

Supplemental Information for

Power of Bayesian and heuristic tests to detect cross-species introgression with reference to gene flow in the *Tamias quadrivittatus* group of North American chipmunks

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Table S1. Posterior means and 95% HPD CIs (in parentheses) of introgression probabilities (φ) and introgression times (τ) in the stepwise construction of the MSci model, applied to datasets of the two halves

Model	First half			Second half		
	φ	$\tau (\times 10^{-3})$	B_{10}	φ	$\tau (\times 10^{-3})$	B_{10}
1 QIRCD \rightarrow U	0.537 (0.247, 0.801)	0.841 (0.702, 0.980)	∞	0.632 (0.332, 0.869)	0.906 (0.740, 1.045)	∞
2 QIRCD \rightarrow U	0.615 (0.427, 0.798)	0.869 (0.773, 0.966)	∞	0.695 (0.501, 0.876)	0.918 (0.802, 1.037)	∞
QI \leftrightarrow D	0.138 (0.094, 0.185)	0.349 (0.311, 0.391)	∞	0.069 (0.038, 0.102)	0.322 (0.282, 0.363)	∞
	0.020 (0.000, 0.047)		0.03	0.018 (0.000, 0.037)		0.03
3 QIRCD \rightarrow U	0.601 (0.369, 0.813)	0.863 (0.759, 0.971)	∞	0.696 (0.480, 0.892)	0.915 (0.782, 1.040)	∞
QI \rightarrow D	0.133 (0.080, 0.191)	0.331 (0.288, 0.372)	53.24	0.085 (0.038, 0.136)	0.331 (0.279, 0.388)	25.06
Q \rightarrow D	0.008 (0.000, 0.021)	0.153 (0.058, 0.261)	0.00	0.008 (0.001, 0.019)	0.100 (0.040, 0.210)	0.00
4 QIRCD \rightarrow U	0.588 (0.360, 0.797)	0.854 (0.746, 0.958)	∞	0.681 (0.470, 0.869)	0.909 (0.787, 1.032)	∞
QI \rightarrow D	0.132 (0.080, 0.188)	0.330 (0.286, 0.373)	∞	0.088 (0.035, 0.149)	0.334 (0.270, 0.396)	35.99
I \rightarrow D	0.007 (0.000, 0.018)	0.120 (0.048, 0.197)	0.00	0.012 (0.001, 0.025)	0.160 (0.090, 0.227)	0.01
5 QIRCD \rightarrow U	0.582 (0.326, 0.818)	0.852 (0.738, 0.961)	∞	0.689 (0.473, 0.883)	0.905 (0.778, 1.026)	∞
QI \rightarrow D	0.126 (0.084, 0.170)	0.307 (0.263, 0.352)	∞	0.099 (0.063, 0.139)	0.336 (0.291, 0.382)	∞
Q \leftrightarrow I	0.036 (0.013, 0.065)	0.099 (0.062, 0.137)	2.90	0.048 (0.023, 0.075)	0.088 (0.051, 0.118)	∞
	0.030 (0.008, 0.055)		0.39	0.014 (0.000, 0.028)		0.02
6 QIRCD \rightarrow U	0.589 (0.338, 0.827)	0.850 (0.738, 0.966)	∞	0.686 (0.491, 0.870)	0.902 (0.782, 1.022)	∞
QI \rightarrow D	0.118 (0.074, 0.165)	0.295 (0.246, 0.345)	∞	0.097 (0.060, 0.136)	0.334 (0.284, 0.381)	∞
Q \rightarrow I	0.041 (0.014, 0.074)	0.100 (0.066, 0.140)	7.90	0.055 (0.026, 0.087)	0.091 (0.053, 0.132)	∞

Note.— Introgression events are added sequentially onto the species tree of figure 4a and those that do not meet our cutoffs ($B_{10} \geq 20$) are grayed out. $B_{10} = \infty$ occurs when there are no MCMC samples with $\varphi < \varepsilon = 1\%$. A bidirectional introgression event, e.g., between Q and I has two introgression probabilities, e.g., $\varphi_{Q \rightarrow I}$ (above) and $\varphi_{I \rightarrow Q}$ (below). The final joint introgression model has three unidirectional introgression events.

Table S2. Bayes factors (B_{10}) for the three introgression probabilities (φ) obtained from BPP analyses of the full data of 1060 loci under the joint MSci model of figure 4b and different beta priors, $\varphi \sim \text{beta}(\alpha, \beta)$

ε & Prior	$\mathbb{P}(\emptyset)$	B_{10}		
		QIRCD \rightarrow U	QI \rightarrow D	Q \rightarrow I
$\varepsilon = 1\%$				
beta(0.2, 0.2)	0.210	∞	∞	∞
beta(0.2, 1)	0.398	∞	∞	∞
beta(0.2, 5)	0.585	∞	∞	∞
beta(1, 0.2)	0.002	∞	∞	∞
beta(1, 1)	0.010	∞	∞	∞
beta(1, 5)	0.049	∞	∞	∞
beta(5, 0.2)	6.0×10^{-12}	∞	∞	∞
beta(5, 1)	1.0×10^{-10}	∞	∞	∞
beta(5, 5)	1.2×10^{-8}	∞	∞	∞
$\varepsilon = 0.1\%$				
beta(0.2, 0.2)	0.132	∞	∞	∞
beta(0.2, 1)	0.251	∞	∞	∞
beta(0.2, 5)	0.371	∞	∞	∞
beta(1, 0.2)	2.0×10^{-4}	∞	∞	∞
beta(1, 1)	0.001	∞	∞	∞
beta(1, 5)	0.005	∞	∞	∞
beta(5, 0.2)	6.0×10^{-17}	∞	∞	∞
beta(5, 1)	1.0×10^{-15}	∞	∞	∞
beta(5, 5)	1.3×10^{-13}	∞	∞	∞

Note.— Bayes factor B_{10} is calculated using eq. 8, where the null region \emptyset for φ is the interval $(0, \varepsilon)$ with $\varepsilon = 1\%$ or 0.1% . $B_{10} = \infty$ occurs when $\varphi > \varepsilon$ in all MCMC samples.

Table S3. Posterior means and 95% HPD CIs (in parentheses) of parameters under the MSci model of figure 4b obtained from BPP analyses of three real datasets (the two halves and the full dataset) and a simulated dataset

Parameters	First half, 530 loci	Second half, 530 loci	Full data, 1060 loci	Simulation, 1060 loci
Population sizes (θ , $\times 10^{-3}$)				
θ_Q	1.119 (0.817, 1.455)	1.032 (0.733, 1.370)	1.059 (0.844, 1.287)	1.098 (0.867, 1.347)
θ_I	1.556 (0.996, 2.191)	2.335 (1.474, 3.387)	1.923 (1.433, 2.473)	2.108 (1.574, 2.701)
θ_R	0.330 (0.266, 0.399)	0.377 (0.311, 0.442)	0.344 (0.295, 0.396)	0.366 (0.313, 0.421)
θ_C	0.478 (0.400, 0.556)	0.474 (0.407, 0.547)	0.478 (0.427, 0.534)	0.491 (0.436, 0.542)
θ_D	3.092 (2.580, 3.633)	3.460 (2.920, 4.016)	3.314 (2.915, 3.705)	3.386 (3.001, 3.781)
θ_U	0.953 (0.843, 1.063)	0.912 (0.814, 1.011)	0.932 (0.857, 1.004)	0.917 (0.844, 0.991)
θ_S	0.792 (0.680, 0.904)	0.934 (0.809, 1.052)	0.866 (0.782, 0.948)	0.817 (0.734, 0.900)
$\theta_{QIRCDUS}$	11.04 (9.516, 12.56)	10.83 (9.357, 12.30)	11.01 (9.924, 12.09)	10.38 (9.368, 11.40)
θ_{QIRCDU}	0.687 (0.332, 1.075)	0.601 (0.274, 0.955)	0.656 (0.367, 0.971)	0.475 (0.229, 0.734)
θ_{QIRCD}	1.963 (0.248, 4.652)	1.595 (0.336, 3.153)	2.203 (0.392, 4.533)	1.340 (0.236, 2.809)
θ_{QIRC}	3.212 (0.296, 6.828)	1.503 (0.232, 3.505)	2.222 (0.295, 4.800)	2.141 (0.192, 5.173)
θ_{QIR}	2.923 (0.724, 5.067)	1.990 (0.755, 3.258)	2.518 (1.266, 3.890)	2.792 (1.523, 4.167)
θ_{QI}	0.727 (0.198, 1.503)	1.033 (0.203, 2.427)	0.773 (0.177, 1.714)	1.157 (0.217, 2.714)
θ_J	1.017 (0.777, 1.272)	1.242 (0.954, 1.545)	1.107 (0.921, 1.298)	1.147 (0.934, 1.372)
θ_K	0.686 (0.177, 1.467)	0.799 (0.177, 1.808)	0.626 (0.170, 1.282)	0.959 (0.185, 2.241)
θ_L	1.911 (0.224, 4.493)	1.280 (0.399, 2.326)	1.568 (0.345, 2.936)	1.381 (0.315, 2.781)
θ_M	0.412 (0.245, 0.569)	0.430 (0.282, 0.578)	0.407 (0.275, 0.529)	0.415 (0.291, 0.543)
θ_N	0.439 (0.310, 0.574)	0.476 (0.350, 0.600)	0.440 (0.342, 0.543)	0.384 (0.301, 0.473)
θ_O	0.291 (0.190, 0.390)	0.422 (0.282, 0.552)	0.325 (0.239, 0.416)	0.350 (0.259, 0.443)
Speciation/introgression times (τ , $\times 10^{-3}$)				
$\tau_{QIRCDUS}$	3.297 (2.830, 3.851)	3.588 (3.062, 4.075)	3.423 (3.061, 3.783)	3.415 (3.066, 3.768)
τ_{QIRCDU}	1.872 (1.299, 2.456)	2.270 (1.703, 2.849)	2.029 (1.569, 2.489)	2.011 (1.673, 2.338)
τ_{QIRCD}	0.749 (0.634, 0.855)	0.750 (0.654, 0.837)	0.731 (0.642, 0.815)	0.753 (0.693, 0.815)
τ_{QIRC}	0.584 (0.469, 0.699)	0.673 (0.573, 0.765)	0.628 (0.542, 0.707)	0.697 (0.615, 0.766)
τ_{QIR}	0.363 (0.283, 0.452)	0.437 (0.360, 0.517)	0.389 (0.322, 0.452)	0.379 (0.312, 0.445)
τ_{QI}	0.267 (0.222, 0.312)	0.321 (0.272, 0.367)	0.290 (0.253, 0.327)	0.274 (0.238, 0.309)
$\tau_J = \tau_K = \tau_{QIRCD \rightarrow U}$	0.850 (0.738, 0.966)	0.902 (0.782, 1.022)	0.871 (0.778, 0.961)	0.832 (0.747, 0.917)
$\tau_L = \tau_M = \tau_{QI \rightarrow D}$	0.295 (0.246, 0.345)	0.334 (0.284, 0.381)	0.307 (0.268, 0.350)	0.298 (0.258, 0.336)
$\tau_N = \tau_O = \tau_{Q \rightarrow I}$	0.100 (0.066, 0.140)	0.091 (0.053, 0.132)	0.102 (0.074, 0.130)	0.094 (0.069, 0.118)
Introgression probabilities (ϕ)				
$\phi_{QIRCD \rightarrow U}$	0.589 (0.338, 0.827) (∞)	0.686 (0.491, 0.870) (∞)	0.625 (0.442, 0.794) (∞)	0.587 (0.440, 0.733) (∞)
$\phi_{QI \rightarrow D}$	0.118 (0.074, 0.165) (∞)	0.097 (0.060, 0.136) (∞)	0.106 (0.074, 0.139) (∞)	0.107 (0.077, 0.140) (∞)
$\phi_{Q \rightarrow I}$	0.041 (0.014, 0.074) (8)	0.055 (0.026, 0.087) (∞)	0.050 (0.028, 0.074) (∞)	0.048 (0.028, 0.069) (∞)

Note.— Bayes factor B_{10} is given in parentheses, calculated using eq. 8: ∞ means that all sampled values of ϕ are $> \epsilon = 1\%$.

Table S4. Power of BPP, HYDE and D-statistic tests of gene flow between sister species and average estimates of introgression probability in 100 simulated replicate datasets (each of 8000 loci) under the model of figure 8a

Methods	Power		$\hat{\phi} \pm \text{SD}$	Proportion of invalid estimates
	$(\alpha = 1\%)$	$(\alpha = 5\%)$		
HYDE				
R→Ua	3%	8%	0.005 ± 0.003	48%
R→Ub	3%	5%	0.004 ± 0.004	51%
D-statistic				
R↔Ua	0%	1%	—	NA
R↔Ub	0%	2%	—	NA
BPP				
R→U	100%	100%	0.623 ± 0.066	0%

Note.— Bayesian test by BPP is considered significant at the 5% (or 1%) level if $B_{10} \geq 20$ (or 100). In the HYDE test, Ua and Ub were regarded as the ‘hybrid’ lineage to detect gene flow R→Ua and R→Ub, respectively, in figure 8a. In some datasets, the HYDE estimate of ϕ was outside the range (0, 1), and only the valid estimates were used to calculate the means.

Table S5. Power of BPP and HYDE tests of gene flow and average estimates of introgression probability in 100 simulated replicates under the three models of figure 8b-d

# loci	BPP			HYDE			Proportion of invalid estimates
	Power ($\alpha = 1\%$)	Power ($\alpha = 5\%$)	$\hat{\phi} \pm SD$	Power ($\alpha = 1\%$)	Power ($\alpha = 5\%$)	$\hat{\phi} \pm SD$	
Outflow asym (fig. 8b)							
500	39%	56%	0.096 \pm 0.026	1%	4%	0.155 \pm 0.111	44%
2000	100%	100%	0.104 \pm 0.025	3%	9%	0.107 \pm 0.057	33%
8000	100%	100%	0.105 \pm 0.013	10%	24%	0.076 \pm 0.042	20%
Inflow asym (fig. 8c)							
500	72%	84%	0.118 \pm 0.030	23%	41%	0.331 \pm 0.110	10%
2000	100%	100%	0.106 \pm 0.014	87%	95%	0.321 \pm 0.068	0%
8000	100%	100%	0.107 \pm 0.009	100%	100%	0.325 \pm 0.037	0%
inflow sym (fig. 8b, HYDE model)							
500	15%	27%	0.115 \pm 0.037	2%	10%	0.124 \pm 0.071	19%
2000	90%	95%	0.110 \pm 0.022	14%	27%	0.101 \pm 0.047	2%
8000	100%	100%	0.108 \pm 0.010	83%	90%	0.108 \pm 0.025	0%

Note.— The true introgression probability is $\phi = 0.106$ (fig. 8b-d). See legend to table S4.