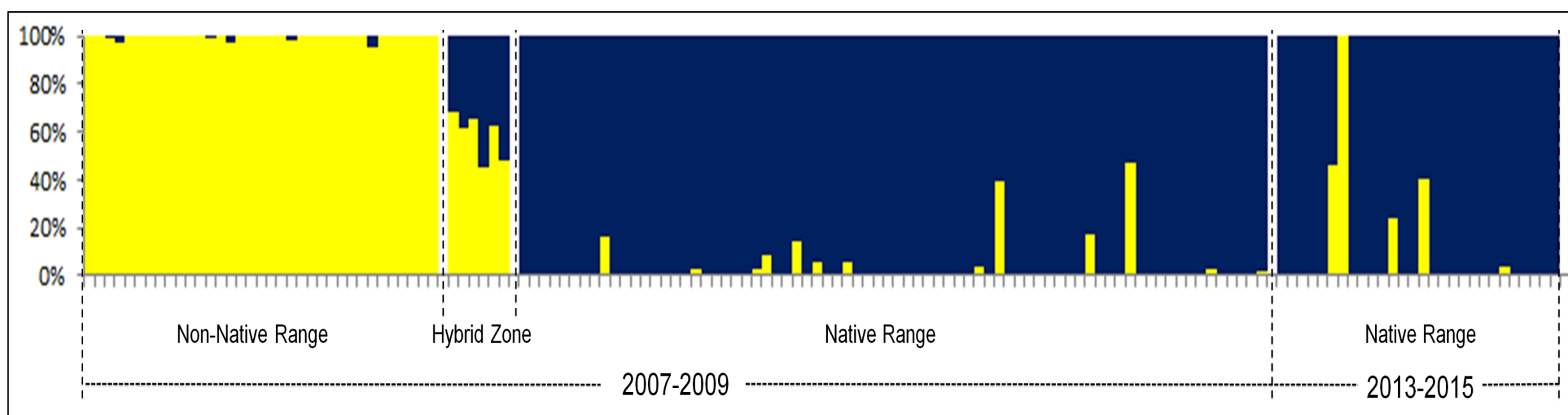
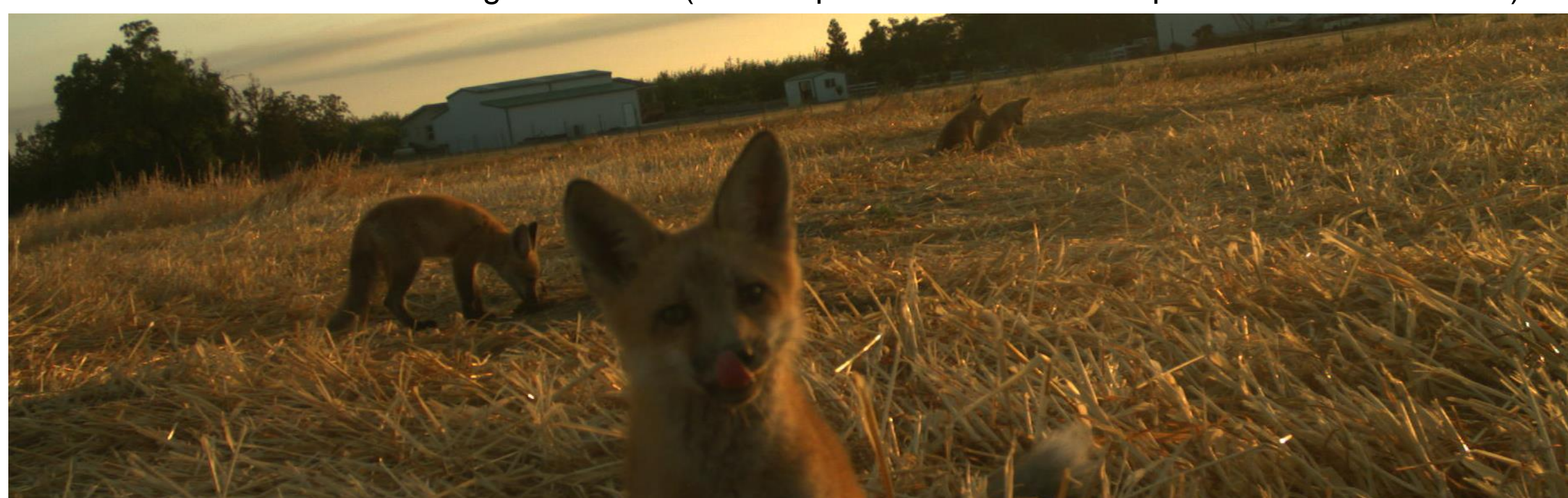


Figure 3. Distribution of estimated proportions of ancestry (q) according to admixture analysis at $K=2$ with prior information using nuclear DNA. Analyses were conducted with multilocus genotypes composed of 33 microsatellite loci in program *Structure* based on 150,000 post-burn-in Markov Chain Monte Carlo cycles. Nonnative ancestry shown in yellow. Native ancestry shown in blue.

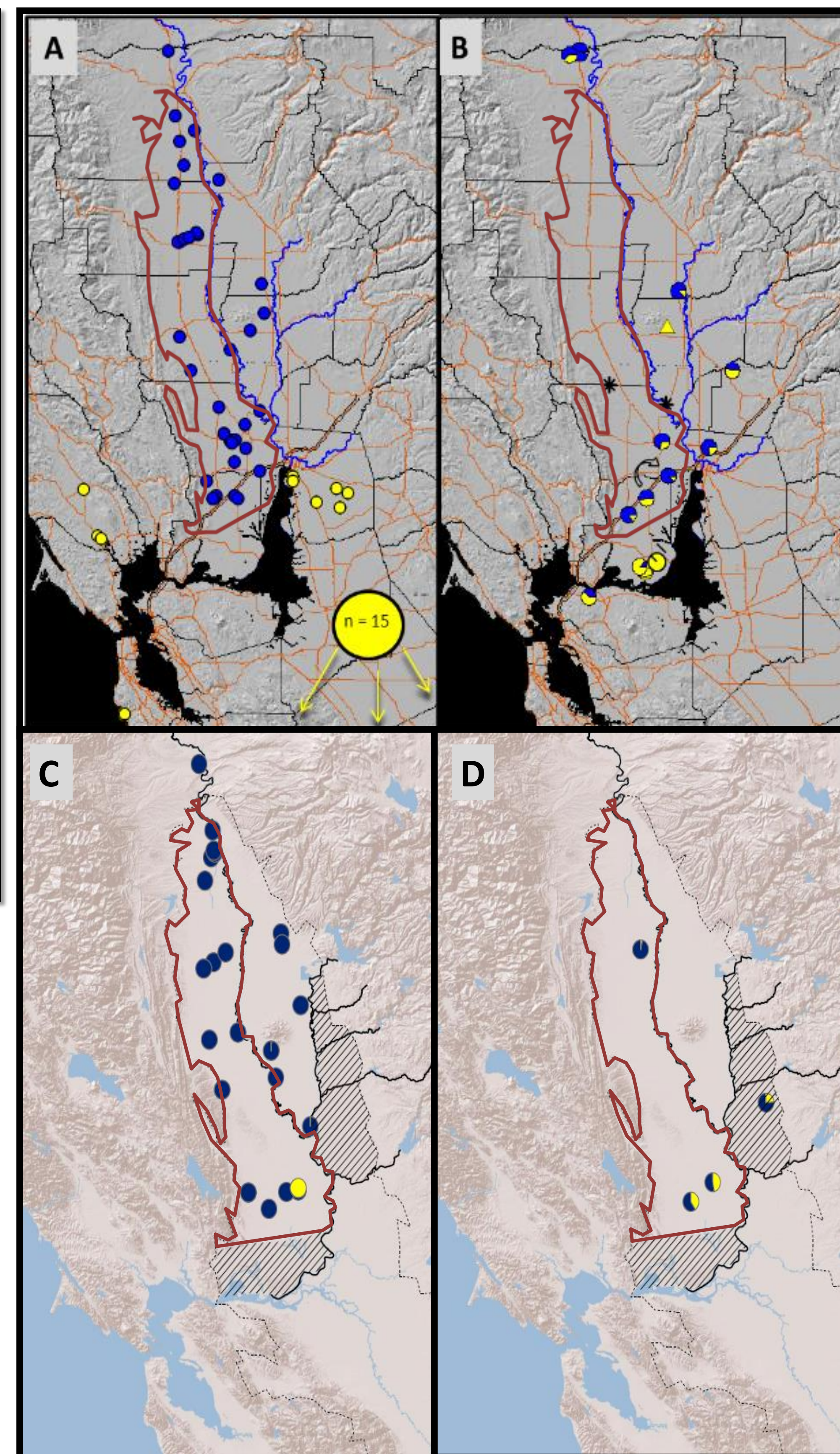


Figure 2. Locations of red fox samples with ancestry assigned fully or partially to native and nonnative populations. (A) 2007-2009 samples assigned to their home population as pure ($q>0.97$ native, $q<0.03$ nonnative) Sacramento Valley red foxes (blue circles) and non native foxes (yellow circles); Large yellow circle reflects 15 samples from further South⁴. (B) 2007-2009 samples identified as hybrids, with pie charts indicating estimated proportions of native (blue) and nonnative (yellow) ancestry. Note: No fully nonnative individuals were detected in the native range. (C) 2013-2015 samples assigned to their home population as pure ($q>0.97$, $q<0.03$) native Sacramento Valley red foxes (blue circles) and nonnative ($q<0.03$, $q>0.97$) foxes (yellow circles). (D) 2013-2015 samples identified as hybrids, with pie charts indicating estimated proportions of native (blue) and nonnative (yellow) ancestry. Note the novel presence of a fully nonnative immigrant (C) and her hybrid offspring (D) within the Southern core area. Both individuals also had a nonnative haplotype.

Preliminary Results

- 154 of 397 red fox samples had nonnative haplotypes
- The core range in 2013-2015 contained 31% nonnative haplotypes compared to 0% nonnative haplotypes from 2007-2009 (Fig. 1)
- 56 of 82 samples identified unique individuals via nuclear DNA (Chart 1)
- 28 genetically and/or geographically independent individuals yielded:
 - 23 "pure" native ($q>0.97$ native, $q<0.03$ nonnative [Fig. 2C]) individuals
 - 4 hybrid ($q<0.097$, $q>0.03$ [Fig. 2D]) individuals
 - 1 nonnative immigrant ($q<0.03$, $q>0.97$ [Fig. 2C]) individual.

Preliminary Conclusions and Future Research Needs

- Nonnative mitochondrial haplotypes increased in both Southern and Northern ends of the core native range.
- Nuclear (microsatellite) genetic introgression was little changed since previous survey except that a pure nonnative individual was sampled for the first time in the core nonnative range.
- Immigrant nonnative in the core area is a novel event and suggests future increase in hybridization and further nonnative encroachment and genetic introgression
- Future research needs:
 - Monitor gene flow between native and nonnative foxes
 - Determine consequences of hybridization to fitness
 - Investigate fine-scale habitat use of native vs. nonnative red foxes
 - Develop management strategies that will encourage native population growth over nonnative expansion/hybridization

References

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