

Title: Analysis of in-plant Factors and Genotyping of Antimicrobial Resistance among Four Organisms Isolated from Swine Processing Plants - **NPB-06-162** revised

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Scientific Abstract

The importance of *Salmonella*, *Campylobacter*, *Escherichia*, and *Enterococcus* as carriers of antimicrobial resistance is well known, but limited work has been done to examine the relationship between this phenotypic characteristic and genotypic attributes among strains isolated in similar settings and time points. The specific objectives of the study were to determine the role of plant size and origin of samples on prevalence of resistant foodborne and commensal organisms, identify the clonality of major foodborne pathogens particularly *Salmonella* and *Campylobacter* recovered from small and large size processing plants in two predominant pig producing geographic locations (NC and IA) and to determine the distribution and similarity of specific antimicrobial resistance genes and class-1 integrons among the four organisms from swine production. Isolates were collected from processing plants in North Carolina and Iowa. Phenotypic characterization of antimicrobial resistance patterns was completed on 1,284 samples. DNA microarray was used for gene detection in 19 selected samples. PCR of resistance genes and class-1 integrons was performed on 128 isolates. Select resistance genes were sequenced based on PCR results. In all four pathogens the proportion of positive samples from lairage was higher (30 to 52%) compared to other locations. It was also found that small plants had a higher percentage of pansusceptible isolates (27.4%) compared to the large processing plants (10.6%). Phenotypically, all organisms were highly resistant to tetracycline, with the lowest prevalence in *Salmonella* at 69.4%. Multidrug resistance was common among isolates from both small and large processing plants, however, relatively higher in later ones. Microarray results showed that 47.3% of resistance genes tested were found in at least two different bacterial organisms. Within the samples that tested PCR positive for *tetA(B)*, *strA*, *strB*, and *aphA1-lab*, there were multiple groups of organisms that were from the same animal. After sequencing, *strB* and *aphA1-lab* genes with 98.6% or greater homology were found in different organisms (*Salmonella* and *E. coli*) from the same animal host. Class-1 integrons were found in 18.2% of the samples. Large (4kb) integrons were found in *Salmonella* serovar Havana. Large integrons among MDR *Salmonella* is of high significance since integrons facilitate the carriage and dissemination of multi-drug resistance. Overlapping of resistance genes found within the four organisms may be the result of horizontal resistance gene transfer within the host. Further characterization via conjugation is planned.

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