

Further Evaluate Bacteria Persistence and Regrowth

Konstantinidis et al. 2011. "Genome sequencing of environmental *Escherichia coli* expands understanding of the ecology and sequencing of the model bacteria species"

[Proceedings of the National Academy of Sciences](#)

Abstract: Defining bacterial species remains a challenging problem even for the model bacterium *Escherichia coli* and has major practical consequences for reliable diagnosis of infectious disease agents and regulations for transport and possession of organisms of economic importance. *E. coli* traditionally is thought to live within the gastrointestinal tract of humans and other warm-blooded animals and not to survive for extended periods outside its host; this understanding is the basis for its widespread use as a fecal contamination indicator. Here, we report the genome sequences of nine environmentally adapted strains that are phenotypically and taxonomically indistinguishable from typical *E. coli* (commensal or pathogenic). We find, however, that the commensal genomes encode for more functions that are important for fitness in the human gut, do not exchange genetic material with their environmental counterparts, and hence do not evolve according to the recently proposed fragmented speciation model. These findings are consistent with a more stringent and ecologic definition for bacterial species than the current definition and provide means to start replacing traditional approaches of defining distinctive phenotypes for new species with omics-based procedures. They also have important implications for reliable diagnosis and regulation of pathogenic *E. coli* and for the coliform cell-counting test.

Satoshi Ishii,¹ Winfried B. Ksoll,³ Randall E. Hicks,³ and Michael J. Sadowsky. 2006. Presence and Growth of Naturalized *Escherichia coli* in Temperate Soils from Lake Superior Watersheds. *Applied and Environmental Microbiology* 72(1): 612-621

The presence of *E. coli* in water is used as an indicator of fecal contamination, but recent reports indicate that soil populations can also be detected in tropical, subtropical, and some temperate environments. In this study, we report that viable *E. coli* populations were repeatedly isolated from northern temperate soils in three Lake Superior watersheds from October 2003 to October 2004. Seasonal variation in the population density of soilborne *E. coli* was observed; the greatest cell densities, up to 3×10^3 CFU/g soil, were found in the summer to fall (June to October), and the lowest numbers, <1 CFU/g soil, occurred during the winter to spring months (February to May). Horizontal, fluorophore-enhanced repetitive extragenic palindromic PCR (HFERP) DNA fingerprint analyses indicated that identical soilborne *E. coli* genotypes, those with $>92\%$ similarity values, overwintered in frozen soil and were present over time. Soilborne *E. coli* strains had HFERP DNA fingerprints that were unique to specific soils and locations, suggesting that these *E. coli* strains became naturalized, autochthonous members of the soil microbial community. In laboratory studies, naturalized *E. coli* strains had the ability to grow and replicate to high cell densities, up to 4.2×10^5 CFU/g soil, in nonsterile soils when incubated at 30 or 37°C and survived longer than 1 month when soil temperatures were $<25^\circ\text{C}$. To our knowledge, this is the first report of the growth of naturalized *E. coli* in nonsterile, nonamended soils. The presence of significant populations of naturalized

populations of *E. coli* in temperate soils may confound the use of this bacterium as an indicator of fecal contamination.

Beth L. Mote,^a Jeffrey W. Turner,^{a,b*} and Erin K. Lippa. 2012. Persistence and Growth of the Fecal Indicator Bacteria Enterococci in Detritus and Natural Estuarine Plankton Communities. *Applied and Environmental Microbiology* 78(8):2569-2577

Enterococci are used to evaluate recreational-water quality and health risks in marine environments. In addition to their occurrence in feces of warm blooded animals, they are also common epiphytes. We investigated the contribution of plankton- or particle-associated enterococci in estuarine and coastal water. Seven water and size-fractionated plankton samples were collected monthly between April 2008 and January 2009 in the tidal reaches of the Skidaway River (Georgia, USA). Each size fraction, along with filtered (<30_μm) and bulk estuarine water, was processed according to U.S. Environmental Protection Agency method 1600. Presumptive enterococci were selected and species were identified using carbon substrate utilization patterns. The highest average densities occurred within the 30-, 63-, 105-, and 150-μm size fractions, which also represented the majority (>99%) of the particles within the sampled water. Particle-associated enterococci accounted for as little as 1% of enterococci in bulk water in April to as much as 95% in July. *Enterococcus faecalis* was the most commonly isolated species from both water and plankton and represented 31% (16/51) and 35% (6/17) of the identified *Enterococcus* species from water and plankton, respectively. *Enterococcus casseliflavus* represented 29% of the selected isolates from plankton and 16% from water. Both *E. faecalis* and *E. casseliflavus* were able to survive and grow in plankton suspensions significantly longer than in artificial seawater. *Enterococcus* spp. may be highly concentrated in plankton and associated particles, especially during summer and fall months. These findings could have implications for the effectiveness of enterococci as an indicator of coastal water quality, especially in particle-rich environments.