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Présentation par affiche (poster)

Analysis of the transmission of *Escherichia coli* as a microbiological marker in a swine production network

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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 functional network they constitute, has not been well characterized. A better understanding of the movement of these *E. coli* between the different steps 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 is 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 profiles both temporally and spatially will help to better understand the evolution of *E. coli* contamination in the farms and in the network.