

Title: Reverse Vaccinology and Genomics Towards Controlling Post-Weaning Diarrhea –
NPB #11-081

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Date Submitted: 5/1/2013

Scientific Abstract.

Enterotoxigenic *Escherichia coli* (ETEC) is the causative agent of post-weaning diarrhea (PWD) in production pigs, which is a disease that continues to be a major cause of morbidity for the swine industry. The primary ETEC types implicated in PWD are well known and characterized and mostly include those that harbor K88 or F18 fimbriae. However, traditional approaches at a vaccine providing protection against PWD have not proven effective. Here, we utilized a global approach known as reverse vaccinology towards the identification of novel vaccine candidates. This approach utilized the first completed genome sequences of K88+ and F18+ porcine ETEC isolates, subsequent mining of their predicted proteins for suitable antigenic candidates, and assessment of the prevalence of the gene sequences encoding for suitable antigenic candidates among porcine *E. coli* collections. Using this approach, we identified approximately 50 antigenic candidates from the K88+ and F18+ genome sequences. We screened a collection of 300 porcine *E. coli* isolates for the presence of these candidates, narrowing this subset to eight genes that are significantly associated with PWD ETEC isolates and possess antigenic potential. This subset of antigens will be used in future studies aimed at developing a recombinant attenuated *Salmonella* vaccine that will elicit a mucosal immune response and protect against ETEC strains implicated in PWD.

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 This report has not been peer-reviewed.

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