

EVALUATION OF *E. FAECALIS* AND *E. FAECIUM* POPULATIONS IN THE UPPER
PASSAIC RIVER, MORRIS COUNTY, NJ.

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Abstract: To determine the prevalence of the nosocomial pathogens *Enterococcus faecalis* (EFS) and *E. faecium* (EFM) in surface water of the upper Passaic River, we isolated enterococci from six equidistant sites along the river in Morris County, NJ, monthly from June through October, 2007. Duplicate samples were collected aseptically; enterococci were isolated by membrane filtration on mEI agar. All enterococcal isolates (n = 1349) were verified, enumerated, speciated and the antibiotic resistance patterns determined. Total enterococcal counts ranged between 19 and 1200 CFU/100 ml. EFS isolates (n = 406) ranged from 14 to 40 % of the total isolates per site while EFM isolates (n = 104) ranged from 3 to 22 %. EFS isolates predominated upstream while EFM isolates were more prevalent at downstream sites. All isolates were tested against a panel of 10 antibiotics at clinically relevant concentrations. Greater than 99% of EFS and EFM isolates were resistant to ampicillin; penicillin resistance varied by sampling date. All EFS isolates were sensitive to gentamycin, nitrofurantoin and vancomycin; all EFM isolates were sensitive to chloramphenicol and vancomycin. Ampicillin/penicillin resistance was the most common Multiple Antibiotic Resistance (MAR) pattern, expressed by 20% of all EFS and EFM isolates. MAR patterns for resistance to three or more antibiotics were observed in 30% of EFM isolates but in only 2% of EFS isolates. Selected EFS and EFM isolates were evaluated for the expression of three virulence factors: gelatinase, hemolysin, and bacteriocin. Eighty-nine percent of EFS isolates (n = 159) and 4.3 % of EFM isolates (n = 92) produced gelatinase. Production of at least one bacteriocin was observed in 58 % of EFS and 32 % of EFM isolates. Beta-hemolysis was observed in 1.9% of EFS isolates. The combination of antibiotic resistance and virulence factor expression increases the pathogenic potential of these microorganisms.