

Raritan River Pathogens Trackdown Collaborative Meeting
September 26, 2022 - Notes

EPA 2022 Sampling Efforts:

Stan Stephansen gave the collaborative an update on EPA’s 2022 pathogen sampling. Zone 3 was split into Sections A, B, and C. (The enterococcus data can be found on the EPA sharepoint site for this project at <https://usepa.sharepoint.com/sites/R2CSOPathogenProject>)

August intense wet weather sampling had high enterococcus values in Zone 3, Sections A and B. EPA is still waiting for the Human Fecal marker genetic sampling data from those samples. These samples will be used to identify potential hotspots, as several of the sites are adjacent to Bound Brook and Ambrose Brook.

Bob Schuster (NJDEP) discussed the wet weather timing of the samples. His sampling work indicates that the first flush after wet weather can have a very high enterococcus values, and that can be very informative to find hotspots.

Heather Fenyk (LRWP) asked if EPA or NJDEP were aware of any dissipation models in a riverine or tidal system. Neither were aware of any. Heather also asked if the EPA data would be available to the public. Stan replied that all the data will be placed into EPA’s water quality portal. Adam Fisher (EPA) stated that 2021 data is in the portal now, and the 2022 data will be uploaded shortly.

USGS Potential Work on the Raritan

Pam Reilly (USGS) stated that the USGS NJWSC uses MST studies in NJ for source trackdown projects and analysis for the following markers are performed at the [USGS Ohio Microbiology Lab](#). Studies were done on the Second, Third and Saddle Rivers of the Passaic River basin as part of the Urban Waters Federal Partnership, in collaboration with PVSC and the EPA. Future work in the Raritan River basin is planned. Below are the markers used:

Target analyte	Description	Reference	Water:		Solids (Known Source Samples):	
			Parameter/method codes	Parameter/method codes	Parameter/method codes	Parameter/method codes
HF183/BacR287	targets 16S rRNA sequence of <i>Bacteroides</i> ; human associated	Bernhard and Field, 2000; Green and others, 2014	31898	PCR95	31899	PCR95

GFD	targets 16S rRNA sequence of <i>Helicobacter</i> ; avian associated	Green and others, 2012	31810	PCR32	31811	PCR32
Rum-2-Bac	targets 16S rRNA sequence of <i>Bacteroides</i> ; ruminant associated	Mieszkin and others, 2010	31808	PCR30	31809	PCR30
CowM2	targets rRNA sequence of <i>Bacteroides</i> ; cattle associated	Shanks and others, 2008	31806	PCR31	31807	PCR31
CL	targets 16S rRNA sequence of <i>Brevibacterium</i> ; poultry associated	Ryu and others, 2014	31902	PCR97	31903	PCR97
Hor-Bac	targets 16S rRNA sequence of <i>Bacteroides</i> ; horse associated	Tambalo and others, 2012	31900	PCR96	31901	PCR96
BacCan	targets 16S rRNA sequence of <i>Bacteroides</i> ; canine associated	Kildare and others, 2007	68206	BACCA	31805	BACCA

Mike Flood (EPA) thought this information would be extremely helpful to understand entero inputs to the Raritan watershed and posited that we may be able to work with USDA to assist farmers to lower agriculture derived entero inputs to the Raritan. Dr. Wu (Montclair State) stated that she is already working with USDA on the Delaware River and agreed that USDA will be a good partner to bring on board after the USGS work is completed.

Microbial Source Trackdown 2021 Genetic Markers

Rosana Pedra Nobre (HEP) discussed that in June 2022, HEP had 5 preserved filters from water samples of EPA's 2021 efforts sent from U.S. EPA Region 2 Laboratory at the Edison to the USGS Ohio Water Microbiology Laboratory (OWML). These samples were analyzed for microbial source tracking (MST) markers associated with human, ruminant, cattle, waterfowl, canine, and horse fecal sources. Those 5 samples had some of the highest enterococcus levels found in the 2021 sampling season and were from Zone 2 near New Brunswick. Below are the results.

Table 2. Water sample information and results.

LIMS #	Sample Date	Station Name	HF183/BacR287	Rum2Bac	CowM2	GFD	BacCan	HorBac
---copies per 100 mL---								
6022-01	6/4/2021	ELR-2-005-060421	59,000	2,500	<1,200	<260	31,000	<340
6022-02	6/4/2021	ELR-2-006-060421	2,900	4,100	<1,200	<260	18,000	<340
6022-03	6/4/2021	ELR-2-007-060421	19,000	2,400	<1,200	<260	14,000	<340
6022-04	7/30/2021	ELR-2-006-073021	8,800	1,200 Eb	<1,200	<530	6,400	<340
6022-05	7/30/2021	ELR-2-007-073021	6,600	1,400 Eb	<1,200	<530	5,000	<340
Simulated Blank	N/A	N/A	<310	<960	<1,200	<260	<550	<340

[HF183/BacR287, human-associated *Bacteroides* marker; Rum2Bac, ruminant-associated *Bacteroides* marker; CowM2, cattle-associated *Bacteroides* marker; GFD, waterfowl-associated *Helicobacter* marker; BacCan, canine-associated *Bacteroides* marker; HorBac, horse-associated *Bacteroides* marker; Remark code: E, estimate; <, less than the sample limit of detection; b, concentration is below the limit of quantification but above the limit of detection; N/A, not applicable

Mike Flood explained that there is not enough data to make any definitive conclusions, however, it indicates the presence of dog and ruminant genetic markers.

Partner Updates:

Jocelyn Palomino (LRWP) stated that the LRWP sampling has been going well, with sampling every week during the summer. The data is placed on the Rutgers University Raritan River Hydrological Observatory mapping tool and on the LRWP website each week.

Nichole Farhenfeld (Rutgers Univ.) stated that Rutgers has been saving paired samples from the LRWP 2022 sampling and will also be doing analysis for genetic markers.

Respectfully,

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