Research

EDITORIAL

MRSA transmission between horses and vets: who's doing the infecting?

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METICILLIN-resistant *Staphylococcus aureus* (MRSA) is a major health problem in people. About 30 per cent of the general population are nasal carriers of *Staphylococcus aureus*, and only a small proportion carry MRSA (Kluytmans and others 1997, Mainous and others 2006). However, in a hospital environment this proportion is generally much higher, although large differences exist between countries. Healthcare workers are regularly colonised (transiently or persistently) and are likely to play a role in the transmission within the hospital setting (Albrich and Harbarth 2008).

In horses, MRSA seems to behave in a similar way. Healthy horses carry MRSA at low prevalence, but in equine hospitals the prevalence is much higher (Van Balen and others 2014, Tirosh-Levy and others 2015) and nosocomial MRSA infections in horses leading to serious and sometimes fatal conditions have previously been described (Kuroda and others 2015). However, the high prevalence of MRSA in equine hospitals is not only a risk for the horses, but also for the personnel involved. Veterinarians are at an increased risk of carrying MRSA compared to the general population, but equine veterinarians are at an even higher risk than veterinarians working with other animal species (Jordan and others 2011, Cuny and others 2016). Transmission from hospitalised horses to their veterinarians therefore seems to occur, but as in the human healthcare situation where healthcare workers may infect patients, vets may also infect their equine patients.

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In recent years, MRSA in horses has been the subject of a substantial number of scientific studies. In a paper summarised on p 473 of this issue of Veterinary Record, Kuroda and others (2016) make an interesting contribution to this growing body of literature by describing the MRSA situation in two large thoroughbred racing horse training centres in Japan. The two training centres have their own equine hospitals and associated veterinary staff. Following up on a series of MRSA infections (mainly cases of keratitis) in nine horses treated in these hospitals, the authors looked into the source of these infections. They initially estimated the prevalence of MRSA carriage in two potential source populations (the horses and people in the training centre), and then used molecular typing tools to further characterise the MRSA strains. The data, particularly the molecular typing results, give important new information regarding MRSA transmission between animals and humans.

By screening a large sample of the racing horse population, the MRSA prevalence in healthy horses was estimated with great precision at 0 per cent (upper 95 per cent confidence limit 0.6 per cent). Then, all veterinarians and office staff were screened for nasal carriage. All the office staff turned out to be negative, but among the veterinarians the prevalence of MRSA was just over 30 per cent. Based on these data, the authors conclude that it is highly unlikely that healthy horses were the source of clinical cases. The question, however, is how to interpret the high prevalence among the vets? Are veterinarians the source of the equine infections? Or in line with other evidence about the occupational risk of MRSA carriage is their high colonisation rate the result of contact with MRSApositive horses? Perhaps the most plausible answer is both.



Strains of MRSA can be shared between horses, the enviroment and veterinarians

Kuroda and others (2016) did not sample any hospitalised horses other than the nine clinical cases. Also, no environmental samples were collected in the study, which in other studies have been shown to be instrumental for transmission within an equine hospital (Van Balen and others 2014). It is therefore possible that the MRSA circulates among hospitalised horses, the environment and veterinarians. As the horse strains and most human strains are indistinguishable by pulsed-field gel electrophoresis, exchange between horses and humans is plausible, but this alone does not give information about the direction of transmission. The strains were, however, also characterised by multilocus sequence typing (MLST) and SCCmec typing. This showed that all equine strains and most veterinarian strains belonged to ST5 and SCCmec type II (ST5/II). MRSA in horses in North America often belongs to ST8/ IV (Weese and others 2005, Lin and others 2011) and in Europe ST398/IV is a dominant equine clone (Abdelbary and others 2014, Loncaric and others 2014), but to the author's knowledge ST5/II MRSA has not been described in horses until now. In people, ST5/II is an epidemic clone, particularly prevalent in hospitals in Japan, sometimes referred to as the New York/Japan clone (Kawaguchiya and others 2013, Chen and Huang 2014, Nakaminami and others 2014, Khokhlova and others 2015). This clone causes a variety of diseases in humans, such as keratitis (Hayashi and others 2014), which has now also been described in equine cases by Kuroda and others (2016). The ST5/II clone was recently detected in dogs and their veterinarians in Japanese veterinary clinics (Ishihara and others 2014), and now Kuroda and others also identify it in horses. This seems to indicate that this human healthcare-associated MRSA clone not only transmits effectively within the human healthcare environment, but also in veterinary healthcare settings. Most likely, a human carrier of the clone first introduced it into equine hospitals. Following that initial human-to-horse transmission event, the

hospital may have acted as an amplifier of the pathogen, resulting in disease among the horses and substantial carriage in veterinarians. Still, it remains elusive how often transmission from humans to horses occurs. Is MRSA primarily circulating within the hospitalised horse population, and are the vets spillover hosts? Or do the colonised vets play a significant role in maintaining the transmission cycle within the hospital? More intensive screening in combination with the use of next generation sequencing of the isolates may help to answer these questions (Paterson and others 2015).

This is not the first time that a human healthcare-associated MRSA clone has entered equine clinics. In a review on the emergence of human-associated MRSA clones in equine clinics, Cuny and Witte (2016) stressed the importance of early identification of new potentially epidemic clones. Whole genome sequencing of the strains identified by Kuroda and others (2016) would allow for comparison with the strains circulating in the human healthcare setting at a much finer resolution (Harrison and others 2014). This may show whether multiple introductions have taken place, or if a single introduction led to circulation within the equine setting. Genome sequencing would also give clues about the potential adaptation of this clone to the equine host, which is relevant to assessing its zoonotic potential. The study by Kuroda and others (2016) is significant, because it identifies a human epidemic MRSA clone as the cause of disease in horses and carriage in their veterinarians. Further genomic research is needed in order to begin to understand the routes and drivers of transmission within and between the equine and human healthcare settings and specifically between horses and their veterinarians.

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