

1. Introduction

Microbial contamination in the United States (US) and abroad continues to impact the many beneficial uses of surface waters (Hall et al., 2014; Herrig et al., 2015; Rochelle-Newall et al., 2015). Public health officials and resource managers are given the challenging task of identifying potential sources of microbial contamination and offering strategies to ensure public safety. For over 80 years, US state and local authorities have used fecal indicator bacteria (FIB), such as fecal coliforms (FC), *Escherichia coli* (EC) and enterococci (EN) as indicators for pathogens that cause human illness. FIB occur naturally in the intestinal track of warm blooded vertebrates, so their occurrence in surface water is believed to be associated with fecal deposition (Atwill et al., 2012; Bradshaw et al., 2016); however, FIB can also become naturalized in the environment and flourish in soils and sediments (Ferguson and Signoretto, 2011).

Over the last two decades there have been many advances in our ability to study FIB in the environment including, but not limited to, microbial source tracking (Boehm et al., 2013; Shanks et al., 2006), genetic fingerprinting (Chandrasekaran et al., 2015; Gobet et al., 2012), and bacterial community sequencing (Whitman et al., 2014). Despite the many promising advances in microbial science, local ambient monitoring programs lack the resources to conduct more robust laboratory analyses and thus generally incorporate the more cost-effective, culture-based, FIB monitoring strategies. These strategies rely on samples being taken at the right place and time to capture microbiological conditions, however samples are typically collected at locations with easy access and at times that are most convenient for personnel (Nevers and Whitman, 2010). The highly dynamic spatial and temporal variability of surface water systems makes finding the right time and place to sample difficult (Boehm et al., 2009).

Some modern FIB monitoring programs have begun incorporating the use of predictive models of microbial concentrations to improve program performance, including but not limited to, hydrodynamic models (Drummond et al., 2015), geospatial analysis (Kelsey et al., 2004), microbial networks (Faust and Raes, 2012), and most commonly, regression analyses (Herrig et al., 2015; Hogan et al., 2012; Lewis et al., 2012; Nevers and Whitman, 2011b). However, nearly a century later, we still lack the ability to reliably predict changes in concentrations of FIB in surface waters across systems. One predominant reason for the lack of reliable predictions is that microbial contamination can come from many sources, both point and non-point (Stewart et al., 2008); including sewage discharges or overflows (Eregno et al., 2016), storm water pulses (Lewis et al., 2005), urban runoff (Arnone and Walling, 2007), agricultural tail-water discharge (Partyka et al., 2016), and the redistribution of upstream sediments (Norman et al., 2013). Once bacteria enter surface water they are subjected to additional mixing and transport mechanisms that can further complicate our ability to predict their occurrence (Bai and Lung, 2005; David and Haggard, 2011; Drummond et al., 2015). Even in well-studied systems like the Great Lakes (Nevers and Whitman, 2011a; Whitman et al., 2006) and Southern California beaches (Griffith et al., 2016), surface water must be continually monitored and modeled regularly to reflect emerging conditions.

The purpose of this study and data presented herein was to provide guidance for monitoring site selection for FIB contamination in the Sacramento-San Joaquin Delta (Delta) and to determine if particular land uses or environmental conditions were associated with higher microbial concentrations. Our experiences in other complex tidal systems (Lewis et al., 2012) had prepared us for the difficulties associated with capturing physiochemical and environmental conditions at appropriate spatiotemporal scales to capture associations with FIB. Our study was designed with these difficulties in mind to include dense spatial sampling over the course of multiple years and the collection of several tiers of ancillary characteristics, allowing for a robust statistical investigation into the dynamism of microbial concentrations in the Delta.

2. Methods and materials

2.1. Study area

California's Sacramento/San Joaquin Delta Estuary located in Central Valley of Northern California, is the confluence of the Sacramento and San Joaquin Rivers which together drain Sierra Nevada Mountain rivers and streams then empties into San Francisco Bay (Fig. 1). The study area covers approximately 1200 km² (~50%) of the Delta estuary which is surrounded by floodplains, densely populated urban areas, crop and rangelands and small rural communities (Hickson and Keeler-Wolf, 2007).

The study area was spatially divided into two distinct regions, the Northern Drainage Region (NDR) which is centered around the Cache Slough and Sacramento River complexes (including the Yolo Bypass Toe Drain) and the Southern Drainage Region (SDR) which is centered on the San Joaquin and Old River complexes and receives water from the Mokelumne and Calaveras Rivers from the east and the Merced, Tuolumne and Stanislaus Rivers from the south. These two regions are roughly divided by the California Highway 12 corridor (Fig. 1).

2.2. Sampling design

A total of 88 sampling sites were chosen throughout the eastern and central Delta (Fig. 2). At each site water samples were taken once a month, between the hours of 0600–1200, over a two-year period. Year one (13 months) began in June 2006 and continued until June of 2007 and the second year (12 months) was sampled from December 2007 until November 2008. Each sampling year was divided into three seasons based on a typical water year: rainfall season (Nov–Mar), snow-melt season (Apr–June), and a dry season (Jul–Oct). In order to prioritize sampling in areas with the highest average bacterial counts, five sites with the lowest average bacterial counts from year one were removed from the sampling schedule and five new sites were added during year two near sites with the highest average year one bacterial counts.

2.3. Sample collection

Locations for all sites were designated by a six-digit latitude and longitude collected a GPS device for repeated sampling (Garmin 76S, Garmin, Inc.). Water collection at each site was performed via boat. Each sample was collected using a custom-made wire-triggered sampling device, the Bond, Atwill, Partyka (BAP) water sampler, which holds and secures three round 500 mL sterilized polypropylene bottles (Nalgene). The BAP sampler was rinsed between sites with 70% alcohol, followed by sterile deionized water in order to reduce the risk of cross contamination between sites.

Along with the water samples, water chemistry measurements (Table 1) were taken using a YSI 556 multiparameter meter (YSI Inc.). In addition to these in situ field measurements, we collected meteorological data from stations operated by California Irrigation Management Information System (CIMIS) at University of California, Division of Agriculture and Natural Resources (Table 1). We also collected tidal stage data using the California Data Exchange Center (CDEC) river stage gauges for waterways nearest to sampling locations. Time of collection was recorded for each water sample so that all data collected from an external independently monitored sensors (CIMIS and CDEC) could be temporally synchronized with in situ measurements (Herrig et al., 2015).

2.4. Land use characteristics

We used geospatial software (ArcGIS 10.3, ESRI, Redlands, CA) in combination with data made publically available through ArcGIS Online

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