

PORK SAFETY

Title: Strain Specific Typing Bacterial Pathogens in the Pork Industry Chain
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Abstract

The incidence of *Listeria monocytogenes*, *Salmonella* spp. and *Yersinia enterocolitica* was assessed at one small and one medium-sized slaughterhouse and five farms supplying hogs to these slaughterhouses. Four hogs from each farm were randomly selected and sampled by swabbing before stunning, after scalding/singeing, after evisceration, after final carcass washing and after chilling. Environmental samples were collected from receiving (truck, holding pens), processing (dehairing machine, band saw, drains) and storage areas (cooler walls). Five composite environmental samples of manure, feed, trough water and pen areas were collected from farms supplying hogs to the slaughterhouses. Samples were examined for *L. monocytogenes*, *Salmonella* and *Y. enterocolitica* using USDA/VIDAS, FDA/VIDAS, and the FDA methods, respectively. *L. monocytogenes* was present in 28 of 565 (5.0%) samples, 17 (60.7%) of which were environmental. Six samples from trucks off-loading hogs for slaughter and four samples from the dehairing machine yielded *L. monocytogenes*. *L. monocytogenes* was recovered from one carcass swab after evisceration in the post-slaughter processing area. *Salmonella* was present in 24 of 509 (4.7%) samples, 12 of which (50%) were environmental, including 4 samples from trucks. Two samples from the dehairing machine yielded *Salmonella*, whereas 4 and 2 samples tested positive for *Salmonella* at evisceration and prechill/final wash, respectively. However, neither *L. monocytogenes* nor *Salmonella* were isolated from carcasses after 16-18 h of chilling. Several floor drain samples from the slaughter and meat-processing/packing areas were positive for *L. monocytogenes* and *Salmonella*. Thirty-one isolates of *S. Typhimurium* were serotyped as O-5 negative. No *Yersinia* spp. was identified from samples collected at the small slaughterhouse after which no further analyses were conducted. PFGE analysis yielded 9 different clusters of *L. monocytogenes*. Three isolates yielded PFGE patterns that were similar to a previously determined clinical pattern from a foodborne outbreak. Eight isolates of *S. Typhimurium* DT 104 were presumptively identified using PFGE.

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