

Innovation Grant: 2A-117, Erysipelothrix Rhusiopathiae Epi-Interface, A New Approach To The Management Of Porcine Erysipelas

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Aims and Objectives: Characterise *E. rhusiopathiae* isolates using Multi Locus Sequence Typing, virulence gene and antibiotic resistance profiles from DNA sequences derived from whole genome sequencing. Integrate this profile with bacteriological data, farm disease and management information in an Epi-Interface database to establish a better understanding of the epidemiology of erysipelas. We aim to establish this as an affordable, ongoing and dynamic ecological and epidemiological tool to (1) improve management of porcine erysipelas in the Australian pig industry and (2) develop a model for disease data collection that can be applied to both pig and other livestock industries. Information from this Epi-Interface will aid future decisions in vaccine development and the judicious use of antibiotics.

Key Findings: In this study, one hundred and eighty *E. rhusiopathiae* isolates underwent whole genome sequencing (WGS) of which 178 were successful. From the whole genome sequences, we were able to generate 46 MLSTs from a range of archived and contemporary isolates. Of these, nine were equivalent to previous studies and 37 were new to this study. WGS were screened for 47 putative virulence genes producing 24 distinct profiles (virotypes). Antibiotic sensitivity testing showed that all strains were susceptible to amoxicillin and a single isolates displayed lincospectin or penicillin resistance. This WGS data and the associated clinical information was integrated into the Epi-Interface (database) and screened systematically. Results demonstrated that Australian and International isolates of *E. rhusiopathiae* are quite distinct. Isolates from 45 farms were associated with suspected vaccine breakdowns of which 29 (64%) were attributable to three MLSTs.

Furthermore, this study identified a bacteriophage, detected in 14% of the studied isolates. Bacteriophages have been identified as potential anti-bacterial agents that may be instrumental in overcoming antimicrobial resistance.

Application to Industry: This innovation study has generated a dynamic resource to improve the understanding of this highly variable pathogen in the Australian pig industry. It has also provided insight into the quantity and quality of metadata that is required nationally for improved management of porcine erysipelas. The Epi-Interface developed in this project will have cumulative commercial value as data is added. The genome sequences generated during this pilot study have stand-alone commercial value for data mining in relation to future diagnostic, vaccine and antibiotic development.

There is growing evidence that environmental data is critical to the understanding of erysipelas. Fortunately, the modular nature of the Epi-Interface allows for the inclusion of new data sets, such as environmental data. Pre-existing data can then be reanalysed in relation to the newly added information.