

*The following supplement accompanies the article*

## **Comparative phylogeography to test for predictions of marine larval dispersal in three amphidromous shrimps**

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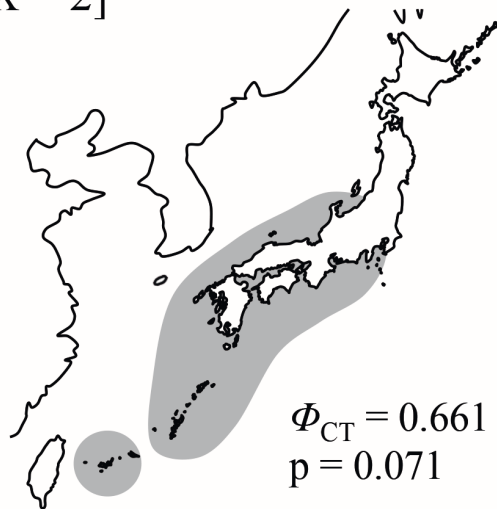
*Marine Ecology Progress Series 560: 105–120 (2016)*

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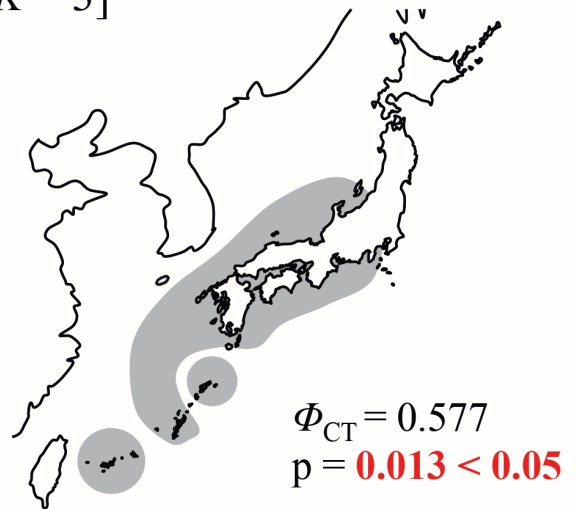
This data supplement includes the following information: the groups of populations used in the spatial analysis of molecular variance (SAMOVA; Fig. S1), Bayesian estimates of the time to the most recent common ancestor (TMRCA; Fig. S2), a global and hierarchical analysis of molecular variance (AMOVA; Table S1), and Bayes factor tests to compare the demographic models (Table S2).

# *Caridina leucosticta*

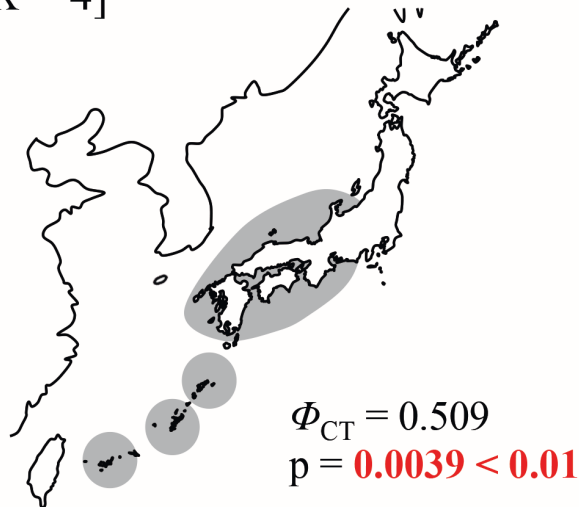
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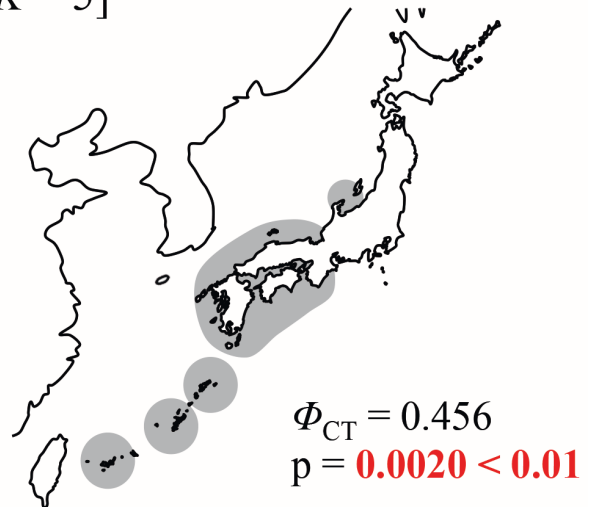
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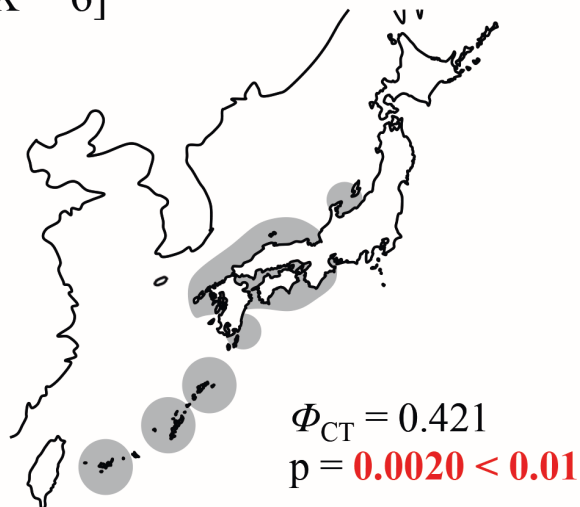
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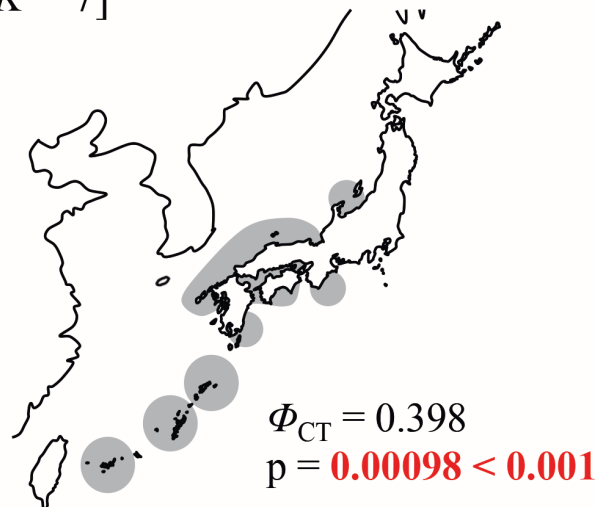
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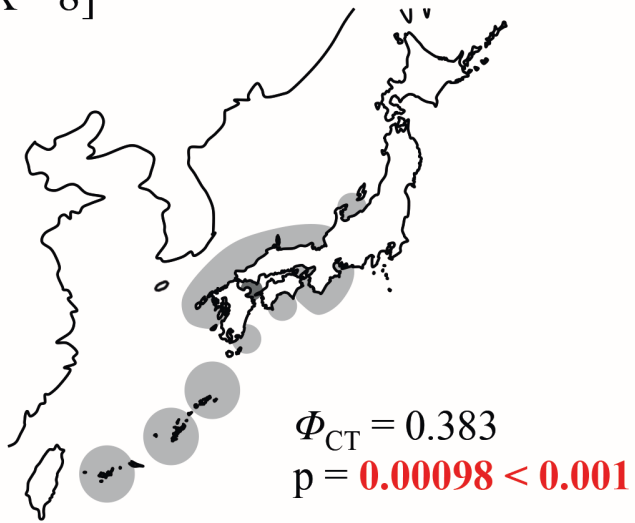
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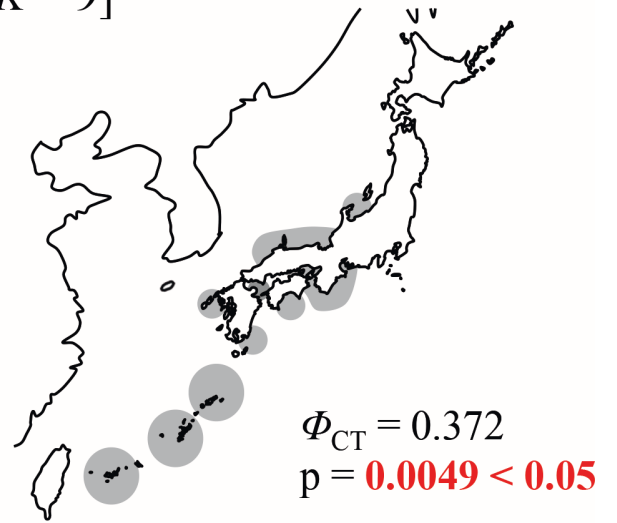
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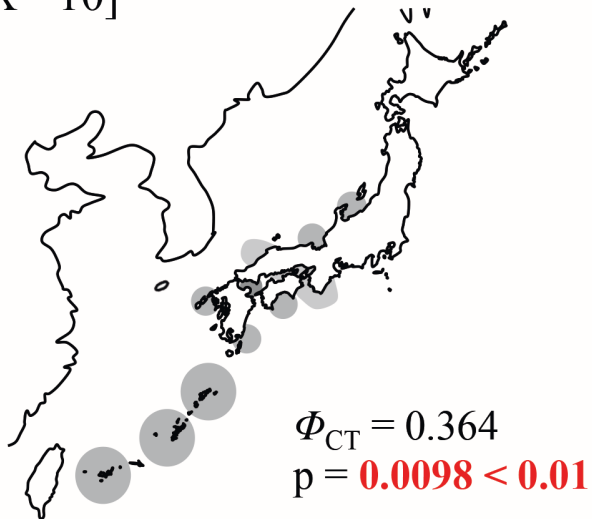
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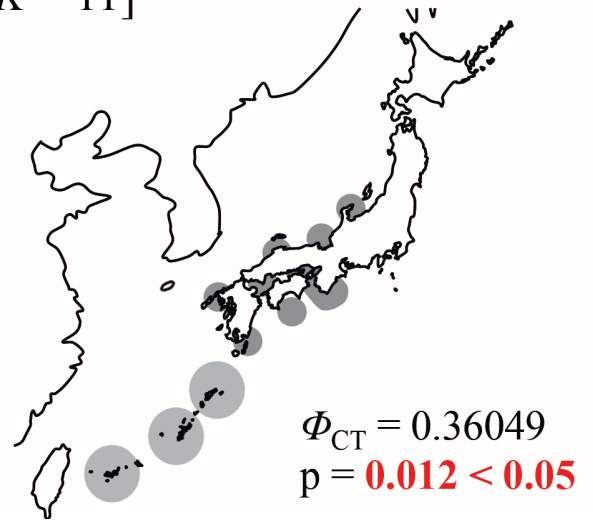
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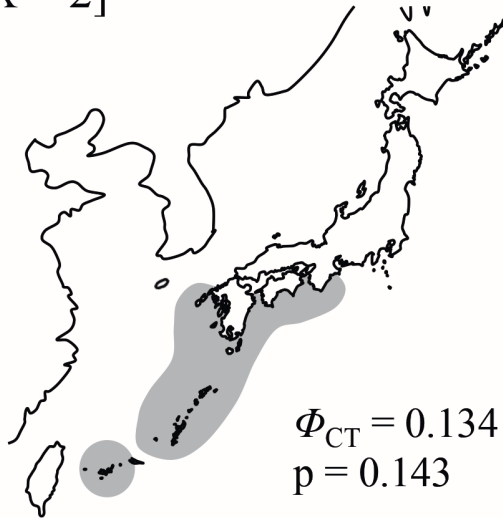


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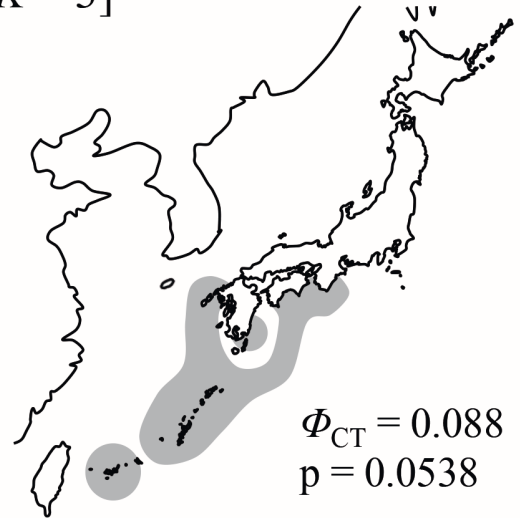


*Caridina typus*

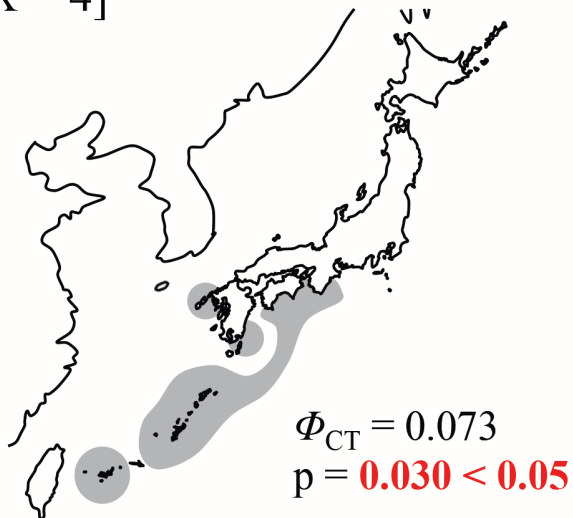
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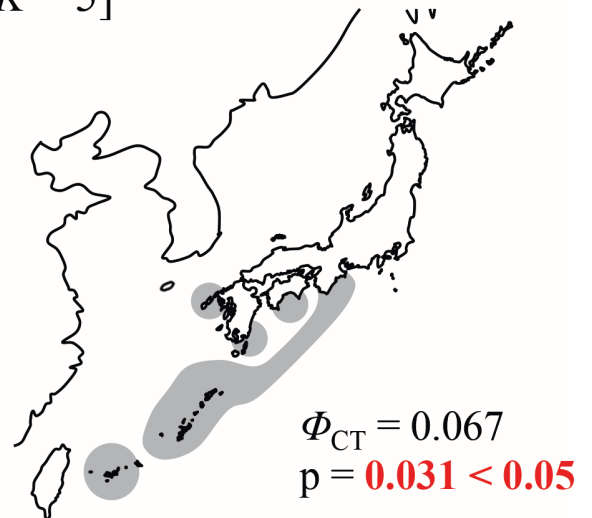
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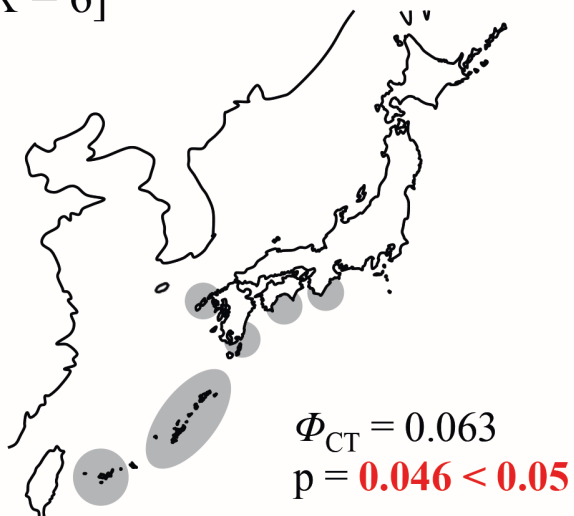
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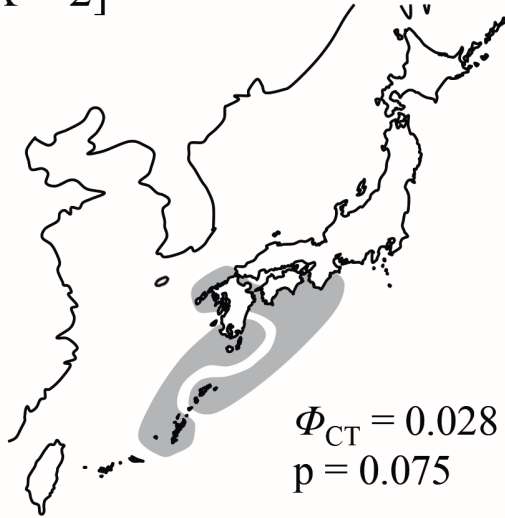


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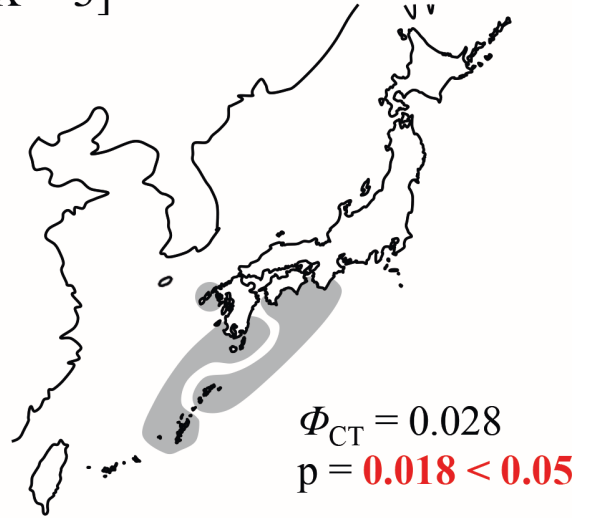


## *Caridina multidentata*

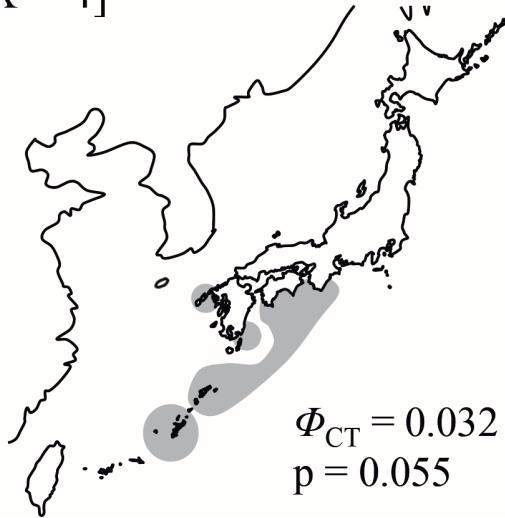
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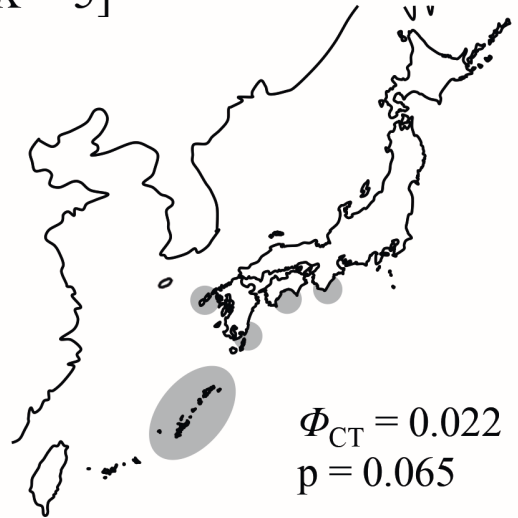
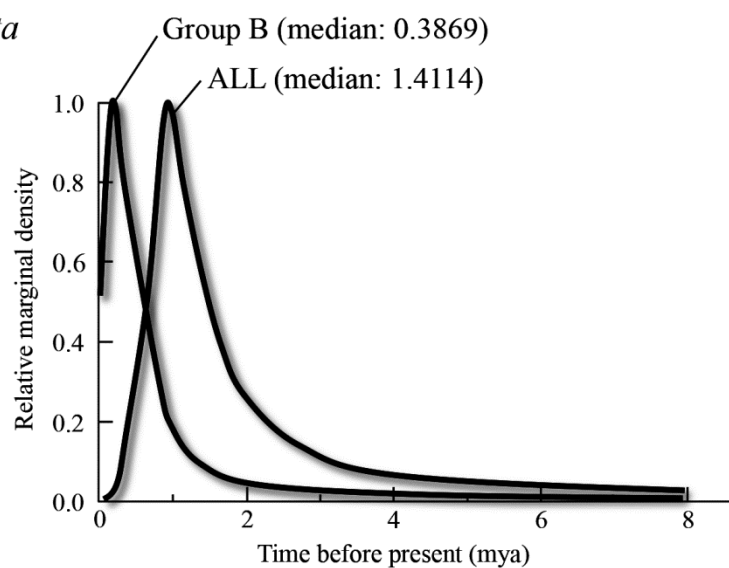
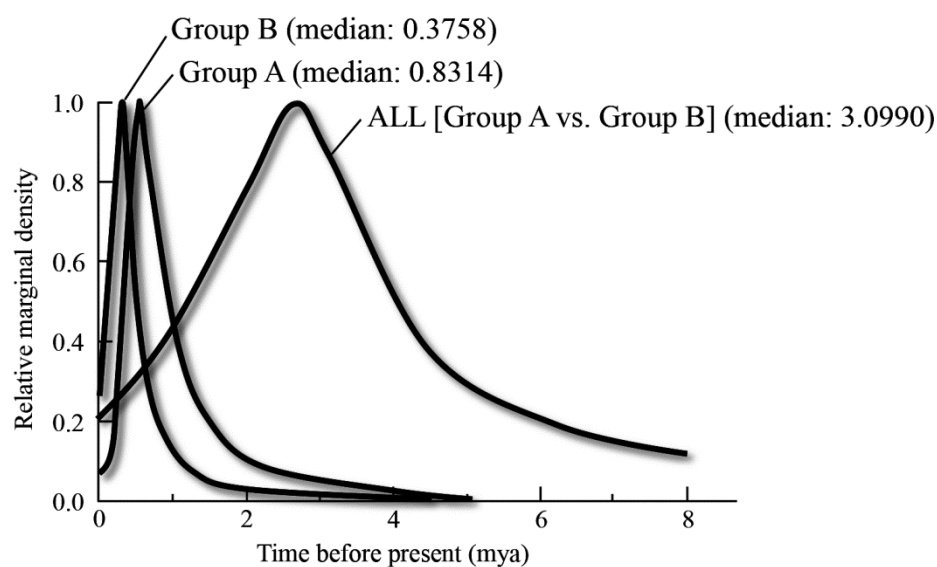


Fig. S1. The populations groups of *Caridina leucosticta*, *C. typus*, and *C. multidentata* used in the spatial analysis of molecular variance (SAMOVA) determined using the criteria of geographical homogeneity and maximal differentiation from each other, with  $K$  varying from 2 to max. Red values indicate significant  $\Phi_{CT}$  values.

*Caridina leucosticta*



*Caridina typus*



*Caridina multidentata*

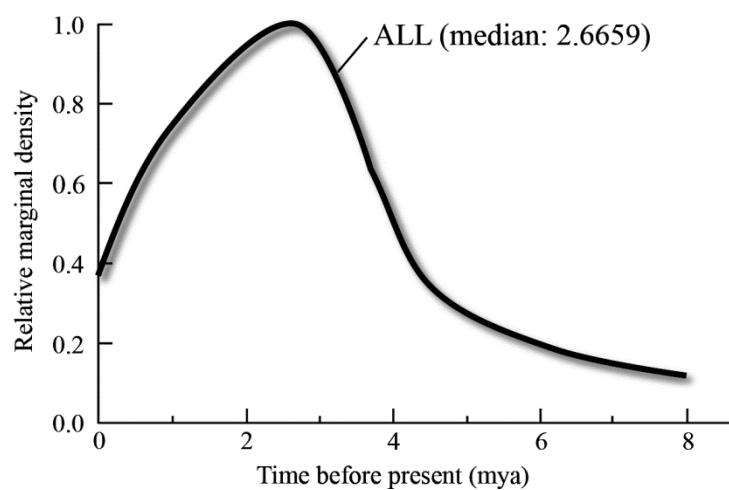


Fig. S2. Bayesian estimates of the time to the most recent common ancestor (TMRCA) for *Caridina leucosticta*, *C. typus*, and *C. multidentata*.

Table S1. Analysis of molecular variance (AMOVA) results based on 10 100 replicates using frequency of *Caridina leucosticta*, *C. typus*, and *C. multidentata* haplotypes. \*\*p < 0.01, \*\*\*p < 0.001, ns = not significant.

Global AMOVA

*Caridina leucosticta*

Source of Variation	d.f.	Sum of squares	Variance components	Percentage of Variation	$\Phi$ -Statistics	p
Among populations	11	121.68	0.495	33.30	$\Phi_{ST} = 0.333$	***
Within populations	232	230.21	0.992	66.7		
Total	243	351.89	1.488			

*Caridina typus*

Source of Variation	d.f.	Sum of squares	Variance components	Percentage of Variation	$\Phi$ -Statistics	p
Among populations	6	25.34	0.058	1.88	$\Phi_{ST} = 0.019$	ns
Within populations	133	406.35	3.055	98.12		
Total	139	431.69	3.114			

*Caridina multidentata*

Source of Variation	d.f.	Sum of squares	Variance components	Percentage of Variation	$\Phi$ -Statistics	p
Among populations	5	20.50	0.011	0.29	$\Phi_{ST} = 0.003$	ns
Within populations	114	441.55	3.873	99.71		
Total	119	462.05	3.885			

Hierarchical AMOVA ~ Japanese mainland vs. Nansei Islands ~

*Caridina leucosticta*

Source of Variation	d.f.	Sum of squares	Variance components	Percentage of Variation	$\Phi$ -Statistics	p
Among groups	1	69.72	0.681	36.22	$\Phi_{CT} = 0.362$	**
Among populations within groups	10	51.96	0.208	11.03	$\Phi_{SC} = 0.173$	***
Within populations	232	230.21	0.992	52.74	$\Phi_{ST} = 0.473$	***
Total	233	351.89	1.881			

*Caridina typus*

Source of Variation	d.f.	Sum of squares	Variance components	Percentage of Variation	$\Phi$ -Statistics	p
Among groups	1	1.93	-0.040	-1.30	$\Phi_{CT} = -0.013$	ns
Among populations within groups	5	23.41	0.081	2.63	$\Phi_{SC} = 0.026$	ns

Within populations	133	406.35	3.055	98.67	$\Phi_{ST} = -0.013$	ns
Total	139	431.69	3.096			
<i>Caridina multidentata</i>						
Source of Variation	d.f.	Sum of squares	Variance components	Percentage of Variation	$\Phi$ -Statistics	p
Among groups	1	2.74	-0.032	-0.83	$\Phi_{CT} = -0.008$	ns
Among populations within groups	4	17.76	0.028	0.73	$\Phi_{SC} = 0.007$	ns
Within populations	114	441.55	3.873	100.09	$\Phi_{ST} = -0.0009$	ns
Total	119	462.05	3.870			



Table S2. Bayes factor (BF) tests comparing demographic models for the three species. The BF's correspond to row-by-column comparisons. Marginal (tree) likelihood of the model [ $\ln P(\text{model})$ ]; standard error of the estimate (SE) using 1000 bootstrap replicates. Bayes factor interpretation based on Kass & Raftery (1995): \*, \*\* and \*\*\* denotes "positive," "strong," and "very strong" evidence in favor of the row model compared with the column model, respectively.

Species	Model	ln <i>P</i> (model)	SE	ln BF compared with:						
				Constant	Exponential	Logistic	Expansion			
				size	growth	growth	growth			
<i>Caridina leucosticta</i>	Constant size	−1492.668	0.09		41.88	***	18.66	***	31.46	***
	Exponential growth	−1534.543	0.11	−41.88			−23.21		−10.41	
	Logistic growth	−1511.33	0.12	−18.66	23.21	***			12.80	***
	Expansion growth	−1524.13	0.09	−31.46	10.41	***	−12.80			
<i>Caridina typus</i>	Constant size	−1324.986	0.20		−0.97		4.19	*	1.49	
	Exponential growth	−1324.018	0.18	0.97			5.16	*	2.45	*
	Logistic growth	−1329.176	0.16	−4.19	−5.16				−2.70	
	Expansion growth	−1326.472	0.21	−1.49	−2.45		2.70	*		
<i>Caridina multidentata</i>	Constant size	−1764.221	0.18		33.48	***	37.40	***	36.83	***
	Exponential growth	−1797.701	0.16	−33.48			3.92	*	3.35	*
	Logistic growth	−1801.621	0.19	−37.40	−3.92				−0.57	
	Expansion growth	−1801.051	0.18	−36.83	−3.35		0.57			

#### LITERATURE CITED

Kass RE, Raftery AE (1995) Bayes Factor. J Am Stat Assoc 90:773–795