Epidemiology of Shiga toxin-producing *Escherichia coli* (STEC) in finishing swine

Tseng, M.[1], Fratamico, P.[2], Manzinger, D.[2], Garman, B.[2] and Funk, J.[1], [1]Michigan State University, College of Veterinary Medicine, East Lansing, MI, USA, [2]United States Department of Agriculture, Agricultural Research Service, Eastern Reginal Research Center, Wyndmoor, PA, USA; tsengmar@cvm.msu.edu

Every year, approximately 200,000 cases of illness are estimated to be associated with Shiga toxin-producing *Escherichia coli* (STEC) in the United States. STEC strains are one of the leading causes of hemorrhagic colitis (HC) and hemolytic uremic syndrome (HUS) in humans. Many STEC outbreaks are attributed to food contaminated by animal feces. Notably, some human cases of STEC O157:H7 and non-O157 infections have been associated with pork products. To this date, little is known about swine STEC. We have conducted a prospective cohort study to achieve our objectives: to provide the first longitudinal descriptive epidemiology of STEC shedding in US finishing swine and to characterize swine STEC isolates. Three cohorts of pigs from one production company were included. In each cohort, 50 pigs were randomly selected and individually identified. Fecal samples were collected from each pig once every two weeks throughout the 16 weeks of the finishing period (eight samples/pig). Fecal samples were assayed for STEC by enrichment (10 min in TSB, pH 3 followed by incubation for 15 h in TYTP at 41 °C) followed by DNA extraction and the polymerase chain reaction (PCR) targeting the Shiga toxin genes (stx) and the intimin protein gene (eae). Shiga toxin gene-positive enrichments were plated onto ChromAgar STEC. Presumptive STEC isolates were recovered, confirmed by PCR, and serotyped. At the time of submission, STEC isolates were recovered at least one time from 90% (45 out of 50) of the pigs in cohort one, 98% (48 out of 50) in cohort 2, and 86% (43 out of 50) in cohort 3. STEC were isolated from swine in this study at relatively high incidence rates with variability of shedding over time and between cohorts. These data will be critical to fill in current gaps in swine STEC epidemiology and determine the association between STEC in swine, pork, and humans.