Seasonal Variability in the Diversity of Microbial Assemblages and Antibiotic Resistance Determinants of an Estuary System

Conference: Alabama NSF EPSCoR Science and Technology Open House., At Renaissance Hotel and Convention Center, Montgomery, Alabama

By Richard M. Mariita, Mohammad J. Hossain, Mark R. Liles, Anthony G. Moss

Abstract

Antibiotic resistance (AR) promoted by heavy metal pollution, is widely found in environmental microbes [1-3]. The mobility and acquisition of AR genes depends on mobile genetic elements (MGEs) [4]. Estuaries are metals sinks and aid with the comingling of AR genes [5,6]. In light of the food and recreational value of estuaries (6), it is important to understand estuarine AR dynamics. Here we demonstrate seasonal changes in 1) microbial assemblages and functional diversity, and 2) AR, for the Mobile Bay Estuary. Seasonal samples were sequenced using Illumina Miseq platform. Annotation was achieved via MG-RAST [7], taxonomic analysis via the SILVA SSU rDNA database [8], functional annotation via the SEED Project and functional graphical analysis via Krona [9]. Analysis revealed seasonal trends in abundance. The predominant microbes were Proteobacteria (1,000,738) reads. Abundances were β-proteobacteria (447,758)>α-proteobacteria (307,924)> γ-proteobacteria (209,704)>δ-proteobacteria (30,565)> ε-proteobacteria (4,340)> ζ-proteobacteria (447). α-diversity followed a similar trend: Sp (436.94), W (405.76); Su and F were <300. Chemotaxis

and motility genes displayed similar trends: Sp (2728) > W (2221) > F (900) > Su (698). Co-Zn-Cd resistance genes were most abundant in the winter: W (1553) > Sp (1345) > F (494) ≈ Su (459). MvirDB [10] BLAST results revealed the greatest number of virulence and AR genes during Summer: Su (79) > Sp (59) > W (48) > F (23). Our study reveals that microbial taxonomic, functional, and AR gene diversity is highest during Sp, possibly because of expanded riverine input. In contrast, the greatest abundance of AR genes occurs summer, during reduced fresh water input. Thus, this study describes distinct trends in seasonal microbial and genetic populations, and forms a basis for future studies of the link between watershed management, estuaries, and public health.

Supported in part by ALA-EPSCoR: NSF EPS-1158862, USDA-Hatch 370225-310100 (AGM, ML) and NSF0348327 (AGM). RMM support: Alabama EPSCoR fellowship, AU-CMB Peaks of Excellence summer graduate research award.

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