

The following supplement accompanies the article

## Long-term vicariance and post-glacial expansion in the Japanese rocky intertidal goby *Chaenogobius annularis*

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**Supplement.** Additional data used to infer the population structure and demographic history of *Chaenogobius annularis*

Table S1. *Chaenogobius annularis*. Hierarchical analysis of molecular variance (AMOVA) based on mitochondrial DNA frequency

Comparison	Source of variation	df	Fixation index	p	Percentage of variation
All localities	Among localities	14	0.926	<0.001	92.64
	Within localities	449			7.36
Two groups (Pacific Ocean/ Sea of Japan)	Among groups	1	0.870	<0.001	87.38
	Within groups	13	0.956	<0.001	8.25
	Within localities	449	0.653	<0.001	4.38
Pacific Ocean group only	Among localities	7	0.710	<0.001	71.02
	Within localities	237			28.98
Three subgroups (north/central/south)	Among groups	2	0.532	0.003	53.23
	Within groups	5	0.749	<0.001	21.69
	Among localities	237	0.464	<0.001	25.08
Sea of Japan group only	Among localities	6	0.478	<0.001	47.79
	Within localities	212			52.21

Table S2. *Chaenogobius annularis*. Hierarchical analysis of molecular variance (AMOVA) based on microsatellite DNA frequency

Comparison	Source of variation	df	Fixation index	p	Percentage of variation
All localities	Among localities	14	0.440	<0.001	44.03
	Within localities	917			55.97
Two groups (Pacific Ocean/ Sea of Japan)	Among groups	1	0.356	<0.001	35.58
	Within groups	13	0.532	<0.001	17.65
	Among localities	917	0.274	<0.001	46.77
Pacific Ocean group only	Among localities	7	0.167	<0.001	16.73
	Within localities	458			83.27
Sea of Japan group only	Among localities	6	0.401	<0.001	40.13
	Within localities	459			59.87
Two subgroups (Japanese/Korean)	Among groups	1	0.291	0.026	29.12
	Within groups	5	0.475	<0.001	18.36
	Within localities	459	0.259	<0.001	52.52

Fig. S1. *Chaenogobius annularis*. (a) Neighbor-joining and (b) maximum likelihood (ML) trees of 92 haplotypes with bootstrap probabilities >80% (the bootstrap probability of the Pacific Ocean clade in the ML tree is shown although the value is <80%)

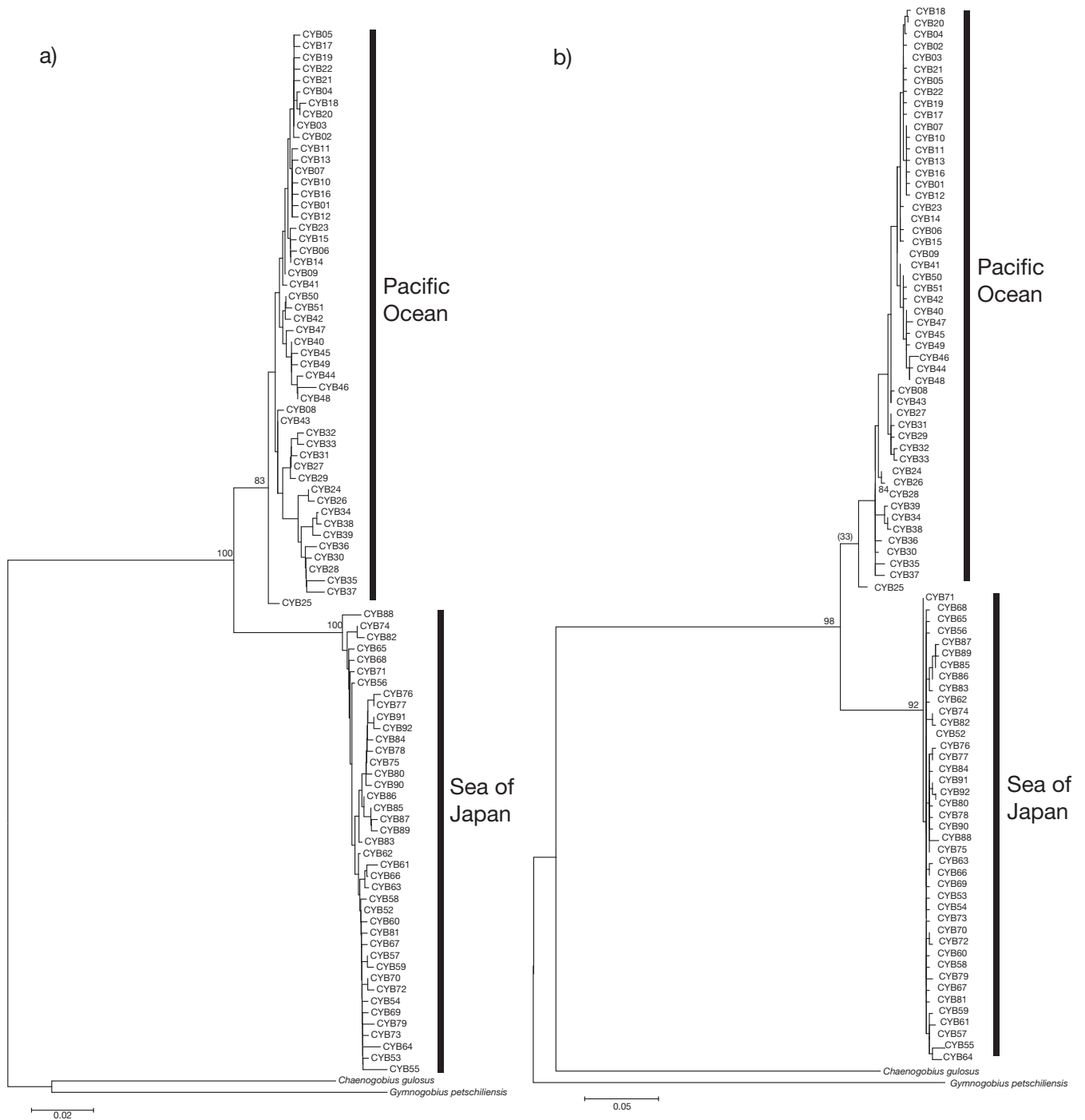


Fig. S2. Unrooted neighbor-joining tree of the 3 clusters of the Sea of Japan group based on  $F_{ST}$  values calculated by Bayesian clustering analysis ( $K = 3$ )

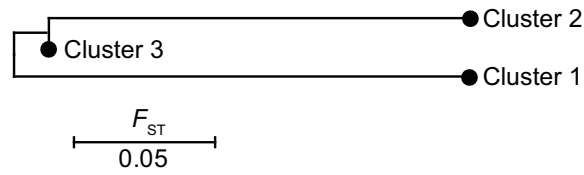


Fig. S3.  $M$ -ratio values for 7 populations (locality codes are given in Table 1 in the main manuscript) of the Sea of Japan group; the line represents  $M = 0.68$

