

Trends in Golden-cheeked Warbler Abundance

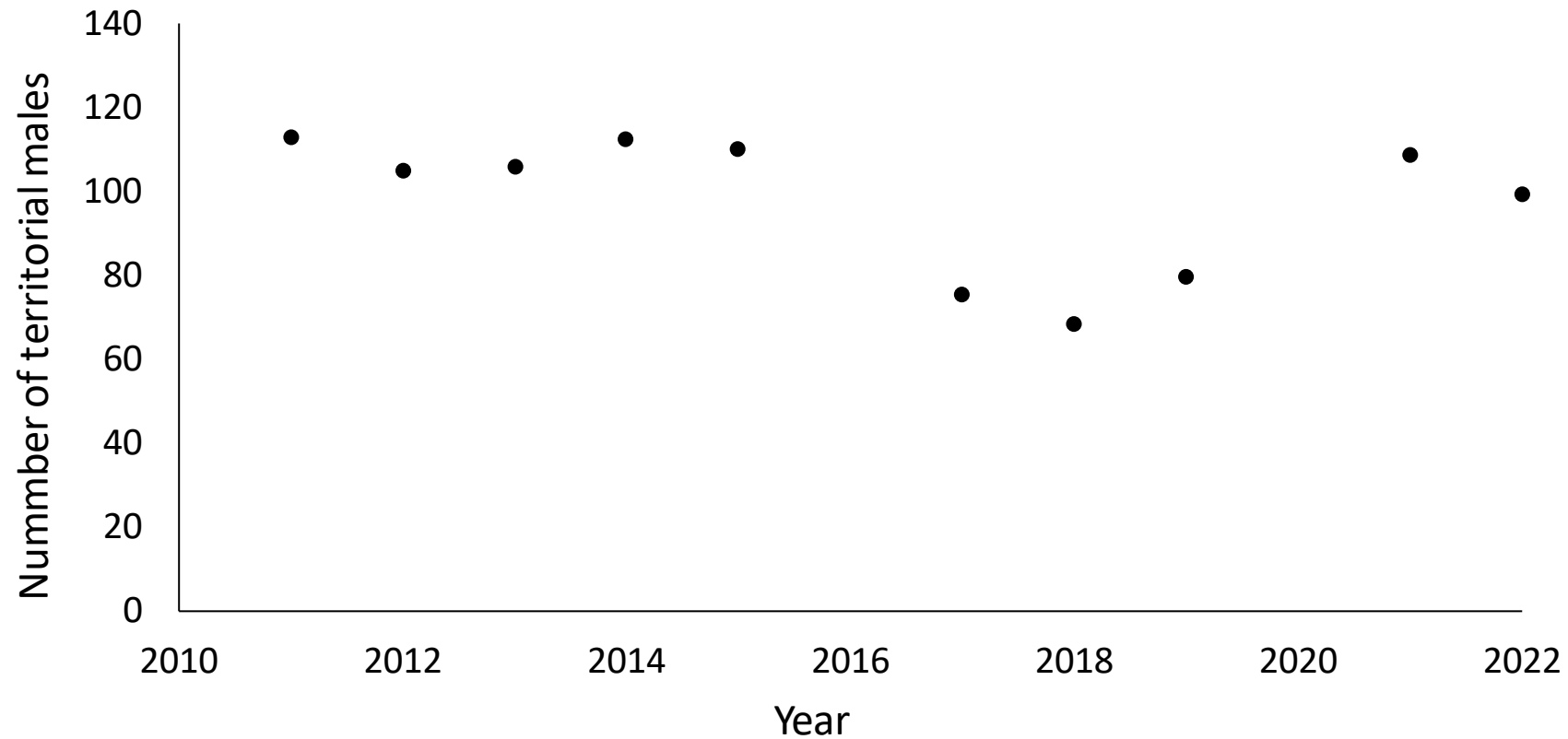
- BCP biologists have been intensively monitoring Golden-cheeked Warbler abundance on 10 study plots across the entire BCP since 2011.



Photo by volunteer Arman Moreno

- While abundance was stable from 2011 to 2015, it declined between 2016 and 2019.
- In 2021, the City of Austin BCP contracted a study to understand possible explanations for the decline.

Number of Territorial Male Golden-cheeked Warblers Across 10 Study Plots on the Balcones Canyonlands Preserve



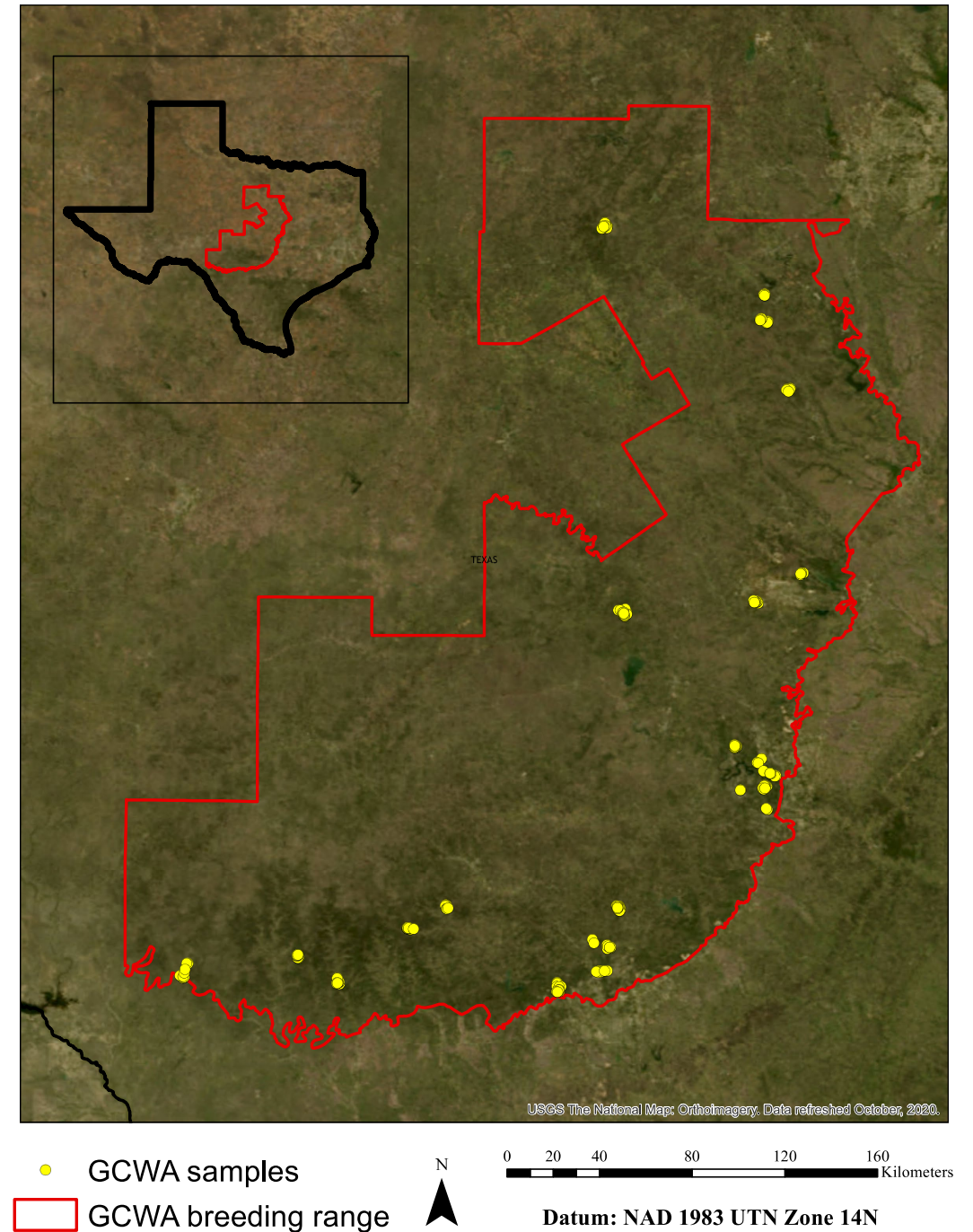
Key Findings:

- The decline in abundance appeared to be in part the result of a single, strong El Niño event that occurred during the winter of 2015 to 2016.
- Management to promote nesting success by protecting, maintaining, and creating high quality Ashe juniper-oak woodlands is critical to overcoming threats that the Golden-cheeked Warbler faces throughout its limited range.

[Urban land cover and El Niño events negatively impact population viability of an endangered North American songbird - Reidy - 2023 - Ecosphere - Wiley Online Library](#)

Updates on population genetics research

- Whole-Genome Sequencing
 - 239 field-sampled GCWA (2018-2021)
 - 14 Texas counties (11 populations clusters)
 - Used open source ANGSD (Analysis Next Generation Sequencing Data) for analyses



Updates on population genetics research

- Overview of results

- low genetic diversity
 - low heterozygosity (0.031 across species)
 - high level of inbreeding (0.099 species average)

- Interpretation

- historically recent, severe genetic bottleneck(s)
- still not fully recovered from prolonged periods with small population sizes

Table 2: Summary of the sample sizes per county, the population-wise inbreeding coefficients (F_i), and the observed heterozygosity (H_o). Genome-wide averages are presented by population, and a final species average is presented.

Population	Sample Size (N)	Avg. F_{IS}	Avg. H_o
Bandera	25	0.097	0.025
Bell/Coryell	23	0.095	0.033
Bexar	42	0.075	0.022
Bosque	15	0.114	0.040
Kendall	25	0.070	0.024
Kinney Edwards	15	0.112	0.041
Palo Pinto	16	0.119	0.034
San Saba	19	0.101	0.035
Somervell	18	0.084	0.030
Travis	15	0.124	0.035
Uvalde/Real	25	0.096	0.025
Total	239	0.099 (Avg.)	0.031 (Avg.)

Updates on population genetics research

• Overview of results

- pairwise F_{ST} values show high differentiation levels (0.008 to 0.02) among populations indicating reduced gene flow
- Bexar, Palo Pinto, and Somervell are most distinct from other pops
- recent demographic estimates of effective population size (N_e) show small genetic effective sizes across the range, suggesting recent severe bottlenecks

• Interpretation

- low heterozygosity, high inbreeding, and low N_e values combined suggest prolonged periods of small effective population size with no evidence of population expansion or recovery from population lows

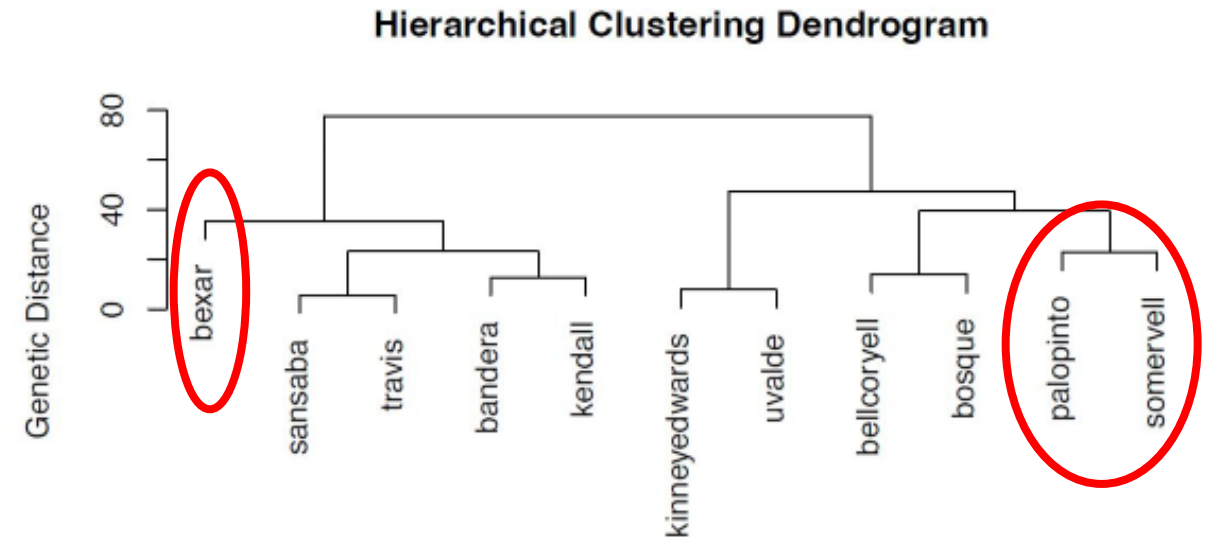


Figure 5: Hierarchical clustering dendrogram showing the grouping of populations based on genetic similarity.

Table 3: Summary of the estimates of effective population sizes using three different methods in this study. When available, the numbers from the temporal estimates (MLNe) generated in the 2011 study are reported alongside.

Population	2011 study	N_e (Coancestry)	N_e (LD)	N_e (Het)
Bandera		152 (108-191)	78	5.9
Bell Coryell		140 (73-178)	72	4.8
Bexar	49 (24-212)	254 (159-361)	130	6.1
Bosque		82 (41-104)	46	4.3
Kendall		156 (110-181)	80	3.9
Kinney Edwards		92 (76-123)	47	2.17
Palo Pinto		98 (66-134)	51	7.75
San Saba		116 (91-133)	59	5.17
Somervell		110 (101-145)	52	4.7
Travis	273 (46-621)	89 (53-99)	49	3.47
Uvalde/Real		110 (93-128)	70	4.8