

Supplementary table 1: Reproductive strategy and geographic extent predict population genetic structure in phylogenetic analyses using unconstrained tree

Model	Terms	Generalized estimating equations ^a				Phylogenetic generalized least squares ^a			
		n = 91, phylogenetic d.f. = 50.4				n = 91			
		Effect size	t	P ^a	QIC ^b	Effect size	t	P ^a	AIC ^b
ln(Rousset F _{ST}) ~ Marker + Egg	Intercept (Marker-allozyme, Egg-benthic)	-1.18	-1.37	0.0176	379.9	-1.18	-0.50	0.6162	510.6
	Marker-microsatellite	-1.46	-4.35	<0.0001		-1.46	-1.59	0.1149	
	Marker-mtDNA sequence	0.68	1.70	0.0960		0.68	0.62	0.5354	
	Reproduction – pelagic spawning	-1.30	-1.72	0.0948		-1.42	-0.78	0.4354	
ln(Rousset F _{ST}) ~ Marker + ln(Km) + Egg	Intercept (Marker-allozyme, Egg-benthic)	-16.10	-12.52	<0.0001	511.5	-16.11	-9.72	<0.0001	408.9
	Marker-microsatellite	-0.58	-1.47	0.1474		-0.58	-1.44	0.2556	
	Marker-mtDNA sequence	-0.30	-0.63	0.5286		-0.30	-0.49	0.6232	
	ln(Km)	2.09	18.39	<0.0001		2.09	14.28	<0.0001	
	Reproduction – pelagic spawning	-3.28	-4.21	0.0001		-3.28	-3.27	0.0015	
ln(Rousset F _{ST}) ~ Marker + ln(Km) + Egg + Marker: ln(Km)	Intercept (Marker-allozyme, Egg-benthic)	-5.89	-1.19	0.2394	414.9	-5.89	-0.96	0.3393	385.7
	Marker - microsatellite	3.44	0.62	0.5352		3.44	0.50	0.6159	
	Marker –mtDNA sequence	-12.99	-2.66	0.1100		-12.99	-2.14	0.0353	
	ln(Km)	0.59	0.90	0.3721		0.59	0.73	0.4695	
	Reproduction – pelagic spawning	-2.66	-3.75	0.0005		-2.66	-3.02	0.0034	
	Marker – msat: ln(Km)	-0.64	-0.88	0.3848		-0.64	-0.71	0.4814	
	Marker – mtDNA seq: ln(Km)	1.71	2.59	0.0131		1.71	2.09	0.0400	

^aPhylogeny is backbone constrained tree. See text for more details.

^bBased on two-tailed tests.

^cAkaike Information Criterion, Quasilikelihood Information Criterion

Supplementary table 2: Reproductive strategy and clade depth predicts species richness of families in phylogenetic analyses using unconstrained tree

		Generalized estimating equations ^a				Phylogenetic generalized least squares ^a			
		n = 91, phylogenetic d.f. = 40.0				n = 55			
Model	Terms	Effect				Effect			
		size	t	P ^a	QIC ^b	size	t	P ^a	AIC ^b
ln(Spp_richness) ~	Intercept (Egg – benthic)	5.15	8.25	<0.0001	115.3	5.15	6.92	<0.001	201.2
Egg	Reproduction – pelagic spawning	-1.48	-3.22	0.0019		-1.48	-2.81	0.007	
ln(Spp_richness) ~	Intercept (Clade_depth = 0)	0.54	1.00	0.3211	73.4	0.54	0.87	0.39	165.6
Clade_depth	Clade_depth	14.12	8.93	<0.0001		14.12	7.70	<0.01	
ln(Spp_richness) ~	Intercept (Clade_depth = 0, Egg – benthic)	1.58	2.57	0.0144	71.1	1.58	2.26	0.0279	160.4
Clade_depth + Egg	Clade_depth	13.34	8.67	<0.0001		13.34	7.63	<0.0001	
	Reproduction – pelagic spawning	-1.03	-3.16	0.0031		-1.03	-2.78	0.00755	

^a Based on two-tailed tests.

^b Akaike Information Criterion, Quasilikelihood Information Criterion