

Geographic sharing of ribotype patterns in *Enterococcus faecalis* for bacterial source tracking

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ABSTRACT

The limited host range of *Enterococcus faecalis* may reduce its clonal diversity and thereby increase its geographic sharing of ribotype patterns. Such sharing would be advantageous for bacterial source tracking (BST). We determined the geographic sharing of ribotype patterns in 752 *E. faecalis* isolates obtained primarily from wastewater treatment plants in Delaware (15 locations; 490 isolates), Georgia (2 locations; 48 isolates), Idaho (1 location; 118 isolates), New York (2 locations; 48 isolates), and Puerto Rico (2 locations; 48 isolates). Isolates were ribotyped with a RiboPrinter. When pooled across all locations and analyzed at a similarity index of 100% and a tolerance level of 1.00%, the 752 *E. faecalis* isolates yielded 652 different ribotypes, of which 429 (66%) were unshared. Even when the matching criterion was relaxed by decreasing the tolerance level from 1% to 10% or lowering the similarity cutoff from 100% to 90%, half or almost half of the ribotypes were unshared. A Mantel test of zero correlation showed no statistically significant correlation between ribotype patterns and geographic distance among the 32 samples (one location at one time) at either the 1.00% ($p = 0.91$) or 10.00% ($p = 0.83$) tolerance levels. Therefore, the percentage of ribotype patterns shared between two locations did not increase as the distance between locations decreased. In the case of BST, a permanent host origin database sufficiently large to encompass these ribotype patterns would be time-consuming and expensive to construct.

Full Text

ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2007AnnualReport/AR07_299_310.pdf