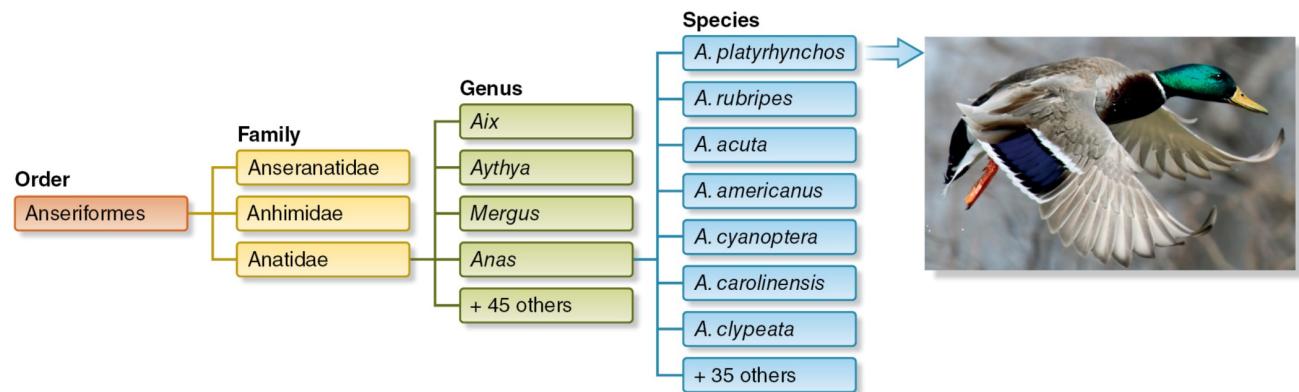


# Classifying Avian Diversity

## Why Classify?

1. Classification provides order, understanding of relatedness
2. Related taxa have ***synapomorphies*** (what are these?)
3. Classifications have always been hierarchical; we now use ***phylogenies*** for classification



# Classifying Avian Diversity

What is in a name?

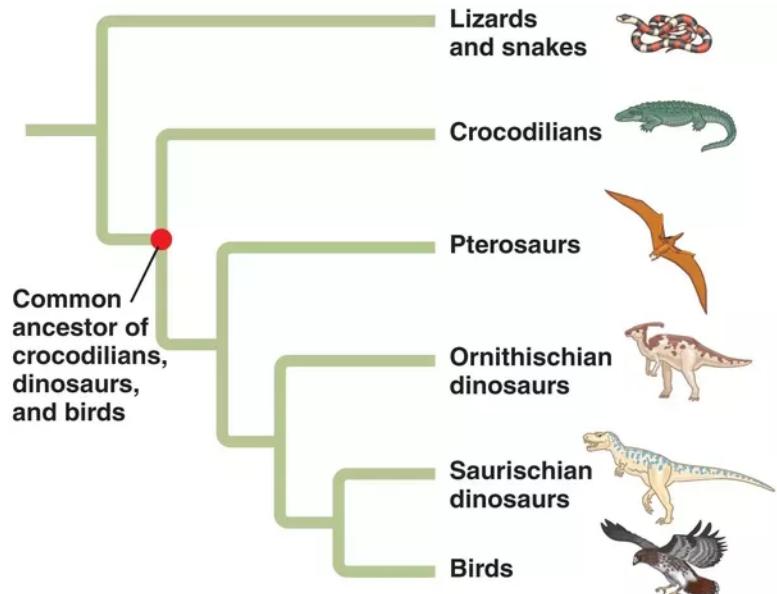
Scissor-tailed Flycatcher  
*Tyrannus forficatus*

*Muscicapa forficata* Gmelin, 1789

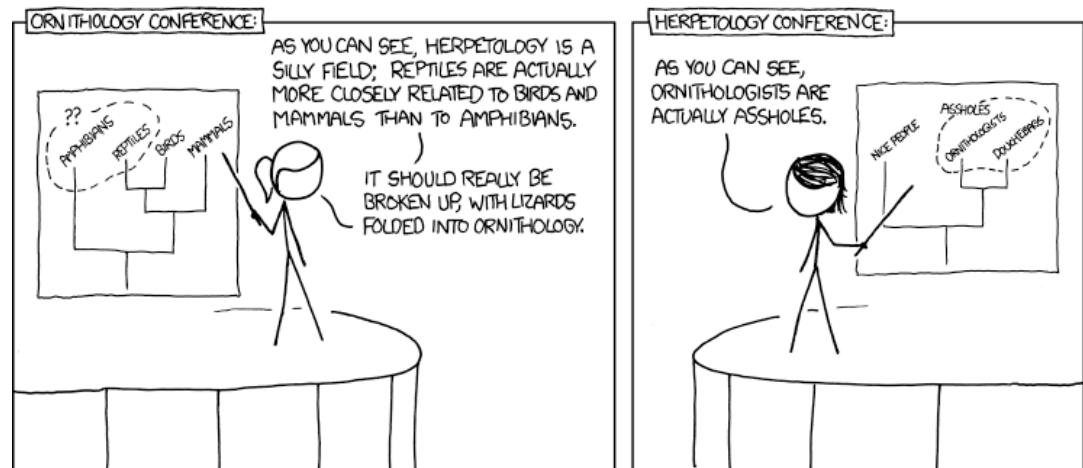


# Classifying Avian Diversity

Where birds fit into the tree of life



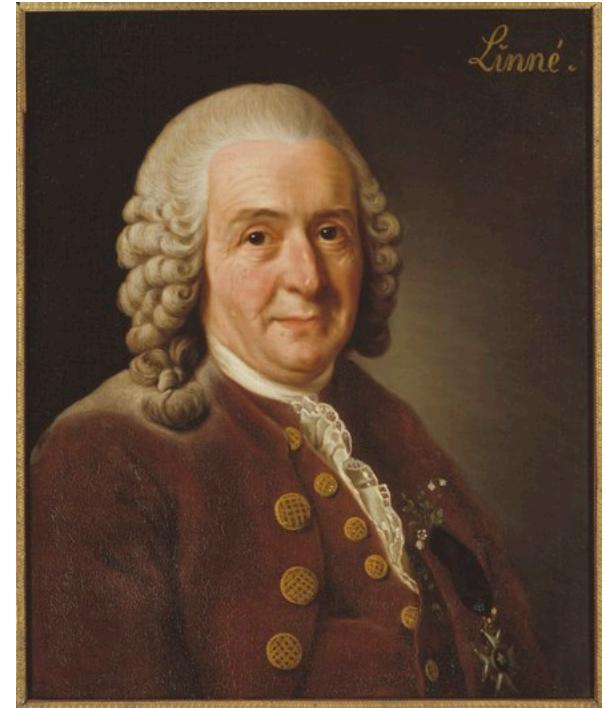
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# Classifying Avian Diversity

## Carl Linnaeus: Role in Bird Classification

1. Birds are: “creatures of the air, gifted in song, winged, loveliest of them all”
2. Linneus was the first to exclude bats from birds!
3. 10<sup>th</sup> edition of *Systema Naturae* introduced binomial taxonomy
  1. 554 birds named; grouped into seven orders
  2. Orders established primarily based on birds' bills and feet. (why?)
    1. Accipitres – Birds of Prey, Owls
    2. Picae – Woodpeckers, Parrots, Toucans, Hummingbirds + Crows
    3. Anseres – Ducks, Geese, Swans,
    4. Grallae – Herons, Flamingos, Sandpipers
    5. Gallinae – Phasians, Chickens, Curassows, Grouse
    6. Passeres – Songbirds + Pigeons, Swifts, Nightjars



A



B



C



D



E



F



G



H



I



Atlantic Puffin



King Vulture



Andean Cock-of-the-Rock



Black-hooded Sunbeam



Red-tailed Tropicbird



Chimney Swift



Summer Tanager



Great Hornbill



Resplendent Quetzal

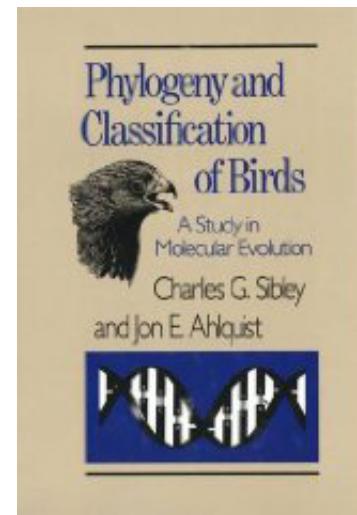
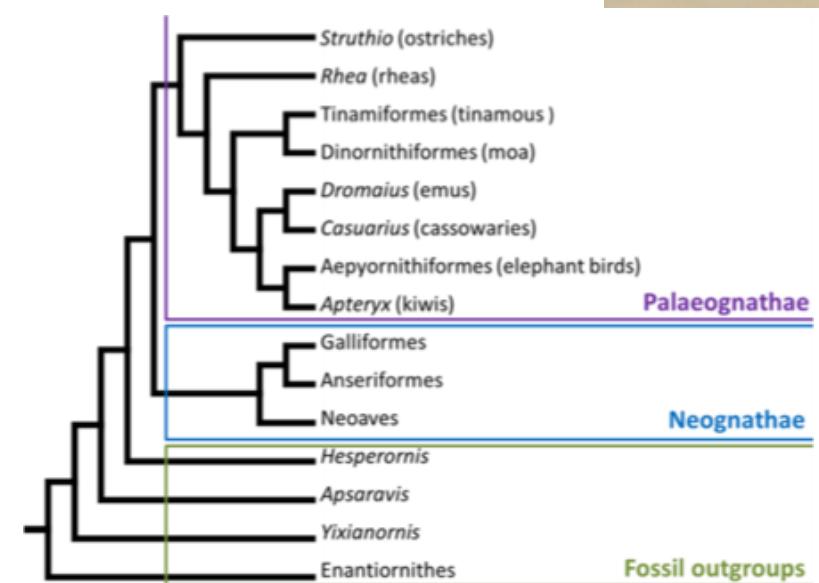
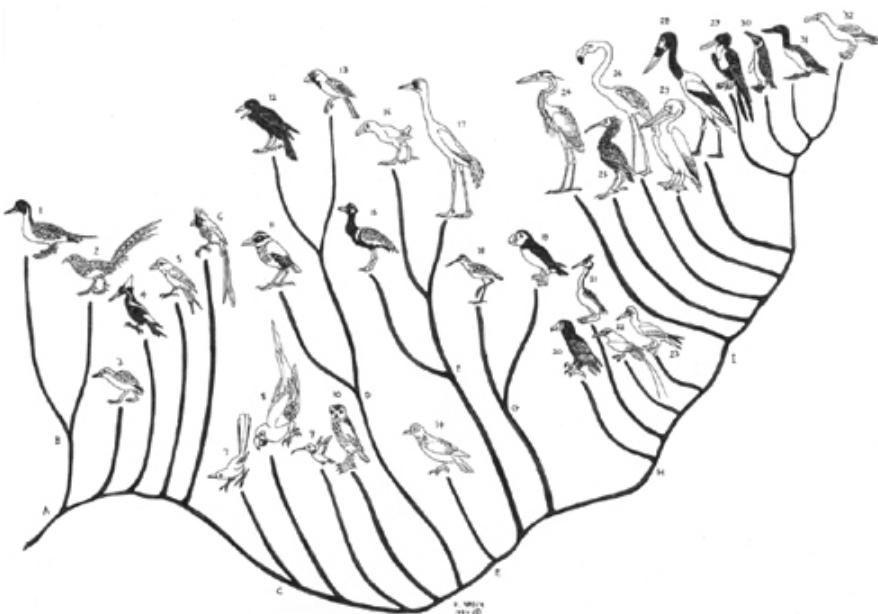


# Classifying Avian Diversity

Modern Bird Taxonomy I: Sibley and Ahlquist (1990)

First attempt to use DNA to generate a comprehensive phylogeny for birds

Used DNA–DNA Hybridization (akin to distance) to create a “tapestry”



# Classifying Avian Diversity



## Modern Bird Taxonomy II: Jarvis et al (*Science* 2014)

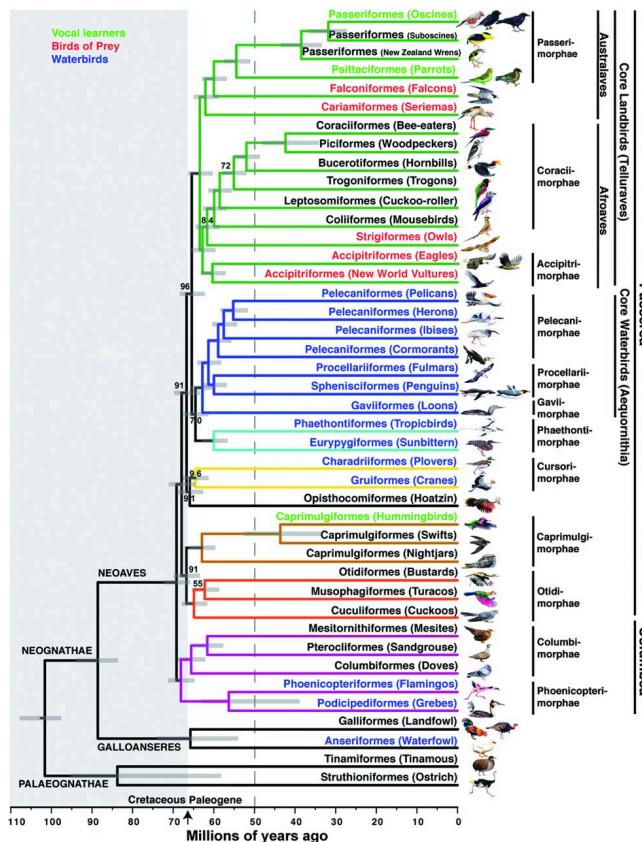
Used whole genomes to generate tree

48 species used to generate the tree

### RESEARCH ARTICLE

#### Whole-genome analyses resolve early branches in the tree of life of modern birds

Erich D. Jarvis,<sup>1,\*†</sup>; Siavash Mirarab,<sup>2\*</sup>; Andre J. Aberer,<sup>3</sup>; Bo Li,<sup>4,5,6</sup>; Peter Houde,<sup>7</sup>; Cai Li,<sup>4,7</sup>; Simon Y. W. Ho,<sup>8</sup>; Brant C. Faircloth,<sup>9,10</sup>; Benoit Nabholz,<sup>11</sup>; Jason T. Howard,<sup>12</sup>; Alexander Suh,<sup>13</sup>; Claudio C. Weber,<sup>12</sup>; Rute R. da Fonseca,<sup>6</sup>; Jianwen Li,<sup>4</sup>; Fang Zhang,<sup>4</sup>; Hui Li,<sup>4</sup>; Long Zhou,<sup>4</sup>; Nitish Narula,<sup>7,13</sup>; Liang Liu,<sup>14</sup>; Ganesh Ganapathy,<sup>1</sup>; Bastien Boussan,<sup>15</sup>; Md. Shamsuzzoha Bayzid,<sup>9</sup>; Volodymyr Zavidovych,<sup>16</sup>; Sanjay Subramanian,<sup>16</sup>; Toni Gabaldón,<sup>21,18,19</sup>; Salvador Capella-Gutiérrez,<sup>17,19</sup>; Jaime Huerta-Cepas,<sup>17,19</sup>; Bhama Rekpeljalli,<sup>20</sup>; Kasper Munch,<sup>20</sup>; Mikkel Schlerup,<sup>21</sup>; Bent Lindow,<sup>6</sup>; Wesley C. Warren,<sup>20</sup>; David Ray,<sup>22,24,25</sup>; Richard E. Green,<sup>26</sup>; Michael W. Bruford,<sup>27</sup>; Xiangjiang Zhan,<sup>27,28</sup>; Andrew Dixon,<sup>29</sup>; Shenghui Li,<sup>23</sup>; Ning Li,<sup>23</sup>; Yinhua Huang,<sup>23</sup>; Elizabeth P. Derryberry,<sup>30,31</sup>; Made Frost Bertelsen,<sup>32</sup>; Frederick H. Sheldon,<sup>33</sup>; Robb T. Brumfield,<sup>33</sup>; Claudio V. Melo,<sup>33,34</sup>; Peter V. Lovell,<sup>35</sup>; Morgan Wirthlin,<sup>35</sup>; María Paula Cruz Schneider,<sup>36,37</sup>; Francisco Prostocinosi,<sup>36,38</sup>; José Alfredo Samaniego,<sup>36</sup>; Ahmed Missael Vargas Velazquez,<sup>36</sup>; Alonso Alvaro-Núñez,<sup>37</sup>; Paula F. Campos,<sup>36</sup>; Bent Petersen,<sup>39</sup>; Thomas Sicheritz-Ponten,<sup>39</sup>; An Pas,<sup>40</sup>; Tom Bailey,<sup>41</sup>; Paul Scelfold,<sup>42</sup>; Michael Bunce,<sup>43</sup>; David M. Lambert,<sup>44</sup>; Qi Zhou,<sup>44</sup>; Polina Pereiman,<sup>45,46</sup>; Amy C. Driskell,<sup>47</sup>; Beth Shapiro,<sup>48</sup>; Zhen Xiong,<sup>49</sup>; Yongli Zeng,<sup>49</sup>; Shiping Liu,<sup>49</sup>; Zhenyu Li,<sup>49</sup>; Binghang Liu,<sup>49</sup>; Kui Wu,<sup>49</sup>; Jin Xiao,<sup>49</sup>; Xiong Yingli,<sup>49</sup>; Qiumei Zheng,<sup>49</sup>; Yong Zhang,<sup>49</sup>; Haizheng Yang,<sup>49</sup>; Jian Wang,<sup>49</sup>; Linnea Smeds,<sup>50</sup>; Frank E. Rheinhardt,<sup>49</sup>; Michael Braun,<sup>51</sup>; Jon Fjeldså,<sup>51</sup>; Lluísori Orlando,<sup>51</sup>; F. Keith Barker,<sup>52</sup>; Knud Andreas Jansson,<sup>51,53,54</sup>; Warren Johnson,<sup>52</sup>; Klaus-Peter Koepfli,<sup>52</sup>; Stephen O'Brien,<sup>57,58</sup>; David Haussler,<sup>59</sup>; Oliver A. Ryder,<sup>60</sup>; Carsten Rahbek,<sup>51,54</sup>; Eske Willerslev,<sup>59</sup>; Gary R. Graves,<sup>51,61</sup>; Travis C. Glenn,<sup>62</sup>; John McCormack,<sup>63</sup>; Dave Burt,<sup>64</sup>; Hans Ellegren,<sup>65</sup>; Per Alström,<sup>63,66</sup>; Scott V. Edwards,<sup>67</sup>; Alexandros Stamatakis,<sup>5,68</sup>; David P. Mindell,<sup>69</sup>; Joel Cracraft,<sup>70</sup>; Edward L. Braun,<sup>71</sup>; Tandy Warnow,<sup>5,72</sup>; Wang Jun,<sup>46,73,74,75,76</sup>; M. Thomas P. Gilbert,<sup>6,69</sup>; Guojie Zhang,<sup>6,77</sup>.



# Classifying Avian Diversity

Modern Bird Taxonomy II: Prum et al (2015 *Nature*)

Used targeted genes (259) from 198 species to generate tree

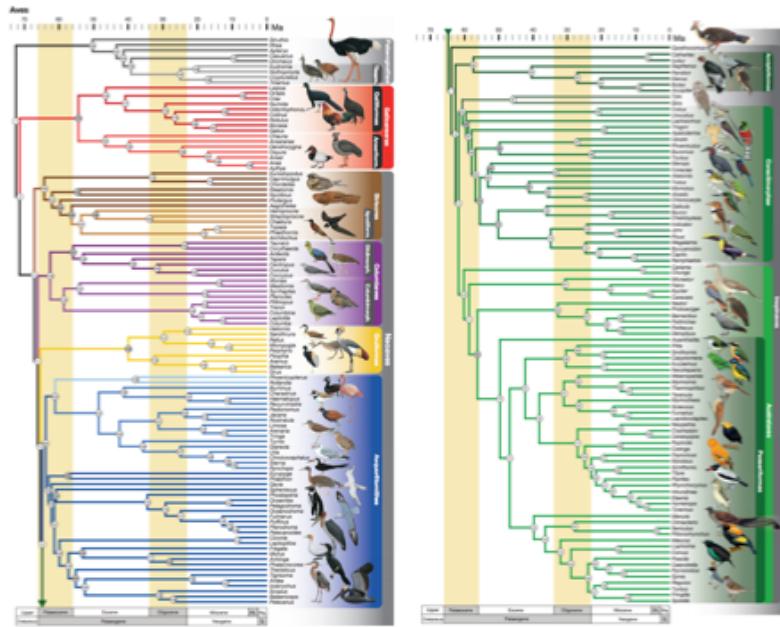


LETTER

doi:10.1038/nature15697

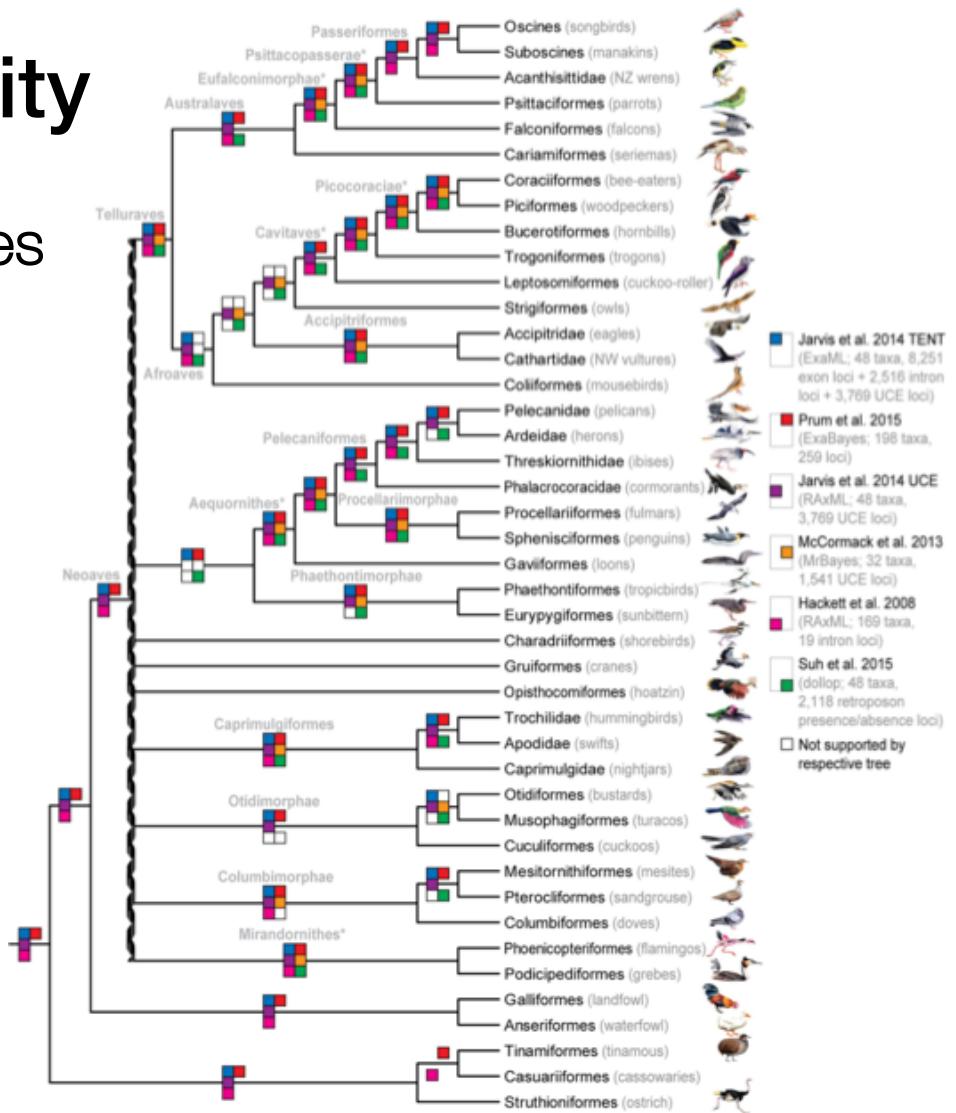
A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing

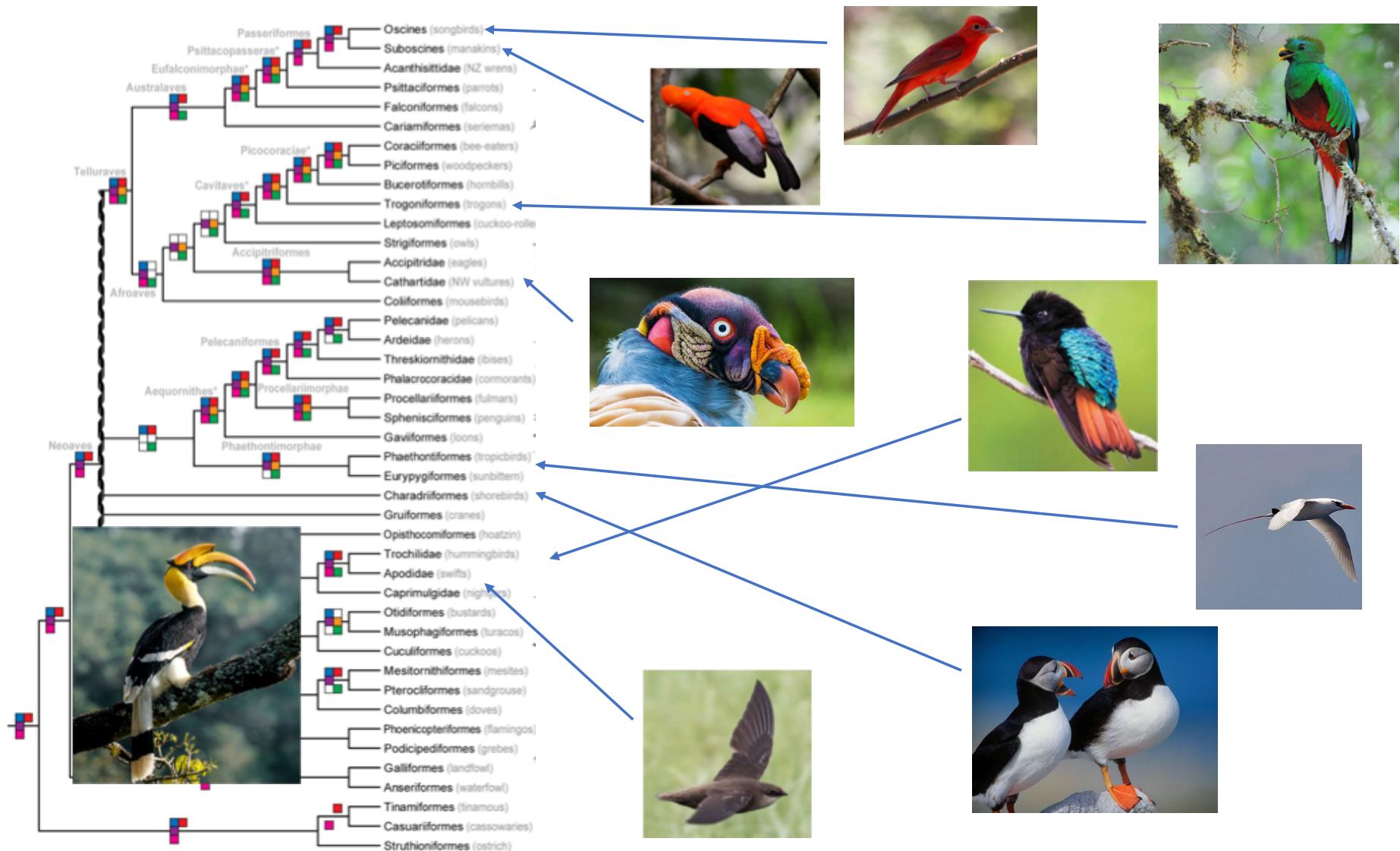
Richard O. Prum<sup>1,2\*</sup>, Jacob S. Berv<sup>3\*</sup>, Alex Dornburg<sup>2,3,4</sup>, Daniel J. Field<sup>2,3</sup>, Jeffrey P. Townsend<sup>1,6</sup>, Emily Moirany Lemmon<sup>2</sup> & Alan R. Lemmon<sup>2</sup>



# Classifying Avian Diversity

Broad consensus among recent trees

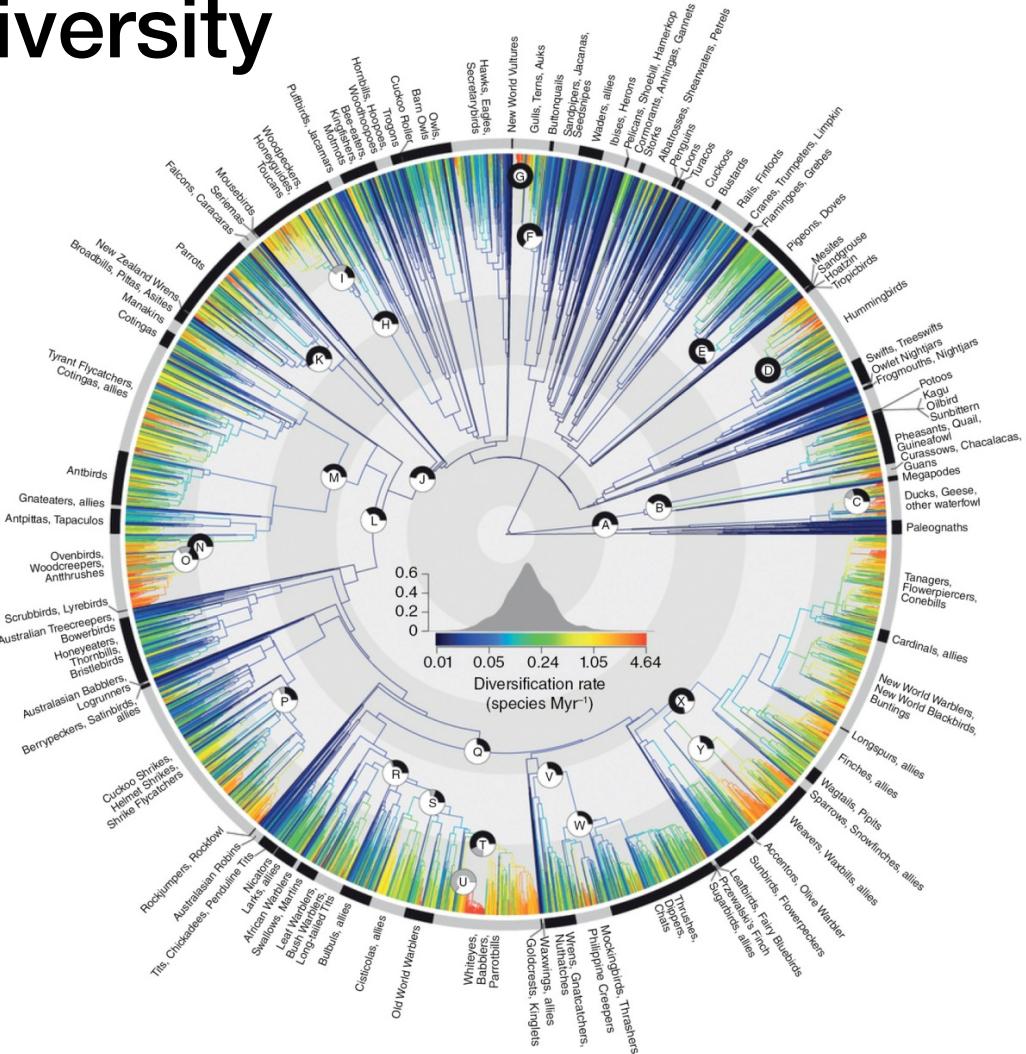




# Classifying Avian Diversity

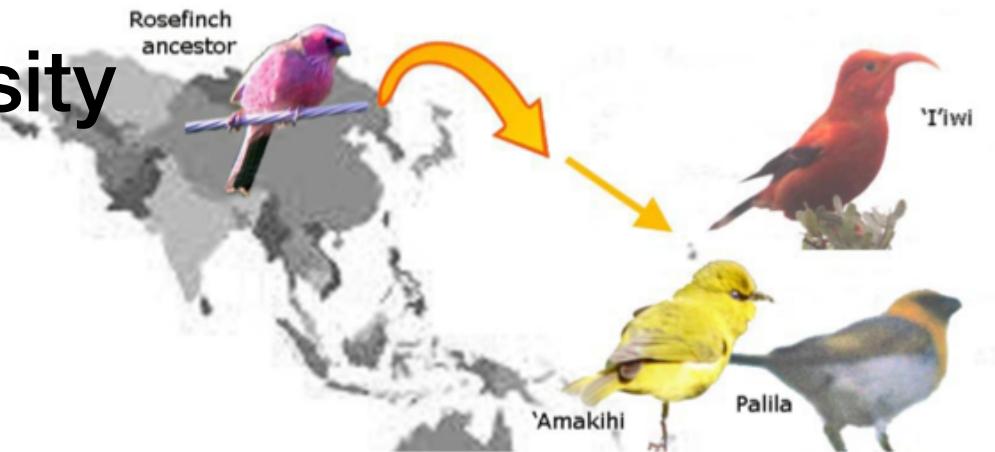
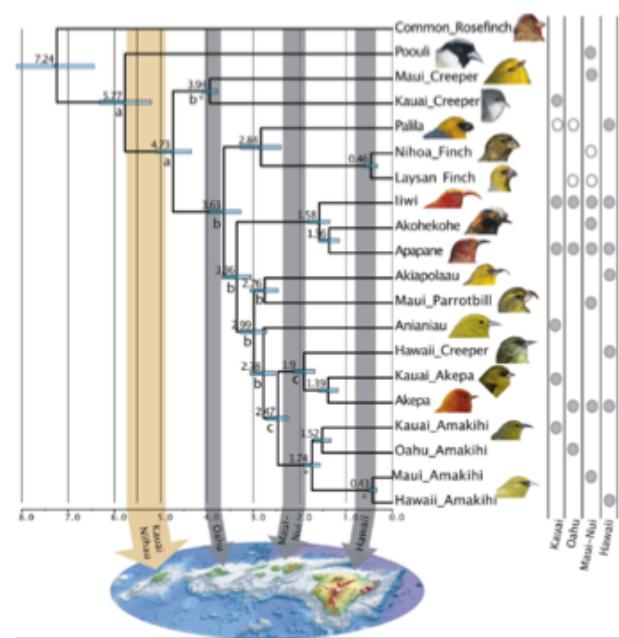
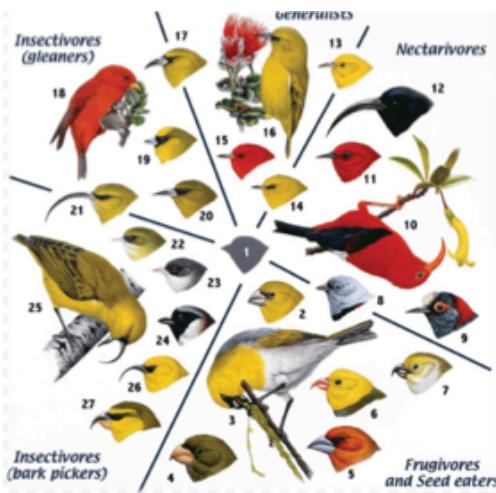
## Differing rates of evolution

We will come back to this!



# Classifying Avian Diversity

## Avian Radiations: Hawaiian Honeycreepers



Lerner et al 2011 *Current Biology*

# Classifying Avian Diversity

Two "species" have different ranges, different vocalizations\*, maybe assortively mate in contact zone



Pacific-slope Flycatcher (*E. difficilis*)



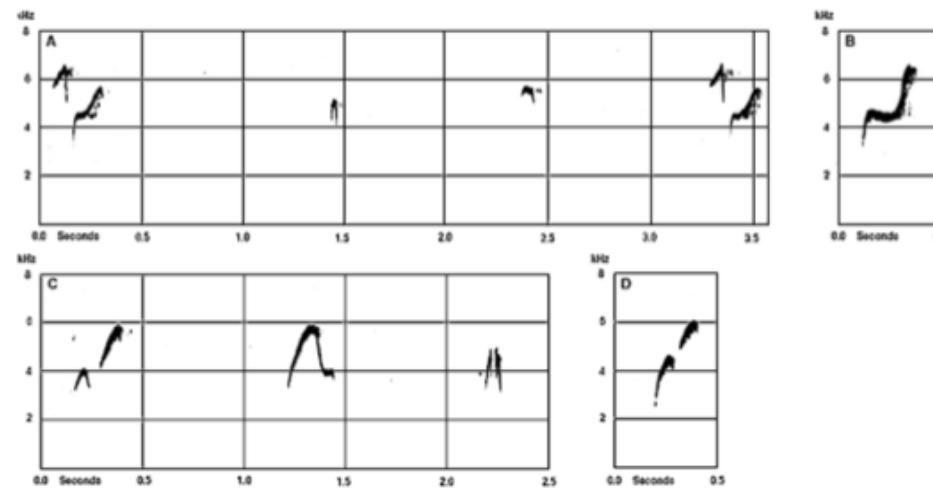
Cordilleran Flycatcher (*E. occidentalis*)



# Classifying Avian Diversity

Taxonomic Splitting:  
the case of *Empidonax difficilis* (Western Flycatcher)

Pacific-slope Flycatcher (*E. difficilis*)



Cordilleran Flycatcher (*E. occidentalis*)



# Classifying Avian Diversity

Taxonomic Lumping: *Ramphocelus*



Scarlet-rumped Tanager



Cherrie's Tanager



# Classifying Avian Diversity

Taxonomic Lumping: *Ramphocelus*

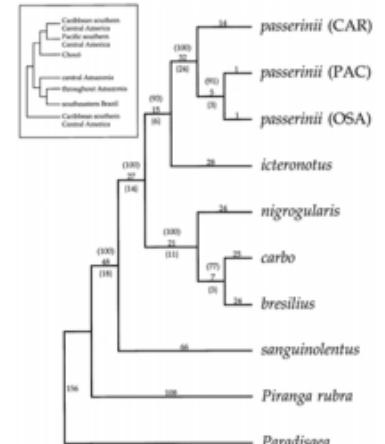
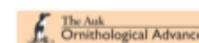


FIG. 2. Parsimony analysis of *Ramphocelus* combined cytochrome b and ND2 sequences. Numbers at nodes are unambiguous branch lengths (using DELTRAN optimization). Numbers in parentheses above branches are bootstrap values; numbers in brackets below branches are decay values. Inset is the hypothesized area relationships based on the *Ramphocelus* phylogeny.

Hackett 1996 *Mol. Phy. Evol.*



AmericanOrnithology.org  
Volume 134, 2017, pp. 857–879  
DOI: 10.1642/AUK-17-451

RESEARCH ARTICLE

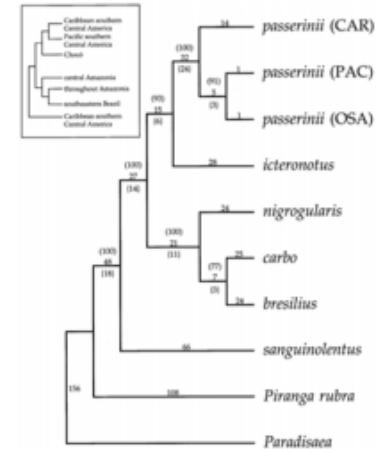
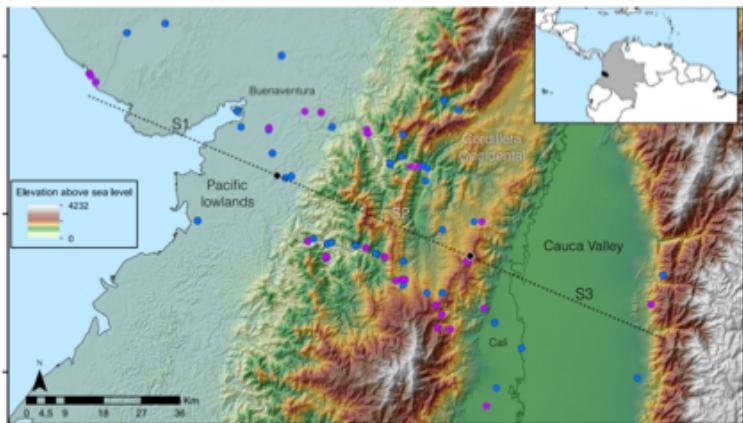
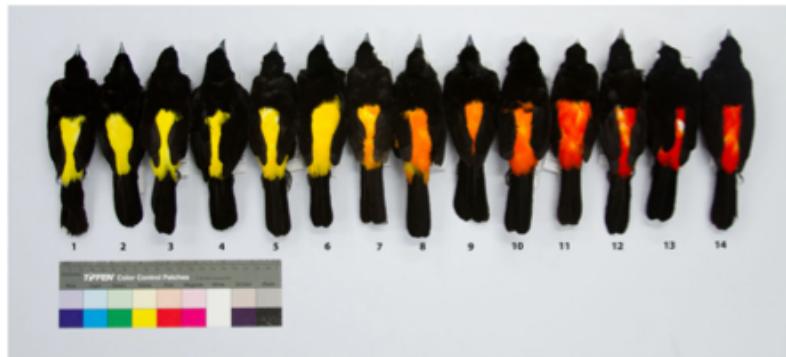
Using song playback experiments to measure species recognition between geographically isolated populations: A comparison with acoustic trait analyses

Benjamin G. Freeman<sup>1,2\*</sup> and Graham A. Montgomery<sup>3</sup>



# Classifying Avian Diversity

Hybrid zones: windows into speciation

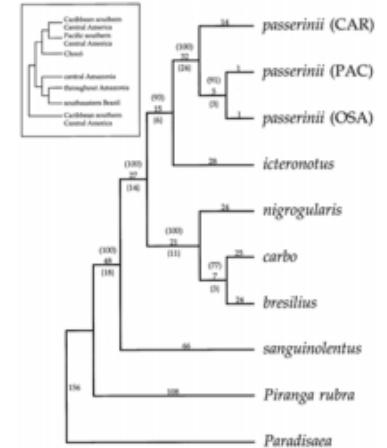
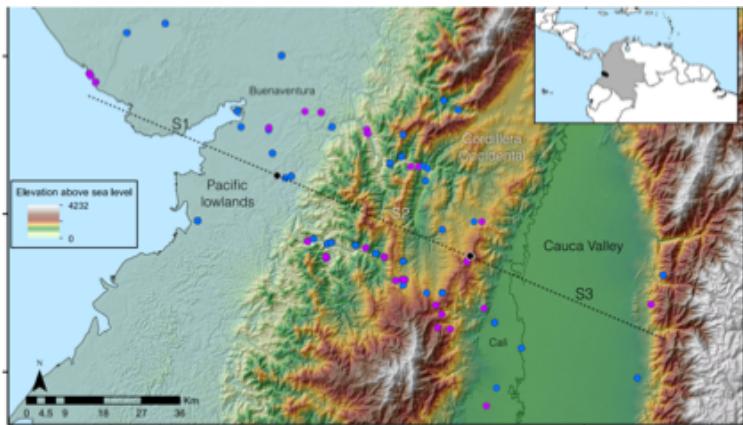
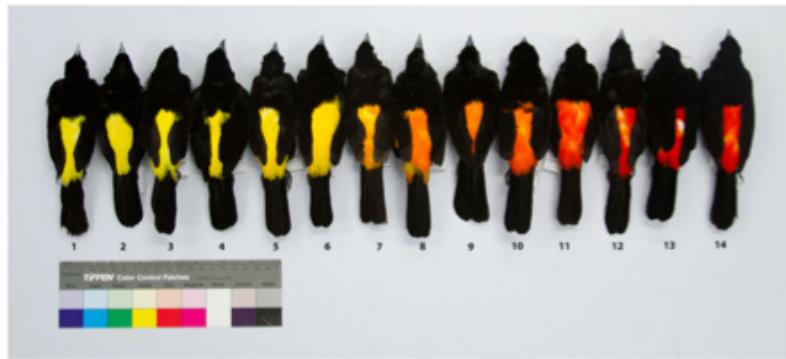


**FIG. 2.** Parsimony analysis of *Ramphocelus* combined cytochrome b and ND2 sequences. Numbers at nodes are unambiguous branch lengths (using DELTRAN optimization). Numbers in parentheses above branches are bootstrap values; numbers in brackets below branches are decay values. Inset is the hypothesized area relationships based on the *Ramphocelus* phylogeny.

Hackett 1996 *Mol. Phy. Evol.*

# Classifying Avian Diversity

Hybrid zones: windows into speciation

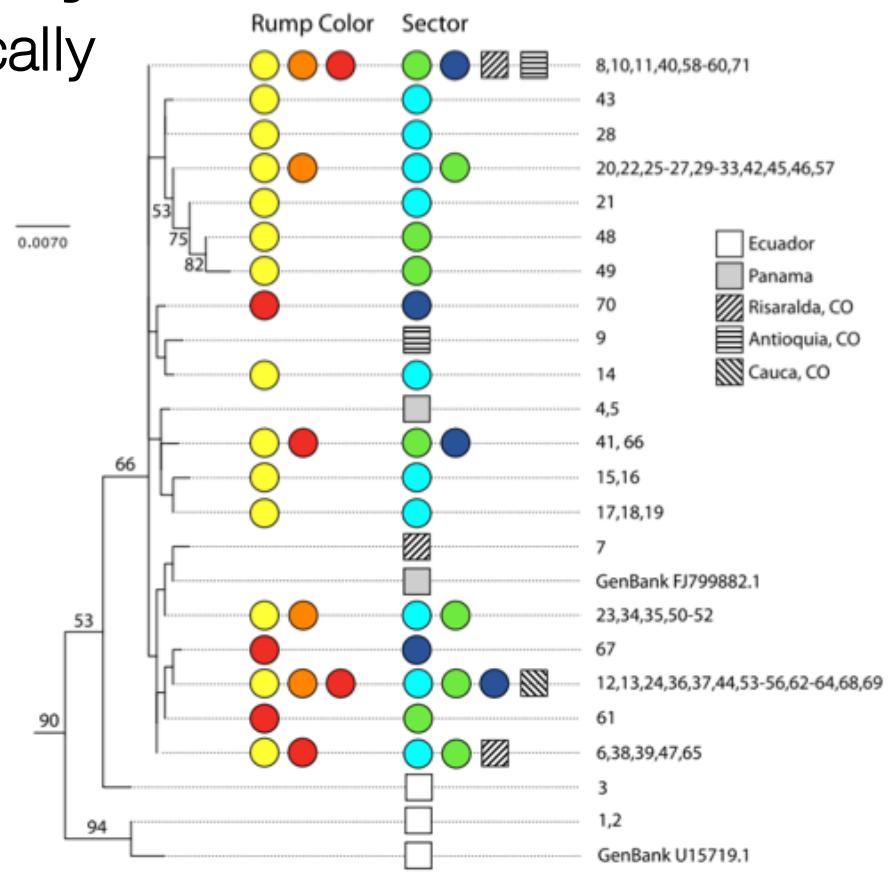
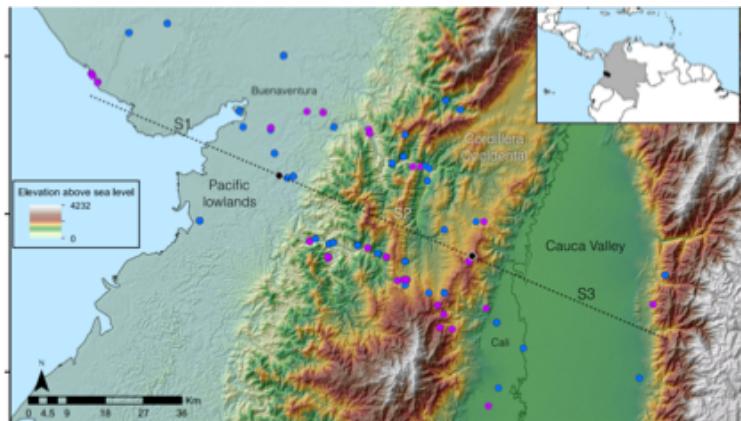


**FIG. 2.** Parsimony analysis of *Ramphocelus* combined cytochrome b and ND2 sequences. Numbers at nodes are unambiguous branch lengths (using DELTRAN optimization). Numbers in parentheses above branches are bootstrap values; numbers in brackets below branches are decay values. Inset is the hypothesized area relationships based on the *Ramphocelus* phylogeny.

Hackett 1996 *Mol. Phy. Evol.*

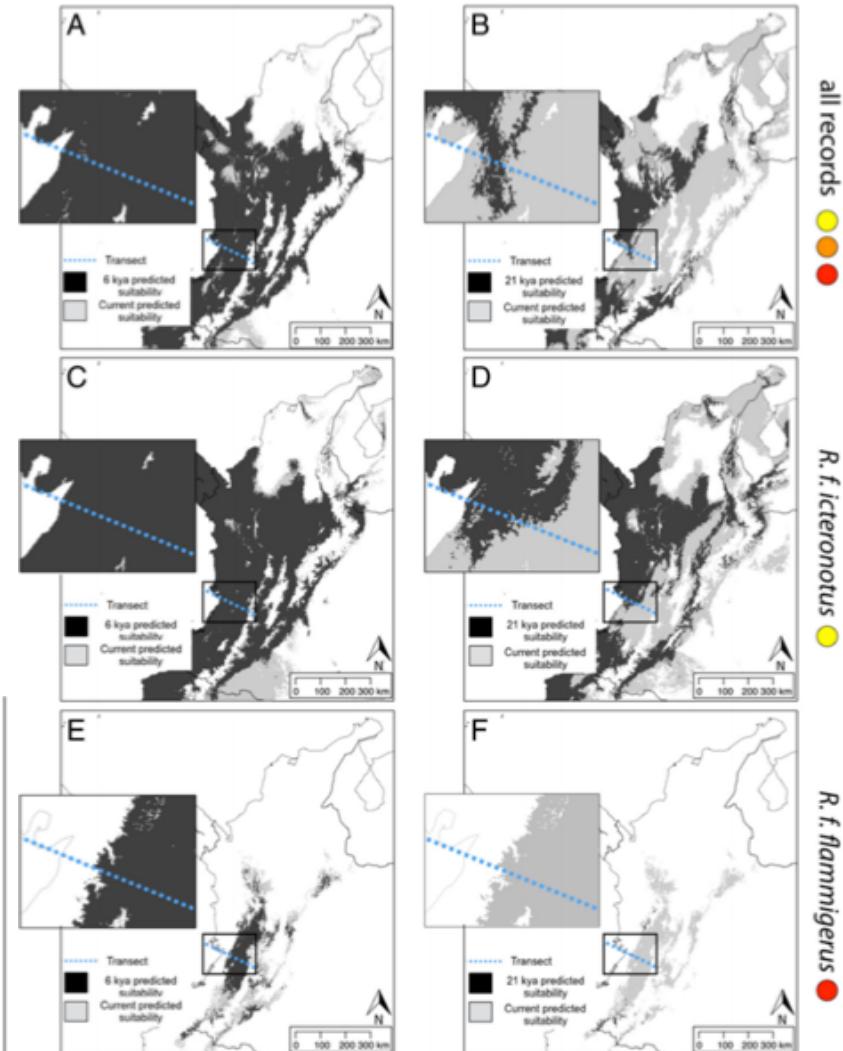
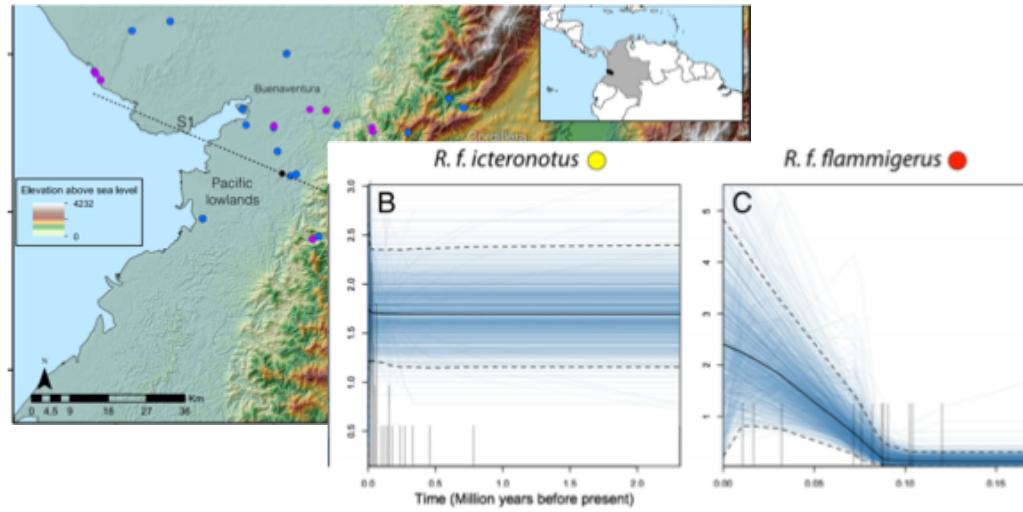
# Classifying Avian Diversity

## Color morphs not defined genetically



# Classifying Avian Diversity

Color morphs reflect historical ranges!



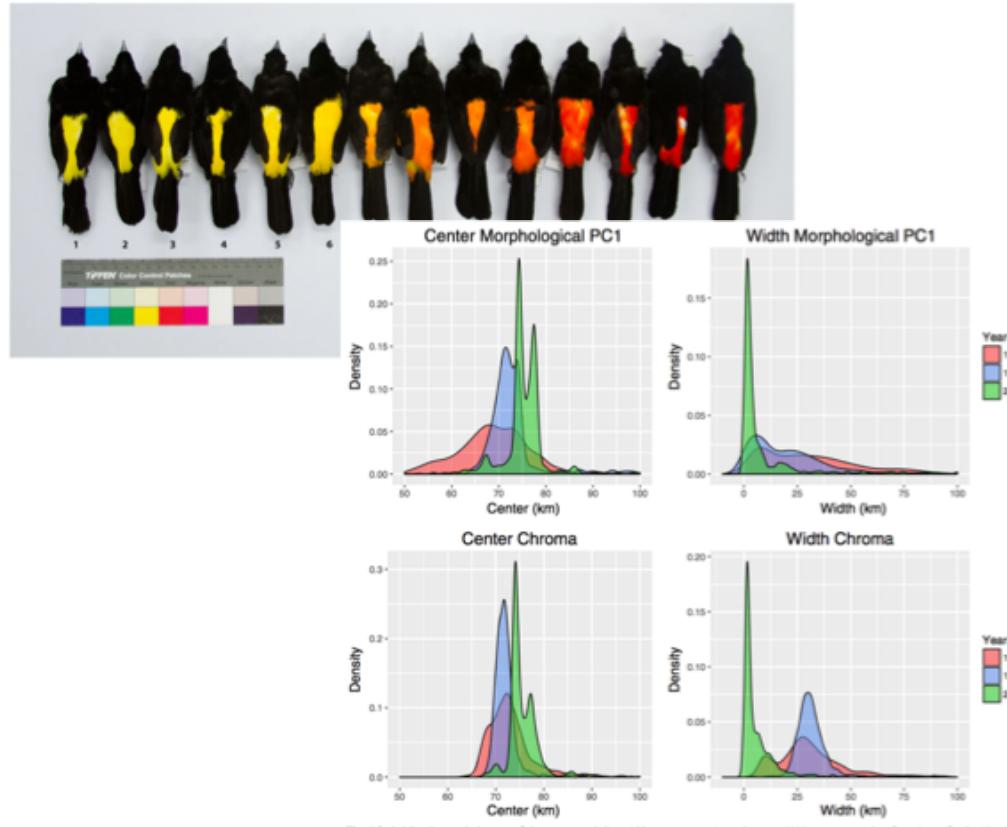
all records

*R. f. icteronotus*

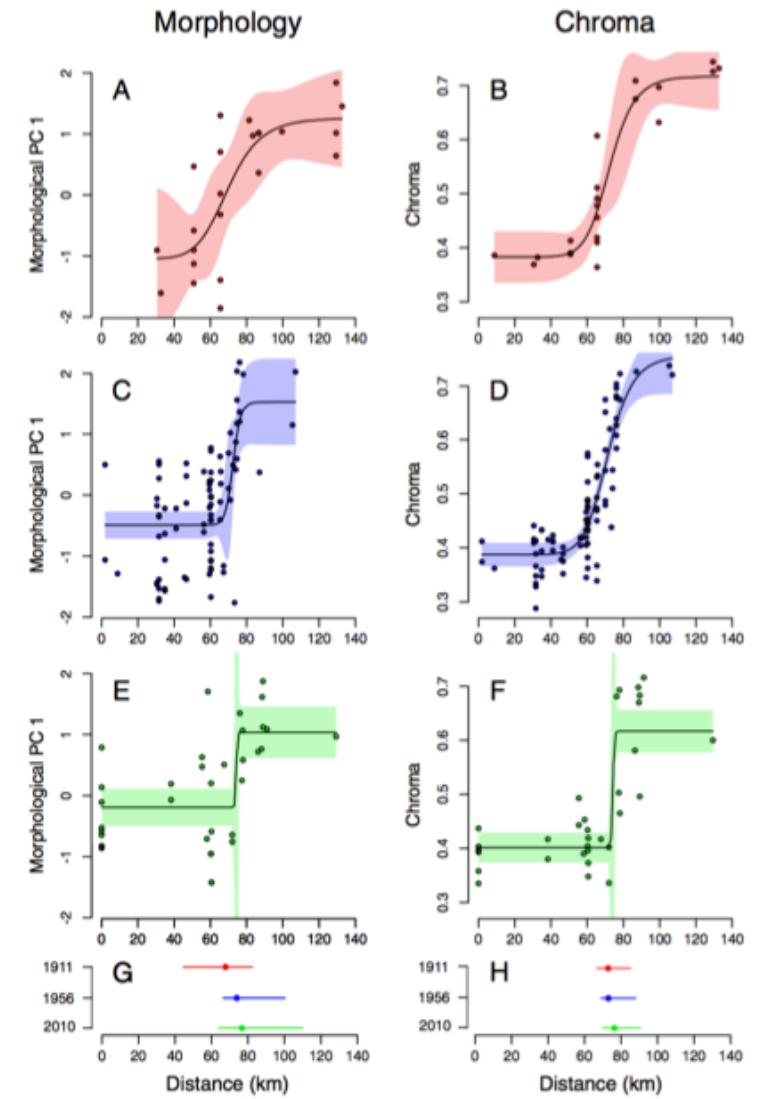
*R. f. flammigerus*

# Classifying Avian Diversity

Hybrid zone moves over a century!

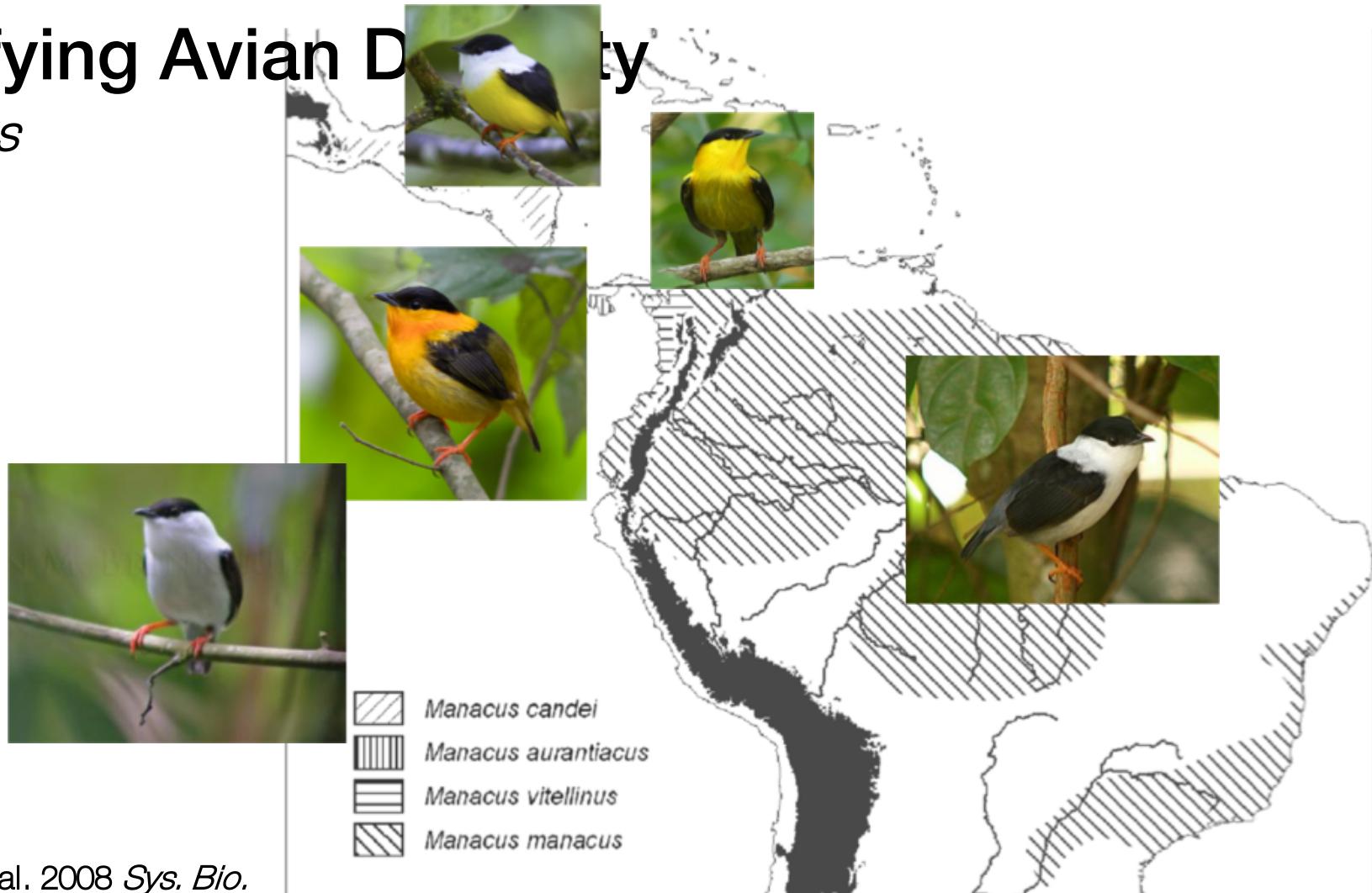


Yet another reason to continue collecting specimens!



# Classifying Avian Diversity

*Manacus*

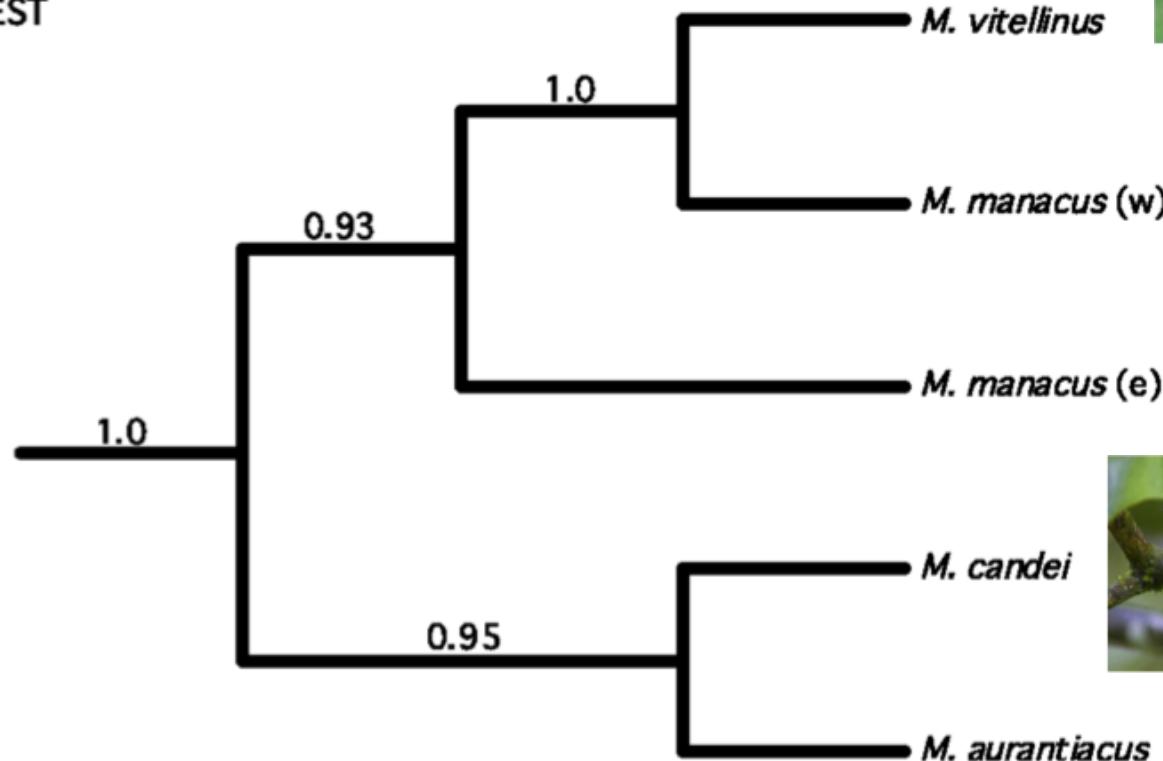


Brumfield et al. 2008 *Sys. Bio.*

# Classifying Avian Diversity

*Manacus*

c) BEST

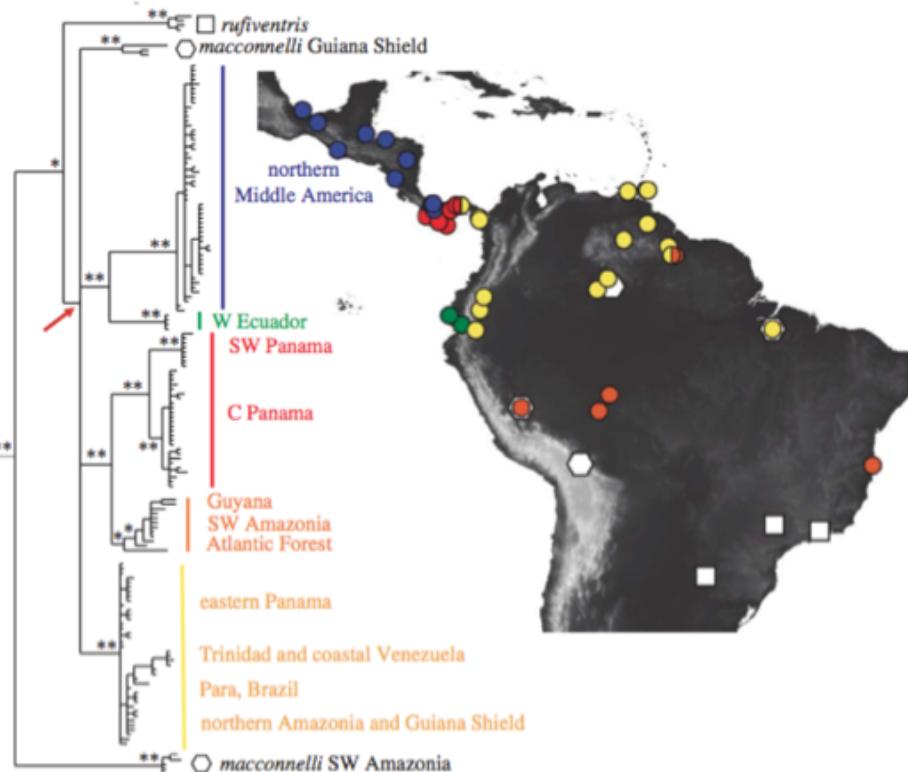


Brumfield et al. 2008 *Sys. Bio.*

# Complex trans-Andes phylogeography of *Mionectes oleagineus*



— 1% sequence divergence

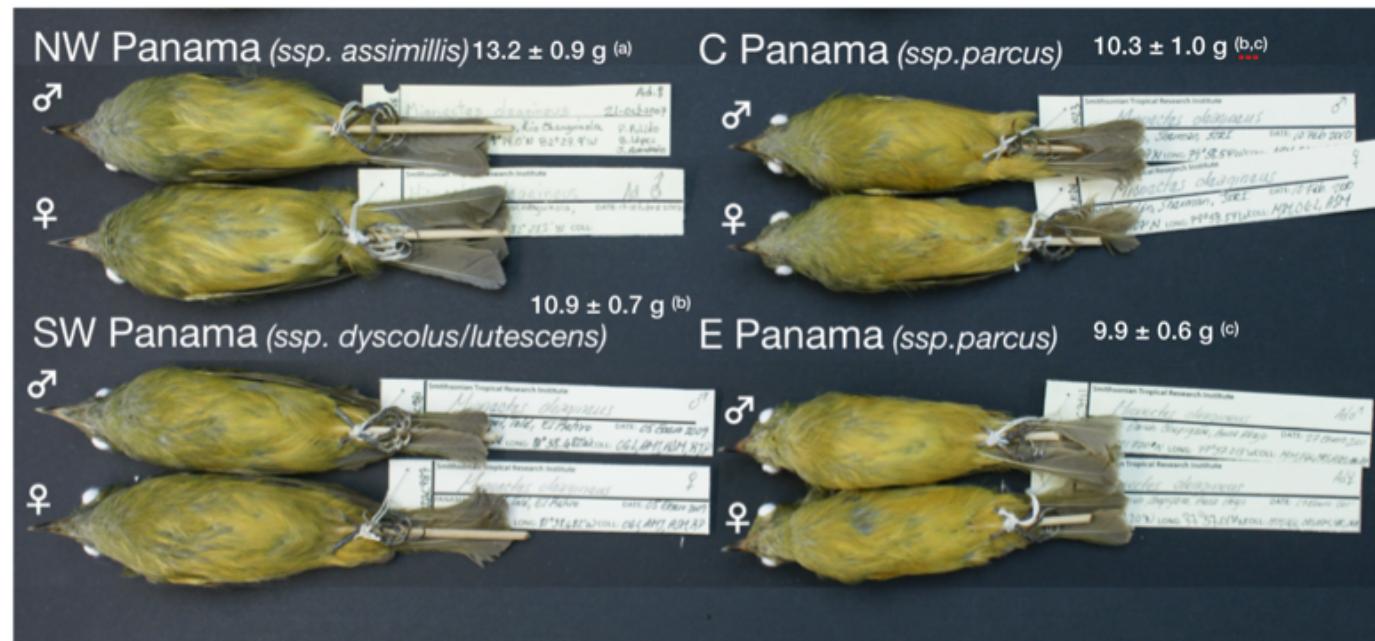


Miller et al. 2008. *Proc Roy. Soc.*

# Four subspecies of *M. oleagineus* occur in Panama

- Wetmore 1972

Subspecies do not concur with Miller et al. mtDNA haplogroups



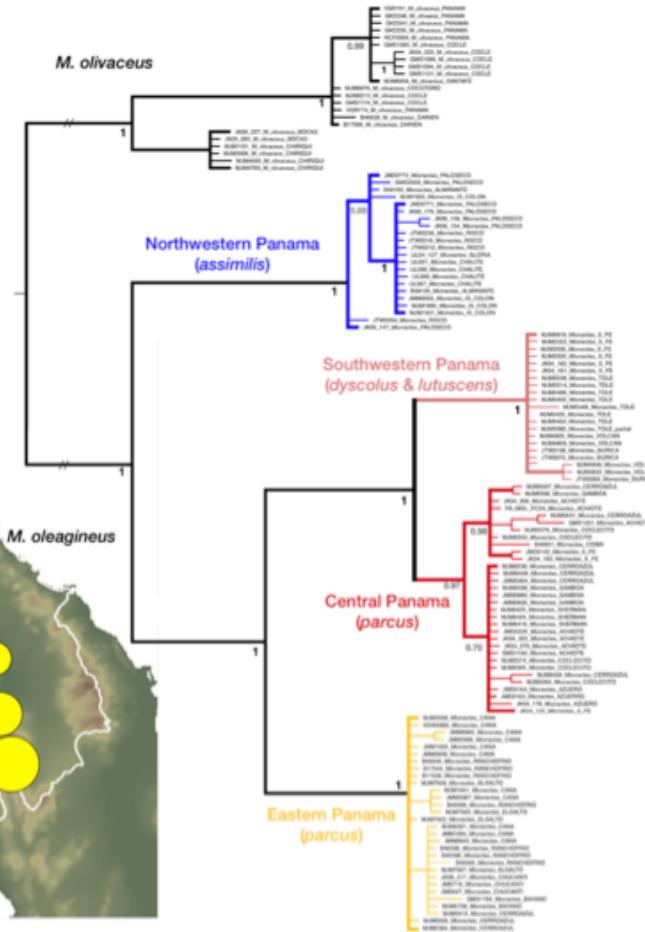
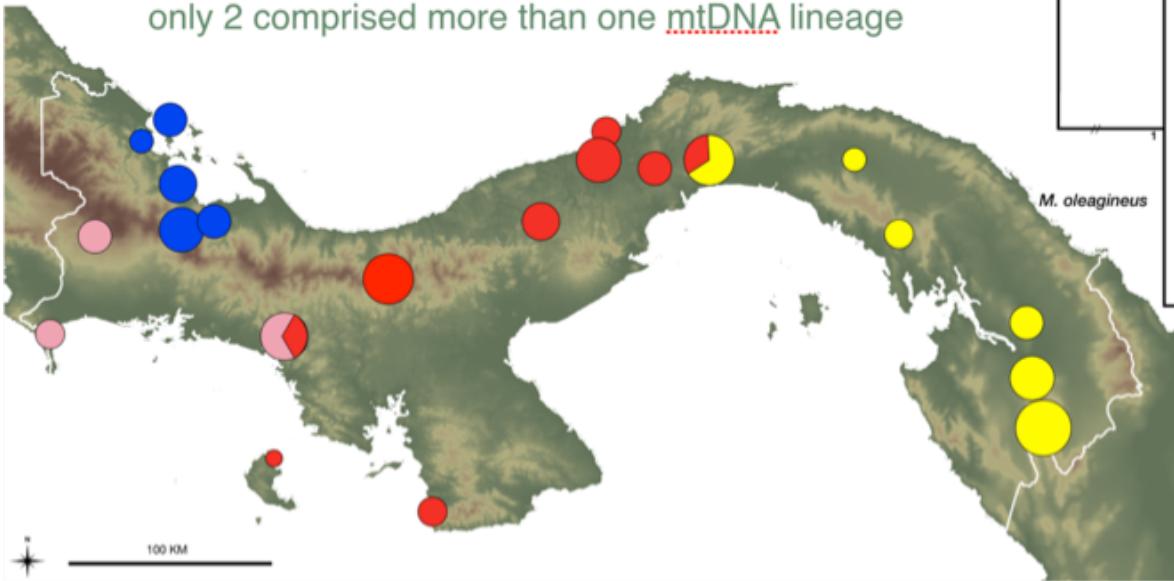
# MrBayes mtDNA tree

complete mtDNA ND2 gene

105 *oleagineus* from Panama

21 sampling locations

only 2 comprised more than one mtDNA lineage



# Model Selection with discriminant functions

Model comparisons performed in JMP on 5 different classification schemes

Model <sub>males</sub>	AIC	Akaike weight	% misclassified
NW vs. SW vs. C vs. E	93.8	0	20%
NW vs. SW vs. C/E	54.3	0	13%
<b>NW vs. SW/C vs. E (*mtDNA)</b>	<b>49.5</b>	<b>0</b>	<b>16%</b>
NW/SW vs. C/E	39.3	0	8%
<b>NW vs. SW/C/E</b>	<b>24.0</b>	<b>1.0</b>	<b>8%</b>
Model <sub>females</sub>	AIC	Akaike weight	% misclassified
NW vs. SW vs. C vs. E	88.7	0	32%
NW vs. SW vs. C/E	61.2	0	18%
<b>NW vs. SW/C vs. E (*mtDNA)</b>	<b>74.2</b>	<b>0</b>	<b>21%</b>
<b>NW/SW vs. C/E</b>	<b>37.0</b>	<b>0.89</b>	<b>6%</b>
NW vs. SW/C/E	41.1	0.11	10%



## SVD Quartets Species Tree (Chifman & Kubatko 2013)

Total concatenated data

