

The limits of mtDNA analysis for determining the provenance of invasive species: a midwife toad example

Chris Vliegenthart^{1,2,*}, Maurits van de Vrede^{1,2,*}, Ingrid den Boer³, Maarten J. Gilbert^{4,5},
Pim Lemmers^{6,7}, James France^{1,2}, Manon C. de Visser^{1,2}, Richard P.J.H. Struijk⁴, Ben
Wielstra^{1,2,**}

1 - Naturalis Biodiversity Center, P.O. Box 9517, 2300 RA Leiden, The Netherlands

2 - Institute of Biology Leiden, Leiden University, P.O. Box 9505, 2300 RA Leiden,
The Netherlands

3- Independent Researcher, The Netherlands

4 - Reptile, Amphibian and Fish Conservation Netherlands (RAVON), P.O. Box 1413,
6501 BK Nijmegen, The Netherlands

5 - Department Biomolecular Health Sciences – Infectious Diseases and Immunology,
Faculty of Veterinary Medicine, Utrecht University, P.O. Box 80.165, 3508 TD Utrecht,
The Netherlands

6 - Natuurbalans – Limes Divergens, Toernooiveld 1, 6525 ED Nijmegen, The
Netherlands

7 - Netherlands Centre of Expertise for Exotic Species (NEC-E), Nature plaza, P.O. Box
9010, 6500 GL Nijmegen, The Netherlands

* These authors contributed equally to this work.

**Corresponding author: ben.wielstra@naturalis.nl

ORCID iD: Wielstra: 0000-0002-7112-5965

Supplementary material

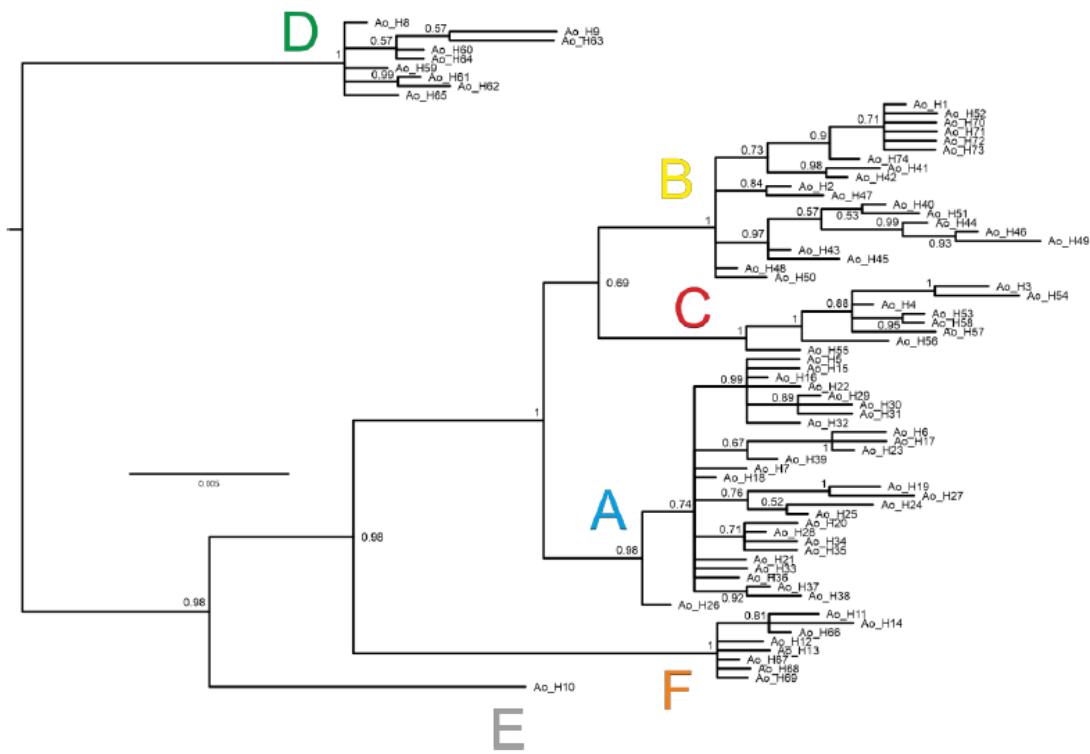


Figure S1. The 50% majority-rule consensus tree from the Bayesian phylogenetic analysis of 74 ND4 mtDNA haplotypes of the common midwife toad (*Alytes obstetricans*). The outgroup is not shown. The letters denote six major mtDNA clades referred to as haplogroups by Gonçalves et al. (2015). Haplotype details can be found in supplementary table S1.