Journal of Equine Veterinary Science 39 (2016) S88–S97

Contents lists available at ScienceDirect

Journal of Equine Veterinary Science

journal homepage: www.j-evs.com

10th IEIDC Abstracts-Respiratory: *Streptococcus equi*

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The global population diversity of *Streptococcus equi* highlights transmission across international boundaries

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The genomes of 499 strains of *S. equi*, which were isolated between 1955 and 2015 from horses across the world, were sequenced to study the phylogenetic relationships of strains of different geographical and temporal origins. Phylogenetic trees were reconstructed based on single nucleotide polymorphisms in the core genome and the genetic diversity of isolates was examined relative to the country of origin. The molecular epidemiology of outbreaks, where information was available, was investigated in greater depth to enable the identification of outbreak sources. Sequencing strains from an outbreak at a rehoming centre in Norfolk, UK, in early 2015 identified that a breakdown in biosecurity measures in the isolation yard was responsible for recent cases of disease. This information enabled rapid remedial actions to be implemented, which minimised further cases and facilitated the resolution of the outbreak. The sequences of isolates recovered from an outbreak of strangles at a rehoming centre in Lincolnshire, UK, during 2007/8 provided evidence that this outbreak was triggered by persistently infected carrier animals, most likely from a previous spate of disease on this site. Following the outbreak, the identification and treatment of persistently infected horses enabled the eradication of *S. equi* from these premises. The transmission of four strains of *S. equi* linked to the import of horses from Europe led to multiple outbreaks of strangles in Dubai. Our data highlight potential benefits of pre-export screening for the effective identification and treatment of carrier animals. Certain groups of *S. equi* were restricted to particular outbreaks or countries, for example isolates in Australia and New Zealand were related. However, the populations of *S. equi* recovered from several European countries (Ireland, Sweden, Belgium, France, the Netherlands, Spain, Italy and the UK) and Dubai were virtually indistinguishable. Our data highlight that the international movement of horses facilitates cross-border transmission of *S. equi*. International transmission is most likely to occur through a failure of pre-import health checks and quarantine procedures to identify outwardly healthy persistently infected animals. Pre-movement screening can identify persistently infected horses and prevent outbreaks of strangles. However, these diagnostic tools do not form part of pre-export testing procedures as strangles is not currently recognised as an OIE-Listed disease that is important for international trade. Strangles is endemic throughout the world and causes significant disruption to the equine industry. However, the international transmission of *S. equi* is preventable. We recommend that strangles should be listed by the OIE and that diagnostic testing for this agent becomes a routine part of pre-export health checks.

Acknowledgements

We are grateful to all those who have contributed isolates to this study.

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Reduced clinical severity of strangles in weanlings associated with restricted seroconversion to optimized *S equi* assays.

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In autumn 2014, clinical strangles occurred in a group of 112 warmblood weanlings. All were sampled by nasal swabs at the peak of the outbreak and four months later 98 of the 112 sampled by nasal swab, nasopharyngeal lavage and guttural pouch lavage for culture and qPCR [(1)] to *Streptococcus equi* ssp. *equi* (hereafter *S. equi*). Clinical signs were recorded serially over the entire outbreak to identify occurrence of clinical strangles. Those with ruptured abscess/es on the head region, and/or, an elevated clinical score based on presence of fever (>38.2°C), presence of mucopurulent nasal discharge and moderate to severe lymph node swellings of the head were classified as disease positive. Serial blood samples also obtained before, during and following the clinical outbreak were analysed for reactivity against antigens A and C of a *S equi* specific ELISA [(2)].

At the outbreak's peak, 14/112 animals were culture positive for *S. equi* and 53/112 positive on qPCR. All culture positives were qPCR positive. Fever was present in 11/53 qPCR positive foals, purulent nasal discharge in 5/53 and swollen submandibular lymph nodes in 6/53 foals (data not shown). Only 26/53 of qPCR positive foals showed any clinical signs suggestive for acute strangles. While 91/112 eventually seroconverted fully to antigen A, 39/91did so without developing any clinical signs suggestive of strangles. On the other hand, while only 7/112 developed antibodies against antigen C; most (5/7) displayed clinical signs of strangles.

0737-0806/$ – see front matter.