



Corrigendum: On a Reef Far, Far Away: Anthropogenic Impacts Following Extreme Storms Affect Sponge Health and Bacterial Communities

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A Corrigendum on

On a Reef Far, Far Away: Anthropogenic Impacts Following Extreme Storms Affect Sponge Health and Bacterial Communities

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In the original article, there was a mistake in the legend for **Figures 1–4** as published. Legends corresponding to previous versions of the Figures were published. The years of salinity data included in **Figure 1D** were written as “2015–2018,” where it should be “2016–2018.”

In **Figure 2** “Empty symbols” and “filled symbols” should be “Squares” and “Triangles,” respectively. “Circles = Seawater samples.” was missing from the original legend and has been added. “Circles” and “squares” have been replaced with “Empty symbols” and “filled symbols,” respectively.

In **Figure 3** “Bars represent mean (\pm sem).” should be “Bars represent mean with individual value dots.” Additionally, the parts were initially listed in alphabetical order (A, B, C, D, etc.) but should correspond to the order of the figure parts (i.e., A, C, E, B, D, F).

In **Figure 4** “Black bars = affected sponges in 2016; red bars = healthy sponges in 2017; green bars = healthy sponges in 2017; blue bars = healthy sponges in 2018 (no flood, baseline year).” should be “Black bars = affected sponges in 2016; red bars = visually healthy sponges in August 2016; orange bars = visually healthy sponges in September 2017; green bars = visually healthy sponges in October 2017; blue bars = visually healthy sponges in October 2018 (no flood, baseline year).”

The corrected legends appear below.

Figure 1. Summary of study site, host taxa, and local abiotic conditions associated with this study. (A) map of Flower Garden Banks National Marine Sanctuary (northwest Gulf of Mexico) with sites of sponge and seawater collection

indicated. Filled circles represent seawater column sample collection sites; filled squares represent Buoy 2 and Buoy 4 (sponge, seawater column, and near reef seawater collection) and open circle represents location of TABS Buoy V (surface salinity data collection); (B) representative *Xestospongia muta* sponge; (C) representative *Agelas clathrodes* sponge; (D) surface Salinity (ppt) at buoy V spanning the months April through October in which sampling occurred for this study. Black lines represent daily means from 2006 to 2018 and gray shaded areas encompass minimum and maximum values from 2006 to 2018. Red lines represent daily means for 2016–2018, individually. Dashed lines with storm icon represent dates of terrestrial flooding. Dotted lines with symbols represent mean daily values on each sample collection date: dark red circle = 6 August 2016, orange circle = 16 September 2017, green circle = 21 October 2017, and blue circle = 23 October 2018.

Figure 2. Principle Coordinate Analysis of the weighted UniFrac distance matrix for bacterial communities analyzed in this study. Squares = *Agelas clathrodes* samples; Triangles = *Xestospongia muta* samples; Circles = Seawater samples. Black symbols = samples from diseased sponges (August 2016); Red symbols = visually healthy sponge samples (August 2016). Orange symbols = samples collected immediately following Hurricane Harvey (Sept. 2017) from visually healthy sponges; Green symbols = samples collected 1 month following Hurricane Harvey (Oct. 2017) from visually healthy sponges. Blue symbols = samples collected in a no-flood (baseline) year from visually healthy sponges (Oct. 2018). Empty symbols = samples collected from East Bank (EB); filled symbols = samples collected from West Bank (WB) of the Flower Garden Banks National Marine Sanctuary (northern Gulf of Mexico).

Figure 3. Sponge-associated bacterial communities differed in composition and variability following extreme storm-derived floods. Principle Coordinate Analysis of the weighted UniFrac distance matrices for (A) visually healthy *Xestospongia muta*, (C) visually healthy *Agelas clathrodes*, and (E) seawater bacterial

communities. Mean (with individual value dots) pairwise dissimilarity values for (B) *X. muta*, (D) *A. clathrodes*, and (F) seawater bacterial communities. Red = August 2016; Orange = September 2017; Green = October 2017; Blue = October 2018 associated with no flooding stress. Bars represent mean with individual value dots. Within a species, bars that do not share a letter are significantly different based on ANOVA with Tukey's multiple comparisons ($p < 0.05$).

Figure 4. Relative abundance of sequences in the Family Enterobacteriaceae (A,B) and to specific human pathogens (*Escherichia coli* and *Klebsiella pneumoniae*) (C,D) across sites and years. Data in (A,B) are based on Illumina MiSeq amplicon sequencing of the V4 region of the bacterial 16S rRNA gene. Data in (C,D) are quantitative PCR amplification of the bacterial *ybbW* and *phoE* genes for *E. coli* and *K. pneumoniae*, respectively. All data are presented as mean with individual value dots. Black bars = affected sponges in 2016; red bars = visually healthy sponges in August 2016; orange bars = visually healthy sponges in September 2017; green bars = visually healthy sponges in October 2017; blue bars = visually healthy sponges in October 2018 (no flood, baseline year). Groups that share a letter in (A,B) are not significantly different based on a Generalized Linear Model with Tukey's multiple comparisons across groups within a species. ND, not detected.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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