
Sponsors

University of Minnesota

College of Veterinary Medicine

College of Food, Agricultural and Natural Resource Sciences

Extension Service

Swine Center

Thank you to **IDEXX Laboratories** for their financial support to reproduce conference proceedings

Production Assistants

Steven Claas

Michael Klatt

Layout and CD-ROM

David Brown

Logo Design

Ruth Cronje, and Jan Swanson;

based on the original design by Dr. Robert Dunlop

The University of Minnesota is committed to the policy that all persons shall have equal access to its programs, facilities, and employment without regard to race, color, creed, religion, national origin, sex, age, marital status, disability, public assistance status, or sexual orientation.

Molecular analysis and diversity of pathogenic *Clostridium perfringens* and *Clostridium difficile* among neonatal pigs in the Midwest
A. Baker^{1*}, K. Novak¹, E. Davis¹, R. Moser², M. Englehart², D. Webel², A. Veldkamp¹ T. Rehberger¹, and D. Rosener¹
**¹Agtech Products, Inc. Waukesha, WI.,
²JBS United, Inc., Sheridan, IN**

Enteric clostridial disease in swine is often caused by pathogenic *Clostridium perfringens* Types A and C as well as *Clostridium difficile*. Infection is most common in neonatal pigs and can lead to scouring, low weaning weights, and pre-weaning mortality. The focus of our study was to evaluate the diversity of *C. perfringens* Type A and *C. difficile*, although all types of *C. perfringens* were screened for. In this study, a total of 180 pigs were sampled from 16 locations across the Midwest region over a period of three months. Clinical pigs were swabbed rectally and samples plated on selective media for *C. perfringens* and *C. difficile*. Isolated colonies were picked from the plates and DNA was extracted for genetic analysis. Multiplex PCR was performed on the isolates targeting the four major toxins in *C. perfringens*: *alpha*, *beta*, *iota*, and *epsilon* and the toxin genes *tcdA* (Toxin A) and *tcdB* (Toxin B) in *C. difficile* to confirm identification. Multiplex PCR confirmed 479 of 502 isolates as *C. perfringens* Type A. Three isolates of *C. perfringens* Type C were identified at one regional site indicating a low incidence of Type C among the farms in this study. No other types of *C. perfringens* were found. A total of 102 *C. difficile* isolates were positive for Toxins A or B. RAPD PCR was used to characterize the toxigenic isolates of *C. perfringens* Type A and *C. difficile*. Isolates were constructed into dendrograms to

evaluate genetic diversity among the isolates. The *C. perfringens* Type A dendrogram consisted of 479 isolates in 97 clusters at an 80% similarity coefficient. The *C. difficile* dendrogram was comprised of 102 isolates grouped into 51 clusters. Diversity indexes were calculated for each dendrogram using the formula: number of isolates/number of clusters. A low index indicates a high degree of diversity. *Clostridium difficile* isolates showed greater diversity than the *C. perfringens* Type A isolates with diversity indexes of 2.0 and 4.93 respectively. The largest cluster in the *C. difficile* dendrogram contained 20 isolates. Nineteen of the 51 clusters contained a single isolate. Conversely, the *C. perfringens* Type A dendrogram contained five large clusters with more than 25 isolates each, the largest cluster being 38 isolates. Overall, the incidence of *C. difficile* was found in the samples less frequently than *C. perfringens* Type A and seemed to be prevalent at only some farms. Many clostridia isolates were common to all farms evaluated in this study. However, the presence of some isolates that were unique to specific farm sites was also evident. These data indicate that enteric clostridial disease likely results from the presence of ubiquitous *C. perfringens* Type A and *C. difficile* strains.