

## **Identification and distribution of an ETEC: F4 contamination marker in a swine production network**

Gabriel DESMARAIS<sup>1</sup>, John M. Fairbrother<sup>1,3,4</sup>, Alexandra Henry<sup>1</sup>,  
Virginie Lachapelle<sup>1,2</sup>, Nadia Bergeron<sup>1</sup>, Ann Letellier<sup>1,3,4</sup>, Philippe Fravalo<sup>1,3,4</sup>

1- Groupe de recherche et d'enseignement en salubrité alimentaire (GRESA)

2- Agence canadienne d'inspection des aliments (ACIA)

3- Centre de recherche en infectiologie porcine et avicole (CRIPA)

4- Groupe de recherche sur les maladies infectieuses du porc (GREMIP)

A number of studies have demonstrated a link between the detection of potentially pathogenic *Escherichia coli* strains and economic loss in the swine industry. The transmission of such *E. coli* between herds and the slaughterhouse and vice versa, in the network they constitute, has not been well characterized. A better understanding of the movement of these *E. coli* between the different stages of food production could lead to better herd health status and contamination control in the slaughter process. *E. coli* strains belong to different clonal groups which may be commensal or pathogenic, the latter being characterized by the presence of specific virulence genes. Thus, the presence of certain of these genes, as detected by molecular techniques, could be used as an indicator of contamination between herds and the slaughterhouse. The objective of this study was to examine the transmission modes of *E. coli* in a defined swine production network. A geographical region containing 10 finishing farms, a slaughterhouse, and a transportation network was selected. Periodic samples were collected at various sites on the farms (3 visits), at the slaughterhouse (2 visits), and on the vehicles of stakeholders linking the farms and slaughterhouse, such as animal transporters and veterinarians. Three consecutive production batches were followed during 8 months. The presence of virulence genes (*eltB*, *estA*, *estB*, *faeG*, *stxA*, *stx2A*, *eae*, *cnf*, *papC*, *iucD*, *tsh*) most commonly associated with pathogenic *E. coli* was examined in the samples by conventional multiplex PCR. The monitoring of the virulence gene distribution profiles both temporally and spatially gave us the opportunity to identify an ETEC: F4 marker. The ETEC: F4 distribution suggests the slaughterhouse yards act as a reservoir of contamination in the network. Further characterization and comparison of ETEC: F4 strains present in the network could identify contamination events between the farms and the associated slaughterhouse.