Adding a further twist to the tail of Leptospirosis in the UK

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Conventional serological typing of the spirochaete *Leptospira* (figure 1) is challenging, particularly when applied to serogroup Pomona. This group being comprised of members of four genospecies, namely *Leptospira interogans* (Kennewicki; Monjakov; Pomona), *Leptospira kirschneri* (Altodouro; Mazdok; Tsaratsova; Kumming), *Leptospira noguchii* and *Leptospira sanarosai*. The latter two species not being endemic to Europe. The significance attributed to these strains is hugely variable with *L. kirschneri* seorvar Mozdock, only rarely resulting in consequences amongst livestock or companion animals, whereas *L. interrogans* serovars Pomona type Kennewicki potentially results in devastating infection consequences (Timoney and others 2011). The pathogenic traits of Kennewicki strains are not shared with other serovars belonging to the *L. interogans* Pomona serogroup such as Monjakov or Pomona. In Europe, within the Pomona serogroup, serovars Pomona and Mozdok correlated pigs (figure 2) and rodent reservoirs respectively are the most commonly encountered members of this group, with occasional spill-over into non-reservoir species. Expansion of reservoir species has been reported for serovar Pomona with its ability infect sea lions, but also cause disease (Prager and others 2013).

Leptospiral infection associated with serogroup Pomona has been associated with haemorrhagic acute febrile manifestations, renal signs, jaundice, and reproductive involvement (Jacobs and others 2015). Equines appear to be particularly susceptible

with several reports of abortion, particularly where serovar Kennewicki is endemic (Timoney and others 2011). Intriguingly, the majority of isolates assessed by Arent et al, are largely derived from equine infection (symptomatic and asymptomatic) over a three-year period (Arent and others 2017a).

Given this backdrop, the description of serogroup Pomona from the UK domestic animals was concerning. This serogroup has been sporadically reported from livestock in the UK, with both Mozdock and Pomona serovars being recovered. Arent and co-workers (this issue), subjected a series of 10 UK-derived isolates to various Leptospiral typing approaches to gain insights into their identity and enable assessment of their potential pathogenic potential. Recovery of isolates is technically challenging, hence our general reliance upon non-cultivation based diagnostics such as serology and molecular detection. Evolution of molecular typing techniques has enabled more highly discriminatory methods to be applied to the Leptospiral group and has highlighted the heterogeneity even within serovars and facilitated analysis of these sub-populations by host and geographical location (Arent and others 2017b) and has been used to describe new strains such as Altodouro (Paiva-Cardoso and others 2013).

Application of molecular typing revealed that the isolates all resembled serovar Pomona, a finding that supports the greater potential of this serovar to spill into livestock species. Interestingly, restriction endonuclease digestion using *Alu*I and *Hpa*II could discriminate between two sub-populations amongst the recovered isolates, splitting those recovered from animals in Northern Ireland and that obtained from a shrew from an adjacent area to a pig farm with possible leptospiral infection in

England. This sub-division could not be resolved by MLVA raising the question of the discriminatory capability of these two typing methods? This conundrum is akin to that which these authors previously assessed with different serovars of *L. interrogans* Bratislava and Muenchen, where again restriction endonuclease digestion offered greater resolution (Arent and others 2016). These data raise the question as to whether restriction endonuclease digestion should be retained as a valued highly discriminatory tool over methods such as MLVA which offers greater transportability of data between laboratories, and requires significantly less DNA as a pre-requisite for typing? Under stringently controlled conditions, restriction endonuclease digestion appears to retain its value for discrimination of sub-types within serotype, but this could also suggest that alternative MLVA approaches need to be further refined with a view of increasing their discriminatory power. It maybe that an alternative typing approach such as use of canonical SNPs might provide a more transferrable and less DNA thirsty highly discriminatory solution for molecular typing of Leptospira?

To conclude, the isolates recovered from sporadic testing in the UK revealed that Pomona was the causative serovar, thus paralleling the observations seen elsewhere in Europe where Pomona serogroup strains infect livestock. Interestingly, a new variant was described. As this currently was based upon a single isolate from a shrew, further investigative studies are essential to map strain epidemiology and assess host correlations and their pathogenic potential.

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