

# Application of nanopore sequencing in Biosecurity surveillance



QR code

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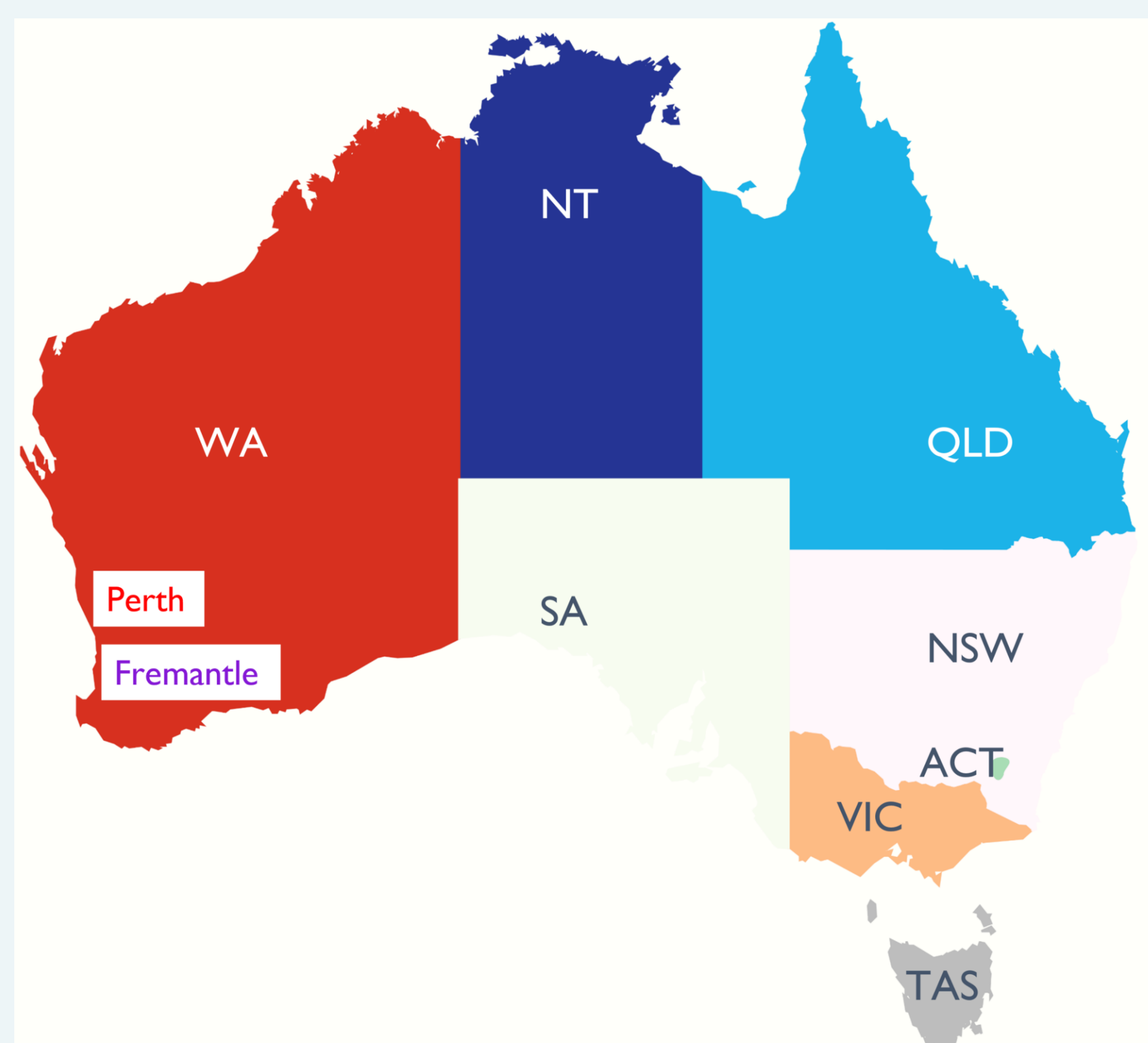
## Introduction

- 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



Photo: Pia Scanlon and Marc Widmer

**Fig 1.** Browsing ant incursion in Australia



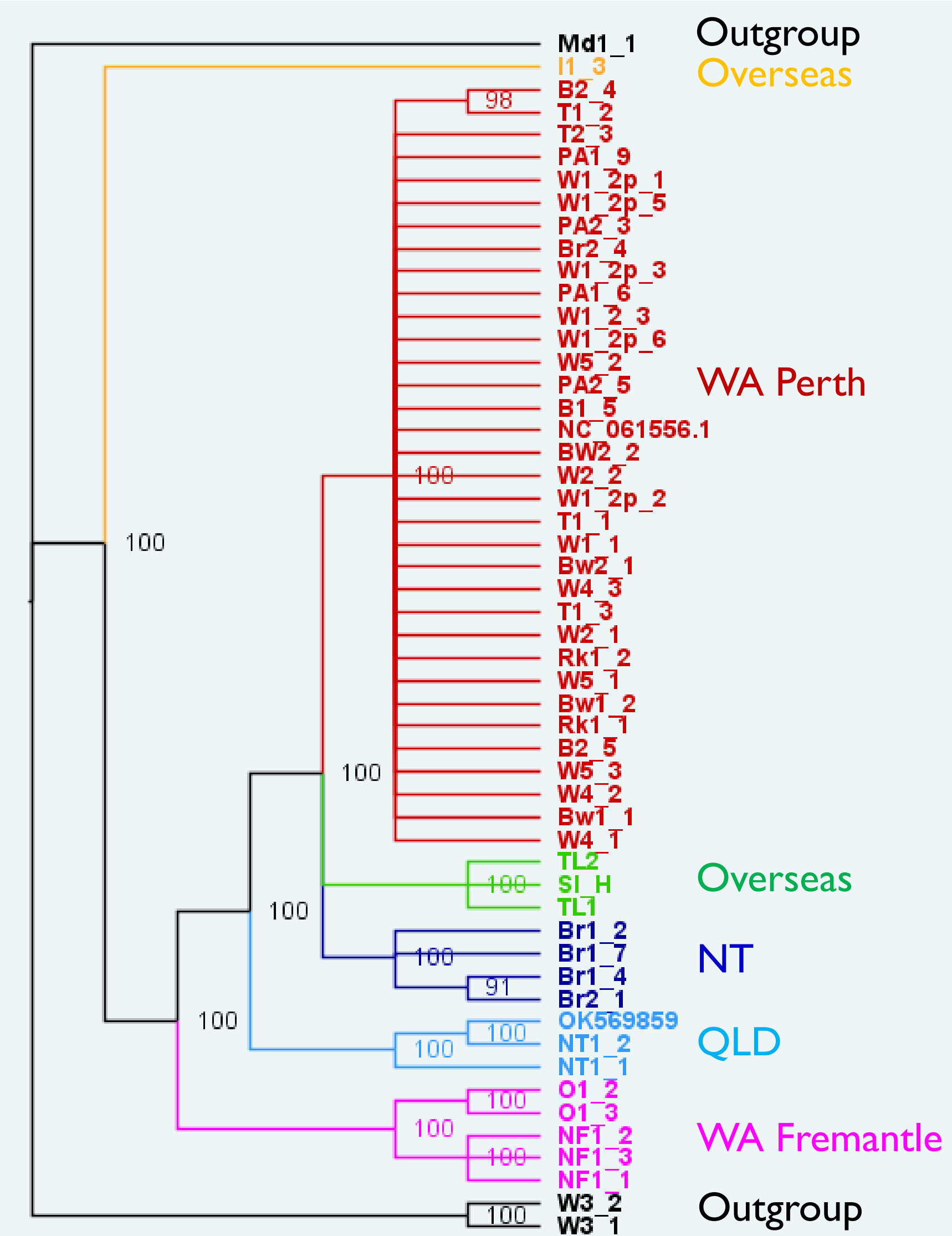
**Fig 2.** Browsing ant detected in WA, NT, and QLD.

## Methods

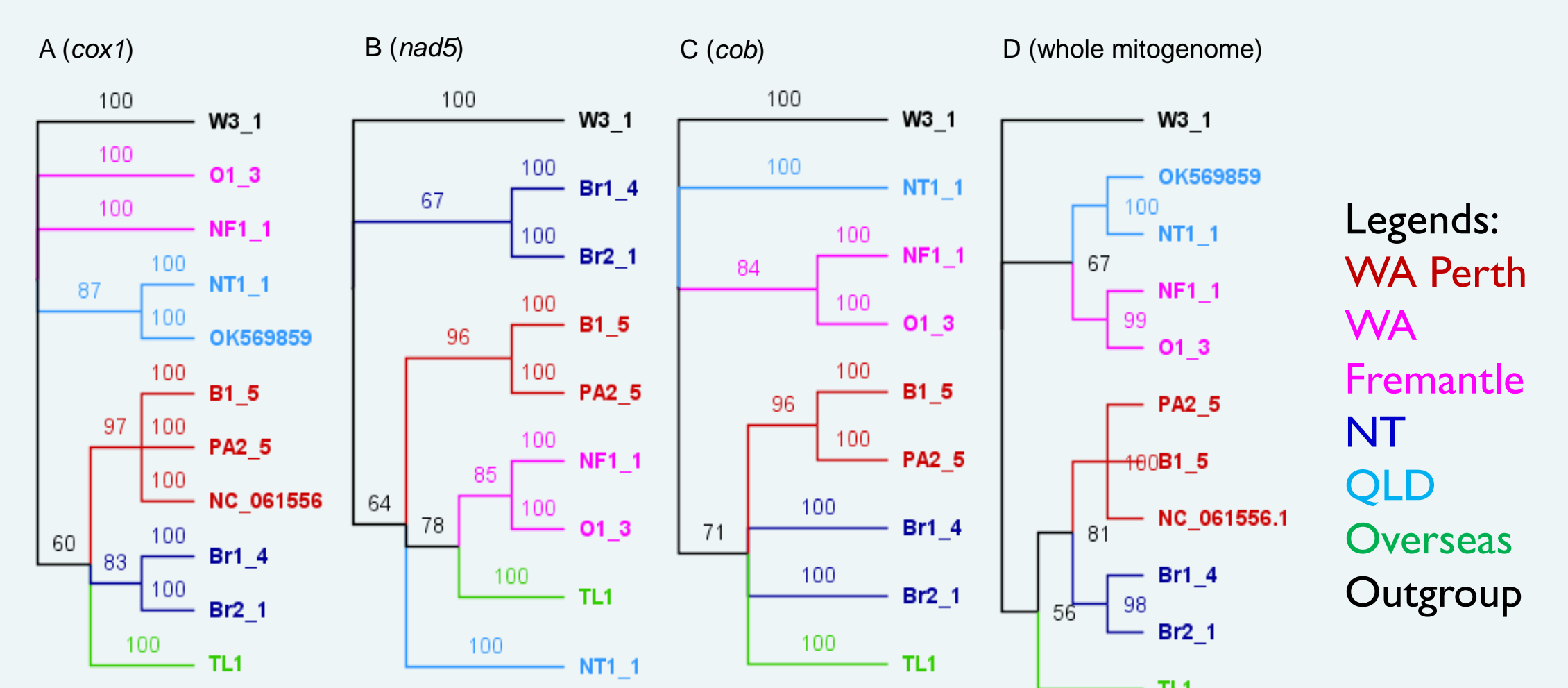
- 48 *L. frauenfeldi* and 3 *L. incisa* mitogenomes
- L. incisa* as outgroup
- Qiagen's DNeasy blood & tissue kits
- SQK-LSK109; R9.5; MinION sequencing
- Reference based assembly, 17 kb mitogenome
- Phylogenetic analysis

## 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

## 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