

SWINE HEALTH

Title: Investigation and characterization of pathogenic and molecular differences in atypical *Brachyspira* spp. clinical isolates versus classic strains - **NPB# 11-178**

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Scientific Abstract:

Classical swine dysentery is associated with the presence of the strongly beta-hemolytic *Brachyspira hyodysenteriae*; however, multiple *Brachyspira* spp. can colonize the porcine colon. Recently, *Brachyspira* spp. not identified as *B. hyodysenteriae* by genotypic and/or phenotypic methods have been isolated from pigs with clinical swine dysentery. In this study, seventeen strains of *Brachyspira*, including multiple strongly beta-hemolytic and weakly beta-hemolytic isolates, were screened for virulence in mice to determine a proposed pathotype for each strain and to select the most appropriate isolates for inoculation into pigs. Following virulence screening, eight clinical isolates, including five strongly beta-hemolytic and three weakly beta-hemolytic *Brachyspira* strains, and a reference strain of *B. hyodysenteriae* (B204) were inoculated into pigs to compare pathogenic potential following oral inoculation. Results revealed that strongly beta-hemolytic isolates induced significantly greater typhlocolitis than those that were weakly beta-hemolytic, regardless of the genetic identification of the isolate, and that strongly beta-hemolytic isolates identified as "*Brachyspira* sp. SASK30446" and *B. intermedia* by polymerase chain reaction (PCR) produced lesions similar to those caused by *B. hyodysenteriae*. These results suggest that the microbial culture characteristics of *Brachyspira* spp. may be a more sensitive indicator of the potential to induce swine dysentery than the identification of the organism by currently available PCR assays alone.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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