



Preliminary Comparison of Genetic Diversity in the Endangered San Joaquin Kit Fox (*Vulpes macrotis mutica*) Before and After a Mange Outbreak

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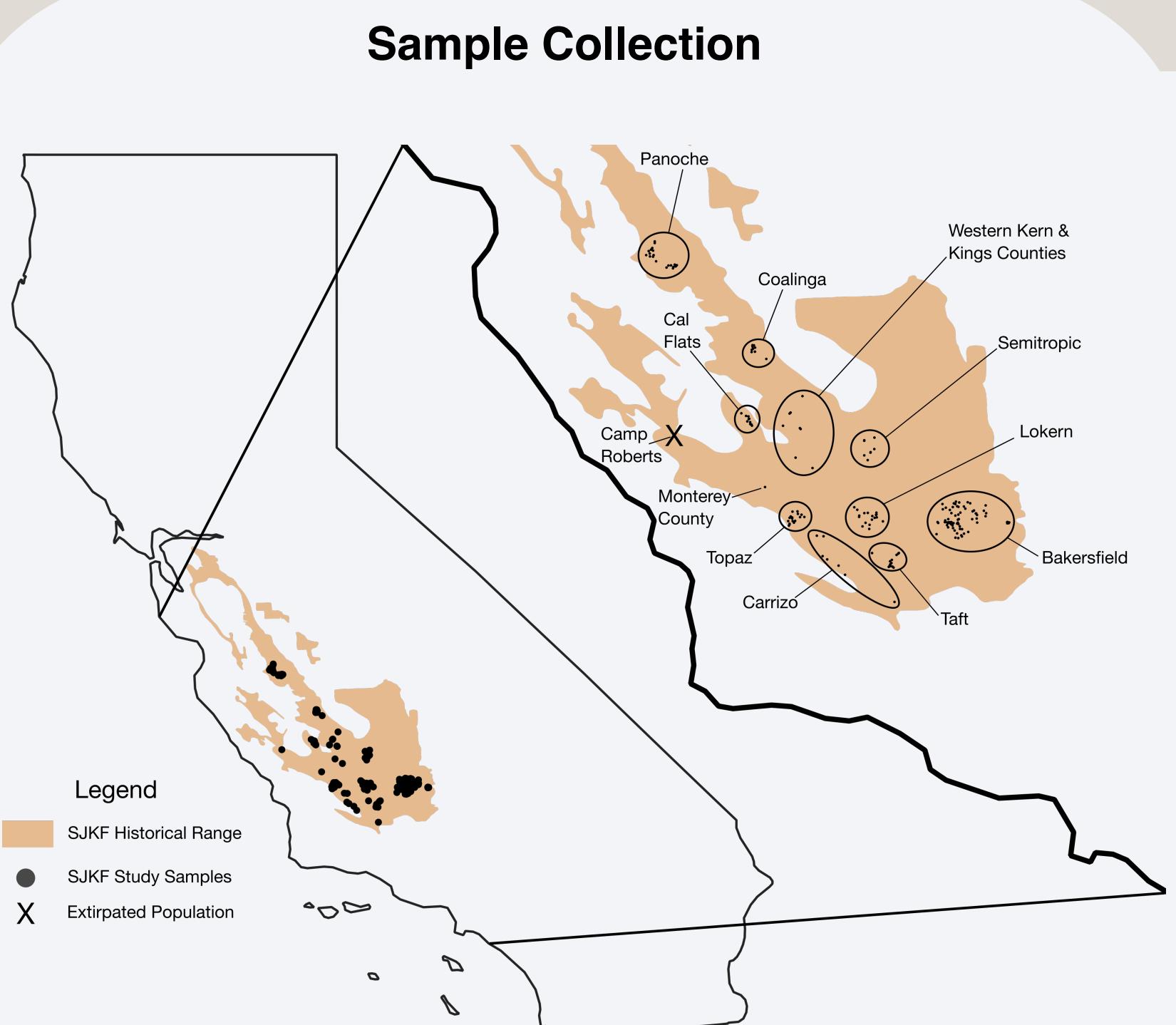
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Introduction

The San Joaquin kit fox (SJJKF; *Vulpes macrotis mutica*) is a federally endangered species.¹ Today, fewer than 5,000 individuals are thought to occur across their range, and the contemporary metapopulation is distributed across three core regions and several smaller satellite populations.^{2,3} While anthropogenic habitat loss is believed to be the fundamental cause of the historical decline of the SJJKF, localized disease outbreaks today proximately threaten remaining populations both demographically and genetically^{4,5}. Two known satellite populations (Camp Roberts, Fort Hunter Liggett) became extirpated, presumably as a result of inbreeding depression or disease.⁶ Additionally, in the last decade, sarcoptic mange has caused significant demographic declines in a formerly abundant urban SJJKF population in Bakersfield.⁵ There has been minimal evidence of mange occurring in exurban kit fox populations outside of the Bakersfield region (small scale outbreak identified in neighboring Taft in 2019), which may indicate that dispersal between urban and exurban regions is low.⁷ We aimed to assess whether there is population structure between kit foxes within Bakersfield and those found in other portions of their range. We then compared differences in genetic diversity and internal relatedness (a proxy metric for quantifying inbreeding) over both geographic space and across time to see whether the mange outbreaks have had a significant impact on genetic diversity and inbreeding. We used reduced-representation genomic sequencing approach to compare population structure, landscape connectivity, genetic diversity, and internal relatedness of historical SJJKF individuals sampled prior to the mange outbreak ($n = 89$) as well as of SJJKF individuals sampled from the contemporary population ($n = 109$), focusing on both urban ($n = 82$) and exurban ($n = 116$) regions.

Methods



We obtained 198 kit fox tissue samples that were collected across California from 1985–2022. These included samples from the urban population in Bakersfield ($n = 82$) as well as from the exurban regions ($n = 116$).



Sample Collection

- DNA extraction using Qiagen DNEasy Blood and Tissue Kit
- Genotyping-by-Sequencing⁸
- We retained 157 SJJKF samples that were sequenced at ~33x coverage across 11,155 nuclear loci

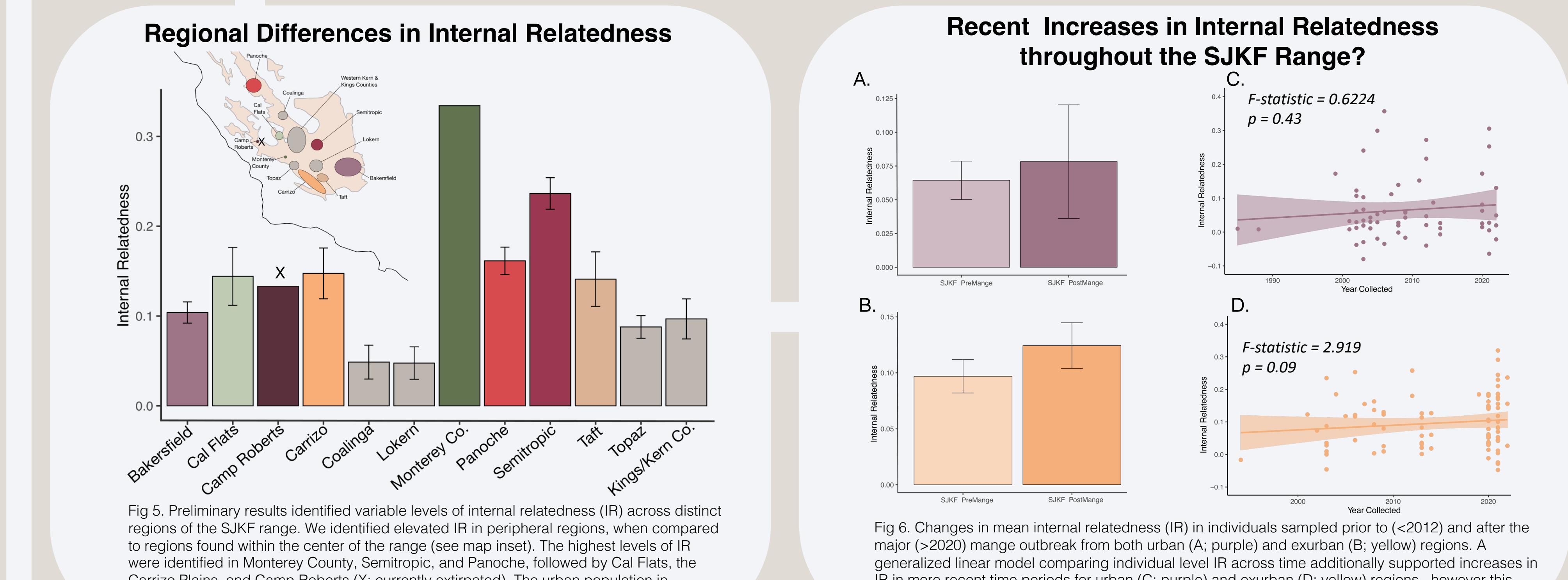
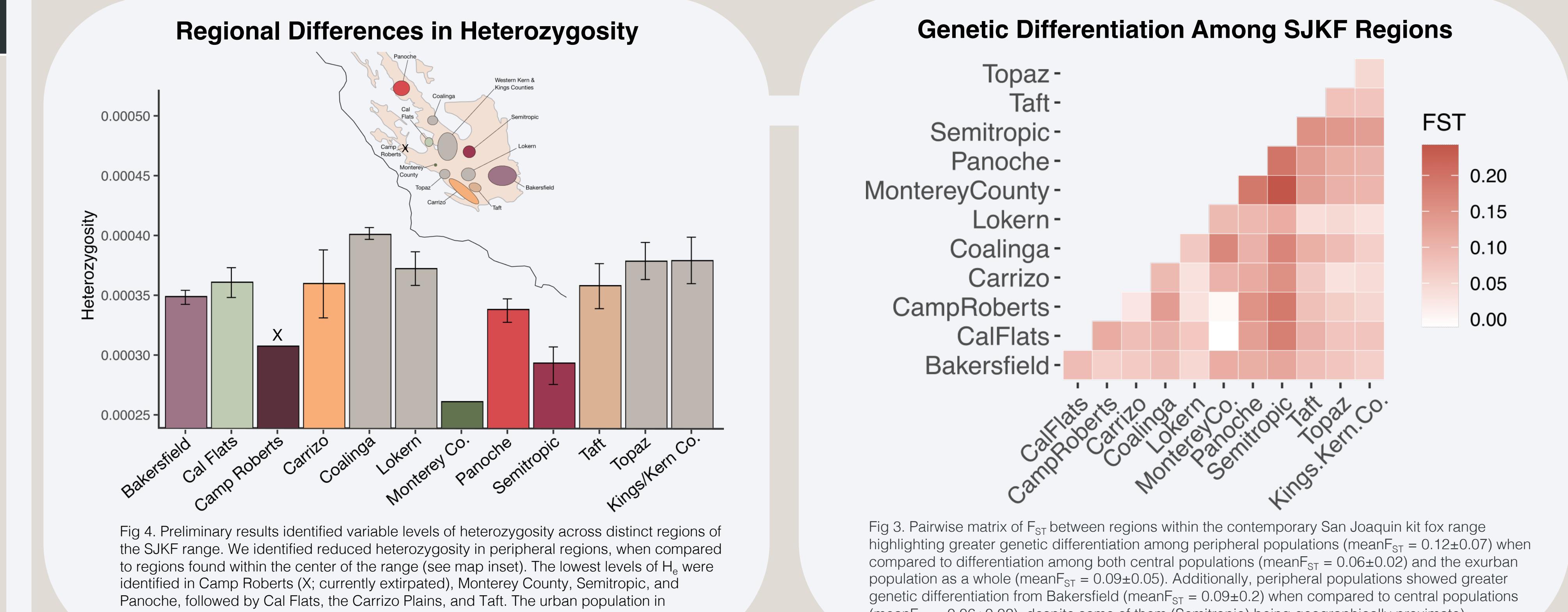
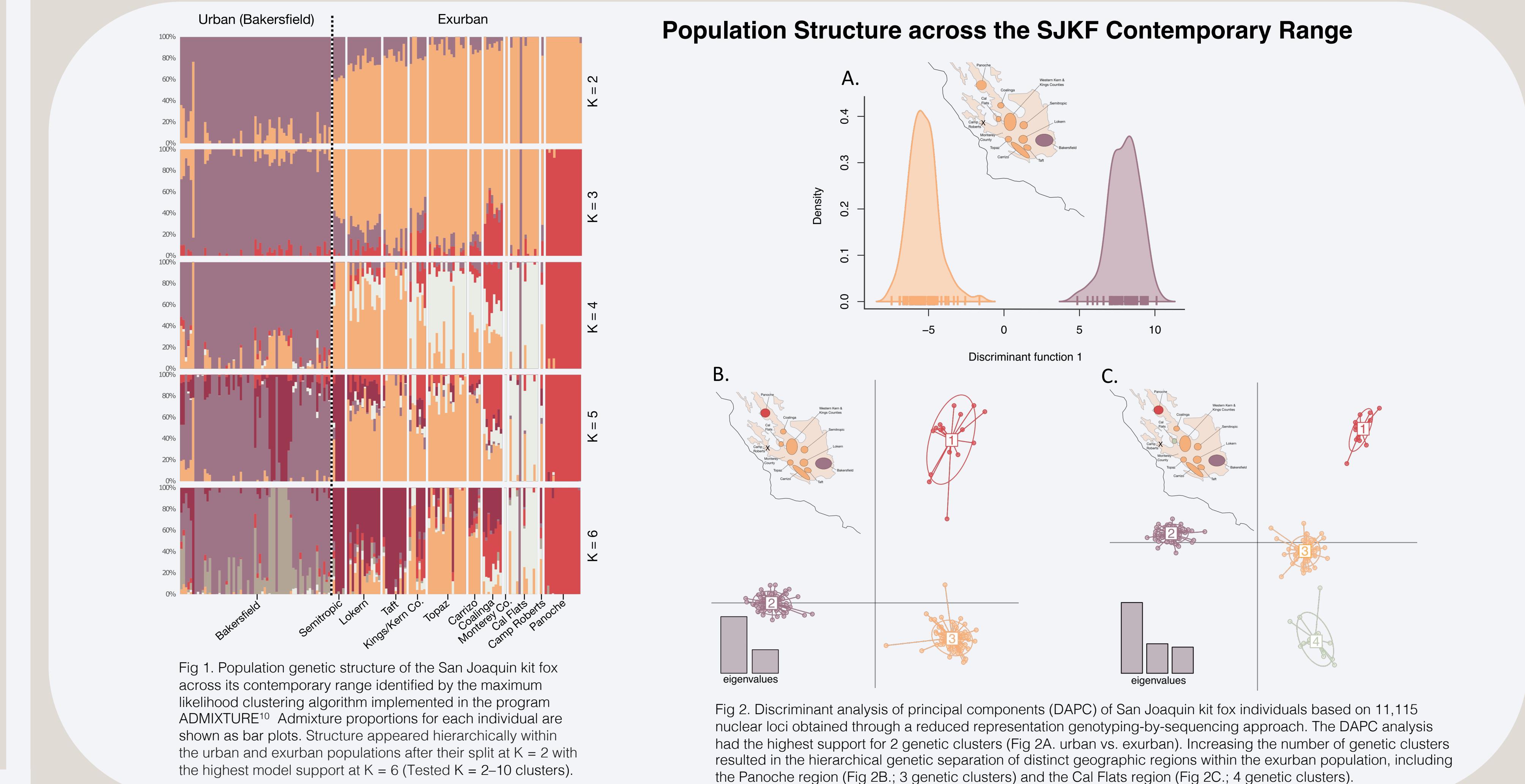
Population Structure

We conducted a discriminant analysis of principal components (DAPC) in adegenet⁹ as well as maximum likelihood population assignment ($K = 2–10$) in the program ADMIXTURE.¹⁰ Additionally, we compared the genetic dissimilarity across the SJJKF range using a pairwise F_{ST} analysis in hierfststat.¹¹

Characterizing Heterozygosity and Internal Inbreeding

To calculate regional differences in H_e we calculated individual H_e from the site frequency spectrum [easySFS]¹² using genotype likelihoods [angsd]¹³. We calculated internal relatedness (IR), which serves as a proxy for inbreeding, using the program GENHET¹⁴.

Preliminary Results



Conclusions and Next Steps

- Preliminary analyses indicate minimal gene flow between Bakersfield and adjacent exurban populations. While reduced movement between disjunct regions of the SJJKF range may effectively limit the transmission of mange from the urban population into exurban regions, it may also result in increased inbreeding and population differentiation which can have negative impacts on the long-term viability of the SJJKF population.
- H_e is reduced and internal relatedness (IR) is elevated in peripheral exurban populations, which may indicate these geographic regions are more isolated, and therefore more susceptible to genetic drift and inbreeding. Whole Genome Sequencing will allow us to quantify levels of inbreeding load and deleterious variation.
- We detected an increase in IR over time across both the urban and exurban populations, but these results were only significant in the exurban group. Additional sampling of both historical and contemporary kit foxes could elucidate whether there is in fact a significant increase in inbreeding in the modern SJJKF population.
- We plan to conduct isolation by environment analyses to determine whether observed population structure in the SJJKF is a result of genetic drift or whether local adaptation contributes to differentiation.



- We will also compare genomic diversity of SJJKF to related populations of Desert kit fox (*Vulpes macrotis* ssp.).

References

QR CODE COMING SOON...

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