

DNA barcodes mapped on multigene phylogenies correctly identify sister-species of birds

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Organization of the talk

Aim is to address the following concerns about DNA barcoding:

- (1) Closely related sister-species might not have unique barcodes
- (2) 10X rule for the ratio of intra- to interspecific distance would fail to detect cryptic sister-species
- (3) More extensive sampling might blur the boundary between within-species and among species variation

I will argue we are forgetting the barcode analogy

Multigene phylogeny of terns

COI:651 bp

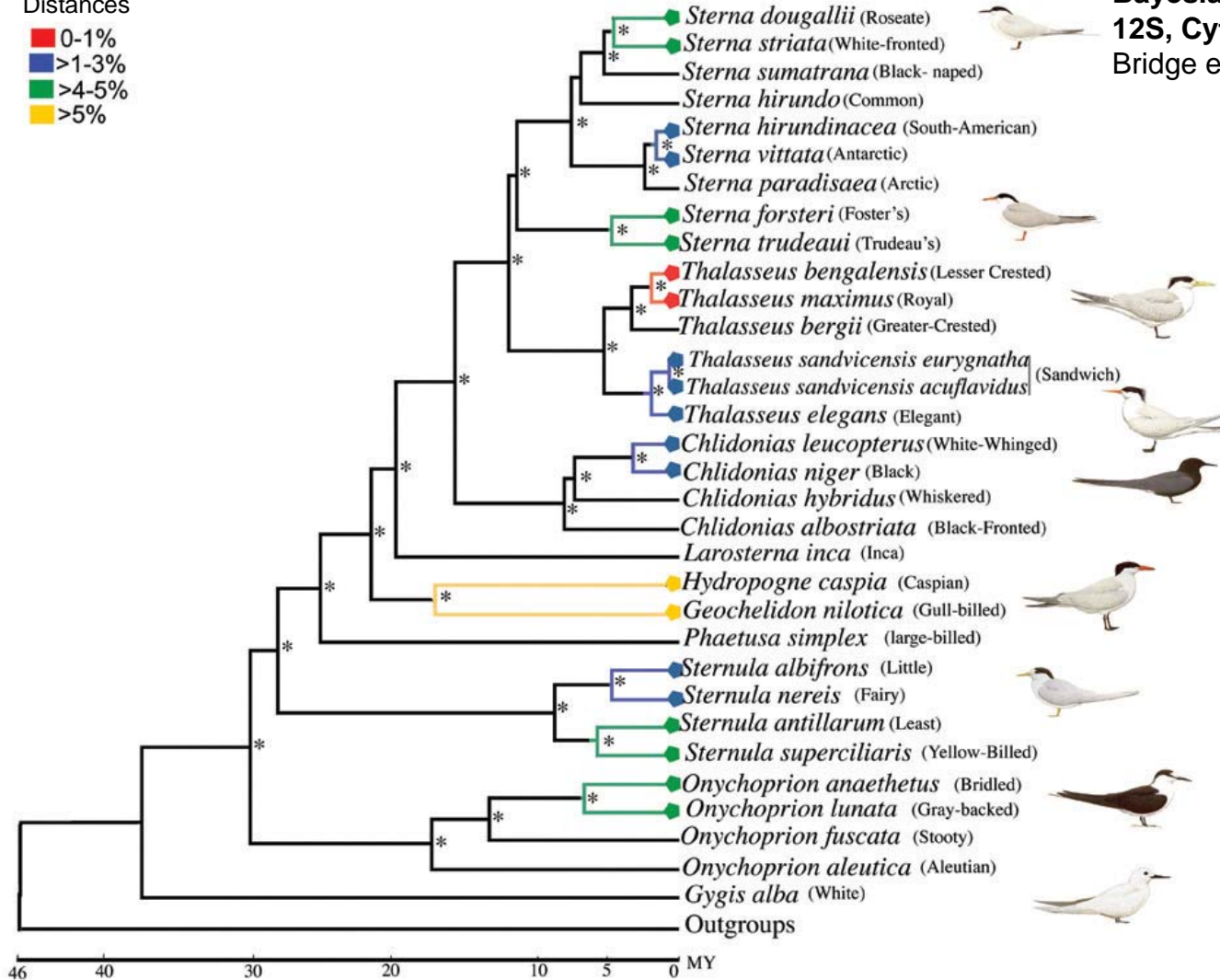
Distances

- 0-1%
- >1-3%
- >4-5%
- >5%

Bayesian analysis

12S, Cytb, ND2, COI :3320 bp

Bridge et al 2005, MPE 35: 459-469



* Posterior Prob. = 1.00

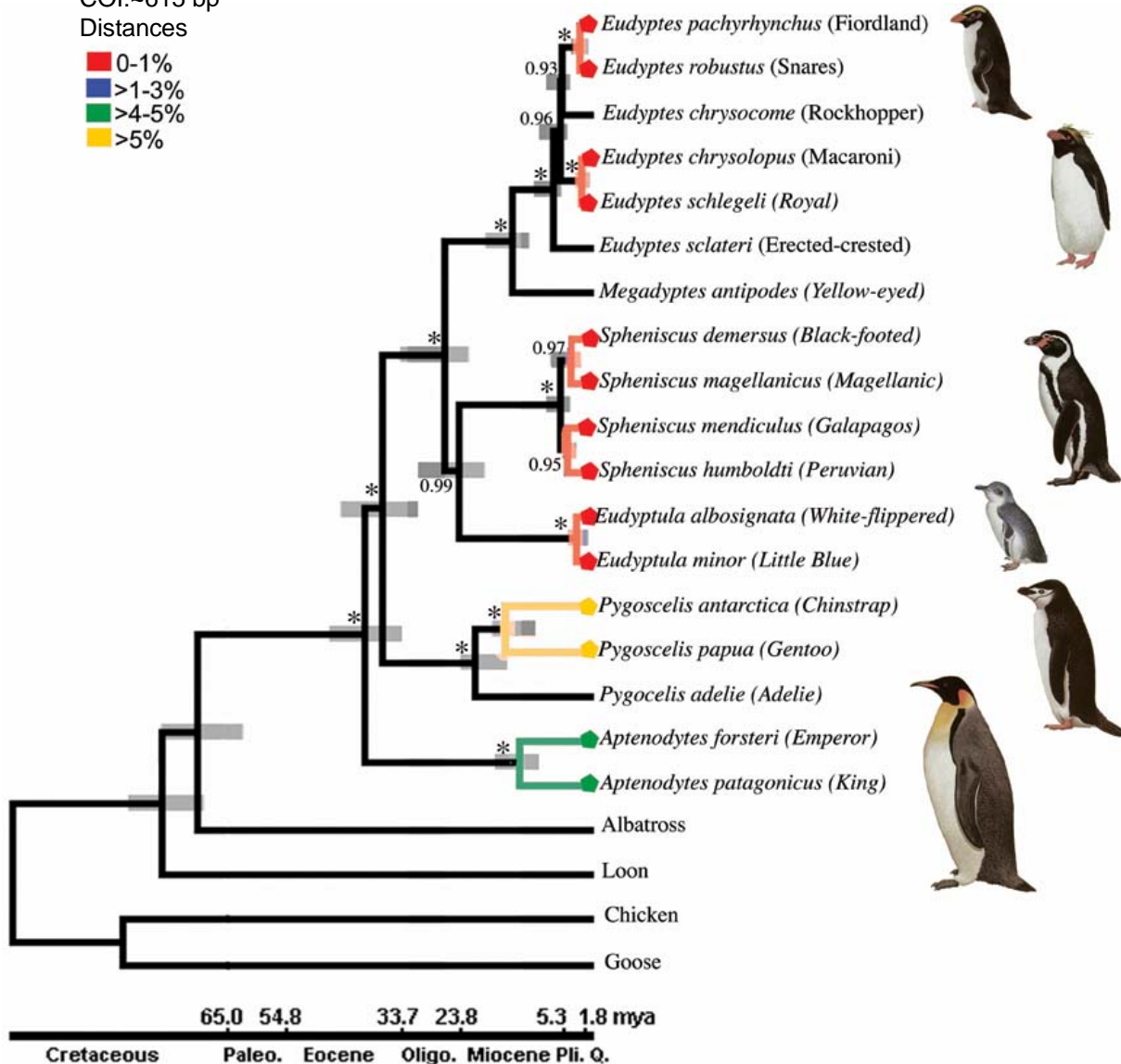
Non-hybridizing species were selected

Multigene phylogeny of penguins

COI: ~615 bp

Distances

- 0-1%
- >1-3%
- >4-5%
- >5%



Bayesian analysis

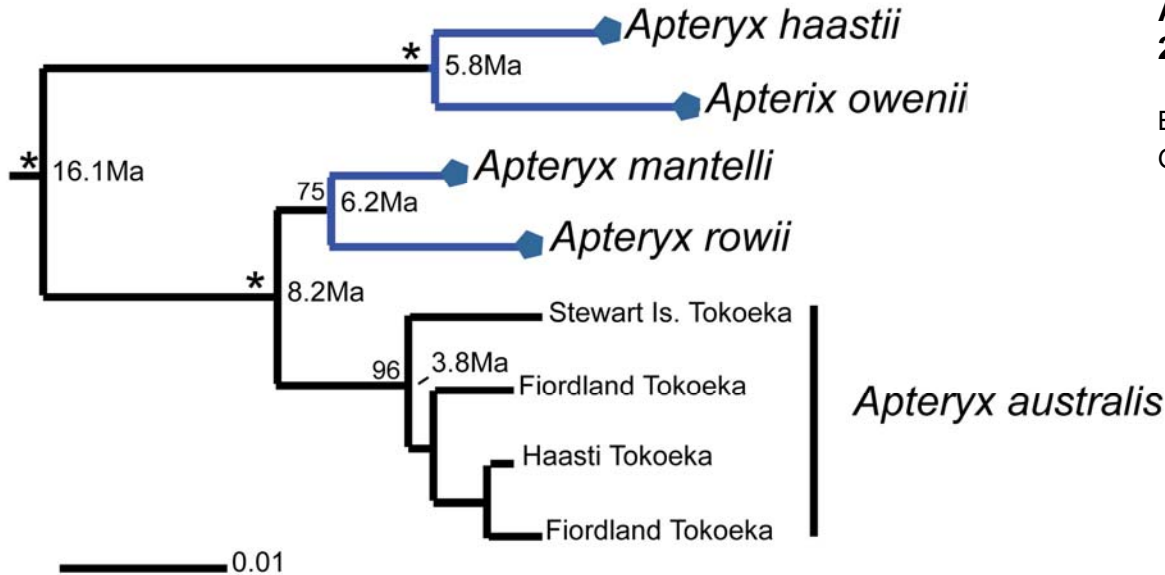
RAG1, 12S, 16S, COI, Cytb: 5571 bp.

Pereira and Baker et al (2006) Proc. Biol. Sci 273.

* Posterior Prob. = 1.00

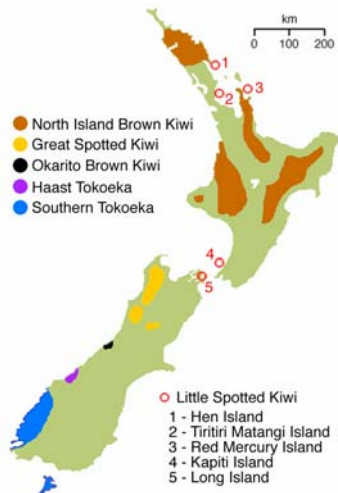
Multigene phylogeny of kiwis

COI:~650 bp
Distances



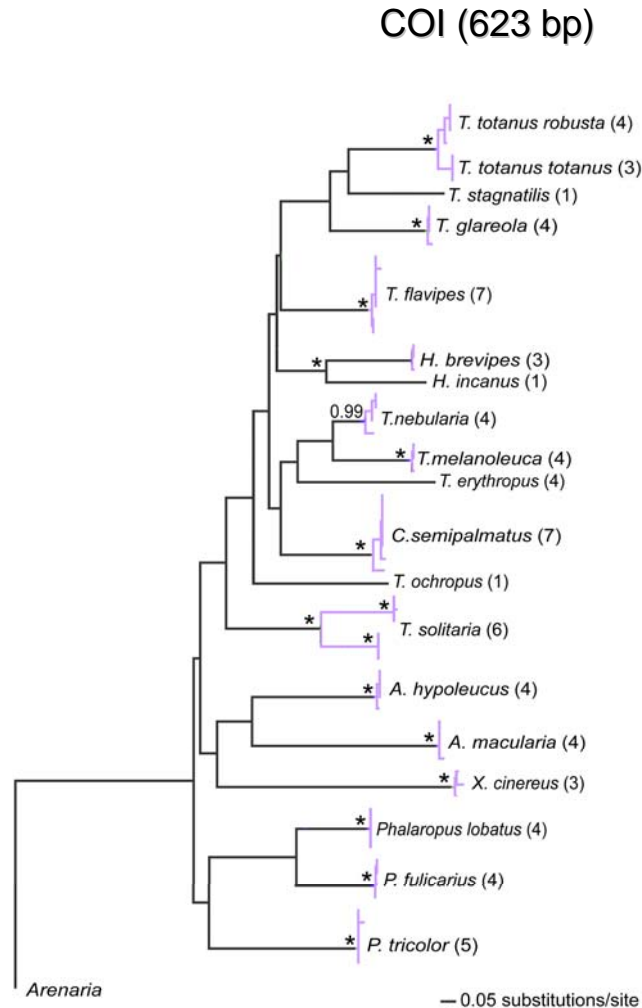
**Maximum Likelihood
ATPase 6, ATPase 8, CR, Cytb:
2267 bp.**

Burbidge et al (2003) Conservation
Genetics 4.



* Bootstrap proportion = 100%

Within-species variation in Tringid sandpipers

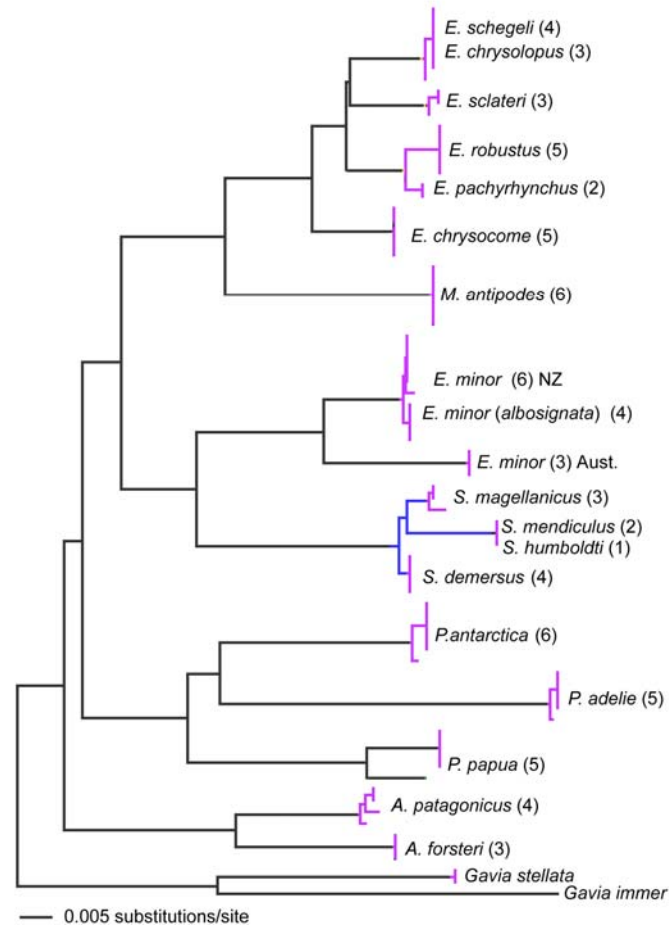


Neighbor-Joining (model Kimura-2P)

Node support: Posterior Prob. Bayesian analysis.

Within-species variation in penguins

COI (650bp)



Neighbour Joining (model Kimura-2P)

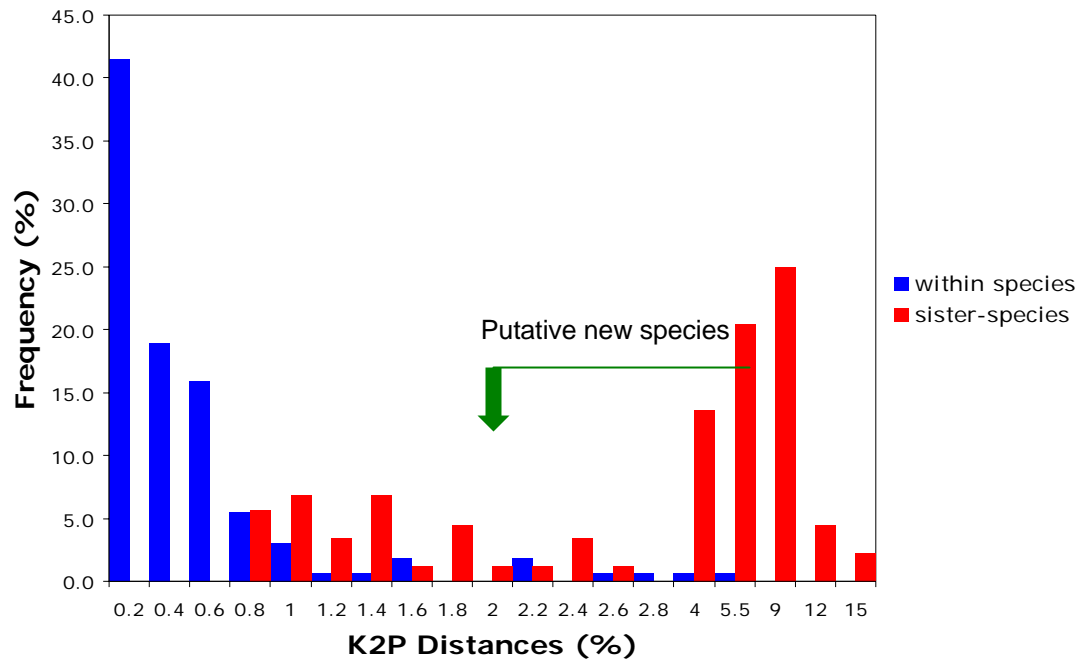
Node support: Posterior Prob. Bayesian analysis.

Reciprocal monophyly

- All non-hybridizing sister-species pairs could be distinguished by monophyletic clusters of barcodes
- Monophyly well supported except in some cases where species comprise more than one phylogroup, or very recent sister species
- ~650 bp of COI is enough to distinguish very closely related birds so we don't need multiple gene barcodes

Within-species versus among sister-species variation

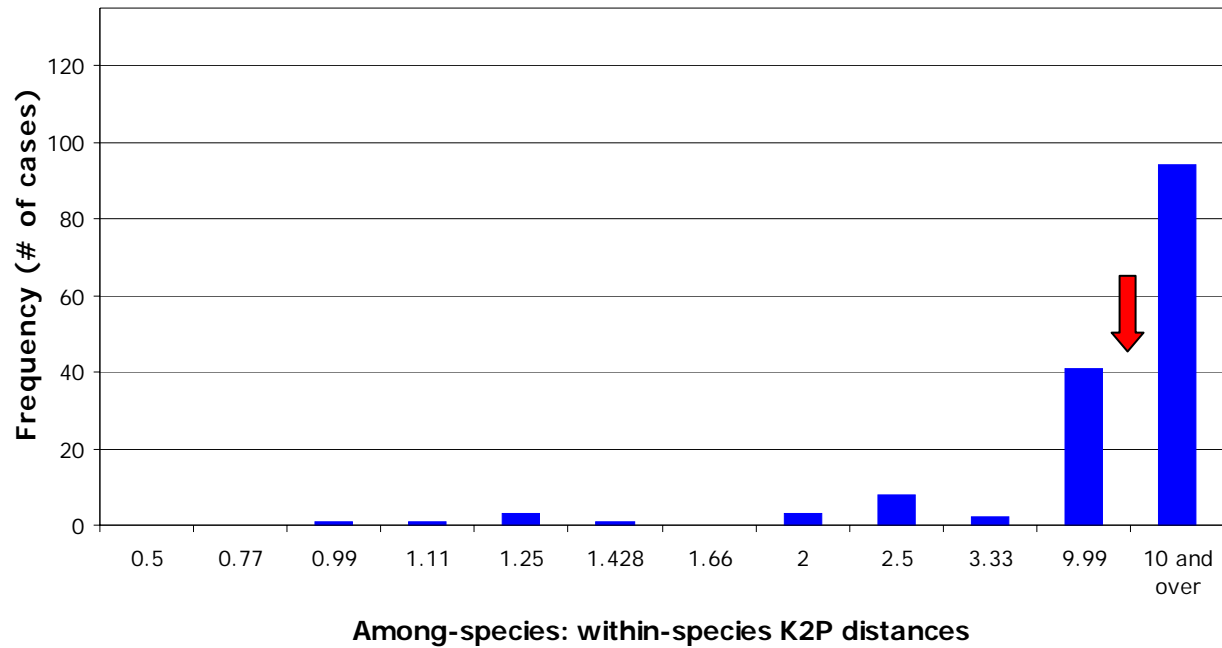
Sample of 745 sequences from 88 sister-species pairs.



Is this a potential problem for barcoding sister-species?

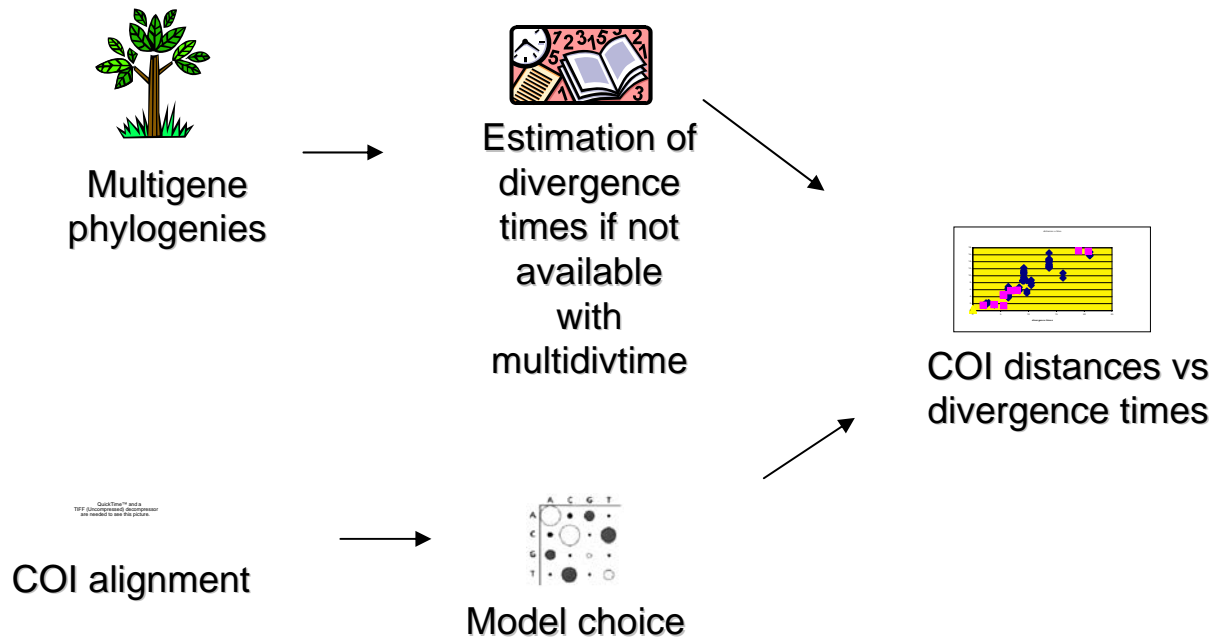
Among sister-species: within species variation

Ratio among:within species variation



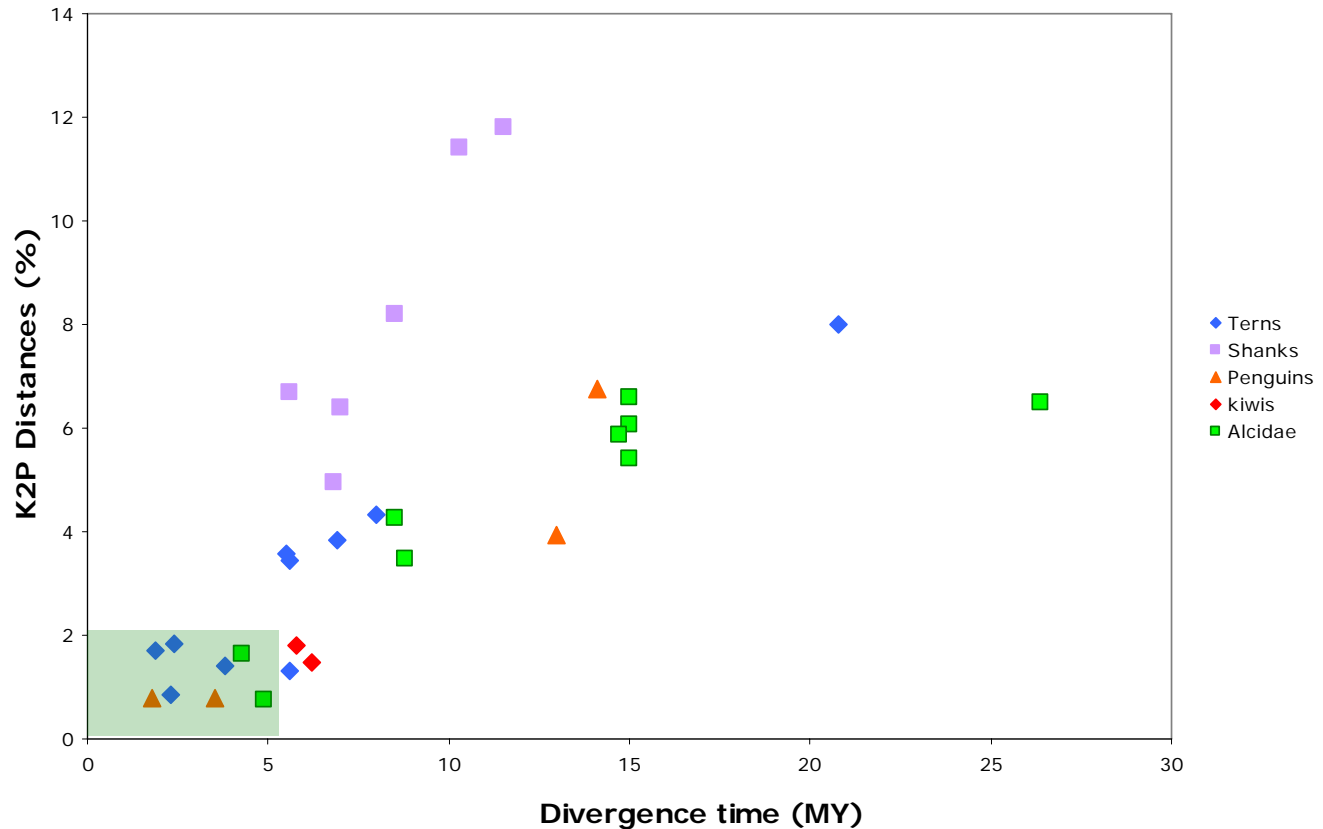
Excluding putative new species about 30% of sister-species have ratios below 10 x rule.

COI barcodes vs time of divergence of species



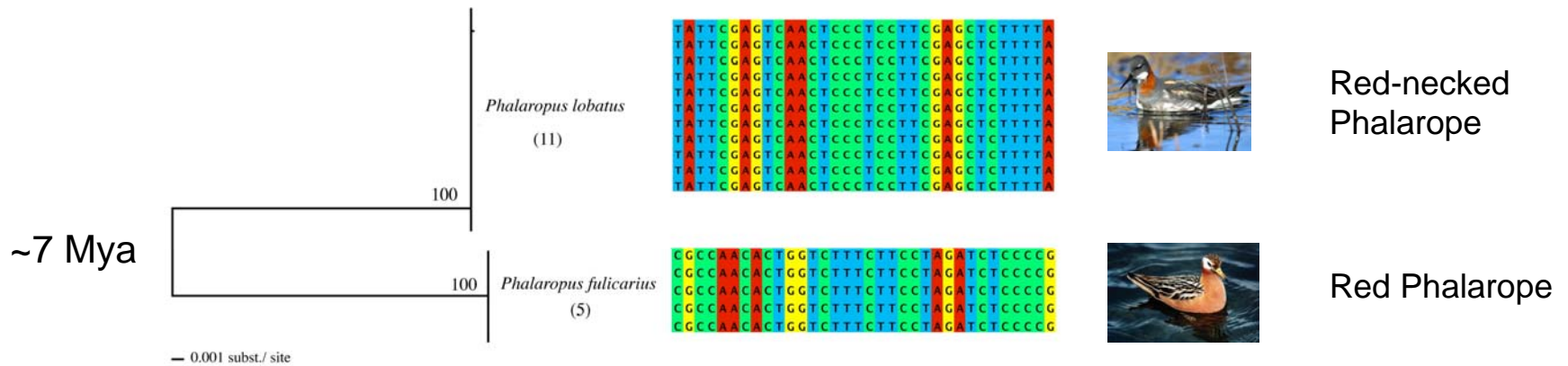
Species barcode value varies with time since speciation

Sister-species distances



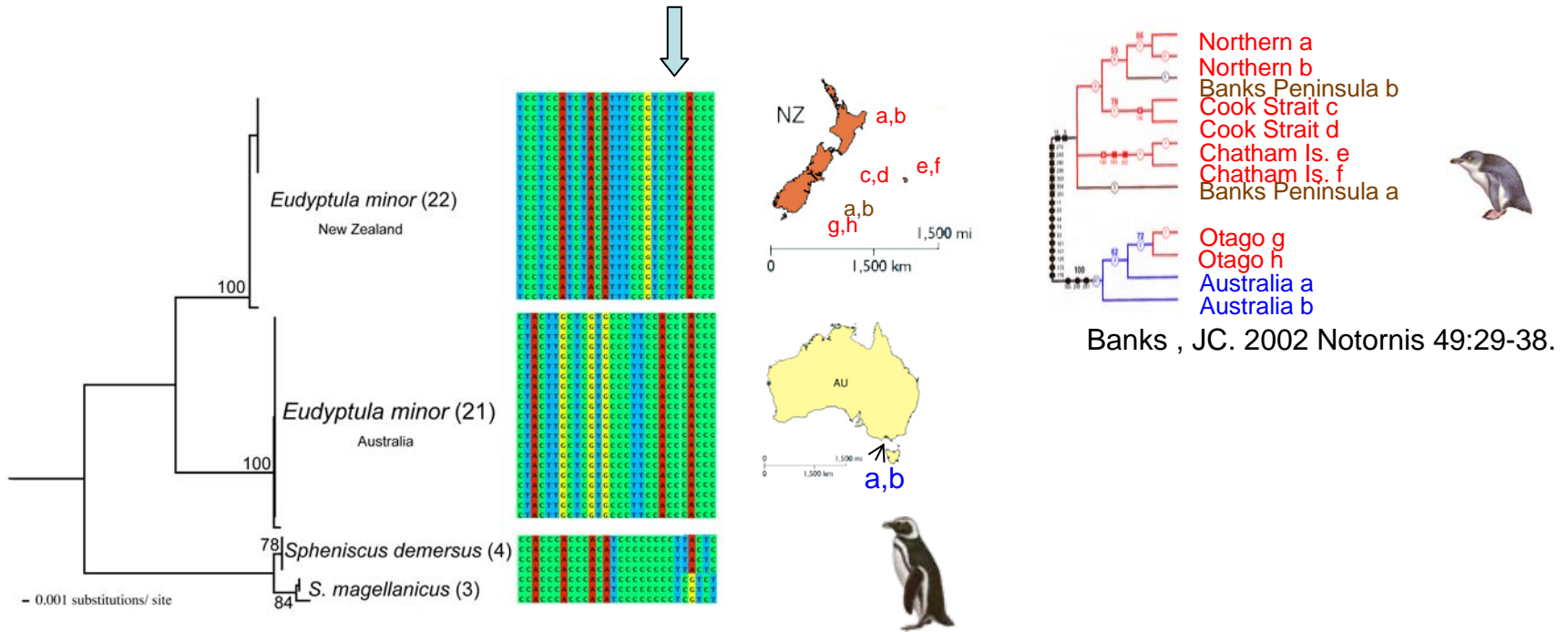
This explains why 10 X rule is a safe species criterion, but is too stringent for recent sister-species

Barcodes provide diagnostic characters



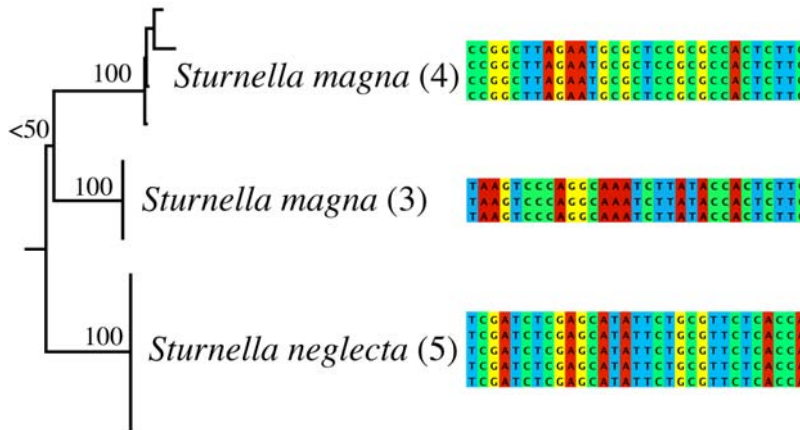
Most sister-species have a good number of species diagnostic substitutions in their barcodes.

Another example in penguins



Even recently diverged sister-species have diagnostic characters.

Diagnostic barcodes in putative new species

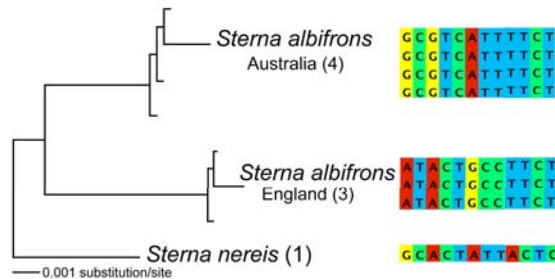


Eastern meadowlark



Western meadowlark

— 0.005 substitutions/site



Little tern

Fairy tern

Diagnostic characters can flag potential new species

Conclusions

- ~650 bp of COI provide enough information to assign individuals to correct species at sister-species levels.
- 30 % of the sister-species have interspecific:intraspecific ratios smaller than 10.
- However, even the most closely related sister-species pairs have diagnostic substitution patterns or DNA barcodes.
- Barcodes of each sister species pair have many more fixed substitution differences than do phylogroups within each species
- We need coalescent approaches that distinguish between expected phylogroup and sister species divergences

Acknowledgements

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