Figure S1. Results of the four demographic models investigated by Approximate Bayesian Computation (ABC) for *Cardamine impatiens* and *C. resedifolia*. For each demographic model we report the marginal densities (a) and modes (b), the bandwidth of the kernel (c), and the posterior probabilities of each of the model parameters (d).
Cardamine impatiens

a

Constant population size

Population size bottleneck

Population size expansion

Population size reduction

Marginal density

Retained simulations (out of 1,000,000)
Cardamine resedifolia

(a) Constant population size
(b) Population size bottleneck
(c) Population size expansion
(d) Population size reduction

Marginal density

Retained simulations (out of 1,000,000)
**Cardamine impatiens**

- **mode**
- **95% highest posterior density interval**

**Log$_{10} N_C$**

- **N$_C$ = Current population size**

**Constant population size (CON)**
**Cardamine impatiens**

- **$N_C$** = Current population size
- **$N_A$** = Ancestral population size
- **$T_R$** = Time of population size reduction
- **$T_E$** = Time of population size expansion

![Graphs showing population size over time](image)

Retained simulations (out of 1,000,000)
**Cardamine impatiens**

- **mode**
- **95% highest posterior density interval**

**Log$_{10} N_C$**

- $N_C = \text{Present population size}$
- $N_A = \text{Ancestral population size}$
- $T_R = \text{Time of population size reduction}$

**Population size reduction (RED)**

- Retained simulations (out of 1,000,000)
**Cardamine impatiens**

$N_C = \text{Current population size}$

$T_E = \text{Time of population size expansion}$

$r = \text{exponential growth parameter}$
**Cardamine resedifolia**

![Graph showing Log$_{10} N_C$](image)

- **Mode**
- **95% highest posterior density interval**

**Retained simulations (out of 1,000,000)**

**Log$_{10} N_C$**

- **$N_C$** = Current population size

**Constant population size (CON)**
Cardamine resedifolia

\[ \text{Log}_{10} N_C \]

\[ \text{Log}_{10} N_{A1} \]

\[ \text{Log}_{10} N_{A2} \]

Population size bottleneck (BOT)

- \( N_C \) = Current population size
- \( N_{A1} \) = Ancestral population size
- \( T_R \) = Time of population size reduction
- \( T_E \) = Time of population size expansion

Retained simulations (out of 1,000,000)
**Cardamine resedifolia**

- **Log$_{10} N_C$**
  - Mode
  - 95% highest posterior density interval

- **Log$_{10} N_A$**

- **$T_R$**

### Population size reduction (RED)

- $N_C$ = Present population size
- $N_A$ = Ancestral population size
- $T_R$ = Time of population size reduction

Retained simulations (out of 1,000,000)
**Cardamine resedifolia**

Population size expansion (EXP)

- $N_C = \text{Current population size}
- T_E = \text{Time of population size expansion}
- r = \text{exponential growth parameter}

**Log Base 10 of $N_C$**

**$T_E$**

Retained simulations (out of 1,000,000)
Cardamine impatiens

Corrected posterior probability

Bandwidth of the kernel
Cardamine resedifolia

Corrected posterior probability vs. Bandwidth of the kernel

Legend:
- Bottleneck
- Constant
- Expansion
- Reduction
**Cardamine impatiens**

Constant population size (CON)

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**Mutation rate**

**Log$_{10} \, N_C$**

**Recombination rate**

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Prior distribution

Posterior distribution

Marginal distribution among the 5,000 retained simulations (0.5% of total)
Cardamine impatiens
Population size bottleneck (BOT)

Mutation rate

$\log_{10} N_A^1$

$\log_{10} N_A^2$

$\log_{10} N_C$

Recombination rate

$T_E$

$T_R$

Prior distribution
Posterior distribution
Marginal distribution among the 5,000 retained simulations (0.5% of total)
Cardamine impatiens

Population size expansion (EXP)

Mutation rate

\( r \)

\( \log_{10} N_C \)

Recombination rate

\( T_E \)

Prior distribution

Posterior distribution

Marginal distribution among the 5,000 retained simulations (0.5% of total)
**Cardamine impariens**

Population size reduction (RED)

Mutation rate

Log$_{10} N_A$

Log$_{10} N_C$

Recombination rate

$T_R$

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Cardamine resedifolia

Constant population size (CON)

Mutation rate

Log$_{10}$ $N_C$

Recombination rate

Prior distribution

Posterior distribution

Marginal distribution among the 5,000 retained simulations (0.5% of total)
Cardamine resedifolia

Population size bottleneck (BOT)

Mutation rate

Log$_{10} N_A^1$

Log$_{10} N_A^2$

Log$_{10} N_C$

Recombination rate

$T_E$

$T_R$

Prior distribution
Posterior distribution
Marginal distribution among the 5,000 retained simulations (0.5% of total)
Cardamine resedifolia

Population size expansion (EXP)

- Mutation rate
- $r$
- $\log_{10} N_C$
- Recombination rate
- $T_C$

Prior distribution
- Posterior distribution
- Marginal distribution among the 5,000 retained simulations (0.5% of total)
Cardamine resedifolia

Population size reduction (RED)

Mutation rate

Log\(_10\) \(N_A\)

Log\(_10\) \(N_C\)

Recombination rate

\(T_R\)

Prior distribution

Posterior distribution

Marginal distribution among the 5,000 retained simulations (0.5% of total)