RESEARCH ABSTRACT
PORK SAFETY

Title: Identifying genes associated with *Salmonella* shedding to increase pork safety through improved genetic resistance - **NPB #08-034** revised

Investigator: Christopher K Tuggle[1]

Co-Investigators: Shawn Bearson[2] Jack Dekkers[1], Annette O'Connor[3], James McKean[3]

Graduate students: Jolita Uthe[1,4], Long Qu[1,5]
Undergraduate students: Yasi Rodriguez[1], Stephen Robinson[1]

Institution: [1]Department of Animal Science, Iowa State University, Ames, IA
[2] USDA, ARS, National Animal Disease Center, Ames, IA
[3]Department of Veterinary Microbiology and Production Animal Medicine, Iowa State University, Ames, IA
[4]Interdepartmental Genetics Graduate Program, Iowa State University, Ames, IA
[5]Department of Statistics, Iowa State University, Ames, IA

Abstract

Salmonella shed from colonized swine can contaminate: slaughter plants and pork products during meat processing (Hurd et al, 2002, Appl Environ Microbiol, 68:2376-2381); edible crops when swine manure is used as a fertilizer; water supplies if manure used as crop fertilizer runs off into streams and waterways (Guan and Holley, 2003, J Environ Qual 32:383-92); and neighboring pigs resulting in a food safety problem and animal health issue. Control of food-borne *Salmonella* within the farm-retail continuum is a complex issue. An essential step in providing pathogen-free products to consumers is reduction of the risk of food-borne disease on the farm level. Reduction of on-farm *Salmonella* contamination by the use of antimicrobials is not a sustainable way of disease control for two reasons: one, antimicrobial overuse can lead bacteria to develop resistance to such antimicrobials which decreases their effectiveness for the producer and rises serious human health-care issues (Perron et al, 2008, PLoS One 3:e3749); and second, pigs can be infected with *Salmonella* not only at the farm, but also during transportation and/or lairage. A potentially more effective method of addressing pre-

harvest food safety is through genetic improvement of disease resistance in animals. Thus, the long-term goals of this project are to use the power of genomics to identify gene variants that are associated with decreased *Salmonella* shedding on farms; and to use these variants to select for animals that shed fewer bacteria and so are less likely to cause contamination in lairage, at the abattoir, or in carcasses during fabrication. To identify genetic components controlling disease resistance differences in pigs, we: 1) created a large resource population of pigs with known *Salmonella* shedding phenotypes; 2) created DNA tests for genetic variation in candidate genes that are involved in swine response to *Salmonella*, 3) genotyped our resource populations for single nucleotide polymorphisms (SNPs) in the candidate genes and 4) analyzed SNPs for associations with *Salmonella* shedding and/or tissue colonization phenotype. Previous work has been successful in identifying an important association between genetic variation in the CCT7 gene and *Salmonella* shedding (Uthe et al, 2009, Vet Microbiol 135:384-8). In the current work using a total of 750 pigs we genotyped 62 SNPs in 53 genes that are involved in porcine response to *Salmonella* infection. We found 28 segregating genetic variants with minor allele frequency of 15 % or higher in at least 2 of our 4 porcine populations. Statistical analysis revealed several SNPs associated with *Salmonella* fecal shedding or tissue colonization, with p-value <0.1 and q-value ≤ 0.2, where q-value is the minimum false discovery rate (FDR) such that the corresponding null hypothesis can be rejected. Fecal shedding associated SNPs were CCT7 #3 (p=0.041), GNG3 (p=0.029), PGD (p=0.047) and HP #2 (p=0.0002) in the field population, AMT (p=0.005) in the NADC-40 pig population and PGD (p=0.001) in the NADC-77 pigs population. In the IAH-Compton population three SNPs in the ACP2 gene were associated with *Salmonella* burden in spleen (ACP2#1, p=0.013, ACP2#2, p=0.026, ACP2#3, p=0.033); and in the NADC-40 pig population, a SNP in the EMP1 (p=0.002) gene was associated with bacterial load in ileo-cecal lymph node. The genotyping and statistical analysis data will be used to generate genetic markers useful in selecting animals that shed fewer bacteria and are less likely to cause pen-mate *Salmonella* contamination in a farm and on a slaughter plant, thus providing novel information for the pig industry to implement in strategies for selecting pigs with reduced shedding and/or disease susceptibility.