Identifying Invasive Alien Species by DNA-barcoding: possibilities, gaps and pitfalls

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Invasive alien species (IAS) have a negative impact on their newly occupied, non-native environments after their accidental or deliberate introduction. In order to protect native biodiversity and ecosystems, and mitigate the potential impact on human health and socio-economic activities, the European Commission issued Regulations for 49 IAS impacting EU member states. The reliability with which these IAS can be identified by molecular data, using the online available sequence data, is now described in concise factsheets, one for each species on the EU list. These factsheets will be made publicly available through BopCo’s webpage.

Project aim:
Investigate and evaluate the usefulness of publicly available DNA sequence data to reliably identify each of the 49 IAS

Factsheets

1 factsheet for each of the 49 IAS:
Arthropods 7
Mammals 11
Fish 2
Birds 4
Herpetofauna 2
Plants 23

PART 1: Overview of taxonomy, classification and native & invasive range distributions to allow the evaluation of the completeness of the DNA sequence datasets.

PART 2: Evaluation of DNA reference databases with regards to the identification of the 49 IAS using DNA barcoding. A conclusion is formulated on how well the data cover the identification needs, on which sequence marker(s) to use and on how the currently available datasets can be improved.

Evaluation criteria, issues & examples

Data availability
- IAS DNA sequences:
  Enough sequences of the IAS need to be available to capture the intra-species genetic variability
- IAS distribution range:
  Sequence data preferably available for both the native and the invasive species range to not miss any intra-species genetic variability
- Data on congenerics:
  Sequence data should be available for all closely related species to capture inter-species sequence divergence

Recovery of supported taxon
- The sequences of the IAS should form one or several supported cluster(s) in the NJ-tree for the marker to be useful

Potential mis-identifications
- DNA sequences may come from misidentified reference specimens confounding the analyses

Future prospects
For some of the listed IAS the identifications can be reliably completed using the current public DNA sequence data. However, other IAS require further investigation of their DNA sequences and/or a completion of the existing data gaps. For the latter BopCo is always looking for collaborations or specimen contributions.

Take a look at the previews