

by Paul Hess

Mojave Raven Populations

Raven taxonomy has long been a source of fascination and frustration. Common Ravens around the world look virtually alike and are notoriously variable in size even within named subspecies. As long ago as 1941, ornithologist George Willett at the Los Angeles County Museum lamented that his specimen collection was “perhaps inadequate” to sort out California’s taxa by measurements. Kimball Garrett, ornithology collections manager at the same museum, voiced a broader lament in September 2007. He reminded readers of the *Frontiers of Field Identification* e-mail list that ravens remain “a taxonomic nightmare.”

Genetic analysis addresses the problem in recent studies by Kevin E. Omland and colleagues. Their seminal report in 2000 reveals a deep genetic divide between a “California clade” in western North America and a “Holarctic clade” encompassing all the world’s other Common Ravens (*Proceedings of the Royal Society of London—B* 267:2175–2182). A clade is an assemblage of related populations whose members have diverged historically from a single shared ancestor.

A report in 2008 casts localized light on these two Common Raven clades in the Mojave Desert (*Molecular Ecology* 17:464–474). Robert C. Fleischer and eight coauthors wondered whether a recent raven population explosion in the desert’s western portion reflects local breeding success or immigration of birds from adjacent areas. They analyzed variations in mitochondrial and nuclear DNA among birds from five regions: coastal northern California, coastal southern California, the western and eastern Mojave Desert, and northern Nevada. Their findings affirm a California/Holarctic division.

The results also show diverse geographic patterns of gene flow (not including northern California ravens, which differ genetically from all the other populations):

- Within the California clade, there is high gene flow between coastal southern California and the western Mojave Desert—suggesting that immigrant ravens from southern coastal areas may at least partly be causing the western desert’s population increase. A small sample of individuals from California’s Central Valley indicates a possibility of gene flow into the desert from the valley, too.
- Within the Holarctic clade, there is high gene flow between the eastern Mojave Desert and northern Nevada—suggesting movement of ravens north and south between those two regions.

- In contrast, there is very little gene flow between the desert’s western region in California and its eastern region in Nevada—indicating that ravens of the California and Holarctic clades are virtually isolated from each other across the desert, perhaps kept apart by the broad central region of inhospitable habitat.

Fleischer and his colleagues offer an interesting speculation. Ravens on both sides of the desert rely on human subsidies such as water and food from agriculture and landfills, as well as nesting sites on structures and recently intro-



A new study of **Common Raven** DNA shows that those in the western Mojave Desert belong to a “California” group and those in the eastern Mojave are part of a worldwide “Holarctic” group. They are separated by inhospitable habitat in the central desert. *Kern County, California; November 2005.* © Bob Steele.

duced trees. Future development in the central desert might open a corridor that would increase the raven population, mix the western and eastern taxa, and close the local genetic division between the clades.

Meanwhile, a conservation issue lurks in the study’s findings. Common Ravens are major predators of the threatened desert tortoise, and the U.S. Fish & Wildlife Service plans to reduce raven populations in the Mojave to protect the tortoise. The authors suggest that if gene flow represents birds moving in from the southern coast and possibly from the Central Valley, then these immigrants could nullify any raven control program that is restricted to the desert. Genetic analysis does not always tell us what we would prefer to hear.

Altamira Oriole Conservation

Altamira Oriole prospects in the Lower Rio Grande Valley looked bright for a few decades after this beautiful immigrant's first Texas nest was discovered in 1951. In favorable breeding habitat (tall trees in open brushland), it became the most common nesting oriole at Santa Ana National Wildlife Refuge and Bentsen–Rio Grande Valley State Park. Then, in the 1980s, the Santa Ana population collapsed after a period of drought and freezes killed many of its preferred nesting trees.

Tim Brush described the collapse in *Birding* (February 1998, pp. 46–53). From more than 20 nests in the 1960s, the population fell to one or two pairs by the 1980s. Christopher Hathcock and Brush reported a modest rebound to nine nests at Santa Ana in the late 1990s (*Southwestern Naturalist* 49:33–38). The valley's only larger increase during that period came in a narrow strip of riparian forest below Falcon Dam between Chapeño and Fronton, where Brush estimated 20–25 pairs. That number reflected adequate water levels and freeze-resistant tree species.

Brush warned in 1998 that the oriole's future existence in Texas would require water management to preserve tall trees, as well as maintenance of suitable habitat amid an onslaught of agricultural and urban development. He tells *Birding* in 2008 that a crucial factor is the total amount of riparian and thorn forest available. Restoration has created some areas of new habitat that are being used by Altamira Orioles, but he adds that “the jury is out as to how much positive impact this will have.”

A recent study of Altamira breeding ecology in the Lower Rio Grande Valley leads to the same conclusion. Scott M. Werner, Sallie J. Hejl, and Brush analyzed habitat characteristics, nest-site selection, nest success, and productivity of young at nine sites in Hidalgo County in 2002–2003 (*Condor* 109:907–919).

Their findings, published in 2007, demonstrate this oriole's preference for tall trees: Nest trees averaged 12.7 meters high, and nest height averaged 8.8 meters. Artificial flooding from Falcon Dam has maintained large trees in a test area at Santa Ana in recent years, and the authors suggest that similar management could be beneficial at Bentsen, where favorable habitats are becoming degraded by lack of water.

Parasitism by Bronzed Cowbirds is worrisome. Of 83 nesting attempts monitored, Werner, Hejl, and Brush observed 11 nest entries by cowbirds, found cowbird eggs in six nests, and documented partial clutch losses of 17 eggs

in 12 nests (some perhaps due to predation). Only two of six nests that fledged cowbirds also fledged orioles, and in those cases only one or two orioles per nest. Overall, 59% of nests fledged young, and those averaged 2.3 fledglings. The Altamira Oriole sometimes ejects cowbird eggs from its nest, which may help it to maintain populations where other oriole species have disappeared—but, of course, only in suitable habitat.



The Lower Rio Grande Valley population of **Altamira Oriole** is threatened by loss of tall trees that the species prefers for nesting. A recent report calls for management to preserve these trees by assuring an adequate water supply. *Hidalgo County, Texas; November 2001.* © Alan Murphy.

Meanwhile, Michael Patrikeev, Jack C. Eitniear, Werner, and Paul C. Palmer report that Altamira Orioles appear to be hybridizing with Audubon's Orioles in South Texas (*Birding*, March/April 2008, pp. 42–46). Apparent hybrids are relatively few, but a troubling question arises: Might the small Texas population of pure Altamira Orioles gradually be swamped by hybrids? Brush believes the situation bears watching.

Yellowthroat Mask and Bib

Morphologically, vocally, and ecologically, the Common Yellowthroat is one of North America's most variable warblers. Research in Wisconsin and New York suggests that some of the variation may be related to a female's choice of a mate. The attraction for females studied in Wisconsin is the size of a male's black facial mask, whereas females studied in New York favor males with more yellow on the throat and breast (the "bib").

Kevin Thusius, Kara Peterson, Peter Dunn, and Linda Whittingham at the University of Wisconsin–Milwaukee



Female preference for a male **Common Yellowthroat** depends on the size of his mask in Wisconsin but on the amount of yellow on his throat and breast in New York. Researchers are attempting to find out the reason for this difference in mate-selection behavior. *Somerset County, Maine; May 2007.* © Garth McElroy.

reported in 2001 that males with larger masks are more likely to obtain a mate and sire more "extra-pair" young with a neighboring male's mate (*Animal Behaviour* 62:435–446). In contrast, unpublished data collected by Corey Freeman-Gallant at Skidmore College in New York showed that males with larger yellow bibs are more likely to obtain a mate and to sire extra-pair young.

Why is the mask more important in Wisconsin and the bib more important in New York? Researchers from both localities teamed up to investigate how these differences in breeding success arose. They used aviary experiments to determine whether males with larger masks or bibs are

more attractive to females, or whether these males are dominant over other males and, thus, are better able to gain access to neighboring females.

In Wisconsin, Scott Tarof, Dunn, and Whittingham demonstrated in 2005 that mask size predicts both female mate choice and male dominance (*Proceedings of the Royal Society of London–B* 272:1121–1127). To test competition between males, the authors placed two males together and measured how often each chased the other. Larger-masked males were nearly always dominant. To test female choice, two males were placed in separate compartments facing a female, and her preference was judged by how long she spent in front of either male. All females preferred the larger-masked male. In another set of tests, males' masks were enlarged with a black marker or reduced with yellow paint. Results were the same: Larger-masked males were dominant over other males and favored by females.

In New York, when the experiments were replicated, the researchers found that males with larger masks were dominant over other males, as in Wisconsin. However, the New York females showed no Wisconsin-type preference for larger masks; they nearly always preferred males with larger yellow bibs. Reporting these results in the *Journal of Avian Biology* (39:66–72) in 2008, Dunn, Whittingham, Freeman-Gallant, and Jonathan DeCoste propose a number of hypotheses for the differences. For example, different environmental factors at the two locations might make different plumage pigments more attractive to females.

As a general rule, females are thought to prefer males whose plumage "ornaments" signal high genetic, reproductive, or behavioral quality. Carotenoid pigments (as in the male's bib) must be obtained intact from the diet, whereas melanin pigments (as in the male's mask) can be synthesized from commonly available amino acids. If carotenoids are difficult to obtain in the diet, then a brighter yellow bib might signal a male's higher quality. Why melanin, relatively easy to produce, might be a more important signal in Wisconsin is unknown. The authors speculate that environmental factors such as differences in habitat, carotenoid abundance, or parasite abundance could be involved. Researchers in both states continue to seek the answer.

Tracking Birds by Parasites

Linking the breeding and wintering areas of migratory songbird populations on a fine scale remains an elusive goal. In a review of the problem in 2002, Michael S. Webster and four coauthors call these links “migratory connectivity”—“the extent to which individuals from the same breeding area migrate to the same nonbreeding area and vice versa” (*Trends in Ecology and Evolution* 17:76–83). They note that genetic markers and stable isotope ratios may indicate birds’ breeding grounds on regional scales but not necessarily at the level of local breeding populations. They look ahead to the promise of satellite telemetry, but only after transmitters are available to track small creatures (see *Birding*, May/June 2008, p. 34). Further, they suggest that analysis of parasites is an “exciting and potentially powerful” method. The idea is that distinct, localized parasite lineages in birds and other animals might establish migratory connectivity with great geographic precision. Thus



Can birds’ parasites aid ornithologists in connecting breeding populations with their wintering locations? Studies of Black-throated Blue Warbler, **American Redstart**, and Common Yellowthroat parasites have not succeeded in showing the connection. *Brazoria County, Texas; October 2006.* © Michael L. Gray.

far, however, investigations of parasites in three wood-warbler species, conducted at the Smithsonian’s Center for Conservation and Evolutionary Genetics, have failed to fulfill the hope.

Sylvia M. Fallon, Robert C. Fleischer, and Gary R. Graves examined malarial *Plasmodium* and *Haemoproteus* parasites in Black-throated Blue Warblers across the breeding range.

Findings published in 2006 show no distinct parasite lineages that are restricted to a particular breeding population or even to a regional group of populations (*Biology Letters* 2:213–216). According to the authors, this absence of geographic differentiation may reflect a spread of lineages by dispersal of young on the breeding grounds or a transmission of lineages among different breeding populations that mix on the wintering grounds. In either case, no local lineages of these two parasites identify Black-throated Blue Warbler breeding populations at a desirable “site-specific” scale.

A study published in 2008 focuses on American Redstarts by investigating relative geographic prevalence of the two parasites as well as the parasites’ lineages. Kate L. Durrant and nine coauthors report in the *Journal of Zoology* (274:318–326) that several distributional features of parasites differentiate redstarts in the southeastern U.S. from those in the rest of the breeding range. Prevalence of parasites is higher overall in the Southeast. *Haemoproteus* is much more common in the Southeast, whereas *Plasmodium* is much more common in the rest of the range. Southeastern redstarts are also more likely to carry *Haemoproteus* lineages that are unique to the region. But Durrant and her colleagues emphasize that differentiation among broad regions solely on the breeding grounds is not sufficient to demonstrate migratory connectivity across continents. Wide sampling of redstarts’ parasite assemblages in the winter range will be needed to determine whether these can be useful markers for connecting the birds’ breeding and wintering locations.

Another paper in 2008 describes patterns in Common Yellowthroat infections by those two parasites and a third one, *Leucocytozoon*. Katrina M. Pagenkopp and four colleagues found significant differences in prevalence and geographic distribution, but only of the most common *Plasmodium* lineages and only among five large regions of the breeding range, as reported in *Conservation Genetics* <doi:10.1007/s10592-007-9497-6>. As with the redstart, differences at a regional level cannot indicate migratory connectivity in a local breeding population. Not discouraged, Pagenkopp and her coauthors suggest research using parasites that are more localized and that have other features which might differ on a fine geographic scale. The potential power of parasites as markers of connectivity is not yet fully tapped.