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.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **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.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **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).

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample replicates** | **Number of raw sequences** | **Treatment** | **Site of origin** |
| |  | | --- | | 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 | | t2M-14 | | t2M-15 | | t2M-16 | | t2M-17 | | t2M-18 | | t2M-19 | | t2M-20 | | t3M-1 | | t3M-2 | | t3M-3 | | t3M-4 | | t3M-5 | | t3M-6 | | t3M-7 | | t3M-8 | | t3M-9 | | t3M-10 | | t3M-11 | | t3M-13 | | t3M-14 | | t3M-15 | | t3M-16 | | t3M-17 | | t3M-19 | | t3M-20 | | t6M-1 | | t6M-2 | | t6M-3 | | t6M-4 | | t6M-5 | | t6M-6 | | t6M-7 | | t6M-8 | | t6M-9 | | t6M-10 | | t6M-11 | | t6M-13 | | t6M-14 | | t6M-15 | | t6M-16 | | t6M-17 | | t6M-18 | | t6M-19 | | t6M-20 | | t9M-1 | | t9m-3 | | t9m-4 | | t9m-5 | | t9m-6 | | t9m-8 | | t9m-10 | | t9m-11 | | t9m-13 | | t9m-15 | | t9m-16 | | t9m-18 | | t9m-19 | | t9m-20 | | |  | | --- | | 158897 | | 34792 | | 47295 | | 36099 | | 49682 | | 114896 | | 107011 | | 101951 | | 111801 | | 110544 | | 101444 | | 27590 | | 33987 | | 62873 | | 100611 | | 75285 | | 135673 | | 117309 | | 110663 | | 64707 | | 156886 | | 121053 | | 103909 | | 51547 | | 58334 | | 37218 | | 12804 | | 29191 | | 80153 | | 79932 | | 24591 | | 132257 | | 111073 | | 60153 | | 33822 | | 104861 | | 140651 | | 54223 | | 20374 | | 159592 | | 95577 | | 119940 | | 17760 | | 121710 | | 133114 | | 122225 | | 93906 | | 157030 | | 101082 | | 95163 | | 34243 | | 155969 | | 149718 | | 118458 | | 37087 | | 93722 | | 84546 | | 51056 | | 55088 | | 105978 | | 84398 | | 32270 | | 35161 | | 137431 | | 97290 | | 83473 | | 84788 | | 164128 | | 143359 | | 97208 | | 106145 | | 118944 | | 127245 | | 52110 | | 142246 | | 25522 | | 88976 | | 130113 | | 86473 | | 148496 | | 74922 | | 98394 | | 81698 | | 47939 | | 39535 | | 123413 | | 120922 | | 103680 | | 108103 | | 134014 | | 88238 | | 181694 | | 117713 | | 163512 | | 151590 | | 220769 | | 162779 | | 170208 | | 144651 | | 99035 | | 110702 | | 91397 | | 78036 | | 139880 | | 75297 | | 105761 | | 21097 | | 168392 | | 162330 | | 140953 | | |  | | --- | | RR | | RR | | RR | | RR | | RR | | RM | | RM | | RM | | RM | | RM | | MR | | MR | | MR | | MR | | MR | | MM | | MM | | MM | | MM | | MM | | RR | | RR | | RR | | RR | | RR | | RM | | RM | | RM | | RM | | MR | | MR | | MR | | MR | | MR | | MM | | MM | | MM | | MM | | MM | | RR | | RR | | RR | | RR | | RR | | RM | | RM | | RM | | RM | | RM | | MR | | MR | | MR | | MR | | MR | | MM | | MM | | MM | | MM | | MM | | RR | | RR | | RR | | RR | | RR | | RM | | RM | | RM | | RM | | RM | | MR | | MR | | MR | | MR | | MM | | MM | | MM | | MM | | RR | | RR | | RR | | RR | | RR | | RM | | RM | | RM | | RM | | RM | | MR | | MR | | MR | | MR | | MM | | MM | | MM | | MM | | MM | | RR | | RR | | RR | | RR | | RM | | RM | | RM | | MR | | MR | | MR | | MM | | MM | | MM | | MM | | |  | | --- | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | reef | | reef | | reef | | reef | | reef | | reef | | reef | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | | mangrove | |

**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.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **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.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **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.

|  |  |
| --- | --- |
| **Taxonomic ID** | ***p*-value (corrected)** |
| |  | | --- | | 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 | | |  | | --- | | 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 | |



**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.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **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.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **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.

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

**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** |
| |  | | --- | | Milano\_WF1B\_44 | | Endozoicomonadaceae | | Cyanobiaceae | | Halieaceae | | Anaerolineaceae | | Desulfocapsaceae | | Methyloligellaceae | | Marinococcaceae | | Kiloniellaceae | | |  | | --- | | 0.0058214 | | 0.0058214 | | 0.0058214 | | 0.0058214 | | 0.012298 | | 0.015457 | | 0.015994 | | 0.030384 | | 0.045709 | |