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What's in a MANE?

By Timothy F. Wright and Michael A. Russello

In Act II, Scene 2 of Shakespeare's Romeo and Juliet, Juliet famously declares "What's in a name? That which we call a rose / By any other name would smell as sweet." While that sentiment is a fine one for star-crossed lovers attempting to slip the bonds of feuding families, in the world of science and conservation names do matter.

THIS IS PARTICULARLY SO when it comes to defining that fundamental unit of biology - the species. While there are varying definitions of what exactly constitutes a species, most scientists understand the term to mean a collection of individuals that represents a distinct evolutionary unit capable of interbreeding.

The science of taxonomy is devoted to the characterization and naming of species. It is an ancient discipline that goes back at least as far as Aristotle, but it has particular relevance when it comes to the very modern discipline of conservation biology.

That is because our framework for protecting biodiversity is based on the concept of species—we devote effort and funds towards the protection of species that are judged to be threatened, and less to species that are not. But what about cases where our taxonomy is not correct? In particular, what about cases in which there are several different unrecognized species lumped together as a single species, perhaps because they look physically similar? And what if one of these so-called 'cryptic species' was rare and threatened and the other was common? Practically speaking, in these cases conservation efforts are limited because what we recognized as a species, the aggregate of two or more cryptic species, does not appear to be threatened.

In such cases we run a very real risk of allowing the extinction of a species simply because we failed to recognize it as such. A recent study we conducted with a graduate student, Ted Wenner, suggests we may be in danger of just such a scenario with the familiar parrot species *Amazona farinosa*, the Mealy Amazon.

The Mealy Amazon is a widespread rainforest species distributed from the Caribbean side of southern Mexico through Central America, northern South America and across the Amazon basin, with a spatially separated population in the highly fragmented Atlantic forests of southern Brazil.

Taxonomists have long recognized several different subspecies based on physical appearances, including *A. f. guatemalae* in southern Mexico and Guatemala, *A. f. virenticeps* from Honduras through western Panama, *A. f. inornata* in eastern Panama and northwestern South America, *A. f. chapmani* in the eastern foothills of the Andes mountains, and *A. f. farinosa* in the Amazon Basin and the Atlantic forest of Brazil.

At various times different taxonomic authorities have advocated recognizing at least some of these subspecies as full species, but most recent taxonomies treated them as a single extensive species. Before our work, there had been no comprehensive study of what the underlying genetic variation might tell us about the evolutionary distinctiveness of different subspecies.



A.f. farinosa © Valdir Hobus

Unlike many of its Amazon parrot cousins, which are listed on the IUCN Red List as Vulnerable or Endangered due to pressures including habitat loss and capture for the pet trade, the Mealy Amazon is listed as a species of Least Concern.

This listing, though, is due primarily to the observation that populations in South America are doing well. In Central America, where both habitat loss and poaching for the pet trade are more extensive, populations are in much worse shape. And critically, this listing is based on the assumption that populations extending from Mexico to southern Brazil are all members of the same species.

In 2011, the World Parrot Trust asked us to test this assumption using modern genetic data. The request was prompted by a study of evolutionary relationships in the genus *Amazona* previously performed by Mike Russello, in which he included four of the subspecies of the Mealy Amazon, two from Central America and two from South America (Russello and Amato, 2004 *Molecular Phylogenetics and Evolution*).

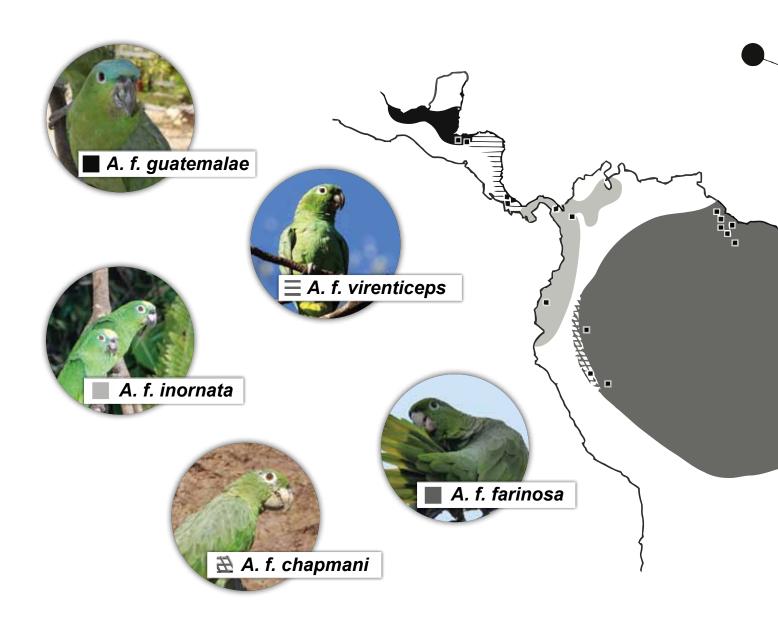
He found a deep genetic split between the Central and South America subspecies. In fact, this split was as deep as that found between other long-recognized species of *Amazona*. This result clearly hinted that the two groups of subspecies should be considered different species. But there were limitations to the study. One was that Mike had included just a single representative of each of 4 subspecies, so it was difficult to judge whether the variation seen between different subspecies might also be detected within a given subspecies.

Furthermore, the samples he used were collected from birds living in captivity with uncertain origins. These limitations left sufficient uncertainty about the species status that taxonomists and the IUCN were unwilling to declare the two groups of subspecies as distinct species, worthy of separate conservation status.

In designing our new study, we determined that vouchered specimens were a critical necessity. Vouchered specimens are tissues saved from birds collected in the wild by natural history museums that are linked to the skins of the birds preserved in the museum collections. Such specimens are the gold standard for studies such as ours because of the extensive data about locality and bird condition that accompany them.

Additionally, the presence of a wellpreserved skin in a collection allows future scientists to cross-check the genetic information from the samples with the physical data available from the skin itself.

The three of us contacted numerous museum collections around the world requesting samples of Mealy Amazons; in all, seven different institutions sent us small bits of tissue from **Fig 1.** The map below illustrates the distributions of the currently recognized subspecies of *Amazona farinosa*. The network to the right of the map illustrates genetic distances between different subspecies, with the length of the branches proportional to the number of mutational steps between samples (up to 6 changes, and illustrated with numbers thereafter).



vouchered specimens they had collected. Importantly, these samples spanned the range of the species, and included multiple representatives from each subspecies.

With samples in hand, Ted got to work in the lab. He quickly extracted DNA from the tissue and amplified sequences from a variety of genes representing both the nuclear and mitochondrial genomes. We then conducted several different analyses to characterize the genetic similarities and differences among these samples. The results provided striking confirmation of Mike's earlier results. We found large genetic distances between the two Central American subspecies on one hand and the three South American subspecies on the other (Fig 1).

These differences were as great as those found between many pairs of well-established bird species. Within South America, we found consistent differences between the *inornata* subspecies in the northwest and the *farinosa* subspecies in central South America, although these differences were smaller than those found between Central and South American subspecies. In contrast, we found no consistent differences among representatives of the *chapmani* subspecies and the neighboring *farinosa* subspecies, nor did we detect any differences between the Amazon basin and Atlantic Forest populations of *farinosa*. Finally, we did not detect any consistent differences between the two Central American subspecies. The results are now published in the journal *Conservation Genetics* (Wenner, Russello and Wright, 2012, *Conservation Genetics*).

How did these genetic differences among subspecies come about? To address this question, we estimated a Fig 1. Adapted from "Cryptic species in a Neotropical parrot: genetic variation within the Amazona farinosa species complex and its conservation implications", by Wenner, TJ and Russello, MA and Wright, TF, 2012, Conservation Genetics, p. 13. Copyright © 2012 Springer, Part of Springer Science+Business Media. Reprinted with kind permission from Springer Science+Business Media B.V.

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general timeframe within which the Central and South American lineages diverged using a molecular clock. This approach takes advantage of the general observation that the number of genetic differences between two groups is related to the amount of time since they have genetically separated.

In the case of the Mealy Amazon, a rough estimate based on the number of genetic differences and a standard molecular clock suggests that the Central American and South American lineages split from a common ancestor about 1.8 to 2.7 million years ago, after the formation of the Isthmus of Panama about 3.5 million years ago. This timing suggests a scenario in which the common ancestral population lived in South America, and the lineage that eventually led to the Central America subspecies split off and dispersed up the Isthmus of Panama.

The South American population later experienced a further split between populations in the central Amazonian basin and the northwestern part of the continent, perhaps influenced by the

Mealy Amazon

Amazona farinosa

The Mealy Amazon occurs in tropical Central America and South America. It frequents humid to semi-humid forest and plantations. Because the Mealy Amazon has been heavily trapped for the wild bird trade and shot for food in French Guiana there is evidence of a decline in the population.

Did You Know? The name Mealy comes from the bird's peculiar colouration, giving it a "dusty" or "powdered" appearance.



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A. f. virenticeps © Luis Guzman

ongoing rise of the Andes mountains. These results emphasize the important fact that evolution, and the different species that result from it, is an ongoing process rather than something that only happened eons ago.

And what do these genetic results tell us about cryptic diversity within the single, currently recognized species of Mealy Amazon? They suggest that, at minimum, this single species should be treated as two distinct species, one in Central America and one in South America and Panama.

An argument might also be made for the *inornata* and *farinosa* subspecies within South America to be each given full species status, but this case is not quite as strong given the smaller genetic distances observed between these two subspecies.

In any case, it is the distinction between Central and South American populations that has the most important conservation implications, given the intense pressures that are currently experienced by the Central American populations. Recognition of these populations as their own species would immediately trigger a reconsideration of conservation status to better reflect the threats they are facing.

So, what's in a name? Sadly, for Romeo and Juliet, names meant tragedy. Unlike Romeo and Juliet, though, this story of a name may have a happy ending. The taxonomic group responsible for naming Central and South American birds has asked us to submit a proposal for reclassifying the Mealy Amazon.

A request to the IUCN for reconsideration of conservation status would follow. Although these proposals require careful consideration, there is a good chance that, with continued attention, the new genetic data we have collected will eventually lead to the naming of a new species of Amazon parrot in Central America.

More importantly, the elevated taxonomic status would offer important opportunities for more accurately recognizing the threats faced by this new proposed species of conservation significance.