Prevalence of *Ureaplasma diversum* in induction cohort animals sampled at two time-points (day 0 and day 14) and hospital pen animals from a Southern NSW feedlot

R. Barnewall[A,B,F], *I. Marsh*[C], *N. Sales*[C], *P. Cusack*[D], *T. Williams*[E], *F. Galea*[C], *V. Vicic*[A,B] *and J. Quinn*[A,B]

[A]School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, NSW 2678, Australia.
[B]Gulbali Institute, NSW 2678, Australia.
[C]NSW DPI, Elizabeth Macarthur Agricultural Institute, NSW 2567, Australia.
[D]Australian Livestock Production Services, NSW 2794, Australia.
[E]School of Health, Medical and Applied Sciences, Central Queensland University, Qld 4701, Australia.
[F]Corresponding author. Email: rbarnewall@csu.edu.au

Bovine respiratory disease (BRD) is the most common disease of feedlot cattle worldwide. It is a complex disease and many bacterial and viral agents have been implicated in its aetiology. *Ureaplasma diversum* is commonly associated with other bovine ailments, such as abortion and infertility, and more recently has been implicated in the pathogenesis of BRD (Szacawa *et al.* 2016). However, the involvement of *U. diversum* in BRD as a non-commensal microorganism is not well understood. To better understand the prevalence of this organism in the Australian feedlot system, we compared the prevalence of *U. diversum* in feedlot cattle at three stages within the feedlot system using quantitative PCR.

Nasal swabs were collected from an induction cohort of animals in a Southern NSW commercial feedlot at induction (day 0) and again after 2 weeks on feed (day 14). Cattle located in the hospital pen on the same collection dates were also sampled. Two hundred and sixteen nasal swabs were collected from the induction cohort and 34 nasal swabs from hospital pen animals for comparison. These collections occurred during the low-risk BRD period between October and November 2020 (Barnes *et al.* 2015), with approval from Charles Sturt University (ACEC Protocol A18070). The swabs were stored in viral transport fluid (VTF, Edwards Group Pty Ltd, Australia) and processed for qPCR analysis using a direct heat extraction method. To determine the presence of *U. diversum,* PCR was performed using published primer sequences (Kishimoto *et al.* 2017) and PerfeCTa® SYBR® Green FastMix® (Quanta BioSciences, USA) with minor modifications. Any samples with a PCR cycle threshold (Cq) value of less than 40 was considered as having detectable *U. diversum*.

There was a low prevalence of *U. diversum* detected in cattle at induction (day 0 $n = 15$, day 14 $n = 21$) and no significant difference between prevalence at day 0 and day 14 (Fisher's exact test, $P = 0.3844$; Fig. 1A). Of the 216 induction cohort animals sampled, 3 had detectable *U. diversum* at both day 0 and day 14 collections. The detection rate of *U. diversum* was significantly higher (61% ± 15) in animals sampled from the hospital pen when compared to that of the induction cohort ($P < 0.001$; Fig. 1A). In addition, *U. diversum* was detectable equally in the 20 hospital pen animals whether treated for BRD or for other ailments (Fig. 1B).

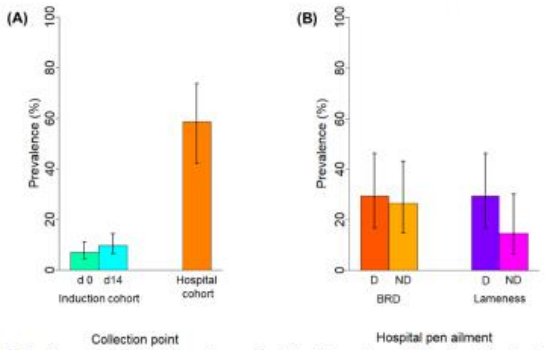

Fig. 1. Prevalence (+/- CI) of *U. diversum* in nasal swabs collected during low-risk period for bovine respiratory disease; (A) comparison between induction cohort animals at two time-points (day 0 (d 0) and day 14 (d 14), $n = 216$) and hospital pen animals ($n = 34$), (B) comparison between detectable (D) and not-detectable (ND) within the hospital cohort ($n = 34$) dependent on disease; BRD (detectable = 10, not-detectable = 9), lameness (detectable = 10, not-detectable = 5).

This study is the first to report on the detection of *U. diversum* from nasal swabs in Australian feedlot cattle. While *U. diversum* was detected at a significantly higher rate in cattle from the hospital pen than those sampled at induction, its prevalence was similar regardless of the hospitalisation ailment. These findings suggest that *U. diversum* may be contributing to disease in feedlot cattle although the contribution to BRD is currently unknown.

References

Barnes T *et al.* (2015) Project code: B.FLT.0225. (Meat & Livestock Australia)
Kishimoto M *et al.* (2017) *Journal of Veterinary Medical Science* **79**, 517–523.
Szacawa E *et al.* (2016) *Journal of Veterinary Research* **60**(4), 391–397.

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