

## Genetic Structure of *Escherichia coli*

### Problem

Horizontal transfer - the the physical movement of DNA between cells via extrachromosomal elements (plasmids, lysogenic bacteriophages, etc) - is a hallmark of bacterial genetics. Examination of bacterial genomic sequences reveals that, for many groups, there is strong evidence for recent acquisition of a significant proportion (>12% for *E. coli*) genomic sequence. At the practical level, horizontal transfer contributes to evolution of antibiotic resistance and virulence among clinically significant bacterial species.

Factors contributing to the evolution of horizontal transfer are complex. On the one hand, horizontal transfer may be a classically infectious process, favoring the reproductive success of the transferred sequences. On the other hand, what one might call "plasmid susceptibility" - a genetic propensity to serve as a recipient - might be selected for in some environments. This would predict that certain phylogenetic lines of a species would be more likely to harbor extrachromosomal elements than others.

Subspecific phylogenetic groups - ECOR groups - have been identified for *E. coli*, and the distribution of phenotypic traits, including virulence, among different ECOR groups, has been studied. Recently, assignment of *E. coli* isolates to ECOR groups has been simplified by the use of multiplex PCR. The objective of this project is to compare distribution of ECOR types between collections of *E. coli* with and without selection for recent horizontal acquisition.

### Specific Aims

1. Collection of *Escherichia coli* with and without selection for horizontal acquisition (e.g., antibiotic resistance).
2. Classification of isolates by ECOR type.
3. Analysis of distribution of ECOR types according between selected and unselected collections.

### Outcomes

Students will acquire experience with methods and strategies of bacterial populations genetics, and insight into the evolution of horizontal transfer.

### Prerequisites

Some familiarity with basic microbiology technique, including aseptic transfer and culture purification, would be helpful, as is the ability to conduct measurements and calculations required for complex buffer preparation.

### References (see <http://journals.asm.org/search.dtl>)

Clermont, O., S. Bonacorsi, and E. Bingen. 2000. Rapid and simple determination of the *Escherichia coli* phylogenetic group. *Appl Environ Microbiol* 66(10): 4555-4558.

Picard, B., J.S. Garcia, S. Gouriou, P. Turiez, N. Brahimi, E. Bingen, J. Elion, and E. Denamur. 1999. The link between phylogeny and virulence in *Escherichia coli* extraintestinal infection. *Infect Immun* 67(2): 546-553.

Watt, S., P. Lanotte, L. Mereghetti, M Moulin-Schouleur, B. Picard, and R. Quentin. 2003. *Escherichia coli* strains from pregnant women and neonates: intraspecies genetic distribution and prevalence of virulence factors. *J Clin Microbiol* 41(5): 1929-1935.