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Patterns of Multi-Antibiotic-Resistant *Escherichia Coli* from Streams with No History of Antimicrobial Inputs

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Abstract

A growing body of evidence suggests that contaminated environments may harbor a greater proportion of antibiotic-resistant microorganisms than unpolluted reference sites. Here, we report the screening of 427 *Escherichia coli* strains isolated from 11 locations on nine streams draining the US Department of Energy's Savannah River Site against a panel of five antibiotics. Streams were chosen to capture a wide range of watersheds from minimally disturbed to highly impacted. Overall, higher levels of resistance were found in waterborne *E. coli* that also generally exhibited low spatial variability. However, 3 of 11 locations also demonstrated elevated resistance levels in sediments. Two of these occurred in highly disturbed tributaries with no obvious sources of antimicrobials. To further investigate these patterns, we screened a subset of isolates obtained from three streams against 23 antibiotics or antibiotic combinations. A large proportion of these isolates (>40 %) demonstrated resistance to 10 or more antimicrobials, suggesting that environmental multi-antibiotic resistance may be prevalent in this bacterial commensal. Only 4 of 87 viable isolates were tested susceptible to all 23 antibiotics and combinations. Among these multi-antibiotic-resistant isolates, several demonstrated resistance to all structural classes of antimicrobial agents tested, including frontline antibiotics such as gatifloxacin and ciprofloxacin.

Keywords

E. coli – Antibiotic resistance – Industrial activity

Electronic supplementary material

The online version of this article (doi:10. 1007/ s00248-015-0678-4) contains supplementary material, which is available to authorized users.

Supplementary Material (4)

248_2015_678_Fig6_ESM.gif (245055)
S1. Proportions of isolates from U4, U8, and U10 resistant to various antibiotic and antibiotic combinations excluding the cephlasporins. (GIF 239 kb)

248_2015_678_MOESM1_ESM.tif (177318)
High resolution image (TIFF 173 kb)

248_2015_678_Fig7_ESM.gif (167208)
S1. Proportions of isolates from U4, U8, and U10 resistant to various antibiotic and antibiotic combinations excluding the cephlasporins. (GIF 239 kb)

248_2015_678_MOESM2_ESM.tif (85456)
High resolution image (TIFF 83 kb)

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