

DNA barcoding of European and African *Accipiter* (ACCIPITRIDAE: FALCONIFORMES)

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A. tachiro

A. unduliventer*

A. toussenelii

A. melanochlamys

A. albogularis

A. rufitorques

A. haplochrous

A. badius

A. brevipes

A. butleri

A. francesiae ?

A. soloensis ?

A. fasciatus

A. castanilius

A. novaehollandiae

A. trinotatus

A. henicogrammus

A. luteoschistaceus

A. imitator

A. trivirgatus

A. griseiceps

A. poliocephalus

A. princeps

A. gentilis

A. melanoleucus

A. meyerianus

A. henstii

A. superciliosus

A. collaris

A. poliogaster

A. minullus

A. erythropus

A. virgatus

A. gularis

A. nanus ?

A. bicolor

A. cooperii

A. gundlachi

A. chilensis

A. nisus

A. rufiventris

A. madagascariensis

A. ovampensis ?

A. striatus

A. ventralis

A. chionogaster

A. erythronemius

A. cirrhocephalus

A. brachyurus

A. erytrauchen

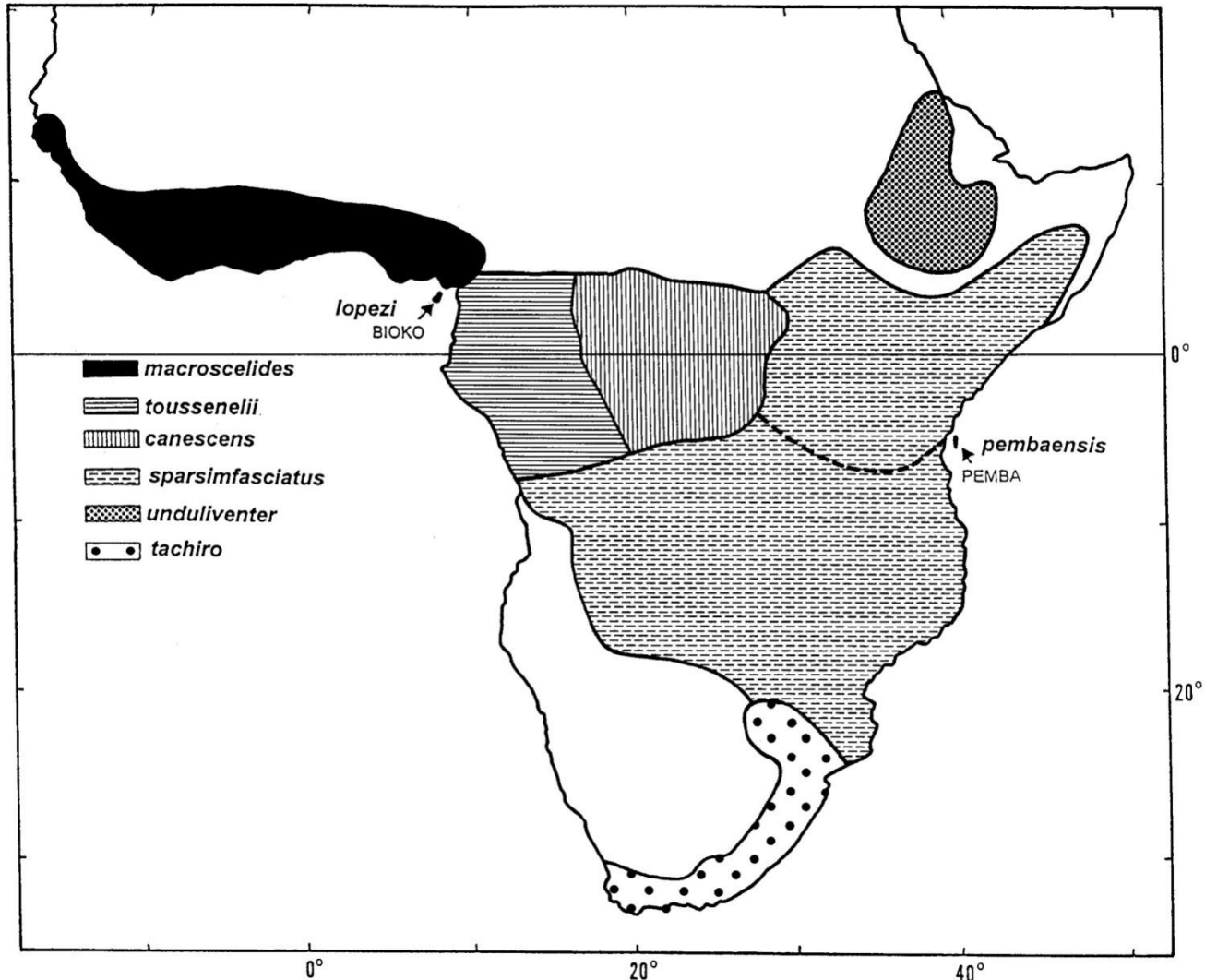
A. rhodogaster ?

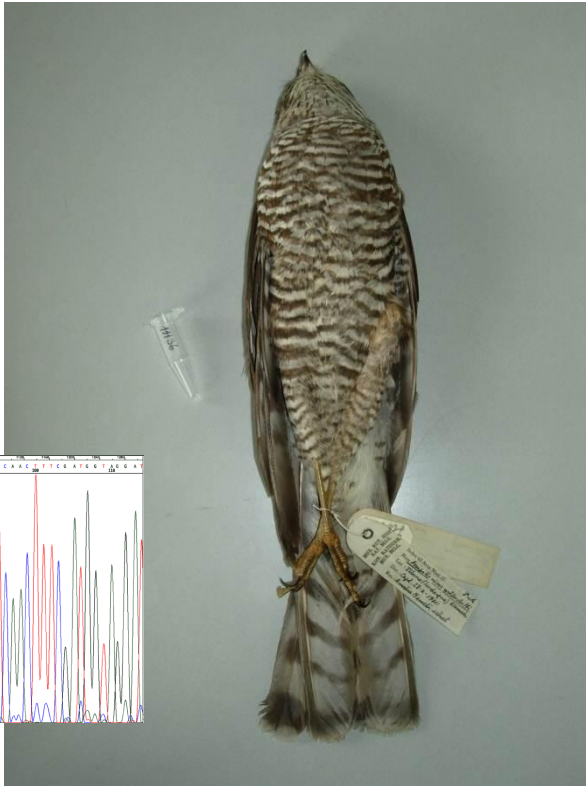
Wattel J (1973) *Geographical differentiation in the genus Accipiter*. *Publ Nuttall Ornithol Club* 1–231.

del Hoyo J, Elliott A, Sargatal JP (eds) (1994) *New world vultures to guinea-fowl. Handbook of the 4 birds of the world, vol. 2*. Lynx, Barcelona, (Spain)



The African goshawk:



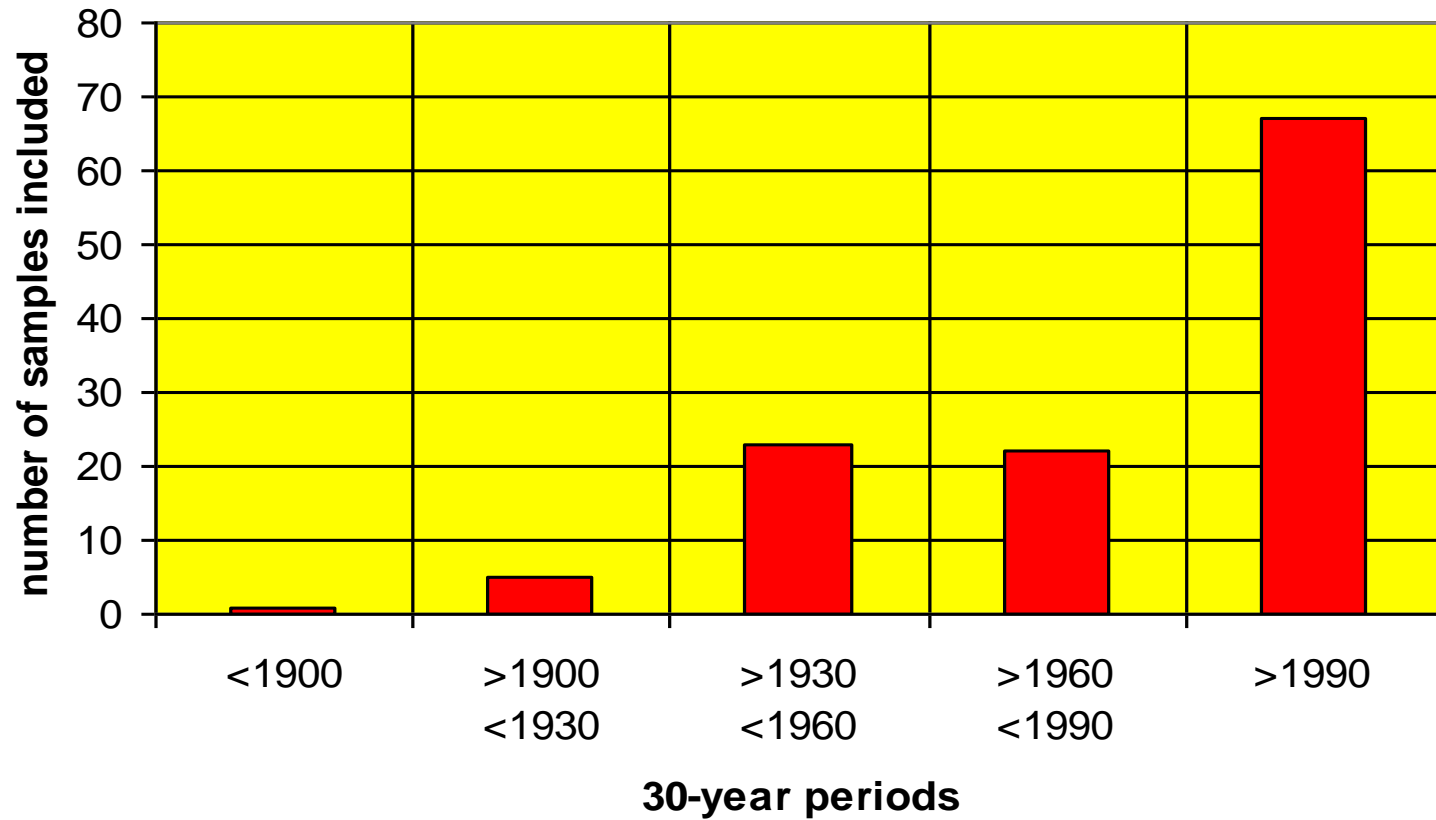


1. To obtain DNA sequences from our bird museum specimens



sample distribution through time

Series1



Objectives



	barcoded	remaining	% barcoded
<i>Accipiter</i>	16	50	32%
Afrotropical region	5	15	33%
Palaearctic region	6	7	86%

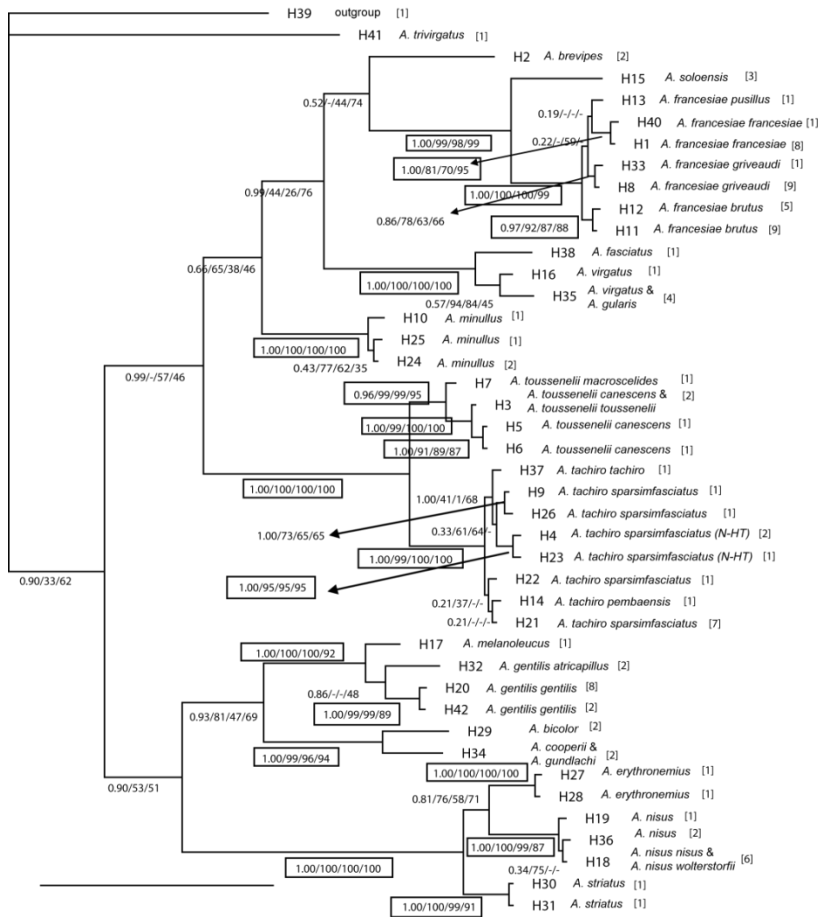
2.

To contribute to the reference library of DNA barcodes (CBOL)

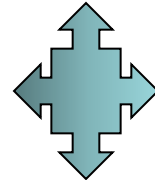
ABBI website <http://www.barcodingbirds.org>
November 2011



Objectives



[trivirgatus]
[badius]
[unplaced]
[virgatus]
[minullus]
[tachiro]
[gentilis]
[cooperii]
[nisus]



A. tachiro	A. fasciatus	A. trivirgatus
A. unduliventer*	A. castanilius	<i>A. griseiceps</i>
A. toussenelii	<i>A. novaehollandiae</i>	<i>A. poliocephalus</i>
<i>A. melanochlamys</i>	<i>A. trinotatus</i>	<i>A. princeps</i>
<i>A. albogularis</i>	<i>A. henicogrammus</i>	A. gentilis
<i>A. rufitorques</i>	<i>A. luteoschistaceus</i>	A. melanoleucus
<i>A. haplochrous</i>	<i>A. imitator</i>	<i>A. meyerianus</i>
A. badius		<i>A. henstii</i>
A. brevipes		<i>A. superciliosus</i>
<i>A. butleri</i>		<i>A. collaris</i>
A. francesiae ?		<i>A. polioaster</i>
A. soloensis ?		

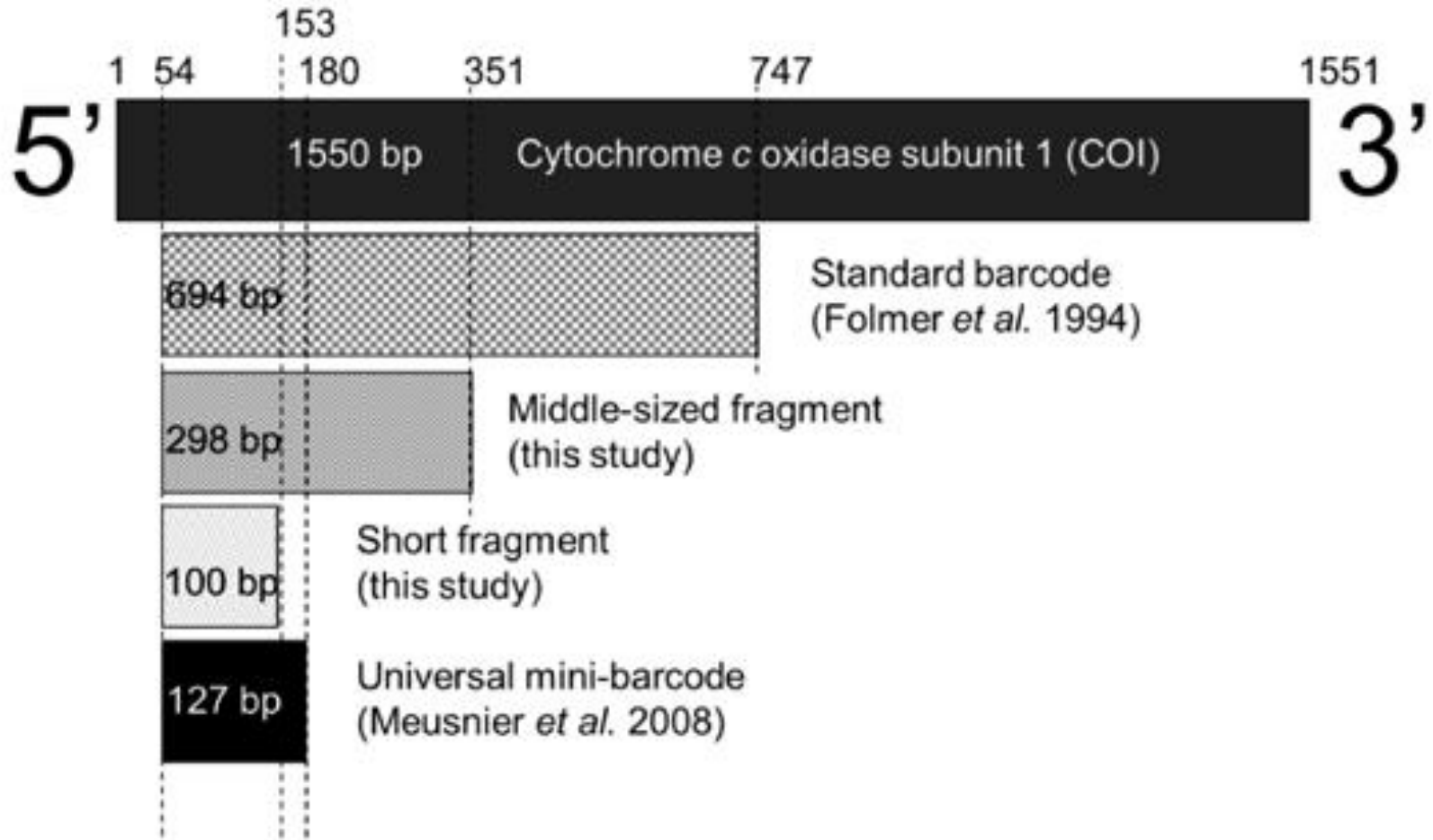
A. minullus	A. nisus
A. erythropus	A. rufiventris
	A. madagascariensis
	A. ovampensis ?
A. virgatus	A. striatus
A. gularis	<i>A. ventralis</i>
<i>A. nanus ?</i>	<i>A. chionogaster</i>
A. bicolor	A. erythronemius
A. cooperii	<i>A. cirrhocephalus</i>
A. gundlachi	<i>A. brachyurus</i>
<i>A. chilensis</i>	<i>A. erytrauchen</i>
	<i>A. rhodogaster ?</i>

3.

To evaluate the utility of the produced DNA barcodes in a group that is well known



Mini barcodes



Sonet et al. in press



Species identification:

Character based identification

- + Easy: detecting unique differences
- + No arbitrary distance threshold used
- May be unreliable with insufficient sampling

29	48	54	63	66	90	105	108	153	174	225	240	276
T	G	C	A	T	C	C	C	T	G	T	T	C
T	A	T	A	C	T	C	T	C	A	T	T	C
C	G	T	G	C	T	T	C	C	A	C	C	A
2nd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd



Species identification: Best Match and Best Close match

- Best Match (BM), assigns the species name of its best-matching sequence regardless of how similar the query and reference sequences were.
- Best Close Match (BCM) also considers a distance threshold.



Determination of a distance threshold: 10 X mean intraspecific distances

- Distances
- Arbitrary
- Does not always hold
- However, works well in birds

DNA Barcoding Korean Birds

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333, Korea;*

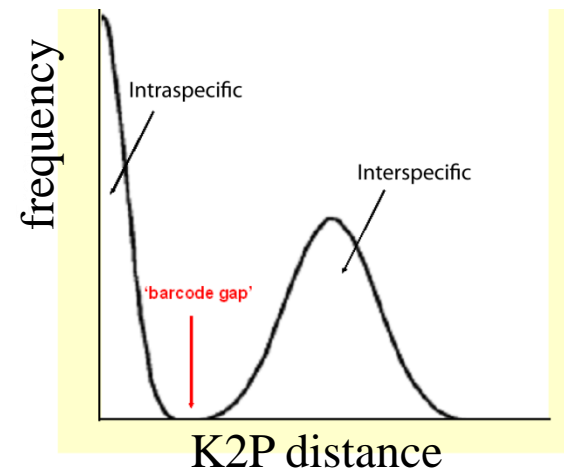
Open access, freely available online [PLoS BIOLOGY](#)

Identification of Birds through DNA Barcodes

Paul D. N. Hebert¹, Mark Y. Stoeckle², Tyler S. Zemlak¹, Charles M. Francis³

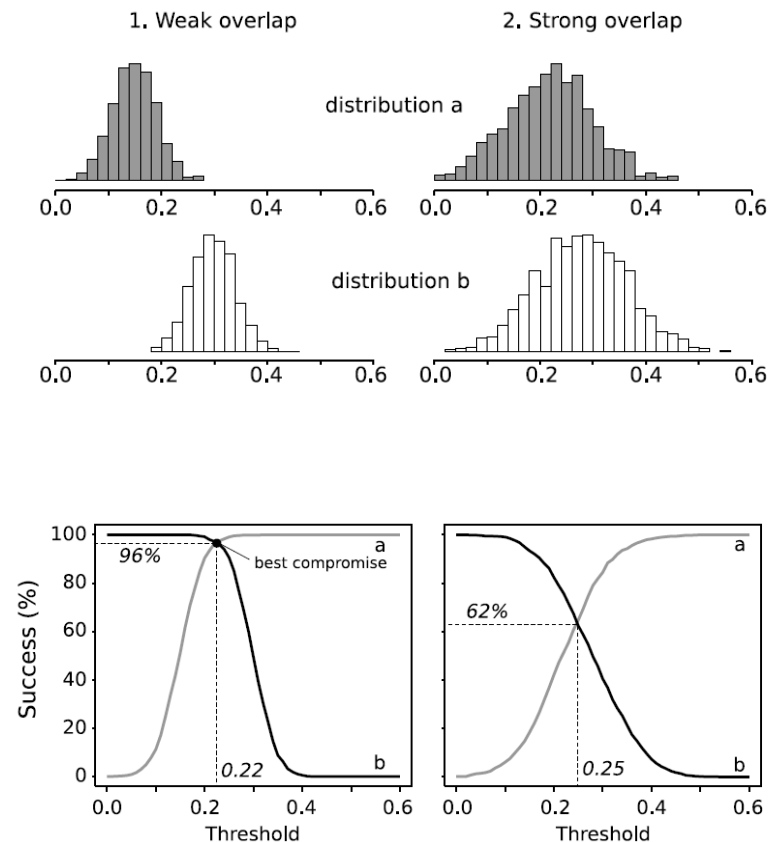
1 Department of Zoology, University of Guelph, Guelph, Ontario, Canada, 2 Program for the Human Environment, Rockefeller University, New York, New York, United States of America, 3 National Wildlife Research Centre, Canadian Wildlife Service, Ottawa, Ontario, Canada

Distribution of pairwise distances



Determination of a distance threshold: The Best compromise threshold (BCTh)

- Based on the intercept between cumulative intra and interspecific distances
- + Based on the dataset under study rather than a predetermined threshold
- Results from one dataset not applicable to another



The obtained dataset

- 25 European and African *Accipiter* species with a total of 140 specimens (including 28 GenBank sequences)
- sequenced for a 291bp (mini) and 647bp (standard) BC fragment of the COI gene
- three datasets analysed:
 - dataset A: 25 species, 291bp
 - dataset B: 19 species, 647 bp
 - dataset C: 19 species, 291bp

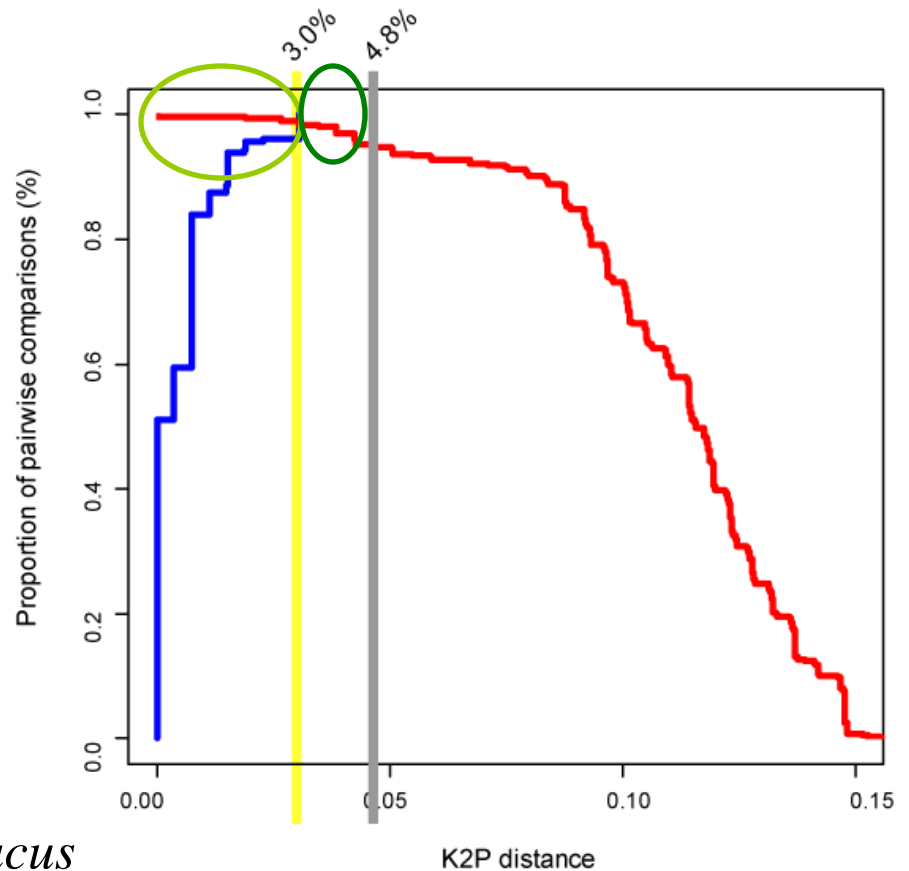


- Partial overlap caused by

- *A. nisus/rufiventris*
- *A. virgatus/gularis*
- *A. cooperii/gundlachi*

- and close to the BC threshold:

- 2x *A. badius* ssp. + *A. brevipes*
- 2x *A. gentilis* ssp. + *A. melanoleucus*



Results: BCTh vs. 10 X distance threshold

a **BM**

dataset	BCTh threshold	correct	ambiguous	incorrect	no match closer than threshold
A	3.00%	124 (84.35%)	19 (12.92%)	4 (2.72%)	–
B	2.80%	90 (90.0%)	6 (6.0%)	4 (4.0%)	–
C	3.00%	90 (90.0%)	5 (5.0%)	5 (5.0%)	–

b **BCM**

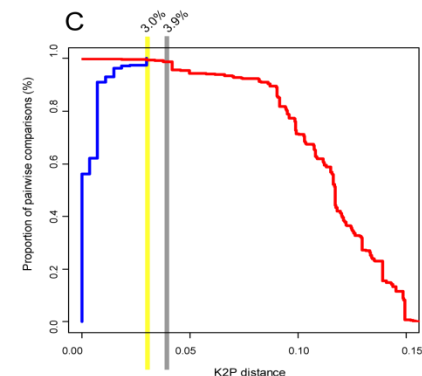
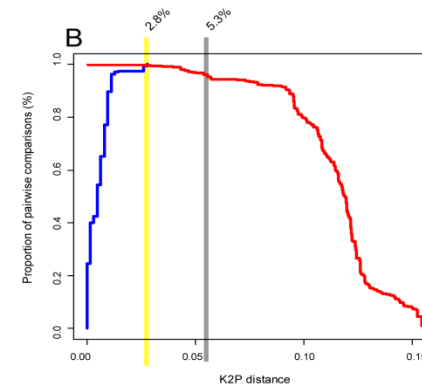
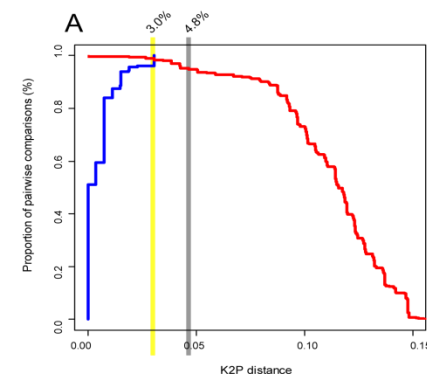
dataset	BCTh threshold	correct	ambiguous	incorrect	no match closer than threshold
A	3.00%	124 (84.35%)	18 (12.24%)	3 (2.04%)	2 (1.36%)
B	2.80%	90 (90.0%)	5 (5.0%)	4 (4.0%)	1 (1.0%)
C	3.00%	90 (90.0%)	5 (5.0%)	4 (4.0%)	1 (1.0%)

c **BM**

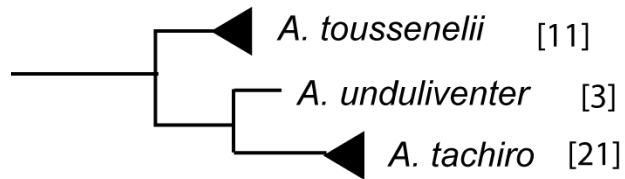
dataset	10 X threshold	correct	ambiguous	incorrect	no match closer than threshold
A	4.80%	124 (84.35%)	19 (12.92%)	4 (2.72%)	–
B	5.30%	90 (90.0%)	5 (5.0%)	5 (5.0%)	–
C	3.90%	90 (90.0%)	6 (6.0%)	4 (4.0%)	–

d **BCM**

dataset	10 X threshold	correct	ambiguous	incorrect	no match closer than threshold
A	4.80%	124 (84.35%)	18 (12.24%)	3 (2.04%)	2 (1.36%)
B	5.30%	90 (90.0%)	5 (5.0%)	4 (4.0%)	1 (1.0%)
C	3.90%	90 (90.0%)	5 (5.0%)	4 (4.0%)	1 (1.0%)



Case 1: African goshawk



	18	63	96	108	117	129	190	198	204	213
<i>A. toussenelii</i>	G	A	T	C	C	C	G	T	C	C
<i>A. unduliventer</i>	A	G	C	T	T	C	G	T	C	A
<i>A. tachiro</i>	A	G	T	T	T	T	A	C	T	A
	3rd	3rd	3rd	3rd	3rd	3rd	1st	3rd	3rd	3rd



A. castanilius



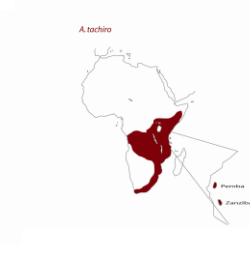
A. toussenelii



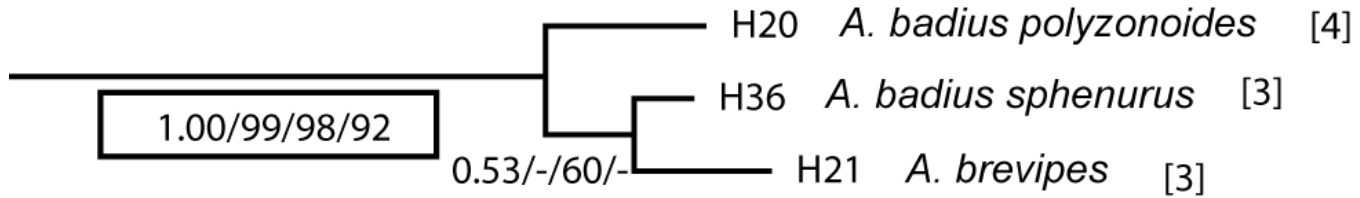
A. unduliventer



A. tachiro



Case 2: *A. Badius* and *A. brevipes*



Accipiter brevipes



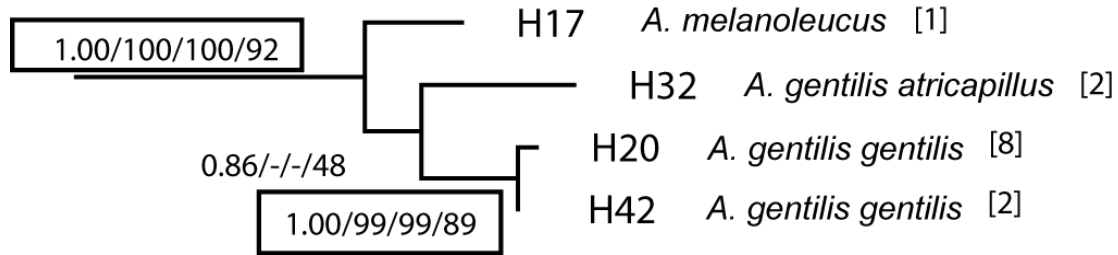
Accipiter badius polyzonoides



Accipiter badius sphenurus



Case 3: *A. gentilis* subspecies



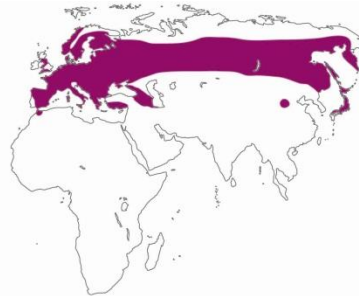
A. melanoleucus



A. gentilis gentilis



A. gentilis atricapillus



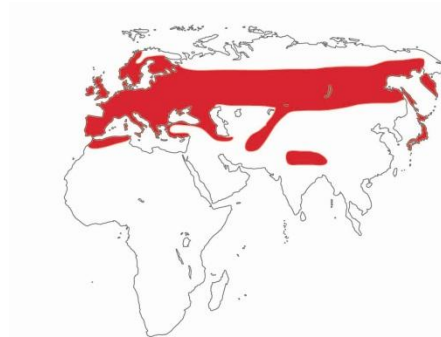
Case 4: *A. nisus* and *A. rufiventris*



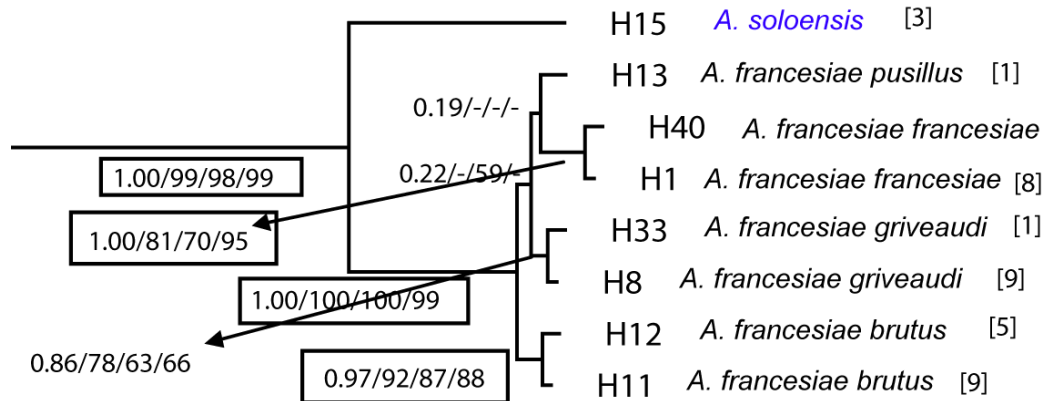
A. nisus



A. rufiventris



Case 5: *A. soloensis* and *A. francesiae*



Accipiter soloensis



Accipiter francesiae francesiae



Accipiter francesiae griveaudi

Accipiter soloensis



A. francesiae



Conclusions

- Museum material works!
- Molecular techniques provide a powerful method for reviewing taxonomy
- COI can identify 19 out of the 25 species included
- The content (size of DNA fragments and species sampling) of the dataset and the methods matter





Gerhard Aubrecht (Ober-Österreichische Landesmuseen, Linz Austria), Marieke Berkvens (Wuustwezel, Belgium), Charles Botha (South Africa), Sebastien Bruaux (RBINS), Kizungu Byamana (Lwiro, DR Congo), Chang Yuong Choi (Migratory Bird Centre of the Korean National Park Service, South Korea), Stijn Cooleman (RMCA), S. Viñas & Lellani Fariñes Crespo (RMCA), René De Roland Lily Arison (Peregrine Fund, Madagascar), Renate van den Elzen (Zoologisches Forschungsmuseum Koenig, Bonn, Germany), Clem Fisher (World Museum Liverpool, UK), Jon Fjeldså (University of Copenhagen Zoological Museum, Denmark), Marc Herremans (Mechelen, Belgium), Jon Bolding Kristensen (University of Copenhagen Zoological Museum, Denmark), Georges Lenglet (RBINS), Danny Meirte (RMCA), Jürgen Plass (Ober-Österreichische Landesmuseen, Linz Austria), Alain Reygel (RMCA), Lucia Liu Severinghaus (The Biodiversity Research Museum Taiwan, Taiwan), Erik Verheyen (RBINS), Malcolm Wilson (South Africa), Reuven Yosef (International Birding & Research Centre in Eilat, Israel). All experiments complied with the laws of Belgium.



Thank you for your attention

