**Supplementary Materials**

**Table S1.** Centrifugation separation of symbionts (S) and their coral host tissue (H).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Coral species | Initial centrifugation (rcf) | Sample type | 1st centrifugation (rcf) | 2nd centrifugation (rcf) | 3rd centrifugation (rcf) |
| *Acropora samoensis* | 300 | S | 200 | 150 | 100 |
| H | 200 | 300 | 450 |
| *Pavona decussata* | 350 | S | 300 | 200 | 150 |
| H | 200 | 300 | 450 |
| *Turbinaria peltata* | 400 | S | 350 | 300 | 200 |
| H | 200 | 300 | 450 |
| *Favites abdita* | 450 | S | 300 | 250 | 200 |
| H | 200 | 300 | 450 |
| *Platygyra carnosa* | 800 | S | 650 | 450 | 350 |
| H | 450 | 650 | 800 |

***Calibration standards for GC-MS***

GC-MS is a highly sensitive, efficient, and reproducible analytical technique which can be used to quantitate fatty acids and has been routinely used for decades. ISTD must be kept constant across all samples and calibration standards as relative responses are used to create calibration curves (Table S2). The responses of the FAME standards are normalized to the response of ISTD (relative response). We applied nonadecanoic acid (19:0) as internal standard.

**Table S2.** Preparation for calibration standards of FAMEs containing INSTD.

|  |  |  |  |
| --- | --- | --- | --- |
| FAME mix (ul) | Dichlroromethane (ul) | ISTD (ul) | Final volume (ul) |
| 5 | 45 | 50 | 100 |
| 10 | 40 | 50 | 100 |
| 20 | 30 | 50 | 100 |
| 40 | 10 | 50 | 100 |
| 50 | 0 | 50 | 100 |

MSD Chemstation Data Analysis software was used to set up the calibration curve and to quantitate fatty acids. For the calibration curve, presence of qualifier ions in the correct amounts relative to the target ion gives evidence of the correct target compound identification. Target ion: qualifier ion response ratio will be automatically calculated (Table S3). For example, C18:0, Retention Time (RT): 12.44, Target 298.3, Q1 255.3, Target ion: qualifier ion response ratio equals 108.7, etc. Please refer to Table S3 for a list of selected specific target ions and qualifiers for the Supelco FAMEs mix. The peaks appeared on the chromatogram but were not included in the 37 FAMEs mix were quantified by semi-quantification method (Agilent Technologies, Inc. 2006). These unknown FA were preliminary identified applying the mass spectral library and determined as 18:4n-3, 22:5n-3 and 22:4n-6 in our samples. These FA were subsequently quantified by their relative response to internal standard (19:0).

**Table S3.** List of target ions and qualifier ions for fatty acids.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Compound | Target | Qualifier 1 | Qualifier 2 | Qualifier 3 |
| C16:1 | 268.3 | 236.3 | 194.2 | 152.2 |
| C16:0 | 270.3 | 239.3 | 227.2 | 143.1 |
| C17:1 | 282.3 | 250.3 | 208.2 | 166.2 |
| C17:0 | 284.3 | 253.3 | 241.2 | 199.2 |
| C18:3n3 | 292.1 | 194.1 | 150.1 | 107.1 |
| C18:2n6c | 294.3 | 263.1 | 150.1 | 123.1 |
| C18:1n9c | 296.3 | 264 | – | – |
| C18:2n6t | 294.3 | 266.2 | – | – |
| C18:3n6 | 292.3 | 222.4 | – | – |
| C18:1n9t | 235.2 | 123.1 | 166.2 | 111.1 |
| C18:0 | 298.3 | 255.3 | 199.2 | 143.1 |
| C20:4n6 | 203.2 | 150.2 | 133.1 | 119.1 |
| C20:5n3 | 201.2 | 180.1 | 133.1 | 119.1 |
| C20:3n3 | 320.3 | 289.3 | 222.2 | 177.2 |
| C20:2 | 322.2 | 391.3 | 150.1 | 123.1 |
| C20:1 | 324.3 | 292.3 | 250.3 | 208.2 |
| C20:3n6 | 320.3 | 289.3 | 264.1 | 149.1 |
| C20:0 | 326.4 | 283.3 | 199.2 | 143.1 |
| C21:0 | 340.4 | 297.3 | 199.2 | 143.1 |
| C22:6n3 | 159.1 | 145.1 | 131.1 | 119.1 |
| C22:2 | 350.4 | 319.3 | 109.1 | 95.1 |
| C22:1n9 | 320.4 | 352.4 | 278.3 | 236.3 |
| C22:0 | 354.4 | 311.3 | 255.3 | 143.1 |
| C23:0 | 368.4 | 325.4 | 269.3 | 143.1 |
| C24:1 | 348.4 | 380.4 | 306.3 | 264.3 |
| C24:0 | 382.5 | 339.4 | 283.3 | 143.1 |

**Table S4.** Similarity percent (SIMPER) analysis within group to evaluate the contribution (shown up to 50% in the table) of abundant fatty acids to the five different groups clustered by non-metric multi-dimensional scaling (nMDS) plot shown in Fig. 3.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Group (similarity) | FA | Av. Abund (%) | Av. Sim | Sim/SD | Con (%) | Cum (%) |
| *Acropora samoensis*  *(93.0)* | 16:0 | 31.1 | 13.7 | 16.2 | 14.7 | 14.7 |
| 18:0 | 14.4 | 9.7 | 13.8 | 10.4 | 25.1 |
| 18:3n-3 | 12.0 | 8.9 | 25.7 | 9.5 | 34.6 |
| 20:4n-6 | 7.2 | 7.1 | 23.4 | 7.6 | 42.2 |
| 22:6n-3 | 6.6 | 6.8 | 18.1 | 7.3 | 49.5 |
| *Pavona decussata*  *(96.10)* | 16:0 | 50.4 | 22.0 | 69.7 | 22.9 | 22.9 |
| 18:0 | 18.4 | 13.2 | 61.4 | 13.7 | 36.6 |
| 18:3n-6 | 5.0 | 6.7 | 25.5 | 6.9 | 43.5 |
| 18:1n-9 | 4.2 | 6.3 | 21.1 | 6.6 | 50.1 |
| *Turbinaria peltata*  *(94.14)* | 18:0 | 35.4 | 19.2 | 19.8 | 20.4 | 20.4 |
| 16:0 | 31.6 | 18.3 | 26.5 | 19.4 | 39.8 |
| 20:4n-6 | 16.3 | 12.6 | 9.4 | 13.4 | 53.2 |
| *Favites abdita*  *(93.46)* | 16:0 | 36.2 | 18.4 | 34.8 | 19.7 | 19.7 |
| 18:0 | 23.1 | 14.2 | 53.1 | 15.2 | 34.8 |
| 20:4n-6 | 13.8 | 10.1 | 12.5 | 10.8 | 45.6 |
| 18:3n-6 | 5.7 | 6.5 | 13.1 | 6.9 | 52.5 |
| *Platygyra carnosa*  *(92.84)* | 16:0 | 36.0 | 17.7 | 34.1 | 19.0 | 19.0 |
| 20:4n-6 | 19.3 | 12.5 | 13.8 | 13.5 | 32.5 |
| 18:0 | 18.0 | 12.5 | 12.0 | 13.4 | 45.9 |
| 22:5n-3 | 6.4 | 7.2 | 13.7 | 7.8 | 53.7 |

All values of each group similarity are expressed in %.

FA: Fatty acids, Av. Abund: average abundance in each group, Av. Sim: the average similarity contributed by FA, Sim/SD: the ratio of similarity to standard deviation, Con: contribution of the FA to the overall similarity, Cum: additive overall similarity.

**Table S5.** Dissimilarity among groups from SIMPER analysis to evaluate the contribution (cut off contribution 50 %) of abundant fatty acids between two groups.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Groups (dissimilarity) | FA | Av. Abund 1 (%) | Av. Abund 2 (%) | Av. Diss | Diss/SD | Con (%) | Cum (%) |
| *Acropora samoensis*  *vs*  *Favites abdita*  *(19.6)* | 18:3n-3 | 12.0 | 2.7 | 3.4 | 8.1 | 17.5 | 17.5 |
| 20:5n-3 | 5.7 | 1.0 | 2.5 | 3.3 | 12.5 | 30.0 |
| 22:6n-3 | 6.6 | 2.5 | 2.2 | 4.1 | 11.0 | 41.1 |
| 20:1n-9 | 2.9 | 0.6 | 1.7 | 19.3 | 8.9 | 49.9 |
| *Acropora samoensis*  *vs*  *Platygyra carnosa*  *(22.3)* | 18:3n-3 | 12.0 | 0.9 | 4.2 | 7.7 | 18.7 | 18.7 |
| 20:5n-3 | 5.7 | 6.4 | 2.6 | 3.6 | 11.6 | 30.3 |
| 22:6n-3 | 6.6 | 2.2 | 2.1 | 6.5 | 9.4 | 39.6 |
| 20:1n-9 | 2.9 | 0.3 | 2.0 | 17.5 | 8.9 | 48.5 |
| 22:5n-3 | 1.0 | 6.4 | 1.9 | 3.8 | 8.3 | 56.8 |
| *Favites abdita*  *vs*  *Platygyra carnosa*  *(12.6)* | 22:5n-3 | 0.3 | 6.4 | 3.3 | 6.0 | 25.8 | 25.8 |
| 20:4n-6 | 13.8 | 19.3 | 1.6 | 1.7 | 12.8 | 38.4 |
| 18:3n-3 | 2.7 | 0.9 | 1.0 | 2.2 | 7.8 | 46.1 |
| 18:1n-9 | 4.7 | 2.2 | 0.9 | 2.7 | 7.1 | 53.3 |
| *Acropora samoensis*  *vs*  *Turbinaria peltata*  *(30.3)* | 18:3n-3 | 12.0 | 0.0 | 6.1 | 18.6 | 20.1 | 20.1 |
| 20:1n-9 | 2.9 | 0.0 | 3.0 | 23.7 | 10.0 | 30.1 |
| 16:0 | 31.1 | 31.6 | 2.8 | 2.0 | 9.3 | 39.3 |
| 18:3n-6 | 5.4 | 1.3 | 2.7 | 8.6 | 9.0 | 48.3 |
| 22:6n-3 | 6.6 | 2.3 | 2.7 | 9.8 | 8.9 | 57.2 |
| *Favites abdita*  *vs*  *Turbinaria peltata*  *(17.8)* | 18:3n-3 | 2.7 | 0.0 | 2.8 | 10.3 | 15.9 | 15.9 |
| 18:3n-6 | 5.7 | 1.3 | 2.3 | 4.1 | 13.2 | 29.1 |
| 16:0 | 36.2 | 31.6 | 1.9 | 3.2 | 10.7 | 39.8 |
| 20:1n-9 | 0.6 | 0.0 | 1.4 | 21.9 | 7.6 | 47.4 |
| 18:2n-6 | 2.1 | 0.7 | 1.2 | 6.5 | 7.0 | 54.4 |
| *Platygyra carnosa*  *vs*  *Turbinaria peltata*  *(19.6)* | 22:5n-3 | 6.4 | 0.6 | 3.3 | 6.0 | 16.9 | 16.9 |
| 16:0 | 36.0 | 31.6 | 2.5 | 3.0 | 12.7 | 29.6 |
| 18:3n-6 | 4.2 | 1.3 | 2.0 | 4.4 | 10.1 | 39.7 |
| 20:4n-6 | 19.3 | 16.3 | 1.9 | 1.9 | 9.9 | 49.6 |
| *Acropora samoensis*  *vs*  *Pavona decussata*  *(19.6)* | 18:3n-3 | 12.0 | 0.0 | 5.5 | 17.9 | 27.4 | 27.4 |
| 20:5n-3 | 1.0 | 0.8 | 2.5 | 3.6 | 12.6 | 40.0 |
| 20:1n-9 | 2.9 | 0.2 | 2.1 | 22.6 | 10.5 | 50.5 |
| *Favites abdita*  *vs*  *Pavona decussata*  *(15.9)* | 20:4n-6 | 13.8 | 2.9 | 2.9 | 3.6 | 18.2 | 18.2 |
| 18:3n-3 | 2.7 | 0.0 | 2.5 | 10.8 | 15.8 | 34.0 |
| 16:0 | 36.2 | 50.4 | 2.1 | 6.3 | 13.0 | 47.0 |
| 16:1 | 1.3 | 3.7 | 1.3 | 8.0 | 8.2 | 55.1 |
| *Platygyra carnosa*  *vs*  *Pavona decussata*  *(15.5)* | 20:4n-6 | 19.3 | 2.9 | 4.3 | 7. 1 | 27.7 | 27.7 |
| 22:5n-3 | 6.4 | 1.3 | 2.3 | 4.8 | 14.8 | 42.5 |
| 18:3n-3 | 0.9 | 0.0 | 1.5 | 4.5 | 9.4 | 51.8 |
| *Turbinaria peltata*  *vs*  *Pavona decussata*  *(22.8)* | 16:0 | 31.6 | 50.4 | 4.2 | 5.8 | 18.5 | 18.5 |
| 20:4n-6 | 16.3 | 2.9 | 3.0 | 4.3 | 13.0 | 31.5 |
| 16:1 | 0.5 | 3.7 | 2.3 | 17.8 | 10.2 | 41.7 |
| 18:3n-6 | 1.3 | 5.0 | 2.3 | 6.6 | 10.0 | 51.7 |

All values between groups dissimilarity are expressed in %

FA: Fatty acids, Av. Abund: average abundance in each group, Av. Diss: the average dissimilarity contributed by FA, Diss/SD: the ratio of dissimilarity to standard deviation, Con: contribution to the FA to the overall dissimilarity, Cum: additive overall dissimilarity.