

Supplementary Information

[illegible]

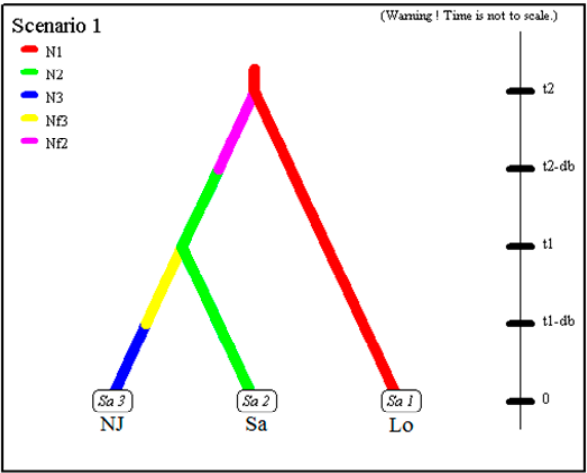
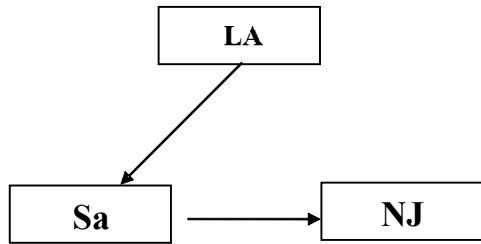
(a)

Figure S1. Cont.

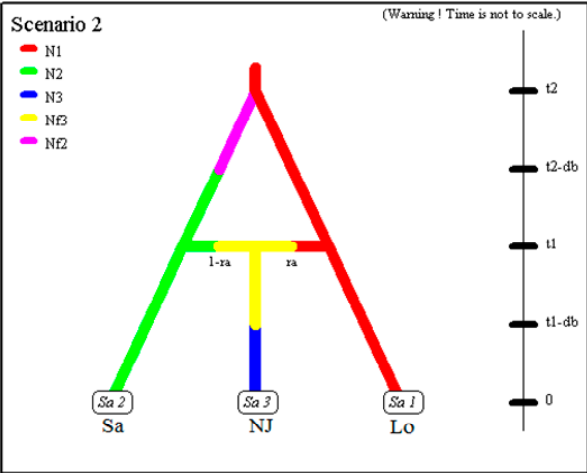
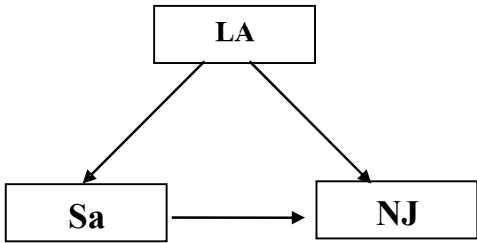
haplotypes	SH	NB	JX	XYc	XYw	WXb	NT	XG	XBv	BGt	WX	WJ	MAS	CJr	CH	HF	DY	SLt	NBp	PYL	NCyl	NHL	YNL	XT	QJ	LZL	HHL	CHL	YJ	NX	DTL	DTLs	CQs	ZX	JY	Sa	Lo		
Hap_i1	1	4	2		1	3	2	5	1	5	3	2	1	3	5	1			5	1				3	3		1	1	3	1	2	1	3	6	4	4	2	2	
Hap_i2	1			3	3	2		2	5	2	1	5		2	2	5	3	5	1	1	3	4	3	3			1		2	1	1			2	2	2	1	2	
Hap_i3	1			3		1	4				3		5												3			1	1	3	1	1	1				1	1	
Hap_i4												1																									1		
Hap_i5																			1																		1		
Hap_i6																										1												1	
Hap_i7																																			1			1	
Hap_i8																																						1	
Hap_i9																																							4

(b)

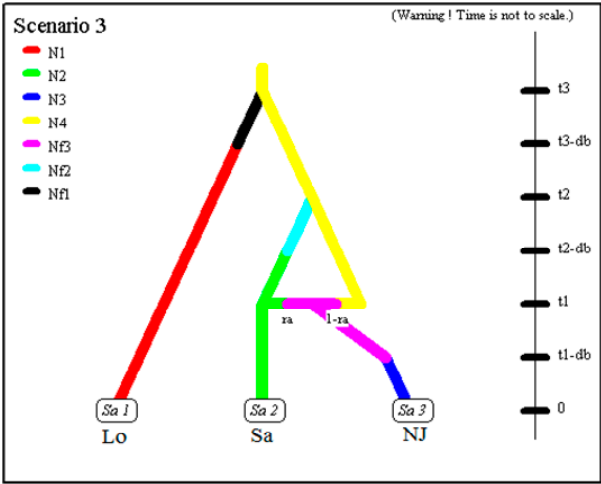
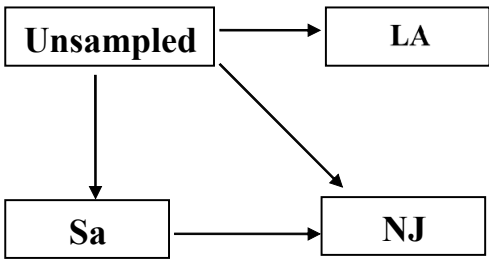
Figure S1. Distribution of all haplotypes obtained. **(a)** Distribution of haplotypes in mitochondrial control region sequences of *P. clarkii*; **(b)** Distribution of haplotypes in *proPOx* intron sequences of *P. clarkii*. The sampling location codes see Table S1 in supplementary material.



Scenario 1

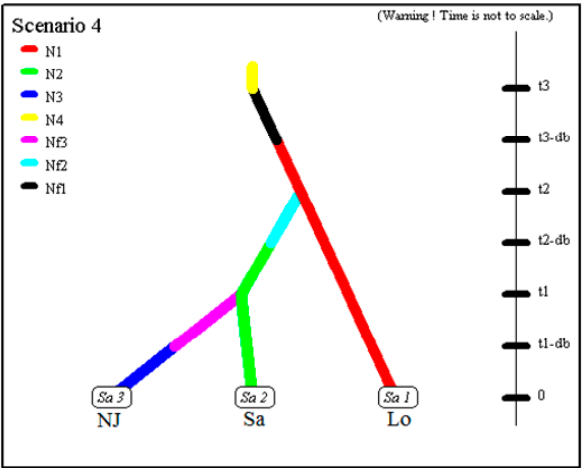
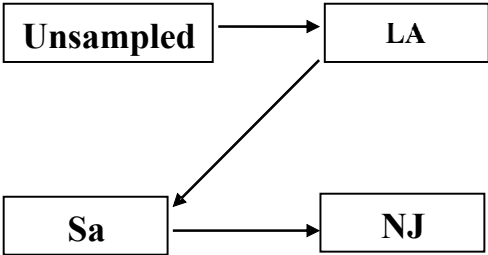


Scenario 2

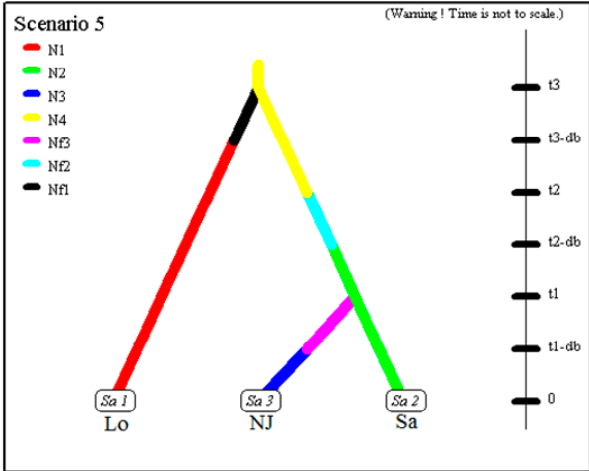
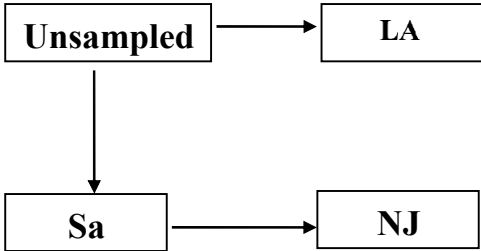


Scenario 3

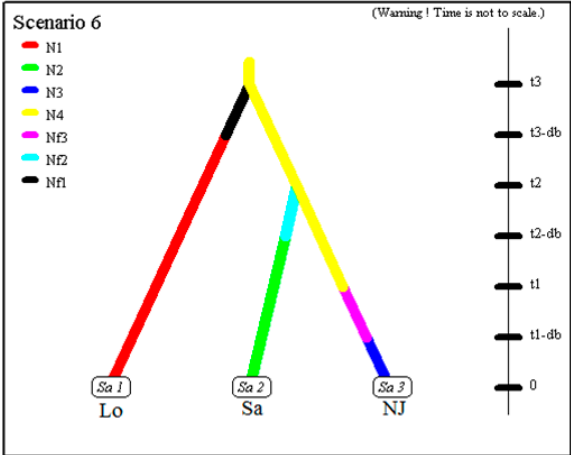
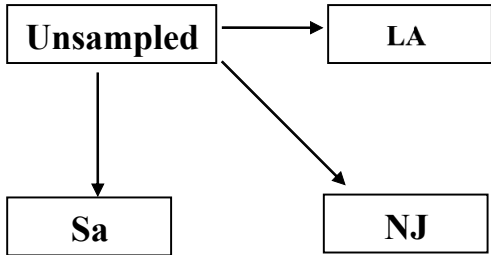
Figure S3. Cont.



Scenario 4

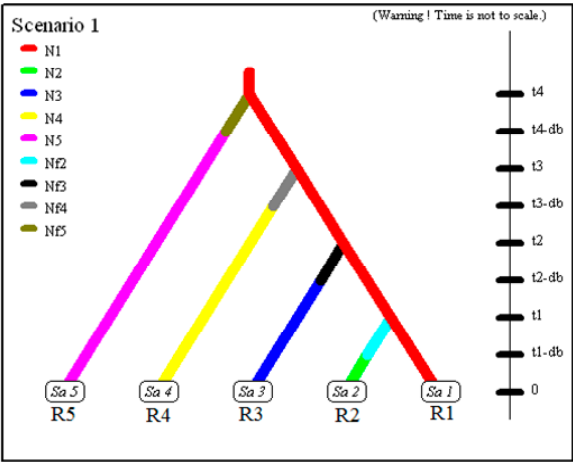
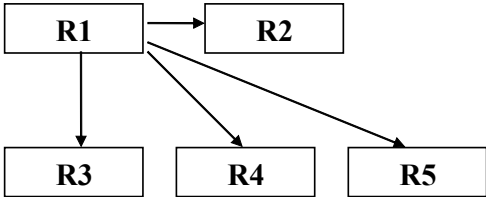


Scenario 5

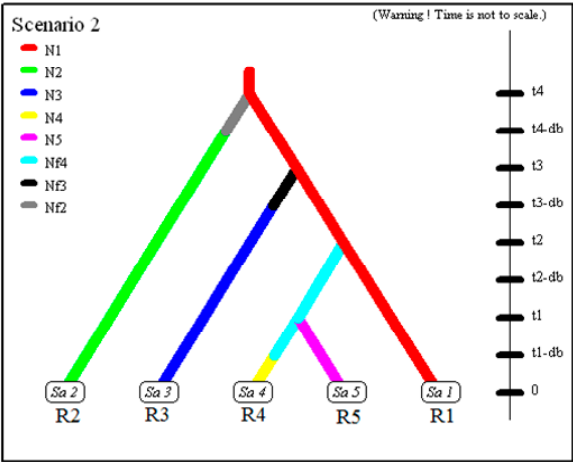
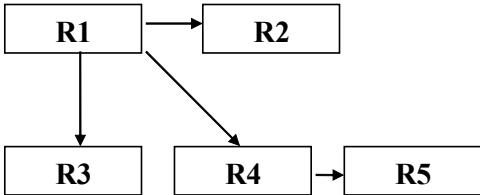


Scenario 6

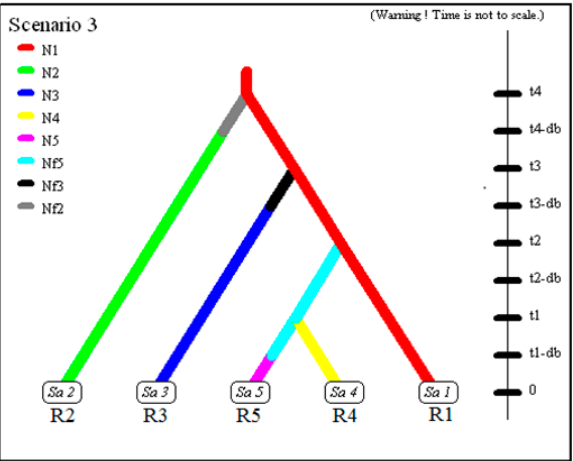
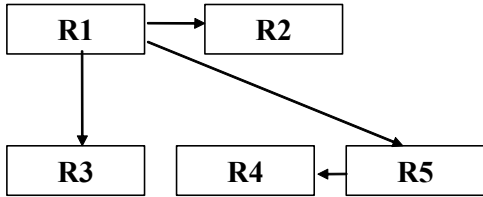
Figure S3. Cont.



Scenario 7

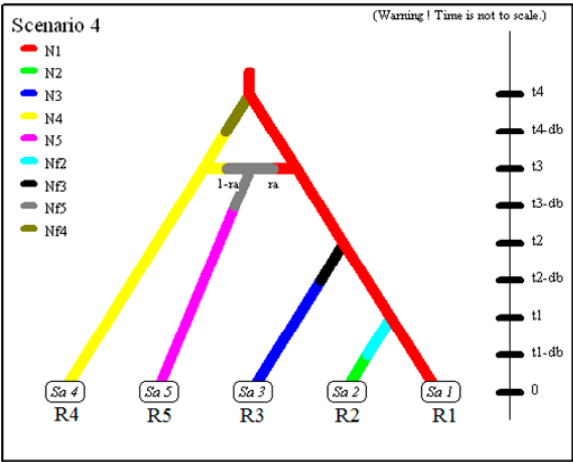
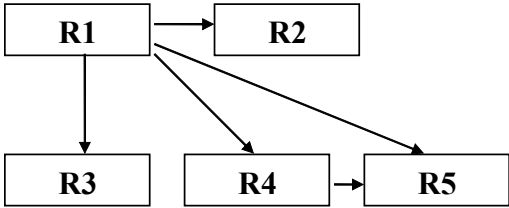


Scenario 8

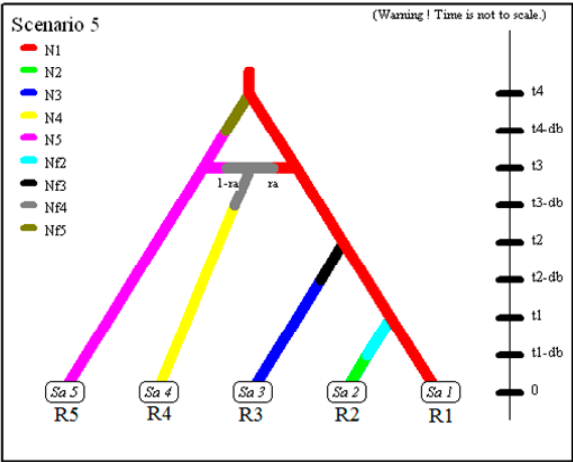
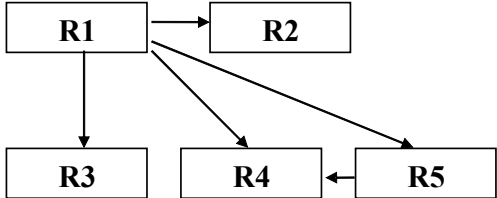


Scenario 9

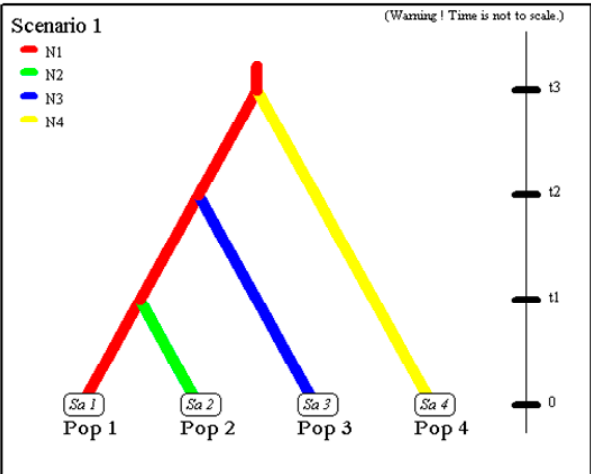
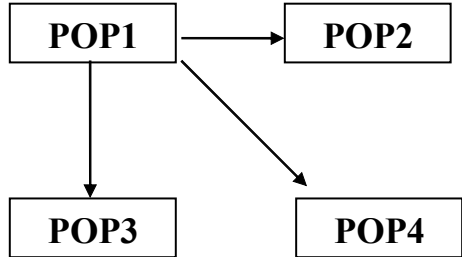
Figure S3. Cont.



Scenario 10

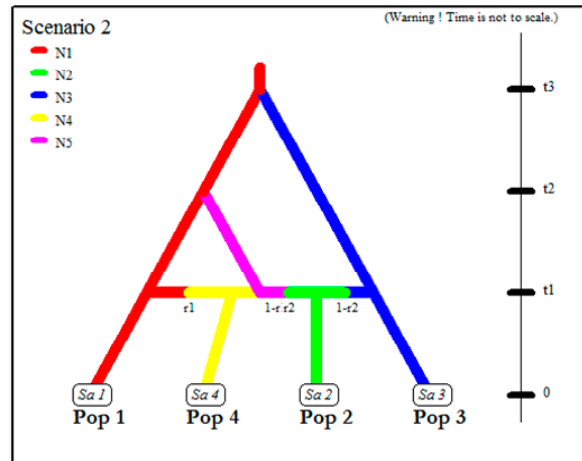
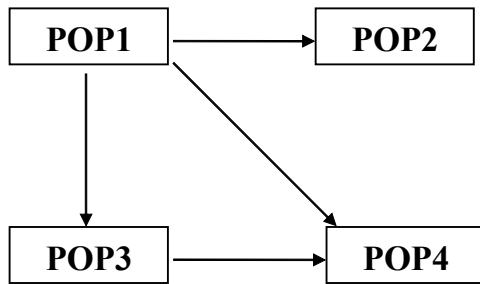


Scenario 11

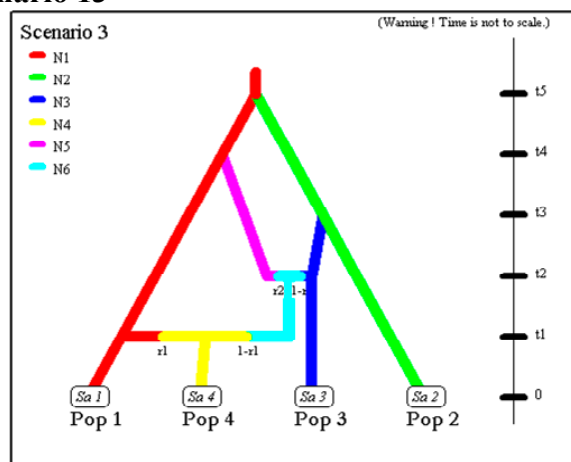
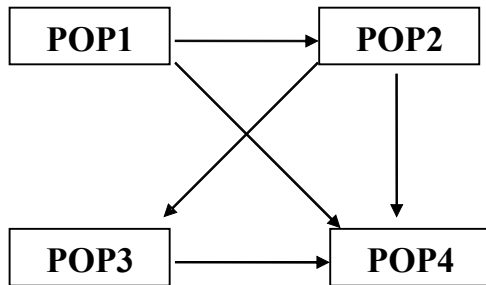


Scenario 12

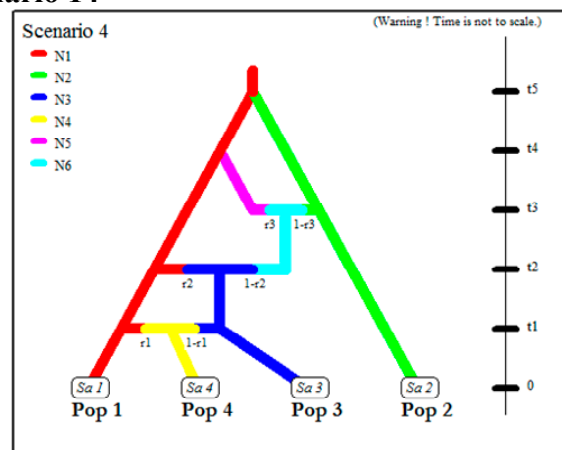
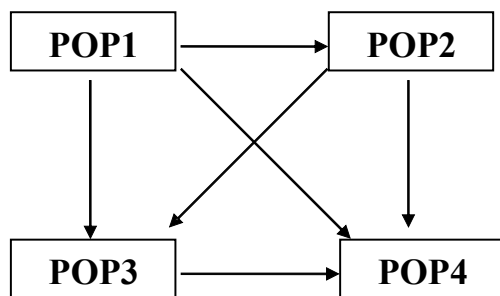
Figure S3. Cont.



Scenario 13

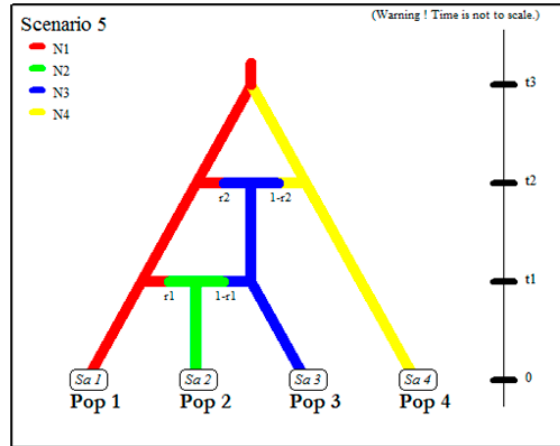
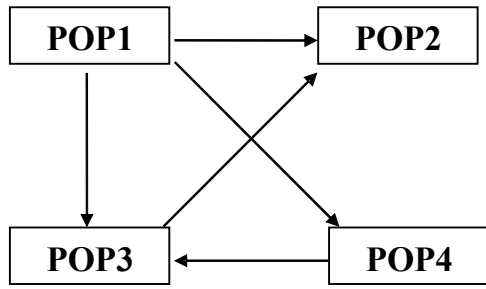


Scenario 14

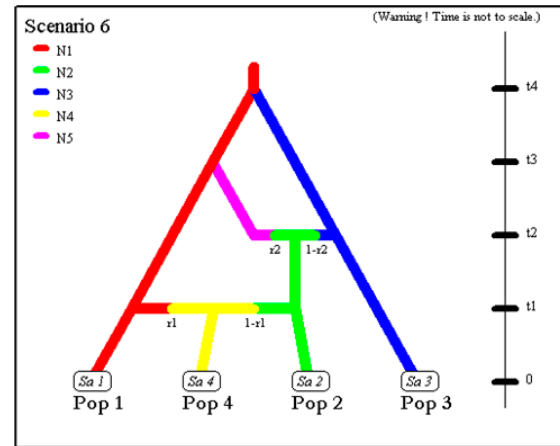
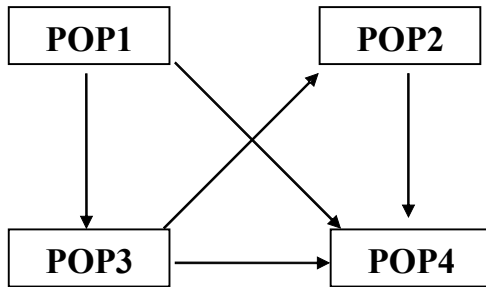


Scenario 15

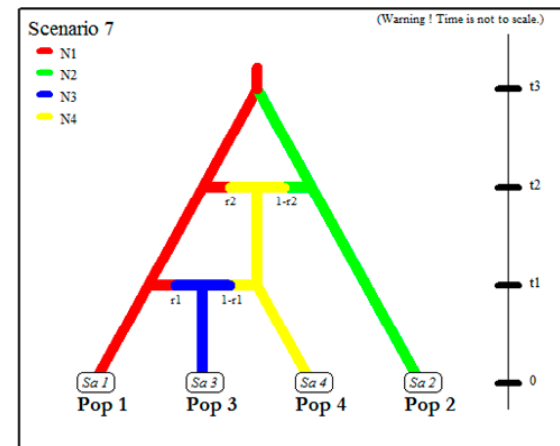
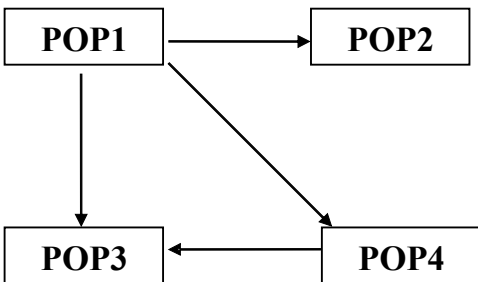
Figure S3. Cont.



Scenario 16

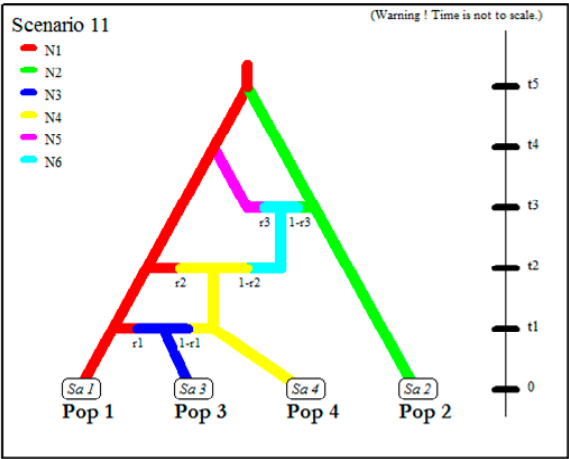
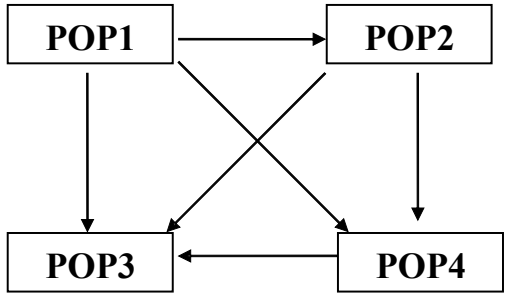


Scenario 17

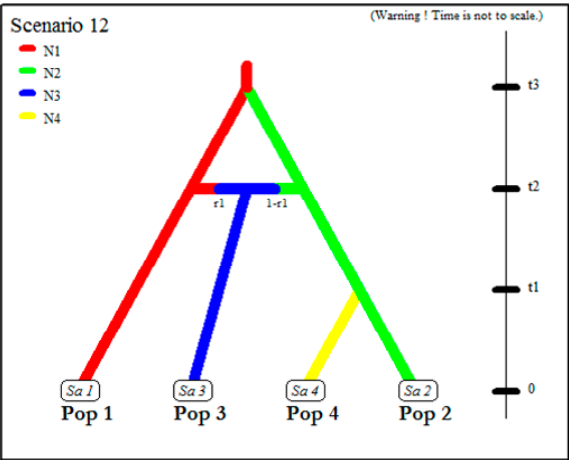
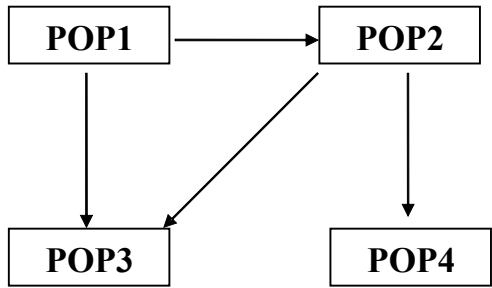


Scenario 18

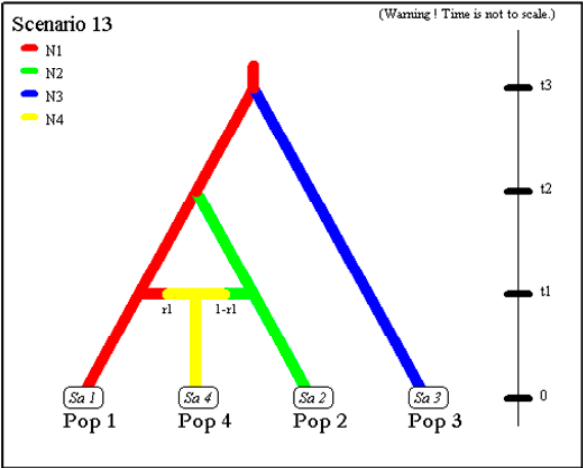
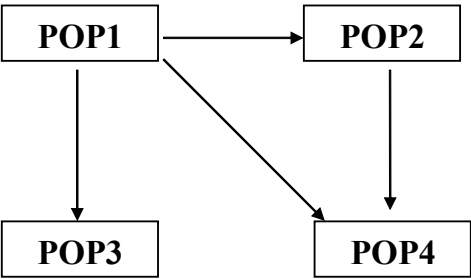
Figure S3. *Cont.*



Scenario 22



Scenario 23



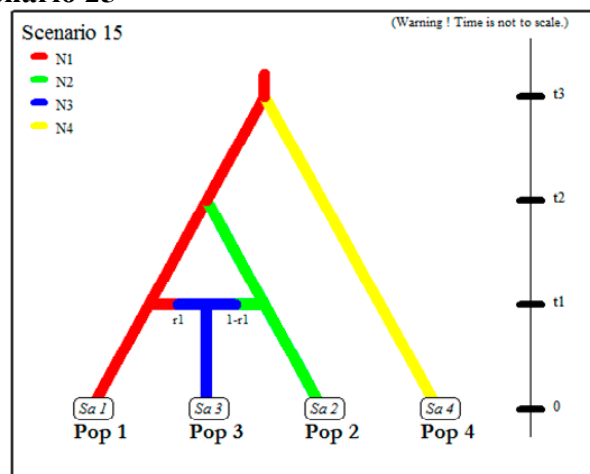
Scenario 24

Figure S3. *Cont.*

The diagram illustrates a four-population model with the following migration pathways:

- POP1 to POP2 (horizontal arrow)
- POP1 to POP3 (vertical arrow)
- POP1 to POP4 (diagonal arrow)
- POP2 to POP4 (vertical arrow)
- POP3 to POP2 (diagonal arrow)

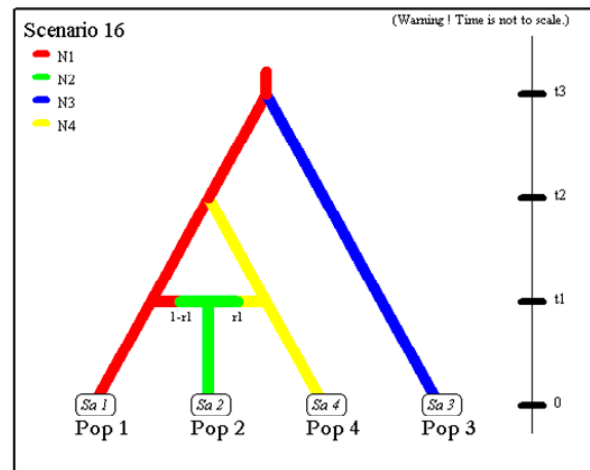
There are no arrows shown between POP2 and POP3, or between POP3 and POP4.



The diagram illustrates a four-population model with the following migration structure:

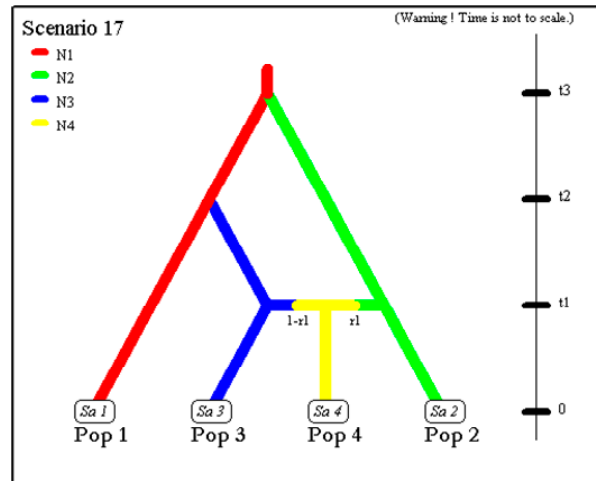
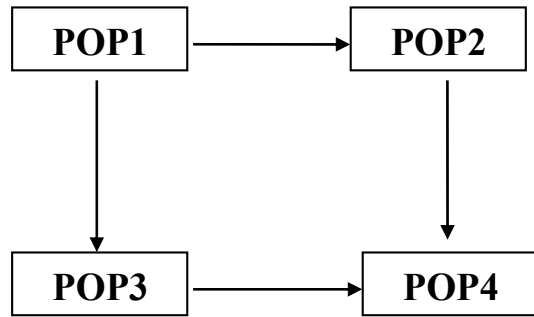
- POP1 has a horizontal arrow pointing to POP2.
- POP1 has a vertical arrow pointing down to POP3.
- POP2 has a diagonal arrow pointing down to POP4.
- POP3 has a diagonal arrow pointing up to POP4.

There are no arrows between POP2 and POP3, or between POP1 and POP4.

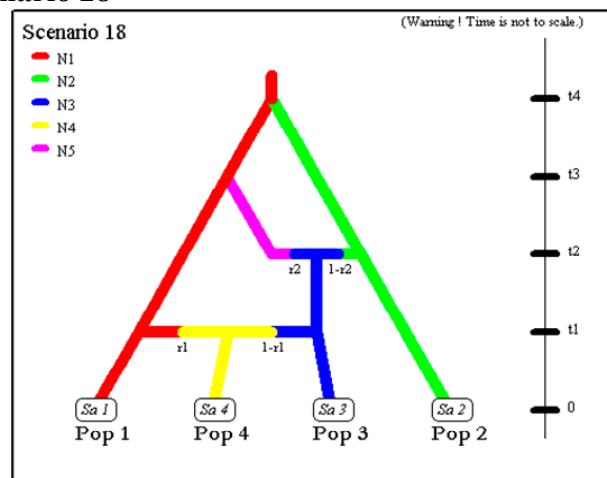
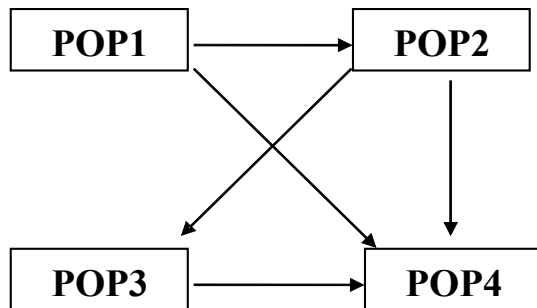


The diagram illustrates a four-population system with migration between POP1, POP2, POP3, and POP4. The populations are arranged in a 2x2 grid. POP1 is at the top-left, POP2 at the top-right, POP3 at the bottom-left, and POP4 at the bottom-right. Migration is indicated by arrows: a horizontal arrow from POP1 to POP2, a vertical arrow from POP1 to POP3, a diagonal arrow from POP1 to POP4, and a diagonal arrow from POP3 to POP2.

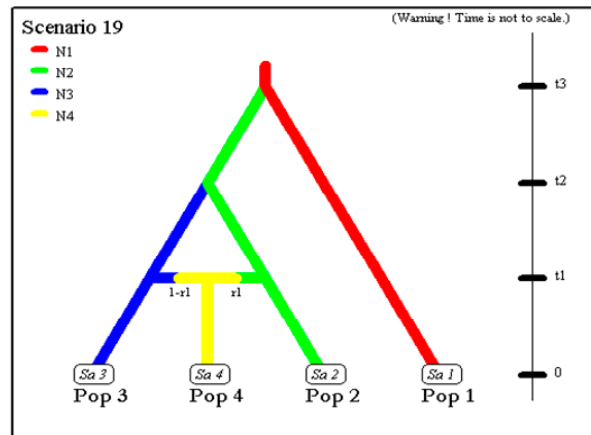
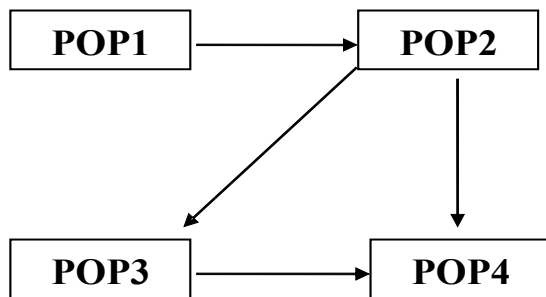
Scenario 27



Scenario 28



Scenario 29



Scenario 30

Figure S3. Distinct scenarios tested using the software DIYABC and schematic representation of the competing scenarios considered for the inference of the invasion routes of *P. clarkii* in China. Scenario 1 to 6: hypothesized for Cluster 1; Scenario 6 to 11: hypothesized for Cluster 2; Scenario 12 to 30: hypothesized for Cluster 3.

Table S1. Analysis of molecular variance within and among *P. clarkii* populations by mitochondrial control region and *proPOx* intron analysis.

Source of Variance	<i>d.f.</i>	Sum of Squares	Variance Components	Percentage of Variation (%)
Control region analysis				
Among populations	36	1732.506	5.54030 Va	54.09
Within populations	254	1194.766	4.70181 Vb	45.91
Total	290	2926.766	10.24211	
<i>ProPOx</i> intron analysis				
Among populations	36	208.138	0.76471 Va	30.45
Within populations	159	277.729	1.74673 Vb	69.55
Total	195	485.867	2.51144	

Table S2. Relative posterior probabilities with 95% confidence intervals for all scenarios compared using Approximate Bayesian Computation, and results of type I and type II error rates. Power analyses were based on 100 datasets simulated under the different scenarios. Calculations were not performed for scenarios 12 to 30, as no scenario had higher posterior probability.

Scenario	Posterior Probability	Type I Error Rate	Type II Error Rate
1	0.0000 [0.0000–0.0000]		
2	0.0000 [0.0000–0.0000]		
3	0.1800 [0.0000–0.5168]		
4	0.1300 [0.0000–0.4248]		
5	0.6900 [0.2846–1.0000]	0.712	Mean: 0.172 (Min.: 0.000; Max.: 0.288)
6	0.0000 [0.0000–0.0000]		
7	0.0300 [0.0000–0.1795]		
8	0.4700 [0.0325–0.9075]	0.178	Mean: 0.158 (Min.: 0.028; Max.: 0.202)
9	0.3600 [0.0000–0.7807]		
10	0.0800 [0.0000–0.3178]		
11	0.0600 [0.0000–0.2682]		
12	0.0400 [0.0000–0.2118]		
13	0.0700 [0.0000–0.2936]		
14	0.0500 [0.0000–0.2410]		
15	0.0500 [0.0000–0.2410]		
16	0.0500 [0.0000–0.2410]		
17	0.0400 [0.0000–0.2118]		
18	0.0200 [0.0000–0.1427]		
19	0.0400 [0.0000–0.2118]		
20	0.1200 [0.0000–0.4048]		
21	0.0400 [0.0000–0.2118]		
22	0.0400 [0.0000–0.2118]		
23	0.0600 [0.0000–0.2682]		
24	0.0600 [0.0000–0.2682]		
25	0.0600 [0.0000–0.2682]		
26	0.0500 [0.0000–0.2410]		

Table S2. *Cont.*

Scenario	Posterior Probability	Type I Error Rate	Type II Error Rate
27	0.0400 [0.0000–0.2118]		
28	0.0500 [0.0000–0.2410]		
29	0.0500 [0.0000–0.2410]		
30	0.0700 [0.0000–0.2936]		