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Letter to the Editor

Tracing Contamination and *Escherichia coli* Diversity

In a recent paper Geornaras et al. (1) describe the genotypic analysis by amplified fragment length polymorphism (AFLP) of *Escherichia coli* strains isolated from poultry carcasses at different stages of processing. This study importantly demonstrated the presence of a high degree of genetic diversity among 50 *E. coli* strains by a technique other than those traditionally used in genotypic studies on bacteria. These authors suggested, "The heterogenous nature of the AFLP fingerprints of these strains possibly indicates a large number of contamination sources of carcasses with *E. coli*. Sources could include the farm and processing environments as well as the processing equipment," and concluded, "To pinpoint these sources, a study including isolates from the environment and equipment, as well as intestinal contents of carcasses and workers' hands, would have to be conducted." However, other studies investigating the extent to which variation among population accounts for the genetic diversity of *E. coli* (2, 3, 6) suggest another, and far likelier, interpretation of these data than those presented by the authors.

Specifically, investigations of commensal *E. coli* from a wide variety of hosts indicated that typically only around 5% of the observed genetic diversity may be attributed to variation among locality (environment) or among the host group (species or population) variation (2, 3, 4). Differences among individuals of the same species living in close proximity (such as a human family or flock of chickens), on the other hand, can account for up to 60% of observed *E. coli* diversity (4, 6). The majority of *E. coli* organisms on the chicken carcasses in the study under discussion were likely to have originated directly or indirectly from incoming live birds. In their study (1), the authors therefore simply determined and reported the genetic diversity of strains inherent among individual birds entering the slaughter facility, with the diversity due to other factors making a nonsignificant contribution. Any suggestion that the diversity indicated by the AFLP analysis in this study points to a large number of sources of contamination, especially from environments such as the farm, or that the data may be used for epidemiological or trace-back studies is therefore neither appropriate nor practical.

Instead, these data give strong practical support by a novel genotyping technique to the view of Gordon (4) that ". . .most of the assumptions in any programme attempting to identify sources of coliform contamination that focuses on commensal *E. coli* appear to be invalid." The study under discussion is important in that it clearly indicated that the genotypic analysis of commensal *E. coli* populations to trace sources of contamination during animal slaughter is of very limited value. Since the pattern of diversity distribution typical for generic *E. coli* is not necessarily the same for all coliforms (4) or even pathogenic *E. coli*, such as the O157:H7 serotype (5), tracing bacteria other than commensal *E. coli* may therefore represent a more valid approach for studies investigating sources of fecal or coliform contamination.

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