Microbial Source Tracking and Dynamics of Bacterial Communities and Pathogens in the Urban Tropical Environment

Abstract

Research aims were (1) to examine general bacterial community composition and specific sequences characteristic of sewage associated taxa and pathogen-like sequences as a function of water quality, (2) to validate host-associated Bacteroidales genetic markers for microbial sources tracking in Singapore, (3) to compare the performance of digital droplet PCR and quantitative PCR in detecting and quantifying markers, and (4) to evaluate sediment-associated decay rates of the best-performing human-associated markers B. thetaiotaomicron α-1-6, mannanase (B. theta) and BacHum and those of fecal indicator bacteria in the presence and absence of grazing protozoa. Four Bacteroidales markers were validated for microbial source tracking in Singapore and Southeast Asia (Human: B. theta and BacHum; Dog: BacCan, and total Bacteroidales: BacUni). Bacteroidales viable cells and DNA had similar decay rate constants in sediments, with two-log reduction times between five and six days, and rates were not affected by the presence of protozoa.