Supplementary Tables and Figures - Thomé et al.

Table S1. Size and percentage of damaged tissue for sampled *Pseudodiploria strigosa* **colonies.** Healthy colonies did not have visual signs of disease. For unhealthy colonies, UCL refers to samples taken close to the lesion; UAL refers to samples taken away from the lesion. Colonies successfully sequenced indicated with an asterisk.

| Healthy | Diameter | Unhealthy | Diameter | Damaged |
|----------|----------|------------|----------|------------|
| colonies | (mm) | colonies | (mm) | tissue (%) |
| H1* | 254 | UCL1/UAL1* | 255 | 23.49 |
| H2* | 255 | UCL2/UAL2* | 255 | 49.84 |
| H3* | 227 | U3CL* | 249 | 55.92 |
| H4 | 255 | U4 | 245 | 66.54 |
| Н5 | 250 | U5 | 253 | 27.81 |
| H6 | 228 | U6 | 254 | 77.18 |

Table S2. Relative abundance of all ASVs, raw data (Excel file, after rarefaction). Uploaded separately.

Table S3. Alpha diversity indexes calculated for all colonies sampled.

| Colony | Obs. | Chao1 | ACE | Shannon | Simpson |
|--------|------|--------|--------|---------|---------|
| H1 | 202 | 203 | 202.29 | 3.57 | 0.91 |
| H2 | 147 | 147.5 | 147.63 | 3.06 | 0.85 |
| Н3 | 111 | 111.25 | 111.43 | 2.14 | 0.72 |
| UAL1 | 155 | 155 | 155 | 3.11 | 0.89 |
| UAL2 | 131 | 131.2 | 131.57 | 2.83 | 0.85 |
| UCL1 | 233 | 233 | 233.21 | 4.15 | 0.97 |
| UCL2 | 115 | 115 | 115 | 2.51 | 0.74 |
| UCL3 | 112 | 117.14 | 115.61 | 2.32 | 0.70 |

H1-3, healthy colonies; UAL1-2, unhealthy colonies sampled away from lesions; UCL1-3, unhealthy colonies sampled close to lesions.

Table S4. Relative abundance (%) in *Pseudodiploria strigosa* colonies and water samples, for two bacterial Orders implicated in WS and SCTLD.¹

| | H1 | H2 | H3 | UAL1 | UAL2 | UCL1 | UCL2 | UCL3 | WH | WD |
|---|------|------|-------|------|-------|------|------|------|-------|-------|
| Rhodobacterales | 5.90 | 2.55 | 11.61 | 7.83 | 10.67 | 2.11 | 0.48 | 0.19 | 11.56 | 17.20 |
| Rhizobiales | 0.05 | 0.12 | 0.14 | 0 | 0.04 | 0.49 | 0 | 0.02 | 0 | 0.14 |
| ¹ According to Pollock et al, 2017; Rosales et al., 2020 | | | | | | | | | | |

All data are for single samples.



Figure S1. Status of *Pseudodiploria strigosa* **colonies.** Colonies sampled on different surveys conducted in a rear reef site near Puerto Morelos in the NE Mexican Caribbean. Colonies (95 total) were mapped and followed within an area of 435 m² throughout 306 days. The proportion of healthy, diseased, and dead colonies is given for 100 colonies per survey day.



Figure S2. *Pseudodiploria strigosa* **tissue sampling.** The photograph illustrates the location of sampling points for unhealthy colonies, at ≤ 1 cm from the lesion border (black arrowhead, UCL samples) and 15 cm away from the lesion border, over healthy-looking tissue (white arrowhead, UAL samples). Photo credit: Eric Jordán-Dahlgren.



Figure S3. Microphotographs of ciliates in the proximity of tissue affected (UAL) by WS in *Pseudodiploria strigosa* colonies. (A) Ciliates (black arrows) in direct contact with necrotic tissue (LN).
(B) Ciliate (black) arrow next to the mesoglea within the mesentery of the individual. (C) Several ciliates (black arrows) next to necrotic tissue (LN) within the mesentery.



Figure S4. Accumulation curves for ASVs resolved per sample. Total number of reads was 261,176 normalized to 16,600 per sample after rarefaction.



Figure S5. Bacterial community associated with the surface mucus layer of *Pseudodiploria strigosa* **colonies.** Relative abundance of assigned (**A**) Phylum and (**B**) Class to ASVs from sampled colonies. Sample identity as follows: Healthy colonies: H1-3, unhealthy colonies sampled away from lesion: UAL1-2, unhealthy close to lesion: UCL1-3, seawater sample close to a healthy colony: WH, seawater sample close to an unhealthy colony: WU. Phyla with < 1% of abundances were grouped in the "Others" category.



Figure S6. Venn diagram showing total number of ASVs for the colonies sampled. The numbers in the center of each colored circle refer to the total number of ASVs for each category; numbers on intersections show shared ASVs between and among categories. Note that the sample size was different for UAL with only 2 samples, while Healthy and UCL conditions had 3 samples each.



Figure S7. Phylogeny analysis for the most abundant ASVs within the six genera identified in unhealthy colonies. This analysis was done using as reference the NCBI RefSeq database.