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Topics :

Public health issues and risk assessment

Foodborne pathogen epidemiology and control strategies

### **Identification and distribution of *E. coli* virulence gene profiles in an operating 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. *E. coli* strains belong to different commensal or pathogenic clonal groups, the latter being characterized by the presence of specific virulence genes. The transmission of such *E. coli* between herds and a slaughterhouse in a network, in particular to illustrate the dissemination of *E. coli* strains in a zoonotic perspective, has not been well characterized. The presence of certain virulence genes could be used as an indicator of contamination between herds and the slaughterhouse. The objective of this study was to examine some transmission modes of such *E. coli* in a well defined swine production network. A defined region containing 10 farms, a slaughterhouse, and a transportation network was selected. Periodic samples (feces, dust, soil...) 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 in the samples of virulence genes (*eltB*, *estA*, *estB*, *faeG*, *stxA*, *stx2A*, *eae*, *cnf*, *papC*, *iucD*, and *tsh*) commonly associated with pathogenic *E. coli* was examined by conventional multiplex PCR. The monitoring of the virulence gene profiles both temporally and spatially resulted in the identification of an ETEC:F4 profile as such a marker. The distribution of ETEC:F4 suggests that the slaughterhouse yard acts as a reservoir of contamination in the network, ETEC:F4 being transmitted back to the farms by mechanical vectors. These results illustrated the need to improve

the biosecurity relationship between herds and slaughterhouse, both playing a role in distribution of pathogens in pig production.

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