



## **FOCUS ARTICLE**

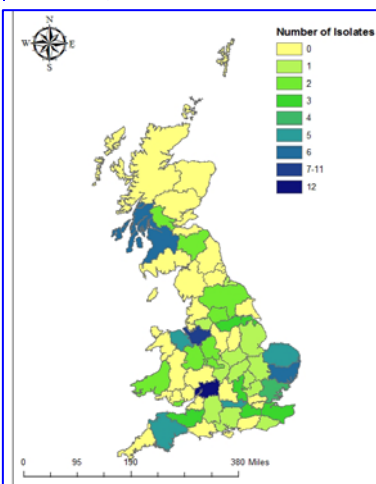
### **The molecular epidemiology of strangles in the United Kingdom**

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*Streptococcus equi* is the causative agent of strangles and is one of the most commonly diagnosed and important infectious disease of horses world-wide. The disease is characterised by pyrexia followed by profuse nasal discharge and abscessation of the lymph nodes of the head and neck. The majority of infected horses recover from strangles and eliminate *S. equi* over a 4–6 week period. However, up to 10% of recovered horses continue to shed *S. equi* intermittently for prolonged periods after clinical signs have resolved. It is increasingly recognised that sub-clinical carriage of *S. equi* is fundamental to the persistence of this infection between outbreaks.

Although strangles has a high welfare and economic cost to the equine industry, very little is so far known about the temporo-spatial and molecular epidemiology of the disease. Strangles is not notifiable in the UK and there are few published data on the geographical locations of strangles outbreaks in the UK and, although it is speculated that they may exist, it is not known whether geographical ‘hot spots’ of disease occur. Since the beginning of 2008 the Animal Health Trust (AHT) and Royal Veterinary College (RVC) have been collecting data to conduct some preliminary studies on the temporo-spatial and molecular epidemiology of strangles in the UK.

‘DNA fingerprinting’ techniques such as multilocus sequence typing (MLST) have been used widely in epidemiological surveillance of bacterial infections, such as those caused by *Staphylococcus aureus*, enabling quick and reliable differentiation of different bacterial strains. However, *S. equi* isolates collected from several continents and spanning a period of 27 years were all found by MLST to be sequence type (ST)-179 or a single locus variant ST-151, suggesting that this method does not have sufficient discriminatory power to study the molecular epidemiology of *S. equi* infection. Variability in a surface protein of *S. equi* called the M-protein (SeM) has recently been found, making the gene encoding SeM potentially suitable for single locus sequence typing (SLST), another molecular epidemiological tool. In human medicine, SLST of the M-protein of the Lancefield group A streptococcus *Streptococcus pyogenes*, has been used to study the epidemiology of this pathogen and in disease surveillance.



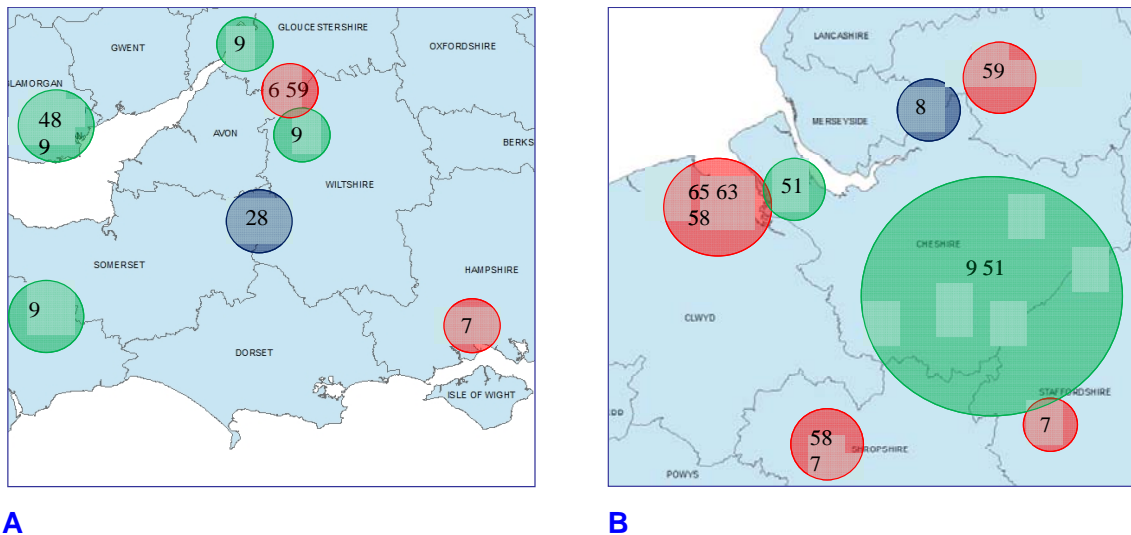
A pilot study conducted by the AHT and RVC applied SLST molecular SeM typing to 95 *S. equi* isolates submitted to the AHT’s diagnostic laboratory during 2008. This preliminary study has provided some provisional evidence for qualitative temporal and geographical clustering of related outbreaks that might be consistent with regional differences in occurrence of strangles in the UK, although obvious caution is required in interpretation of these pilot data from only a single testing laboratory.

**Figure 1:** County-level distribution of veterinary practices submitting 95 *S. equi* positive clinical isolates examined by the AHT diagnostic laboratory during 2008.



It is emphasised, however, that the way that these data have been collected (i.e. from only a single laboratory) means that they cannot be taken to indicate the likely relative frequency of strangles occurrence in individual counties but more likely reflects biases in the submission to the laboratory that collected the isolates.

The 95 SeM typed *S. equi* samples were collected from 92 horses on 78 premises and were submitted from 53 veterinary practices. The median age of affected horses was 9 years old and they were of a mixture of breeds and genders. The 95 *S. equi* isolates represented 18 different SeM alleles, with the most frequent being SeM-9 and SeM-7, which were distributed throughout the UK. Less frequently identified alleles were restricted to defined geographical areas. At a more local level it was possible to see apparent phylogenetic clustering and clear differentiation of outbreaks based on these clusters (Figure 2, which shows colour coding of SeM alleles that share greatest sequence identity).



**Figure 2:** Evidence for temporal and spatial clustering or exclusion of *S. equi* SeM types in A) south west and B) north west England in 2008

These data demonstrate the discriminatory capability of SeM typing as some outbreaks in relatively close geographical proximity were clearly associated with different alleles, precluding any likely epidemiological link between them. For example, a SeM-8 outbreak in Cheshire was unrelated to a SeM-59 isolate recovered by a vet in Greater Manchester or other SeM-9 and SeM-51 isolates recovered from Cheshire (Figure 2 B).

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