

Large scale analysis of virulence genes in *Escherichia coli* strains isolated from Avalon Bay, CA

Matthew J. Hamilton^{1,2}, Asbah Z. Hadi^{1,3}, John F. Griffith⁴, Satoshi Ishii³ and Michael J. Sadowsky^{2,3}

¹Department of Microbiology, University of Minnesota, Minneapolis, MN

²BioTechnology Institute, University of Minnesota, St. Paul, MN

³Department of Soil, Water, and Climate, University of Minnesota, St. Paul, MN

⁴Southern California Coastal Water Research Project, Costa Mesa, CA

ABSTRACT

Contamination of recreational waters with *E. coli* and *Enterococcus* sp. is a widespread problem resulting in beach closures and loss of recreational activity. While *E. coli* is frequently used as an indicator of fecal contamination, and has been extensively measured in waterways, few studies have examined the presence of potentially pathogenic *E. coli* strains in beach waters. In this study, a combination of high-throughput, robot-assisted colony hybridization and PCR-based analyses were used to determine the genomic composition and frequency of virulence genes present in *E. coli* isolated from beach water in Avalon Bay, Santa Catalina Island, CA. A total of 24,493 *E. coli* isolates were collected from two sites at a popular swimming beach between August through September 2007 and from July through August 2008. All isolates were examined for the presence of shiga-like toxins (*stx1/stx2*), intimin (*eaeA*), and enterotoxins (ST/LT). Of the 24,493 isolates examined, 3.6% contained the *eaeA* gene, indicating that these isolates were potential EPEC strains. On five dates, however, greater than 10% of the strains were potential EPEC, suggesting that incidence of virulence genes at this beach has a strong temporal component. No STEC or ETEC isolates were detected, and only eight (<1.0%) of the potential EPEC isolates were found to carry the EAF plasmid. The potential EPEC isolates mainly belonged to *E. coli* phylogenetic groups B1 or B2, and carried the beta intimin subtype. DNA fingerprint analyses of the potential EPEC strains indicated that the isolates belonged to several genetically diverse groups, although clonal isolates were frequently detected. While the presence of virulence genes alone cannot be used to determine the pathogenicity of strains, results from this study show that potential EPEC strains can be found in marine beach water and their presence needs to be considered as one of the factors used in decisions concerning beach closures.

Due to distribution restrictions, the full-text version of this article is available by request only.

Please contact pubrequest@sccwrp.org to request a copy.