SUPPLEMENTARY MATERIAL

Strong linkages between depth, longevity and demographic stability across marine sessile species

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Figure S1. Long-term population trends at nine red coral populations in the NW Mediterranean.

Figure S2. *Corallium rubrum* mean and maximum longevity estimates depending on matrix dimensions**.**

Figure S3. *Corallium rubrum* normalized age-dependent vital rates and size-dependent elasticity patterns.

Table S1. Red coral populations in the NW Mediterranean Sea studied in this work.

Table S2. Correlation coefficients between maximum depth and maximum lifespan in marine sessile species.

Table S3. Best fit models for different longevity estimates based on matrix models of octocorals, hexacorals and sponges.

Table S4. Summary statistics of best supported multiple linear regression model between maximum depth occurrence and maximum lifespan marine sessile species

Table S5. Summary statistics of best-supported multiple linear models for the effect of maximum depth occurrence on maximum lifespan of marine sessile species, including the potential effects of different ageing methods (annual ring counts, radiocarbon dating, demographic simulations and growth curves) and taxonomic levels (Phylum, Class, Order). Model support was based on Akaike Information Criteria corrected for small sample sizes (AICc).

Table S6. Summary statistics of quantile linear regression models between maximum depth occurrence and maximum lifespan across all marine sessile species (n = 223).

Table S7. Multiple linear regression models used to assess the effects of maximum longevity on temporal variance in population size in terrestrial plant species (n=25) and marine sessile invertebrates (n=9).

Table S8. Mean fecundity values of marine sessile species (n = 28). Fecundity values correspond to the mean annual recruitment rate per adult and were computed based on the F values of each size-class of the population matrix (first row), weigthed by the proportion of each class at the Stable Stage Distribution. We only included species in which the first stage corresponded to recruits.

Table S9. Source studies of longevity estimates and maximum occurrence depth for marine sessile species included in the comparative analysis.

Table S10. Source studies of long-term demographic variability estimates included in the comparative analysis.

Supplementary Methods (I): Model Construction
Supplementary Methods (II): R Code

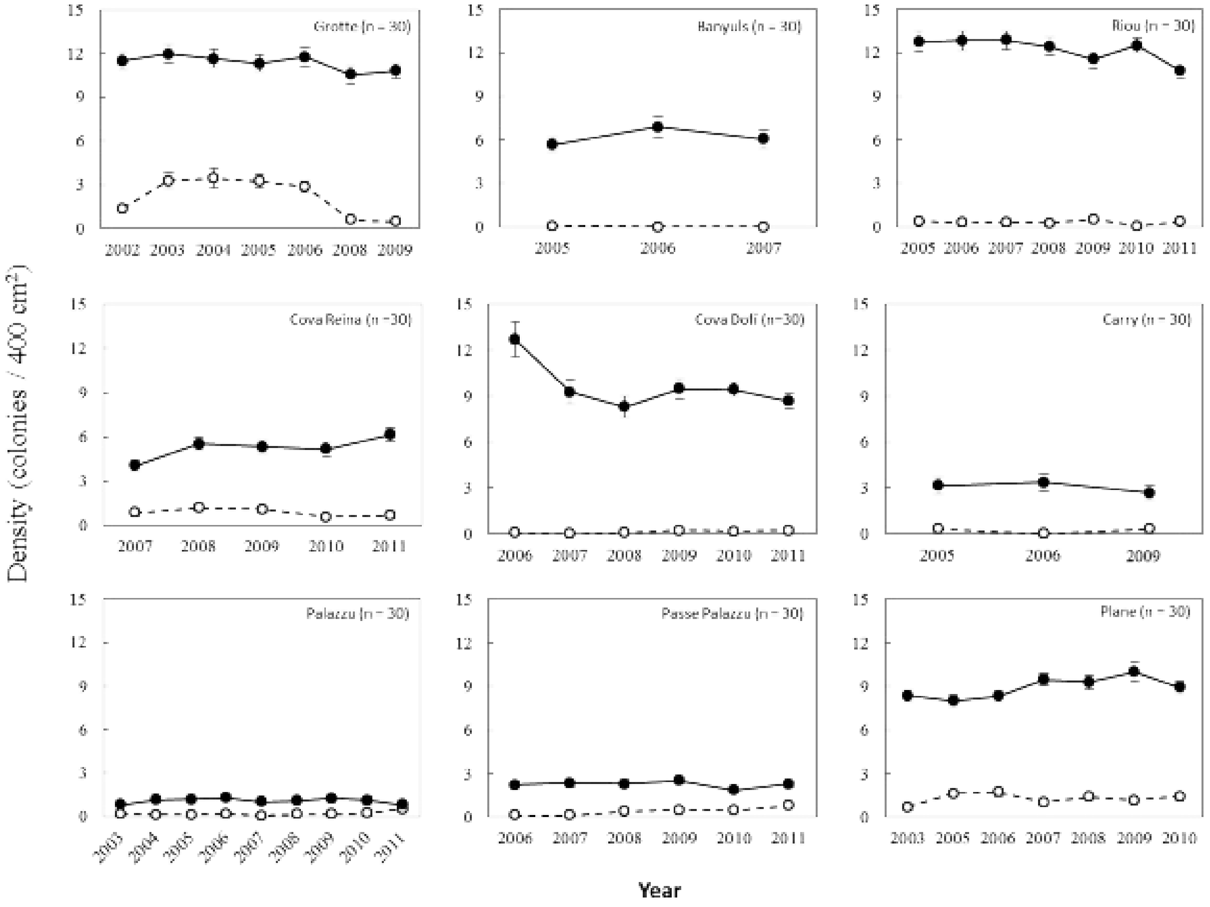

Figure S1. Long-term population trends at nine red coral populations in the NW Mediterranean. Black dots indicate adult and white dots recruit densities.

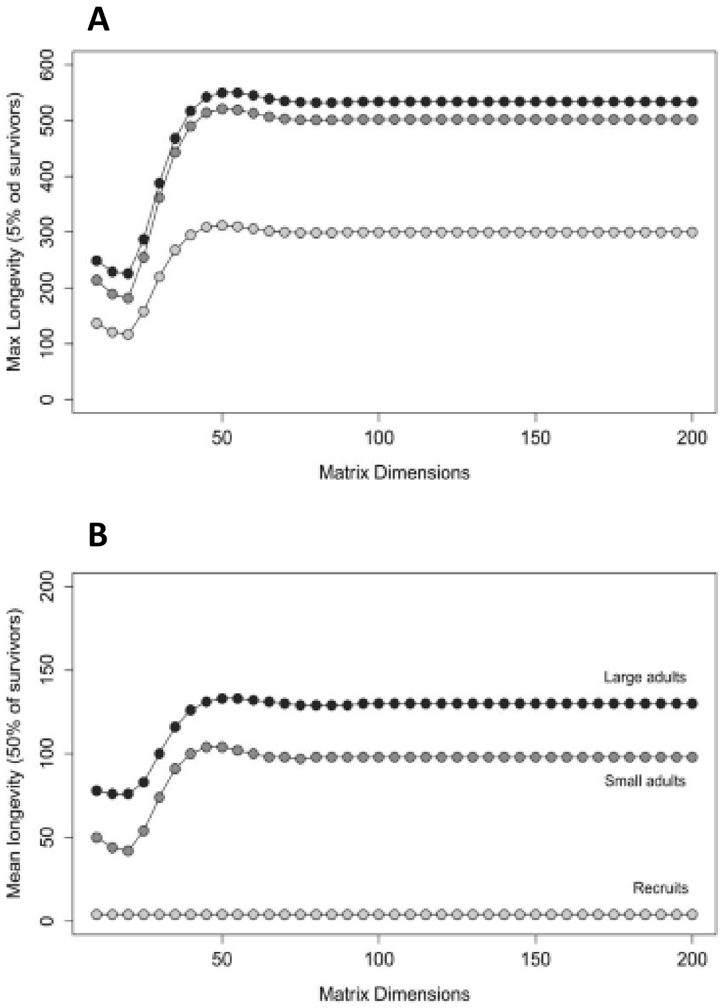

Figure S2. *Corallium rubrum* mean and maximum longevity estimates depending on matrix dimensions**.** A. Shows maximum potential lifespan, the number of years until 5% of the initial population remains alive. B. Shows the mean lifespan, the number of years until the 50% of the initial population remains alive. Simulations were performed based on 100 individuals starting as recruits (light grey), adults of the smallest size class (grey), and adults of the largest size class (black).

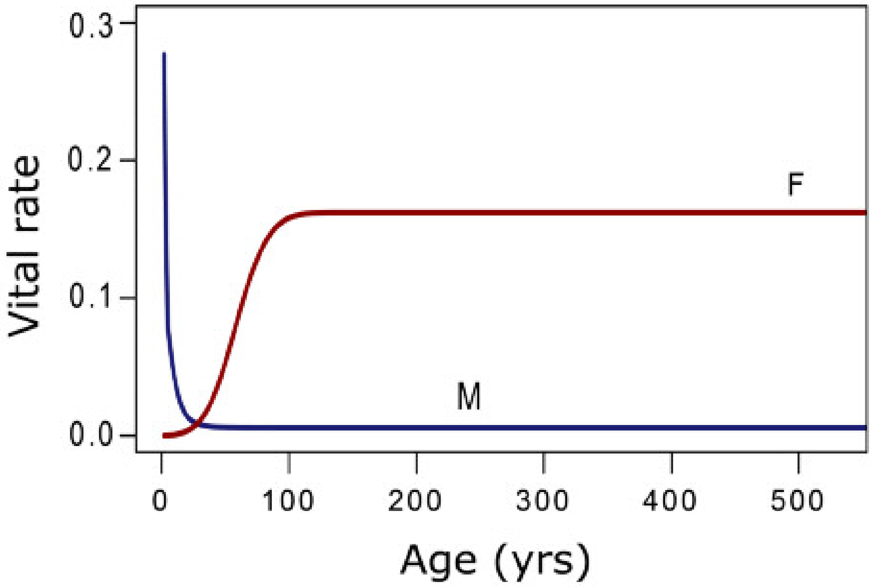

Figure S3. *Corallium rubrum* Normalized age-dependent vital rates: mortality (M) and fecundity (F).

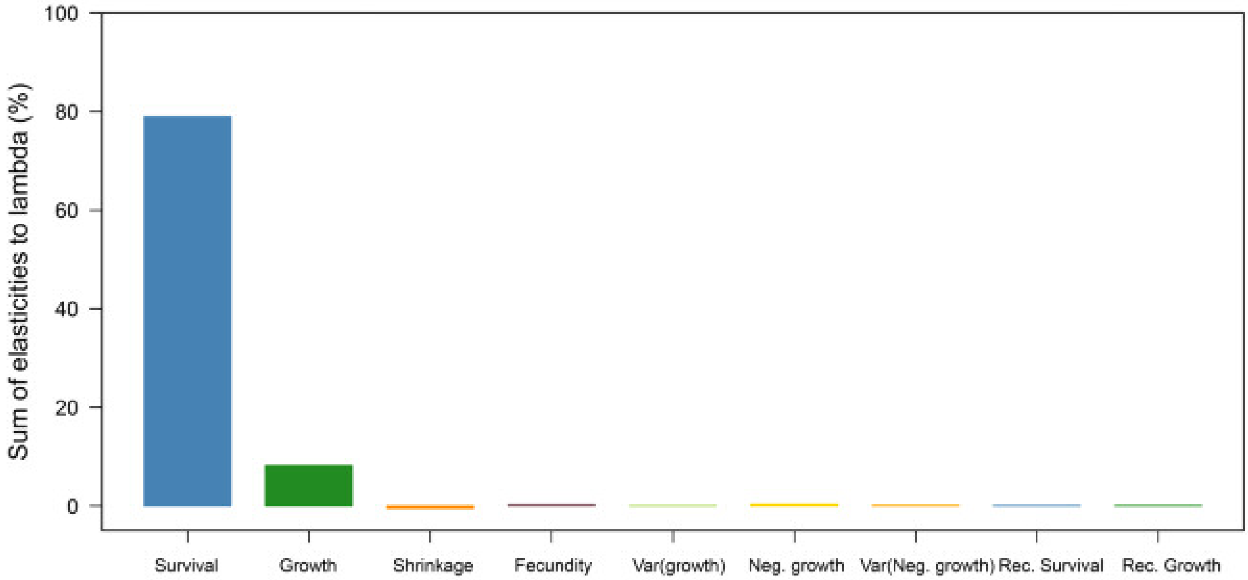

Figure S4. Patterns of sum of elasticity values to the asymptotic population growth rates of different vital rates in the red coral *Corallium rubrum*. From left to right: survival of adult colonies, mean normal growth of adult colonies, probability of extreme shrinkage, fecundity, variance in normal growth of adult colonies, mean negative growth, variance in mean negative growth, recruits survival, and recruits growth.

Table S1. Red coral (*Corallium rubrum*) populations in the NW Mediterranean Sea used in this study.

Name	**Longitude**	**Latitude**	**Depth (m)**	**Area**	**Protection Level**	**N**	**Years Surveyed**
Dofí	3° 13' 44" E	42° 2' 29" N	17 - 22	Catalan Sea	Partial Protection	148	2006 to 2011
Reina	3° 13' 34" E	42° 2' 49" N	17 - 24	Catalan Sea	Partial Protection	140	2007 to 2011
Banyuls	3°7'50" E	42°28' 60" N	23 - 25	Catalan Sea	Integral Protection	108	2005 to 2007
Maire	5°20'14" E	43°12'32" N	15 - 18	Marseille	Unprotected	140	2002 to 2009
Riou	5° 14' 3" E	43° 6' 13" N	17 - 24	Marseille	Unprotected	204	2005 to 2009
Plane	5° 14' 3" E	43° 11' 54" N	17 - 24	Marseille	Unprotected	154	2003 to 2010
Passe	8° 33' 27" E	42°21' 35" N	24 - 27	Corsica	Integral Protection	145	2006 to 2011
Palazzu	8° 33' 27" E	42° 21' 35" N	19 - 22	Corsica	Integral Protection	137	2003 to 2011

Table S2. Correlation coefficients between maximum depth and maximum lifespan in marine sessile species. The category "All Marine Sessile" includes data on species in five most-represented taxa plus those fromother taxa, including bryozoan, hydrozoan, polychaeta, cirripeds and one tunicate species. Statistics shown are: n = number of species included in the analysis, rho = Spearman's correlation coefficient; P = Pearson's correlation coefficient.

Spearman's rank correlation

Taxa	**Maximum Lifespan vs. Maximum Depth Occurrence**			**Maximum Lifespan vs. Depth at the Study Site**		
	n	**rho**	**P value**	**n**	**rho**	**P value**
Octocorals	35	0.673	P < 0.001	34	0.546	P = 0.008
Hexacorals	40	0.592	P < 0.001	34	0.704	P < 0.001
Sponges	17	0.647	P < 0.001	16	0.729	P = 0.001
Bivalves	93	0.358	P < 0.001	34	0.700	P < 0.001
Macroalgae	14	0.600	P = 0.023	9	0.597	P = 0.089
All Marine Sessile	223	0.503	P < 0.001	138	0.695	P < 0.001

Pearson's R correlation

Taxa	**Maximum Lifespan vs. Maximum Depth Occurrence**			**Maximum Lifespan vs. Depth at the Study Site**		
	n	**R**	**P value**	**n**	**R**	**P value**
Octocorals	35	0.714	P < 0.001	34	0.594	P = 0.0002
Hexacorals	40	0.650	P < 0.001	34	0.790	P < 0.001
Sponges	17	0.739	P < 0.001	16	0.727	P = 0.0014
Bivalves	93	0.456	P < 0.001	34	0.679	P < 0.001
Macroalgae	14	0.620	P = 0.018	9	0.674	P = 0.046
All Marine Sessile	223	0.547	P < 0.001	138	0.674	P < 0.001

Table S3. Sumary of the four best supported models predicting longevity estimates based on matrix models of octocorals, hexacorals and sponges.

Model	Predictors / Levels	Estimate	Std. Error	P value	AICc	deltaAIC
Maximum Longevity Adults ~ Depth + Dimensions	Intercept	0.849207	0.278340	0.0072	67.219	0
	Maximum Depth	0.020635	0.008199	0.0222		
	Dimensions	-0.157308	0.082079	0.0723		
	Overal Model: $R^2 = 0.4298$; F = 8.161; df = 17; P = 0.0033					
Maximum Longevity Adults ~ Depth	Intercept	0.956596	0.292187	0.0042	67.965	0.746
	Maximum Depth	0.005170	0.001558	0.0038		
	Overal Model: $R^2 = 0.\ 3796$; F = 11.01; df = 18; P = 0.0038					
Mean Longevity Recruits ~ Depth + Dimensions + Depth*Dimensions	Intercept	2.0324517	1.0345084	0.067	68.833	1.613
	Maximum Depth	0.0143110	0.0088083	0.124		
	Dimensions	-0.6189497	0.2300075	0.016		
	Maximum Depth*Dimensions	0.0006347	0.0002998	2.117		
	Overal Model: $R^2 = 0.\ 5463$; F = 8.625; df = 18; P = 0.001232					
Mean Longevity Adults ~ Depth + Dimensions + Depth*Dimensions	Intercept	1.9999077	1.0460125	0.074	69.275	2.056
	Maximum Depth	0.0164804	0.0089062	0.083		
	Dimensions	-0.4057816	0.2325653	0.100		
	Maximum Depth*Dimensions	0.0003458	0.0003032	0.271		
	Overal Model: $R^2 = 0.\ 4397$; F = 5.97; df = 16; P = 0.00624					

Table S4. Summary statistics of best supported multiple linear regression model between maximum depth occurrence and maximum lifespan for all marine sessile species (n = 223). Model support was based on Akaike Information Criteria corrected for small sample sizes (AICc). The second-best model had deltaAICc of 3.568. Data were log-transformed.

Best Fit Model	**Predictors / Levels**	**Estimate**	**Std. Error**	**t value**	**P value**
Longevity ~ Depth + Taxa + Method + Depth*Taxa	Intercept	0.67424	0.14385	4.687	< 0.001
	Maximum Depth	0.29642	0.07414	3.998	< 0.001
	Taxa (Hexacoral)	-0.01922	0.34657	-0.055	0.9558
	Taxa (Macroalgae)	-0.43510	0.33371	-1.304	0.1939
	Taxa (Octocoral)	0.62504	0.36226	1.725	0.0861
	Taxa (Sponge)	-0.71140	0.56550	-1.258	0.2100
	Method (Matrix/Survival)	-0.17426	0.09751	-1.787	0.0756
	Method (Oxygen)	0.33719	0.09751	0.883	0.3785
	Method (Radiometric Age)	0.39427	0.38196	2.492	0.0136
	Maximum Depth * Taxa (Hexacoral)	0.21700	0.15820	1.223	0.2228
	Maximum Depth * Taxa (Macroalgae)	0.59011	0.17740	2.176	0.0308
	Maximum Depth * Taxa (Octocoral)	-0.05002	0.27123	-0.294	0.7689
	Maximum Depth * Taxa (Sponge)	0.74739	0.29825	2.506	0.0131
	Overall model statistics: $R^2 = 0.5105$; F = 18.12; df = 185; P < 0.0001				

Table S5. Summary statistics of best supported multiple linear regression models between maximum depth occurrence and maximum lifespan in marine sessile species, including the potential effects of different ageing methods (annual ring counts, radiocarbon dating, demographic simulations and growth curves) and taxonomic levels (Phylum, Class, Order). Model support was based on Akaike Information Criteria corrected for small sample sizes (AICc).

Formula	**Intercept**	**Depth slope (P value)**	**df**	**AICc**	**Delta AICc**
Longevity ~ Depth + Class + Method	1.0129	0.3633 (>0.0001)	15	315.0721	0
Longevity ~ Depth + Class + Method + Depth*Class	0.8859	0.4299 (0.00101)	21	316.2796	1.2075
Longevity ~ Depth + Phylum + Depth*Phylum	-2.0621	1.4262 (0.2853)	15	316.8752	1.803146
Longevity ~ Depth + Method + Phylum	-2.8295	1.8155 (0.175)	12	319.1589	4.086796
Longevity ~ Depth + Class + Depth*Class	0.4153	0.6715 (>0.0001)	18	322.0485	4.0868

Table S6. Summary statistics of quantile linear regression models between maximum depth occurrence and maximum lifespan across all marine sessile species (n = 223)

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Quantile	Intercept (IC 95%)	Slope (IC 95%)
10%	-0.0682 (-0.516 – 0.083)	0.441 (0.361 – 0.677)
20%	0.0691 (-0.174, 0.173)	0.486 (0.427 – 0.593)
80%	0.811 (0.547 – 0972)	0.628 (0.570 – 0.791)
90%	0.9031 (0.691 – 1.071)	0.715 (0.550 – 0.918)

Table S7. Multiple linear regression models used to assess the effects of maximum longevity on temporal variance in population growth (realized log-lambda values) in terrestrial plant species (n=25) and marine sessile invertebrates (n=9).

Model	**R^2**	**AICc**	**Delta**	**Weight**
log(Variance) ~ log(Longevity) + Habitat	0.543	125.4652	0	0.6222
log(Variance) ~ log(Longevity) + Habitat + log(Longevity)*Habitat	0.528	128.1723	2.707	0.1607
log(Variance) ~ log(Longevity)	0.466	130.2689	4.804	0.0671
log(Variance) ~ Habitat	0.224	142.9632	17.498	0.0001

Table S8. Mean fecundity values of marine sessile species (n = 28). Fecundity values correspond to the mean annual recruitment rate per adult and were computed based on the F values of each size-class of the population matrix (first row), weigthed by the proportion of each class at the Stable Stage Distribution. We only included species in which demographic data in the form of standar matrix population models, including fecundity were available. To allow standard comparisons, we did not include matrices in which the first stage corresponded to larvae or eggs.

Species Name	**Taxa**	**Fecundity**	**Source**
A. islandica	Mollusca	0.001	Ripley & Caswell 2008
P. abrupta	Mollusca	0.004	Ripley & Caswell 2008
X. muta	Mollusca	0.006	McMurray *et al.* 2010
T. gigas	Mollusca	0.013	Ripley & Caswell 2008
A. colbecki	Mollusca	0.040	Ripley & Caswell 2008
A. compressa	Mollusca	0.071	Mercado-Molina 2011
C. rubrum	Cnidaria	0.077	Present study
A. palmata	Cnidaria	0.077	Vardi *et al.* 2012
P. astreoides	Cnidaria	0.083	Edmunds 2010
L. digitata	Macroalgae	0.126	Chapman 1990
S. graminea	Porifera	0.135	Cropper 1999
G. demissa	Mollusca	0.254	Ripley & Caswell 2008
N. obscurata	Mollusca	0.261	Dudas. et al. 2007
H. iris	Mollusca	0.547	Somerville *et al*. 2014
H. sorenseni	Mollusca	0.727	Roggers-Bennett 2006
H. rufenses	Mollusca	0.794	Roggers-Bennett 2006
P. caesia	Cnidaria	0.847	Tanner 1997
B. annulata	Cnidaria	0.875	Nelsen 2008
A. nana	Macroalgae	0.966	Pfister 2005
L. notorcadensis	Mollusca	1.176	Ripley & Caswell 2008
L. miliaris	Mollusca	1.639	Ripley & Caswell 2008
H. laevigata	Mollusca	1.654	Fordham et al. 2013
M. mactroides	Mollusca	1.791	Brazeiro & Defeo 1999
M. californianus	Mollusca	2.314	Carson *et al*. 2011
M. galloprovincialis	Mollusca	2.768	Carson *et al*. 2011
Alcyonium sp.	Cnidaria	3.257	McFadden 1991
F. distichus	Macroalgae	8.001	Ang & De Wreede 1993
L. rubra	Mollusca	115.314	Ripley & Caswell 2008

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Table S9. Source studies of longevity estimates and maximum occurrence depth for marine sessile species included in the comparative analysis (n = 241) (See completed references list below).

Name	Family	Taxa	Lifespan Method	Source Lifespan	Source Depth
Acropora cervicornis	Acroporidae	Hexacoral	Matrix/Survival	1	37, 44
Acropora hyacinthus	Acroporidae	Hexacoral	Matrix/Survival	2	38, 44
Acropora palmata	Acroporidae	Hexacoral	Matrix/Survival	3	37, 44
Agaricia agaricites	Agariciidae	Hexacoral	Matrix/Survival	4	37, 44
Leptoseris cucullata	Agariciidae	Hexacoral	Matrix/Survival	9	49, 50, 44
Bartholomea annulata	Aiptasiidae	Hexacoral	Matrix/Survival	19	42
Antipathes dendrochristos	Antipathidae	Hexacoral	Radiometric Age	69, 70	69
Antipathes dichotoma	Antipathidae	Hexacoral	Radiometric Age	58	NA
Antipathes griggi	Antipathidae	Hexacoral	Radiometric Age	70	NA
Caryophyllia inornata	Caryophylliidae	Hexacoral	Growth	76, 86	87
Desmophyllum cristagalli	Caryophylliidae	Hexacoral	Radiometric Age	60	NA
Lophelia pertusa	Caryophylliidae	Hexacoral	Radiometric Age	131	130
Solenosmilia variabilis	Caryophylliidae	Hexacoral	Radiometric Age	132	133
Leptosammia pruvoti	Dendrophylliidae	Hexacoral	Growth	84, 76	81
Balanophyllia elegans	Dendrophylliidae	Hexacoral	Matrix/Survival	79	78
Balanophyllia europea	Dendrophylliidae	Hexacoral	Growth	80	81, 82
Enallopsammia rostrata	Dendrophylliidae	Hexacoral	Radiometric Age	134	135136
Ctenactis echinata	Fungiidae	Hexacoral	Growth	52	44
Diaseris distorta	Fungiidae	Hexacoral	Growth	52	37,44
Fungia actiniformis	Fungiidae	Hexacoral	Growth	52	44
Fungia fungites	Fungiidae	Hexacoral	Growth	52	44
Fungia granulosa	Fungiidae	Hexacoral	Growth	52	49, 44
Fungia paumotensis	Fungiidae	Hexacoral	Growth	52	49, 44
Leiopathes glaberime	Leiopathidae	Hexacoral	Radiometric Age	58,70	70
Leiopathes sp.	Leiopathidae	Hexacoral	Radiometric Age	57	133
Goniastrea aspera	Merulinidae	Hexacoral	Matrix/Survival	7	44
Goniastrea favulus	Merulinidae	Hexacoral	Matrix/Survival	7	258
Orbicella annularis	Merulinidae	Hexacoral	Matrix/Survival	9	37, 44
Platygyra sinensis	Merulinidae	Hexacoral	Matrix/Survival	7	237
Diploria strigosa	Mussidae	Hexacoral	Matrix/Survival	6	45
Antipathella fiordensis	Myriopathidae	Hexacoral	Growth	71, 70	41
Plumapathes pennacea	Myriopathidae	Hexacoral	Growth	72,70	NA
Kulamanamana haumeaae	Parazoanthidae	Hexacoral	Radiometric Age	57, 59	59
Parazoanthus axinellae	Parazoanthidae	Hexacoral	Matrix/Survival	75	74
Pocillopora damicornis	Pocilloporidae	Hexacoral	Matrix/Survival	2	48, 44
Alveopora japonica	Poritidae	Hexacoral	Growth	181	181
Porites astreoides	Poritidae	Hexacoral	Matrix/Survival	6	49, 50, 44

Fannyella rossii	Primnoidae	Hexacoral	Radiometric Age	64	NA
Stauropathes artica	Schizopathidae	Hexacoral	Radiometric Age	62	NA
Palythoa caesia	Sphenopidae	Hexacoral	Matrix/Survival	11	41
Alcyonium acaule	Alcyoniidae	Octocoral	Matrix/Survival	75, 76	77
Anthomastus ritteri	Alcyoniidae	Octocoral	Growth	179	179
Gorgonia ventalina	Anthothelidae	Octocoral	Matrix/Survival	88	91
Chrysogorgia sp.	Chrysogorgiidae	Octocoral	Radiometric Age	177	177
Corallium niobe	Corallidae	Octocoral	Radiometric Age	67	NA
Corallium secundum	Corallidae	Octocoral	Radiometric Age	58	NA
Corallium rubrum	Coralliidae	Octocoral	Matrix/Survival	Present Study	55
Eunicella singularis	Gorgoniidae	Octocoral	Growth	66	73
Leptogorgia sarmentosa	Gorgoniidae	Octocoral	Growth	85	123
Leptogorgia virgulata	Gorgoniidae	Octocoral	Matrix/Survival	8	259
Pseudopterogorgia	Gorgoniidae	Octocoral	Matrix/Survival	14	NA
Pseudopterogorgia acerosa	Gorgoniidae	Octocoral	Matrix/Survival	88	41
Pseudopterogorgia americana	Gorgoniidae	Octocoral	Matrix/Survival	88	91
Halipteris willemoesi	Halipteridae	Octocoral	Radiometric Age	63	NA
Halipteris willemoesi	Halipteridae	Octocoral	Growth	176	176
Isidella tentaculum	Isididae	Octocoral	Radiometric Age	129	NA
Keratosis ornata	Isididae	Octocoral	Radiometric Age	62	NA
Keratosis sp.	Isididae	Octocoral	Radiometric Age	128	NA
Acanella arbuscula	Isididae	Octocoral	Radiometric Age	62	NA
Eunicea laxispica	Plexauridae	Octocoral	Matrix/Survival	88	NA
Eunicea succinea	Plexauridae	Octocoral	Matrix/Survival	88	92
Eunicea tourneforti	Plexauridae	Octocoral	Matrix/Survival	88	NA
Muricea californica	Plexauridae	Octocoral	Growth	83	NA
Muricea fruticosa	Plexauridae	Octocoral	Growth	83	NA
Muriceopsis flavida	Plexauridae	Octocoral	Matrix/Survival	88	92
Paramuricea biscaya	Plexauridae	Octocoral	Growth	177	177
Paramuricea clavata	Plexauridae	Octocoral	Matrix/Survival	12	56
Paramuricea spp.	Plexauridae	Octocoral	Radiometric Age	62	NA
Plexaura A	Plexauridae	Octocoral	Matrix/Survival	13	NA
Plexaura flexuosa	Plexauridae	Octocoral	Matrix/Survival	88	91
Plexaurella dichotoma	Plexauridae	Octocoral	Matrix/Survival	88	91
Pseudoplexaura porosa	Plexauridae	Octocoral	Matrix/Survival	88	91
Pseudoplexaura wagenaari	Plexauridae	Octocoral	Matrix/Survival	88	91
Primnoa resedaeformis	Primnoidae	Octocoral	Radiometric Age	60, 65	62
Thouarella variabilis	Primnoidae	Octocoral	Radiometric Age	64	NA
Fannyella abies	Primnoidae	Octocoral	Radiometric Age	64	NA
Aplysina cavernicola	Aplysinidae	Sponge	Growth	76	104
Amphimedon compressa	Chalinidae	Sponge	Matrix/Survival	5	102
Haliclona fulva	Chalinidae	Sponge	Growth	76	103
Chondrosia reniformis	Chondrosiidae	Sponge	Growth	76	99
Crambe crambe	Crambeidae	Sponge	Matrix/Survival	76	101
Desmapsamma anchorata	Desmacididae	Sponge	Matrix/Survival	105	106

Monorhaphis chuni	Monorhaphididae	Sponge	Radiometric Age	94	NA
Mycale fistulifera	Mycalidae	Sponge	Matrix/Survival	170	NA
Petrosia ficiformis	Petrosiidae	Sponge	Growth	76	97, 98, 100
Xestospongia muta	Petrosiidae	Sponge	Growth	89	124
Rhabdocalyptus dawsoni	Rossellidae	Sponge	Growth	96	NA
Rosella spp.	Rossellidae	Sponge	Oxigen_Size	93	NA
Rossella racovitzaeracovitzae	Rossellidae	Sponge	Radiometric Age	95	NA
Spirastrella cunctatrix	Spirastrellidae	Sponge	Growth	76	100
Spongia graminea	Spongiidae	Sponge	Matrix/Survival	32	261
Stylocordyla borealis	Stylocordylidae	Sponge	Oxigen_Size	93	NA
Cinachyra antarctica	Tetillidae	Sponge	Oxigen_Size	93	NA
Scalarispongia scalaris	Thorectidae	Sponge	Growth	76	100
Glossus humanus	Glossidae	Bivalve	Growth	212	213
Panopea generosa	Hiatellidae	Bivalve	Growth	216	190, 217
Perna perna	Mytilidae	Bivalve	Growth	236	2237
Pedum spondyloideum	Pectinidae	Bivalve	Growth	180	248
Anadara tuberculosa	Anadarinae	Bivalve	Growth	207	211
Arca noae	Arcidae	Bivalve	Growth	208	195, 209
Arctica islandica	Arcticidae	Bivalve	Growth	127	121
Astarte arctica	Astartidae	Bivalve	Growth	240	41
Astarte borealis	Astartidae	Bivalve	Growth	240	215
Astarte elliptica	Astartidae	Bivalve	Growth	240	241
Astarte montagui	Astartidae	Bivalve	Growth	240	215
Astarte sulcata	Astartidae	Bivalve	Growth	234	234
Clinocardium californiense	Cardiidae	Bivalve	Growth	240	241
Clinocardium ciliatum	Cardiidae	Bivalve	Growth	240	241
Serripes gloenlandicus	Cardiidae	Bivalve	Growth	240	215
Tridacna gigas	Cardiidae	Bivalve	Matrix/Survival	16	205
Cardita affinis	Carditidae	Bivalve	Growth	226	227
Cyclocardia ventricosa	Carditidae	Bivalve	Growth	240	41
Donax denticulatus	Donacidae	Bivalve	Growth	173	215
Donax denticulatus	Donacidae	Bivalve	Growth	233	215
Donax trunculus	Donacidae	Bivalve	Growth	235	225
Mytilopsis leucophaeata	Dreissenidae	Bivalve	Growth	228	215
Glycymeris bimaculata	Glycymerididae	Bivalve	Growth	210	195
Glycymeris pilosa	Glycymerididae	Bivalve	Growth	194	195
Neopycnodonte zibrowii	Gryphaeidae	Bivalve	Radiometric Age	246	246
Haliotis iris	Haliotidae	Bivalve	Matrix/Survival	24	157
Haliotis laevigata	Haliotidae	Bivalve	Matrix/Survival	33, 34	158
Haliotis rufescens	Haliotidae	Bivalve	Matrix/Survival	25	159
Haliotis sorenseni	Haliotidae	Bivalve	Matrix/Survival	171	160
Cyrtodaria kurriana	Hiatellidae	Bivalve	Growth	240	272, 41
Hiatella arctica	Hiatellidae	Bivalve	Growth	240	273
Panomya ampla	Hiatellidae	Bivalve	Growth	240	41
Panopea abrupta	Hiatellidae	Bivalve	Growth	16, 151	152, 168

Hiatella arctica	Hiatellidae	Bivalve	Growth	119	167
Lasaea rubra	Lasaeidae	Bivalve	Matrix/Survival	16	278
Mysella kurilensis	Lasaeidae	Bivalve	Growth	240	240
Laternula elliptica	Laternulidae	Bivalve	Growth	148	150
Keletistes rhizoecus	Lucinidae	Bivalve	Growth	245	245
Lyonsia arenosa	Lyonsiidae	Bivalve	Growth	240	274
Lyonsia vniroi	Lyonsiidae	Bivalve	Growth	240	NA
Mactromeris polynyma	Mactridae	Bivalve	Growth	240	243
Spisula sachalinensis	Mactridae	Bivalve	Growth	240	244
Spisula solidissima	Mactridae	Bivalve	Growth	172	NA
Spisula subtruncata	Mactridae	Bivalve	Matrix/Survival	224	225
Mesodesma mactroides	Mesodesmatidae	Bivalve	Growth	175	174
Mya arenaria	Myidae	Bivalve	Growth	148	149, 196
Mya baxteri	Myidae	Bivalve	Growth	240	NA
Mya pseudoarenaria	Myidae	Bivalve	Growth	240	41
Mya truncata	Myidae	Bivalve	Growth	240	215
Mytilus trossulus	Mytilidae	Bivalve	Growth	240	242
Arvella manshurica	Mytilidae	Bivalve	Growth	240	240
Crenella decussata	Mytilidae	Bivalve	Growth	240	215
Crenomytilus grayanus	Mytilidae	Bivalve	Growth	240	192
Geukensia demissa	Mytilidae	Bivalve	Matrix/Survival	16	156
Limnoperna fortunei	Mytilidae	Bivalve	Growth	218	219
Lithophaga lithophaga	Mytilidae	Bivalve	Growth	206	195
Lithophaga patagonica	Mytilidae	Bivalve	Growth	214	215
Musculus discors	Mytilidae	Bivalve	Growth	240	215
Musculus niger	Mytilidae	Bivalve	Growth	240	215
Mytilus californianus	Mytilidae	Bivalve	Matrix/Survival	35	161
Mytilus galloprovincialis	Mytilidae	Bivalve	Matrix/Survival	35	162
Perna viridis	Mytilidae	Bivalve	Growth	231	232
Adamussium colbecki	Pectinidae	Bivalve	Matrix/Survival	16	278
Aequipecten opercularis	Pectinidae	Bivalve	Radiometric Age	147	146
Argopecten irradians irradians	Pectinidae	Bivalve	Growth	137	143144
Argopecten purpuratus	Pectinidae	Bivalve	Growth	139140	145
Placopecten megellanicus	Pectinidae	Bivalve	Growth	141, 142	153
Siliqua alta	Pharidae	Bivalve	Growth	240	41
Lissarca miliaris	Philobryidae	Bivalve	Matrix/Survival	16	155
Lissarca notorcadensis	Philobryidae	Bivalve	Matrix/Survival	16	154
Zirfaea pilsbryi	Pholadidae	Bivalve	Growth	240	NA
Pinna nobilis	Pinnidae	Bivalve	Matrix/Survival	122	120
Nuttallia obscurata	Psammobiidae	Bivalve	Matrix/Survival	31, 164	241
Pinctada imbricata	Pteriidae	Bivalve	Growth	229	230
Abra alba	Semelidae	Bivalve	Growth	247	41
Macoma balthica	Tellinidae	Bivalve	Growth	240	241
Macoma calcarea	Tellinidae	Bivalve	Growth	240	241
Macoma lama	Tellinidae	Bivalve	Growth	240	241

Macoma loveni	Tellinidae	Bivalve	Growth	240	215
Macoma middendorffi	Tellinidae	Bivalve	Growth	240	41
Tellina lutea	Tellinidae	Bivalve	Growth	240	41
Tellina tenuis	Tellinidae	Bivalve	Growth	238	239
Thracia septentrionalis	Thraciidae	Bivalve	Growth	240	215
Tindaria callistifomis	Tindariidae	Bivalve	Radiometric Age	138	NA
Tindaria callistiformis	Tindariidae	Bivalve	Radiometric Age	169	NA
Diplodonta aleutica	Ungulinidae	Bivalve	Growth	240	240
Callista brevisiphonata	Veneridae	Bivalve	Growth	197, 200	17, 18
Callista chione	Veneridae	Bivalve	Growth	201	203, 204, 222
Gemma gemma	Veneridae	Bivalve	Matrix/Survival	16	215
Liocyma fluctuosum	Veneridae	Bivalve	Growth	240	272
Mercenaria mercenaria	Veneridae	Bivalve	Growth	101	215
Protothaca euglypta	Veneridae	Bivalve	Growth	221	220, 221
Ruditapes philippinarum	Veneridae	Bivalve	Growth	201, 223	202
Yoldia eightsi	Yoldiidae	Bivalve	Growth	191	193
Yoldia myalis	Yoldiidae	Bivalve	Growth	240	215
Yoldia seminuda	Yoldiidae	Bivalve	Growth	240	241
Alaria nana	Alariaceae	Macroalgae	Matrix/Survival	17	267
Leathesia difformis	Chordariaceae	Macroalgae	Matrix/Survival	263	270
Lithothamnium crassiusculum	Corallinaceae	Macroalgae	Radiometric Age	187	187
Ascophyllum nodosum	Fucaceae	Macroalgae	Matrix/Survival	18	41
Fucus distichus	Fucaceae	Macroalgae	Matrix/Survival	23	268
Pelvetia fastigiata	Fucaceae	Macroalgae	Matrix/Survival	264	116
Iridaea splendens	Gigartinaceae	Macroalgae	Matrix/Survival	26	NA
Gracilaria gracilis	Gracilariaceae	Macroalgae	Matrix/Survival	265	
Halimeda incrassata	Halimedaceae	Macroalgae	Matrix/Survival	182	249
Hormosira banksii	Hormosiraceae	Macroalgae	Matrix/Survival	183	NA
Laminaria digitata	Laminariaceae	Macroalgae	Matrix/Survival	27	NA
Laminaria hyperborea	Laminariaceae	Macroalgae	Growth	117	117
Laminaria hyperborea	Laminariaceae	Macroalgae	Matrix/Survival	184	41
Macrocystis pyrifera	Laminariaceae	Macroalgae	Matrix/Survival	30	266
Petrocelis middendorffii	Phyllophoraceae	Macroalgae	Growth	113	NA
Pterocladia capillacea	Pterocladiaceae	Macroalgae	Growth	112	269
Petrocellis middendorffi	Rhodymeniophycidae	Macroalgae	Growth	186	NA
Cystoseira zosteroides	Sargassaceae	Macroalgae	NA	114	115
Clathromorphum nereostratum	Hapalidiaceae	Macroalgae	Growth	185	188
Adeonellopsis sp	Adeonidae	Bryozoan	NA	189	NA
Cellepora pumicosa	Celleporidae	Bryozoan	Matrix/Survival	22	262
Mucropetraliella ellerii	Petraliellidae	Bryozoan	Matrix/Survival	10	10
Watersipora subtorquata	Watersiporidae	Bryozoan	Matrix/Survival	20	107
Semibalanus balanoides	Archaeobalanidae	Cirriped (Crustacea)	Matrix/Survival	21	NA
Onithochiton quercinus	Chitonidae	Cirriped (Crustacea)	Growth	271	41
Chthamalus montagui	Chthamalidae	Cirriped (Crustacea)	Matrix/Survival	21	NA

Plaxiphora albida	Mopaliidae	Cirriped (Crustacea)	Growth	271	41
Cantellius sp.	Pyrgomatidae	Cirriped (Crustacea)	NA	180	41
Botrylloides violaceous	Styelidae	Tunicate	Matrix/Survival	20	110
Botryllus schlosseri	Styelidae	Tunicate	Matrix/Survival	20	111
Campanularia everta	Campanulariidae	Hydrozoan	NA	125	NA
Campanularia flexuosa	Campanulariidae	Hydrozoan	NA	126	NA
Corymorpha nutans	Corymorphidae	Hydrozoan	NA	250	250
Corymorpha palma	Corymorphidae	Hydrozoan	NA	250	41
Eutima japonica	Eirenidae	Hydrozoan	NA	253	NA
Helecium petrosum	Haleciidae	Hydrozoan	Growth	108	NA
Helecium pusillum	Haleciidae	Hydrozoan	Growth	108	NA
Nemertesia antennina	Plumulariidae	Hydrozoan	NA	251	41,
Errina novaezelandiae	Stylasteridae	Hydrozoan	Growth	178	178, 41
Tubularia indivisa	Tubulariidae	Hydrozoan	NA	125	NA
Tubularia indivisa	Tubulariidae	Hydrozoan	NA	252	41
Galeolaria hystrix	Serpulidae	Polychaete	NA	255	276
Circeis armoricana	Serpulidae	Polychaete	NA	256	41
Ficopomatus enigmaticus	Serpulidae	Polychaete	NA	254	41
Hydroides elegans	Serpulidae	Polychaete	NA	256	NA
Janua pagenstecheri	Serpulidae	Polychaete	NA	256	277
Neodexiospira brasiliensis	Serpulidae	Polychaete	NA	256	41
Pomatoceros triqueter	Serpulidae	Polychaete	NA	256	257
Pseudochitinopoma occidentalis	Serpulidae	Polychaete	NA	256	41
Spirobranchus cariniferus	Serpulidae	Polychaete	NA	255	NA
Spirobranchus giganteus	Serpulidae	Polychaete	NA	256	41

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Table S10. Source studies of long-term demographic variability estimates included in the comparative analysis (n = 34) (See completed references list below).

Species Name	**Family**	**Habitat**	**Study Period**	**# Populations**	**Source ID**
Actaea spicata	Ranunculaceae	Terrestrial	1999 - 2005	2	1
Alliaria petiolata	Brassicaceae	Terrestrial	2003-2008	6	2
Arabis fecunda	Brassicaceae	Terrestrial	1987-1993, 2009	3	3, 4
Astragalus scaphoides	Fabaceae	Terrestrial	1986-2009	3	3, 5
Astragalus tyghensis	Fabaceae	Terrestrial	1991-1998, 2008	5	3, 6
Cimicifuga elata	Ranunculaceae	Terrestrial	1992–1996, 1992–1997	3	3, 6
Cirsium pitcheri	Asteraceae	Terrestrial	1998-2009	4	3, 7
Cypripedium fasciculatum	Orchidaceae	Terrestrial	1999-2007	3	3
Dicerandra frutescens	Lamiaceae	Terrestrial	1988-2008	6	3, 8, 9
Eryngium cuneifolium	Apiaceae	Terrestrial	1990-2008	6	10
Gentiana pneumonanthe	Gentianaceae	Terrestrial	1987-1993, 2009	7	3, 11
Haplopappus radiatus	Asteraceae	Terrestrial	1992-1999, 2009	4	3, 6
Horkelia congesta	Rosaceae	Terrestrial	1994-1999, 2009	1	3, 12
Hypericum cumulicola	Hypericaceae	Terrestrial	1994-2007	6	3, 13
Lathyrus vernus	Fabaceae	Terrestrial	1988-1991, 2009	10	3, 14
Liatris scariosa	Asteraceae	Terrestrial	1995-2000, 2008	1	3
Lomatium cookii	Apiaceae	Terrestrial	1994-1999, 2009	2	3, 6
Lomatium bradshawii	Apiaceae	Terrestrial	1988–1994, 1996–1997	7	3, 6
Neobuxbaumia macrocephala	Cactaceae	Terrestrial	1997-2002, 2009	1	3, 15, 16
Opuntia macrorhiza	Cactaceae	Terrestrial	1999-2005	5	17
Phyllanthus emblica	Phyllanthaceae	Terrestrial	1999-2004, 2009	1	3
Phyllanthus indofischeri	Phyllanthaceae	Terrestrial	1999-2004, 2009	1	3
Silene acaulis	Caryophyllaceae	Terrestrial	1995-2000, 2009	4	3, 18
Silene spaldingii	Caryophyllaceae	Terrestrial	1987-2009	1	3, 19, 20
Trillium grandiflorum	Orchidaceae	Terrestrial	1998-2002, 2010	12	3, 21, 22
Plexaura A	Plexauridae	Marine	1984-1987	1	23
Corallium rubrum	Coralliidae	Marine	2003-2011	8	Present Study
Montastrea annularis	Merulinidae	Marine	2001-2009	1	24
Porites astreoides	Poritidae	Marine	1999-2007	1	25
Diploria strigosa	Mussidae	Marine	2002-2007	1	25
Acropora palmata	Acroporidae	Marine	2004-2010	1	26

Paramuricea clavata	Plexauridae	Marine	1999-2003	1	27
Mesodesma mactroides	Mesodesmatidae	Marine	1983-1990	1	28
Yoldia notabilis	Yoldiidae	Marine	1973-1989, 1977-1989	2	29

Complete references list of Table S10

ID	Reference
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SUPPLEMENTARY METHODS

Integral Projection Model: data collection and model construction

Demographic monitoring of natural Corallium rubrum populations

A total of 1144 coral colonies from nine *C. rubrum* populations along the North-Western Mediterranean region were individually monitored using photographic techniques over periods ranging from 3 to 9 years between 2003 and 2011 (Montero-Serra *et al. in preparation*).

Six populations were located within Marine Protected Areas (MPA) where harvesting is not allowed but other human uses are allowed with some restrictions. Recreational diving is allowed in Parc Natural del Montgrí, Illes Medes i Baix Ter (Spain) and completely forbidden except for scientific studies in the Réserve Naturelle Marine Cerbère-Banyuls (France), in Parc Marine Côte Bleue (France), and the Réserve Naturelle de Scandola (France). The last three populations are located in the archipelago of Riou near Marseilles (France), where harvesting and recreational diving was allowed during the study (Fig. S1).

To individually identify and track each coral colony during the study period, two to four permanent transects were installed at each population. Transects were monitored once a year using a photographic sampling design. During sampling, a cord was deployed between permanently set screws and a 20 x 20 cm quadrat, sequentially positioned and photographed along the length of each transect. Two photographs were taken from each quadrat using different angles. This allowed us to obtain precise measurements of colony heights using photogrammetric techniques (Drap *et al*. 2013).

Estimation of vital rates

Vital rates (survival, growth, and reproduction) were estimated by fitting size-based continuous functions to long-term data on survival, post-recruit survival, growth and variance in growth (Easterling et al. 2000, Morris and Doak 2002). Survival was described by a logistic mixed effects model (GLMM) including colony size and year as fixed factors and population as a random factor.

Growth data from two populations over variable length periods (7 and 8 yrs) were used to fit a model characterizing annual growth rate depending on size. Processed height data from all annual photographs were not available, and growth is so slow in this species that even 7 to 8 year time periods only result in mean growth on the order of 10 to 40mm in maximum height (2.74 ± 0.19 $\mathrm{mm \cdot yr^{-1}}$, see Fig. S2). As for many other clonal species, red coral can both grow and shrink over time. Shrinkage or negative growth is a common process in plants and sessile invertebrates that is usually accounted for by assuming normally distributed variation in size changes around a mean rate (e.g., Easterling *et al.* 2000, Salguero-Gomez & Casper 2010). However, for many species assuming normally distributed growth variance is problematic, because a few individuals experience sporadic extreme shrinkage events and these results in a highly skewed distribution of growth rates (Shriver *et al*. 2012). We accounted for these two types of growth following the procedures proposed by Shriver and colleagues (2012), describing normal growth and extreme shrinkage as a two-part process. First, we estimated the probability of each colony undergoing “normal growth” (pn) and “extreme shrinkage” (1 - pn). These probabilities are size- and year-dependent according to the data.

For each type of growth (normal and extreme shrinkage) we first calculated mean annual change in size as.

$G = (\text{Size}_T - \text{Size}_0) / T$

where T is the time between the first and final census, Size_0 is the initial size measurement, and Size_T is the final size measurement.

We then extracted the residuals from the best-fitting model and divided the residuals by the number of years to predict annual variance in growth:

$\text{VAR} = \{(\text{Residuals}) / T\}^2$

We then used a linear regression model to fit the squared residuals to size, which showed a marginally significant positive relationship for normal growth ($P = 0.08$) and shrinkage ($P < 0.001$).

Recruitment rates were annually quantified from 30 fixed quadrats for each population. We considered effective recruits to be the button-like colonies observed for the first time in a quadrat. We calculated post-recruitment survival by monitoring recruits that we observed for the first time within a quadrat and tracked during the study period. Our data allowed for a robust estimation of survival within the range from 1 to 4 years. Further, we estimated the probability of recruits growing to an adult stage by direct observations in three populations where this process could be clearly identified**.**

Molecular studies have revealed a fine-scale genetic structure within *C. rubrum* populations and almost negligible dispersal among populations (Ledoux *et al.* 2010). Thus, new recruits were assigned to past individual parents assuming a relationship between colony size and the relative rate of reproduction. Past work has shown that there is an exponential relationship between *C. rubrum* size and polyp number

(Santangelo *et al.* 2003), proportion of fertile colonies, and frequency of larvae per polyp in *C. rubrum* (Torrents *et al*. 2005). Thus, we used the squared adult colony size (height) as an approximation for polyp number. We then corrected these data by the proportion of fertile colonies and percentage of fertile polyps, because both parameters have been shown to increase along with colony size (Torrents et al. 2005).

Fecundity was calculated as follows:

(1)

$$\text{Recruits/Size} = \text{New Recruits per quadrat (t1)} \,/\, \sum((\text{Colony Size})^2 * \text{Colony Fertility} * \text{Polyp Fertility})\ (\text{t0})\ \text{per quadrat}$$

(2)

$$\text{Fecundity values} = [(\text{Adult Colony Size})^2] * (\text{Colony Fertility} * \text{Polyp Fertility}) * (\text{Rec/Size})$$

Model construction

We coupled continuous size-based vital rates estimates for adults to four age-based stages for recruits to build an IPM for red coral. We simulated the model using 60 classes (where the first four classes are age-based categories for recruits and the rest are size-based). The number of size classes was chosen after calculating asymptotic population growth under multiple matrices constructed using a range of size-classes from 3 to 200. The results of these simulations showed that matrices with a number of size-classes larger than 60 showed a consistent value for population growth rate (Fig S2).

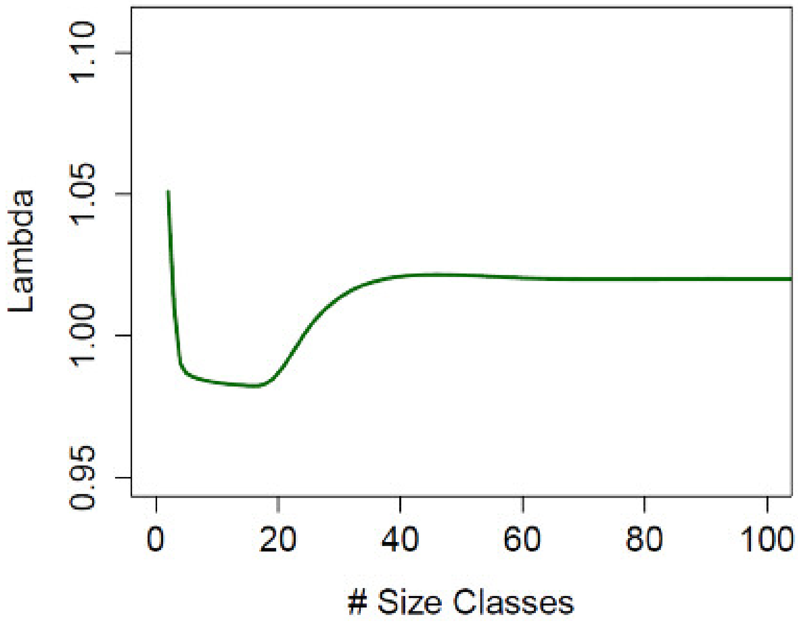

Figure S2. Asymptotic population growth rate (lambda) based on matrix approximations to a continuous IPM model constructed using a range of size-classes from 3 to 200.

We parameterized eight annual matrices that were derived based on the models previously fit; the fecundity and survival functions varied between these years, while growth was not estimated on an annual basis. All the a_{ji} matrix elements below the top row (the reproductive elements) were estimated as:

(3)

$$a_{ji} = s_i \, (p_{n,i} \, n_{ji} + (1 - p_{n,i}) \, m_{ji})$$

where s_i is the probability of survival for the ith size class, $p_{n,i}$ is the probability of ‘‘normal growth or shrinkage’’ for the ith class, n_{ji} is the probability of normally growing or shrinking from the ith class to the jth class, and m_{ji} is the probability of moving from the ith to the jth class with extreme shrinkage. To estimate n_{ji} and m_{ji} values, we used the mid-point size for class i as the starting size, and a normal CDF to calculate the total probability of falling within the range of sizes in the jth class.

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R Code

```
# Deterministic IPMs to quantify life-history traits of the red coral Corallium rubrum #####

# I. Montero Serra et al. 2018.


rm(list=ls())

require(dplyr)
require(popbio)
require(plyr)
require(lme4)
require(MASS)


#########################################################################

#1.# Fitting regression models to empirical data to describe vital rates

#########################################################################

## Mean growth rate model
dataGrowth <- read.csv("DataGrowth.csv", sep=";")
dataG <- na.omit(dataGrowth[,c(2,4,5)]) # Keeping only needed data
colnames(dataG) <- c("t0", "growth", "years")

## Linear Growth Model
dataG$t1 <- dataG$t0+dataG$growth
growthlm1 <- lm(t1 ~ t0, data = dataG)

## Variance in Growth Model -  residuals of the NL Growth Model
dataG$residuals_lm <- (resid(growthlm1)^2)/dataG$years
vargrow_lm1 <- lm(residuals_lm~ t0, data= dataG)

## Fecundity and Survival Models
data=read.csv("AllPopulations.csv", sep=";")
dataS1 <- read.csv("AllPopulations_Shrinkage.csv", sep=";")

tmax <- length(data$Population)

size <- arrange(data,Size_t)
data$Year_t = as.factor(data$Year_t)
data$Size_t = as.numeric(data$Size_t)

data$Pop_Year = paste(data$Population, data$Year, sep="_")

## Mixed Model for survival
glmmSurv = glmmPQL(Survival_t_t1~Size_t,random=list(Population=~1, Year_t=~1), family=binomial,
data=data)

## Mixed Model for fecundity
glmmFec = glmmPQL(Fecundity_t~Size_t,random=list(Population=~1, Year_t=~1),
family=quasipoisson(link="log"), data=data)

## Modeling shrinkage events #
dataS2 = dataS1[dataS1$Survival_t_t1==1,] # Only colonies that survive

## Probability of Shrinking
dataS2$Year_t = as.factor(dataS2$Year_t)
```

```
glmmSh = glmmPQL(Shrinkage~Size_t, random=list(Population=~1, Year_t=~1), family=binomial,
data=dataS2)

## If shrinking, negtive growth and variance models
dataS3 = dataS2[dataS2$Shrinkage==1,1:7] # Only data of shrinkage events
dataS3 = na.omit(dataS3)

## Negative growth (shrinakge) model
lmSh = lm(as.numeric(Size_t1)~as.numeric(Size_t), data=dataS3)

## Variance of Shrinkage Model
dataS3$ReslmSh = resid(lmSh)^2
varlmSh = lm((ReslmSh)~Size_t, data=dataS3)

## Standard deviation of the Shrinkage model
sd_lmSh = lm(abs((resid(lmSh)))~Size_t, data=dataS3)

## Early stage vital rates: age-based survival and growth
Data <- read.csv("DataRecruits.csv", sep=";")
Data$Age_tb <- Data$Age_t

## four categories: 1yr; 2yrs; 3yrs; +3yrs
for(i in 1:391) {
 if (Data$Age_t[i] > 4) {Data$Age_tb[i]=4}
}

glmRecSurv <- glm(Survival_t~as.numeric(Age_tb),data= Data, family=binomial(link = "logit"))


##################################################

#2.# Discretizing vital rates into stage-classes

##################################################

# set matrix dimensions
matDim = 80

bin=(matDim-3)

maxsize <- max(data$Size_t)
minsize <- 0
binedges <- minsize + seq(0,(bin-1),1)*((maxsize-minsize)/(bin-1))
binmids <- 0.5*(binedges[2:length(binedges)] + binedges[1:(length(binedges)-1)])

predictor = binmids

## Predicting vital rates based on reegression models previously fitted to demographic data

## Mean fecundity values from a glmm for the deterministic mean matrix model
indata = data.frame(Size_t=predictor)
predictedF = exp(predictor*fixef(glmmFec)[2] + fixef(glmmFec)[1])

## Mean survival rates from a glmm for the deterministic mean matrix model
predictedS = plogis(predictor*fixef(glmmSurv)[2] + fixef(glmmSurv)[1])

## Mean shrinkage rates
predictedSH = plogis(predictor*coef(glmSh)[2] + coef(glmSh)[1])
predictedSh = plogis(predictor*fixef(glmmSh)[2] + fixef(glmmSh)[1])
```

```
## Predicting values from the age-based model for each age-class of early stages (1yr, 2yr, 3yr, +3yrs)
predictorR <- seq(from=1, to=4, by=1)
predicted <- plogis(predictorR*glmRecSurv$coefficients[2] + glmRecSurv$coefficients[1])
recSurvival <- predicted


##############################
#3.# Big Matrix Construction
##############################

maxsize1 <- max(data$Size_t)
maxsize <- maxsize1
minsize <- 0

bin=(matDim-3)

binedges <- minsize + seq(0,(bin-1),1)*((maxsize-minsize)/(bin-1))
binmids <- 0.5*(binedges[2:length(binedges)] + binedges[1:(length(binedges)-1)])

indata <- as.data.frame(cbind(binmids, binmids^2))
names(indata) <- c("t0", "t0sq")

#Growth Linear Model
growth <- predict(growthlm1,indata, type='response')
growthVAR <- predict(vargrow_lm1,indata, type='response')

growthb = growth+binmids
gmx <- matrix(data=NA, nrow=bin-1, ncol=bin-1)

#Growth Matrix
for (ss in 1:(bin-1)) {
  growcdf <- pnorm(binedges,growth[ss],sqrt(growthVAR[ss])) #Mean and Variance for each size class
(ej. at x size class, the mean growth and the var are xxx)
  grows <- growcdf[2:length(binedges)]-growcdf[1:(length(binedges)-1)]
  grows2=grows/sum(grows)
  gmx[,ss]=grows2 } ## Cumulative distribution function

#Shrinakge Matrix
indata2 <- as.data.frame(cbind(binmids, binmids^2))
names(indata2) <- c("Size_t", "t0sq")

shrinkage <- predict(lmSh,indata2, type='response')
shrinkage_SD<- predict(sd_lmSh,indata2, type='response')
shrinkageVAR = (shrinkage_SD)^2
shmx <- matrix(data=0, nrow=bin-1, ncol=bin-1)

#Shrinkage CDF
for (ss in 1:(bin-1)) {
  shcdf <- pnorm(binedges,shrinkage[ss],sqrt(shrinkageVAR[ss])) #Mean and Variance for each size class
(ej. at x size class, the mean growth and the var are xxx)
  shcdf2 <- shcdf[2:length(binedges)]-shcdf[1:(length(binedges)-1)]
  shcdf3=shcdf2/sum(shcdf2) #
  shmx[,ss]=shcdf3 } ## Cumulative distribution function


shmx2<- shmx*t(matrix(rep(predictedSH,(bin-1)),(bin-1),(bin-1))) # survs*growth

NormalGrow = 1-predictedSH
```

```
#Adding normal growth matrix*(1-S) + shrinking*(S)
gmx3 = matrix(data=0, nrow=bin-1, ncol=bin-1)
gmx3 = gmx*t(matrix(rep(NormalGrow,(bin-1)),(bin-1),(bin-1)))
sh_g_mx = gmx3 + shmx2

#Adding growth+Shrinkage matrix to survival
survgmx2 <- sh_g_mx*t(matrix(rep(predictedS,(bin-1)),(bin-1),(bin-1))) # survs*growth

#Adding fecundityto the matrix t=1
fecundityrow <- predictedF*predictedS

gmxsh2 = rbind(fecundityrow,rep(0, bin-1),rep(0, bin-1),rep(0, bin-1),survgmx2)

#Recruits' probability of growing into adult stage (from empirical observations across all surveyed
populations)
Gr1 <- 0.0312
Gr2 <- 0.0476

#Recruit survival
predictor2 <- seq(from=1, to=4, by=1)
recSurvival <- plogis(predictor2*glmRecSurv$coefficients[2] + glmRecSurv$coefficients[1])

age1 <- c(0,recSurvival[1]*(1-Gr1),recSurvival[1]*Gr1,0, rep(0, bin-1))
age2 <- c(0,0,recSurvival[2]*(1-Gr1),recSurvival[2]*Gr1,rep(0, bin-1))
age3 <- c(0,0,0,recSurvival[3]*(1-Gr2),recSurvival[3]*Gr2, rep(0, bin-2))
age4 <- c(0,0,0,(recSurvival[4]*(1-Gr2)),(recSurvival[4]*Gr2),rep(0, bin-2))

gmxsh3 <-cbind(age1,age2,age3,age4,gmxsh2)

Big_Matrix = gmxsh3


############## ############## ############## ##############
############## PERTURBATION ANALYSIS ########################
############## ############## ############## ##############


perturbation = c(0.95,0.99, 1.01,1.05)

Matrix = gmxsh3
#save(Matrix, file="C_rubrum_Det_Mx.rda")

DetLam = eigen.analysis(Matrix)$lambda
Elasticties = matrix(nrow=matDim-4, ncol=length(perturbation))
vital_rates = seq(1:7)
ElasticitiesSummary = matrix(nrow=matDim-4, ncol=length(vital_rates))

vital_ratesRec = seq(1:6) #s1,s2,s3,s4,g1,g2
ElastictiesRec = c()
ElastictiesSummary_Rec = c()

predictedS_Rec_S2=c()
predictedS_Rec_G2=c()


predictedS2=c()
predictedSH2=c()
growth2=c()
growthVAR2=c()
shrinkage2=c()
```

```
shrinkageVAR2=c()


#Start of the pertorbation loops

for(k in 1:length(c(vital_rates,vital_ratesRec))){
for(j in 1:length(perturbation)){
for(i in 1:length(binmids)){

#Adult vital rates perturbation (size-based)
if(k == 1) {predictedS2[i] = predictedS[i]*perturbation[j]} else {predictedS2 = predictedS}
if(k == 2) {growth2[i] =  growth[i]*perturbation[j]} else {growth2 = growth}
if(k == 3) {predictedSH2[i] =  predictedSH[i]*perturbation[j]} else {predictedSH2 = predictedSH}
if(k == 4) {predictedF2[i] = predictedF[i]*perturbation[j]} else {predictedF2 = predictedF}
if(k == 5) {growthVAR2[i] =  growthVAR[i]*perturbation[j]} else {growthVAR2 = growthVAR}
if(k == 6) {shrinkage2[i] =  shrinkage[i]*perturbation[j]} else {shrinkage2 = shrinkage}
if(k == 7) {shrinkageVAR2[i] =  shrinkageVAR[i]*perturbation[j]} else {shrinkageVAR2 =
shrinkageVAR}

#Recruits vital rates perturbation (age-based growth & survival)
if(k == 8 || k == 9 || k == 10|| k == 11) {recSurvival2[k-7] =  recSurvival[k-7]*perturbation[j]} else
{recSurvival2 = recSurvival}
if(k == 12) {Gr1_2 =  Gr1_2*perturbation[j]} else {Gr1_2 = Gr1}
if(k == 13) {Gr2_2 =  Gr2_2*perturbation[j]} else {Gr2_2 = Gr2}




  gmx <- matrix(data=NA, nrow=bin-1, ncol=bin-1)

#Growth Matrix
for (ss in 1:(bin-1)) {
  growcdf <- pnorm(binedges,growth2[ss],sqrt(growthVAR2[ss])) #Mean and Variance for each size class
(ej. at x size class, the mean growth and the var are xxx)
  grows <- growcdf[2:length(binedges)]-growcdf[1:(length(binedges)-1)]
  grows2=grows/sum(grows)
  gmx[,ss]=grows2 } ## Cumulative distribution function

#Shrinakge Matrix

shmx <- matrix(data=0, nrow=bin-1, ncol=bin-1)

#Shrinkage CDF
for (ss in 1:(bin-1)) {
  shcdf <- pnorm(binedges,shrinkage2[ss],sqrt(shrinkageVAR2[ss])) #Mean and Variance for each size
class (ej. at x size class, the mean growth and the var are xxx)
  shcdf2 <- shcdf[2:length(binedges)]-shcdf[1:(length(binedges)-1)]
  shcdf3=shcdf2/sum(shcdf2) #
  shmx[,ss]=shcdf3 } ## Cumulative distribution function


shmx2<- shmx*t(matrix(rep(predictedSH2,(bin-1)),(bin-1),(bin-1))) # survs*growth

NormalGrow = 1-predictedSH2


#Adding normal growth matrix*(1-S) + shrinking*(S)
gmx3 = matrix(data=0, nrow=bin-1, ncol=bin-1)
gmx3 = gmx*t(matrix(rep(NormalGrow,(bin-1)),(bin-1),(bin-1)))
sh_g_mx = gmx3 + shmx2
```

```
#Adding growth+Shrinkage matrix to survival
survgmx2 <- sh_g_mx*t(matrix(rep(predictedS2,(bin-1)),(bin-1),(bin-1))) # survs*growth

#Adding fecundityto the matrix t=1
fecundityrow <- predictedF2*predictedS2 #afegim una fila i columna pels recruits (aquí s'hauria d'afegir
4 files i 4 columnes per incloure la part "age-based")



gmxsh2 = rbind(fecundityrow,rep(0, bin-1),rep(0, bin-1),rep(0, bin-1),survgmx2)

#Recruit survival & growth

age1 <- c(0,recSurvival2[1]*(1-Gr1_2),recSurvival2[1]*Gr1_2,0, rep(0, bin-1))
age2 <- c(0,0,recSurvival2[2]*(1-Gr1_2),recSurvival2[2]*Gr1_2,rep(0, bin-1))
age3 <- c(0,0,0,recSurvival2[3]*(1-Gr2_2),recSurvival2[3]*Gr2_2, rep(0, bin-2))
age4 <- c(0,0,0,(recSurvival2[4]*(1-Gr2_2)),(recSurvival2[4]*Gr2_2),rep(0, bin-2))

gmxsh3 <-cbind(age1,age2,age3,age4,gmxsh2)

NewLam = eigen.analysis(gmxsh3)$lambda

Dif_Lam = (NewLam-DetLam)/DetLam

Dif_Parameter = perturbation[j]-1

ElasticityParameter = Dif_Lam / Dif_Parameter
Elasticties[i,j] = ElasticityParameter
ElastictiesRec[j] = ElasticityParameter

}
}
if(k == 1 || k == 2 || k == 3 || k == 4 || k == 5 || k == 6 || k == 7) {ElastictiesSummary[,k]=
rowMeans(Elasticties)}

if(k == 8 || k == 9 || k == 10 || k == 11 || k == 12 || k == 13) {ElastictiesSummary_Rec[k-7]=
mean(ElastictiesRec)}

}

# Sum of elasticities #

ElasticitiesSummary2 = c(colSums(ElastictiesSummary), sum(ElastictiesSummary_Rec[-c(5,6)]),
sum(ElastictiesSummary_Rec[c(5,6)]))


##### Barplot #####

colors = c("steelblue", "forestgreen","darkorange","pink4","yellowgreen" ,"gold","orange")

xbars = barplot(ElasticitiesSummary2, space=0.4,horiz = T)

barplot(ElasticitiesSummary2,
        col=colors, space=0.4, ylab="Sum of elasticities to lambda (%)", horiz = T,axes=F, border = colors)
box()
axis(1, at=xbars,
     labels=c("Survival",  "Growth", "Shrinkage", "Fecundity",
              "Var(growth)", "Neg. growth", "Var(Neg. growth)", "Rec. Survival", "Rec. Growth"),
cex.axis=.5)
```

```
axis(2, las=2, cex.axis=0.8)


## Only main vital rates ##

colors2 = c("steelblue", "forestgreen","darkorange","pink4")
xbars2 = barplot(ElasticitiesSummary2[1:4], space=0.4)

barplot(ElasticitiesSummary2[1:4], ylim=c(-5,100),
      col=colors2, space=0.4, ylab="Sum of elasticities to lambda (%)", axes=F, border = colors)
abline(h=0, lwd=1, col="grey20")
box()
axis(1, at=xbars2,labels=c("Survival",  "Growth", "Shrinkage", "Fecundity"), cex.axis=1)

axis(2, las=2, cex.axis=1)
```