

Supporting Information

Ziemert et al. 10.1073/pnas.1324161111

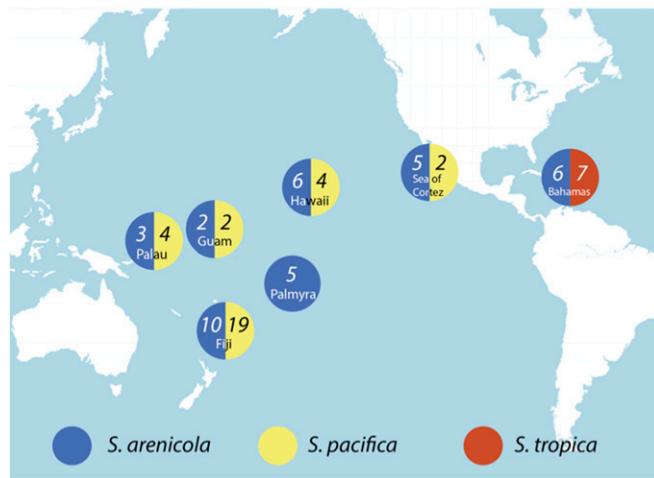


Fig. S1. Geographic origin and numbers of *Salinispore* strains used in this study.

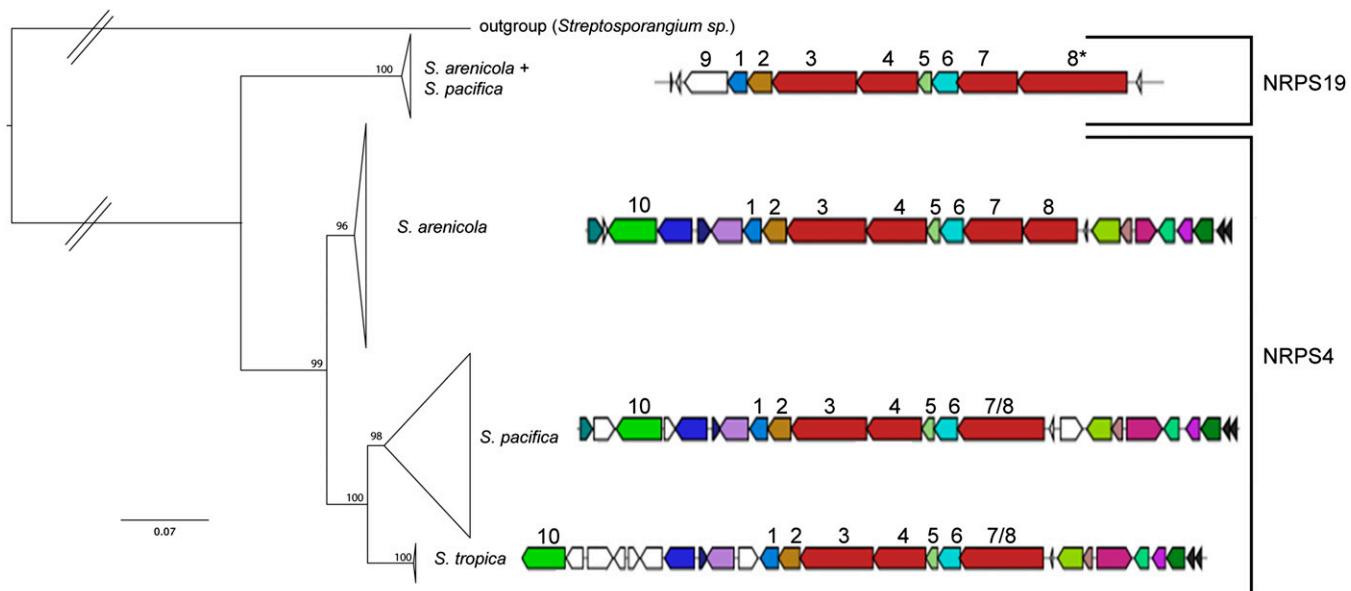


Fig. S2. Operational biosynthetic unit (OBU) phylogeny supports duplication followed by divergence. Nonribosomal peptide synthetase (NRPS)4 was detected in all but one of the 75 *Salinispore* strains. NRPS19 was placed in a separate OBU that shared ca. 80% homologous C-domain sequence identity with NRPS4. It possesses an additional C domain in the NRPS gene Orf8 and was observed in 16 *S. arenicola* and *S. pacifica* strains. Individual phylogenies of the NRPS genes orf3 and 4 and the kynurenine monooxygenase orf6 from these two pathways all revealed a sister relationship between the NRPS4 and NRPS19 clades, which can best be explained by a duplication event. The products of these pathways have yet to be identified. 1, methyltransferase; 2, major facilitator superfamily; 3, NRPS; 4, NRPS; 5, MbtH; 6, kynurenine-3-monooxygenase; 7, NRPS; 8, NRPS; 9, lantibiotic dehydratase; 10, penicillin amidase.

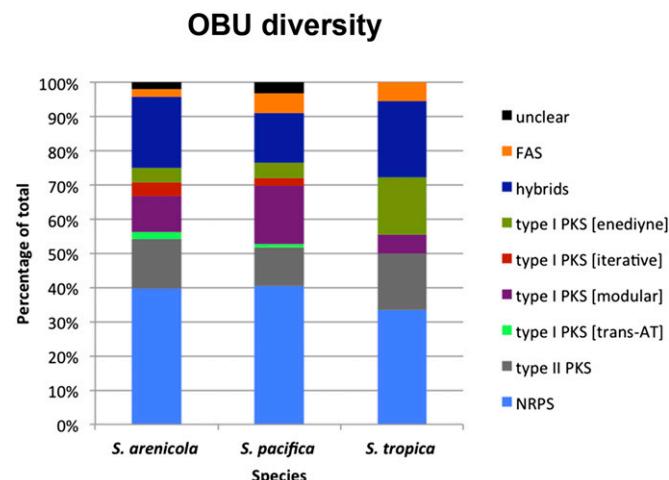


Fig. S3. Polyketide synthase (PKS) and NRPS relative abundance and NaDPoS PKS classification (1). FAS, fatty acid synthase.

1. Ziemert N, et al. (2012) The natural product domain seeker NaPDoS: A phylogeny based bioinformatic tool to classify secondary metabolite gene diversity. *PLoS ONE* 7(3):e34064.

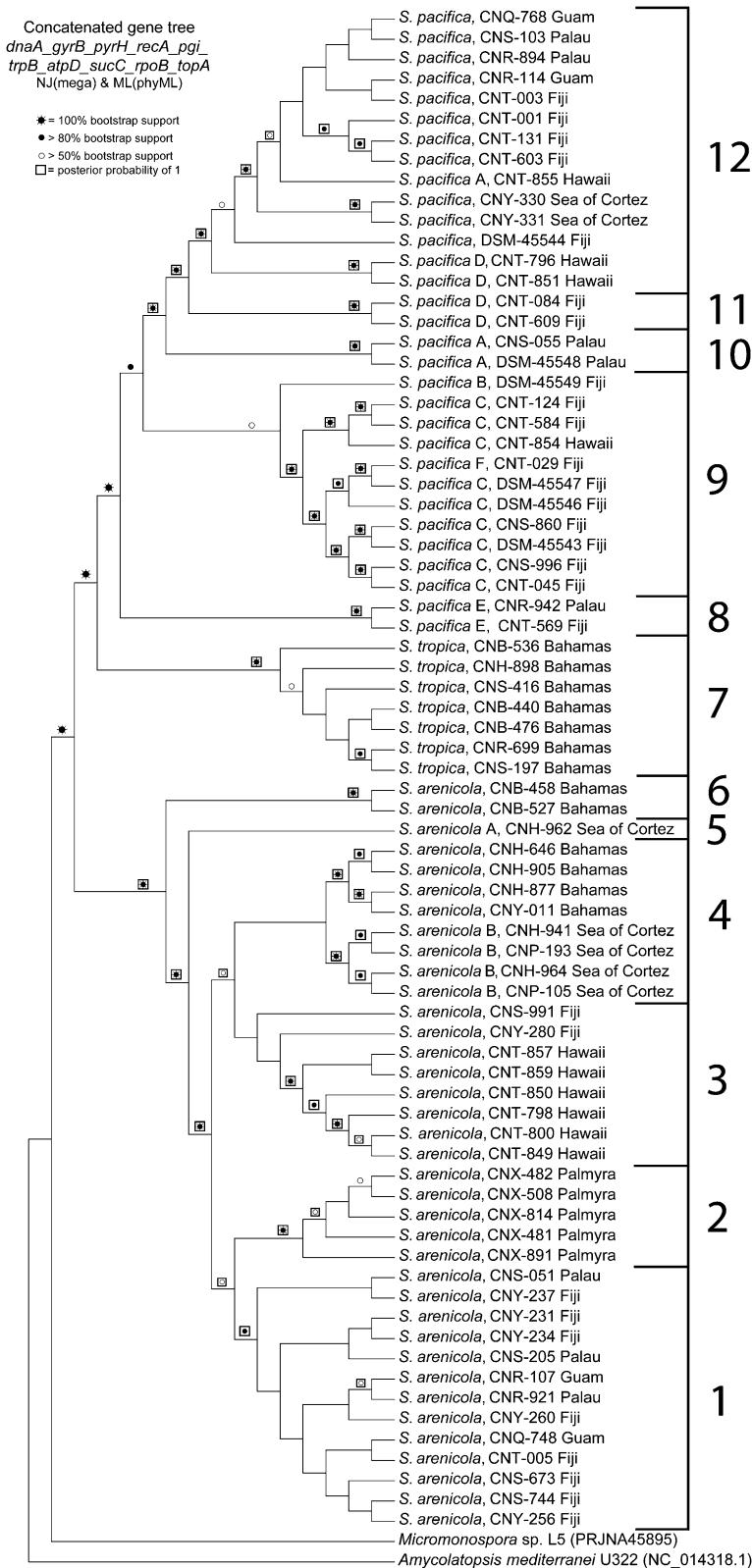


Fig. S4. *Salinispore* species phylogeny. Concatenated maximum-likelihood phylogeny based on 10 loci (*dnaA*, *gyrB*, *pyrH*, *recA*, *pgi*, *trpB*, *atpD*, *sucC*, *rpoB*, *topA*) derived from the genome sequence data. Strain names are followed by a capitalized letter, which indicates the 16S rRNA sequence type and geographic origin. No letter indicates standard (ST) sequence type as previously described (1). Bootstrap support for maximum-likelihood and neighbor-joining methods was the same and is indicated along with Bayesian posterior probabilities. Numbers on the right indicate major clades used in Fig. 5.

1. Frell KC, Edlund A, Jensen PR (2012) Microdiversity and evidence for high dispersal rates in the marine actinomycete '*Salinispore pacifica*'.' *Environ Microbiol* 14(2):480–493.

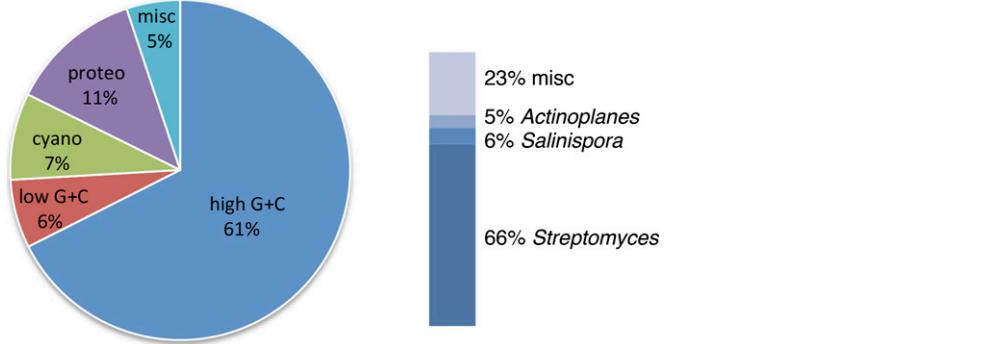


Fig. S5. Taxonomic assignments of top BLAST matches for OBUs observed in one strain (singletons). Cyano, cyanobacteria; proteo, proteobacteria.

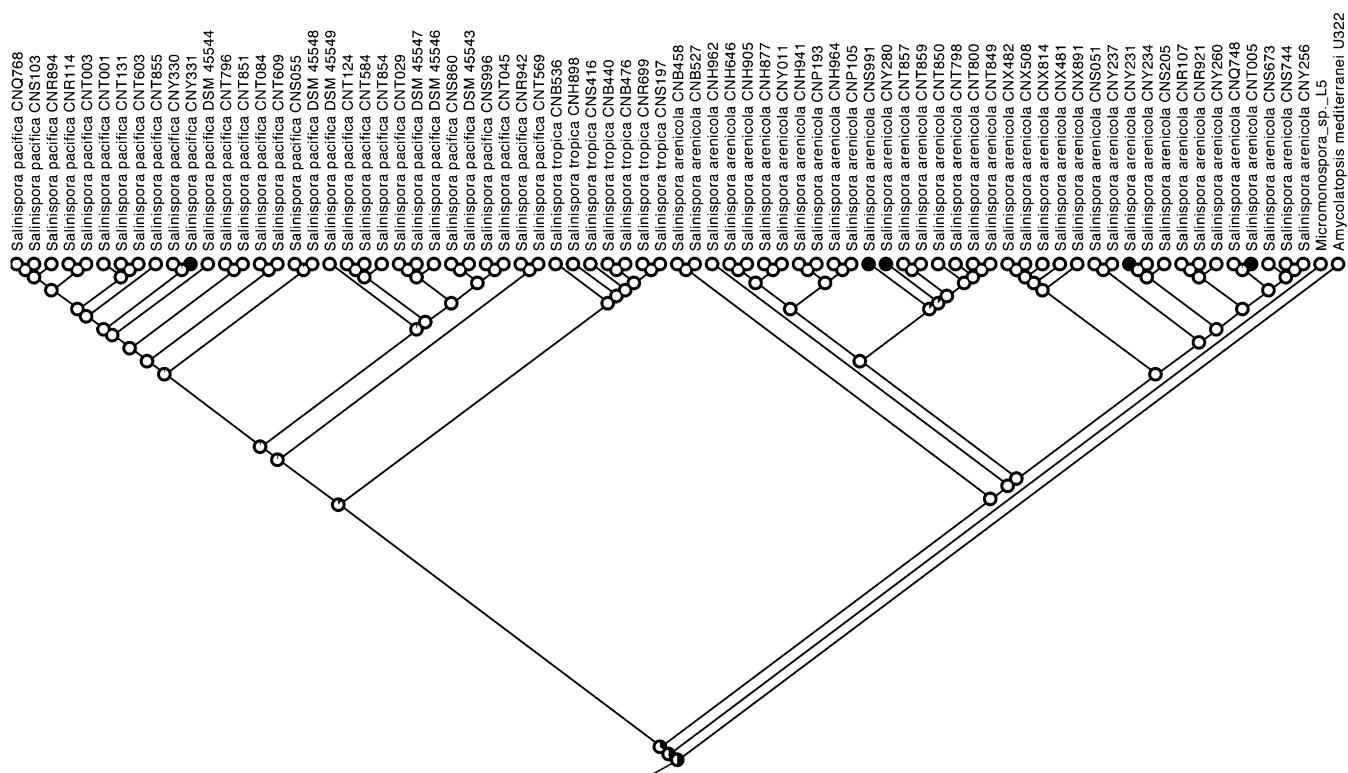


Fig. S6. Location-specific pathway acquisition. Likelihood analysis showing multiple ancestral nodes for PKS17 on the *Salinisporea* species tree (black circles). This result was used to infer that the OBU had been acquired independently by four *S. arenicola* strains from Fiji (CNS-991, CNT-005, CNY-231, and CNY-280) and one *S. pacifica* strain from the Sea of Cortex (CNY-331).

Table S1. *Salinisporea* strains and sequence accession numbers

Species and strain	IMG genome ID	NCBI taxon ID
<i>S. arenicola</i> CNB-458	2517572210	1136425
<i>S. arenicola</i> CNB-527	2515154093	1137250
<i>S. arenicola</i> CNH-646	2515154181	1136427
<i>S. arenicola</i> CNH-877	2519103192	1169176
<i>S. arenicola</i> CNH-905	2515154183	1137251
<i>S. arenicola</i> CNH-941	2515154193	1137252
<i>S. arenicola</i> CNH-962	2519103193	1169175
<i>S. arenicola</i> CNH-964	2515154125	1136430
<i>S. arenicola</i> CNP-105	2518285551	1169174
<i>S. arenicola</i> CNP-193	2518285552	1169170
<i>S. arenicola</i> CNQ-748	2515154180	1144929
<i>S. arenicola</i> CNR-107	2519103194	1169167
<i>S. arenicola</i> CNR-921	2515154203	1136429
<i>S. arenicola</i> CNS-205	641228504	391037
<i>S. arenicola</i> CNS-991	2516143022	999546
<i>S. arenicola</i> CNS-051	2518285553	1169178
<i>S. arenicola</i> CNS-673	2519103185	1144930
<i>S. arenicola</i> CNS-744	2518285554	1169168
<i>S. arenicola</i> CNT-005	2517572137	1137255
<i>S. arenicola</i> CNT-798	2515154186	1137256
<i>S. arenicola</i> CNT-800	2515154088	1137253
<i>S. arenicola</i> CNT-850	2515154135	1136428
<i>S. arenicola</i> CNT-857	2515154127	1137254
<i>S. arenicola</i> CNT-859	2517572233	1169163
<i>S. arenicola</i> CNX-481	2518285555	1169169
<i>S. arenicola</i> CNX-482	2515154137	1136426
<i>S. arenicola</i> CNX-508	2515154188	1137257
<i>S. arenicola</i> CNX-814	2517572152	1169171
<i>S. arenicola</i> CNX-891	2515154187	1137258
<i>S. arenicola</i> CNY-011	2517572153	1169162
<i>S. arenicola</i> CNY-231	2518285558	1169179
<i>S. arenicola</i> CNY-234	2519103195	1169165
<i>S. arenicola</i> CNY-256	2518285559	1169166
<i>S. arenicola</i> CNY-260	2518285560	1169177
<i>S. arenicola</i> CNY-280	2517572154	1169173
<i>S. pacifica</i> CNQ-768	2517572155	1169193
<i>S. pacifica</i> CNR-114	2515154178	1137260
<i>S. pacifica</i> CNR-894	2515154194	1137261
<i>S. pacifica</i> CNR-942	2518285561	1169187
<i>S. pacifica</i> CNS-055	2518285562	1169182
<i>S. pacifica</i> CNS-103	2515154129	1137262
<i>S. pacifica</i> CNS-860	2518285563	1169186
<i>S. pacifica</i> CNS-996	2517572157	1169189
<i>S. pacifica</i> CNT-001	2515154184	1136416
<i>S. pacifica</i> CNT-003	2515154126	1136417
<i>S. pacifica</i> CNT-029	2515154177	1136418
<i>S. pacifica</i> CNT-045	2517572158	1169190
<i>S. pacifica</i> CNT-084	2515154202	1136419
<i>S. pacifica</i> CNT-124	2517572159	1169188
<i>S. pacifica</i> CNT-131	2515154200	1136420
<i>S. pacifica</i> CNT-569	2515154124	1137263
<i>S. pacifica</i> CNT-584	2517572160	1169191
<i>S. pacifica</i> CNT-603	2515154185	1136424
<i>S. pacifica</i> CNT-609	2517572161	1169184
<i>S. pacifica</i> CNT-796	2515154182	1206102
<i>S. pacifica</i> CNT-849	2518285550	1137264
<i>S. pacifica</i> CNT-851	2517572162	1169180
<i>S. pacifica</i> CNT-854	2515154170	1137265
<i>S. pacifica</i> CNT-855	2515154128	1137266
<i>S. pacifica</i> CNY-237	2517572163	1169185
<i>S. pacifica</i> CNY-330	2518645626	1169192
<i>S. pacifica</i> CNY-331	2518645627	1169181
<i>S. pacifica</i> DSM-45543	2517572194	168694

Table S1. Cont.

Species and strain	IMG genome ID	NCBI taxon ID
<i>S. pacifica</i> DSM-45544	2517287019	999543
<i>S. pacifica</i> DSM-45546	2516653042	1050198
<i>S. pacifica</i> DSM-45547	2516493032	1050199
<i>S. pacifica</i> DSM-45548	2517287023	999544
<i>S. pacifica</i> DSM-45549	2517434008	999545
<i>S. tropica</i> CNB-440	640427140	369723
<i>S. tropica</i> CNB-476	2517572211	1137247
<i>S. tropica</i> CNB-536	2517572212	1136431
<i>S. tropica</i> CNH-898	2515154094	1137248
<i>S. tropica</i> CNR-699	2518645624	1169198
<i>S. tropica</i> CNS-197	2515154163	1137249
<i>S. tropica</i> CNS-416	2517572164	1169195

IMG, Integrated Microbial Genomes database; NCBI, National Center for Biotechnology Information.

Table S2. Pathway (OBU) distributions among *Salinispore arenicola* strains

Table S3. Pathway (OBU) distributions among *Salinispora tropica* strains

Pathway	Strain						
	CNB-440	CNB-476	CNB-536	CNH-898	CNS-197	CNS-416	CNR-699
PKS4	1	1	1	1	1	1	1
FAS1	1	1	1	1	1	1	1
NRPS4	1	1	1	1	1	1	1
lym	1	1	1	1	1	1	1
Sid1	1	1	1	1	1	1	1
lom	1	1	1	1	1	1	1
slm	1	1	1	1	1	1	1
sal	1	1	1	1	1	1	1
Sid3	1	1	1	1	1	1	1
Sid4	1	1	1	1	1	1	1
NRPS3	1	1	0	1	1	1	1
spo	1	1	0	1	1	1	1
STpks1	1	0	0	0	1	0	1
FAS5	0	0	1	1	0	0	0
NRPS36	0	0	1	1	0	0	0
cya	0	0	1	0	0	0	0
PKS41	0	0	1	0	0	0	0
PKS42	0	0	0	1	0	0	0
NRPS41	0	0	0	1	0	0	0

Table S4. Pathway (OBU) distributions among *Salinispora pacifica* strains

Pathway	PK54	CNY-331
	FA51	CNY-330
NRP54	1	1
cya	1	1
lym	1	1
lom	1	1
NRP520	0	1
PK516	1	1
slm	1	1
NRP519	1	1
NRP516	1	1
NRP519	1	1
PK525	0	1
NRP528	0	1
NRP51	0	1
sal	0	1
SID1	0	1
NRP527	0	1
PK512	1	1
FAS3	0	1
NRP543	0	1
PK544	0	1
NRP521	0	1
NRP522	0	1
NRP542	0	1
SID3	0	1
SID4	0	1
PK59	0	1
PK531	0	1
NRP510	0	1
NRP537	0	1
PK52	0	1
NRP53	0	1
spo	0	1
STPK51	0	1
PK528	0	1
PK510	0	1
PK520	0	1
FA52	0	1
PK522	0	1
PK524	0	1
PK526	0	1
PK527	0	1
PK532	0	1
PK533	0	1

Table S4. Cont.

Pathway	Strain
PKS34	CNY-331
PKS35	CNY-330
PKS43	CNT-796
PKS47	CNT-855
PKS49	CNT-854
PKS53	CNT-851
PKS54	CNT-609
PKS56	CNT-603
PKS26	CNT-584
NRPS32	CNT-569
NRPS33	DSM45549
NRPS49	DSM45548
PKS17	DSM45547
FAS5	DSM45546
NRPS36	CNT-131
PKS8	CNT-124
PKS23	CNT-084
FAS4	CNT-045
PKS29	CNT-029
PKS30	CNT-003
PKS36	CNT-001
PKS37	CNS-996
PKS38	DSM45544
PKS39	DSM45543
PKS40	CNS-860
PKS41	CNS-103
PKS42	CNR-942
PKS43	CNR-894
PKS44	CNR-114
PKS45	CNS-055
PKS46	CND-768
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