



Pork Information Gateway



Research Project: Impact of Diet and Gut Microbial Ecology on Foodborne Bacterial Pathogens and Antimicrobial Resistance in Farm Animals

Location: Pre-Harvest Food Safety and Enteric Diseases

Title: Antibiotic Resistant Microbiota in the Swine Intestinal Tract

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Technical Abstract: The healthy swine intestine is populated by upwards of 500 bacterial species, mainly obligate anaerobes. Our research focuses on the roles of these commensal bacteria in antimicrobial resistance and on interventions to reduce the prevalence of antibiotic resistant bacteria. In comparisons of intestinal microbial populations, 16% of the anaerobes from organically raised swine were resistant to chlortetracycline (CTC), whereas 0.3%, from feral swine were resistant. Of *Megasphaera elsdenii* isolates, 49% (264/540) from organic swine were CTC-resistant, whereas none (0/91), from feral swine were resistant. *M. elsdenii* strains exhibited high levels of CTC-resistance (greater than or equal to 256 ug/ml) and carried novel `mosaic` tetracycline resistance genes. One strain carried seven different antibiotic resistance genes, including genes previously found in the foodborne pathogen *Campylobacter jejuni*. As an intervention strategy, we tried to block sow-to-piglet transmission of *M. elsdenii* antibiotic resistant strains by dosing newborn piglets with five antibiotic sensitive strains. The dosing of piglets with antibiotic sensitive strains delayed, but did not prevent, colonization by maternal resistant strains which were highly diverse. Our studies indicate that antibiotic resistant commensal anaerobes persist in the absence of antibiotic use. *M. elsdenii* strain diversity suggests an explanation for the persistence of antibiotic resistance in this species. The presence of mosaic CTC resistance genes in *M. elsdenii* suggests commensal bacteria may not only be reservoirs of antibiotic resistance but also sites for the evolution of resistance.

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