

**Table S1.** Definitions of different parameters and prior distributions with DIYABC.

Parameter	Distribution	Interval
Effective population size, $N_i$	Uniform	10–10,000
Rates of admixture, $r_a$	Uniform	0.001–0.999
Mean mutation rate (MEANMU)	Uniform	$10^{-4}$ – $10^{-3}$
Mean parameter of the geometric distribution of the number of repeats (MEAN P)	Uniform	0.1–0.3
Mean single nucleotide insertion/deletion mutation rate (MEANSNI)	Log-uniform	$10^{-8}$ – $10^{-5}$

**Table S2.** Assumed 33 demographic history scenarios among four snail populations.

Analysis	Number	Scenario		
		t3	t2	t1
No admixture (t1 t2 t3)	1	2014→2015	2014→2016	2014→2017
	2	2014→2015	2014→2016	2015→2017
	3	2014→2015	2014→2016	2016→2017
	4	2014→2015	2015→2016	2014→2017
	<b>5</b>	<b>2014→2015</b>	<b>2015→2016</b>	<b>2015→2017</b>
	6	2014→2015	2015→2016	2016→2017
Admixture (t1 t2 t3)	7	2014→2015	2014→2016	2014 + 2015→2017
	8	2014→2015	2014→2016	2014 + 2016→2017
	9	2014→2015	2014→2016	2015 + 2016→2017
	10	2014→2015	2015→2016	2014 + 2015→2017
	11	2014→2015	2015→2016	2014 + 2016→2017
	<b>12</b>	<b>2014→2015</b>	<b>2015→2016</b>	<b>2015 + 2016→2017</b>
	13	2014→2015	2014 + 2015→2016	2014→2017
	14	2014→2015	2014 + 2015→2016	2015→2017
	15	2014→2015	2014 + 2015→2016	2016→2017
	16	2014→2015	2014 + 2015→2016	2014 + 2016→2017
	17	2014→2015	2014 + 2015→2016	2015 + 2016→2017
No admixture (t1 t2)	18	2014→2015; 2014→2016		2014→2017

	19	2014→2015; 2014→2016	2015→2017
	20	2014→2015; 2014→2016	2016→2017
	21	2014→2015	2014→2016; 2014→2017
	22	2014→2015	2015→2016; 2014→2017
	23	2014→2015	2014→2016; 2015→2017
	24	2014→2015	2015→2016; 2015→2017
Admixture (t1 t2 )	25	2014→2015; 2014→2016	2014 + 2015→2017
	26	2014→2015; 2014→2016	2015 + 2016→2017
	27	2014→2015; 2014→2016	2014 + 2016→2017
	28	2014→2015	2014→2016; 2014 + 2015→2017
	<b>29</b>	2014→2015	2015→2016; 2014 + 2015→2017
	30	2014→2015	2014 + 2015→2016; 2014→2017
	31	2014→2015	2014 + 2015→2016; 2015→2017
	32	2014→2015	2014 + 2015→2016; 2014 + 2015→2017
No admixture(t1)	33		2014→2015; 2014→2016; 2014→2017

**Table S3.** Posterior probabilities of the 33 demographic history scenarios evaluated in DIYABC analysis.

Analysis	Number	Posterior Probability 95% CI	
No admixture (t1 t2 t3)	1	0.0001	[0.0000,0.0033]
	2	0.0096	[0.0052,0.0140]
	3	0.0026	[0.0000,0.0058]
	4	0.0003	[0.0000,0.0035]
	<b>5</b>	<b>0.8506</b>	<b>[0.8298,0.8714]</b>
	6	0.1368	[0.1164,0.1572]
Admixture (t1 t2 t3)	7	0.0001	[0.0000,0.0106]
	8	0.0002	[0.0000,0.0106]
	9	0.0034	[0.0000,0.0138]
	10	0.0208	[0.0095,0.0320]
	11	0.0111	[0.0003,0.0218]
	<b>12</b>	<b>0.7133</b>	<b>[0.6705,0.7560]</b>
	13	0.0000	[0.0000,0.0105]
	14	0.1990	[0.1579,0.2402]
	15	0.0140	[0.0032,0.0248]
	16	0.0016	[0.0000,0.0120]
	17	0.0365	[0.0241,0.0488]
No admixture (t1 t2)	18	0.0008	[0.0003,0.0013]

	19	0.0275	[0.0201,0.0348]
	20	0.0083	[0.0056,0.0111]
	21	0.0025	[0.0009,0.0040]
	22	0.0014	[0.0007,0.0022]
	23	0.0023	[0.0010,0.0036]
	<b>24</b>	<b>0.9572</b>	<b>[0.9483,0.9661]</b>
Admixture (t1 t2 )	25	0.0047	[0.0000,0.0524]
	26	0.0456	[0.0000,0.0915]
	27	0.0035	[0.0000,0.0512]
	28	0.0005	[0.0000,0.0486]
	<b>29</b>	<b>0.4901</b>	<b>[0.4404,0.5397]</b>
	30	0.0005	[0.0000,0.0486]
	31	0.4363	[0.3848,0.4879]
	32	0.0188	[0.0000,0.0656]
No admixture(t1)	33		
<b>The second round</b>			
No admixture VS Admixture	5	0.2561	[0.2376,0.2747]
	12	0.1964	[0.1811,0.2116]
	<b>24</b>	<b>0.5326</b>	<b>[0.5114,0.5538]</b>
	29	0.0138	[0.0045,0.0230]
	33	0.0011	[0.0000,0.0102]

**Table S4.** Posterior distributions of population demographic parameters from Scenario 24 with the highest posterior probability inferred by DIY ABC analysis.

Parameter	Mean	Median	Mode	Quantile 2.50%	Quantile 5.00%	Quantile 95.00%	Quantile 97.5%
N1	$2.38 \times 10^3$	$2.13 \times 10^3$	$1.82 \times 10^3$	$6.94 \times 10^2$	$8.55 \times 10^2$	$4.70 \times 10^3$	$5.88 \times 10^3$
N2	$3.85 \times 10^3$	$3.59 \times 10^3$	$3.29 \times 10^3$	$1.19 \times 10^3$	$1.47 \times 10^3$	$7.33 \times 10^3$	$8.37 \times 10^3$
N3	$6.21 \times 10^3$	$6.29 \times 10^3$	$7.02 \times 10^3$	$2.21 \times 10^3$	$2.79 \times 10^3$	$9.41 \times 10^3$	$9.71 \times 10^3$
N4	$2.76 \times 10^3$	$2.31 \times 10^3$	$1.44 \times 10^3$	$5.46 \times 10^2$	$6.95 \times 10^2$	$6.69 \times 10^3$	$7.85 \times 10^3$
t1	$8.04 \times 10^2$	$6.16 \times 10^2$	$3.32 \times 10^2$	$1.04 \times 10^2$	$8.95 \times 10^1$	$2.08 \times 10^3$	$2.78 \times 10^3$
t2	$8.09 \times 10^3$	$8.42 \times 10^3$	$9.75 \times 10^2$	$4.51 \times 10^2$	$5.10 \times 10^2$	$9.86 \times 10^3$	$9.93 \times 10^3$
$\mu_{mic}$	$2.28 \times 10^{-4}$	$1.91 \times 10^{-4}$	$1.43 \times 10^{-4}$	$1.09 \times 10^{-4}$	$1.15 \times 10^{-4}$	$4.72 \times 10^{-4}$	$5.89 \times 10^{-4}$
$p_{mic}$	$1.90 \times 10^{-1}$	$1.85 \times 10^{-1}$	$1.49 \times 10^{-1}$	$1.06 \times 10^{-1}$	$1.11 \times 10^{-1}$	$2.82 \times 10^{-1}$	$2.90 \times 10^{-1}$
$sn_{mic}$	$5.25 \times 10^{-6}$	$5.47 \times 10^{-6}$	$1.00 \times 10^{-5}$	$8.36 \times 10^{-8}$	$1.57 \times 10^{-7}$	$1.00 \times 10^{-5}$	$1.00 \times 10^{-5}$

N1, N2, N3 and N4, effective population sizes of the corresponding populations;

t1, divergence of 2016 and 2017 from 2015; t2, divergence of 2016 from 2015;

$\mu_{mic}$ , the mean mutation rate of SSR;

$p_{mic}$ , the mean distribution of the number of repeats of microsatellites;

$sn_{mic}$ , the mean rate of single nucleotide insertions/deletions.