Supplementary Material

**Rapid shifts in bacterial communities and homogeneity of Symbiodiniaceae in colonies of *Pocillopora acuta* transplanted between reef and mangrove environments**

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**Supplementary Figures and Tables**

**Supplementary Table S1.** Environmental parameters in the mangrove and reef environments at each time point ( t0, t3D, t2M, t3M, t6M, t9M) during the nine month transplant experiment. N=3 for pH, salinity, oxygen and temperature measurements, SE = standard error of the mean.

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| **Mangrove** |
|  | **pH** | **Salinity** | **O2 (mg/L)** | **Temp (°C)** |
|  | **Average** | **SE** | **Average** | **SE** | **Average** | **SE** | **Average** | **SE** |
| **t0** | 7.759 | 0.005 | 34.167 | 0.033 | 3.180 | 0.020 | 24.4 | 0.066 |
| **t3D** | 7.744 | 0.007 | 34.200 | 0.000 | 3.303 | 0.124 | 24.4 | 0.01 |
| **t2M** | 7.781 | 0.014 | 33.933 | 0.033 | 3.043 | 0.003 | 24.0 | 0.066 |
| **t3M** | 7.807 | 0.004 | 34.000 | 0.000 | 4.106 | 0.012 | 23.0 | 0.033 |
| **t6M** | 7.625 | 0.012 | 34.167 | 0.033 | 2.516 | 0.013 | 29.5 | 0.066 |
| **t9M** | 7.717 | 0.007 | 33.900 | 0.000 | 3.393 | 0.308 | 29.8 | 0.033 |
| **Reef** |
|  | **pH** | **Salinity** | **O2 (mg/L)** | **Temp (°C)** |
|  | **Average** | **SE** | **Average** | **SE** | **Average** | **SE** | **Average** | **SE** |
| **t0** | 8.064 | 0.012 | 35.133 | 0.067 | 6.37 | 0.040 | 24.1 | 0.00 |
| **t3D** | 8.100 | 0.005 | 35.100 | 0.000 | 6.18 | 0.055 | 24.1 | 0.06 |
| **t2M** | 8.079 | 0.001 | 35.033 | 0.033 | 6.80 | 0.046 | 23.7 | 0.03 |
| **t3M** | 8.111 | 0.005 | 35.167 | 0.033 | 6.52 | 0.03 | 22.8 | 0.03 |
| **t6M** | 8.084 | 0.006 | 35.033 | 0.033 | 6.62 | 0.035 | 28.3 | 0.00 |
| **t9M** | 8.095 | 0.005 | 35.167 | 0.067 | 6.44 | 0.037 | 28.9 | 0.03 |

**Supplementary Table S2.** PERMANOVA analysis of Symbiodiniaceae communities associated with *Pocillopora acuta* between mangrove (n=10) and reef environments (n=9) prior to transplantation (t0). df = degrees of freedom; SS = sum of squares; MS = mean sum of squares; Pseudo-F = F-value by permutation, *p* = *p*-value

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| **Source** | **df** | **SS** | **MS** | **Pseudo-F** | **R2** | **P (perm)** |
| **Sites** | 1 | 37985 | 37985 | 39.861 | .996 | .001 |
| **Residuals** | 18 | 171.53 |  |  |  |  |

**Supplementary Table S3.** Two-factorial PERMANOVA analysis of Symbiodiniaceae communities associated with *Pocillopora acuta* between transplantation time points (t0 and t9M) of treatments; mangrove-mangrove (MM), mangrove-reef (MR), reef-reef (RR) and reef-mangrove (RM). df = degrees of freedom; SS = sum of squares; MS = mean sum of squares; Pseudo-F = F-value by permutation, *p* = *p*-value.

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| **Main PERMANOVA Test** | **Pairwise (t0-t9M)** |
| **Source** | **df** | **SS** | **MS** | **Pseudo-F** | **R2** | ***p* (perm)** | **Groups** | ***t*** | ***p* (perm)** |
| **Timepoint** | 1 | 354.38 | 354.38 | 0.47304 | .005 | .712 | MM | 0.12869 | 0.948 |
| **Site** | 3 | 64607 | 21536 | 28.747 | .982 | 0.001 | MR | 0.7637 | 0.636 |
| **Timepoint x Site** | 3 | 652.26 | 217.42 | 0.29022 | .010 | 0.987 | RR | 0.64504 | 0.691 |
| **Residuals** | 25 | 187.29 |  |  |  |  | RM | 0.59985 | 0.677 |

**Supplementary Table S4.** Summary of sequence counts from 16S rRNA Illumina sequencing in bacterial communities of *Pocillopora acuta* samples among treatments; mangrove-mangrove (MM), mangrove-reef (MR), reef-reef (RR) and reef-mangrove (RM).

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| --- | --- | --- | --- |
| **Sample replicates** | **Number of raw sequences** | **Treatment** | **Site of origin** |
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| t0-1 |
| t0-2 |
| t0-3 |
| t0-4 |
| t0-5 |
| t0-6 |
| t0-7 |
| t0-8 |
| t0-9 |
| t0-10 |
| t0-11 |
| t0-12 |
| t0-13 |
| t0-14 |
| t0-15 |
| t0-16 |
| t0-17 |
| t0-18 |
| t0-19 |
| t0-20 |
| t3D-1 |
| t3D-2 |
| t3D-3 |
| t3D-4 |
| t3D-5 |
| t3D-6 |
| t3D-7 |
| t3D-9 |
| t3D-10 |
| t3D-11 |
| t3D-12 |
| t3D-13 |
| t3D-14 |
| t3D-15 |
| t3D-16 |
| t3D-17 |
| t3D-18 |
| t3D-19 |
| t3D-20 |
| t2M-1 |
| t2M-2 |
| t2M-3 |
| t2M-4 |
| t2M-5 |
| t2M-6 |
| t2M-7 |
| t2M-8 |
| t2M-9 |
| t2M-10 |
| t2M-11 |
| t2M-12 |
| t2M-13 |
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| t2M-16 |
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| t2M-18 |
| t2M-19 |
| t2M-20 |
| t3M-1 |
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| t3M-13 |
| t3M-14 |
| t3M-15 |
| t3M-16 |
| t3M-17 |
| t3M-19 |
| t3M-20 |
| t6M-1 |
| t6M-2 |
| t6M-3 |
| t6M-4 |
| t6M-5 |
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| t6M-16 |
| t6M-17 |
| t6M-18 |
| t6M-19 |
| t6M-20 |
| t9M-1 |
| t9m-3 |
| t9m-4 |
| t9m-5 |
| t9m-6 |
| t9m-8 |
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| 158897 |
| 34792 |
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| 132257 |
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**Supplementary Table S5.** PERMANOVA analysis of Amplicon Sequence Variant (ASVs) richness (Chao1) and diversity (Shannon’s) present in *Pocillopora acuta* between mangrove (n=10) and reef (n=10) environmentsprior to transplantation(t0). df = degrees of freedom; SS = sum of squares; MS = mean sum of squares; Pseudo-F = F-value by permutation, *p* = *p*-value.

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| **Chao1**  | **Source** | **df** | **SS** | **MS** | **Pseudo-F** | **R2** | ***p* (perm)** |
|  | **Sites** | 1 | 9698.8 | 9698.8 | 13.127 | .416 | 0.001 |
|  | **Residuals** | 18 | 13573 |  |  |  |  |
| **Shannon’s** | **Source** | **df** | **SS** | **MS** | **Pseudo-F** | **R2** | ***p* (perm)** |
|  | **Sites** | 1 | 1378.2 | 1378.2 | 19.443 | .519 | 0.001 |
|  | **Residuals** | 18 | 1275.9 |  |  |  |  |



**Supplementary Figure S1.** Bacterial community composition of the coral *Pocillopora acuta* shown as relative abundance (%) across transplantation treatments; mangrove-mangrove, mangrove-reef, reef-mangrove and reef-reef, and between timepoints t0 (prior to transplantation) and t9M (nine months after transplantation). Each proportion is > 1% relative abundance of bacterial families based on 16S rRNA sequencing (Illumina MiSeq) that matched to one phylogenetic group from the Silva v138 database. Top grey bars represent all other families < 1% relative abundance. Each bar represents an individual replicate.

**Supplementary Table S6.** PERMANOVA analysis of bacterial communities (beta diversity) present between mangrove (n=10) and reef (n=10) environments at t0. df = degrees of freedom; SS = sum of squares; MS = mean sum of squares; Pseudo-F = F-value by permutation, *p* = *p*-value.

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| --- | --- | --- | --- | --- | --- | --- |
| **Source** | **df** | **SS** | **MS** | **Pseudo-F** | **R2** | ***p* (perm)** |
| **Site** | 1 | 9969.1 | 9969.3 | 2.6004 | .126 | 0.001 |
| **Residuals** | 18 | 69007 | 3833.7 |  |  |  |

**Supplementary Table S7.** MetagenomeSeq analysis of significantly differentially abundant bacterial families (*p* < 0.05, following FDR corrections) present in the microbiome of *Pocillopora acuta* between mangrove (n=10) and reef (n=10) environments. Family name is provided where possible.

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| **Taxonomic ID** | ***p*-value (corrected)** |
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| Sulfurovaceae |
| Endozoicomonadaceae |
| Milano\_WF1B\_44 |
| Desulfocapsaceae |
| B2M28 |
| Thermoanaerobaculaceae |
| Woeseiaceae |
| Methyloligellaceae |
| UC\_bacteria |
| Cyanobiaceae |
| Sporichthyaceae |
| UBA10353 |
| Thiomicrospiraceae |
| Bacillaceae |
| Anaerolineaceae |
| Marinococcaceae |
| Carnobacteriaceae |
| Lachnospiraceae |
| Rubritaleaceae |
| Microbulbiferaceae |
| Chromatiaceae |
| KI89A |
| Acaryochloridaceae |
| Microtrichaceae |
| Legionellaceae |
| Thiotrichaceae |
| Sedimenticolaceae |
| Rhizobiales |
| Vicinamibacteria |
| Saprospiraceae |
| KD4\_96 |
| Crocinitomicaceae |
| Flavobacteriaceae |
| Ectothiorhodospiraceae |
| HOC36 |
| Pseudomonadaceae |
| Cyclobacteriaceae |
| OM190 |
| Sandaracinaceae |
| Leuconostocaceae |
| Burkholderiaceae |
| Oxyphotobacteria |
| Geoalkalibacteraceae |
| Bacteroidetes |
| Corynebacteriaceae |
| Kiloniellaceae |
| Micrococcaceae |
| Oligoflexales |
| Sphingomonadaceae |
| Enterobacteriaceae |
| Thermaceae |
| Caldilineaceae |
| Halomonadaceae |
| PS1 |
| Prevotellaceae |
| Rhizobiaceae |
| Ilumatobacteraceae |
| PeM15 |
| Francisellaceae |
| Moraxellaceae |

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| 8.27E-13 |
| 8.27E-13 |
| 9.21E-12 |
| 1.89E-11 |
| 4.19E-11 |
| 6.32E-11 |
| 3.88E-10 |
| 3.98E-10 |
| 5.37E-10 |
| 6.01E-08 |
| 1.89E-06 |
| 2.12E-06 |
| 2.12E-06 |
| 2.59E-06 |
| 3.29E-06 |
| 3.90E-06 |
| 4.94E-06 |
| 1.07E-05 |
| 1.25E-05 |
| 1.31E-05 |
| 1.31E-05 |
| 1.31E-05 |
| 1.31E-05 |
| 1.32E-05 |
| 2.01E-05 |
| 2.88E-05 |
| 3.40E-05 |
| 4.90E-05 |
| 5.49E-05 |
| 8.57E-05 |
| 0.00013393 |
| 0.00013585 |
| 0.00014514 |
| 0.00015943 |
| 0.00015943 |
| 0.00017888 |
| 0.00017888 |
| 0.00024914 |
| 0.00027583 |
| 0.00034664 |
| 0.0015407 |
| 0.0018492 |
| 0.0019321 |
| 0.0024897 |
| 0.0030128 |
| 0.0038452 |
| 0.0038452 |
| 0.0055182 |
| 0.0067008 |
| 0.0067008 |
| 0.0070076 |
| 0.0081229 |
| 0.010025 |
| 0.014583 |
| 0.014583 |
| 0.016388 |
| 0.027788 |
| 0.038251 |
| 0.042801 |
| 0.045132 |

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**Supplementary Figure S2.** Bacterial diversity of ASVs associated with *Pocillopora acuta* between transplantation time points (t0 and t9M) and treatments; mangrove-mangrove (MM), mangrove-reef (MR), reef-mangrove (RM) and reef-reef (RR). Data based on chao1 and Shannon’s diversity index. Box plots represent 25th to 75th percentile range, lines show medians, error bars represent IQR and + represents the mean. N = 3-5 coral colonies (denoted with grey dots).

**Supplementary Table S8.** Two-factorialPERMANOVA analysis of Amplicon Sequence Variant (ASVs) richness (Chao1) and diversity (Shannon’s) present in *Pocillopora acuta* between transplantation time points (t0 and t9M) of treatments; mangrove-mangrove (MM), mangrove-reef (MR), reef-reef (RR) and reef-mangrove (RM). df = degrees of freedom; SS = sum of squares; MS = mean sum of squares; Pseudo-F = F-value by permutation, *p* = *p*-value.

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| **Chao1 index** |
| **Main PERMANOVA Test** | **Pairwise (t0-t9M)** |
| **Source** | **df** | **SS** | **MS** | **Pseudo F** | **R2** | ***p* (perm)** | **Groups** | ***t*** | ***p* (perm)** |
| **Site** | 3 | 7334.3 | 2444.8 | 3.6118 | .226 | 0.005 | MM | 1.1784 | 0.209 |
| **Time** | 1 | 720.19 | 720.19 | 1.064 | .022 | 0.335 | MR | 1.5035 | 0.172 |
| **Site x timepoints** | 3 | 6736.2 | 2245.4 | 3.3173 | .208 | 0.012 | RR | 2.1051 | 0.063 |
| **Residuals** | 26 | 17599 |  |  |  |  | RM | 1.7588 | 0.088 |
| **Shannon’s Index** |
| **Main PERMANOVA Test** | **Pairwise (t0-t9M)** |
| **Source** | **df** | **SS** | **MS** | **Pseudo F** | **R2** | ***p* (perm)** | **Groups** | ***t*** | ***p* (perm)** |
| **Site** | 3 | 270.97 | 90.324 | 4.1134 | .224 | 0.011 | MM | 1.2355 | 0.268 |
| **Time** | 1 | 3.7964 | 3.7946 | 0.17281 | .003 | 0.715 | MR | 4.3222 | 0.021 |
| **Site x timepoints** | 3 | 363.17 | 121.06 | 5.5129 | .30 | 0.005 | RR | 1.1569 | 0.276 |
| **Residuals** | 26 | 570.92 |  |  |  |  | RM | 0.1688 | 0.127 |

**Supplementary Table S9.** Two-factorial PERMANOVA analysis of bacterial communities (beta diversity) associated with *Pocillopora acuta* between transplantation time points ( t0, t3D, t2M, t3M, t6M, t9M) of treatments; mangrove-mangrove (MM), mangrove-reef (MR), reef-reef (RR) and reef-mangrove (RM), and additional comparisons of treatments; (RM and MM) and (MR and RR) at timepoint t9M. df = degrees of freedom; SS = sum of squares; MS = mean sum of squares; Pseudo-F = F-value by permutation, *p* = *p*-value.All pairwise comparison *p*-values have undergone FDR corrections.

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| **Main PERMANOVA test** |
| **Source** | **df** | **SS** | **MS** | **Pseudo-F** | **R2** | ***p* (perm)** |
| **Sites** | 1 | 9969.1 | 9969.3 | 2.6004 | .102 | .001 |
| **Timepoints** | 5 | 8867 | 8933.2 | 2.4501 | .091 | .001 |
| **Sites x timepoints** | 6 | 9925 | 9934.2 | 2.5498 | .102 | .001 |
| **Residuals** | 18 | 69007 |  |  |  |  |
| **Pairwise**  |
| **Factor** |  | **Groups tested** | ***t*** | ***p* (perm) corrected** |
| **Sites** | **Mangrove-mangrove** |  |  |  |
| t0-t3D | 1.3092 | .037 |
| t0-t2M | 1.2039 | .010 |
| t0-t3M | 1.2105 | .018 |
| t0-t6M | 1.2387 | .008 |
| t0-t9M | 1.2092 | .014 |
| **Mangrove-reef** |  |  |  |
| t0-t3D | 1.3609 | .038 |
| t0-t2M | 1.209 | .021 |
| t0-t3M | 1.1261 | .026 |
| t0-t6M | 1.1233 | .055 |
| t0-t9M | 1.1177 | .021 |
| **Reef-reef** |  |  |  |
| t0-t3D | 1.1816 | .112 |
| t0-t2M | 1.3436 | .035 |
| t0-t3M | 1.1455 | .110 |
| t0-t6M | 1.245 | .041 |
| t0-t9M | 1.1155 | .133 |
|  |  |  |
| **Reef-mangrove** | t0-t3D | 1.1052 | .302 |
| t0-t2M | 1.1119 | .109 |
| t0-t3M | 1.306 | .046 |
| t0-t6M | 1.2437 | .037 |
| t0-t9M | 1.2014 | .032 |
| **Timepoint** | **t9M** |  |  |  |
| RM-MM |  | .709 |
| MR-RR |  | .401 |

**Supplementary Table 10.** MetagenomeSeq analysis of significantly differentially abundant bacterial families (*p* < 0.05, following FDR corrections between timepoints (t0 vs t9M) in reef-mangrove *Pocillopora acuta* colonies. Family name is provided where possible.

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| **Taxonomic ID** | ***p*-value corrected** |
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| Endozoicomonadaceae |
| Microcystaceae |
| Pseudomonadaceae |
| Francisellaceae |
| Lachnospiraceae |
| Thermaceae |
| Rhizobiaceae |
| Halomonadaceae |
| Microtrichaceae |
| Ectothiorhodospiraceae |
| Micrococcaceae |
| Amoebophilaceae |
| Hyphomicrobiaceae |
| Thiotrichaceae |
| Bacillaceae |
| Kiloniellaceae |
| Rubritaleaceae |

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| --- |
| 0.00043821 |
| 0.0012067 |
| 0.0037592 |
| 0.0082632 |
| 0.0082632 |
| 0.0082632 |
| 0.020627 |
| 0.023417 |
| 0.024735 |
| 0.024735 |
| 0.024735 |
| 0.024735 |
| 0.024735 |
| 0.025288 |
| 0.027044 |
| 0.042917 |
| 0.048142 |

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**Supplementary Table S11.**  MetagenomeSeq analysis of significantly differentially abundant bacterial families (*p* < 0.05, following FDR corrections between timepoints (t0 vs t9M) in mangrove-reef ) *Pocillopora acuta* colonies. Family name is provided where possible.

|  |  |
| --- | --- |
| **Taxonomic ID** | ***p*-value corrected** |
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| Milano\_WF1B\_44 |
| Endozoicomonadaceae |
| Cyanobiaceae |
| Halieaceae |
| Anaerolineaceae |
| Desulfocapsaceae |
| Methyloligellaceae |
| Marinococcaceae |
| Kiloniellaceae |

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| --- |
| 0.0058214 |
| 0.0058214 |
| 0.0058214 |
| 0.0058214 |
| 0.012298 |
| 0.015457 |
| 0.015994 |
| 0.030384 |
| 0.045709 |

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