

Assessment of Golden-cheeked Warbler Genetic Recovery

Giri Athrey

Texas A&M University



TEXAS A&M
UNIVERSITY



Paul Leberg



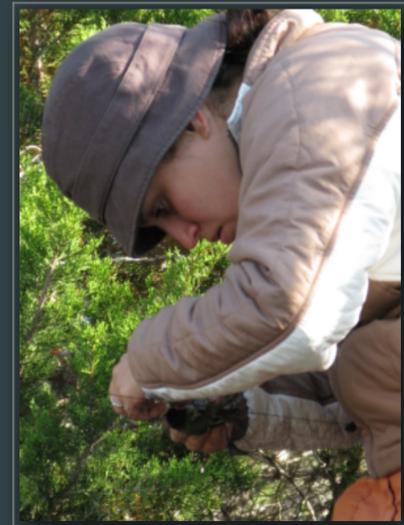
Rick Lance



Kelly Barr



Denise Lindsay



Joy Hernandez



Christina Goates

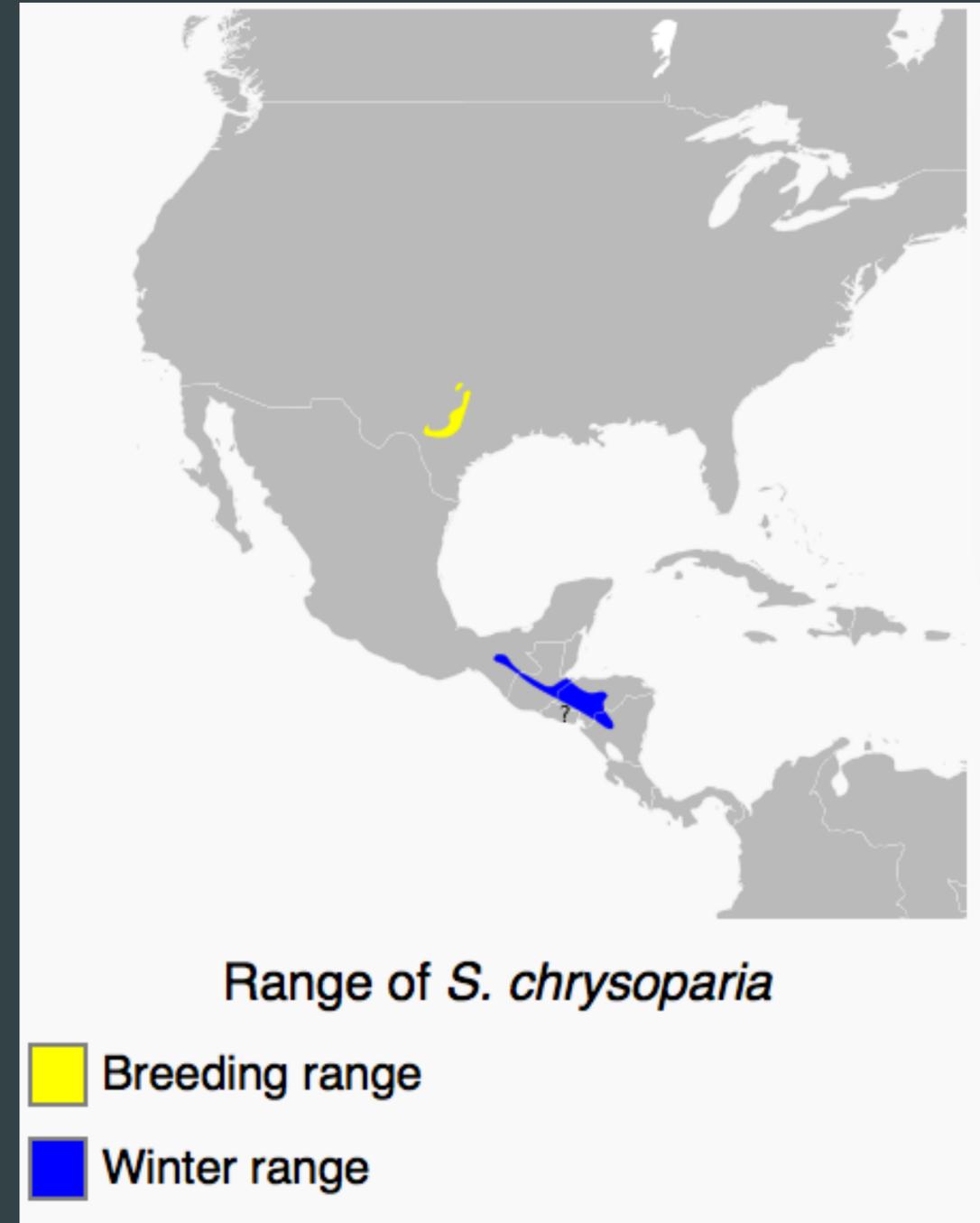


Lisa O'Donnell



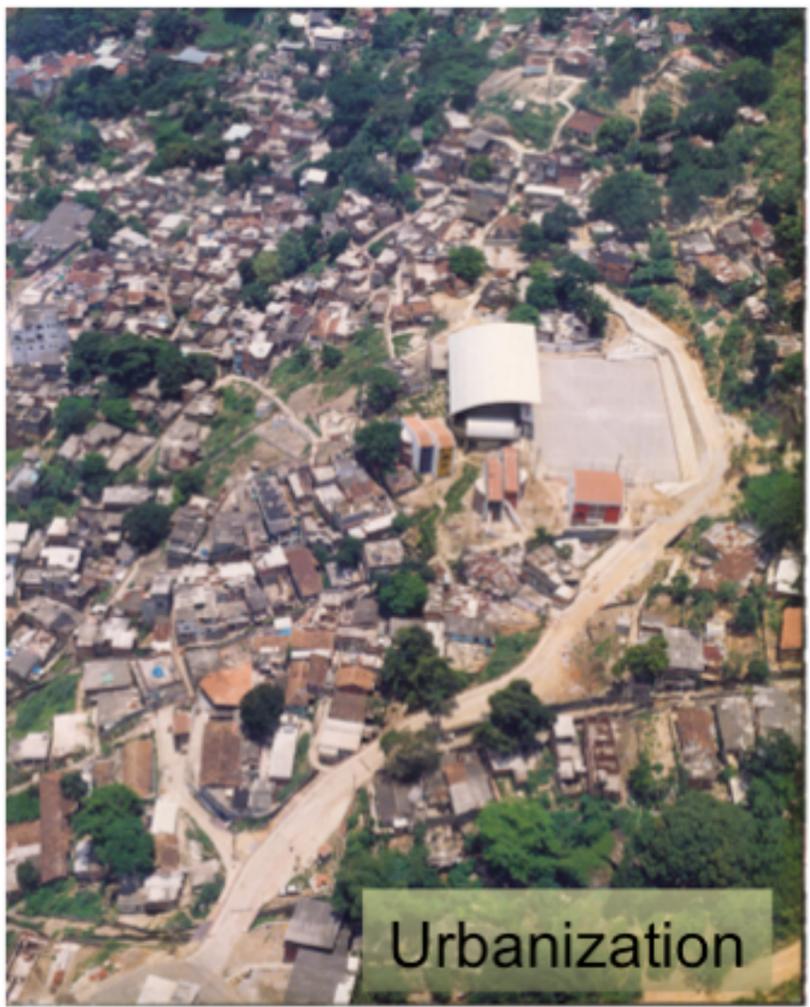
Laurel Moulton

Setophaga chrysoparia
The Golden-cheeked Warbler



The old growth Ashe-Juniper/Oak forests necessary for GCWA nesting success





Urbanization



Parasitism



Agriculture

Images: Google

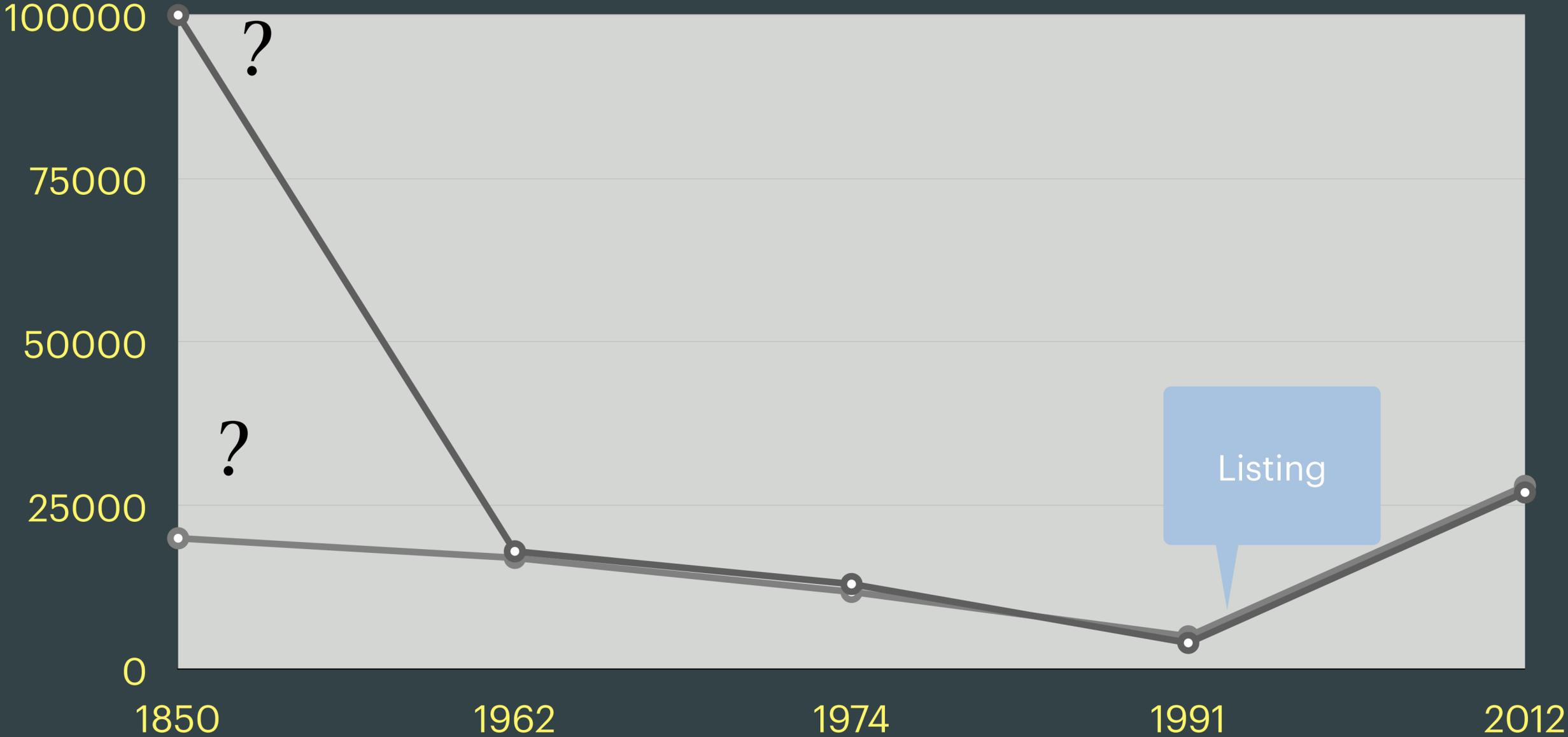


Ranching

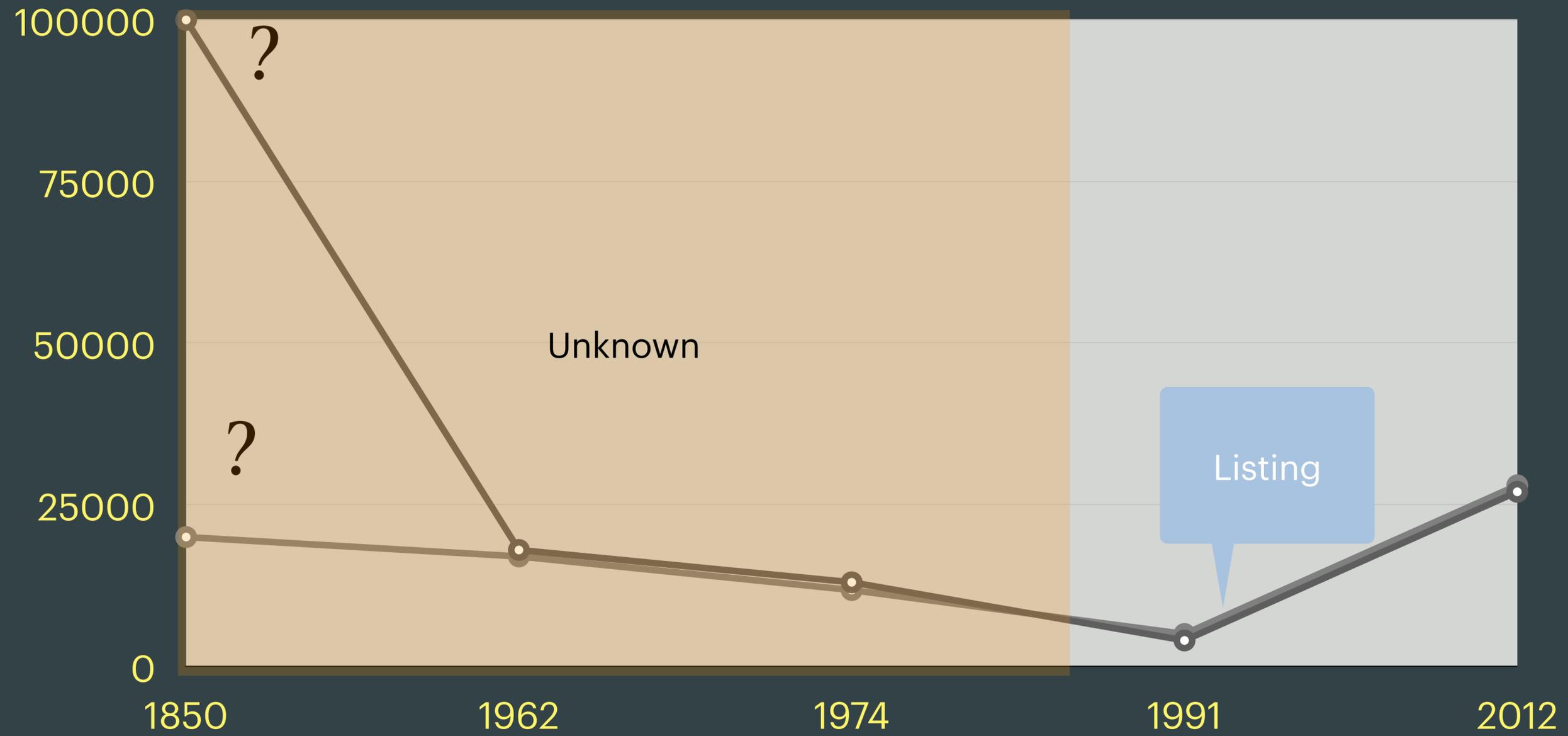


Fire Suppression

Population estimates of GCWA



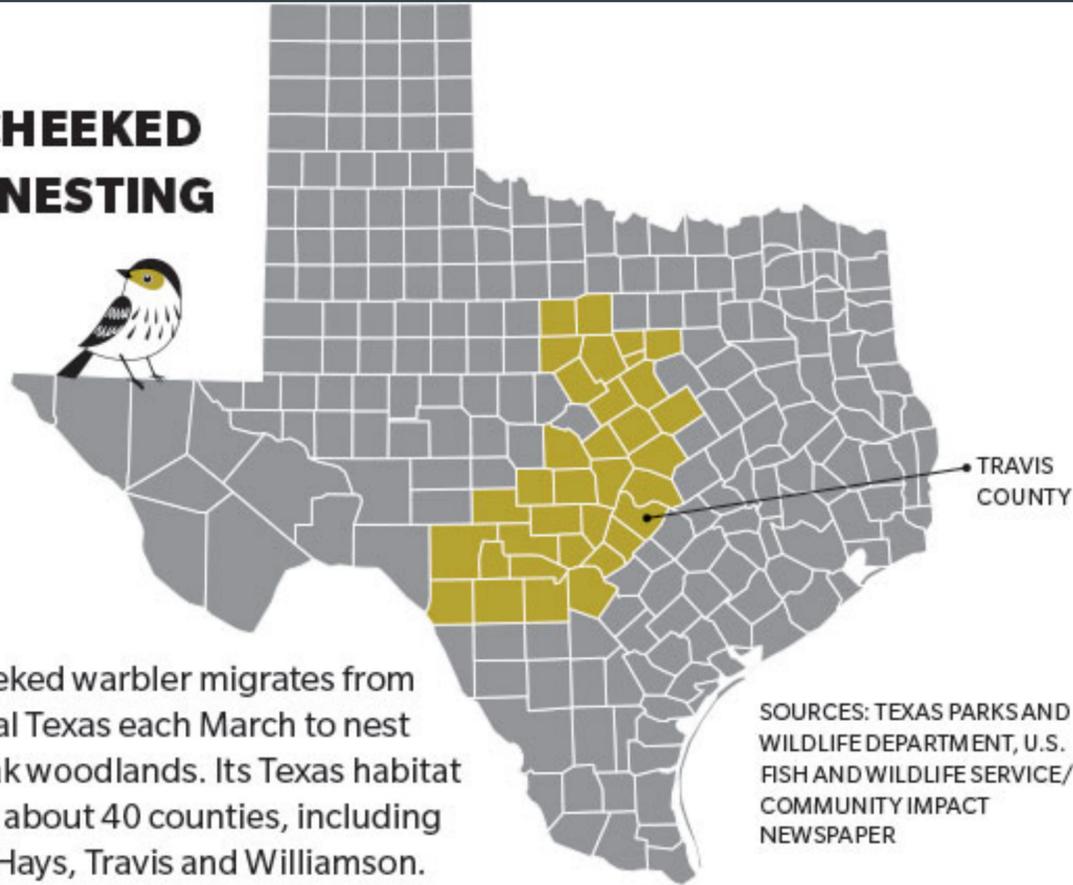
Population estimates of GCWA



Management and Recovery Status

Management and Recovery Status

GOLDEN-CHEEKED WARBLER NESTING RANGE



The golden-cheeked warbler migrates from Mexico to Central Texas each March to nest in juniper and oak woodlands. Its Texas habitat stretches across about 40 counties, including Burnet, Blanco, Hays, Travis and Williamson.

SOURCES: TEXAS PARKS AND WILDLIFE DEPARTMENT, U.S. FISH AND WILDLIFE SERVICE/COMMUNITY IMPACT NEWSPAPER

GOLDEN-CHEEKED WARBLER RECOVERY

POPULATION

1990	2016
13,800	263,339

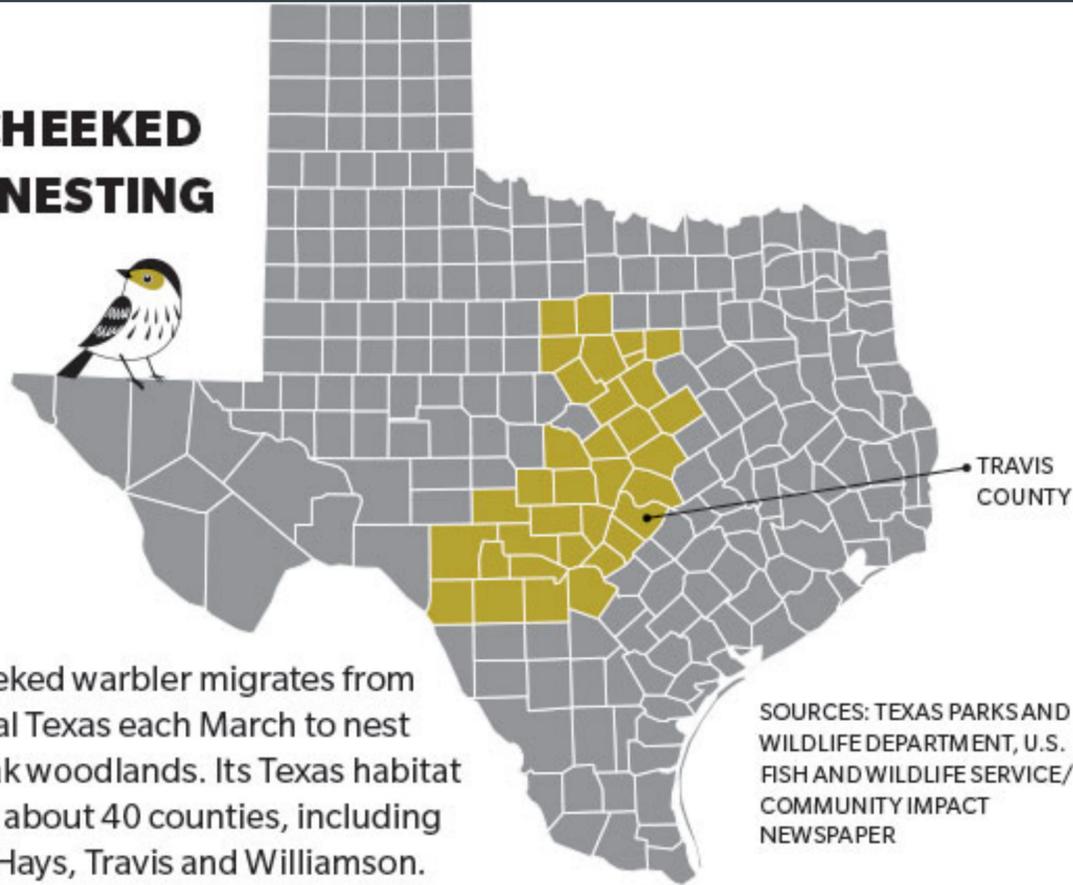
HABITAT

1990	2016
1,270 sq. miles	6,480 sq. miles

SOURCE: TEXAS PUBLIC POLICY FOUNDATION'S CENTER FOR THE AMERICAN FUTURE/COMMUNITY IMPACT NEWSPAPER

Management and Recovery Status

GOLDEN-CHEEKED WARBLER NESTING RANGE



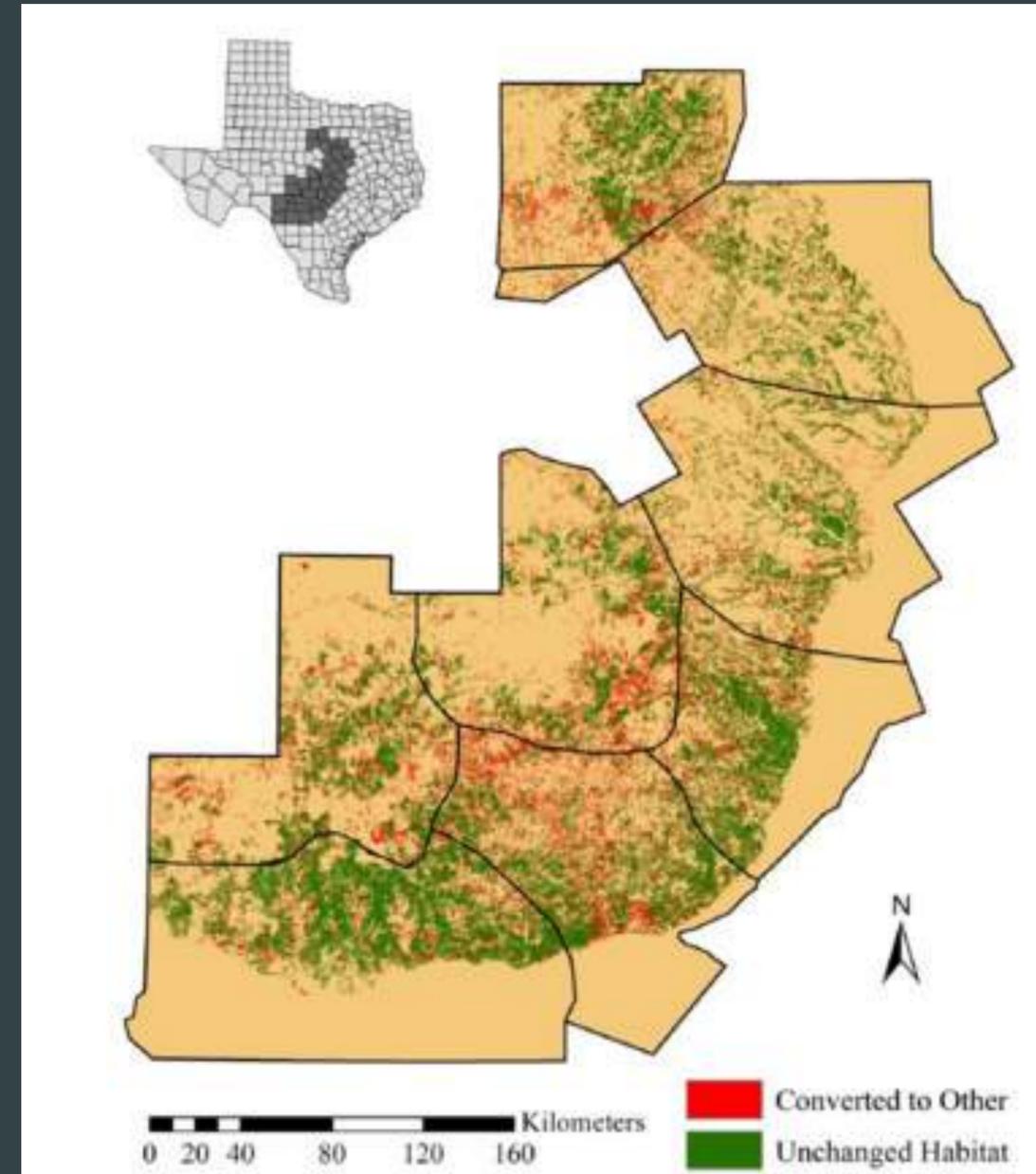
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GOLDEN-CHEEKED WARBLER RECOVERY

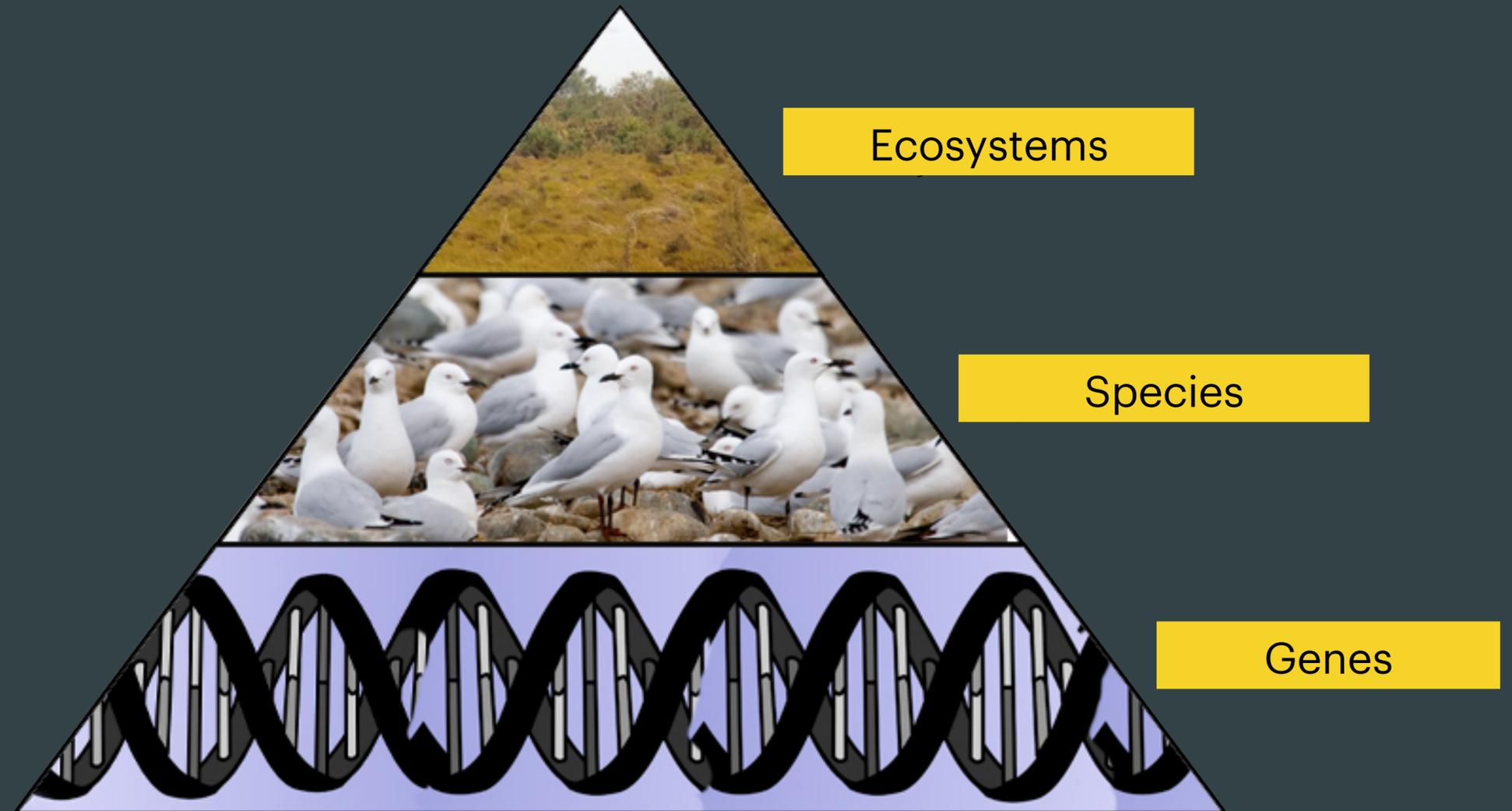
POPULATION		HABITAT	
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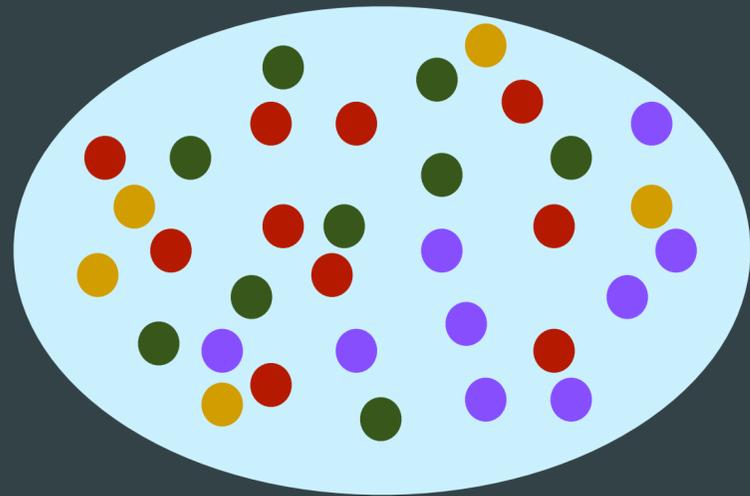
Estimated ~30% reduction in warbler breeding habitat between 2001-2011.

Genetic diversity is an important dimension of biodiversity



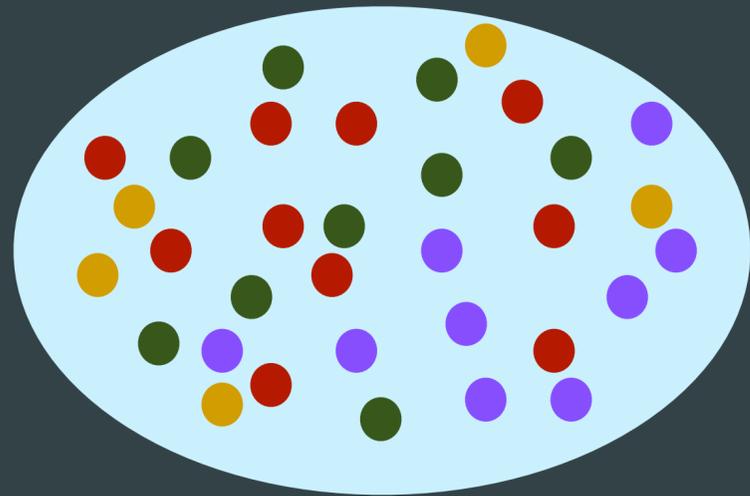
Assessment of Genetic Diversity and Genetic Structure are key elements of the species action plan

Genetic diversity and differentiation

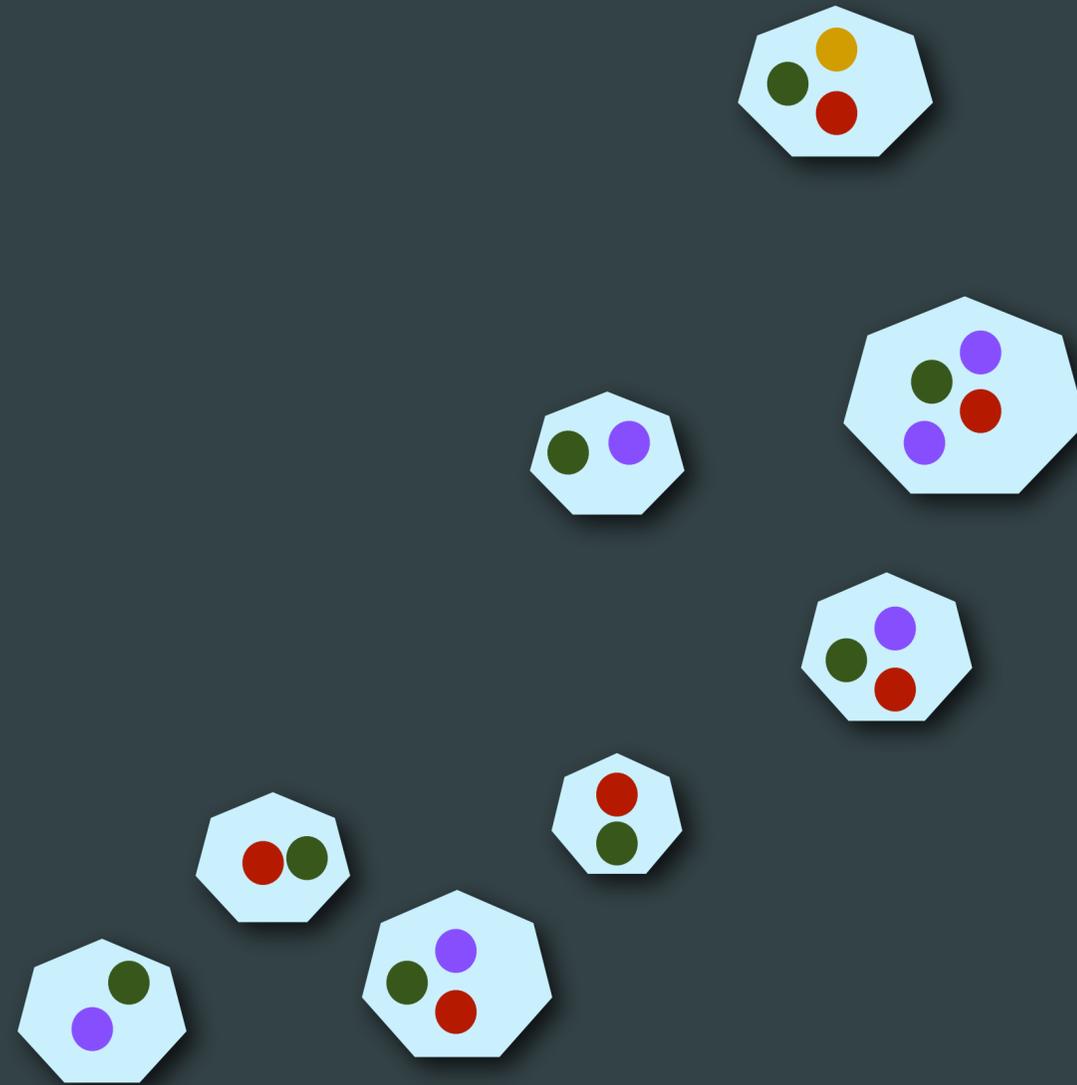


Genetic Diversity

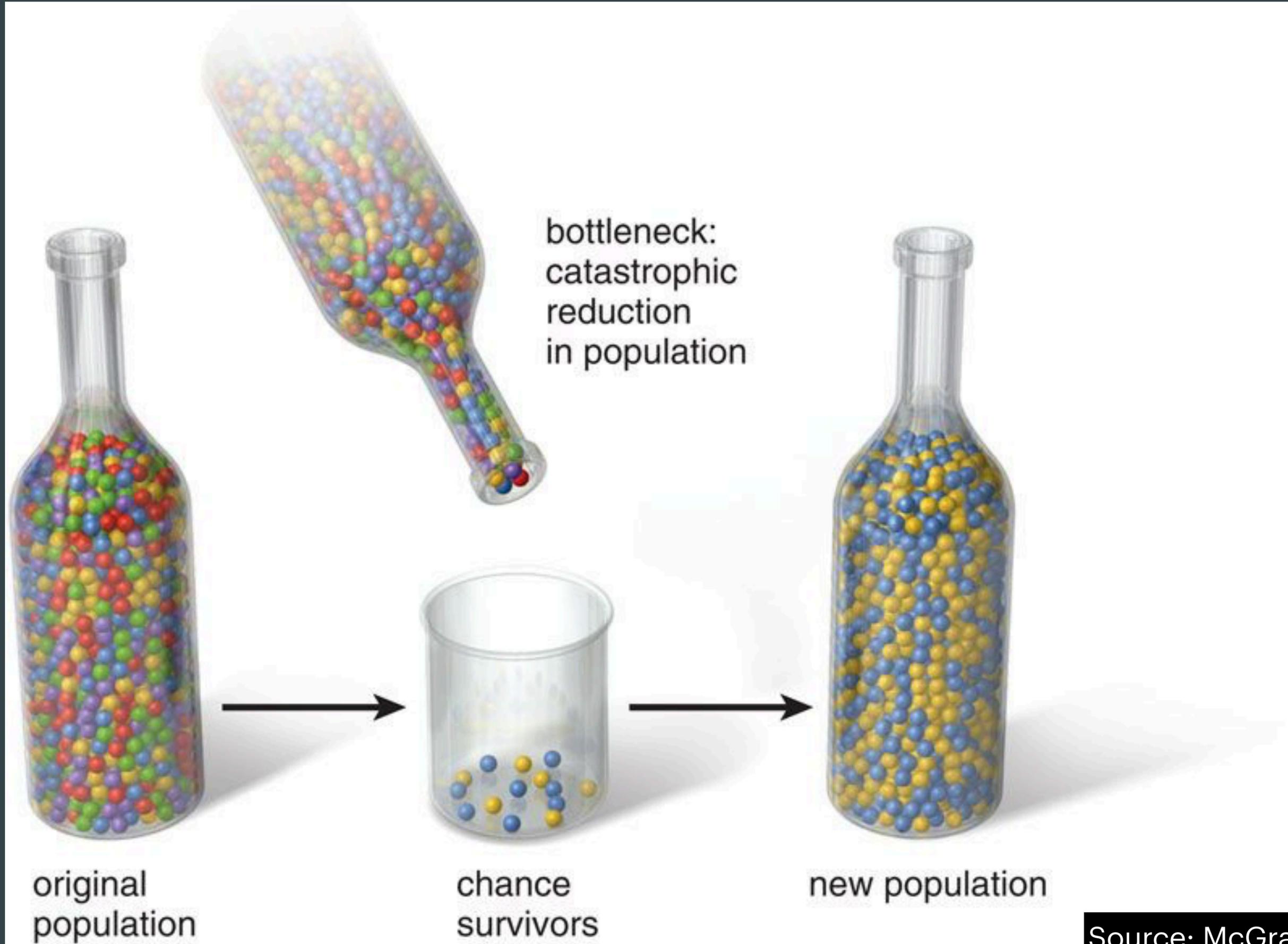
Genetic diversity and differentiation



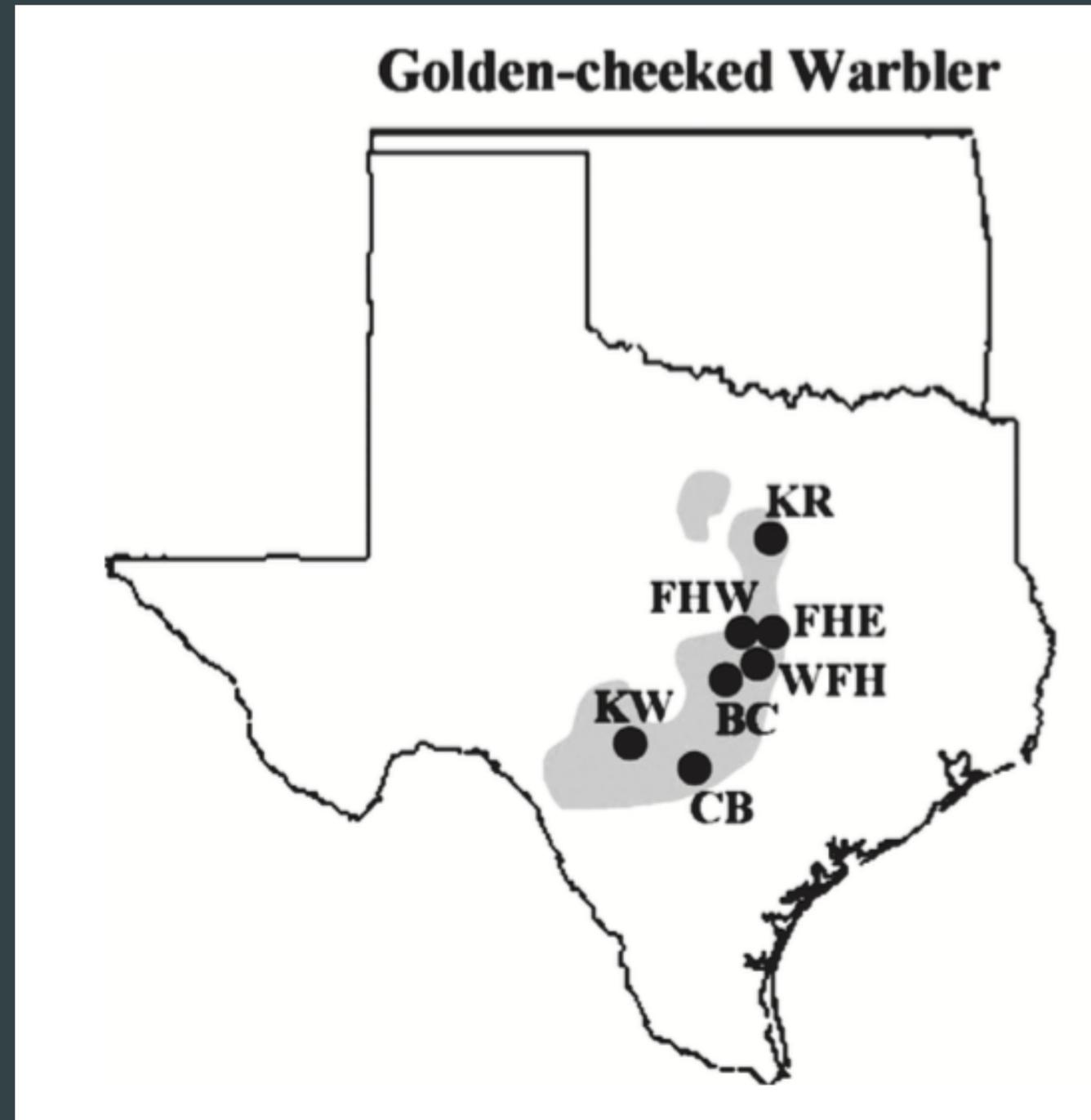
Genetic Diversity



Genetic Differentiation



The first genetic studies



Genetic diversity



$A_R=7.69, H=0.75$

Genetic diversity



$A_R=7.69, H=0.75$

Cardellina pusilla



$A_R=8.36, H=0.75$

Setophaga cerulea



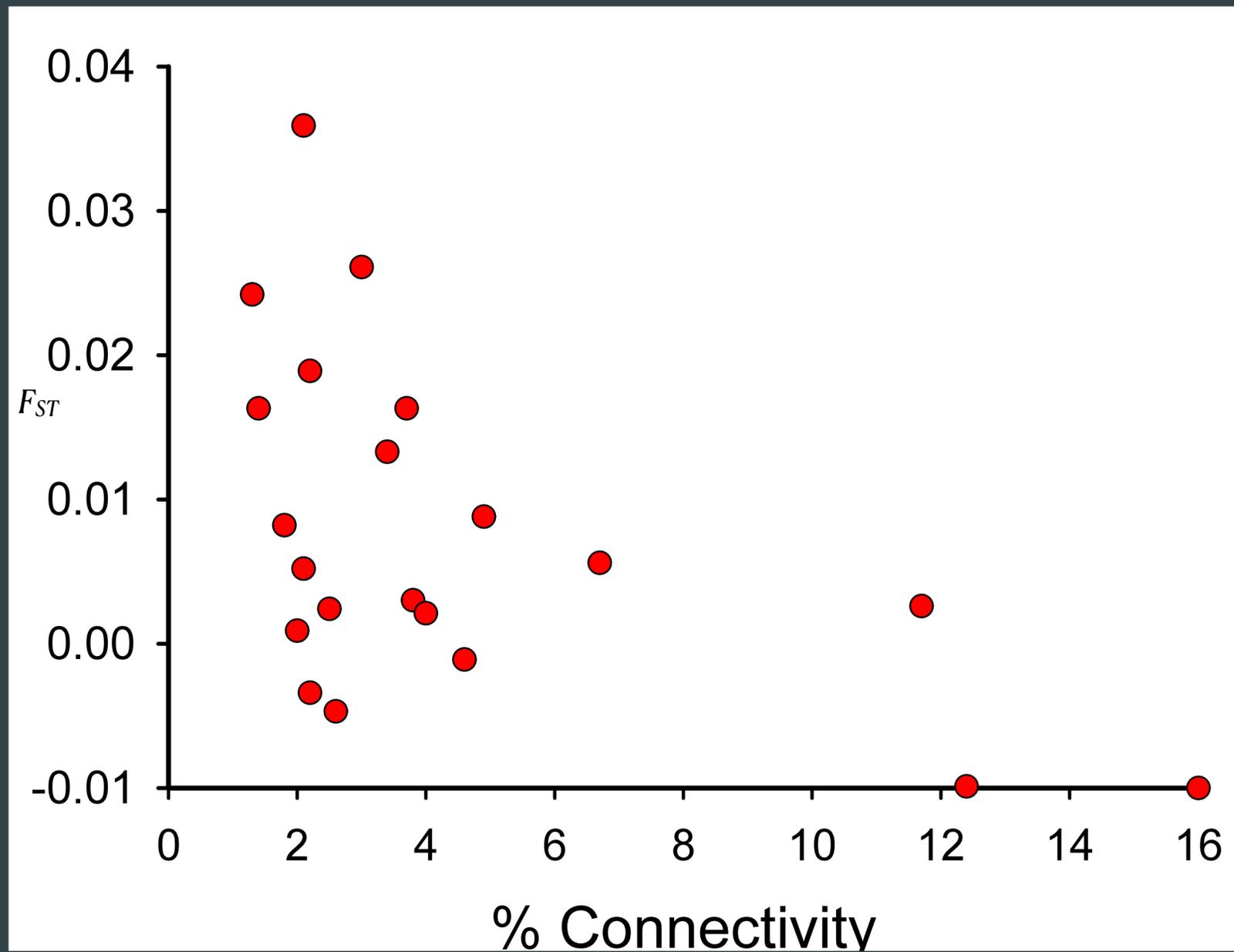
$A_R=10.4, H=0.77$

Setophaga petechia

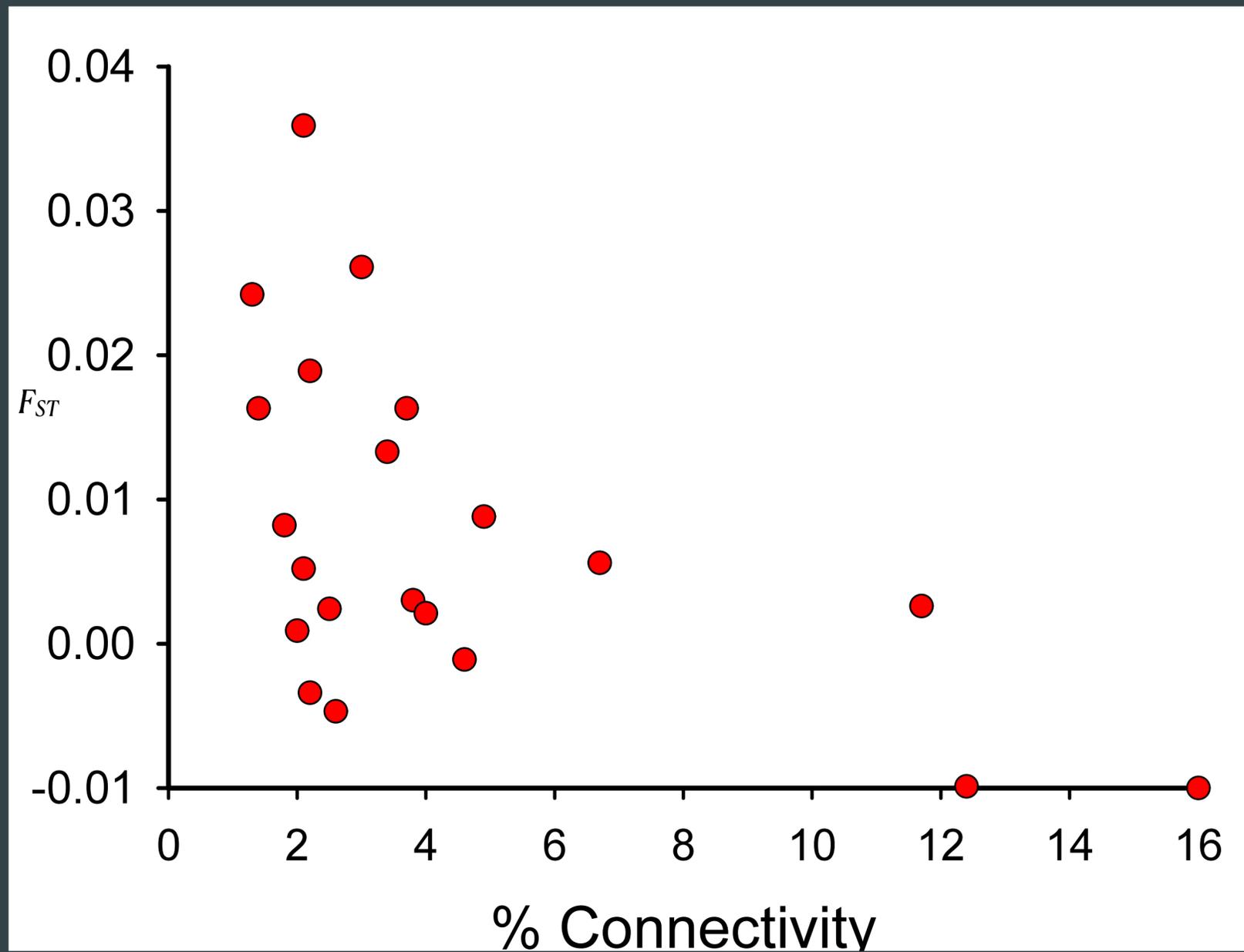


$A_R=11.2, H=0.69$

The first studies



The first studies



No strong correlation
between habitat
connectivity and genetic
differentiation

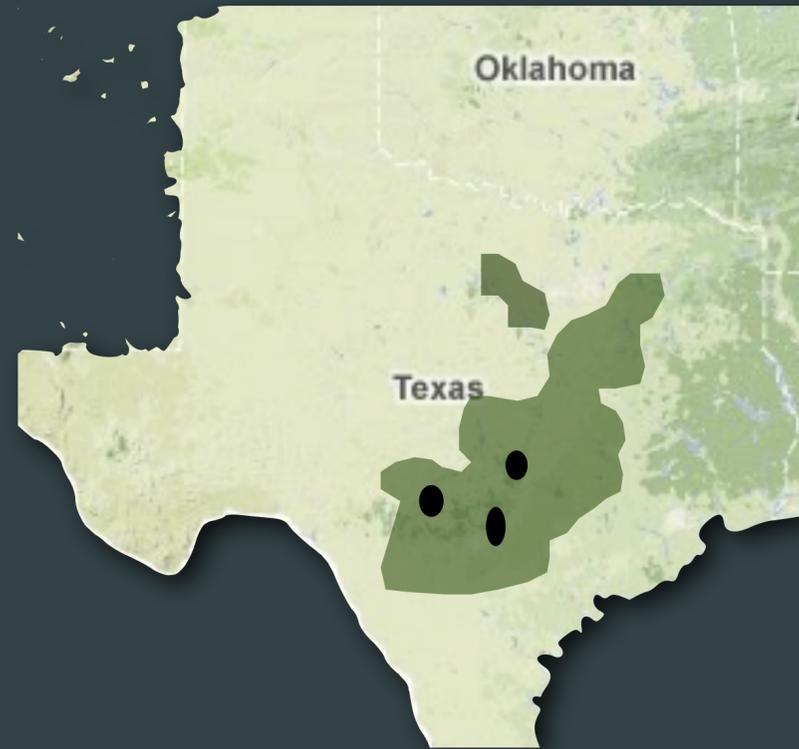
Are contemporary population sizes the
historical norm?

Are contemporary population sizes the
historical norm?

How did habitat changes and population
size changes impact genetic diversity?

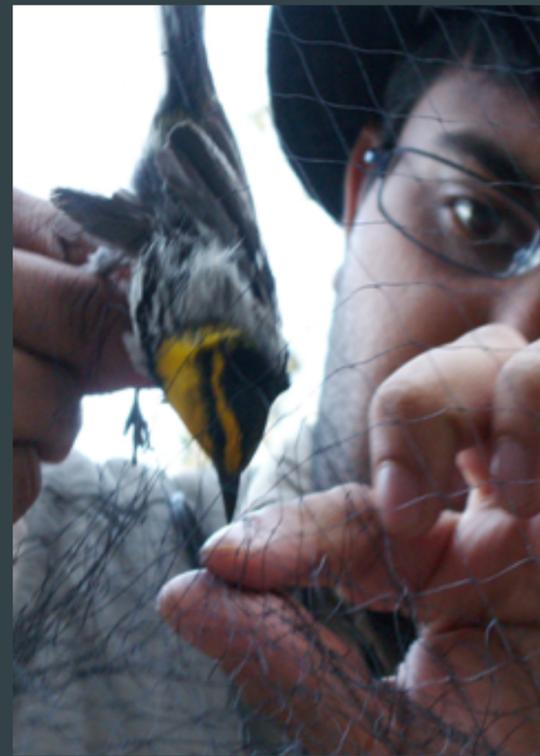
**Historical context needed to answer
this question**

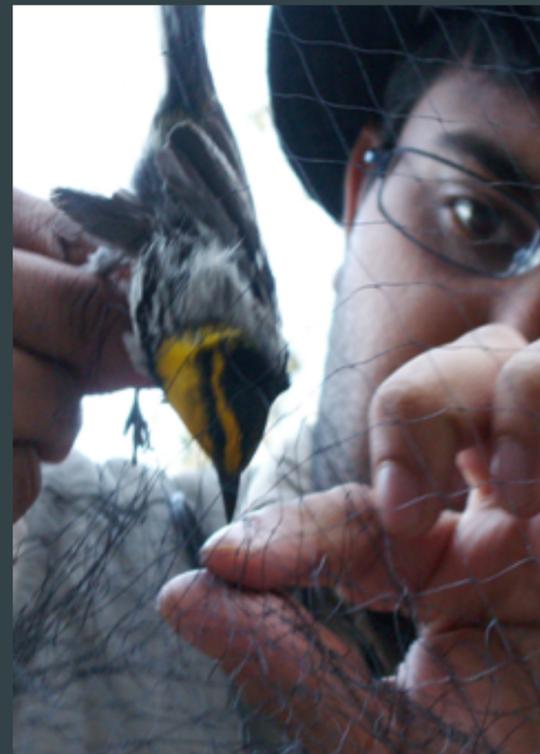


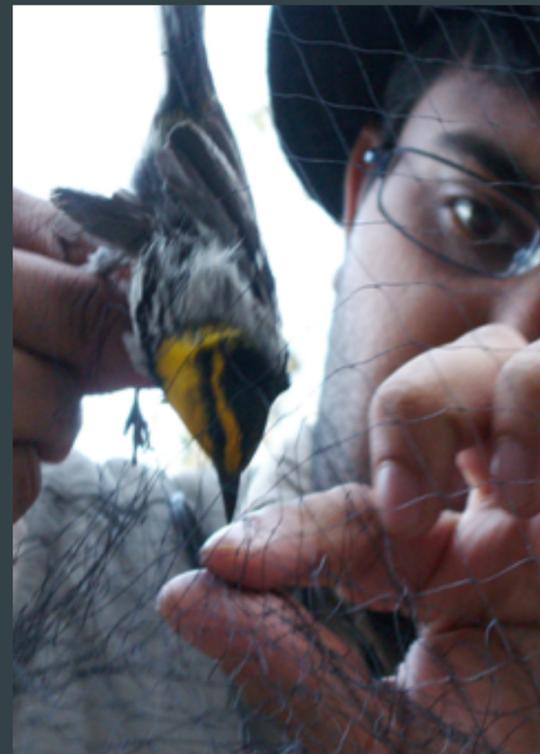


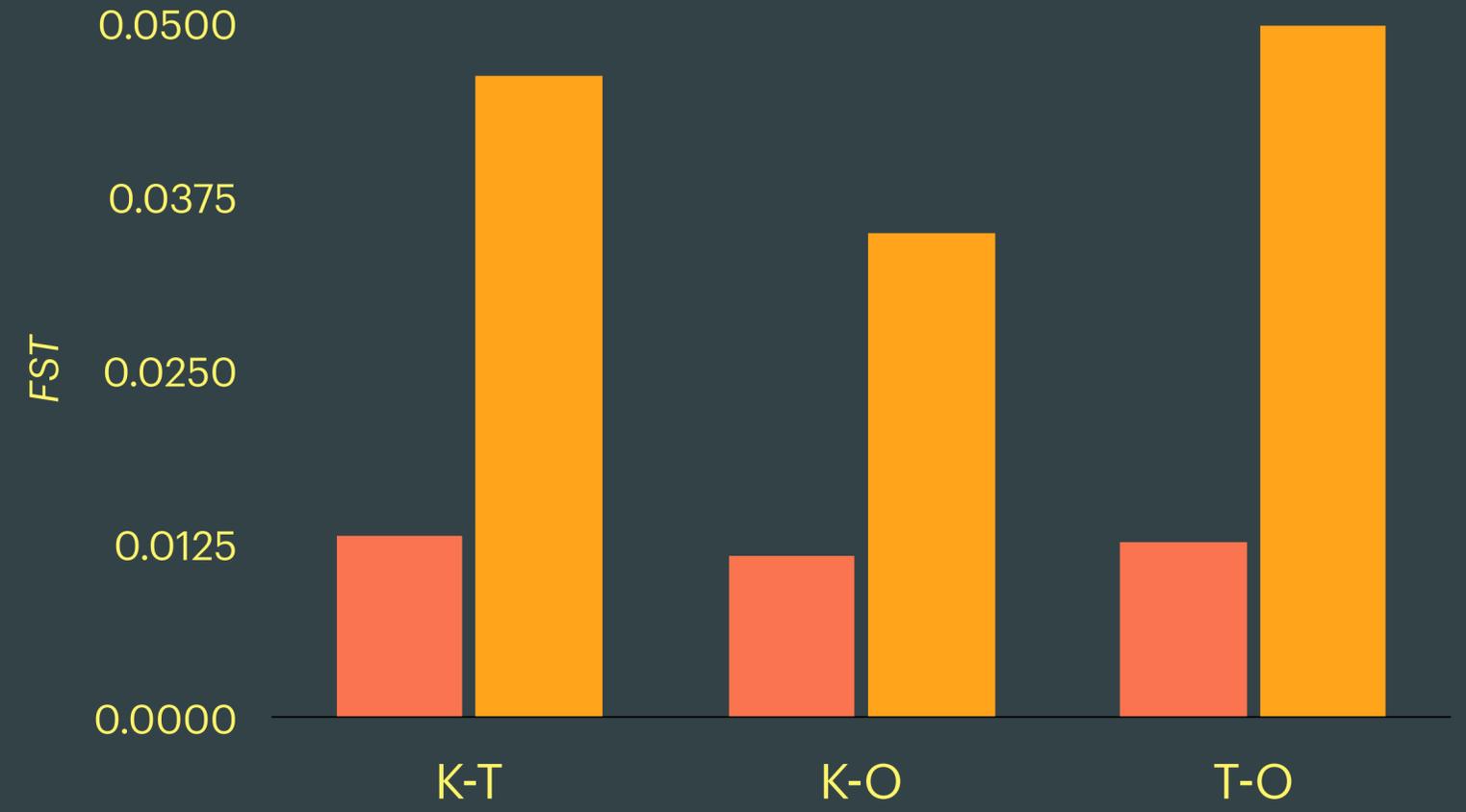
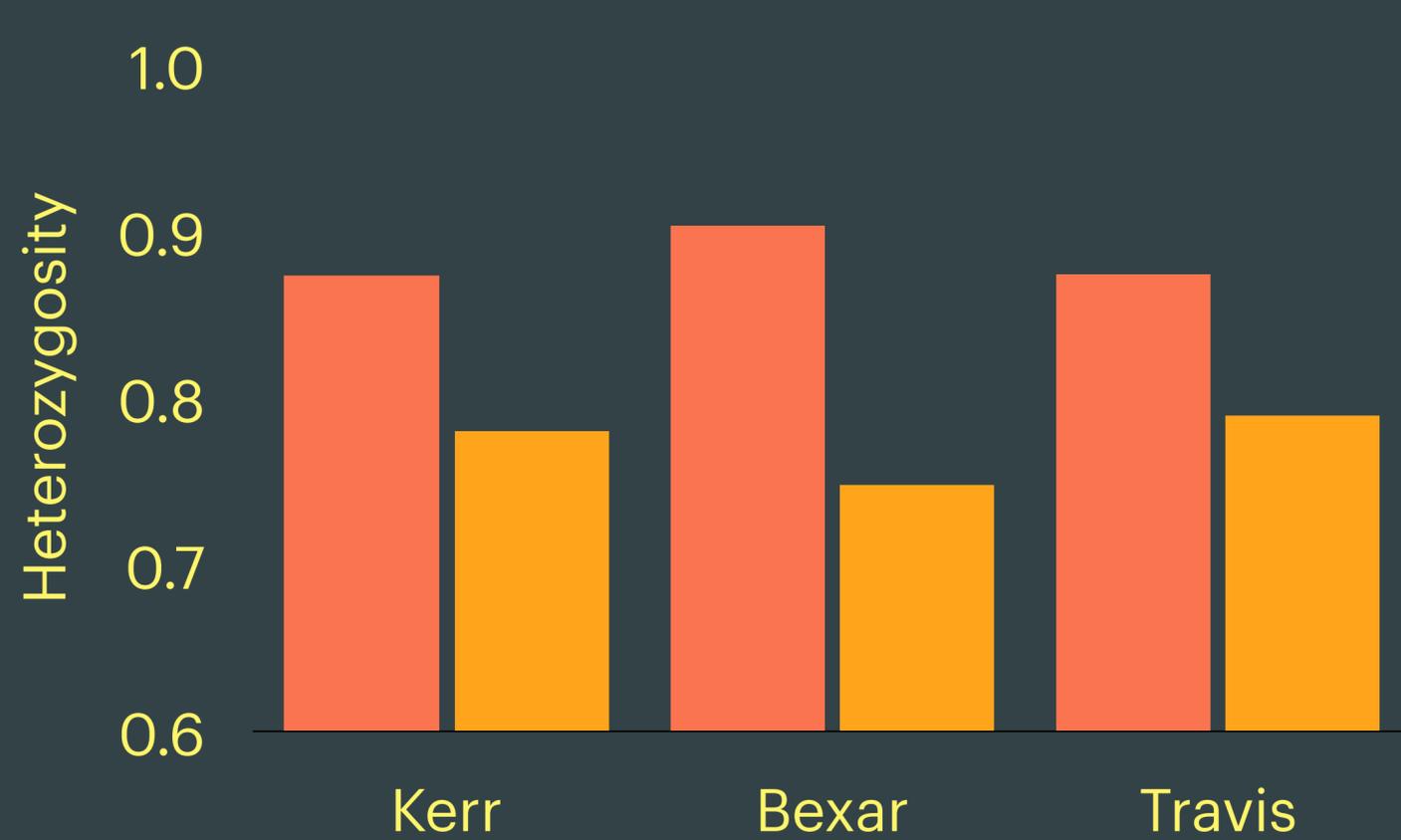
Location	Historical (N)	Contemporary (N)
Bexar	1890 (11)	2005 (17)
Kerr	1900, 1915 (9, 33)	2005 (17)
Travis	1913 (16)	2005 (17)



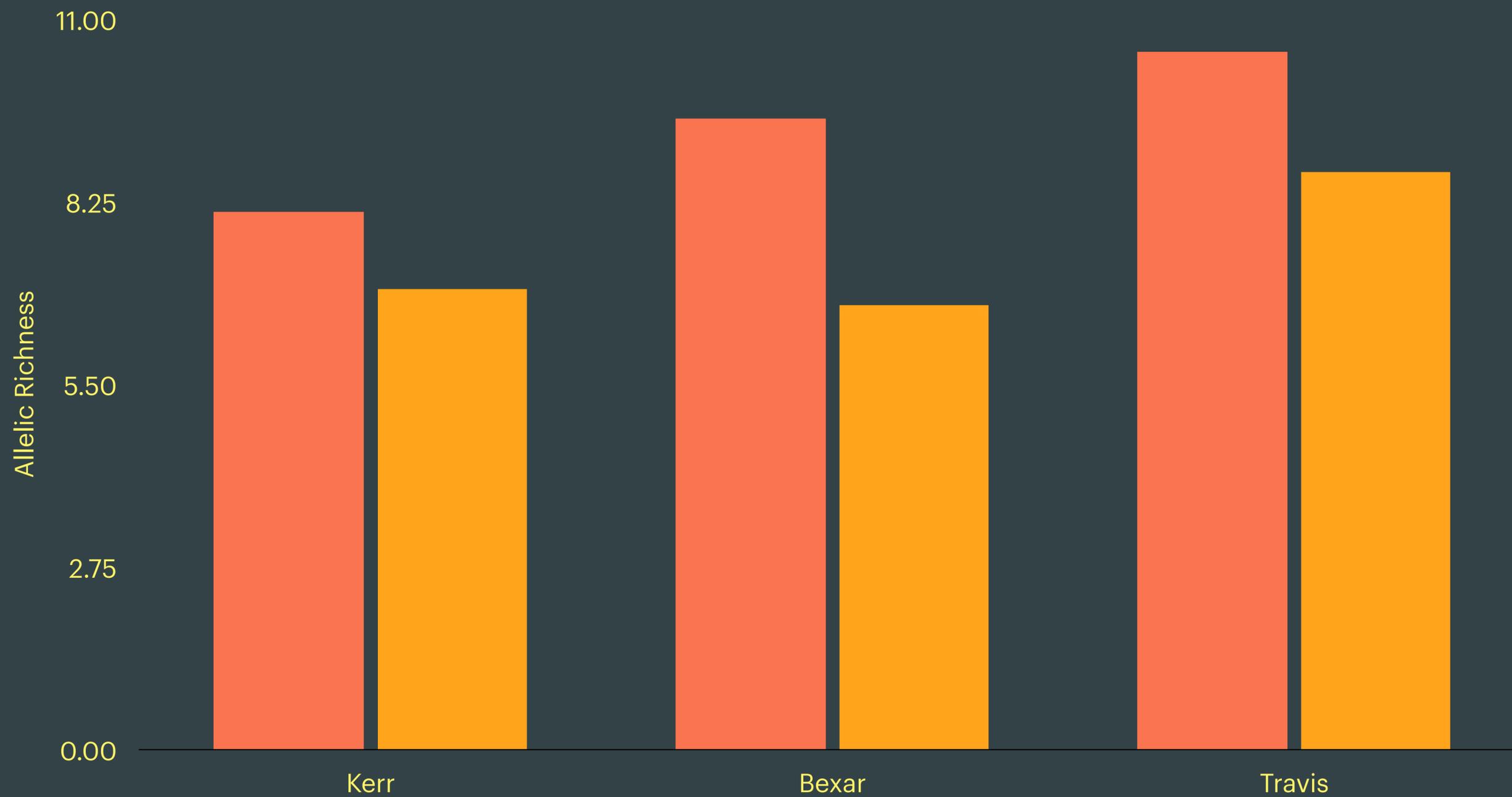




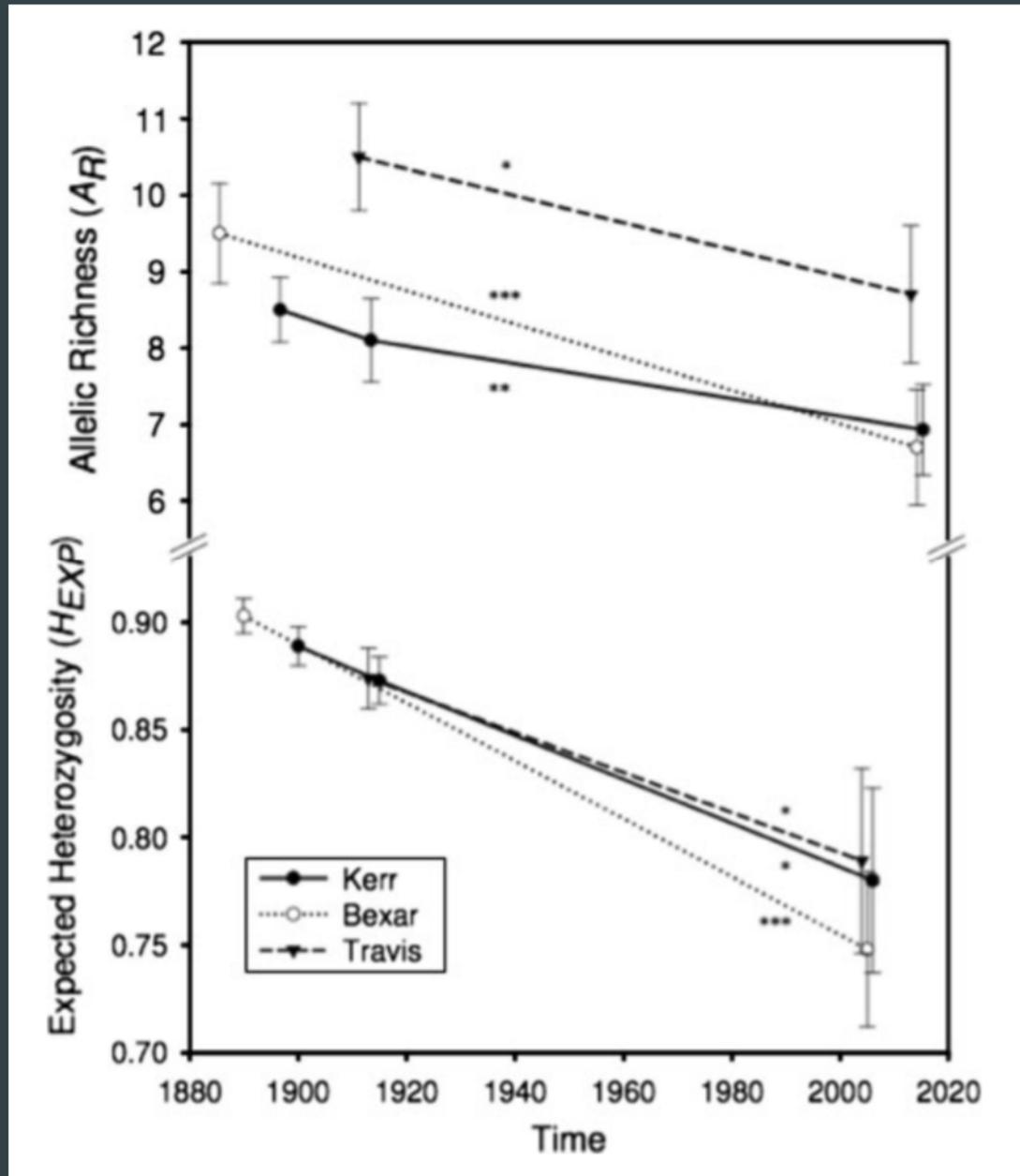




■ Historical Period
 ■ Contemporary Period



How steep was the decline?



20-30% decline in measures of genetic diversity (on average)

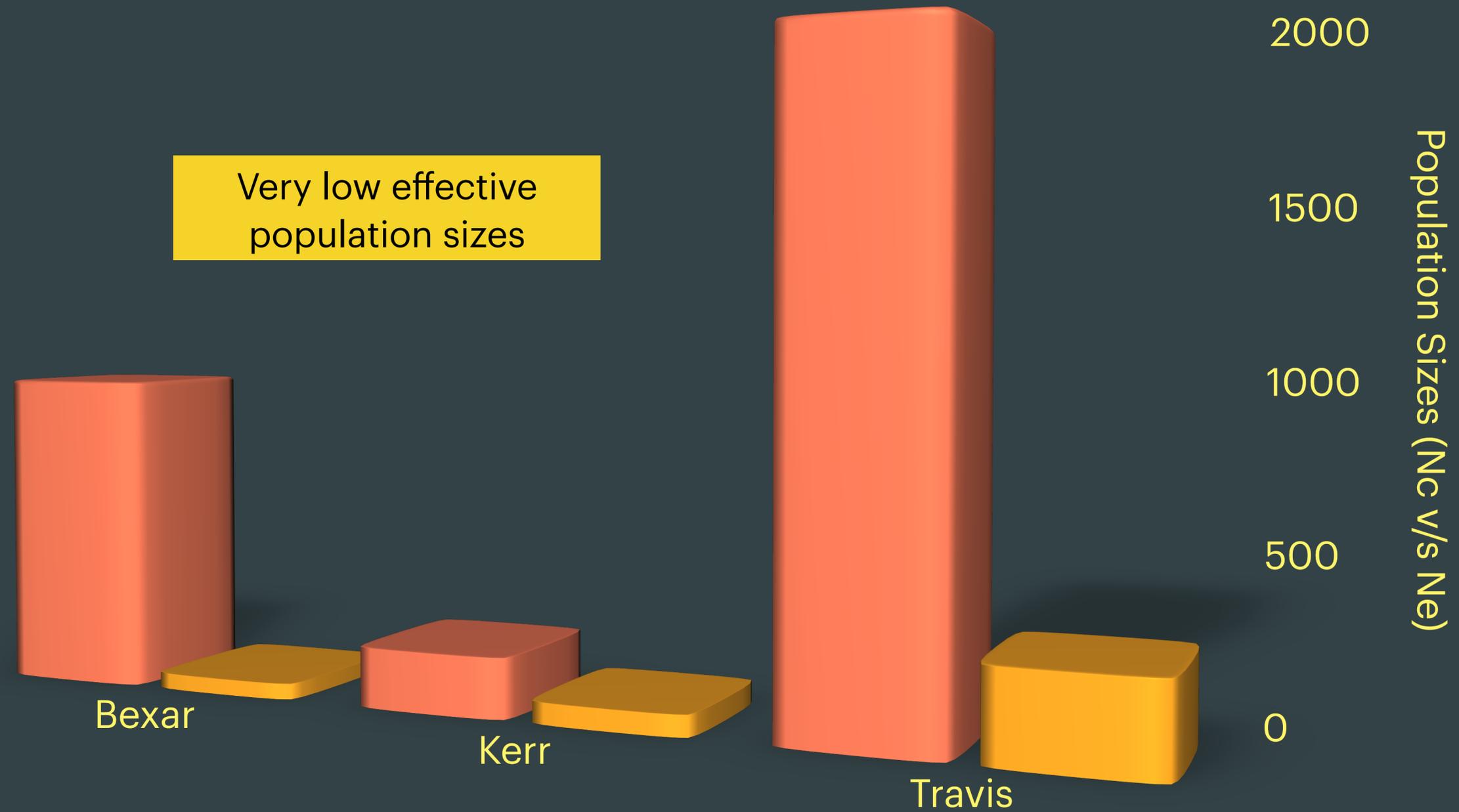
Effective population size

Number of individuals versus number of 'reproductively successful' individuals



even at large numbers, the effective size (N_e) can be very small.

Effective population size



Important findings

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- The studies demonstrated
 - one of the largest recorded reductions in genetic diversity in a vertebrate species
 - One of the lowest N_e/N_c ratios!!
 - N_e results indicate that genetic decline may be ongoing
 - It may take a long time for genetic diversity to recover

So what if genetic diversity declined?

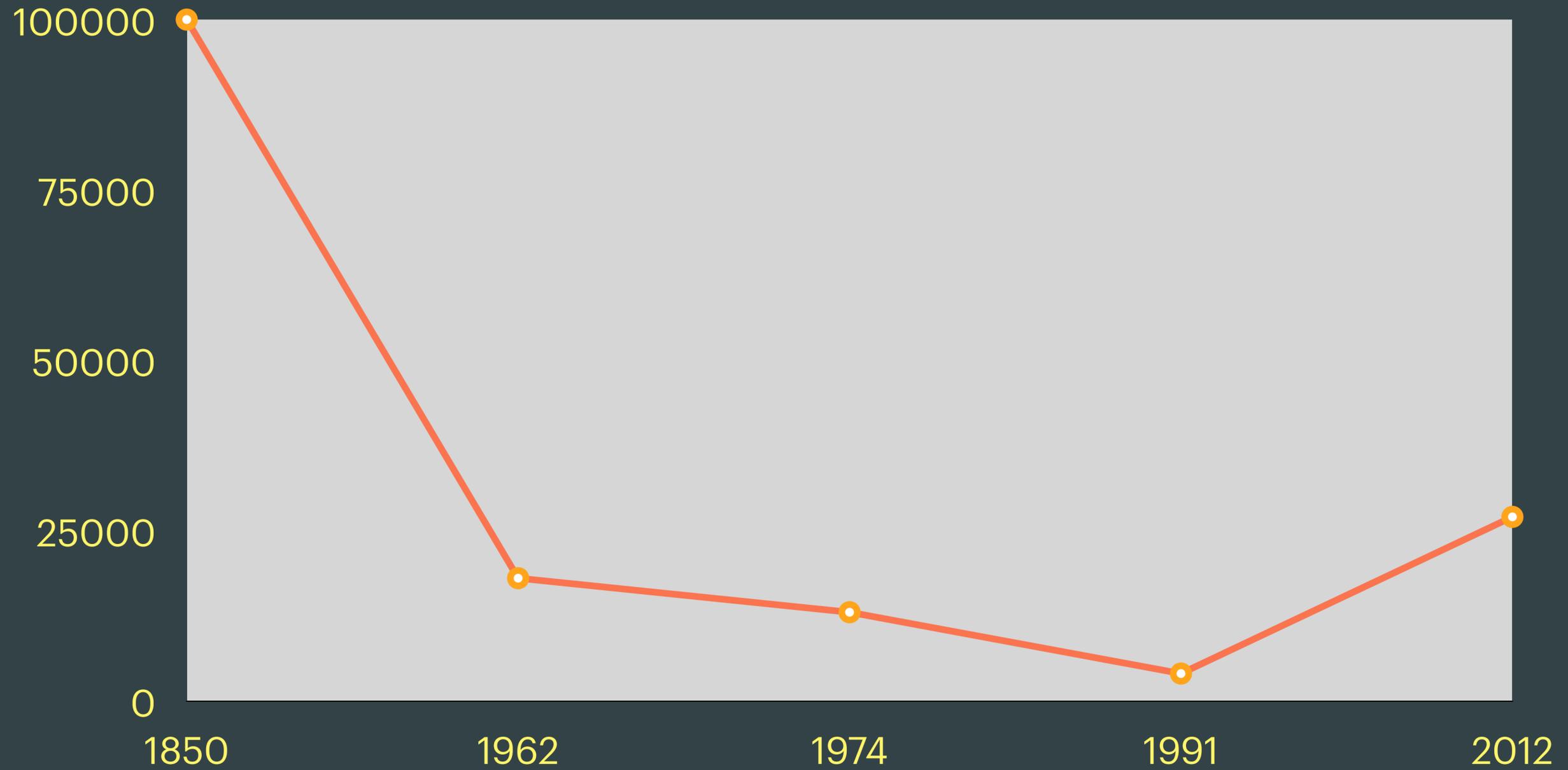
Focusing only on the number of birds does not consider the loss in genetic diversity, said Giridhar Athrey, a Texas A&M University professor of avian genetics.

Athrey said he has compared the genes of museum samples of warblers from 100 to 120 years ago with warblers living today. He found that the species has much lower diversity than it did in the past, leaving it more vulnerable to threats.

“Genetic variation has consequences for the individual every single day if you are a wild bird,” he said in an email. It influences metabolic health, immune response, competing for mates or territories, knowing when to begin migration and when to start laying eggs and eggshell thickness, he said.

“Reduced genetic diversity is going to have a negative impact on one or several of these traits,” he said.

Can genetic diversity have recovered?



Objective 1

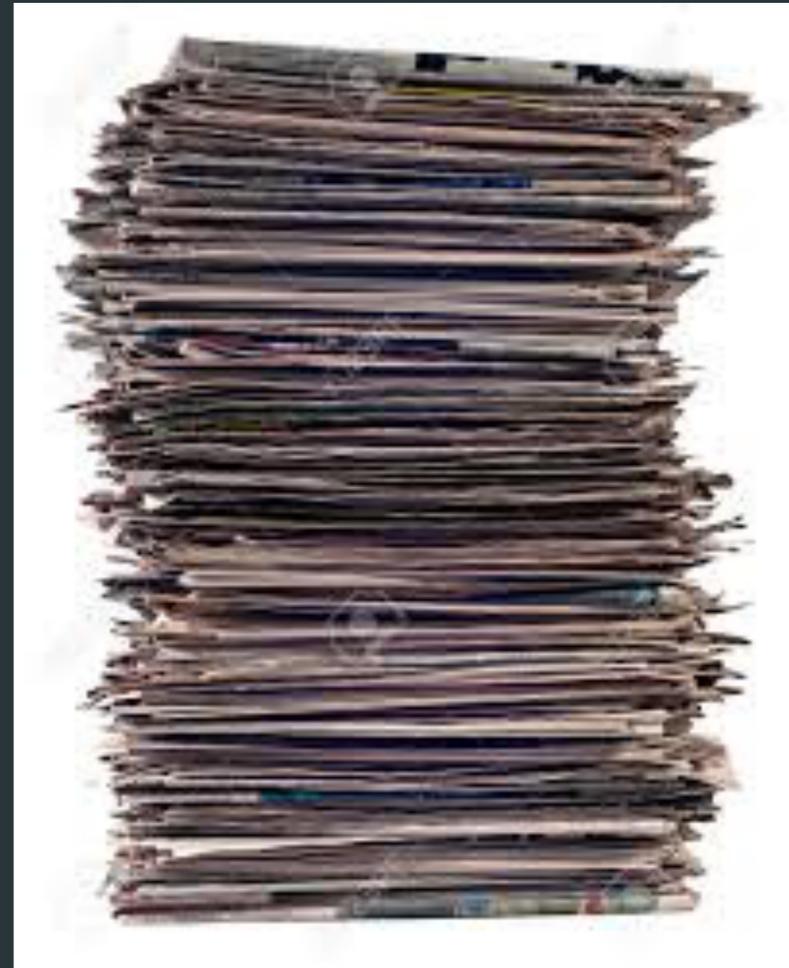
To generate a de novo assembly of the GCWA genome using a combination of short-read and long-read sequencing technologies to be made freely to the public for future studies of GCWA and closely related species.



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What is a genome reference?

- A reference genome is a **haploid representation** of a species' genome
- Can be constructed from a single individual (more common now), or from a pool (common earlier)
- Alternate alleles (when known from population data) are assembled alongside reference locus
- Organized into chromosomes (best), or scaffolds (better), or contigs/supercontigs (ok).



Copies of genomic DNA



Sequence reads



Assembled Genome

Assembly from WGS

Actual Genome sequence



*** Unknown and perhaps unknowable!**

sequenced READS



Perfect Assembly



Typical Assembly



Repetitive regions
and or poor sequencing
leave gaps

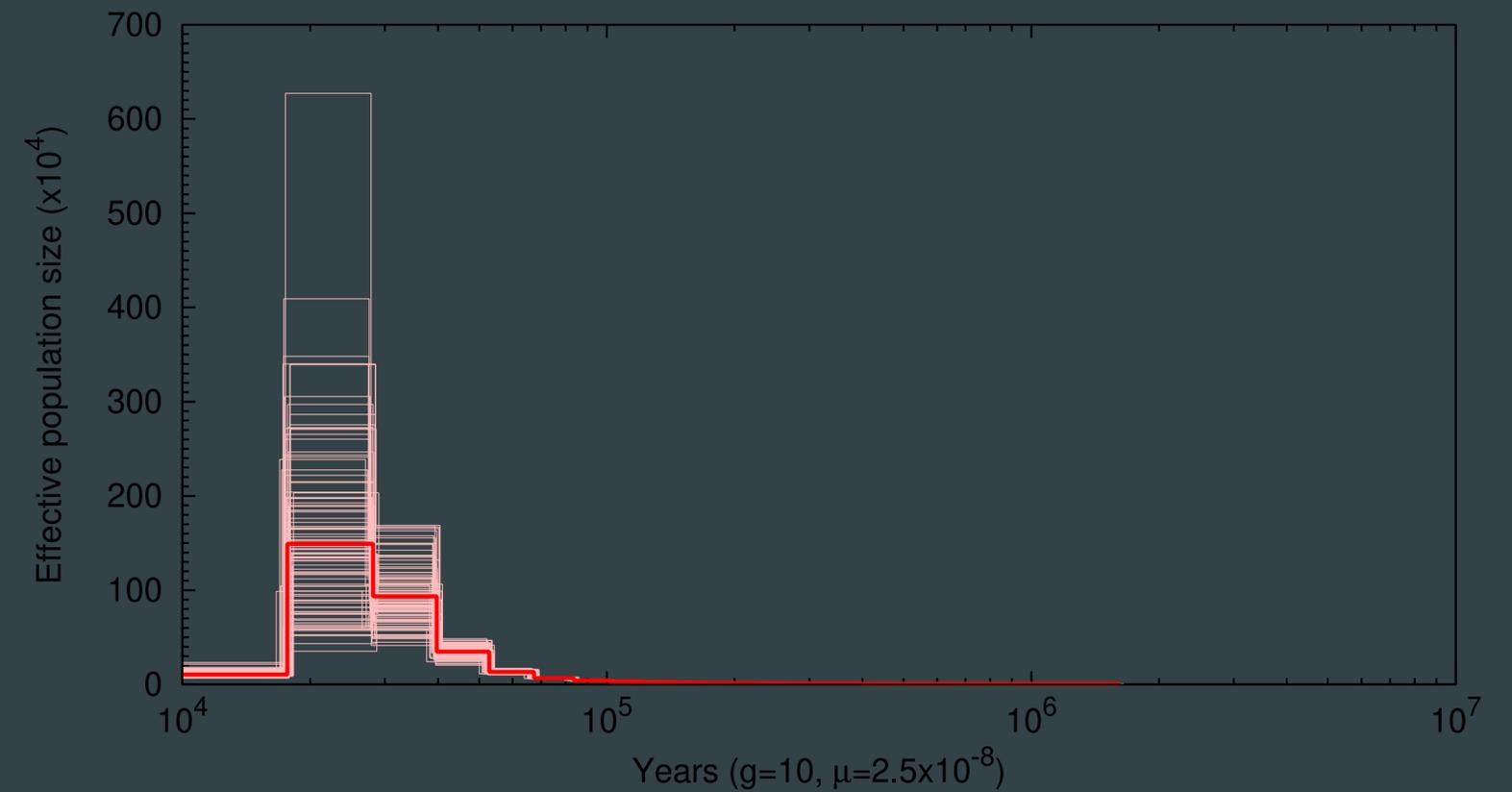
Repeats or un-sequenced



Rationale

The availability of a genome reference can help standardize all future assessments. Additionally, tremendous amount of functional data – that impact bird fitness can be revealed with knowledge of the full genomic sequences

Eg. WHCR population history reconstructed from de novo assembly



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Variant Type	Number
Total SNPs	16,431,629
InDels	218,151
Ts/Tv	1.84



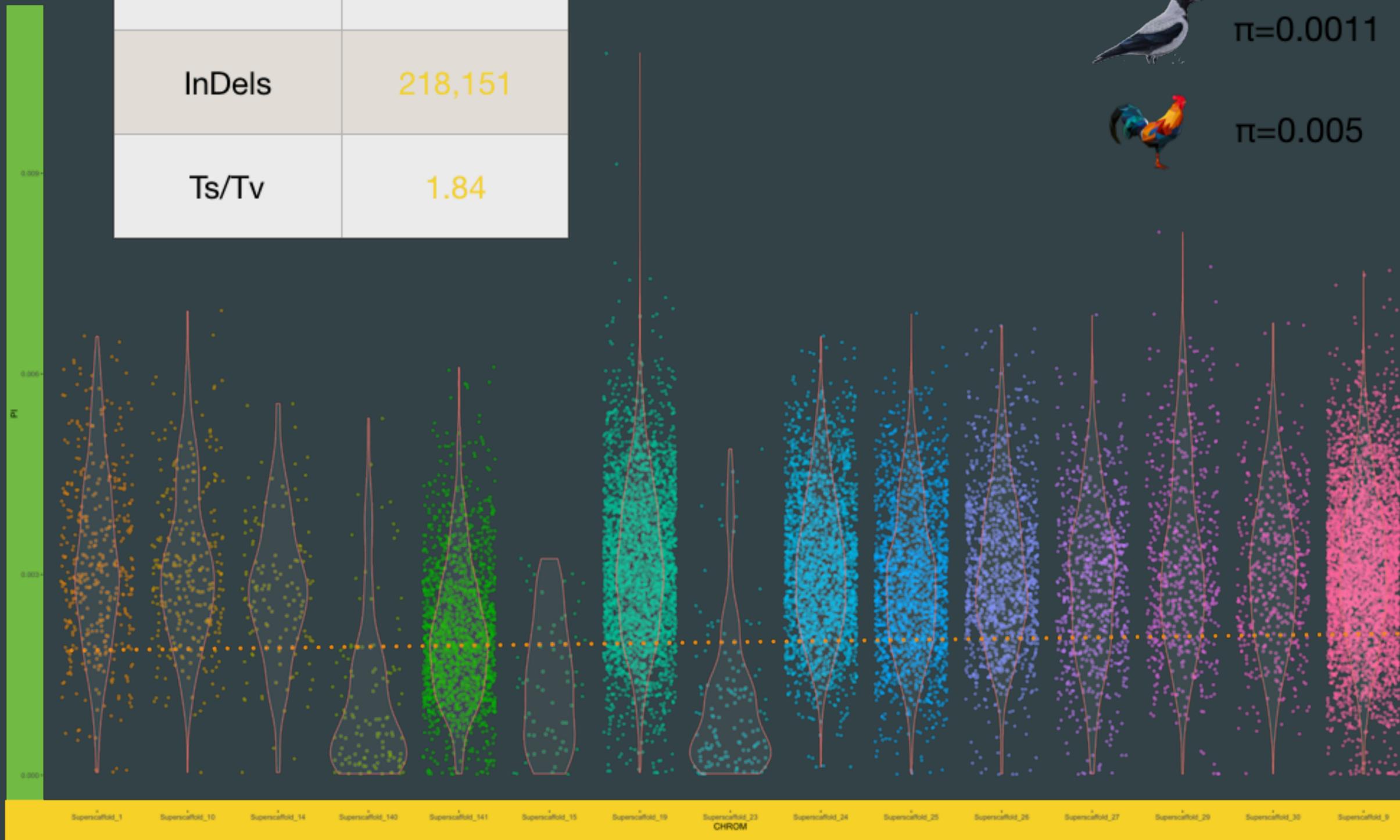
$\pi=0.0039$



$\pi=0.0011$



$\pi=0.005$

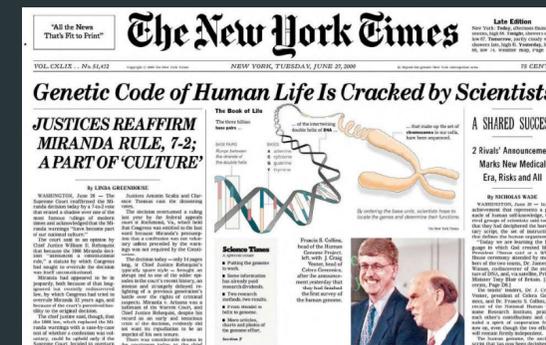


$\pi=0.002$

Species data from Dutoit *et al*, 2017, Ellegren 2013

GCWA Assembly quality*

Ref Free metric	Haslr Hybrid Assembly	Scaffolded	Gapped Scaffolds
N. Contigs	4719	3862	2450
Longest Contig	4.95 Mbp	6.283 Mbp	12.6 Mbp
N50	703 Kbp	957 Kbp	1.518 Mpb
N/100kpb	0	0.61	414
Total Length	982.98 Mbp	982.57 Mbp	817.252 Mbp



Objective 2

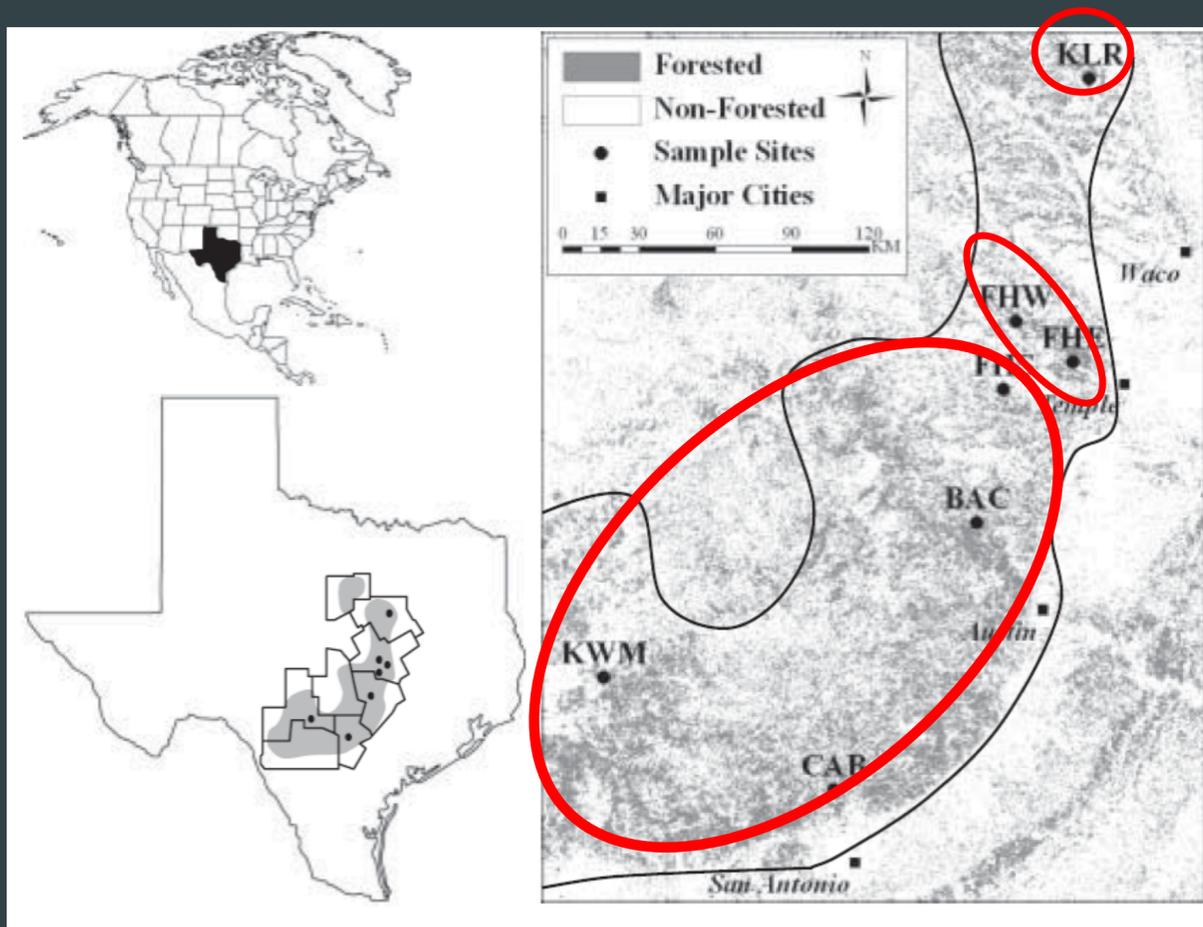
Perform a genetic assessment of GCWA population genetic diversity, structure, and population size history across the breeding range to inform species action plan and upcoming USFWS status review.



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Rationale

Update work done by Lindsay et al. 2008 and Athrey et al. 2011 and to inform species action plan and upcoming USFWS status review.



Lindsay et al. 2008:

From Athrey et al. 2011:

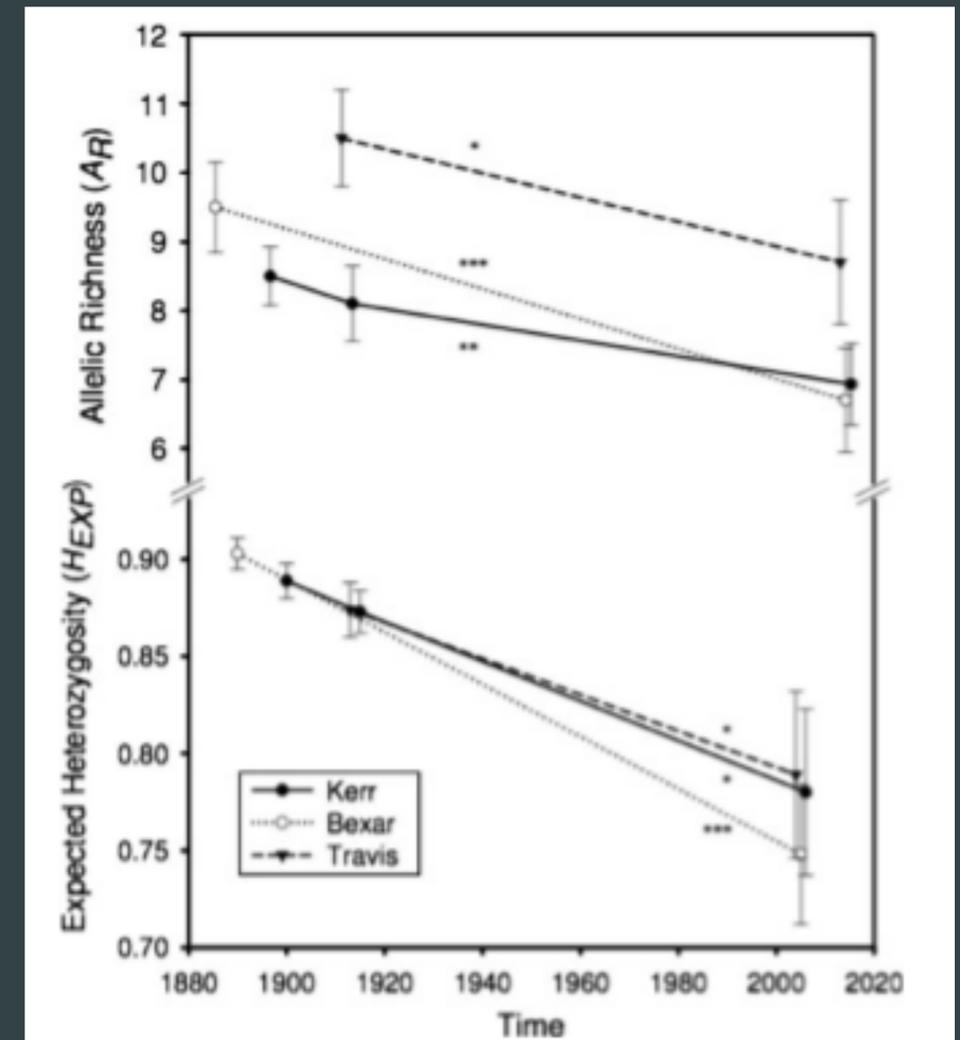
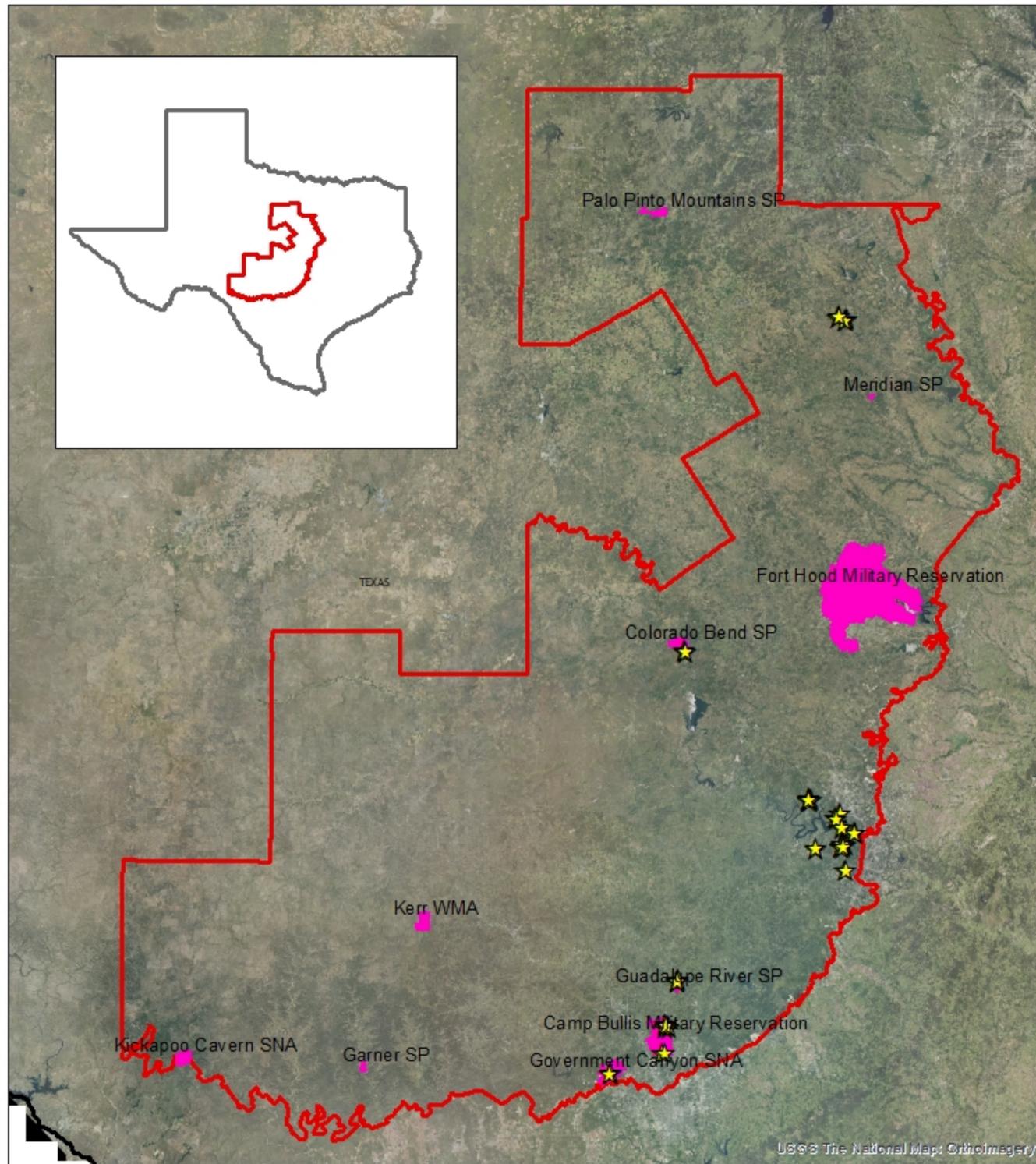


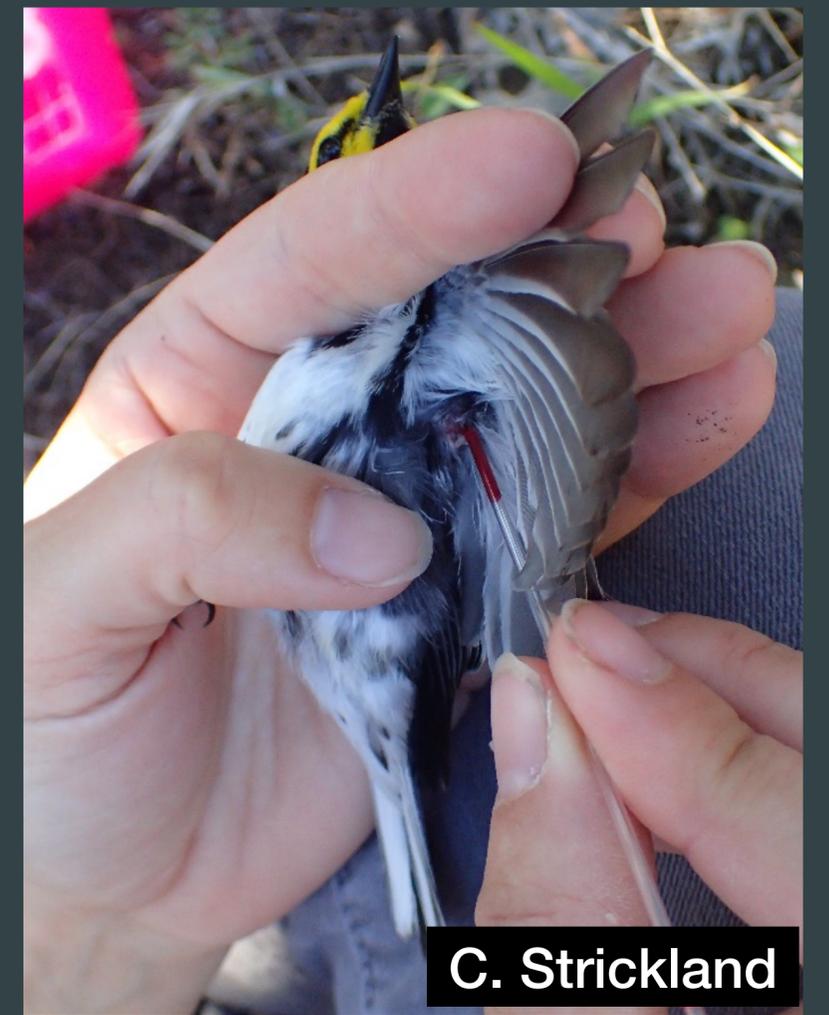
Fig. 2 Estimates of mean genetic diversity (with SEs) for historical and contemporary populations of *D. chrysoparia*. The hypotheses of no difference in estimates of allelic richness (A_R) and expected heterozygosity (H_{EXP}) were evaluated with a *T*-test ($\alpha = 0.05$). Symbols above each bar indicate significant pairwise differences (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$)



☆ GCWA samples
 ■ Sampling locations
 □ Golden-cheeked Warbler breeding range

Author: Laurel Moulton Date: 11/13/19
 Datum: NAD 1983 UTM Zone 14N

0 15 30 60 90 120 Kilometers



C. Strickland



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Expected outcomes

- Establish new genetic resources for long term monitoring.
- Long term demographic history can answer questions about what GCWA may have experienced long before land conversion expanded in the breeding range
- Near term histories can help understand population history in the last 100-200 generations
- Population genetic data can help understand if the ongoing management is promoting gene flow among populations

Expected outcomes

- Reconstruction and analysis of mitochondrial genomes and functional genes (MHC, other immune genes) can illuminate if the past population decline and genetic bottleneck have affected fitness.
- Provide policy makers and managers with actionable information that captures both historical and recent dynamics.
- Establish an updated template for assessing genetic diversity in endangered populations and other species.

Thanks to these people who help support
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Ms. Lisa O'Donnell
Ms. Zia Burns
Mr. Greg Bonnell
Mr. Ryan Orndorff
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Research
Dr. Byron Stone
Travis Audubon and TOS
Land owners across the state

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