

SWINE HEALTH

Title: Development of a genus-specific virulence gene PCR panel for *Brachyspira* spp. –
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Scientific Abstract:

In recent years the swine industry has observed a resurgence of swine dysentery and dysentery-like disease although the reason(s) for this increase in dysentery diagnoses is poorly understood. Classically, swine dysentery has been attributed to infection by *Brachyspira hyodysenteriae*, but recent research by this group and others has identified at least two potentially novel species of *Brachyspira*, “*Brachyspira hampsonii*” and “*Brachyspira suanatina*”, with strong hemolytic potential that induce dysentery-like disease but are not positive by *B. hyodysenteriae*-specific PCR assays. These potentially novel species have proven to be diagnostically challenging. In this study, whole genome sequencing of multiple putatively novel pathogenic *Brachyspira* isolates along with several officially recognized species with a recognized virulence phenotype *in vivo* was completed. The obtained sequences can be used for ongoing analyses and investigations into genetic differences that may underlie the potential to induce dysentery in susceptible swine. This will provide critical insight into future diagnostic and prevention strategies.

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 This report has not been peer-reviewed.

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