Connecting Hudson River Estuary water quality to microbial aerosols at the urban waterfront

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Introduction

Aerosols produced from bubbles bursting in surface waters in coastal and estuarine areas carry chemical and microbial content to shore, forming a connection between oceanic, atmospheric and terrestrial systems that is potentially relevant to coastal microbial ecology and human health [1-2]. Because of long atmospheric residence times (days to weeks) and long distance transport potential (100's to 1000's km), fine aerosols (PM2.5) are the usual focus of atmospheric aerosol studies [3]. Bacterial aerosols, however, are most often associated with particles in the inhalable coarse aerosol fraction (PM10-PM2.5) [4]. While the microbial component of atmospheric aerosols has long been recognized as a source for human allergies and disease transmission [5] and is thought to play an important role in the observed cosmopolitan distribution of some species of bacteria [6], the ocean contribution of bacteria to the atmosphere has yet to be fully characterized, especially in the near-shore environment.

A recent review estimated that 50 – 1000 bacterial cells m^{-2} s^{-1} are emitted from marine waters globally [4]. This most likely underestimates emissions from coastal waters, where microbial abundances can be higher than the open ocean [7], and aerosol production is increased by wind-wave and wave-shore interactions, recreational activities (e.g. boat wakes) and management efforts (e.g. aeration of polluted waters). Today, about half of the world's population lives within 200 kilometers of a coastline, and by 2025, that figure is likely to double [8]. In 2003, 23 of the 25 most densely populated U.S. counties were coastal [9]. With subsequent increases in wastewater input to rivers, estuaries and coastal waters [10], microbial aerosol production at these coastlines should be a pressing concern. Studies have shown a connection between proximity to polluted waters and respiratory illness [11-13] and between asthma and airborne bacterial cell concentrations [14]. The scope of this issue may broaden with climate change, given that storm frequency is expected to increase at many coastlines, which will result in greater sewage delivery to urban water bodies and elevated winds to drive aerosol production [15]. Also, anthropogenic influences on global atmospheric water content [16] can profoundly affect aerosol particle size (and therefore transport) and microbial aerosol viability [17-20].

In coastal settings, coarse aerosol particles are primarily products of bursting bubbles in surface waters [21-23]. Once formed, onshore winds transport these particles over land, where they are eventually deposited through gravitational settling, inhalation, or surface interception. Upon release into saline waters, fresh water sewage (containing human pathogens) remains in a lens at the surface, where bubbles can release this material into the air [6]. Probability of human contact with airborne pathogens can be expressed as the concentration of infective material in a given atmosphere at a given time and the number of susceptible individuals in that locale [24]. The likely high concentration of infective agents in raw sewage CSO discharges [25-26] coupled with the high density of people in coastal urban environments implies the potential for airborne infection if aerosol formation is efficient at the water's edge.

Despite increasing evidence that air quality and water quality may be linked in coastal settings, the abundance of microbial aerosols, the factors that determine their aerosolization, concentrations, viability and dispersal have yet to be characterized. To address these current knowledge gaps, the study outlined here was conducted on two waterfronts of the Hudson River

Estuary (HRE), which has a long history of degraded water quality [27], and a dense waterfront population [28] potentially exposed to microbial aerosol discharge from estuarine waters.

This study had three goals:

- to quantify the role of aeration remediation in production and deposition of coarse and viable microbial aerosols at the urban waterfront
- to characterize the viable microbial aerosol community at the urban waterfront
- to quantify the role of wind speed in production and deposition of coarse and viable microbial aerosols at the urban waterfront.

The data briefly outlined in this report will be used to construct the final two chapters of my dissertation, to be deposited Spring 2012. Long term plans for the full findings from this study include modeling of wind speed and aeration remediation effects on coarse and microbial aerosol production and delivery at the waterfront. These models coupled with microbial aerosol species identities will be useful not only for assessing air quality and exposure risks at the urban waterfront, but also for understanding how air quality and water quality may be interconnected in coastal ecosystems globally.

Materials and Methods

Study sites and dates. To assess effects of aeration remediation on coarse and microbial aerosols, sampling was conducted at an inner-city aeration remediation site in the English Kills of Newtown Creek (Newtown Creek Aeration (NTA)) (Fig. 1). To assess effects of wind speed on coarse and microbial aerosols, sampling was conducted at Louis Valentino Pier (LVP) on the NY Harbor (Fig. 1). NTA sampling (8 September 2010 – 20 November 2010) was conducted from the R/V Riverkeeper, which was moored to a bulkhead adjacent to the aeration site. LVP sampling (6 April 2011 – 8 June 2011) was land-based, with all sampling conducted from the furthest end of the pier.

Meteorological Data. One-minute wind speed, wind direction, humidity, and temperature were collected using a Vantage Pro2 Plus Weather Station (Davis Instruments, Hayward, CA). At NTA, the weather station was placed at 4 m above water level. At LVP, the weather station was placed at 2.0 m above the pier floor (which was 2.5 - 5 m above water-level, depending on tidal height). Wind direction was used to assess local origin of sampled aerosols (marine vs. terrestrial influence). Sampling for both sites was conducted only under conditions with no wind or onshore winds (from the NW, WNW, W, SW, or SSW). At LVP, these winds provided varying fetch over water surface: NW: 3.0 km unobstructed fetch; WNW, W, WSW: 4.0 - 4.3 km unobstructed fetch; SW, SSW: 5.7-7.3 km unobstructed fetch. To assess wind speed influence on coarse aerosol concentrations and microbial aerosol deposition at LVP, results were binned by wind speed and wind direction. According to the Beaufort Wind Scale, wind speeds above 3.3 m s^{-1} are required before observing breaking waves on surface waters (which indicate new aerosol particle production). Also, previous research has shown linear increases in coastal coarse aerosol concentrations with wind speeds over 4 m s^{-1} [29]. Therefore, to detect wind speed effects on coarse aerosols at the LVP site, regression analyses were performed on samples gathered under wind speeds $\geq$ 3.3 m s^{-1}.

Aerosol particle size concentrations. Aerosol particle concentrations were measured using a stationary Met One 9012 Ambient Aerosol Particulate Profiler (Met One Instruments, Grants Pass, OR, USA). At NTA, the profiler was placed at 2.5 m above water level. At LVP, the profiler was placed at 2.0 m above the pier floor (2.5 - 5m above water level). One-minute data from this monitor were recorded in bins of 0.3, 0.7, 1, 2, 3, 5, 7 and 10 μm diameter (D_p), with a particle cut-off of ~30μm. This range of particle sizes covers both the fine (D_p = 0.3 - 2 μm) and coarse (D_p = 2- 30 μm) aerosol particle modes [3].

Microbial Aerosols and Surface Water Bacteria. I sampled the relative viability of microbes falling out of the air column by exposing triplicate agar plates for 5-50 minutes to ambient aerosols (depending on sample location and wind speed). The use of growth media plate exposures, as opposed to culture independent approaches, ensures that the microbes enumerated and characterized using molecular genetic approaches are viable and therefore able to contribute to infective load or ecological function after transport. Although this approach results in relative viability, it will also underestimate the total numbers of viable microbes. To reduce media-selection bias of microbial aerosol collection, I used both LB (Luria Broth, high nutrient media with salt) and R2A (low-nutrient media used in most aerosol studies) media. Both of these media have grown diverse microbial assemblages from aerosols and water samples in preliminary studies. At the NTA site, plates were exposed at 2.5 m above water surface. At LVP, the plates were exposed from a platform 2.0 m above the pier floor (2.5 – 5 m from water surface according to tide).

After exposure, plates were incubated for 5 days at 25ºC (room temperature) and then colony forming units (CFU) were counted and individually characterized. Microbial aerosol settling rate (CFU m^{-2} s^{-1}) was calculated using the surface area of the exposed petri dishes (0.0079 m^2) and the duration of exposure. To assess culturability of ocean surface bacteria at the site, near-shore surface water (< 1 m depth) was spread on triplicate LB and R2A plates using sterile technique. These plates were incubated and enumerated under the same conditions described for aerosol exposures. After enumeration, all media plates were stored at 4°C until colonies were sampled for molecular analysis. Material picked from colonies was suspended in 50 μl of HyClone sterile water (ThermoScientific, Logan, UT, USA) and boiled for 5 minutes to lyse the cells. This suspension was immediately frozen at -20°C until PCR was performed. All LB plates from NTA site were picked. Analysis of LVP site bacteria is currently underway.

To discern surface water and microbial aerosol community diversity and structure, 16S rRNA genes were amplified from picked colony suspensions using universal bacterial primers 8F (5'-AGRGTTTGATCCTGGCTCAG -3') and 1492R (5'-CGGCTACCTTGTTACGACTT-3') [30] with 35 PCR cycles of 45 seconds of denaturation at 94°C, 45 seconds of annealing at 55°C, and 1 minute elongation at 72°C. Agarose gel electrophoresis was conducted to confirm amplification of a single-sized DNA fragment, and to ensure that DNA-free controls did not yield amplification product. Single-read sequencing using the 8F primer was performed on amplified PCR products by SeqWright Laboratories (Houston, TX, USA). Sequences were quality-checked and edited using Geneious software [31]. Edited sequences yielding less than 300 base pairs of high quality sequence were removed from further downstream analyses. Remaining sequences were aligned using the Ribosomal Database Project (RDP) [32] and taxonomically classified using RDP's naive Bayesian rRNA classifier at an 80% confidence level [33]. Using this classification, dominant genera from the library were identified as genera

representing 5% or greater of the entire sequence library. Significant differences between sequence libraries were determined using RDP's LibCompare tool ($p < 0.05$). All other statistical analyses were performed using R statistical software (R Development Project 2008).

Results

Newtown Creek Aeration (NTA)

Five full sampling days were completed at NTA aboard the R/V R. Ian Fletcher, a Riverkeeper (www.riverkeeper.org) patrol boat. The aerator was operating on 3 days, and not operating on 2. During microbial aerosol sampling, the NTA site experienced relatively low mean wind speeds (2.67 m s^{-1}) (Table 1). Because of these low wind speeds, and the short fetch over which winds traveled before reaching samplers, wind was not expected to be a major new source of coarse aerosols from the water surface, allowing the aeration mode (on or off) to be isolated as a factor. Coarse aerosol concentrations at this site were significantly increased when the aerator was on (Welch's t-test, $p << 0.01$) (Fig. 2).

Culturable microbes both in aerosols and surface waters were abundant at this site. I measured a mean microbial fallout of 8.38 ± 0.77 cfu m^{-2} s^{-1} on R2A media and 3.81 ± 0.43 cfu m^{-2} s^{-1} on LB media (Table 1). Microbial aerosol fallout on both types of media was linearly related ($R^2 = 0.71$, $p << 0.01$, slope = 0.34 ± 0.051 (Fig. 3). Mean surface water concentrations were 2.1 (± 0.3) x 10^4 cells ml^{-1} on R2A plates, and 1.0 (± 0.2) x 10^4 cells ml^{-1} on LB plates (Table 1).

Although microbial aerosol fallout was increased with the aerator on, the increase was not statistically significant from fallout when the aerator was off (Fig. 4). When the aerator was off, there was a significant relationship between coarse aerosol concentrations and both LB and R2A microbial aerosol fallout rates (Fig. 5). For R2A, $R^2 = 0.54$, $p < 0.01$, m = 0.033 ± 0.009 and for LB, $R^2 = 0.42$, $p = 0.013$, m = 0.016 ± 0.005. When the bubbler was operating this relationship was not present.

Molecular analysis of the colonies growing on aerosol and surface water plates resulted in 549 total sequences after quality control. This sequence library included bacteria from 4 phyla: Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria (Fig. 6). The microbial aerosols were dominated by Firmicutes, whereas the surface water sequences were dominated by Proteobacteria. At the phylum level, Proteobacteria were significantly decreased (LibCompare, $p < 0.05$) in the microbial aerosols library when the aerator was on (Fig. 6).

Microbacterium sp., *Bacillus* sp., *Pseudomonas* sp. and *Shewanella* sp. dominated the total sequence library (Table 2). Although each of these dominant genera were present in both surface waters and aerosol samples, *Microbacterium* and *Bacillus* were more commonly found in surface waters, and *Pseudomonas* and *Shewanella* were more commonly found in aerosols (Table 2). According to RDP's LibCompare, there were significantly more ($p < 0.05$) Microbacteriacea (particularly *Microbacterium*) in surface waters when the aerator was on compared to when the aerator was off. Aerosols also contained significantly more *Microbacterium* ($p << 0.05$) when the aerator was on. As evidenced by Table 3, potential human pathogens were abundant both in surface waters and microbial aerosols at this site.

Louis Valentino Pier (LVP)

Nine sampling days were completed at the LVP site, which allowed for sampling of the full range of onshore wind directions (2,290 minutes of onshore winds logged) and a wide range of wind speeds (0.99 - 9.92 m s^{-1}), with a mean wind speed of 4.82 m s^{-1} (Table 4). Coarse aerosol concentrations at this site were significantly related both to wind direction and wind speed (Fig 7). Coarse aerosol concentrations at the pier initially decreased with the onset of onshore winds. When winds increased at or above 3.3 m s^{-1}, coarse aerosol concentrations increased as W and S wind speeds increased. At wind speeds at or above 3.3 m s^{-1}, aerosol concentrations were linearly related to W winds with $R^2 = 0.67$, $p << 0.01$, $m = 7.53 \pm 1.34$. S winds had an $R^2 = 0.72$, $p < 0.01$, $m = 8.96 \pm 1.92$. Winds from the N, however, showed a decreasing coarse aerosol concentration as wind speeds increased, $R^2 = 0.74$, $p << 0.01$, $m = -11.92 \pm 1.92$.

Mean microbial fallout, regardless of wind speed, was 1.98 ± 0.15 cfu m^{-2} s^{-1} with R2A media and 0.66 ± 0.05 cfu m^{-2} s^{-1} with LB media (Table 4). LB and R2A counts were linearly related with an $R^2 = 0.60$, $p << 0.01$, $m = 0.252 \pm 0.033$ (Fig. 8). At wind speeds ≥ 3.3 m s^{-1}, R2A microbial fallout showed a linear relationship to wind speed (Fig. 9A), with an $R^2 = 0.49$, $p << 0.01$, $m = 0.571 \pm 0.109$. LB counts, however, did not show a linear relationship to wind speed ($R^2 = 0.13$, $p = 0.032$, $m = 0.103 \pm 0.045$) (Fig. 9B).

Discussion

The Effect of Aeration Remediation on Coarse Aerosol Concentrations and Microbial Aerosol Fallout at an Urban Waterfront Site (NTA)

While Newtown Creek, and particularly English Kills, is known to sustain elevated surface water bacterial counts as a result of massive CSO inputs [34], the microbial aerosols data presented here is the first confirmation that the air at this site also supports high bacterial loads. The microbial fallout rates on LB media (mean of 3.81 ± 0.43 cfu m^{-2} s^{-1}) (Table 1) were several orders of magnitude higher than those encountered in Maine (0.06 ± 0.05 cfu m^{-2} s^{-1}) [2] and one order of magnitude higher than those encountered at LVP (0.66 ± 0.05 cfu m^{-2} s^{-1}) (Table 4). The sequence library from this site represents an unprecedented molecular look at the microbial communities in water and air at an inner-city urban site. The large number of viable, potentially pathogenic bacteria both in its surface waters and aerosols (Table 3) underscores the need for further research into the sources of these potential pathogens.

The aeration remediation of these polluted waters affected physical and biological aerosol dynamics at this site. When the aerator was off, microbial fallout and coarse aerosol concentrations were significantly positively associated (Fig. 5). This relationship implies a steady background source of bacteria to ambient aerosols at this site. Coarse aerosol concentrations were significantly higher on days that the aerator was on (Fig. 2), but there was not an accompanying statistically significant increase in microbial fallout (Fig. 4). This may be due to the following factors: (1) low winds resulted in reduced aeration-produced particle residence times, (2) the surface water signal (bacteria from surface waters) was overwhelmed by high concentrations of background microbial aerosols.

Because coarse aerosols were increased when the aerator was operating (Fig. 2), it implies that the aeration process is producing new aerosols from surface waters. As is well documented in bubble-delivery of aerosols from ocean surface to the air, the droplets created when bubbles burst at the surface waters vary greatly in size, and have varying residence times based on size and lofting of these particles by wind conditions at the site [35-36]. The low winds present at the time of sampling (Table 1) may have resulted in reduced residence times for larger, bacteria-containing surface water aerosols. These larger particles may simply have settled back onto the water surface before reaching fallout samplers. The surface water bacterial signal in sampled aerosols may also be overwhelmed by a high background bacterial concentration. This site is situated in one of the densest neighborhoods in Brooklyn in terms of both population and industrial activity. This may generate a general inner-city bacterial background so highly concentrated that the bacterial contribution of surface waters at this site would not drive microbial fallout rates.

On a phylum level, surface water bacteria were diverse at this site, and were generally similar to previously characterized culturable bacteria in ocean surface waters (Dueker, unpublished). Aeration activity did not appear to significantly shift the phylum-level structure of surface water communities, but did result in a significant decrease in Proteobacteria in the aerosol communities. The mechanism behind this shift is unclear, but may be related more to shifts in background bacteria rather than pertaining to aeration mode. On a finer taxonomic level, the significant increase in *Microbacterium* sp. in both surface waters and aerosols when the aerator was on suggests a connection between surface water and aerosols. *Microbacterium* sp. is a gram-positive potential pathogen that is most commonly isolated from soils. At NTA, *Microbacterium* may primarily have been associated with dust in the general background aerosol, or may have been associated with urban runoff in NTA waters. The direction of flow in this case is not clear, given that these bacteria could be coming from the surface waters through aerosol creation by the aerator, or could be falling into surface waters from background aerosols.

The Effect of Wind Speed and Wind Direction on Coarse Aerosol Concentrations and Microbial Fallout at an Urban Waterfont (LVP site)

Wind speed and wind direction were important factors in coarse aerosol concentrations and microbial fallout at the Louis Valentino Pier. Unlike NTA, media type also appears to have played a role in microbial fallout results at this site. Also, winds from the N appeared to have an opposite interaction with coarse aerosols than winds from the W and S, but the same dynamic wasn't evident in microbial fallout counts.

For coarse aerosols, increasing low wind speeds (< 3.3 m s^{-1}) decreased concentrations, most likely representing a clearing away of high-concentration coarse aerosol air packets and the onshore movement of low-concentration Harbor air packets. This pattern is similar to patterns found during sampling in coastal Maine (Dueker et al., unpublished) and coastal Denmark [29]. Higher wind speeds at coastal sites result in increasing coarse aerosol concentrations due to the addition of newly-created aerosols from the water surface [22, 29]. Above 3.3 m s^{-1}, increases in W and S wind speeds result in linear increases in coarse aerosol concentrations, with similar slopes. N winds, however, had the opposite relationship with coarse aerosols. This may be due to the following factors: (1) N winds have shorter fetch (3 km) than S and W winds (4 - 7.3km) over the harbor, reducing the opportunity for new coarse aerosol creation over surface waters; (2) N winds may represent a different type of aerosol source than S and W winds, one that is quickly

pushed out by low winds and then not replenished through major new aerosol creation. Regardless, this dynamic did not seem to carry over into microbial fallout response to wind speed and wind direction. Using pooled wind direction data, increased wind speeds correlated with increased microbial fallout rates on R2A plates. A similar trend is evident on LB plates, but the relationship to wind speed does not appear to be strong. This may indicate different sources for the bacteria growing on these two media. Compared to microbial fallout rates in NTA, the relationship between R2A and LB plate counts at LVP in general was not as strong (NTA R^2 = 0.71 compared to LVP R^2 = 0.60). Molecular analyses of the LVP microbial aerosols will help to discern community and source differences as they relate to media type and wind direction.

Conclusion

This study provided unique evidence for connections between water and air quality in the HRE. At both a heavily polluted inner-city tributary and the NY Harbor, coarse aerosols and microbial aerosol fallout responded to activities known to create aerosols from water surfaces, including aeration remediation and high wind speeds. NYC is not alone in struggling to remediate highly polluted and nutrient overenriched waterways experiencing eutrophication and hypoxia. In 2005, at least two-thirds of the coastal rivers and bays in the United States were degraded from nutrient pollution as a result of agricultural runoff, concentrated animal feeding operations, atmospheric deposition from fossil fuel combustion, and sewage and septic wastes. As resource managers in these areas contemplate aeration remediation of these waters, it is key that they have a full understanding of the potential for delivery of surface water materials to the waterfront spaces adjacent to these waterways.

The potential for wind delivery of surface water materials to the urban waterfront may increase through climate change, as extreme weather events become more common in many coastal areas [37]. Given that counties with the highest population densities in the US are primarily coastal, and human interface with these degraded waters is common and increasing [8-9], the urban waterfront is an important arena in which to explore the linkages between human health and environmental degradation. As evidenced from this study, and recently reported by Athanasopoulou et al. [38], air quality in coastal urban centers may be greatly influenced by coastal water quality. The mechanisms behind this flow of surface water materials to the air in coastal areas are quantifiable and should be studied on a broader spatial scale.

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Figure 1. The Lower Hudson River Estuary, with study sites circled (Newtown Creek Aeration (English Kills) (NTA), and Louis Valentino, Jr. Pier (LVP).

Table 1. Mean meteorological conditions, microbial aerosol fallout rates, and surface bacteria concentrations during microbial sampling at the Newtown Creek Aeration (NTA) site.

	Mean	Standard Error
Temperature (°C)	20.73	3.01
Relative Humidity (%)	45.09	6.80
Wind Speed ($m\ s^{-1}$)	2.67	0.17
Coarse Aerosols (m^{-3} air)	3.93×10^{5}	1.58×10^{4}
R2A Microbial Fallout (cfu $m^{-2}\ s^{-1}$)	8.38	0.77
LB Microbial Fallout (cfu $m^{-2}\ s^{-1}$)	3.81	0.43
R2A Surface Water Bacteria (cells ml^{-1})	2.09×10^{4}	3.12×10^{3}
LB Surface Water Bacteria (cells ml^{-1})	1.02×10^{4}	1.80×10^{3}

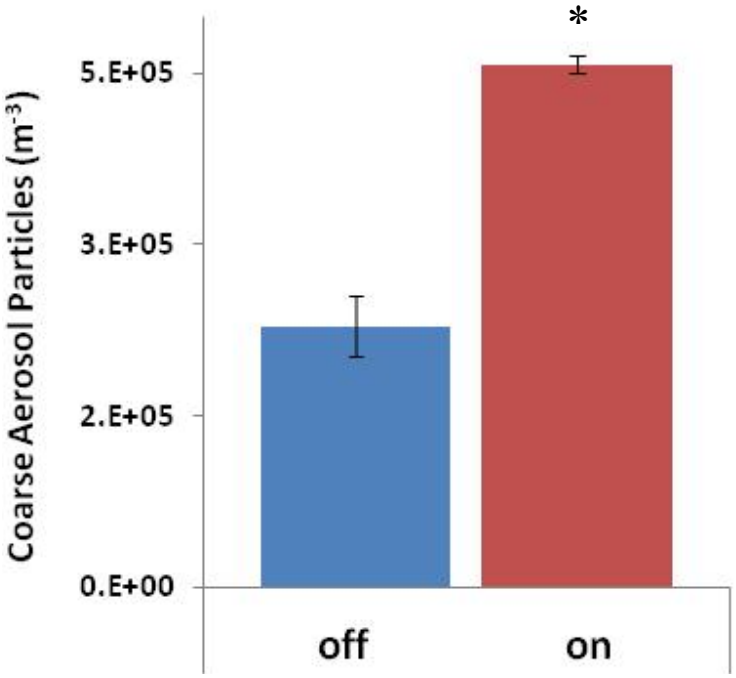


Figure 2. Coarse aerosol concentrations (per m^3 air) at Newtown Creek Aeration (NTA) site, according to aerator mode (off, on). An * indicates significant difference in coarse aerosol concentration ($p < 0.01$).

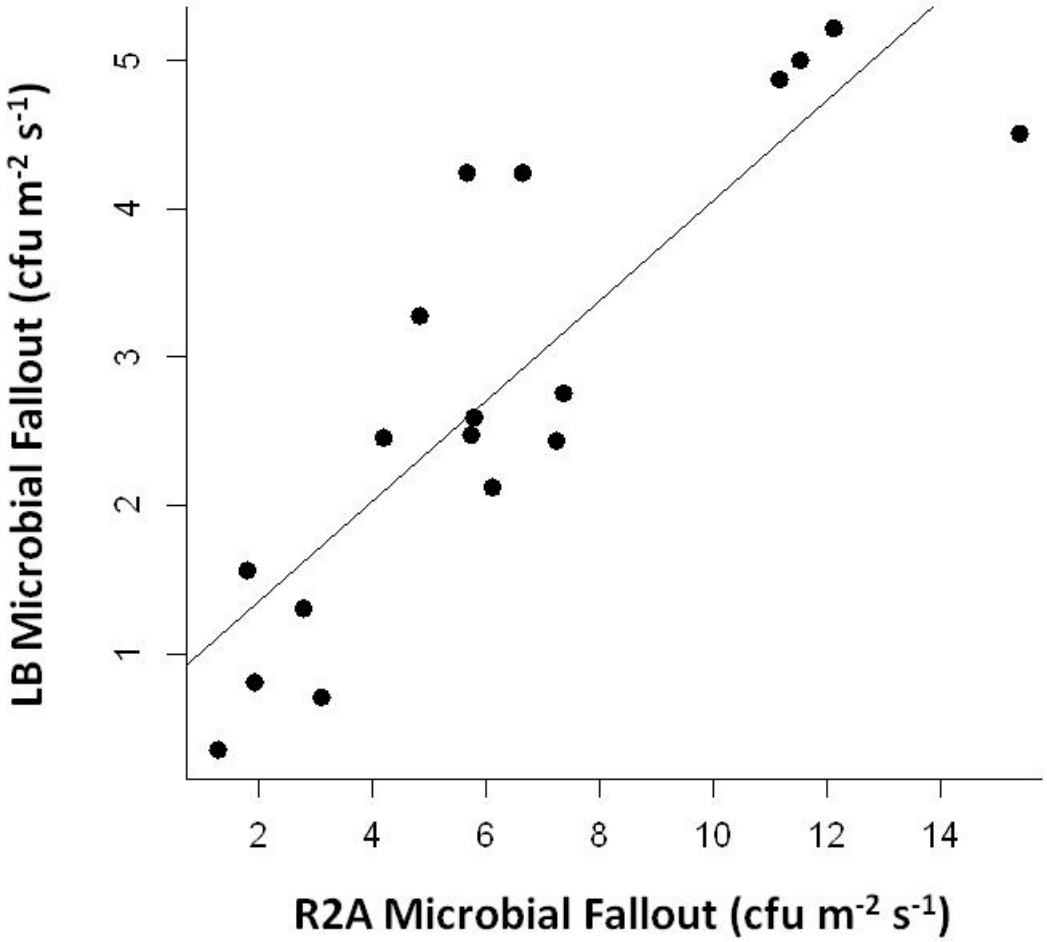


Figure 3. The relationship between LB and R2A microbial fallout rates at the Newtown Creek Aeration (NTA) site. R2A = low nutrient aerosol media, LB = high nutrient, salty media. Points are means for exposure events. The relationship is significant and linear, as shown by the solid curve representing a linear regression model, $R^2 = 0.71$, $p << 0.01$, $m = 0.34 \pm 0.051$.

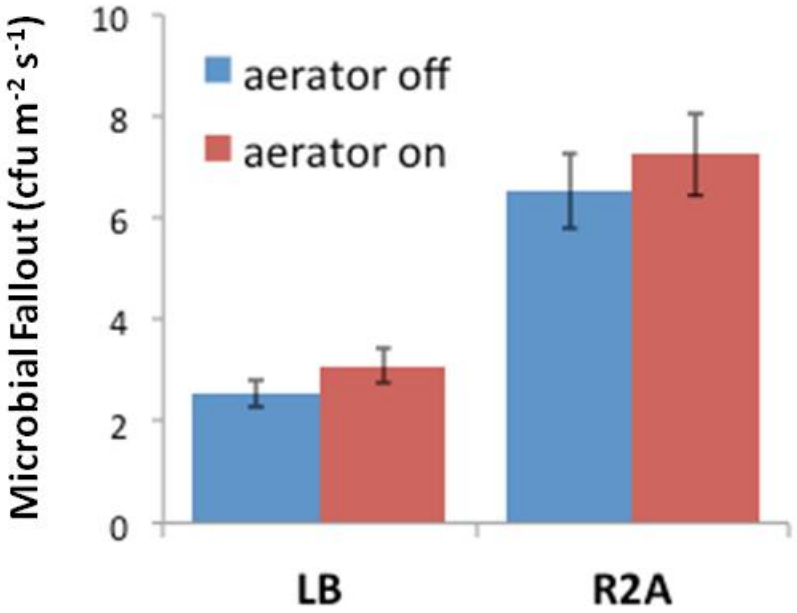


Figure 4. Newtown Creek Aeration (NTA) site microbial aerosol fallout by aeration mode (off, on). R2A = low nutrient aerosol media, LB = high nutrient, salty media.

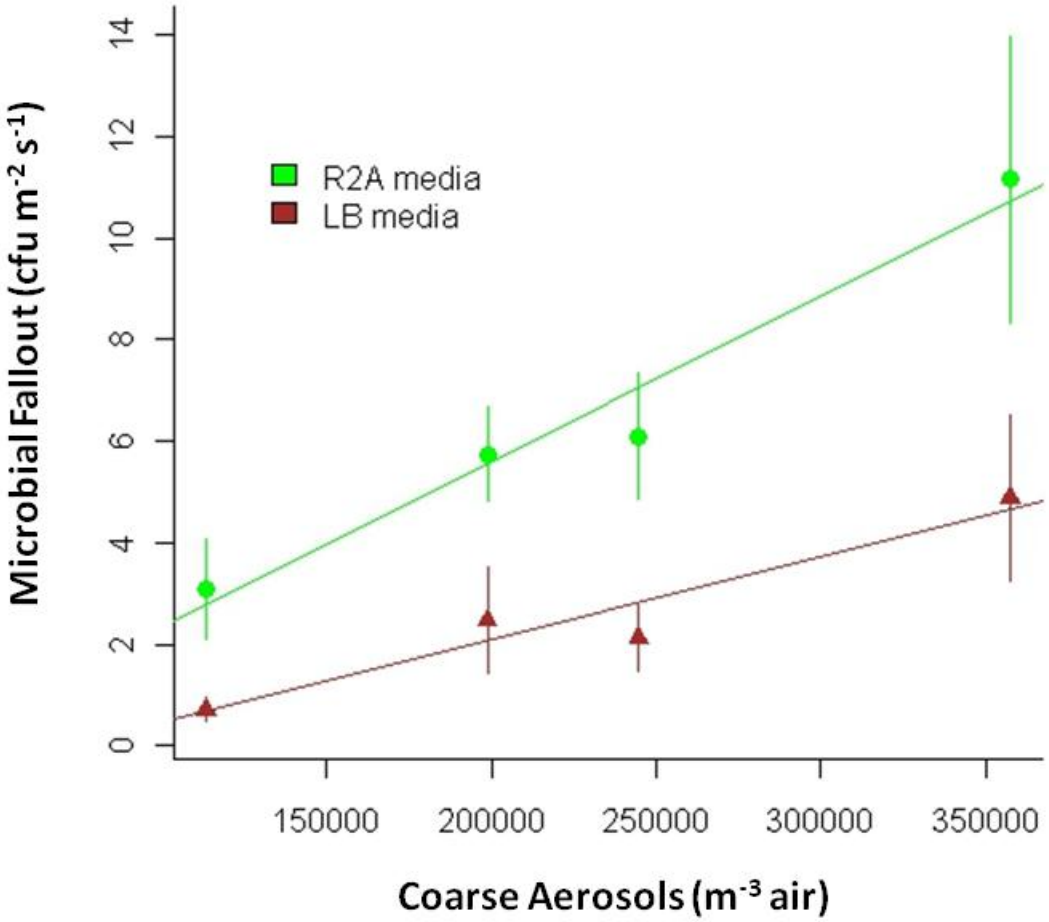


Figure 5. Relationship between LB and R2A microbial aerosol fallout (cfu m^{-2} s^{-1}) and coarse aerosol concentrations (m^{-3} air)at the Newtown Creek Aeration (NTA) site when aerator was off. R2A = low nutrient aerosol media, LB = high nutrient, salty media. Solid curves represent linear regression models: R2A $R^2 = 0.54$, $p < 0.01$; LB $R^2 = 0.42$, $p = 0.013$.

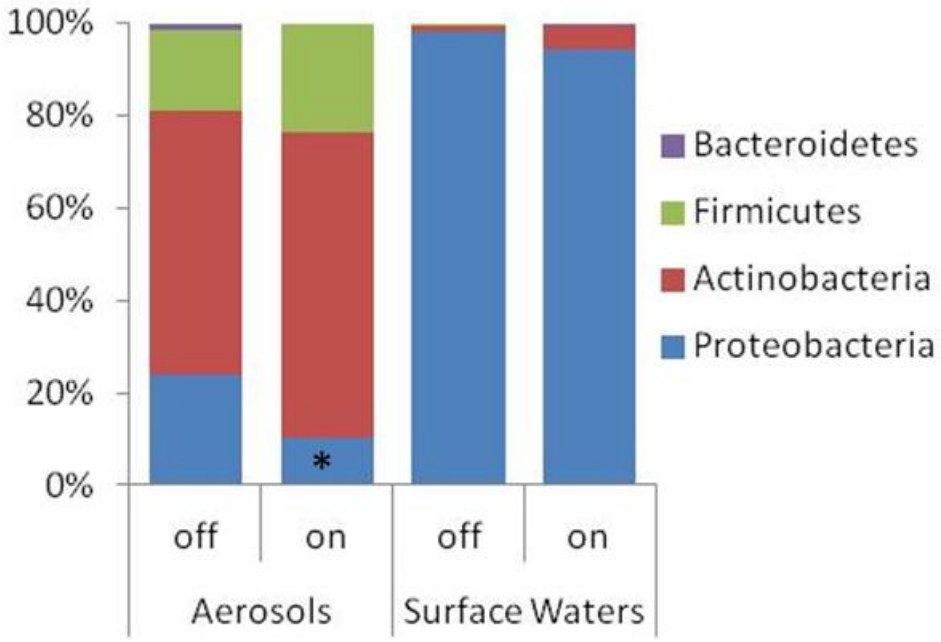


Figure 6. Phylum-level breakdown of Newtown Creek Aeration (NTA) sequence library, by type (Aerosols or Surface Waters) and by aeration mode (aerator off, aerator on). An * indicates significant difference ($p < 0.05$) regarding aeration mode. Note that NTA sequences were extracted from colonies growing on LB media only.

Table 2. Dominant bacterial genera (making up 5% or more of total sequence library) at Newtown Creek Aeration (NTA) site, with % of total sequence library (ocean + aerosol) and distribution of sequences between sources and according to aeration mode (off, on).

		Source Distribution			
	total	ocean		aerosol	
	library	aerator off	aerator on	aerator off	aerator on
Microbacterium	17%	1%	5%	15%	79%
Pseudomonas	13%	54%	37%	3%	6%
Shewanella	9%	82%	16%	2%	0%
Bacillus	6%	0%	0%	25%	75%

Table 3. Potential pathogenic genera present at Newtown Creek Aeration (NTA) site, in both surface waters and aerosols. Aerator mode (on or off) noted for each source.

	Aerosol		Surface Water	
Potential Pathogen	**on**	**off**	**on**	**off**
Acinetobacter sp.		x	x	x
Aerococcus sp.	x			
Aeromonas sp.			x	
Bacillus sp.	x	x		
Brevundimonas sp.	x	x		
Buttiauxella sp.	x			
Citrobacter sp.	x		x	x
Comamonas sp.			x	x
Enterobacter sp.				x
Enterococcus sp.	x			x
Exiguobacterium sp.	x	x		
Francisella sp.			x	
Kocuria sp.	x	x		
Massilia sp.	x			
Microbacterium sp.	x	x	x	x
Micrococcus sp.	x			
Nocardiopsis sp.		x		
Paenibacillus sp.	x			
Paracoccus sp.		x		
Pseudomonas sp.	x	x	x	x
Psychrobacter sp.		x	x	x
Rhodococcus sp.		x		
Roseomonas sp.	x			
Sphingobacterium sp.		x		
Sphingomonas sp.	x			
Staphylococcus sp.	x			
Streptomyces sp.	x	x		
Vibrio sp.			x	
Total	**17**	**13**	**9**	**8**

Table 4. Mean meteorological conditions, microbial aerosol fallout rates, and surface bacteria concentrations during microbial sampling at the Louis Valentino Pier (LVP) site.

	Mean	Standard Error
Temperature (°C)	16.88	1.59
Relative Humidity (%)	63.92	4.96
Wind Speed ($m\ s^{-1}$)	4.82	0.99
Coarse Aerosols (m^{-3} air)	1.28×10^{5}	2.51×10^{4}
R2A Microbial Fallout (cfu $m^{-2}\ s^{-1}$)	1.98	0.15
LB Microbial Fallout (cfu $m^{-2}\ s^{-1}$)	0.66	0.05
R2A Surface Water Bacteria (cells ml^{-1})	891.48	132.60
LB Surface Water Bacteria (cells ml^{-1})	475.93	62.23

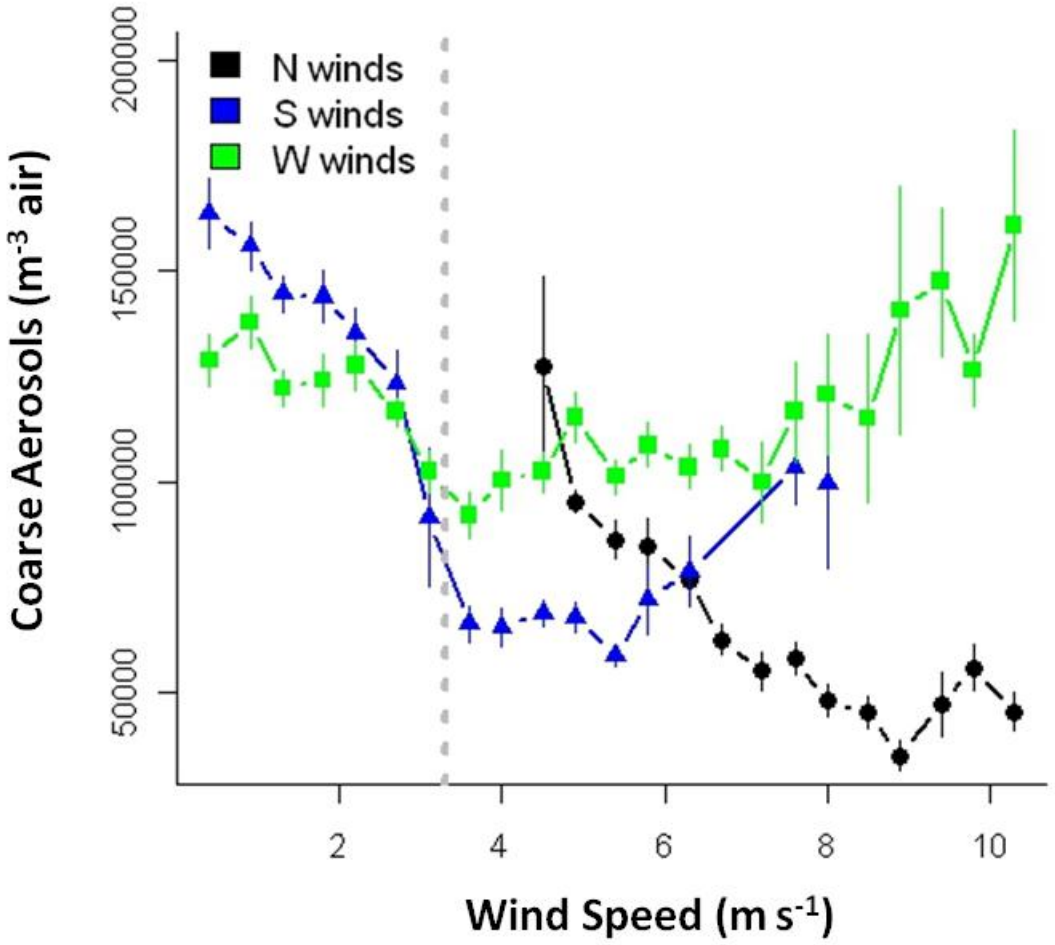


Figure 7. One-minute coarse aerosol concentrations (m^{-3} air) (binned by wind speed) under N (n = 425), S (n = 793), and W (n = 1,072) onshore wind conditions at Louis Valentino Pier (LVP) as a function of one-minute wind speed (m s^{-1}). Grey dashed line denotes 3.3 m s^{-1} wind speed, which is the speed above which wind-water interactions are expected to produce aerosols from surface waters.

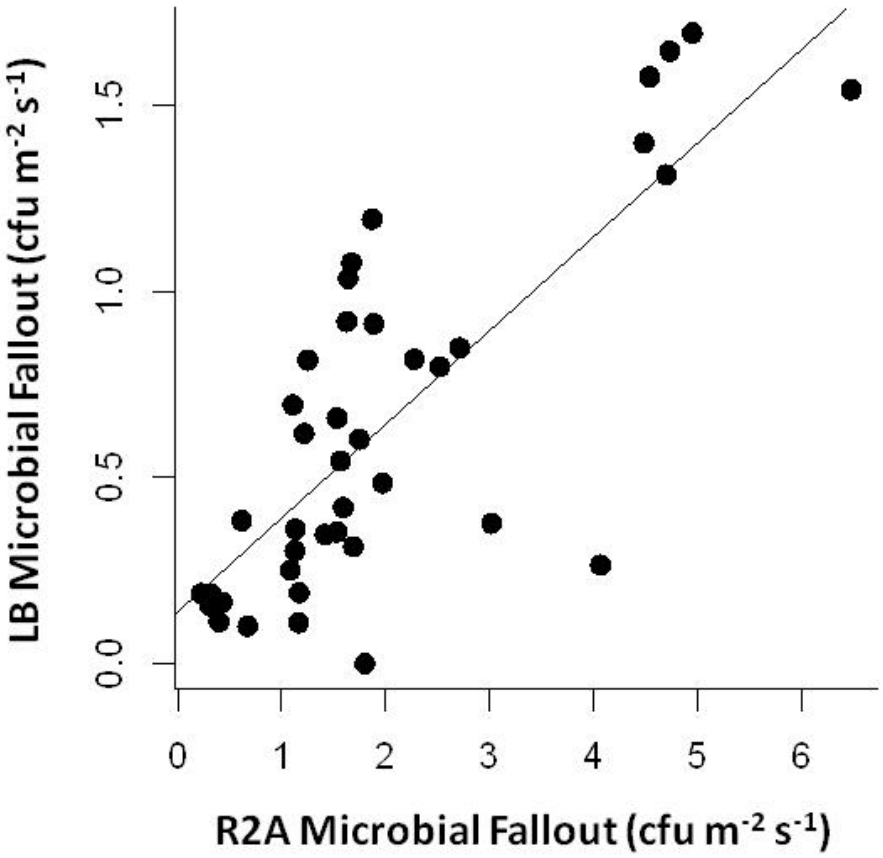
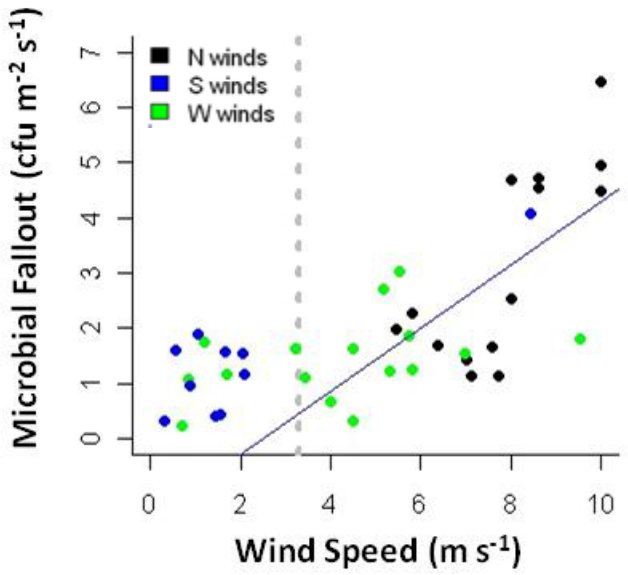


Figure 8. The relationship between LB and R2A microbial fallout rates at the Louis Valentino Pier (LVP) site. R2A = low nutrient aerosol media, LB = high nutrient, salty media. Points are means for exposure events. The relationship is significant and linear, as shown by the solid curve representing a linear regression model, $R^2 = 0.60$, $p << 0.01$, $m = 0.252 \pm 0.033$.

A.



B.

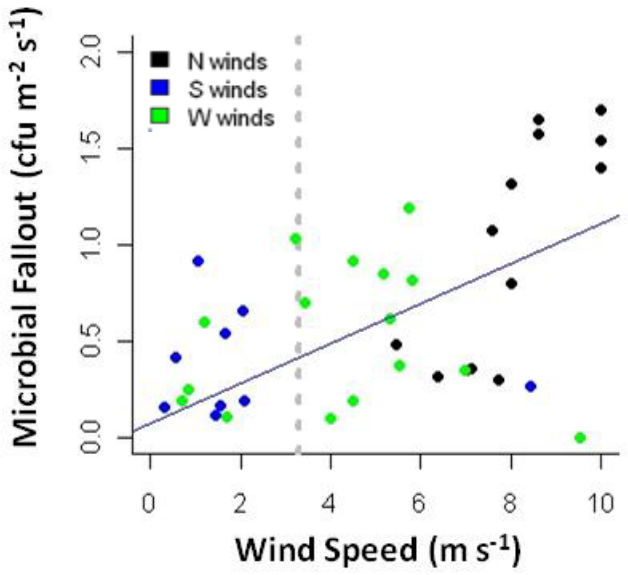


Figure 9. (A) R2A and (B) LB microbial fallout at Louis Valentino Pier (LVP) as a function of wind speed and wind direction. R2A = low nutrient aerosol media, LB = high nutrient, salty media. Solid curves represent linear regression models constructed using microbial fallout rates measured during winds ≥ 3.3 m s^{-1} (grey dashed line). (R2A model: $R^2 = 0.49$, $p << 0.01$, $m = 0.571 \pm 0.109$; LB model: $R^2 = 0.13$, $p = 0.032$, $m = 0.103 \pm 0.045$)