

SCCWRP Annual Report 2010

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

Matthew J. Hamilton, Asbah Z. Hadi, John F. Griffith and Michael J. Sadowsky

ABSTRACT

Contamination of recreational waters with *Escherichia coli* and *Enterococcus* species 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 analyses based on polymerase chain reaction (PCR) was used to determine the genomic composition and frequency of virulence genes present in *E. coli* isolated from beach water at Avalon Bay, Santa Catalina Island, CA. A total of 24,493 *E. coli* isolates were collected from two sites at a popular swimming beach August through September 2007 and 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 enteropathogenic *E. coli* (EPEC) strains. However, after 5 days, more than 10% of the strains were potentially EPEC, suggesting a strong temporal component associated with incidence of virulence genes. No shiga toxin producing *E. coli* (STEC) or enterotoxigenic *E. coli* (ETEC) isolates were detected, and only eight (<1.0%) of the potential EPEC isolates were found to carry the EPEC adherence factor (*EAF*) plasmid. The potential EPEC isolates primarily belonged to *E. coli* phylogenetic groups B1 or B2, and carried the beta intimin subtype. Deoxyribonucleic acid (DNA) fingerprint analyses of the potential EPEC strains indicate that the isolates belong 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.

Full Text

ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2010AnnualReport/ar10_113_125.pdf