

PORK SAFETY

Title: Prevalence of *Yersinia enterocolitica* in US Market Weight Hogs
NPB# 00-135

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Abstract: *Y. enterocolitica* is a major human food-borne pathogen which accounts for ~87,000 human cases and ~1,100 hospitalizations each year in the US. The purpose of this study was to estimate the individual animal and herd prevalence of *Y. enterocolitica* in hogs sampled during National Animal Health Monitoring System (NAHMS) Swine 2000. Tonsil and fecal swabs were collected on farms (n=122) located in the 17 pork producing states. Tonsil (n=1,218) and fecal (n=2,033) samples were tested by our laboratory at the National Animal Disease Center (NADC) for the *ail* gene. Results from an additional 814 fecal samples analyzed by Dr. S. Bhaduri, USDA-ARS-Eastern Regional Research Center (ERRC) were incorporated into the final analysis of fecal samples (total=2,847). The *ail* gene of *Y. enterocolitica* encodes the adherence and invasion protein which is a major virulence factor. The fluorogenic 5' nuclease PCR assay, which was developed earlier in this laboratory with financial support of the National Pork Producers Council, was further optimized and used to screen hogs for the *ail* gene of *Y. enterocolitica*. For tonsils (122 of 1,218 samples), 10% were positive in irgasan tiracillin chlorate (ITC) enrichment broth whereas 5.6% (68 of 1,218) of samples were positive after subculture to the more selective cefsulodin-irgasan-novobiovin (CIN) agar. This indicates that growth in ITC broth is more permissive for pathogenic strains than the more selective CIN agar. Thus, data based solely on results obtained by CIN culture may under estimate the prevalence of *Y. enterocolitica*. When tonsils were sampled to monitor the hog carrier status, the herd prevalence based on ITC data is ~32% (32 of 100 premises sampled) whereas the prevalence based on growth on CIN is ~20% (20 of 102 premises). When feces were used to gauge *Y. enterocolitica* prevalence, an estimated 13% of hogs harbored the *ail* gene, after ITC enrichment (372 of 2,847). The overall herd prevalence is estimated at 45.08% (55 of 122 premises), based on the detection of the *ail* gene in ITC broth enrichments of tonsils and combined laboratory data of feces. We have correlated herd prevalence data with farm management practices. Initially, 12 factors were selected on the basis of passing the cut-off value of $p < 0.25$. Next, five factors were identified as correlated with herd prevalence at the 90% probability level ($p < .10$). These included antibiotics in the feed ($p = 0.07$), previous history of vaccination for *E. coli* ($p = 0.09$), deaths reported on the premises which were due to scours ($p = 0.07$), failure of pigs to thrive because of the porcine respiratory distress complex (age at which pigs "hit the wall") ($p = 0.07$), and use of meat/bone meal in grower-finisher diet ($p = 0.10$). Ultimately, four factors were identified in the final regression model. These included, with their accompanying odds ratio (OR), location in a non-central state (OR=0.3), vaccination for *E. coli* (OR 3.0), % deaths due to scours (OR 3.5), and presence of meat/bone meal in grower-finisher diet (OR 4.1).

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