A preliminary study of the molecular epidemiology of *Brachyspira hyodysenteriae* isolates in Australia

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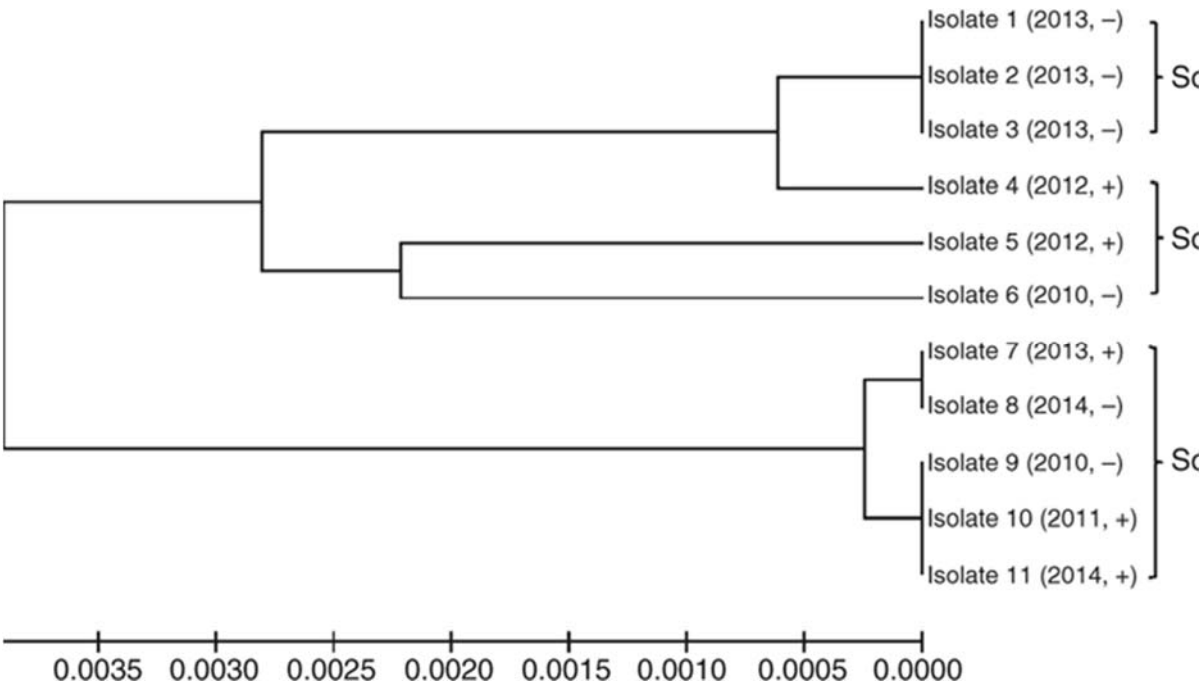
Swine dysentery (SD) is a mucohaemorrhagic colitis of grower-finisher pigs. Affected pigs have faeces ranging from soft, yellow-grey to mucoid, bloody diarrhoea. Swine dysentery is one of the most economically significant enteric diseases of pigs in Australia due to its effect on growth rate, feed efficiency, mortality and the associated medication control costs. The classical causative agent is a strongly β-haemolytic anaerobic intestinal spirochaete *Brachyspira hyodysenteriae*. Diagnosis of SD requires bacterial isolation and (or) identification using polymerase chain reaction (PCR). A number of PCR methods have been described for identifying *B. hyodysenteriae*. In this study, a multiplex PCR for *B. hyodysenteriae*, *B. pilosicoli*, *L. intracellularis* and Salmonella *spp*. including primers described by Elder *et al*. (1997) was compared with the PCR targeting NADH oxidase (*nox*) as described by La *et al*. (2006). Multi-locus sequence typing (MLST) was used to determine the relatedness of the *B. hyodysenteriae* isolates (La *et al*. 2009). The hypothesis was that isolates that were test-negative using the multiplex PCR but test-positive using the simple PCR were related but different to those positive on both PCR tests.

A total of 11 *B. hyodysenteriae* isolates from grower pigs from 11 farms having clinical signs of SD and collected over the period 2010–2014 was tested. Isolates were cultured to demonstrate pure cultures for MLST. The pigs originated from three genetic sources (Sources A, B and C). Isolates 1–3 were from three different farms supplied by Source A. Isolates 4, 5 and 6 were from three farms supplied by Source B. Isolates 7–11 were from five different farms supplied by Source C.

The multiplex PCR detected six (55%) of the *nox* PCR positive isolates. There was no clear relationship between the enteric PCR positive and negative isolates (Fig. 1). Isolates from different farms that obtained pigs from the same source generally were closely related, with isolates 1–3 (Source A) and isolates 7–11 (Source C) being identical or nearly identical, but different from those recovered elsewhere.

Fig. 1. A multi-locus sequence typing tree of the 11 *B. hyodysenteriae* isolates cultured from pigs from 11 farms. The year of isolation is indicated in parentheses, as well as the positive (+) and negative (–) multiplex PCR results for each isolate. The source of the pigs for each farm is indicated. The scale bar represents 5 nucleotide substitutions in 1000 base pairs of the sequenced gene fragment.



This study showed that there were no consistent strain-related patterns among multiplex PCR negative or positive isolates. Isolates from pigs from the same sources were similar in MLST, demonstrating

that this method can reliably be used to map the movement of *B. hyodysenteriae* isolates between farms.

References

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