Deep Roots

Tracing the past of an invading plant

GREAT LAKES

ANCESTRAL

NOVA SCOTIA
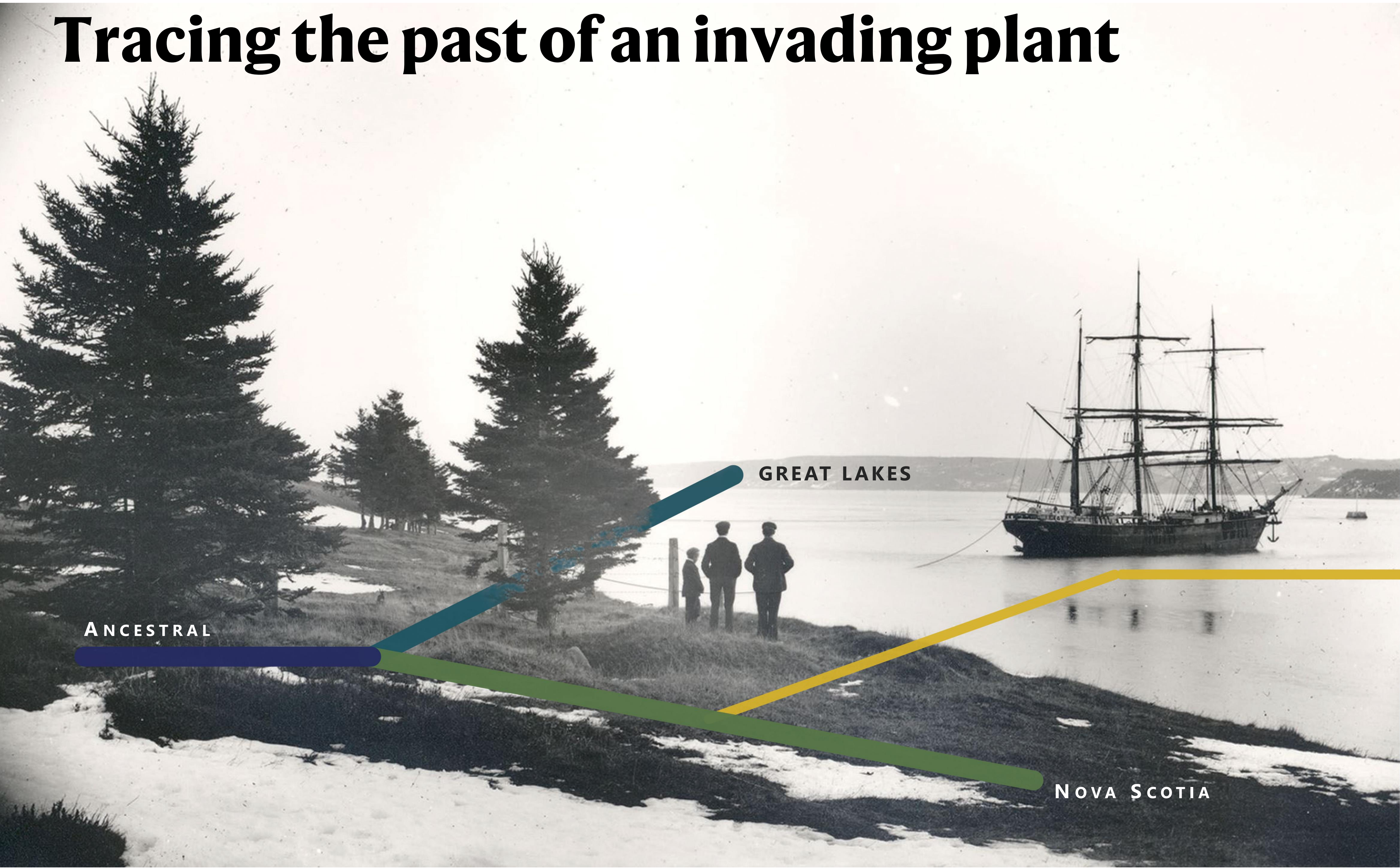
AUSTRALIA

Introduction

- Knowing where a species came from **helps anticipate where it goes next.**
- *Cakile edentula*'s invasion of Australia has been inferred through genetic structuring and Bayesian Inference phylogenetics. However, **simulation-based methods can strengthen and refine these inferences.**
- Identifying the source of invasion strengthens comparisons between native and invading populations - **grounding measures of evolutionary response**.
- Establishing the events of a species' introduction helps characterise the **genetic consequences of invasion**.
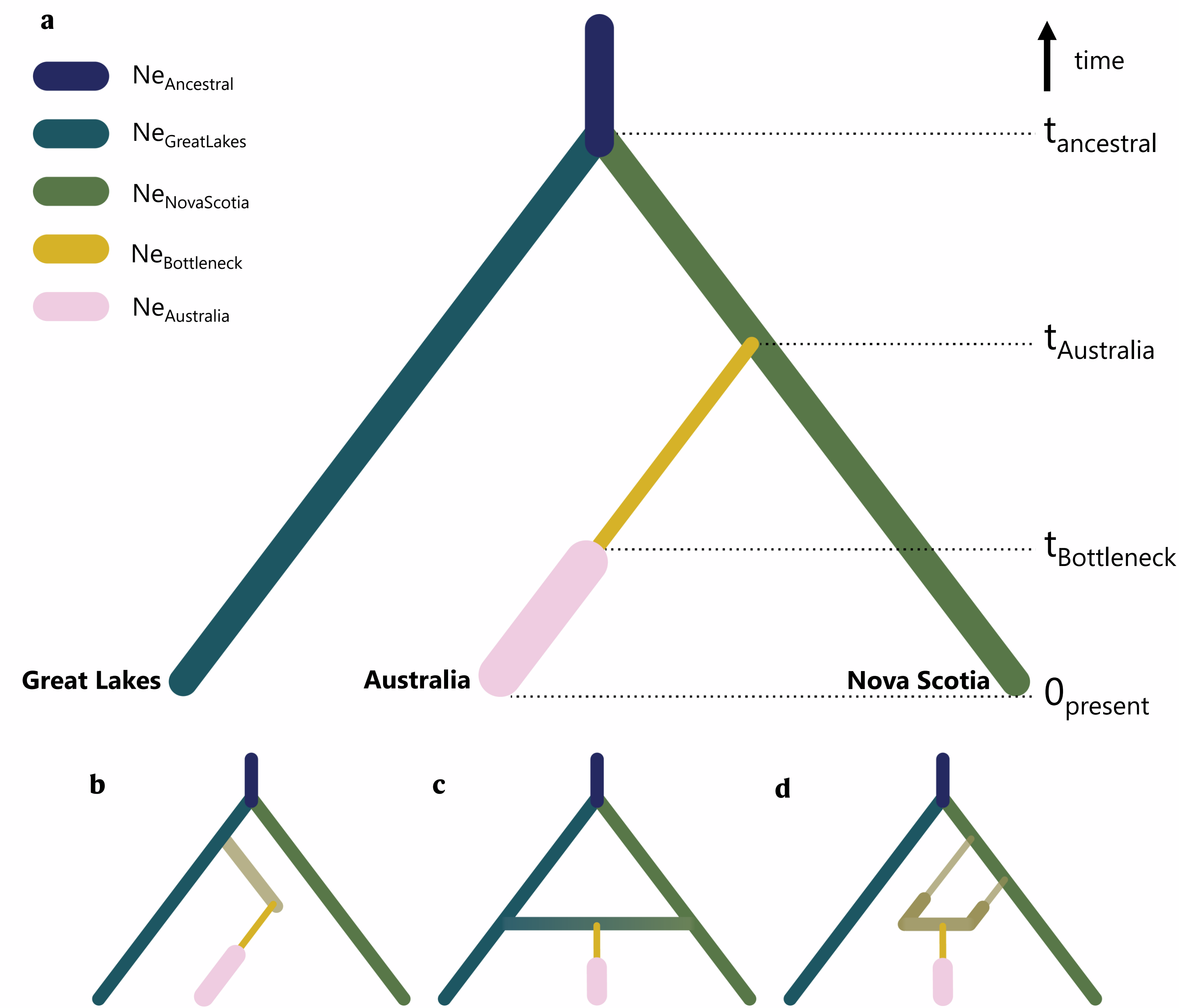
Aims

- Determine the source and timing of Australian invasion.
- Estimate the presence, duration, and impact of bottlenecks during invasion.

Methods

- **Data:** 3877 SNPs from 90 non-hybrid *Cakile edentula* sampled from Eastern North America and Australia.
- **Analysis:** Random-forest approximate Bayesian computation on 25 scenario pooled by topology.
- Pool-winning scenarios directly competed to determine best-supported scenario.
- Parameter estimation conducted on best-supported scenario.

Results

a

- $Ne_{Ancestral}$
- $Ne_{GreatLakes}$
- $Ne_{NovaScotia}$
- $Ne_{Bottleneck}$
- $Ne_{Australia}$

time

$t_{ancestral}$

$t_{Australia}$

$t_{Bottleneck}$

Great Lakes   Australia   Nova Scotia $0_{present}$

b   **c**   **d**

Figure 1. Invading population source, divergence time and bottleneck duration scenario topology using random-forest approximate Bayesian computation. **a** Best-supported scenario (posterior probability = 0.637) of three scenario pools (**b**, **c**, **d**). Parameter values and confidence intervals for best-supported scenario are shown in Table 1. Best-supported scenarios within pools predominantly involved a Nova Scotian source population.

Table 1. Posterior parameter estimates and quantile distributions (0.05-0.95) for the introduction of a novel Australian population of *Cakile edentula* from its native Nova Scotian population (Fig.1), based on the scenario with the highest posterior probability (0.637).

Parameter	Prior	Median	Q(0.05)	Q(0.95)
$Ne_{Ancestral}$	1-10,000	596	59	1858
$Ne_{GreatLakes}$	1-10,000	914	298	1903
$Ne_{NovaScotia}$	1-10,000	1273	500	3562
$Ne_{Bottleneck}$	1-1,000	15	3	69
$Ne_{Australia}$	1-10,000	6780	2509	9789
$t_{Ancestral}$	177-10,000	4730.23	1598	9229
$t_{Australia}$	156-176	166	157	175
$t_{Bottleneck}$	1-176	111	46	157

Conclusions

- *Cakile edentula*'s invasion of Australia most likely **originates from a single introduction from Nova Scotia**. This is congruent with previous inferences on the source of the invasion.
- *Cakile edentula* endured a prolonged bottleneck. However, **despite a bottleneck, present-day effective population has surged**.
- This study highlights how simulation-based methods can be used to strengthen inferences on population source and demographic parameters.

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