Southeast Florida and Florida Keys Antibiotic Resistance Study Final project report

Dale Warren Griffin¹, Kenneth Banks², Kurtis Gregg³ and Brian Walker⁴

¹U.S. Geological Survey, 600 4th Street South, St. Petersburg, Florida 33772. <u>dgriffin@usgs.gov</u>

²Broward County, Environmental Protection and Growth Management Department, 115 South Andrews Avenue, Room 329-H, Fort Lauderdale, Florida 33301. kbanks@broward.org

³ERT, Inc., NOAA-Fisheries Service, 400 North Congress Avenue, Suite 270, West Palm Beach, Florida 33401. <u>kurtis.gregg@noaa.gov</u>

⁴Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, 8000 North Ocean Drive, Dania Beach, Florida 33004. <u>walkerb@nova.edu</u>

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Objective

Antibiotic resistance has recently been recognized as an emerging contaminant and has molecular methods that identify these genes in microbial populations that have proven to be useful tools in assessing anthropogenic impacts on terrestrial and aquatic environments (1). Analyzing microbial communities for the presence of antibiotics enable researchers to demonstrate at the genetic level, the influences of antibiotic laden sources such as septic systems, shallow injection wells, storm sewer overflows and outfalls on regional ecosystems. As antibiotic resistance can affect pathogen virulence, these sources of antibiotic laden pollutants can sustain the presence of these pathogens that can in turn present human recreational and ecosystem health risks.

The objective of this project is to determine the prevalence of antibiotic resistance genes in bacterial populations in impacted (close to and alongside outfall pipes and within the wastewater stream) and reference (along transect extending away from the outfalls) sediment samples around the Hollywood, FL wastewater treatment plant's ocean outfall. Two sample sets of coral mucus, the water column and reef sediment were also collected from a Florida Keys coral reef, pre, and

post treatment with amoxicillin, and were also analyzed for the presence of antibiotic resistance genes. Sediment and wastewater samples were analyzed for 15 different antibiotic resistant gene targets via polymerase chain reaction presence/absence assays in Southeast Florida coral reef environments. Approximately 38 samples per season (June = wet season, March = dry season) were collected by the Florida Department of Environmental Protection, Broward County and NOAA research teams and shipped to and analyzed at the USGS St. Petersburg Environmental and Public Health Microbiology Laboratory.

"This work is a follow-on to the pilot study results from 14ESFUSAFDEP3519 completed between 10/2014 & 9/2016. This project is a continuation of the SE Florida Coral Reef Initiative (SEFCRI) Technical Advisory Committee's recently concluded Outfall Biomarker Pilot Project (LBSP 28/29 Phase I) and builds upon the results and outcomes of that initial work." (current FLDEP/USGS FUSA agreement for this project)

Equipment

- 1. Applied Biosystems StepOne and StepOnePlus Real-Time PCR Systems. Life Technologies catalog #'s 4376373 and 4376598, respectively.
 - a. TaqMan Fast Advanced Master Mix, catalog # 4444556 (ABR PCR).
 - b. TaqMan Fast Virus 1-Step Master Mix, catalog # 4444432 (Viral PCR).
 - c. MicroAmp Fast 96-Well Reaction Plate (0.1ml), catalog # 4346907.
 - d. MicroAmp Fast Optical 48-Well Reaction Plate (0.1ml), catalog # 4375816.
 - e. MicroAmp Optical 8-Cap Strip, catalog # 4323032.
- 2. Eppendorf Reference Pipettes, 0.1-2.5µl, 0.5-10µl, 2-20µl, 20-100µl, 50-200µl, 100-1000µl and 500-2500µl.
- 3. Microfuge tube and 96-well microplate cold plates.
- 4. Master mix boats/Reagent Reservoir. Corning Incorporated COSTAR # 4870 or equivalent.
- 5. Sterile pipette tips and 1.8ml or 2.0ml microfuge tubes.
- 6. Fifty and 15ml conical tubes. Sterile Falcon or Fisher brand equivalent.
- 7. Tube racks for 15, 50 and 2.0ml tubes.
- 8. Ten, 25 and 50ml pipettes with autopipette and/or bulb.
- 9. IEC Centra MP4R centrifuge with swinging 250ml bucket rotor and 50ml tube adapters.
- 10. Beckman Coulter, Avanti J-E centrifuge with rotor/adaptors for 50ml conical tubes.
- 11. Eppendorf 5415 D microcentrifuge (24 place).
- 12. Incubator capable of 56°C.
- 13. Mettler Toledo AL54 scale and weigh boats.
- 14. MoBio PowerSoil DNA Isolation Kit, MoBio's catalog # 12888-100 (now owned by Qiagen).
- 15. MoBio Vortex Genie 2, catalog # 13111-V and 24 place tube holder, catalog # 13000-V1-24.
- 16. pH Meter with reference solutions at 4.0, 7.0 and 10.0 pH.
- 17. Millipore MF membrane filters, 0.45um HA. Fisher Scientific catalog # HAWP04700.
- 18. Sulfuric Acid, Fisher Scientific catalog # A300-500.
- 19. Sodium Hydroxide, Fisher Scientific catalog # S392-212.
- 20. Potassium Citrate, Fisher Scientific catalog # P218-500.
- 21. Potassium phosphate, monobasic, ACROS # 42420-5000.
- 22. Sodium Phosphate Dibasic Heptahydrate, Fisher Scientific catalog # S373-500.
- 23. Tris, Fisher Scientific catalog # T393-212.
- 24. Sodium (Tetra) Ethylenediamine Tetraacetate, Fisher Scientific catalog # S657-500.

- 25. Sodium Thiosulfate, Fisher Scientific catalog # S474-500.
- 26. Ethanol 200 proof, Decon Labs Inc. catalog # 2716.
- 27. Water, D.I.U.F., Fisher Scientific catalog # W2-20.
- 28. Qiagen AE buffer (10mM Tris-Cl, 0.5mM EDTA, pH 9.0).
- 29. Primer/probe sets and corresponding gene target clone (target sequence with ~15bp of random sequences on each end Integrated DNA Technologies (IDT) gBlock) synthesized by Eurofins, IDT or Applied Biosystems.

Sample sites and collection

Sample sites are illustrated in the wet and dry season heatmap figures (Figures 1 and 3). Samples included sediment and water column samples collected along transects centered on a regional ocean outfall and from regional wastewater treatment plants.

Sediment samples were collected by SCUBA divers who navigated to the sample site by descending an anchored center-point buoy line (centroid) and attaching a measuring tape to the anchor. Divers collected one sediment sample at the centroid of the array near the anchor (beneath the outfall pipe) and then navigated to the cardinal and ordinal directions (N, NW, W, SW, S, SE, E, NE) by dive scooter or by self-propulsion to collect samples at 25m and 50m from the centroid. One diver ran out the tape to 50m. The other diver collected sediment at 25m then the 50m site. Samples at 100, 200, 400 and 800m north and south of the centroid were collected on single dives at those intervals. Samples collected at 100, 200, and 400m, west of the centroid were collected by one diver team using scooters to move from site to site along the pipeline with anchored floats deployed from the boat marking the collection location. Samples at 800, and 1,600m from the centroid were collected on individual dives at those sites. Sediment samples were collected by divers using a 50ml centrifuge tube to scoop sediment from the seabed. Divers wore single-use nitrile gloves to prevent cross-contamination of sediment samples. Nitrile gloves were changed between samples (underwater) if more than one sample was collected on a dive. Outfall water samples were collected by opening an empty sterile 50ml centrifuge tube in the plume at the mouth of the pipe. Wastewater treatment samples were collected using sterile technique.

Sample storage and shipping

Wet Season:

Field sediment and water samples were brought to the surface where they were kept on ice on the boat and during transport to the FDEP CRCP office in Miami, FL, where they were placed in a freezer. Effluent water samples from the three wastewater treatment plants were collected while wearing Nitrile gloves. They were collected from spigots directly into sterile 50ml centrifuge tubes. Samples were placed in plastic Ziploc bags, and kept on ice during transport to the FDEP CRCP office where they were placed in a freezer with the field samples. Once all samples were collected, they were shipped frozen, on dry ice, overnight to the USGS lab in St. Petersburg, FL.

Dry Season:

Field sediment and water samples were brought to the surface where they were kept on ice on the boat and during transport to the FDEP CRCP office in Miami, FL, where they were placed in a refrigerator. Effluent and influent water samples from the three wastewater treatment plants were collected while wearing Nitrile gloves. They were taken from spigots directly into sterile 50ml centrifuge tubes. Samples were placed in Ziploc bags, and kept on ice during transport in the car to the FDEP CRCP office where they were placed in a refrigerator with the field samples. Once all samples were collected, they were shipped on ice, overnight to the USGS lab in St. Petersburg, FL.

Table 1. Primer and Probe Sequences

| | Upstream Primer | Downstream Primer | Label-Probe | Reference |
|--------------|------------------------------|---------------------------|------------------------------------|-----------|
| Antibiotic R | esistance Genes | | | |
| tetB | ACACTCAGTATTCCAAGCCTTTG | GATAGACATCACTCCCTGTAATGC | FAM- AAAGCGATCCCACCACCAGCCAAT | (2) |
| tetL | GGTTTTGAACGTCTCATTACCTGAT | CCAATGGAAAAGGTTAACATAAAGG | FAM- CCACCTGCGAGTACAAACTGGGTGAAC | (2) |
| tetM | GGTTTCTCTTGGATACTTAAATCAATCR | CCAACCATAYAATCCTTGTTCRC | VIC- ATGCAGTTATGGARGGGATACGCTATGGY | (2) |
| tetO | AAGAAAACAGGAGATTCCAAAACG | CGAGTCCCCAGATTGTTTTAGC | FAM- ACGTTATTTCCCGTTTATCACGG | (2) |
| tetQ | AGGTGCTGAACCTTGTTTGATTC | GGCCGGACGGAGGATTT | VIC- TCGCATCAGCATCCCGCTC | (2) |
| tetW | GCAGAGCGTGGTTCAGTCT | GACACCGTCTGCTTGATGATAAT | VIC-TTCGGGATAAGCTCTCCGCCGA | (2) |
| ampC | GGGAATGCTGGATGCACAA | CATGACCCAGTTCGCCATATC | VIC- CCTATGGCGTGAAAACCAACGTGCA | (2) |
| vanA | CTGTGAGGTCGGTTGTGCG | TTTGGTCCACCTCGCCA | VIC- CAACTAACGCGGCACTGTTTCCCAAT | (2) |
| ermB | GGATTCTACAAGCGTACCTTGGA | GCTGGCAGCTTAAGCAATTGCT | FAM- CACTAGGGTTGCTCTTGCACACTCAAGTC | (3) |
| mecA | CATTGATCGCAACGTTCAATTTAAT | TGGTCTTTCTGCATTCCTGGA | VIC- CTATGATCCCAATCTAACTTCCACATACC | (3) |
| blaSHV | AACAGCTGGAGCGAAAGATCCA | TGTTTTTCGCTGACCGGCGAG | FAM- TCCACCAGATCCTGCTGGCGATAG | (3) |
| blaPSE | GATTTGGTGCTCGGAGTATT | CATTGAAGCCTGTGTTTGAG | VIC- CTTGATGCTCACTCCA | (4) |
| floR | GGCAGGCGATATTCATTACT | CGAGAAGAAGACGAAGAAGG | FAM- CTAAAGCCGACAGTGTA | (4) |
| aadA2 | CAGCCAYGATCGACATTGATCT | CCAAGGCAACGCTATGTTCTC | VIC- CTGCTTACAAAAGC | (4) |
| tetG | CGGTACTTCTGGCTTCTCTT | GAATCGGCAATGGTTGAG | FAM- CAGGAGCCGCAGTCGATTACACG | (4) |

Positive controls were gene target sequences synthesized with ~15-25 base pair extensions beyond the 5' and 3' ends of the primer binding sequences. The controls were synthesized by Integrated DNA Technologies (gBlock double-stranded DNA fragments).

Master mix recipes

| reactions – 20µl reactions - row 1 Internal Po | sitive Control (IPC) co | ntrol |
|--|--|---|
| | | <u>13rxns</u> |
| 2x TaqMan Fast Universal Master Mix – | 10µ1 | 130µ1 |
| Template – | 2µ1 | |
| Primer/probe (10µM/5µM working stock) | 2µ1 | 26µ1 |
| 10x Exo Internal Positive Control | 2µ1 | 26µ1 |
| 50x Exo IPC DNA | 0.4µl | 5.2µl |
| PCR grade H2O | 3.6µl | 46.8µl |
| eactions row 8 (4 reactions) | | <u>5rxns</u> |
| 2x TaqMan Fast Universal Master Mix – | 10µ1 | 50µ1 |
| Template – | 2µ1 | |
| 10x Exo Internal Positive Control | 2µ1 | 10µ1 |
| 50x Exo IPC DNA | 0.4µ1 | 2µ1 |
| PCR grade H ₂ O | 5.6µl | 28µl |
| | 2x TaqMan Fast Universal Master Mix – Template – Primer/probe (10µM/5µM working stock) 10x Exo Internal Positive Control 50x Exo IPC DNA PCR grade H2O eactions row 8 (4 reactions) 2x TaqMan Fast Universal Master Mix – Template – 10x Exo Internal Positive Control 50x Exo IPC DNA | Template –2μlPrimer/probe (10μM/5μM working stock)2μl10x Exo Internal Positive Control2μl50x Exo IPC DNA0.4μlPCR grade H2O3.6μleactions row 8 (4 reactions)2x TaqMan Fast Universal Master Mix –10μl2μl10x Exo Internal Positive Control2μl50x Exo IPC DNA0.4μl |

Single probe reactions (when utilized for startup testing and repeats if needed) – $20\mu l$ reactions - rows 2 - 7

| a. | 2x TaqMan Fast Universal Master Mix – | 10µ1 |
|----|---------------------------------------|-------|
| b. | Template – | 2µ1 |
| c. | Primer/probe (10µM/5µM working stock) | 2µ1 |
| d. | PCR grade H ₂ O | 6.0µ1 |

Multiplex (two primer and probe sets) – 20µl reactions

| a. | 2x TaqMan Fast Universal Master Mix – | 10µ1 | <u>13rxns</u> 130µ1 |
|----|---------------------------------------|----------|------------------------|
| b. | Template – | 2µ1 | |
| c. | Primer/probe (10µM/5µM working stock) | 2µl each | 26µ1 |
| d. | PCR grade H ₂ O | 4.0µ1 | 52µl |

Amplification profile

Sixty^oC for 0.5min, 50^oC for 2min and 95^oC for 5min, then 45 cycles of 95^oC for 0.25min and 60^oC for 1min, then a final step at 60^oC for 0.5min

PCR plate layouts (wet season)

Plate 1 multiplex duplicate sample layout (tetB/IPC, tetL/M, tetO/W, ampC/vanA, ermB/mecA, blaSHV/blaPSE, floR/aadA2) and Plate 2 (tetG/tetQ) are samples in columns x2 and rows of gene target using a 96-well plate. Use bottom right four wells for negative control (PCR grade water for template – columns 9 and 10, row 8) and IPC

negative control (2µl of IPC block – columns 11 and 12, row 8). Two dyes used, FAM and VIC. FAM labeled probes are tetB, tetL, tetO, ampC, ermB, blaSHV, floR, and tetG. VIC labeled probes are the IPC, TetM, TetW, vanA, mecA, blaPSE, aadA2, and tetQ.

PCR plate layouts (dry season)

Each combination of target/IPC or target/target were run for all the samples in duplicate on an individual 96-well plates with negative (PCR grade H_2O) and positive (gBlock) controls.

Work Flow

27 June 2018

Florida Keys pre-treatment sample set

Received samples (Florida Keys coral antibiotic treatment study, #'s 1-12. These are pretreatment samples, meaning the sample set collected prior to the diseased corals within the reef being treated with amoxicillin) and placed in the refrigerator.

6 July 2018

Centrifuged 25mls of water and mucus samples at 5900g x 30 min at 15°C and pipetted off all but ~500µl of supernatant. Vortexed the samples and transferred 250µl to Qiagen's PowerSoil bead beating tubes. Also transferred ~0.25g of sediment from each sediment sample to bead beating tubes. Extracted DNA from the samples using the PowerSoil protocol and eluted DNA in 100µl of Qiagen's AE buffer. Placed the extracts in the -20°C freezer until analysis.

Florida Keys post-treatment sample set

Received samples 13 - 24 and placed in the refrigerator.

9 July 2018

Set up new primer and probe mixes for the 15 targets. Then set up a polymerase chain reaction (PCR) assay using the above single and multiplex reactions to verify the gBlock synthetic positive control templates and the new primer/probe mixes. First reaction all checked OK except tetL and floR. Remake 10^{-3} dilutions of positive controls from the 10^{-2} frozen stock and rerun both dilutions for these targets. All amplified as expected. Set up and run plate 1 for samples 1 through 6. Extract DNA from samples 13 - 24 using the same protocol as utilized for the first sample set and placed in the refrigerator.

10 July 2018

Set up and run plate 1 for samples 7-12, 13-18 and 19-24. Set up and run plate 2 for samples 1 through 24.

24 July 2018

Received 38 frozen samples from DEP and placed in -20°C freezer. Samples included 6 water and 32 sediment samples collected near three ocean outfalls and their corresponding wastewater treatment plants (WWTP) during Southeast Florida's wet

season. Three effluent water samples were taken at the North Broward, Hollywood, and North Miami-Dade WWTP. At the mouth of the ocean outfall pipes associated with each of the three WWTP a sediment sample was taken from directly underneath the pipe, and a water sample was taken from inside the mouth of the pipe. At the Hollywood outfall only, sediment samples were taken in a rosette pattern 25 and 50 m N, S, E, W, NE, NW, SE and SW from the mouth of the pipe. Sediment samples were also taken along N and S transects at 100, 200, 400 and 800 m from the mouth of the pipe, and along W transect at 100, 200, 400, 800 and 1,600 m from the mouth of the pipe. The W transect was meant to follow along the outfall pipe.

| Collection Date | Site | Sample/Site ID | Site Lat | Site Long | Depth | Water Temp. | Weather | Note (where sample collected) | Divers |
|-----------------|-------------------------------------|----------------|-----------|------------|-------|-------------|---------------------------|--|--------|
| 5/11/2018 | Broward North WWTP Outfall (pipe) | BRN_Sed | 26.251347 | -80.062208 | 111' | 79F | Seas 1-2'/Wind<5 mph | Sandy bottom beneath outfall pipe | AR/PQ |
| 6/11/2018 | Broward North WWTP Outfall pipe) | BRN_H2O | 26.251347 | -80.062208 | 111' | 79F | Seas 1-2'/Wind<5 mph | From inide mouth of outfall pipe | AR/PQ |
| 6/11/2018 | Hollywood outfall (south transect) | HOL_S_100 | 26.018319 | -80.086023 | 84' | 82F | Seas<1'/Wind<5mph | Sandy bottom next to patch reef | DC/KG |
| 6/11/2018 | Hollywood outfall (south transect) | HOL_S_200 | 26.017518 | -80.086005 | 84' | 82F | Seas<1'/Wind<5mph | Sandy bottom next to patch reef | JW/KB |
| 6/11/2018 | Hollywood outfall (south transect) | HOL_S_400 | 26.015895 | -80.086023 | 85' | 80F | Seas<1'/Wind<5mph | Sandy bottom next to patch reef | DC/KG |
| 6/11/2018 | Hollywood outfall (south transect) | HOL_S_800 | 26.011918 | -80.085936 | 90' | 80F | Seas<1'/Wind<5mph | Sandy bottom next to patch reef | JW/KB |
| 6/12/2018 | Hollywood outfall (pipe) | HOL_Sed | 26.019126 | -80.08602 | 86' | 81F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom beneath outfall pipe | KB/MV |
| 6/12/2018 | Hollywood outfall (pipe) | HOL_H2O | 26.019126 | -80.08602 | 86' | 81F | Seas 2-3'/Wind SE 5-10mph | From inide mouth of outfall pipe | KB/MV |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_E_25 | n/a | n/a | 92' | 77F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom, adjacent to/next to patch reef | KG/PQ |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_E_50 | n/a | n/a | 95' | 78F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom, adjacent to/next to patch reef | KG/PQ |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_SE_25 | n/a | n/a | 89' | 77F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom, adjacent to/next to patch reef | KG/PQ |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_SE_50 | n/a | n/a | 94' | 77F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom, adjacent to/next to patch reef | KG/PQ |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_N_25 | n/a | n/a | 85' | 81F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom near minimal patch rreef | KB/MW |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_N_50 | n/a | n/a | 86' | 81F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom, open | KB/MW |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_NE_25 | n/a | n/a | 90' | 81F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom next to patch reef | KB/MW |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_NE_50 | n/a | n/a | 94' | 81F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom next to patch reef | KB/MV |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_NW_25 | n/a | n/a | 82' | 81F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom, adjacent to/next to patch reef | ND/MS |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_NW_50 | n/a | n/a | 79' | 81F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom, adjacent to/next to patch reef | ND/MS |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_W_25 | n/a | n/a | 77' | 81F | Seas 2-3'/Wind SE 5-10mph | Pipe trench, sandy spot | ND/MS |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_W_50 | n/a | n/a | 73' | 81F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom next to and on north side of pipe | ND/MS |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_SW_25 | n/a | n/a | 78' | 82F | Seas 2-3'/Wind SE 5-10mph | Sandy spot in open depression on reef ridge | DC/SW |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_SW_50 | n/a | n/a | 70' | 82F | Seas 2-3'/Wind SE 5-10mph | Sandy spot in open depression on reef ridge | DC/SW |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_S_25 | n/a | n/a | 85' | 82F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom next to reef | DC/SW |
| 6/12/2018 | Hollywood outfall (rosette) | HOL_S_50 | n/a | n/a | 821 | 82F | Seas 2-3'/Wind SE 5-10mph | Sandy bottom in channel between reef ridges | DC/SW |
| 6/12/2018 | Hollywood outfall (west transect) | HOL_W_100 | 26.019111 | -80.086922 | 64' | 81F | Seas 1-2'/Wind ESE<5mph | Pipe trench, sandy spot | AR/MW |
| 6/12/2018 | Hollywood outfall (west transect) | HOL_W_200 | 26.019094 | -80.087816 | 60' | 81F | Seas 1-2'/Wind ESE<5mph | Pipe trench, sandy spot | AR/MW |
| 6/12/2018 | Hollywood outfall (west transect) | HOL_W_400 | 26.019055 | -80.089598 | 60' | 81F | Seas 1-2'/Wind ESE<5mph | Pipe trench, sandy spot | AR/MV |
| 6/12/2018 | Hollywood outfall (west transect) | HOL_W_800 | 26.018996 | -80.093201 | 67' | 82F | Seas 1-2'/Wind ESE<5mph | Sandy bottom next to concrete mat covering pipe | KG/PQ |
| 6/12/2018 | Hollywood outfall (west transect) | HOL_W_1600 | 26.018778 | -80.100384 | 25' | 82F | Seas 1-2'/Wind ESE<5mph | Next to trench, sandy bottom | KG/PQ |
| 6/12/2018 | Hollywood outfall (north transect) | HOL_N_100 | 26.019935 | -80.086031 | 83' | 81F | Seas 1-2'/Wind ESE<5mph | Sandy bottom, next to patch reef | ND/MS |
| 6/12/2018 | Hollywood outfall (north transect) | HOL_N_200 | 26.020742 | -80.086049 | 83' | 81F | Seas 1-2'/Wind ESE<5mph | Sandy bottom, next to patch reef | DC/SW |
| 6/12/2018 | Hollywood outfall (north transect) | HOL_N_400 | 26.022358 | -80.086091 | 82' | 81F | Seas 1-2'/Wind ESE<5mph | Sandy bottom, next to patch reef | ND/MS |
| 6/12/2018 | Hollywood outfall (north transect) | HOL_N_800 | 26.026376 | -80.086081 | 85' | 81F | Seas 1-2'/Wind ESE<5mph | Sandy bottom, next to patch reef | DC/SW |
| 6/19/2018 | Haulover outfall (Miami-Dade North) | MDN_Sed | 25.92005 | -80.086467 | | | | Sandy bottom beneath outfall diffuser pipe | |
| 6/19/2018 | Haulover outfall (Miami-Dade North) | MDN_H2O | 25.92005 | -80.086467 | | | | From inide mouth of 1 of 12 outfall diffuser pipes | |
| 6/20/2018 | Broward North WWTP | BRN_WWTP_H20 | n/a | n/a | n/a | n/a | n/a | From WWTP | DC |
| 6/20/2018 | Hollywood WWTP | HOL_WWTP_H20 | n/a | n/a | n/a | n/a | n/a | From WWTP | DC |
| 6/20/2018 | Miami-Dade North WWTP | MDN WWTP H2 | | | n/a | n/a | n/a | From WWTP | DC |

7 August 2018

Thaw the water samples (Broward North, Hollywood and Miami-Dade North WWTP and matching water column samples collected from the outfall pipe labeled H2O). Start lab sample number system below. Centrifuge 12ml of each sample using Amicon Ultra 15s at 5000 x g for 30 minutes. Transfer retentate ~100 μ l to 1.5ml microfuge tube and freeze the sample at -20°C. Additionally, centrifuge 2ml at 16000 x g for 10 minutes and pipette off 1.8ml. Resuspend the pellet in the remaining 200 μ l and freeze the samples at -20°C.

- 1. Broward North WWTP
- 2. Broward North outfall H₂O
- 3. Hollywood WWTP
- 4. Hollywood outfall H₂O
- 5. Miami-Dade North WWTP
- 6. Miami-Dade North outfall H₂O

Week of 6 and 13 August 2018

Extract DNA (same DNA extraction protocol as used for the Florida Keys sample sets) from ~0.26g of each sediment sample and the 7 August concentrated wastewater samples. Elute each in 100 μ l of Qiagen's AE buffer and store at -20°C.

27 August 2018

Set up and run gBlock positive controls for each antibiotic gene primer set. All target controls amplified.

28 August 2018

Set up and run ABR plate 1 for samples 1 through 6.

29 August 2018

Set up and run ABR plate 1 for samples 7 through 12, 13 through 18 and 19 through 24.

30 August 2018

Set up and run ABR plate 1 for samples 25 through 30, 31 through 36 and 37 and 38.

31 August 2018

Set up and run ABR plate 2 for samples 1 through 38.

6 September 2018

Repeat samples 1 through 6 to see if same detects occur without using the Amicon Ultra centrifugation units with these wastewater stream samples. Extract DNA using centrifugation of 15ml at 5900 x g for 30 minutes. Discard all but ~200 μ l of the supernatant. Vortex the sample to suspend the pellet and extract DNA from the entire volume. Store the 100 μ l AE extracts in the -20°C.

13 September 2018

Set up and run ABR PCR for the 6 September 2018 samples.

12 March 2019

Received 42 samples on ice (not frozen) from DEP and placed in the refrigerator. Samples included 10 water and 32 sediment samples collected during Southeast Florida's dry season. The samples were collected in the same manner as the Southeast Florida wet season samples, except 4 influent water samples were also taken from the Hollywood and North Miami-Dade WWTP. An image of the sample data spreadsheet with our laboratory identification numbers is pasted below.

Table 3. Field and laboratory sample data spreadsheet (dry season)

| Collection Date | Site | Semple/Site 10 | Depth | Water Temp | s. Weather | Note (where sample collected) | Divers/Sampler | USGS Laboratory sample number | wt/volume assayed | |
|-----------------|------------------------------------|------------------------|-------|------------|--|---|----------------|-------------------------------|-----------------------------------|-----|
| /4/19 | Haulover outfall (Mami-Dade North) | MDN_Sed | 1.0 | 98 | 75 Seas 1-2, sunny/clear skies, wind SW 10-15k | In between rubble below mouth of pipe | KK/AR | A CONTRACTOR OF A CONTRACTOR | 1 0.25g | |
| 4/19 | Haulover outfall (Mami-Dade North) | MDN_H2D | | 98 | 75 Seas 1-2;sunny/clear skies;wind 5W 10-15k | From inside mouth of pipe | KK/AR | | 2 2504 | |
| 4/19 | Hellywood outfall (south transect) | HOL_5_800 | | 89 | 79 Seas 1-2 sunny/clear skies wind SW 10-15k | | M5/ND | | 3 0.25g | |
| 4/19 | Heilywood outfall (south transect) | HOL 5 400 | | 84 | 78 Seas 1-2, wnnyfclear skies, wind SW 10-15k | Sandy spot next to reef ledge | AS,KK | | 4 0.25g | |
| 4/19 | Hellywood outfall (south transect) | HOL 5 200 | | 86 | 77 Seas 1-2 symmetriclear skies wind SW 10-15k | | KK/PQ | | 5 0.25g | |
| 4/19 | Hellywood outfall booth transect) | HOL 5 100 | | 82 | 77 Seas 1-2 sunny/clear skies wind SW 10-15k | | M5/N0 | | 6 0.25g | |
| 4/19 | Hellywood outfall (north transect) | HOL_N_200 | | 82 | 75 Seas 1-2 sunny/clear skies/wind SW 10-15k | | AS/KK | | 7 0.25g | |
| 4/19 | Hellywood outfall (north transect) | HOL N 100 | | 87 | 75 Seas 1-2 sunny/clear skies wind SW 10-15k | | POJAR | | 8 0 25g | |
| /4/19 | Hellywood outfall (north transect) | HOL N 400 | | 77 | 78 Seas 1-2 sunnulciear skies wind SW 10-15k | | M5/ND | | 9 0 25g | |
| 4/19 | Hellywood outfull (north transect) | HOL N 800 | | 78 | 77 Seas 1-2 summariclear skies wind SW 10-15k | | ASJACE | | 10 0.25e | |
| /4/19 | Hollywood outfall (west transect) | HOL W 800 | | 69 | Seas 1-2 summiliar skies wind SW 10-15k | Couldn't see ploe, sampled in sand next to coordinate | KK/PQ | | 11 0.25# | |
| /4/19 | Hollywood outfall (west transect) | HOL W 1800 | | 20 | Sean 1-2 summaiclear skietswind SW 10-15k | Could see pipe, sampled in sand next to it | KK/PO | | 12 0.25g | |
| 1/5/19 | Broward North WWTP Dutfail (plot) | DRN Sed | 3 | DIS | 73 Seat 3-2 sunna/part cloud;wind W/NW 5-50k | Below mouth of pipe | KK/KG | | 13 0.25g | |
| 0.0.9 | Broward North WWTP Dutful pipel | BRN H20 | 1 | D6 | 78 Sea 1-2 sunne/part cloud wind W/NW 5-10k | From inside mouth of pipe | KK/KG | | 14 2504 | |
| 1/5/19 | Hellywood outfall (pipe) | HOL_Sed | | 99 | 75 Seas 3-2;sunny/part cloud;wind W/NW 5-50k | Below mouth of pipe | AR/PQ | | 15 0.35g | |
| 1/5/19 | Hellywood outfall (alpe) | HOL H20 | | 99 | 75 Seat 5-2 sunny/part cloud, wind W/NW 5-53k | From inside mouth of pipe | AR/PQ | | 16 250ul | |
| 1/5/19 | Hollywood outfall (resettal) | HOL 5.25 | | 99 | Seas 3-2 sunna/part cloud, wind W/NW 5-10k | | AR/PQ | | 17 0.25g | |
| 15/39 | Hellywood outfail insettel | HOLE SO | | 99 | Seas 3-2 sunna/part cloud wind W/NW 5-10k | | AR/PO | | 18 0.25e | |
| 6/19 | Hollywood outfall (resette) | HOL 54 25 | | 99 | Seas 1-2 winne/part cloud/wind W/NW 5-50k | | AR/PO | | 19 0.25g | |
| /5/19 | Hollywood outfall (resette) | HOL SE SD | | 99 | Seas 1-2 sunny/part cloud/wind W/NW 5-50k | | AR/PQ | | 20 0.35g | |
| 5/15 | Hellywood outfall (resette) | HOL 5.25 | | 99 | Sees 3-2 sunny/part cloud wind W/NW 5-50k | | AR/PO | | 21 0.25g | |
| 15/14 | Hollywood outfall (resette) | HOL 5.50 | | 99 | Seas 1-2, write/part cloud/wind W/NW 5-50k | | AR/PO | | 22 0.35g | |
| 15/19 | Heilywood outfull (resette) | HOLN 25 | | 68 | Seas 3-2 swnmelpart cloud, wind W/NW 5-50k | | ND/KK | | 23 0.25g | |
| 6/19 | Hellywood outfull (resette) | HOL N SO | | 68 | Sees 1-2 sunnelpart cloud wind W/NW 5-50k | | ND/KK | | 24 0.25g | |
| 5/19 | Hellywood outfall (resetted | HOL NW 25 | | 68 | Seas 3-2 sunny/part cloud wind W/NW 5-128 | | ND/KK | | 25 0.25g | |
| 5/19 | Hellywood outfull (resette) | HOL NW 50 | | 68 | Sees 1-2 sunnelpart cloud, wind W/NW 5-10k | | ND/KK | | 26 0.25g | |
| 5/19 | Hellywood outfall (resette) | HOLSW_25 | | 88 | Sees 1-2 sunnulpart cloud, wind W/NW 5-50k | | AS/EH | | 27 0.25e | |
| 5/19 | Hellywood outfall (resette) | HOL SW 50 | | 88 | Sees 1-2 summilizert cloud/wind W/NW 5-50k | | ALOH | | 28 0.25e | |
| 5/39 | Hellywood outfull (resette) | HOL W 25 | | 88 | Sees 3-2 sunmilizert cloud, wind W/NW 5-32k | | A5/DH | | 29 0.25g | |
| (5/19 | Hellywood outfall (resette) | HOL W S0 | | 68 | Seas 3-2 sunmilizert cloud, wind W/NW 5-30k | | A5/D1 | | 30 0.25¢ | |
| 15/19 | Hellywood outfall (resette) | HOL NE 25 | | 95 | Seas 1-2 submy/part cloud wind W/NW 5-10k | | KK/KQ | | 31 0.25¢ | |
| 5/19 | Hellywood outfull (resette) | HOL NE 50 | | 95 | See 1-2 summinant cloud wind W/NW 5-10k | | KK/KG | | 32 0.25e | |
| 5.0.9 | Hellywood outfall (west transect) | HOL W 100 | | 85 | Seas 1-2 sunnulpart cloud, wind W/NW 5-50k | | AR/PO | | 33 0.25e | |
| 6/19 | Hellywood outfall (west transect) | HOL W 200 | | 85 | Seas 3-2 sunnelpart cloud, wind W/NW 5-30k | | AL/PO | | 34 0.254 | |
| 6/19 | Hollywood outfall (west transect) | HOL W 400 | | 65 | Seas 3-2 sunny/part cloud wind W/NW 5-30k | | AN/PO | | 35 0.234 | |
| 7/15 | Broward North WWTP | DRN WWTP effluent | 0/4 | nia | n/a | effluent, right before goes to outfall pipe, outside tank | AS | | 36 250al | |
| 003 | Hellywood WWTP | HOL WWTP efficient | n/s | n/a | n/a | effuent, from spigot inside building | AS | | 37 2504 | |
| 0/19 | Hellywood WWTP | HOL WWTP influent | n/a | n/a | n/a | influent, from spigot inside building | AS | | 38 2504 | |
| /11/19 | Mami-Oade North WWTP | MON WWTP efficient | 0/2 | n/a | n/a | effuent, from spleot inside building | AS | | 39 250pl | |
| /11/19 | Mami-Dade North WWTP | MON WWTP influent high | n/a | 0,0 | n/a | influent, from spigot outside* | AS | *these the | 40 250vl | |
| /11/19 | Mami-Oade North WWTP | MDN WWTP influent med | n/a | n/a | n/a | influent, from spigat outside* | AS | | 41 250vl | |
| /11/19 | Mami-Gade North WWTP | MDN WWTP influent low | n/a | nia | n/a | influent, from spigot outside* | AS | | 42 250sl | |
| 0.455.55 | | | | | - X | | 170 | | | |
| | | | | | | | | | water samples + 250ul out of a St | 004 |
| | | | | | | | | | sediment samples = "0.25g | |

20 March 2019

Weighed out ~0.25 grams of each sediment sample and placed in Qiagen bead beating tubes. Placed in the -20°C freezer. Processed the 10 water/sewage samples as described on 6 July 2018 and placed in the -20°C freezer.

22 March 2019

Extracted DNA from all the samples using Qiagen's Powersoil Kit. Eluted DNA with 100µl of Qiagen's AE buffer and placed in -20°C freezer.

4 April 2019

Set up and run positive control reactions for each primer/probe target set and its corresponding IDT gBlock target clone. aadA2 gBlock did not amplify. Reordered primers/probe and gBlock clone. All other target clones resulted in amplification.

15 April 2019

Set up and run positive control reactions aadA2. Successful amplification required new primer set. Set up and run PCR for tetB/IPC, tetL/tetM and tetO/tetW PCR assays for all 42 samples. Include negative and positive controls as well as the IPC for the tetB plate. Each target set required one 96-well plate.

16 April 2019

Set up and run PCR for ampC/vanA, ermB/mecA, blaSHV/blaPSE and floR/aadA2 PCR assays for all 42 samples. Included negative and positive controls.

17 April 2019

Set up and run PCR for tetG/tetQ PCR assays for all 42 samples. Included negative and positive controls.

Results

Wet season

Florida Keys sample sets

The 24 Florida Keys samples were composed of two 12 sample sets (one pretreatment and one post-treatment with amoxicillin) with each set containing 4 sediment, 4 coral mucus and 4 water column samples (see the following spreadsheet – greyed area is pretreatment samples, no color is post-treatment samples). The tetB resistance target was detected in all of the water and coral mucus samples but not in the pre-treatment sediments. None of the other antibiotic resistance gene targets were detected in this pre-treatment sample set. Following treatment of the diseased corals with amoxicillin (2-weeks post-treatment) the same number and sample types were collected. In this sample set the tetB target was again detected but in only one of the mucus samples. In addition, the blaSHV target which imparts resistance to amoxicillin was detected in one water column and one coral mucus sample.

| Α | В | C D | E | F | G | н | 1 | 1 | K | L | M | N | 0 | P | Q | R |
|--------|------------------|--------------|-------|------|------|------|------|------|------|------|--------|--------|------|-------|------|------|
| ube # | Sample type Samp | le site tetB | teti. | tetM | tetO | tetW | ampC | vanA | ermB | mecA | blaSHV | blaPSE | floR | aadA2 | tetG | tetQ |
| Keys 1 | mucus - pret | 2 (++) | | | | | | | | | | | | | | |
| | 2 water - pretr | 1 (++) | | | | | | | | | | | | | | |
| | 3 sediment - r | 2 | | | | | | | | | | | | | | |
| | 4 water - pret | 1 (++) | | | | | | | | | | | | | | |
| | 5 water - pretr | 2 (++) | | | | | | | | | | | | | | |
| | 6 water - pret | 2 (++) | | | | | | | | | | | | | | |
| | 7 sediment - ; | 1 | | | | | | | | | | | | | | |
| | 8 mucus - pre | 1 (++) | | | | | | | | | | | | | | |
| | 9 mucus - pre | 1 (++) | | | | | | | | | | | | | | |
| | 10 sediment - ; | 2 | | | | | | | | | | | | | | |
| | 11 sediment - p | 1 | | | | | | | | | | | | | | |
| | 12 mucus - pret | 2 (++) | | | | | | | | | | | | | | |
| | 13 sediment - p | 2 | | | | | | | | | | | | | | |
| | 14 sediment - p | 2 | | | | | | | | | | | | | | |
| | 15 water - post | 2 | | | | | | | | | | | | | | |
| | 16 sediment - p | 1 | | | | | | | | | | | | | | |
| | 17 sediment - p | 1 | | | | | | | | | | | | | | |
| | 18 mucus - pos | 2 (++) | | | | | | | | | | | | | | |
| | 19 mucus - post | 2 | | | | | | | | | | | | | | |
| | 20 water - post | 1 | | | | | | | | | | | | | | |
| | 21 water - post | 2 | | | | | | | | | | | | | | |
| | 22 water - post | 1 | | | | | | | | | (++) | | | | | |
| | | | | | | | | | | | (++) | | | | | |
| | 23 mucus - post | 1 | | | | | | | | | | | | | | |

Table 4. Florida Keys PCR data

Blank = negative reaction, (+/+) = positive reaction.

Southeast Florida sample set

The Southeast Florida wet season sample set was composed of 6 wastewater samples (samples highlighted in yellow in the following spreadsheet) collected at three different wastewater treatment plants, their respective outfalls, and 32 sediment samples collected at those outfalls and in an array and along transects centered on the Hollywood outfall. Nine of the antibiotic resistance genes were detected in the sample set. The most prevalent antibiotic resistance genes detected in the samples were tetW and aadA2 at 68.4 and 60.5%, respectively. Seven (tetB, tetW, ampC, vanA, ermB, mecA and tetQ) of the fifteen antibiotic resistance genes were detected in the wastewater samples and six (tetO, tetW, ampC, vanA, mecA and aadA2) were detected in the sediment samples. tetB, ermB and tetQ were only detected in the wastewater samples and tetO and aadA2 were only detected in the samples. A following heatmap illustrates the occurrence of the different numbers of antibiotic resistance genes detected at each site.

Table 4. Southeast wet season PCR data

| Α | В | C D | E | F | G | н | 1 | J | K | L | M | N | 0 | Р | Q | R |
|-------------|-------------|-----------------------|-------------------|------|-------|-------|-------|-------|-------|--------|--------|--------|------|-------|------|-------|
| ube # | Sample type | Sample site tetB | tetL | tetM | tetO | tetW | ampC | vanA | ermB | mecA | blaSHV | blaPSE | floR | aadA2 | tetG | tetQ |
| Broward 1 | water | Broward Nor (+/+) | | | | | | | | | | | | | | (+/+) |
| 2 | water | Broward North WW1 | P outfall pipe - | H2O | | | | | | | | | | | | |
| 3 | water | Hollywood W (+/+) | | | | | (+/+) | (+/+) | (+/+) | (+/+) | | | | | | (+/+) |
| 4 | water | Hollywood WWTP ou | tfall pipe - H2O | | | (+/+) | | | (+/+) | | | | | | | (+/+) |
| 5 | water | Miami Dade (+/+) | | | | | | | (+/+) | | | | | | | (+/+) |
| 6 | water | Miami Dade (+/+) | | | | | | | (+/+) | | | | | | | (+/+) |
| 7 | sediment | Broward North WWT | P outfall pipe - | sed | | (+/+) | | | | | | | | (+/+) | | |
| 8 | sediment | Hollywood outfall - S | (transect) sed1 | 100 | | (+/+) | | | | (+/+) | | | | | | |
| 9 | sediment | Hollywood outfall - S | (transect) sed | 200 | | (+/+) | | | | | | | | (+/+) | | |
| 10 | sediment | Hollywood outfall - S | (transect) sed | 400 | | (+/+) | | | | | | | | (+/+) | | |
| 11 | sediment | Hollywood outfall - S | (transect) sed | 800 | | (+/+) | | | | | | | | (+/+) | | |
| 12 | sediment | Hollywood WWTP ou | tfall pipe - sed | | | (+/+) | | | | | | | | (+/+) | | |
| 13 | sediment | Hollywood outfall - E | (rosette) sed25 | 5 | | | | | | (+/+) | | | | | | |
| 14 | sediment | Hollywood outfall - E | (rosette) sed50 |) | | | | | | | | | | | | |
| 15 | sediment | Hollywood outfall - S | E (rosette) seda | 25 | | | | | | | | | | | | |
| 16 | sediment | Hollywood outfall - S | E (rosette) sed5 | 50 | | | | | | | | | | | | |
| 17 | sediment | Hollywood outfall - N | (rosette) sed2 | 5 | | | | | | | | | | | | |
| 18 | sediment | Hollywood outfall - N | (rosette) sed5 | 0 | | | | | | | | | | | | |
| 19 | sediment | Hollywood outfall - N | E (rosette) sed | 25 | | (+/+) | | (+/+) | | (+/+) | | | | (+/+) | | |
| 20 | sediment | Hollywood outfall - N | E (rosette) sed | 50 | | (+/+) | (+/+) | | | | | | | (+/+) | | |
| 21 | sediment | Hollywood outfall - N | W (rosette) see | d25 | (+/+) | (+/+) | (+/+) | | | (+/+) | | | | (+/+) | | |
| 22 | sediment | Hollywood outfall - N | W (rosette) see | d50 | | (+/+) | (+/+) | | | | | | | (+/+) | | |
| 23 | sediment | Hollywood outfall - V | V (rosette) sed2 | 25 | | (+/+) | (+/+) | | | | | | | (+/+) | | |
| 24 | sediment | Hollywood outfall - V | V (rosette) sed5 | 50 | | (+/+) | (+/+) | | | | | | | | | |
| 25 | sediment | Hollywood outfall - S | W (rosette) sed | 125 | (+/+) | (+/+) | (+/+) | | | | | | | (+/+) | | |
| 26 | sediment | Hollywood outfall - S | W (rosette) sed | 150 | | (+/+) | | | | | | | | (+/+) | | |
| 27 | sediment | Hollywood outfall - S | | | (+/+) | (+/+) | | | | | | | | (+/+) | | |
| 28 | sediment | Hollywood outfall - S | (rosette) sed5 | 0 | (+/+) | (+/+) | | | | (+/+) | | | | (+/+) | | |
| 29 | sediment | Hollywood outfall - V | V (transect) see | d100 | (+/+) | (+/+) | (+/+) | | | | | | | (+/+) | | |
| 30 | sediment | Hollywood outfall - V | V (transect) sed | 200 | | (+/+) | | | | (+/+) | | | | | | |
| 31 | sediment | Hollywood outfall - V | V (transect) sed | 400 | (+/+) | (+/+) | (+/+) | | | (+/+) | | | | (+/+) | | |
| 32 | sediment | Hollywood outfall - V | V (transect) sed | 800 | (+/+) | | (+/+) | | | | | | | (+/+) | | |
| 33 | sediment | Hollywood outfall - V | V (transect) sed | 1600 | (+/+) | (+/+) | | | | | | | | (+/+) | | |
| 34 | sediment | Hollywood outfall - N | (transect) sed: | 100 | (+/+) | (+/+) | | | | | | | | (+/+) | | |
| 35 | sediment | Hollywood outfall - N | (transect) sed | 200 | | (+/+) | (+/+) | | | | | | | (+/+) | | |
| | sediment | Hollywood outfall - N | | | | (+/+) | (+/+) | | | | | | | (+/+) | | |
| | sediment | Hollywood outfall - N | | | | (+/+) | | | | | | | | (+/+) | | |
| | sediment | Miami Dade North W | | | | (+/+) | (+/+) | | | | | | | (+/+) | | |
| | | | | | | | | | | | | | | | | |
| percent pos | tive | | 10.5 | 0 | 0 23. | 7 6 | 8.4 | 34.2 | 5.2 1 | 0.5 21 | .1 | 0 | 0 0 |) 6 | 0.5 | 0 1 |

Blank = negative reaction, (+/+) = positive reaction.

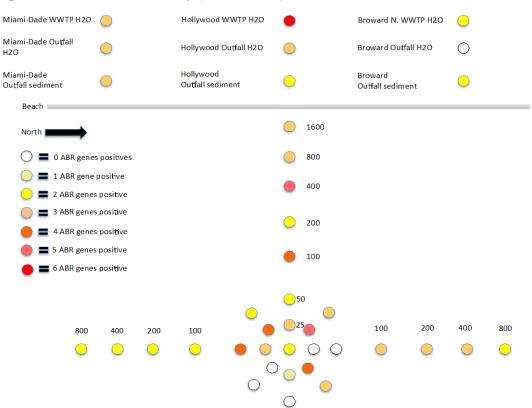


Figure 1. Wet season heatmap (not to scale)

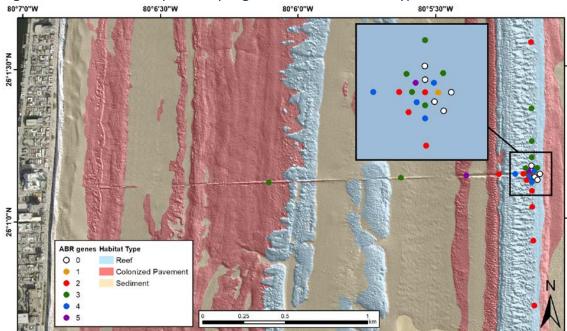


Figure 2. Wet season map of sampling locations and habitat type

Dry season

The dry season sample set was composed of 10 wastewater samples (samples highlighted in yellow in the following spreadsheet) collected at three different wastewater treatment plants, their respective outfalls, and 32 sediment samples collected at those outfalls and in an array and along transects centered on the Hollywood outfall. Ten of the antibiotic resistance genes were detected in the sample set. The most prevalent antibiotic resistance genes detected in the samples were ermB and tetW at 35.7 and 31.0%, respectively. Ten (tetB, tetM, tetO, tetW, ampC, vanA, ermB, mecA, blaSHV and tetQ) of the fifteen antibiotic resistance genes were detected in the sediment samples. tetB, tetM, tetO, mecA, blaSHV and tetQ were only detected in the wastewater samples and all of the four antibiotic resistance genes found in the sediment samples were also detected in the wastewater samples. A following heatmap illustrates the occurrence of the different numbers of antibiotic resistance genes detected at each site.

| A | 8 | C | D | E | F | G | н | 1 | 1 | к | 1 L | M | N | 0 | P | Q | R 5 |
|-------------|---|-------|-------|-------|-------|-------|-------|-------|-------|-------|-----------|--------|--------|-------|-------|-------|-----------------------|
| ample typ | e Sample site | tet8 | teti. | tetM | tetO | tetW | ampC | vanA | ermB | mecA | blaSHV | blaPSE | floR | aadA2 | tetG | tetQ | USGS lab sample numbe |
| water | Broward North WWTP - effluent | (+/+) | | | | (+/+) | (+/+) | | (+/+) | | | | | | | (+/+) | 35 |
| water | Broward North WWTP outfall pipe - H2D | (+/+) | | | | (+/+) | (+/+) | | (+/+) | (+/+) | | | | | | (+/+) | 14 |
| water | Hollywood WWTP - influent | (+/+) | | (+/+) | (+/+) | (+/+) | | | (+/+) | (+/+) | | | | | | (+/+) | 38 |
| water | Hollywood WWTP - effluent | | | | | (+/+) | (+/+) | (+/+) | (+/+) | | | | | | | | 37 |
| water | Hollywood WWTP outfall pipe - H2O | (+/+) | | | (+/+) | (+/+) | (+/+) | | (+/+) | (+/+) | (+/+) | | | | | (+/+) | 16 |
| water | Miami Dade North WWTP - influent - high | (+/+) | | (+/+) | (+/+) | (+/+) | (+/+) | (+/+) | (+/+) | (+/+) | (+/+) | | | | | (+/+) | 40 |
| water | Miami Dade North WWTP - Influent - medium | (+/+) | | | (+/+) | (+/+) | (+/+) | (+/+) | (+/+) | (+/+) | | | | | | (+/+) | 41 |
| water | Miami Dade North WWTP - Influent - low | (+/+) | | | (+/+) | (+/+) | (+/+) | (+/+) | (+/+) | (+/+) | | | | | | (+/+) | 42 |
| water | Miami Dade North WWTP - effluent | (+/+) | | | | (+/+) | | | (+/+) | (+/+) | | | | | | (+/+) | 39 |
| water | Miami Dade North WWTP outfall pipe - H2O | (+/+) | | | (+/+) | (+/+) | (+/+) | | (+/+) | (+/+) | (+/+) | | | | | (+/+) | 2 |
| sedment | Broward North WWTP outfall pipe - sed | | | | | (+/+) | | | (+/+) | | | | | | | | 13 |
| sedment | Hollywood outfail - 5 (transect) sed100 | | | | | | | | (+/+) | | | | | | | | 6 |
| sediment | Hollywood outfail - 5 (transect) sed200 | | | | | | | | (+/+) | | | | | | | | 5 |
| sediment | Hollywood outfall - S (transect) sed400 | | | | | | | | | | | | | | | | 4 |
| sediment | Hollywood outfall - S (transect) sed800 | | | | | | | | | | | | | | | | 3 |
| sediment | Hollywood WWTP outfall pipe - sed | | | | | (+/+) | | | (+/+) | | | | | | | | 15 |
| sedment | Hollywood outfall - E (rosette) sed25 | | | | | | | | | | | | | | | | 17 |
| ediment | Hollywood outfall - E (rosette) sed50 | | | | | | | | | | | | | | | | 18 |
| ediment | Hollywood outfall - SE (rosette) sed25 | | | | | | | | | | | | | | | | 19 |
| sediment | Hollywood outfall - SE (rosette) sed50 | | | | | | | | | | | | | | | | 20 |
| sediment | Hollywood outfall - N (rosette) sed25 | | | | | | | | | | | | | | | | 23 |
| sediment | Hollywood outfall - N (rosette) sed50 | | | | | | | | | | | | | | | | 24 |
| sediment | Hollywood outfall - NE (rosette) sed25 | | | | | | | | | | | | | | | | 31 |
| sediment | Hollywood outfall - NE (rosette) sed50 | | | | | | | | | | | | | | | | 32 |
| sedment | Hollywood outfall - NW (rosette) sed25 | | | | | | | | | | | | | | | | 25 |
| sedment | Hollywood outfall - NW (rosette) sed50 | | | | | | | | | | | | | | | | 26 |
| sedment | Hollywood outfall - W (rosette) sed25 | | | | | | | | | | | | | | | | 29 |
| sediment | Hollywood outfall - W (rosette) sed50 | | | | | | | | | | | | | | | | 30 |
| sediment | Hollywood outfail - SW (rosette) sed25 | | | | | | | | | | | | | | | | 27 |
| sedment | Hollywood outfall - SW (rosette) sed50 | | | | | | | | | | | | | | | | 28 |
| sediment | Hollywood outfall - S (rosette) sed25 | | | | | | | | | | | | | | | | 21 |
| sediment | Hollywood outfall - S (rosette) sed50 | | | | | | | | (+/+) | | | | | | | | 22 |
| sedment | Hollywood outfall - W (transect) sed100 | | | | | | | | | | | | | | | | 33 |
| sedment | Hollywood outfall - W (transect) sed200 | | | | | | | | | | | | | | | | 34 |
| sediment | Hollywood outfall - W (transect) sed400 | | | | | | (+/+) | (+/+) | | | | | | | | | 35 |
| sedment | Hollywood outfall - W (transect) sed800 | | | | | | 1000 | 1000 | | | | | | | | | 11 |
| sediment | Hollywood outfall - W (transect) sed1500 | | | | | | | | | | | | | | | | 12 |
| sediment | Hollywood outfall - N (transect) sed100 | | | | | | | | | | | | | | | | 8 |
| sediment | Hollywood outfall - N (transect) sed200 | | | | | | | | | | | | | | | | 7 |
| sedment | Hollywood outfall - N (transect) sed400 | | | | | | | | | | | | | | | | 9 |
| sediment | Hollywood outfall - N (transect) sed800 | | | | | | | | | | | | | | | | 10 |
| sediment | Miami Dade North WWTP outfall pipe - sed | | | | | (+/+) | | | (+/+) | | | | | | | | 1 |
| percent por | sitive | 2 | 1.4 | 0 | 4.8 1 | 4.3 | 31 2 | 1.4 1 | 1.9 3 | 5.7 | 19 3 | 2.4 | 0 | 0 | 0 | 0 21 | A |
| | IPC (control) at 27 cycles to an Rn of 0.1, all IPC | | | | | | | 500g | | 2004 | -500 Grid | | 1. Sec | 117 | 1.7.8 | | |

Table 5. Dry season PCR data

Blank = negative reaction, (+/+) = positive reaction.

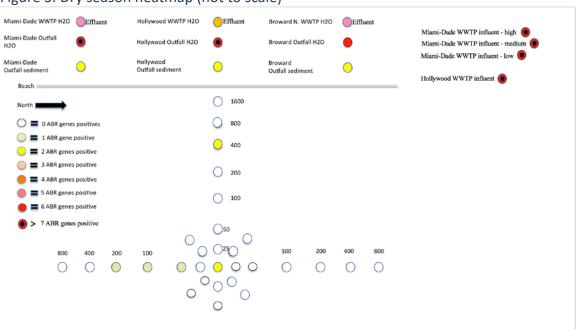
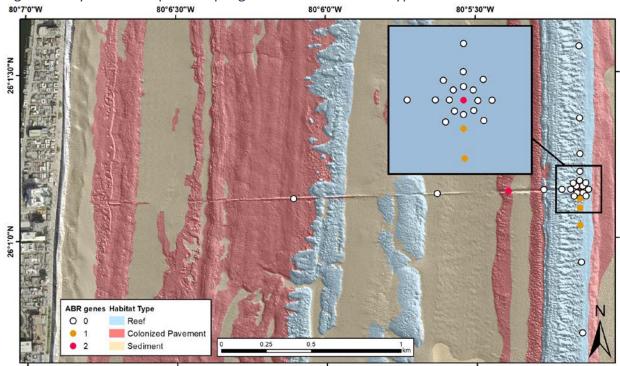


Figure 3. Dry season heatmap (not to scale)





Conclusion

The Southeast Florida data illustrates that antibiotic resistance genes are readily detectable in the wastewater stream and in sediments close to and alongside the outfall and outfall pipe. The wet season data set illustrates widespread occurrence of multiple antibiotic resistance genes with the highest occurrences occurring in the wastewater stream and alongside the Hollywood outfall pipe and in close proximity to the outfall. The dry season data illustrates concentrated occurrence in the wastewater stream but less offshore occurrence relative to the wet season data. The offshore positive samples are associated along the outfall pipe, the outfall and along the southern transit. The prevalence flip between the seasons is interesting, with the wet season showing a lower prevalence in the wastewater stream and higher prevalence in the sediment samples and the opposite trend occurring in the dry season. The Florida Keys data set illustrates little background occurrence, but it does demonstrate acquisition of resistance following a specific (amoxicillin) exposure event.

Sewage associated wastewater is well known to carry numerous antibiotics due to public health use. Microbial communities under the influence or stress of antibiotic laden wastewater will acquire resistance. Microbial communities are known to share resistant genes within and across genera when there is an exposure source, even at a heightened metabolic cost (5, 6). These data illustrate that type of microbial response. The data indicate that there is a heightened prevalence of these genes in the wet season that may be due to factors such as seasonal water temperatures, seasonal wastewater discharge rates, seasonal antibiotic usage and coastal flow dynamics. Members in these coastal microbial communities may present risks to recreational water use and to the ecosystem itself. It should be acknowledged that there are very few scientific journal articles published on the topic of antibiotic resistant bacteria in coastal environments that would allow us to contrast the outfall related data reported here. The Florida Keys sample set may illustrate a more normal profile that would be expected given a lower human population and no local outfall influences. The Florida Keys data does however illustrate the possible consequences of releasing or using antibiotics in coastal marine and coral reef environments.

Recommendations

"This work is a follow-on to the pilot study results from 14ESFUSAFDEP3519 completed between 10/2014 & 9/2016. This project is a continuation of the SE Florida Coral Reef Initiative (SEFCRI) Technical Advisory Committee's recently concluded Outfall Biomarker Pilot Project (LBSP 28/29 Phase I) and builds upon the results and outcomes of that initial work." (current FLDEP/USGS FUSA agreement for this project)

The LBSP 28/29 Phase 1 data indicated a degree of toxicity in samples collected near the outfall. This current project was undertaken to further investigate that observation and more specifically to demonstrate if genetic based changes could be observed due to association with a contaminant source.

I would recommend screening sites in the future where antibiotics may be utilized in coral disease trials. This particular approach of using antibiotic resistance genes as a marker for anthropogenic sources of pollution may also be very useful in addressing the extent of inlet influences into our coral reef communities in Southeast Florida. To contrast this current data set given the stark seasonal change, a four-season study may provide additional insight. Additionally, a heatmap of the Southeast Florida Coral Reef Ecosystem Conservation Area in peak and/or low prevalence season would be of global significance. It may also be helpful in regard to potential remediation pathways to analyze samples where wastewater is being released into the environment from a system that utilizes a more advanced level of sewage treatment (e.g., soils from the sprayfields utilized by the City of Tallahassee).

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