

by Paul Hess

Two Ivory-bill Species?

More than one species of Ivory-billed Woodpecker may be on the brink of extinction or already over the edge. Currently classified as subspecies, the North American population (*Campephilus principalis principalis*) and the Cuban population (*C. p. bairdii*) are extremely similar morphologically. Specimens from Cuba average smaller in overall size and bill length, with the white neck stripe usually extending farther forward on the cheek, and the black crown



The **Imperial Woodpecker** (*Campephilus imperialis*) of Mexico and the Ivory-billed Woodpecker are distinctly different genetically, according to a recent analysis. North American and Cuban Ivory-bills are equally distinct from each other, suggesting that these may be separate species. *Painting by © Norman Arlott / Rare Bird Club; courtesy of BirdLife International.*

feathers typically slightly longer in front of the red crest; but there is overlap in those characters, and in other field-discernible respects the two populations are virtually alike. Genetically, however, they appear to be distinct—suffi-

ciently so that Robert C. Fleischer and nine colleagues suggested in 2006 that both may merit reconsideration for species status (*Biology Letters* 2:466–469). The American Ornithologists' Union had ranked the two as species before merging them in 1976.

The authors reached their conclusion after molecular analysis of skin pared from the toe pads of old museum specimens: seven North American Ivory-billed, three Cuban Ivory-billed, and three Imperial Woodpeckers (*C. imperialis*) from mountains in Mexico, all collected between 1861 and 1923. Comparison of mitochondrial DNA sequences revealed that the two Ivory-bill subspecies in these samples differ from each other as much as each differs from the presumably extinct Imperial Woodpecker, whose classification as a separate species has seldom been questioned.

Further analysis indicated that the three taxa are a monophyletic group (i.e., they share a common ancestor that is shared by no other species). To reconstruct the group's phylogenetic history, the researchers compared mitochondrial DNA sequences in the specimens with sequences in newly sampled South American and Central American *Campephilus* species and in four species from other woodpecker genera. The results suggest that ancestral *Campephilus* woodpeckers originated in South America and spread northward after the Isthmus of Panama formed about three million years ago. Next, lineages leading to *imperialis* and to the two separate *principalis* taxa evidently split from a common ancestor in Central America or Mexico during the Pleistocene epoch approximately one million years ago. In this scenario of divergence, the population that became the Imperial Woodpecker moved into the mountains of Mexico and the population that became the North American Ivory-billed Woodpecker spread into northern Mexico and around the Gulf Coast to Florida.

When and how did the Ivory-bill reach Cuba? Jerome A. Jackson summarized three possibilities—two ancient routes, one recent arrival—in his *Birds of North America* species account in 2002. Perhaps the birds traveled there either from the Yucatan peninsula or from Florida during the peak of Pleistocene glaciation, when sea levels were lower and distances over water from the mainland were less formidable. Alternatively, Jackson suggested, Cuba's original Ivory-bills might have been introduced in recent pre-Columbian times during trade in live birds between Native Americans and Cubans. By showing divergence of the Cuban Ivory-bill in the distant past, the Fleischer team's molecular clock puts that last speculation to rest.

Fleischer and his colleagues have done more than describe evolutionary history. They have provided a resource of immense practical value: a reference set of Ivory-billed and Imperial Woodpecker DNA “bar codes”. Mitochondrial DNA sequences in newly molted feathers or other material collected in current field work could be compared with sequences from the old specimens. With a match, the presence of an Ivory-bill or an Imperial Woodpecker might be proven even without a desperately-sought diagnostic photograph of the bird. In effect, we could see the bird plainly in a picture of its genes.

Tracking Sooty Shearwaters

It is time to revise the bird-migration record book. Erase Arctic Tern and replace it with Sooty Shearwater as the world’s annual long-distance travel champion. Nineteen shearwaters were tracked in 2005 on a 65,000-kilometer journey from two nesting colonies in New Zealand to summer feeding grounds in the North Pacific and back again. Scott A. Shaffer and ten colleagues reported the headline-grabbing news in 2006 (*Proceedings of the National Academy of Sciences* 103:12799–12802). Arctic Terns might be contenders for the title with a direct round trip estimated at 40,000 kilometers between Arctic breeding grounds and the Antarctic—an estimate that does not include daily foraging flights, as the shearwaters’ distance does. No one knows the terns’ total distance because no one has ever tracked them through the complete post-breeding cycle. For now, the Sooty Shearwater is the confirmed record-holder, documented by Shaffer’s team in the longest animal migration ever recorded telemetrically.

A miniature electronic “tag” attached to a leg on the breeding grounds archived daily data on each bird’s location and activities—even how deep it dived for food (as deep as 68 meters). Meanwhile, sensors in orbiting weather satellites measured primary organic productivity in oceanic regions along the birds’ routes, enabling the researchers to relate a bird’s feeding activity to food availability. The authors described the overall migration, which lasted an average of 198 days, as the “pursuit of an endless summer” to regions where food is most abundant in different seasons.

The shearwaters’ overall route was an oddly indirect figure-eight that took them through much of the Pacific Basin thousands of kilometers away from the shortest distance between two points. In April they traveled eastward from New Zealand, some as far as South America, and then

swung northwestward across the equator toward one of three discrete summer feeding areas in the North Pacific: one near Japan, one in the Aleutians and the Gulf of Alaska, and one in the California Current. Each bird remained within one of those areas, and mates in some pairs migrated to separate areas. In October the birds completed the figure-eight by flying southwestward back to New Zealand, crossing over their April path.

The authors speculated that the roundabout route enables the birds to take energy-saving advantage of prevailing tailwinds. Flight speeds varied considerably, averaging 536 kilometers per day eastbound from New Zealand, 910 on the long leg northwestward, 220 within the North Pacific feeding areas, and then 837 on the long return flight. The fastest legs were marathon passages across vast, virtually foodless regions of the ocean where the birds rarely stopped to dive.



Sooty Shearwaters were recently tracked on a 65,000-kilometer migration covering much of the Pacific Ocean—the longest one-year journey ever documented for a bird. An electronic “tag” enabled researchers to follow the shearwaters’ travels through an entire non-breeding cycle. *Off Monterey, California; October 2006.* © Bob Steele.

Shaffer and his group studied the migration as part of an international research project named Tagging of Pacific Pelagics (TOPP). An animated map on the TOPP website <toppcensus.org> depicts the tagged shearwaters’ migration pattern in color-coded detail and provides links to publications explaining research and development behind the tracking technology. A second round of tracking was conducted in 2006 to learn whether these individual birds used the same or different migration flyways and North Pacific areas in the following year, Shaffer said (personal communication).

A detailed summary of online resources for tracking pelagic birds is provided in a WebExtra <aba.org/pubs/birding/archives/vol39no2p33w1.pdf> that accompanies this article.



Ruddy Duck Hybrids

Could the descendants of seven Ruddy Ducks imported from North America drive Eurasia's endangered White-headed Duck (*Oxyura leucocephala*) to extinction? Wildfowl experts consider this outcome possible unless the Ruddy Duck, a congeneric relative of the White-headed Duck, is eradicated from the Palearctic. A potentially critical threat is interbreeding by the non-native Ruddy Ducks with native White-headed Ducks. Genetic introgression could lead to loss of the White-headed Duck's specific behavioral and ecological adaptations, eventually causing its extinction. Research by the Wildfowl & Wetlands Trust (WWT) in England shows that Ruddy × White-headed hybrids are fertile through at least two generations of male hybrids backcrossed with White-headed females.

One of the world's rarest waterfowl, the White-headed Duck has a global population of fewer than 15,000. Most are in central Asia, where loss of critical wetland habitat and over-hunting have already caused a severe decline. An exception to the grim picture is Spain, where protection from habitat loss, hunting, and hybridization has increased western Europe's only population of White-headed Ducks from



Wildfowl experts fear that hybridization with the non-native Ruddy Duck could destroy the pure gene pool of Eurasia's endangered White-headed Duck (*Oxyura leucocephala*). Shown here is a first-generation male **Ruddy Duck × White-headed Duck** in definitive alternate plumage. *Slimbridge, Gloucestershire, United Kingdom.*
© Wildfowl & Wetlands Trust.

22 in 1977 to more than 2,500 today—a bright spot, though not nearly bright enough to ensure recovery of the species.

It has long been assumed that Europe's Ruddy Duck population originated in 1948 from seven birds imported into England for captive breeding. Many descendants of the seven subsequently escaped, and despite recent control efforts,

the current population is estimated at 4,000 in Britain. However, could some of Europe's present-day Ruddy Ducks be natural vagrants? Violeta Muñoz-Fuentes and four coauthors offered an answer in 2006 (*Molecular Ecology* 15:1441–1453). Patterns of mitochondrial DNA (mtDNA) in a sample of 107 Ruddy Ducks and characteristics of nuclear microsatellite genotypes in a sample of 142 point to ancestry from the introduced flock. Four lines of evidence suggest that conclusion:

- If Ruddy Duck populations in Europe originated from a small founding group, the European ducks should be less diverse genetically than those of the immense North American population. Indeed, the Muñoz-Fuentes team found relatively high mtDNA and microsatellite diversity in the North American sample, whereas no mtDNA variation and much lower diversity of microsatellite alleles appeared in the European birds.
- The pattern of low genetic diversity among European birds is consistent with a population deriving from just seven North American founders.
- Microsatellite alleles in the feral European population were also found in Britain's current captive birds, which are direct descendants of the seven original aliens.
- The European Ruddy Ducks were so clearly differentiated from the North American sample that none was likely to be a recent immigrant or its offspring.

Origins are an important consideration when drastic controls are proposed. It is easier to gain support for measures to eliminate descendants of captive-bred birds than those of natural immigrants. For example, the Royal Society for the Protection of Birds and the WWT support a government program to eradicate Britain's Ruddy Ducks, which are the primary source of continental Europe's growing population. More than 5,000 have been eliminated from Britain since 1999, and other nations are taking similar measures—an international effort that ornithologists believe is essential to the White-headed Duck's survival. It is urgently recommended by Baz Hughes, head of WWT's Species Conservation Department, who chairs the Threatened Waterfowl Specialist Group of the World Conservation Union and Wetlands International (personal communication): "Now that the United Kingdom has moved to eradicate its large feral population, governments across Europe should ensure that all Ruddy Duck populations, both feral and captive, are eradicated."

Evolution in Darwin's Finches

Ecological character displacement may seem easy to imagine for someone looking in from outside the realm of rigorous research in evolutionary biology. The chain of events is conceptually straightforward. Two similar species in separate ranges may require the same resource, such as a certain type of food, and have no competitor for it. But if the two come into contact and their ranges overlap, they must compete—intensely, if the required resource is extremely limited. Alternative results are possible. If one species is superior in exploiting the resource, eventually the inferior competitor may be extirpated from their shared range. Or natural selection may favor variations within one or both species that allow each to use different resources, reducing competition. If a favored variation, the “displaced” character, is genetically inherited, the two species can diverge sufficiently to share the overlapping range.

The actual occurrence of inherited character displacement is very difficult to demonstrate, but Peter R. Grant and B. Rosemary Grant took the demonstration an unprecedented step forward in 2006 (*Science* 313:224–226). They documented for the first time in nature, beyond laboratory experiments, an entire process of character displacement from initial competitive encounter to evolutionary change in one species. The character is bill size, and the species is the Medium Ground Finch (*Geospiza fortis*)—one of the “Darwin’s finches” that have embodied evolution in action during the Grants’ legendary 33 years of research on the tiny Galapagos island of Daphne Major.

The Grants had previously documented swift evolutionary changes in Galapagos finches’ bill size when unfavorable environmental conditions affected the food supply. A classic case occurred in 1977 when drought severely depleted the small seeds that were *fortis*’s usual food. Seeds that remained were larger and harder on average, and only rela-

tively large-billed *fortis* individuals could crack them open. A greater proportion of these large individuals survived to reproduce. By 1978—only a single generation later—bills inherited by their offspring averaged 4 percent larger than those of pre-drought *fortis*. Peter Grant described the phenomenon effusively in his book *Ecology and Evolution of Darwin’s Finches* as “[the] outstanding episode of natural selection that we have been fortunate enough to witness.”

At that time *fortis* had no competitor for its food; thus, character displacement was not involved. Instead, the adaptation was simply a direct response to food availability.



Where they are sympatric on the Galapagos Islands, the **Medium Ground Finch** (*Geospiza fortis*, left) and **Large Ground Finch** (*G. magnirostris*, right) compete for large seeds. When these seeds were scarce during a recent drought, *fortis* individuals with relatively small bills survived better by switching to small seeds without competition. Bill size is inherited, and in just one generation the average *fortis* bill size decreased significantly—a swift evolutionary response. Daphne Major, Galapagos Islands. © Peter R. Grant and B. Rosemary Grant.

ty. The Grants’ newly reported evolutionary change in *fortis* was different, although it stemmed from a similarly severe drought and food shortage in 2003. This time *fortis* faced a strong competitor for dwindling food, the Large Ground Finch (*G. magnirostris*), which had immigrated to Daphne Major, established a breeding population in 1982, and become abundant by 2003. In the new episode, selection pressure from competition with the larger species shifted the average bill size of *fortis* in the opposite direction: smaller. Unlike the situation in 1977, relatively large-billed *fortis* individuals were at a disadvantage. They competed more directly with *magnirostris* for large seeds, while smaller-billed individuals could switch to very small seeds without facing competition. More small-billed birds survived to reproduce, and in 2005—after just one generation of inheritance—the average bill of *fortis* offspring was approximately 4 percent smaller than the 2004 sample before the drought’s effect.

How important are the new findings? “This study will be an instant textbook classic,” evolutionary biologist Jonathan B. Losos told writer Elizabeth Pennisi in an article accompanying the Grants’ report (*Science* 313:156).