

Addendum: Genetic structure in the Cactus Wren in coastal southern California.

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The purpose of this addendum is to update results and conclusions reported in Barr et al. 2013 based on the addition of new genetic samples to the original dataset. The additional samples include five samples from Palos Verdes in 2013 that were collected incidental to other projects there, and three samples from a new site, West Coyote Hills, that we were approved for access in 2013. Three other additional samples came from those collected in 2012 but not analyzed in Barr et al. 2013, including one that originally failed to genotype but was amplified with additional attempts and two that were removed from the previous analyses using a very conservative interpretation of sibship results. Original analyses did not include these samples though the probabilities of these sibship relationships were low (<0.95 ; Hauser et al. 2011), thereby preventing spurious population structure from being detected because of potential biases from closely-related individuals in the dataset. With further analyses and a thorough understanding of overall population structure in Cactus Wrens, these lower probability sibships were determined to have no effect on population structure patterns and were hence returned to the dataset.

Clustering analyses performed in GENELAND including these additional samples helped to resolve the LASB cluster (Barr et al. 2013, Fig. 2) into three clusters. These include PALOS VERDES, REDLANDS, and an extended cluster along the southern slope of the San Gabriel Mountains (LASB, Fig. 1). The cluster we originally reported as DBCH is also resolved to include the Whittier area, West Coyote Hills, and Phillips Ranch Park (WHITTIER/CHINO HILLS).

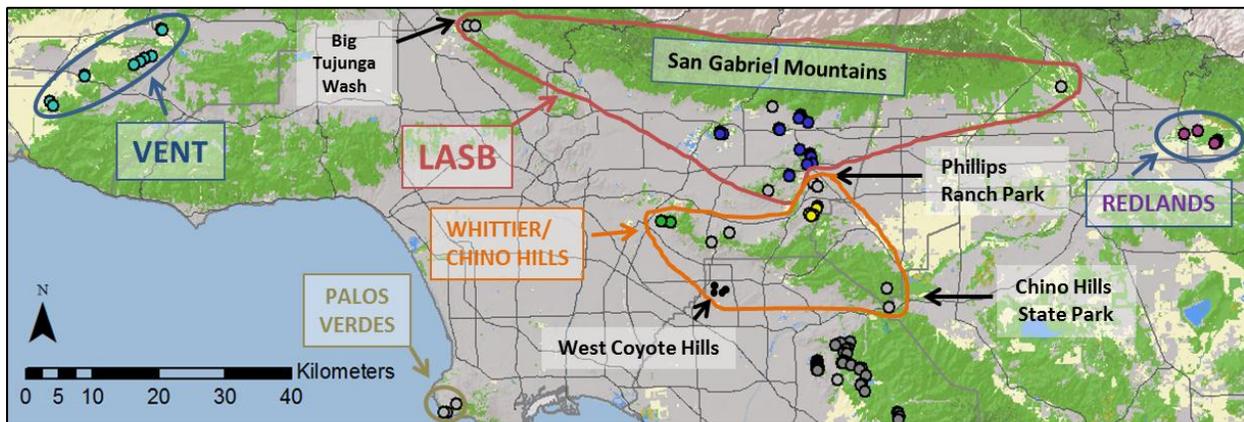


Figure 1. Map of sample locations (colored dots) and fine-scale clusters detected in GENELAND (colored polygons) from substructure analyses within the broadscale clusters in Figure 1. Gray indicates urban development, yellow agriculture, and green sage scrub, chaparral, and otherwise undeveloped open space.

Even with additional samples in areas we previously reported as having low genetic diversity (Barr et al. 2013, Table 2), these areas still exhibited low levels. For instance, at VENT, where three samples were added in these recent analyses, allelic richness (3.75) was still much lower than the mean among clusters over the full study extent (4.313). Allelic richness at PALOS VERDES and REDLANDS, both areas known to have very low census sizes, were also much lower than the overall mean (Table 1). Significant bottleneck signatures (ie, heterozygote excess) were detected at VENT, PALOS VERDES, and WHITTIER/CHINO HILLS. Though further sampling in these areas might change the individual genetic diversity estimates, it seems unlikely that the overall trends would be altered. Genetic diversity at VENT, PALOS VERDES, and REDLANDS is lower than much of the rest of the range.

Table 1. Genetic diversity indices for the clusters detected in GENELAND. N = number of samples, A = allelic richness, H_O = observed heterozygosity, $LD-N_e$ = effective population size from LDNE. Significant bottleneck signatures (H -excess) are indicated with *. In a few locations, not enough information is available in the data to estimate the upper limit of the confidence interval for N_e or the upper limit of the confidence interval (∞).

CLUSTER	N	A	H_O	$LD-N_e$	H -excess
VENT	15	3.75	0.587	23.6 (13.5 - 58.3)	*
PALOS VERDES	8	3.34	0.589	36.8 (13.2 - ∞)	*
LASB	30	4.26	0.562	51 (30.4 - 116.7)	
WHITTIER/CHINO HILLS	22	4.38	0.640	41.7 (28.7 - 69.7)	*
REDLANDS	8	3.65	0.568	51 (17.5 - ∞)	

Adding these samples addresses one of the limitations of our report, which was that we had so few samples from Palos Verdes. Adding better resolution in this area provides results consistent with the patterns detected in Orange and San Diego Counties, where sampling efforts were much more intense. It is now clear that PALOS VERDES, for instance, stands alone in its own cluster, as would be expected given the extreme urbanization enveloping the area and distance from other known aggregations (Fig. 1). Furthermore, this resolution infers connectivity between aggregations of Cactus Wrens near Whittier and Chino Hills (WHITTIER/CHINO HILLS), between which there is extensive open space. Our conclusions about the cluster along the southern slope of the San Gabriel Mountains remains the same as in Barr et al. 2013, namely that because of low sample size in the area of Big Tujunga Wash, for instance, we cannot necessarily assume high levels of connectivity throughout the area.

CITATIONS

Barr, Kelly R, Amy G. Vandergast, and Barbara E. Kus (2013) Genetic structure in the Cactus Wren in coastal southern California. Data summary report, California Department of Fish and Wildlife.

Hauser, Lorenz, Melissa Baird, Ray Hilborn, Lisa W. Seeb, and James E. Seeb (2011) An empirical comparison of SNPs and microsatellites for parentage and kinship assignment in a wild sockeye salmon (*Oncorhynchus nerka*) population. *Molecular Ecology Resources* 11, p. 150-161.