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Supplementary Materials for

Deep reefs are not universal refuges: Reseeding potential varies among coral species

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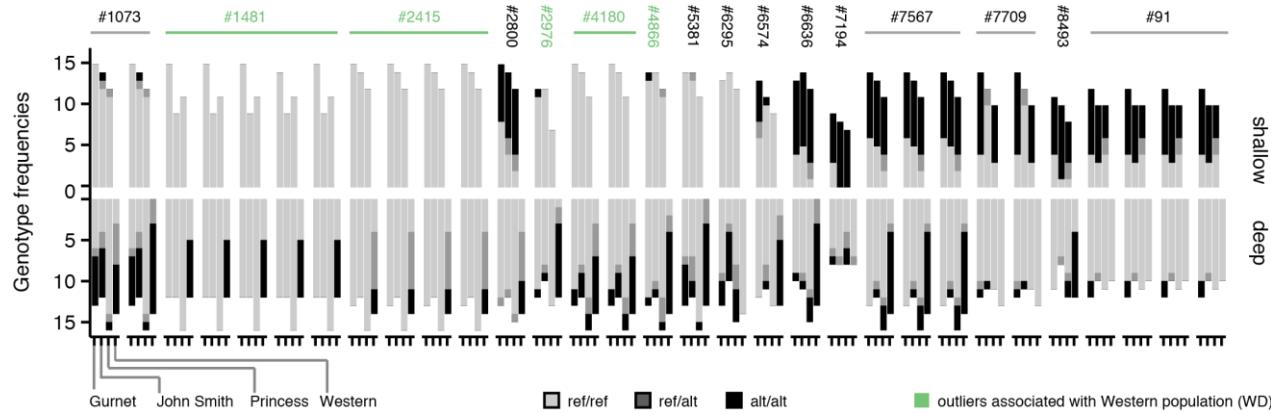


fig. S1. Genotype frequencies of SNP outliers for *A. fragilis*. Genotype frequencies of outlier SNPs (excluding those associated with depth) grouped by RAD locus (indicated by locus identifier) for shallow and deep populations. Hue of stacks indicate genotype (ref/ref = homozygote for the reference allele, ref/alt = heterozygote, alt/alt = homozygote for the alternative allele). Green labels indicate outlier loci in association with the “Western Blue Cut” (WD) population.

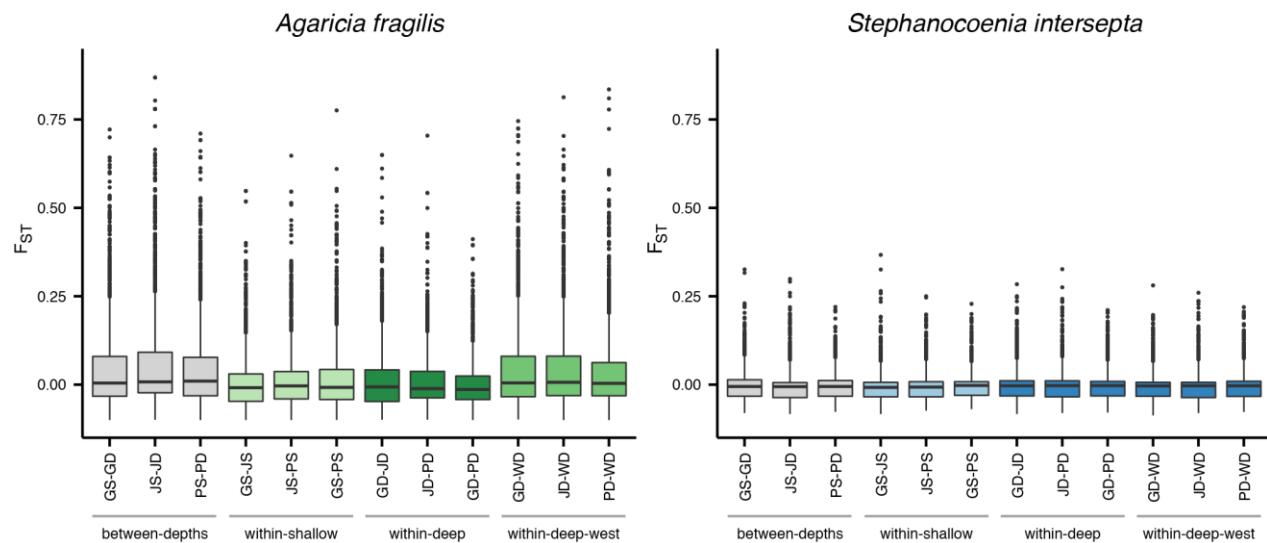


fig. S2. Genome-wide pairwise differentiation (F_{ST}) of populations. Colors correspond to those of STRUCTURE clusters in Fig. 2, except for “gray” indicating between-depth comparisons.

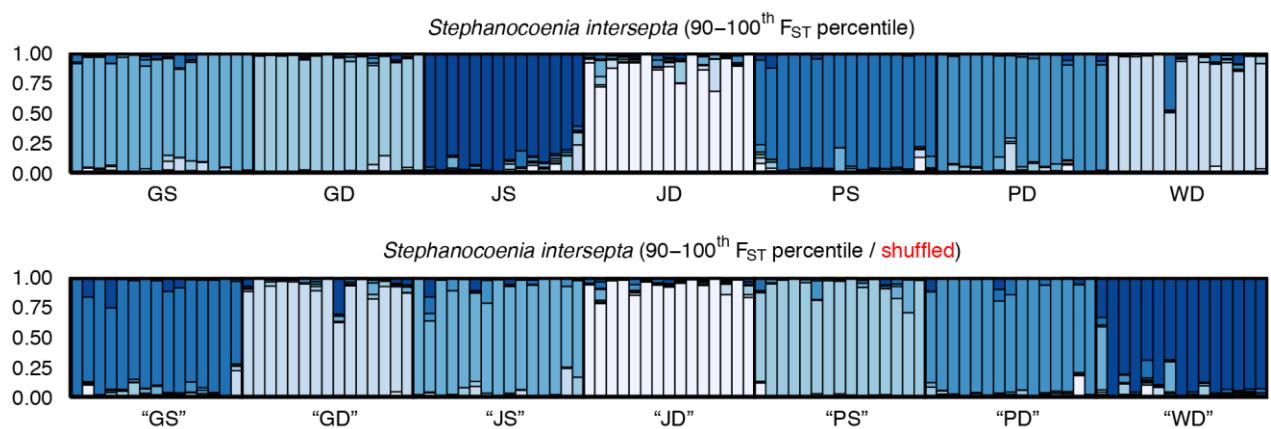


fig. S3. Genetic structuring of *S. intersepta* populations based on most divergent SNPs.

STRUCTURE diagrams for as inferred from the overall 90-100th F_{ST} percentile, for the actual dataset (top) and for the same dataset but with individuals “randomly” shuffled across populations prior to calculating F_{ST} (bottom).

table S1. Details of the sampled *A. fragilis* and *S. intersepta* populations. Details (code, name, depth and coordinates) of sampling locations, as well as the number of samples successfully sequenced (at each of these locations) and the genetic diversity (expected heterozygosity) as calculated from these sequenced samples.

Site code	Site name	Sampling Depth (m)	Coordinates (decimal degrees)	<i>Agaricia fragilis</i>		<i>Stephanocenia intersepta</i>	
				Samples (N)	Genetic diversity (He)	Samples (N)	Genetic diversity (He)
GS	Gurnet Rock	12 m ±2 m	N32 19.981 W64 40.201	15	0.1615541	16	0.1635142
GD	Gurnet Rock	40 m ±2 m	N32 19.816 W64 39.333	15	0.1672369	15	0.1618783
JS	John Smith’s Bay	12 m ±2 m	N32 18.795 W64 42.615	14	0.1618625	14	0.1660883
JD	John Smith’s Bay	40 m ±2 m	N32 18.113 W64 42.130	15	0.1658039	15	0.1622547
PS	Princess Beach	12 m ±2 m	N32 14.679 W64 49.212	13	0.1641213	16	0.1627970
PD	Princess Beach	40 m ±2 m*	N32 13.796 W64 49.110	18	0.1781947	15	0.1622498
WD	Western Blue Cut	40 m ±2 m	N32 22.204 W64 56.952	14	0.2103866	14	0.1620870

*Two samples of *Agaricia fragilis* were collected from 63 m at this location.

table S2. Estimators of the number of STRUCTURE clusters for *A. fragilis* and *S. intersepta*.

K	<i>Agaricia fragilis</i>								<i>Stephanocoenia intersepta</i>							
	overall				“neutral”				overall				“neutral”			
	Med MeaK	Max MeaK	Med MedK	Max MedK	Med MeaK	Max MedK	Med MeaK	Max MedK	Med MeaK	Max MedK	Med MeaK	Max MedK	Med MeaK	Max MeaK	Med MedK	Max MedK
2	2.0	2	2.0	2	2.0	2	2.0	2	1.0	1	1.0	1	1.0	1	1.0	1
3	3.0	3	3.0	3	3.0	3	3.0	3	0.5	1	0.5	1	1.0	1	1.0	1
4	3.0	3	3.0	3	3.0	4	3.0	4	1.0	2	1.0	2	1.0	2	1.0	2
5	3.0	4	3.0	4	2.0	4	2.0	4	1.0	2	1.0	2	*	*	*	*
6	3.0	4	3.0	4	2.0	3	2.0	3	1.0	2	1.0	2	*	*	*	*
7	2.5	3	2.5	3	1.0	2	1.0	2	0.7	2	0.0	2	*	*	*	*
Max	3	4	3	4	3	4	3	4	1	2	1	2	1	2	1	2

*Given an apparent lack of structure, no further analyses were conducted for these K values.

table S3. Genome-wide pairwise differentiation (F_{ST}) of populations.

Category	Code	Comparison	<i>Agaricia fragilis</i>		<i>Stephanocoenia intersepta</i>	
			Pairwise Fst	SD	Pairwise Fst	SD
Between-depths	Habt.G	GS vs GD	0.044362993	0.13073676	0.0006686492	0.04543634
	Habt.J	JS vs JD	0.058421089	0.15207999	-0.0029964692	0.04681601
	Habt.P	PS vs PD	0.044208650	0.12486853	-0.0013645180	0.04008300
Within-shallow	Shal.GJ	GS vs JS	0.003175759	0.08125830	-0.0031695622	0.04477598
	Shal.JP	JS vs PS	0.012652416	0.09337787	-0.0041312842	0.04012289
	Shal.GP	GS vs PS	0.013741802	0.09850756	-0.0011748328	0.03819686
Within-deep	Deep.GJ	GD vs JD	0.011968014	0.09466032	0.0018560410	0.04751326
	Deep.JP	JD vs PD	0.011920970	0.07991237	0.0010777546	0.04670673
	Deep.GP	GD vs PD	0.001320425	0.06945603	0.0006181086	0.04393596
Within-deep-west	West.GW	GD vs WD	0.041809349	0.12038205	-0.0012076287	0.04448286
	West.JW	JD vs WD	0.041948989	0.11847511	-0.0013961982	0.04609704
	West.PW	PD vs WD	0.034801295	0.10693032	-0.0001315717	0.04390589