

Supplementary Materials

Table S1. Details of the lethal equivalent estimates for marine animals from Figure 1.^aLethal equivalents in a haploid genome estimated from *B*, the rate of decline in fitness with inbreeding or from molecular marker data. ^bLethal equivalent estimates from molecular marker data (haploid). Estimates from Launey and Hedgecock 2001 are from four different lines, while estimates from Plough and Hedgecock 2011 are from 2 different inbred families. See File S1 for full citation information.

Group	Species	Inbreeding	Trait	LE ^a	Citation
<i>Invert</i>	Purple sea urchin	0, 0.25	larval growth	1.32	Anderson and Hedgecock 2010
	Catarina scallop	0, 0.25	larval survival	1.06	Ibarra et al., 1995
	Pacific abalone	0, 0.25	post set survival	2.53	Kobiashi and Kijima 2010
	Pacific abalone	0, 0.25	% metamorphosis	1.15	Deng et al., 2005
	White shrimp	0, 0.25, 0.375	hatch rate	1.68	Moss et al., 2009
	White shrimp	0, 0.25, 0.375	hatchery survival	1.38	Moss et al., 2009
	Eastern oyster	0, 0.25	larval survival	0	Mallet and Haley 1983
	Eastern oyster	0, 0.25	survival to day 2	6.08	Longwell and Stiles 1973
	Pacific oyster	0.25	viability	3.77 ^b	Launey and Hedgecock 2001
	Pacific oyster	0.25	viability	2.27 ^b	Launey and Hedgecock 2001
	Pacific oyster	0.25	viability	4.03 ^b	Launey and Hedgecock 2001
	Pacific oyster	0.25	viability	3.77 ^b	Launey and Hedgecock 2001
	Pacific oyster	0.25	viability	3.02 ^b	Plough and Hedgecock 2011
	Pacific oyster	0.25	viability	2.67 ^b	Plough and Hedgecock 2011
<i>Fish</i>	Atlantic Cod	0, 0.25	hatch survival	0.94	Puckrin 2015
	Rainbow trout	0, 0.25, 0.5	fry survival	0.08	Kincaid 1983
	Steelhead Salmon	0, 0.25	0–3 month survival	0.2	Thrower and Hard 2009

File S1. List of references used to generate LE estimates for marine animals in table S1

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Table S2. Summary of segregation distortion studies in wild crosses of marine animals

Author	Species	Taxa group	Segregation Distortion	Proportion of Markers	Marker type	Comments
Wang et al. 2007a	Bay scallop	bivalve	yes	0.19	μsats ¹ and AFLPs ²	
Wang et al. 2012	Bay scallop	bivalve	yes	0.60	μsats	No linkage map
Qin et al. 2007	Bay scallop	bivalve	yes	0.14	μsats and AFLPs	Clustered across three linkage groups
Lallias et al. 2007b	Blue mussel	bivalve	yes	0.28	AFLPs	
Yu and Guo 2003	Eastern oyster	bivalve	yes	0.08	μsats and AFLPs	
Lallias et al. 2007a	Flat oyster	bivalve	yes	0.33	AFLPs	
Peterson et al. 2012	Pacific lion-paw scallop	bivalve	yes	0.07	μsats and AFLPs	
Yuan et al. 2010	Noble scallop	bivalve	yes	0.11	μsats and AFLPs	
Hedgecock et al. 2015	Pacific oyster	bivalve	yes	0.49	μsats and SNPs ³	
Li and Guo 2004	Pacific oyster	bivalve	yes	0.27	AFLPs	
Plough et al. 2016	Pacific oyster	bivalve	yes	0.56	μsats and SNPs	
Bai et al. 2015	Pearl mussel	bivalve	yes	0.20	μsats	
Jones et al. 2013	Pearl oyster	bivalve	yes	0.14	SNPs	121/877 SNPs across 16 families - FDR corrected
Li and He 2014	Pearl oyster	bivalve	yes	0.31	RADseq ⁴	
Shi et al. 2009	Pearl oyster	bivalve	yes	0.13	μsats and AFLPs	
Xu et al. 2008	Yellow scallop	bivalve	yes	0.08	μsats and AFLPs	
Wang et al. 2003	Zhikong scallop	bivalve	yes	0.35	AFLPs	
Wang et al. 2005	Zhikong scallop	bivalve	yes	0.06	AFLPs	
Zhan et al. 2009	Zhikong scallop	bivalve	yes	0.30	μsats	
Nossa et al. 2014	Horseshoe crab	crustacean	not reported	NA	Whole genome SNPs	Tested, but results not reported
Cui et al. 2015	Mitten crab	crustacean	culled/not reported	NA	RADseq	
Liu et al. 2012b	Swimming crab	crustacean	yes	0.10	μsats	
Baranski et al. 2014	Tiger shrimp	crustacean	yes	0.07	SNPs	
Staelens et al. 2008	Tiger shrimp	crustacean	yes	0.21	AFLPs	Averaged across three families
You et al. 2010	Tiger shrimp	crustacean	yes	0.14	μsats and AFLPs	28/85 aflp, 19/256 μsats

PLOUGH: Genetic load in marine animals

Author	Species	Taxa group	Segregation Distortion	Proportion of Markers	Marker type	Comments
Du et al. 2010	White Shrimp	crustacean	not reported	NA	SNPs	apparently tested but not reported
Zhang et al. 2007	White shrimp	crustacean	yes	0.39	μsats and AFLPs	
Tian et al. 2015	Sea cucumber	echinoderm	not reported	NA	RADseq	Filtering for % geno and Mendel: SNP # reduced from 32,000 to 11,000
Yan et al. 2013	Sea cucumber	echinoderm	yes	0.22	μsats and SNPs	
Wang et al. 2007b	Asian seabass	fish	yes	0.11	μsats	Clustered on 3 lgs.
Wang et al. 2015a	Asian seabass	fish	yes	0.15	RADseq	removed, culled before mapping
Hubert et al. 2010	Atlantic cod	fish	low	0.03	SNPs	
Reid et al. 2007	Atlantic halibut	fish	low	0.02	μsats and AFLPs	
Gonen et al. 2014	Atlantic salmon	fish	not reported	NA	RADseq	
Wang et al. 2010	Blue gill sunfish	fish	yes	0.02	AFLPs	
Hermida et al. 2014	Brill	fish	yes	0.18	μsats	
Li et al. 2014	Channel catfish	fish	not reported	NA	SNPs	
Lui et al. 2003	Channel catfish	fish	yes	0.17	AFLPs	
Christiakov et al. 2005	European seabass	fish	not reported	NA	μsats	
Palaiokostas et al. 2015	European seabass	fish	not reported	NA	RADseq	
Kai et al. 2005	Fugu	fish	not reported	NA	μsats	
Tsigenopoulos et al. 2014	Gilthead sea bream	fish	not reported	NA	μsats and SNPs	Not reported, likely culled by Crimap
Kai et al. 2014	Japanese eel	fish	low	0.01	RADseq	
Nomura et al. 2011	Japanese eel	fish	low	0.05	μsats and AFLPs	
Castano-Sanchez et al. 2010	Japanese flounder	fish	not reported	NA	μsats and SNPs	
Coimbra et al. 2003	Japanese flounder	fish	not reported	NA	μsats and AFLPs	
Song et al. 2012b	Japanese flounder	fish	yes	0.38	μsats	
Kessuwan et al. 2016	Kelp grouper	fish	not reported	NA	μsats	not reported, but apparently tested
Liu et al. 2013	Kelp grouper	fish	not reported	NA	μsats	

PLOUGH: Genetic load in marine animals

Author	Species	Taxa group	Segregation Distortion	Proportion of Markers	Marker type	Comments
Naruse et al. 2000	Medaka	fish	not reported	NA	μsats, AFLPs, RAPDs ⁵	
You et al. 2013	Orange spotted grouper	fish	yes	0.30	MSG ⁶	Could be other artifacts (nulls, non-Mendelian segregation)
Hollenbeck et al. 2015	Red drum	fish	low	~0.00	μsats	
Diopere et al. 2014	Common sole	fish	yes	0.04	μsats and SNPs	
Liao et al. 2009	Half-smooth sole	fish	yes	0.33	μsats and AFLPs	
Song et al. 2012a	Half-Smooth sole	fish	yes	0.31	μsats	
Amores et al. 2011	Spotted gar	fish	not reported	NA	RADseq	
Liu et al. 2012a	Striped bass	fish	not reported	NA	μsats	
Piechel et al. 2001	three-spine stickleback	fish	not reported	NA	μsats	
Bouza et al. 2007	Turbot	fish	yes	0.10	μsats	Reported as "scattered"
Bouza et al. 2012	Turbot	fish	yes	0.27	μsats and SNPs	
Wang et al. 2015b	Turbot	fish	culled/not reported	NA	RADseq	
Dor et al. 2014	White grouper	fish	low	0.02	μsats	Reported at $\alpha = 0.01$ level
Ao et al. 2015	Yellow croaker	fish	culled/not reported	NA	RADseq	From 30K to 10K snps that fit Mendel
Ning et al. 2007	Yellow croaker	fish	yes	0.33	μsats and AFLPs	
Xiao et al. 2015	Yellow croaker	fish	not reported	NA	Transcriptome SNPs	23,000 to 8,300 SNPs passing test for Mendel?
Aoki et al. 2015	Yellowtail	fish	not reported	NA	SNPs	not reported, but they tested for chi-square
Portnoy et al. 2010	Red drum	fish	low	0.04	μsats	Only Bonferroni corrected reported; distortions clustered on a few linkage groups
Liu et al. 2006	Pacific abalone	gastropod	low	0.05	μsats, AFLPs, RAPDs	Only Bonferroni corrected reported

Web of Science (WOS) search was performed for articles with titles containing words about segregation/linkage (any of the following key words; linkage map*, genetic map*, QTL, QTL-map*, segregation, segregation distortion, transmission ratio distortion) and marine animal groups (any key words; *fish, fish*, shellfish, oyster, mussel, mollus*, shrimp, crab, decapod, clam, crustacean, scallop, hexapod, lobster, marine, ocean, sea*, barnacle, copepod, *bass, urchin, snail, echinoderm), where 'word*' denotes a match of the proceeding word and any length string of any characters after it. Studies that used specific common or scientific names (e.g. Halibut or Salmo) were not identified with this search but were retrieved manually with more specific searches (see text for detail). Up to three data points per species were included and only outbred F₁ segregation data was considered. ¹microsatellite markers; ²amplified fragment length polymorphisms; ³single nucleotide polymorphisms; ⁴restriction digest associated DNA markers; ⁵multiplexed shotgun sequencing; ⁶random amplified DNA polymorphisms.

File S2. List of references used in literature survey of segregation distortion

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