

# Application of nanopore sequencing in Biosecurity surveillance

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## Introduction

- Browsing ant (*Lepisiota frauenfeldi*) is an exotic pest in Australia (Fig. 1), a **national biosecurity risk**.
- It is a potential threat to agriculture, environment, and households.
- Thirty-four incursions have been detected in Australia since 2013 (Fig. 2).
- Are these incursions from a same origin? Or multiple?
- This information is key to taking effective biosecurity measures and keep the pest at bay



Fig 1. Browsing ant incursion in Australia

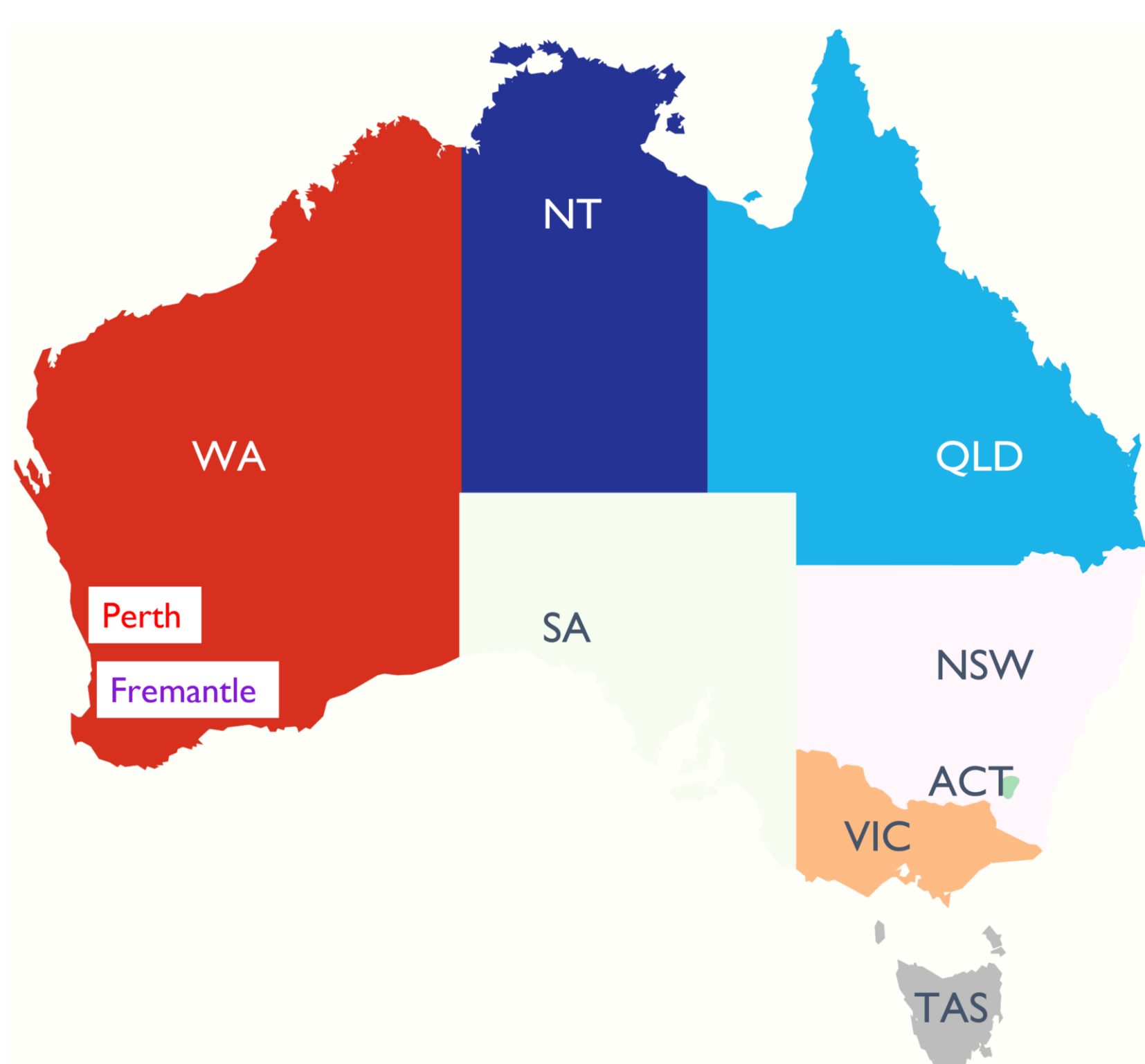


Fig 2. Browsing ant detected in WA, NT, and QLD.

## Results

- QLD, NT and WA incursions are separate (Fig. 3)
- Within WA, possibly two incursions: Perth & Fremantle
- Perth incursions could be a spread of an incursion or multiple incursions from the same source/origin
- Among the 13 mitochondrial protein coding genes, only *cox1*, *nad5* and *cob* (Fig. 4A-C, respectively) showed a topology
- However, none could not reveal the relatedness like the whole mitogenome-based tree (Figs. 3 and 4D).

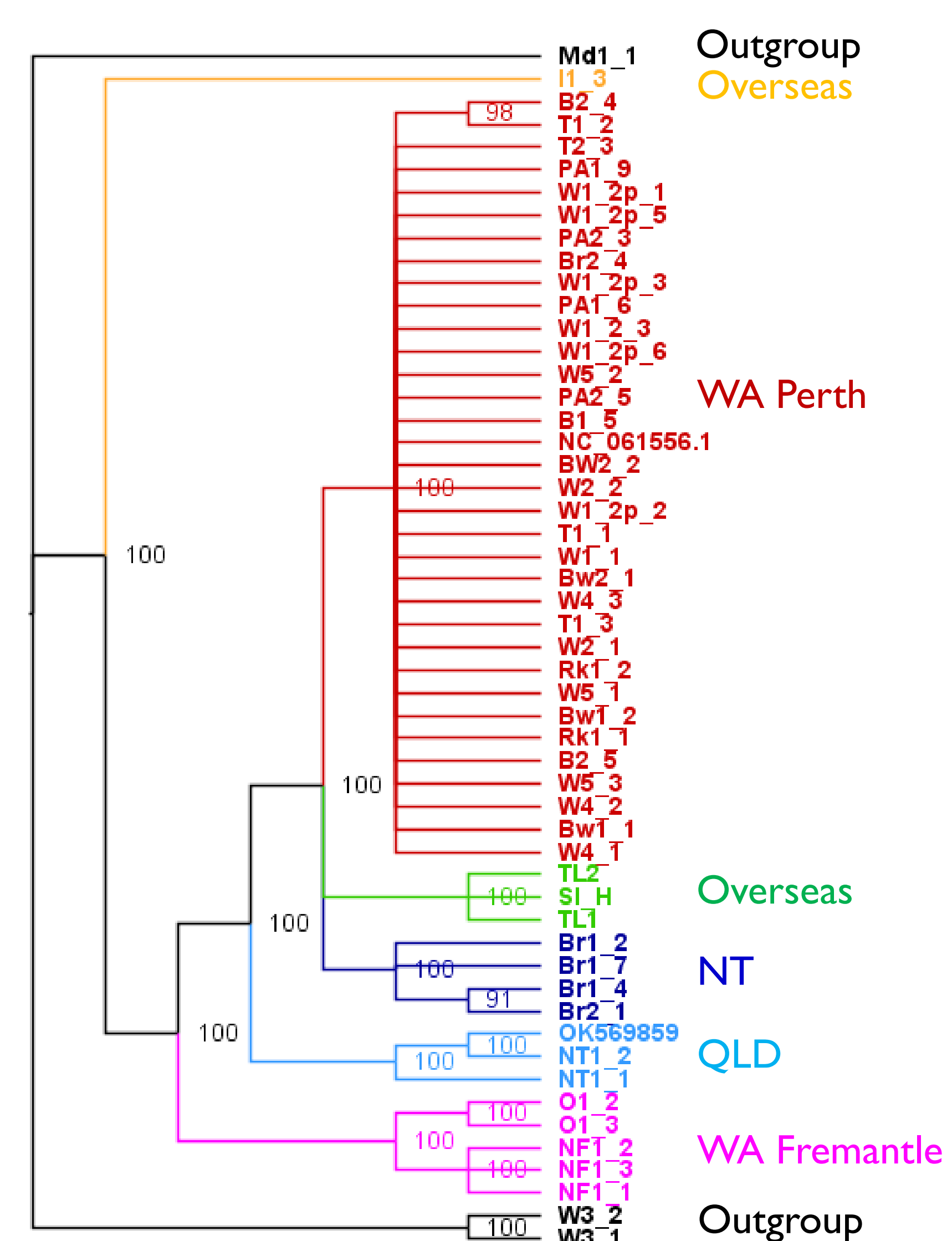


Fig 3. Phylogenetic tree based on Bayesian Inference

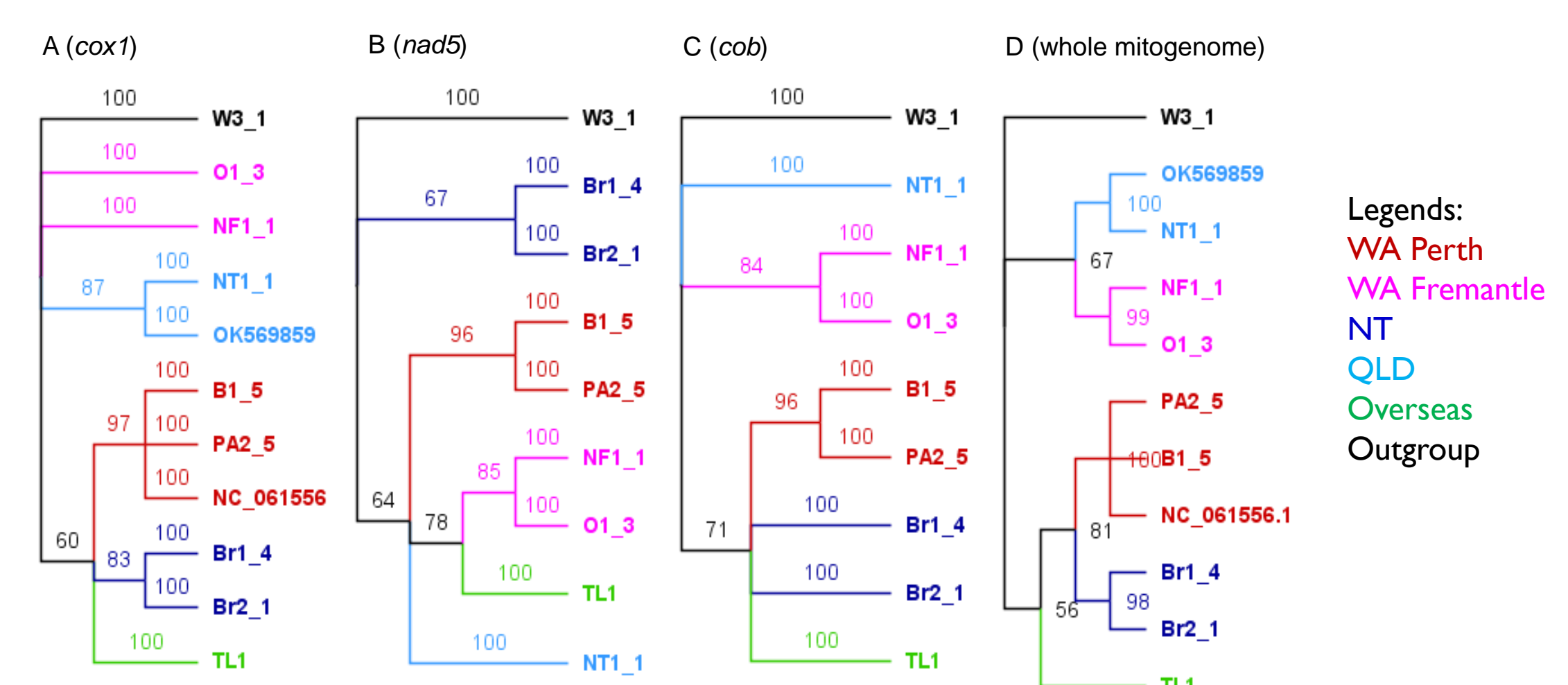


Fig 4. (A) *cox1*, (B) *nad5*, (C) *cob*, and (D) whole mitogenome based Bayesian Inference trees

## Methods

- 48 *L. frauenfeldi* and 3 *L. incisa* mitogenomes
- L. incisa* as outgroup
- SQK-LSK109, MinION sequencing
- Reference based assembly, 17 kb mitogenome
- Phylogenetic analysis

## Take-home message

- Australian browsing ant incursions are not from a single overseas origin suggesting to scrutinise all possible avenues
- However, only whole mitochondrial genome analysis could reveal the above resolution; not by a single gene analysis