



Identification of Invasive Alien Species using DNA barcodes

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General introduction to this factsheet

The Barcoding Facility for Organisms and Tissues of Policy Concern (BopCo) provides an expertise forum to facilitate the identification of biological samples of policy concern in Belgium and Europe. BopCo is funded by the Belgian Science Policy Office (Belspo), and it represented part of the Belgian federal contribution to the European Research Infrastructure Consortium LifeWatch (November 2015 – February 2022).

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. However, to implement the proposed actions, 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, with 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 using DNA barcoding to the taxonomic level stated in the EU list. For further information about the reasoning behind the applied approach and details on the materials and methods utilised, please see below and Smitz *et al.* [1].

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

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

Procyon lotor

(Linnaeus, 1758)

Common names:

English: raccoon, common raccoon, northern raccoon

French: raton laveur

German: Waschbär

Dutch: wasbeer

Last update: October 2019



General information on *Procyon lotor*

Classification

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

Species in the same genus: N = 3 [2-6]

Infra-species level: N = 22 [5-6]

Note: Twenty-two subspecies have been recognised: *P.I. auspicatus*, *P.I. elucus*, *P.I. excelsus*, *P.I. fuscipes*, *P.I. gloveralleni*, *P.I. grinnelli*, *P.I. hernandezii*, *P.I. hirtus*, *P.I. incautus*, *P.I. inesperatus*, *P.I. insularis*, *P.I. litoreus*, *P.I. lotor*, *P.I. marinus*, *P.I. maynardi*, *P.I. megalodous*, *P.I. pacificus*, *P.I. pallidus*, *P.I. psora*, *P.I. pumilus*, *P.I. simus*, and *P.I. vancouverensis*.



Native range: [3], [7-10]

North and Central America.

Invasive range: [3], [7-12]

Europe (geographical):

Austria, Belarus, Belgium, Croatia, Czech Republic, Denmark, Estonia, France, Germany, Hungary, Italy, Ireland, Liechtenstein, Lithuania, Luxembourg, Netherlands, Norway, Poland, Romania, Russia (European part), Serbia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Ukraine and United Kingdom.

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

<https://easin.jrc.ec.europa.eu/spexplorer/species/factsheet/R12260>

<https://www.gbif.org/species/5218786>

<https://www.iucnredlist.org/species/41686/45216638>

<https://www.cabi.org/isc/datasheet/67856>

Outside Europe (geographical):

Azerbaijan, Georgia, Guadeloupe, Japan, Martinique, Russia (Asian part) and Uzbekistan.

Morphology, biology, invasion, negative effects and remedies

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



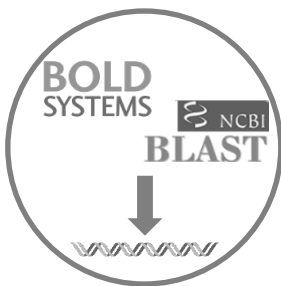
Species identification based on DNA barcodes

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. However, to assure correct species identifications, reference libraries need to include a sufficiently large number of sequences of (i) the IAS under investigation to assess the intraspecific genetic divergence, (ii) the closely related species to evaluate the interspecific genetic divergence, and (iii) the different geographical areas covering the distribution range (native and invasive) of the IAS to detect potential population structure or local hybrids.

In this context, 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/nuccore/) to estimate the reliability with which a species identification can be obtained using DNA barcoding.

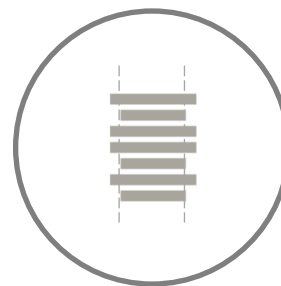
Material and Methods [1]



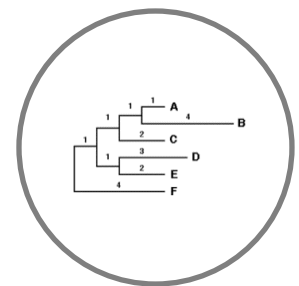
Download all sequence data available for the genus



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 *Procyon lotor*. To allow for a better evaluation of the performance of this marker for species identification, the missing species, especially *P. pygmaeus*, should be added to the analyses.

Discussion

Since the genus *Procyon* comprises only three species, DNA markers for which *Procyon* sequences were available, were downloaded from GenBank and BOLD for all represented species of the family Procyonidae (as defined by Koepfli [13]). In current databases no DNA sequences could be found for *Procyon pygmaeus*. Eight DNA markers were evaluated (Table 1).

In the NJ-tree for *cytb*, almost all Procyonidae species are represented and the *P. lotor* sequences cluster together with maximum support. However, this cluster also contains one *P. cancrivorus* sequence (GenBank accession number AB285333) which is not clustering with the other *P. cancrivorus* sequences. This sequence might involve a misidentification. If so, *cytb* currently represents the most promising DNA marker for the identification of *P. lotor*.

The *P. lotor* COI sequences cluster together, yet only eight out of the fourteen Procyonidae species are represented in the NJ-tree (Table 2). Adding sequences for the missing species will allow to better evaluate the performance of COI for the identification of *P. lotor*.

For **16S**, **ND5**, **ATP6**, **PNOC**, **Rag 1** and **Rag2** either: fewer *P. lotor* sequences are available, none cover the native region and/or less Procyonidae species are represented compared to other markers (Tables 1 & 2). Therefore it is currently not advisable to apply these markers for species identification.



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.

Markers analysed	1	2	3	4	5
COI					X
cytb				X	X
ND5		X			X
ATP6		X			X
PNOC	X	X			X
Rag 1	X	X			X
Rag 2	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 [13]. An 'X' indicates that at least one sequence was used in the final alignment. A '1' indicates only one sequence was available.

Species in family	COI	cytb	ND5	ATP6	PNOC	Rag 1	Rag 2	16S
<i>Bassaricyon alleni</i>	X	X	1	1	X	1	X	1
<i>Bassaricyon gabbii</i>	1	X	1		1	1	1	
<i>Bassaricyon medius</i>		X	1					X
<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>Nasuella meridensis</i>		1						
<i>Nasuella 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	8/14	13/14	10/14	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/41686/45216638>

<https://www.cabi.org/isc/datasheet/67856>

<https://www.pbs.org/wnet/nature/raccoon-nation-raccoon-fact-sheet/7553/>

<http://www.nonnativespecies.org/factsheet/factsheet.cfm?speciesId=2839>

https://www.nobanis.org/globalassets/speciesinfo/p/procyon-lotor/procyon_lotor.pdf

<https://ias.biodiversity.be/species/show/29>

Picture credits

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Page 2 (right): *Procyon lotor*_(Linnaeus_1758) By Michael Gäbler [CC-BY-3.0]

References

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