



Identification of Invasive Alien Species using DNA barcodes

Royal Belgian Institute of Natural Sciences
Rue Vautier 29,
1000 Brussels, Belgium
+32 (0)2 627 41 23



Royal Museum for Central Africa
Leuvensesteenweg 13,
3080 Tervuren, Belgium
+32 (0)2 769 58 54



General introduction to this factsheet

The Barcoding Facility for Organisms and Tissues of Policy Concern (BopCo) aims at developing an expertise forum to facilitate the identification of biological samples of policy concern in Belgium and Europe. The project represents part of the Belgian federal contribution to the European Research Infrastructure Consortium LifeWatch.

Non-native species which are being introduced into Europe, whether by accident or deliberately, can be of policy concern since some of them can reproduce and disperse rapidly in a new territory, establish viable populations and even outcompete native species. As a consequence of their presence, natural and managed ecosystems can be disrupted, crops and livestock affected, and vector-borne diseases or parasites might be introduced, impacting human health and socio-economic activities. Non-native species causing such adverse effects are called Invasive Alien Species (IAS). In order to protect native biodiversity and ecosystems, and to mitigate the potential impact on human health and socio-economic activities, the issue of IAS is tackled in Europe by EU Regulation 1143/2014 of the European Parliament and Council. The IAS Regulation provides for a set of measures to be taken across all member states. The list of Invasive Alien Species of Union Concern is regularly updated. In order to implement the proposed actions, however, methods for accurate species identification are required when suspicious biological material is encountered.

Because morphology-based species identifications are not always possible (e.g. cryptic species, trace material, early life-stages), the purpose of the present work is to investigate and evaluate the usefulness of DNA sequence data to identify each of the IAS included in the EU Regulation. The results are presented as factsheets (one per IAS) compiled using publicly available DNA sequence data and information aggregated from various sources. Each factsheet consists of two major parts; (i) a short introduction to the specific IAS compiling information on its taxonomy and current occurrence/distribution in Europe; (ii) an investigation with respect to the usefulness of publicly available DNA sequences to identify this IAS to the taxonomic level stated in the EU list using DNA barcoding. For further information about the reasoning behind the applied approach and details on the materials and methods utilised, please see below and Smits *et al.* [1].

More info about BopCo on <http://bopco.myspecies.info/> or contact us via bopco@naturalsciences.be.

More info on the EU Regulation on http://ec.europa.eu/environment/nature/invasivealien/index_en.htm.

Nasua nasua

(Linnaeus, 1766)

Common names:

English: South American coati, brown nosed coati, ring-tailed coati

French: coati roux, coati brun, coachi

German: Südamerikanischen Nasenbär

Dutch: rode neusbeer, Zuid-Amerikaanse coati

Last update: October 2019



General information on *Nasua nasua*

Classification

Kingdom	Phylum	Class	Order	Family	Genus
Animalia	Chordata	Mammalia	Carnivora	Procyonidae	<i>Nasua</i>

Species in the same genus: N = 2 [2-3]

Infra-species level: N = 13 [4-6]

Note: Thirteen subspecies have been recognised: *N.n. aricana*, *N.n. boliviensis*, *N.n. candace*, *N.n. cinerascens*, *N.n. dorsalis*, *N.n. manium*, *N.n. molaris*, *N.n. montana*, *N.n. nasua*, *N.n. quicha*, *N.n. solitaria*, *N.n. spadicea* and *N.n. vittata*.



Native range: [2, 7-10]

Argentina, Bolivia, Brazil, Colombia, Ecuador, French Guiana, Guyana, Paraguay, Peru, Suriname, Uruguay and Venezuela.

Invasive range: [2, 8, 11 –13]

Europe (geographical):

Mallorca (Spain) and United Kingdom.

For more detailed locality information and the most recent distribution updates, please visit:

<http://alien.jrc.ec.europa.eu/SpeciesMapper#>

<https://www.gbif.org/species/2433530>

<https://www.iucnredlist.org/species/41684/45216227>

Outside Europe (geographical):

Chile.

Morphology, biology, invasion, negative effects and remedies

For more information on *Nasua nasua* please see the references and online information listed at the end of this document.



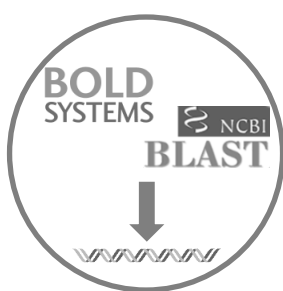
Species identification based on DNA barcodes

Introduction

DNA barcoding is a species identification method that uses a short genetic sequence (DNA barcode) to compare an unknown sample to a database of reference sequences with known species affiliations. The underlying rationale is that the divergence of nucleotide sequences among different species is larger than the nucleotide divergence between sequences within a species. DNA barcoding can facilitate the identification of IAS samples, especially when morphological characteristics are absent or useless. To assure correct species identifications, however, reference libraries need to include a sufficiently large number of sequences of (i) the IAS under investigation, in order to assess the intraspecific genetic divergence; (ii) the closely related species, in order to evaluate the interspecific genetic divergence; (iii) the different geographical areas covering the distribution range (native and invasive) of the IAS in order to detect potential population structure or local hybrids.

Against this background, BopCo evaluated the inclusion of the IAS and their close relatives in both publicly available reference libraries BOLD (www.boldsystems.org/) and GenBank (www.ncbi.nlm.nih.gov/nucleotide/) to estimate the reliability with which a species identification can be obtained using DNA barcoding.

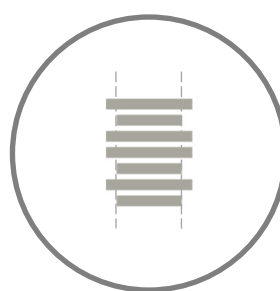
Material and Methods [1]



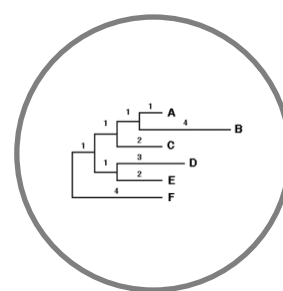
Download all sequence data available for the genus



Filtering the data and selecting 'promising' markers



Aligning and trimming of the sequences



Building Neighbour-Joining tree with Bootstrap support

Conclusion

Based on the present evaluation of the available sequence data, *cytb* is the most reliable DNA marker for the identification of *Nasua nasua*. To allow for a better evaluation of the performance of this marker for species identification, additional sequences for *N. nasua* from the invasive regions should be added to analyses.

Discussion

Since the genus *Nasua* comprises only two species, DNA markers for which *Nasua* sequences were available, were downloaded from GenBank and BOLD for all represented species of the family Procyonidae (as defined Wozencraft [6]). Five DNA markers were evaluated (Table 1).

In the NJ-tree for **cytb**, almost all Procyonidae species are represented (Table 2) and the *N. nasua* sequences cluster together with near maximum support. *Cytb* represents a promising DNA marker for the identification of *N. nasua*. Adding sequences for *N. nasua* collected from the invasive regions will allow for a better evaluation of the performance of marker *cytb*.

N. nasua is clearly distinguished from *N. narica* and all other Procyonidae species in the NJ-trees using the **COI**, **ND5** and **16S** marker datasets, yet not all genera are well represented for these markers (Table 2). For markers **ATP6**, **PNOC**, **Rag 1** and **Rag 2**, the genus *Nasua* has only three or less unique sequences available. In addition, sequences of markers **Rag2** appear to be misidentified, for which the current database cannot offer clarification due to underrepresentation of both *N. nasua* and *N. narica*. Adding the missing species (Table 2), will allow for a better evaluation of the performance of these DNA markers.

Table 1: Overview of the encountered issues concerning the DNA-based identification of the IAS [1]: (1) Insufficient publicly available DNA sequences of the IAS to capture the intra-species divergence; (2) Poor geographical coverage of the IAS sequences (native or invasive range missing); (3) The IAS sequences do not form supported clusters; (4) Potential misidentification of a specimen which influences the clustering of the IAS sequences; and (5) Not all species of the family are represented in the final NJ-tree. An 'X' indicates that the issue was encountered, a '1' indicates only one unique *N. nasua* sequence was available.

Markers analysed	1	2	3	4	5
COI		X			X
cytb		X			X



ND5		X			X
ATP6	X	X			X
PNOC	X	X			X
Rag1	1	X	1		X
Rag2	X	X	X	X	X
16S		X			X

Table 2: Publicly available sequences downloaded (October 2019) from BOLD and GenBank (including sequences extracted from mitochondrial genomes) which were withheld as reliable and informative in the final alignment that was used for building the NJ-trees. The species names follow [6]. An 'X' indicates that at least one sequence was used in the final alignment. A '1' indicates only one unique sequence was available. Species names with * are not mentioned in [6] but used on GenBank.

Species in family	COI	Cytb	ND5	ATP6	PNOC	Rag1	Rag 2	16S
<i>Bassaricyon alleni</i>	1	X	1	1	X	1	X	1
<i>Bassaricyon beddardi</i>	1	1						
<i>Bassaricyon gabbii</i>	1	X	X		1	1	1	X
<i>Bassaricyon lasius</i>								
<i>Bassaricyon pauli</i>								
<i>Bassaricyon neblina*</i>		X						
<i>Bassariscus astutus</i>	1	1	1	1	X	1	X	
<i>Bassariscus sumichrasti</i>		1	1		1	1		
<i>Nasua narica</i>	X	X	X		1	1	1	X
<i>Nasua nasua</i>	X	X	X	X	X	1	X	X
<i>Nasua meridensis*</i>		1						
<i>Nasua olivacea</i>		X						
<i>Potos flavus</i>	X	X	1		X	1	X	
<i>Procyon cancrivorus</i>	X	X	1	X	1	X	1	
<i>Procyon lotor</i>	X	X	X	X	X	X	X	X
<i>Procyon pygmaeus</i>								
TOTAL species	9/14	11/14	9/14	5/14	9/14	9/14	8/14	5/14

For a more elaborate discussion of the available databases, the sequence selection process, the outcome of the NJ-tree analyses, the usefulness of the investigated DNA sequences for species identification, as well as information on how to send samples for analyses please contact BopCo directly.



References and online information

Online information

<https://www.iucnredlist.org/species/41684/45216227>
<https://www.cabi.org/isc/datasheet/74001>
<http://www.nonnativespecies.org/factsheet/factsheet.cfm?speciesId=2324>
https://animaldiversity.org/accounts/Nasua_nasua/

Picture credits

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Page 2 (right): South American Coati (*Nasua nasua*) male By Bernard Dupont [CC BY-SA 2.0]
Page 2 (left): A coati family in Iguazu Falls By Murray Foubister [CC BY-SA 2.0]

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