Risk Assessment on Meticillin-Resistant *Staphylococcus aureus* (MRSA), with a focus on Livestock-associated MRSA, in the UK Food Chain

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Meticillin-Resistant *Staphylococcus aureus* (MRSA)

Data collected ranges from November 1992 to December 2016.

1.0 Statement of Purpose

- To assess the risk to UK consumers associated with the preparation, handling and/or consumption of foodstuffs in the UK which may be contaminated with MRSA, in particular LA-MRSA.

2.0 Definition of Terms Used

1. For the purpose of this risk assessment, a case is inclusive of both carriers and infected individuals (human and animals). A carrier is a person who is asymptomatically colonised with MRSA; an infected individual includes those displaying signs of infection, ranging from superficial infections to invasive disease.

3.0 Executive Summary

2. The focus of this risk assessment is livestock-associated meticillin-resistant *Staphylococcus aureus* (LA-MRSA) as it originates in livestock animals and can potentially be transmitted along the food chain. Other lineages are also covered as there is the potential for these to contaminate foodstuffs *via* other transmission routes, such as by food handlers.

3. In assessing the risk to UK consumers, surveillance data has been collated on carriage and infection of LA-MRSA and/or other MRSA variants in humans and animals in the UK. Data on the presence of LA-MRSA in UK foodstuffs, such as raw meat and milk has also been collated. In addition, given the lack of available data for the UK to fully assess the risk, surveillance data from other European countries and countries outside of Europe has been included as appropriate, although a comprehensive review of all data for all countries was beyond the scope and remit of the current work. Accordingly, the range of countries has therefore been restricted to those with more data available, while ensuring that a wide geographical area has been covered (Europe, North America, Asia and Australia, 1992-2016). This risk assessment is based on the best available evidence; it is however recognised that there is a lack of data in this area, some of which is based on research carried out more than 10 years ago.

4. MRSA in the food chain may be a source for MRSA carriage in humans. Current data suggest that LA-MRSA infection is rare in humans in the UK and such organisms are not readily transmitted from person to person. To our knowledge there have been no reported foodborne outbreaks of LA-MRSA in humans in either the UK or worldwide.

5. Unlike other European countries where LA-MRSA has been isolated from animals since 2007, the first isolation of LA-MRSA from food-producing animals in the UK was from a poultry farm in November 2013 and following that the first isolation from a pig was in May 2014. Current data suggest that LA-MRSA CC398 is the predominant lineage in animals in the UK and other European countries, whereas LA-MRSA CC9 appears to be the predominant lineage in animals in Asia. The prevalence of LA-MRSA in animals in other European countries appears to be significantly higher than in animals in the UK.

6. Current data suggest that the prevalence of food contaminated with LA-MRSA is low in the UK. LA-MRSA has been shown to enter the food chain and survive on raw meat up to the point of retail, although thorough heat treatment of raw meat is sufficient to destroy LA-MRSA and other vegetative bacteria. LA-MRSA CC398 has distinct genotypic and phenotypic features that separate it from other MRSA variants. For example it generally lacks the genes encoding classical enterotoxins, so is unlikely to be associated with cases of staphylococcal food poisoning/intoxication. Based on current evidence, there are no reported cases of LA-MRSA being contracted through ingestion of contaminated foodstuffs, in the UK.

7. In conclusion the risk to human health from the preparation, handling and/or consumption of LA-MRSA/MRSA contaminated foodstuffs in the UK is very low, especially when compared to other routes of transmission. There are, however, uncertainties surrounding the prevalence of LA-MRSA in food and food animals. Although some of these uncertainties are reduced if data from the continent are extrapolated, there is clearly a need to revisit this risk assessment as new data become available.

8. FSA advice remains unchanged - i.e. that raw food should be stored appropriately, handled hygienically and cooked thoroughly. In combination, these measures should be sufficient to ensure that any harmful bacteria present are destroyed.

4.0 Hazard Identification

9. *Staphylococcus aureus* is a Gram-positive bacterium present on skin and in mucous membranes in 20-30% of healthy people, and is also carried by a wide range of animals and birds. It may cause minor infections in humans, typically local skin and wound infections but can occasionally cause more severe infections in the body. *S. aureus* is also found on food and can cause food poisoning via the production of enterotoxins in food, where there is a lack of appropriate temperature/time control. Some strains of *S. aureus* have developed resistance to beta-lactam antibiotics, including meticillin, used for the treatment of a range of infections. Such strains are called meticillin-resistant *S. aureus* (MRSA).[1] Within the general UK population, 30% carry meticillin-sensitive *S. aureus* (MSSA) in their noses, and <2% carry MRSA.[2]

10. Three distinct lineages of MRSA clones have been identified: from humans in hospitals (healthcare-associated MRSA [HA-MRSA]), from humans in the wider external community (community-associated MRSA [CA-MRSA]) and from livestock (livestock-

associated MRSA [LA-MRSA]) suggesting the adaptation of this species to diverse ecological niches. The main transmission route of HA-MRSA and CA-MRSA to humans is through direct contact with individuals colonised or infected with MRSA. Transmission of LA-MRSA to people may occur via direct contact with colonised or infected food-producing animals, companion animals (including horses), wild birds, watercourses and via contaminated dusts and aerosols.[3] In Europe, clonal complex (CC) 398 is the LA-MRSA lineage most often associated with asymptomatic carriage in intensively reared food-producing animals, particularly pigs, veal calves and chickens but has been found in horses and companion animals.[4] EFSA's Panel on Biological Hazards in 2009 reported that food may be contaminated by CC398, but this clonal complex has not been associated with foodborne intoxications. In areas where MRSA prevalence in food-producing animals is high, people in contact with live animals are at greater risk of acquiring CC398 than the general population, although infections are rare.[5] The risk to human health from different levels (dose response) of MRSA during carriage in animals (and in the environment) is not known.

5.0 Hazard Characterisation

11. The main route of transmission of *S. aureus* is through contact with humans or animals that are colonised/infected with *S. aureus*. Indirect transmission could also occur from the environment, as well as through ingestion and/or colonisation *vi*a the consumption and handling of contaminated food.

12. *Staphylococcus aureus* is able to survive and grow in food over quite a wide temperature and pH range of 7-48°C and 4.0-9.8 respectively. The optimum temperature for growth of *S. aureus* is 35-37°C and the optimum pH is 6.0-7.0. The range of temperature over which *S. aureus* is able to produce enterotoxin is narrower, ranging from 10-45°C and has an optimum at 35-40°C. Salt concentration is also particularly important for the survival of *S. aureus* in food as this organism is salt tolerant, surviving and growing readily in concentrations of 5-7% salt.[6] To our knowledge, there are no data available to suggest that MRSA displays any differences from MSSA in its growth and survival characteristics in food.[7]

13. The presence of *S. aureus* in ready-to-eat food is common as the organism is ubiquitous in the environment and a contamination level of $<10^4$ cfu/g is not usually considered to pose a risk to health. Staphylococcal food poisoning mainly occurs via the ingestion of preformed enterotoxins in contaminated food, where the food has a water activity of 0.88 or above and is stored at temperatures of 10°C or above. If levels of *S. aureus* in food exceed 10^5 cfu/g, there is a risk of sufficient enterotoxin to cause illness.[8] The infectious dose for staphylococcal enterotoxin is less than 1.0 mg in contaminated food.[9]

14. *S. aureus* food poisoning is a self-limiting disease, which usually lasts 24-48 hours and the main symptoms include vomiting and diarrhoea. Rarely, *S. aureus* food poisoning can develop into systemic disease, causing symptoms such as fever and hypotension. Strains of *S. aureus* resistant to meticillin appear to be no more virulent than those strains that are sensitive to this antimicrobial, and meticillin resistance is not linked to

the production of enterotoxins.[10] In addition, only some strains of *S. aureus* contain the enterotoxin genes required to produce the toxins, and LA-MRSA CC398 rarely possesses these toxin genes. This has been shown *via* molecular analysis of this clonal lineage, and many of the virulence-associated factors that are sometimes found in HA- and CA-MRSA strains are missing, including the genes encoding for enterotoxins and the immune-evasion cluster.[11,12,13]. As toxin genes may be present on mobile elements such as bacteriophage or plasmids, it is possible that strains of CC398 may acquire such genes.[14] In addition, food poisoning is not usually treated with antibiotics, as such treatment may favour the presence and/or persistence of a range of pathogens.

15. Foodborne transmission of *S. aureus* following the consumption of contaminated food and the development of invasive disease is considered rare. One example in the literature describes an outbreak of MRSA phage type III29 (MRSA non-CC398), which occurred in a hospital in the Netherlands between November 1992 and April 1993, probably caused by food contaminated by a healthcare worker. One patient, who was immunocompromised, developed severe sepsis and died. The development of invasive disease under such conditions therefore appears to be possible.[15,16]

16. Healthy individuals can be asymptomatically colonised with LA-MRSA and other MRSA variants. If the colonised individual then undergoes surgery, cuts their skin or becomes immunocompromised, infection with LA-MRSA/MRSA may occur. It has been reported that non-LA-MRSA is two to three times more frequently associated with bloodstream infections than LA-MRSA.[17]

17. Colonisation with LA-MRSA is primarily an occupational risk for those in contact with LA-MRSA colonised livestock. European studies[18,19] suggest that nasal colonisation of people with LA-MRSA is common after short-term exposure to colonised livestock, but this colonisation is generally short-lived and is lost within 24 hours of ceasing contact with affected livestock. Livestock workers in regular contact with infected stock may become colonised or regularly re-colonised for longer periods. Studies have concluded that LA-MRSA is a poor persistent coloniser of humans. The levels of *S. aureus* and/or MRSA required for human colonisation following exposure are not known. Colonisation may be influenced by a number of factors, in particular colonisation is likely to be host-specific and depend on the susceptibility of the individual. Factors related to the bacterial organism have also been described, which are considered to affect the ability of LA-MRSA to colonise man, for example the immune evasion cluster of genes.[20]

6.0 Exposure Assessment

6.1 Surveillance data on carriage and infection in humans in the UK

18. The first reported isolation of LA-MRSA CC398 from humans in the UK was in 2007. This involved three infants in Scotland with no epidemiological links to pigs.[21] In 2008, surveillance for LA-MRSA was enhanced, as Public Health England (PHE) invited submissions of MRSA isolates recovered from individuals involved in animal husbandry and those with an LA-MRSA-like phenotype (specifically, resistance to tetracyclines).

19. To date, 3 cases of LA-MRSA CC398 were identified in humans in England. All three cases had superficial skin infections, which responded to antibiotic treatment. None of the cases reported agricultural links and the mode of transmission remains unclear. These data suggest that LA-MRSA infection is rare in humans in England.[22]

20. There have been no reported foodborne outbreaks of LA-MRSA in humans in either the UK or worldwide.

6.2 Surveillance data on carriage and infection in humans in other European countries

21. A systematic literature review looked at the prevalence of MRSA carriage in people in contact with livestock between January 1990 and May 2014, and the factors influencing MRSA carriage. This review included 33 studies, of which 29 were cross-sectional studies (n=5,036 participants) and four were longitudinal studies (n=425 participants. Eight studies were from North America (n=600 participants), three were from Asia (n=567 participants), and 22 were from Europe (n=4,294 participants). These studies were conducted on farms, slaughterhouses, agricultural conferences, or markets. Twenty-two studies sampled farmers; eight sampled veterinarians, six sampled slaughterhouse workers and one sampled butchers. The results found that the prevalence of MRSA carriage in people in contact with livestock ranged from 0.0-85.8%, with a pooled prevalence of 14.2%. The prevalence of MRSA carriage was significantly higher in longitudinal studies (38.9%) than in cross-sectional studies (11.8%). Significant differences in prevalence were also found among farmers (18.2%), veterinarians (9.4%), slaughterhouse workers (2.6%) and butchers (5.7%). No significant differences were found among studies conducted in Asia (5.5%), North America (12.9%) and Europe (15.9%). The risk factors influencing MRSA carriage among people in contact with livestock included the type of livestock animals, type of protective measures, intensity of animal contact, gender, age and smoking. The greatest risk factor was working directly with livestock animals (especially pigs and cattle) followed by intensity of animal contact. In summary, this review suggests that the prevalence of MRSA in people in contact with livestock (14.2%) is much higher than that of the general population (0.8-1.3%). Moreover, animal contact and intensity of animal contact were associated with increased risk of MRSA carriage.[23] This study did not distinguish between LA-MRSA and all other MRSA lineages.

6.2.1 Denmark

22. The first human cases of LA-MRSA CC398 were reported in 2004, in Denmark. Since then, the numbers of cases have increased significantly with 643 cases identified in 2013 (compared to 42 in 2009, 111 in 2010, 164 in 2011 and 232 in 2012).[24] LA-MRSA CC398 comprised 31% of all new MRSA-positive cases in 2013, and is now considered the most commonly occurring clone. The increase in prevalence of LA-MRSA CC398 is suggested to be related to a change in the MRSA guidelines issued by the Danish Health and Medicines Authority in November 2012, which required active questioning and screening upon hospitalisation if a person themselves or a household member worked

on a pig farm. This is further supported by the finding that a large portion of the cases in 2013 were from healthy carriers.

23. The proportion of people infected with LA-MRSA CC398 at the time of diagnosis is also increasing. Table 1 shows these data alongside the total number of LA-MRSA CC398 cases (carriers and infections) during the period 2007-2013. It is important to note that although the total number of LA-MRSA CC398 cases and the number of infections are increasing each year, the actual percentage of infections varies year-on-year.[25,26]

Table 1. Total number of cases and infections of LA-MRSA CC398 in Denmark, 2007-2013

	2007	2008	2009	2010	2011	2012	2013
Total number of LA-MRSA CC398 cases	14	65	42	111	164	232	643
Number of Infections	6	16	16	38	63	92	156
Percentage of Infections	43	25	38	34	38	40	24

24. During the period 2007-2013, a total of seven people positive for LA-MRSA CC398 had bacteraemia compared with a total of 10,426 *S. aureus* bacteraemia cases (including MRSA and non-MRSA) in the same time period. In the first nine months of 2014, six cases of bacteraemia caused by LA-MRSA CC398 were identified. Table 2 shows a comparison of LA-MRSA CC398 against all other MRSA strains with regards to carriers, those with infection, bacteraemia and deaths, between 2007 - 3rd quarter 2014.[27]

Table 2. Comparison of the number of cases, infections, bacteraemia and deaths from LA-MRSA CC398 and all other MRSA strains, 2007-3rd quarter 2014

	Total MRSA cases of carriage & infection	Cases of infection	Cases of bacteraemia (%)	Number of deaths within 30 days* (%)
LA-MRSA CC398	2130	553	13 (2.4)	5 (38)
Other MRSA Types	8300	4657	167 (3.6)	39 (23)

*****within 30 days of diagnosis of bacteraemia

25. A recently published study investigated the epidemiology of all LA-MRSA CC9/CC398 cases in Denmark and used whole genome analysis to compare the Danish isolates with a European collection of CC9/CC398 isolates from humans, animals and retail foods.

26. The national MRSA database at Statens Serum Institut was reviewed for all MRSA isolates collected from 1 January 1999 to 31 December 2015. Those isolates with *spa* type t899 were investigated further to determine CC9/CC398 and 12 positive cases (10 urban cases, 2 mink farmers) were identified between 2009 and 2015. For comparative

purposes, 110 CC9/CC398 isolates were also obtained from different laboratories across Europe. These isolates were collected from humans, animals and retail foods during 2006-2012.

27. Whole genome phylogenetic analysis showed that the CC9/CC398 isolates from the 12 Danish cases formed a separate group within the livestock-associated CC398 subpopulation, together with the 110 CC9/CC398 isolates from other European countries. Isolates from the 10 urban cases were identified as belonging to a clade of 49 CC9/CC398 isolates, which harboured a ΦSa3 phage and isolates from 7 of the urban cases were found to belong to a distinct subclade within the ΦSa3 clade. This subclade contained isolates from humans (n=15), animals (n=5) and retail foods (n=17). Notably, it contained 95% (18/19) of all CC9/CC398 isolates from poultry and poultry meat, compared with only 7% (4/56) of the CC9/CC398 isolates from other animal species and retail foods. Three isolates belonging to this poultry-associated subclade were recovered from distinct chicken meat products sold in Denmark. EU labelling showed these three products originated from French production facilities, but there was no information on the origin of the animals before slaughter.

28. This study describes a novel hybrid LA-MRSA CC9/CC398 genotype, which has been observed among persons living in urban areas in Denmark. This genotype has never been detected in Danish livestock and epidemiological investigations showed that none of the 10 urban cases had direct livestock exposure. In contrast to Denmark, CC9/CC398 has been isolated from pigs, cattle, poultry and retail foods in other European countries, including France, Germany, Italy, the Netherlands and Spain. Seven of the 10 urban isolates were closely related to poultry and poultry meat isolates from these countries.

29. In summary, it is unclear how these urban cases became colonised or infected with CC9/CC398, however transmission is likely to be either foodborne or human-to-human. The presence of CC9/CC398 in poultry meat sold in Denmark suggests that cases may have been exposed through consumption or handling of contaminated meat products. Alternatively, CC9/CC398 may have arrived in Denmark through chains of person-to-person transmission where the first link in each chain was a colonised or infected livestock worker. However, the ability to sustain this chain of transmission is considered to be rare and thus it is believed that the most likely source is contaminated poultry meat.[28]

6.2.2 Germany

30. A study carried out in Germany between September 2007 and January 2009 determined the prevalence of human LA-MRSA CC398 colonisation on farms with LA-MRSA CC398 positive pigs. The results showed that up to 86% of humans with regular occupational exposure to pigs are nasal carriers of LA-MRSA CC398, and that antibiotic treatment prior to sampling had no impact on colonisation. Further transmission to humans living on farms with MRSA positive animals but without direct animal contact was found to be uncommon, approximately 4-5%.[29,30]

31. It has been suggested that LA-MRSA can be transferred to the external environment in the exhaust air from animal houses on conventional farms, and can be subsequently detected in soil up to 300m distance downwind.[31,32] A study in Northern Germany found low frequency of colonisation of LA-MRSA in humans residing in close vicinity to conventional farms.[33]

32. In North-western Germany a point prevalence study reported a low incidence of nasal carriage of LA-MRSA CC398 among pupils attending a school in a high density pig farming area. A total of 405 individuals were screened of whom only three (0.7%) were positive for LA-MRSA, and all three had family members with direct farm animal contact. In conclusion, given that humans with no occupational exposure in the community were not found to be colonised with LA-MRSA CC398, it would seem that LA-MRSA is not readily transmitted from human-to-human.

33. Other studies in Germany, suggest that regions with a high density of livestock production holdings provide a greater opportunity for the introduction of LA-MRSA CC398 into hospital settings. In such areas, LA-MRSA CC398 clones represented between 17 and 30% of MRSA isolates detected at hospital admission, compared to the overall German pattern of 0.08 to 0.2% of LA-MRSA detected at hospital admission. In addition, between 2008-2010 LA-MRSA CC398 represented approximately 2% of all MRSA associated with nosocomial infections.[34,35,36]

6.2.3 Italy

34. An Italian study during 2010-2011 aimed to investigate the prevalence of LA-MRSA human colonisation and the occurrence of infections in an area of the Lombardy region. This area has the highest density of pig farming, with 48.2% of all pigs reared in Italy.

35. In terms of colonisation, nine (1%) of 879 nasal swabs taken from people following admission to a local hospital between March-April 2010, were MRSA positive, of which more than half (56%, n=5) were LA-MRSA CC398. The overall LA-MRSA colonisation rate was 0.56%. The remaining four MRSA isolates were characterised as CC8 (3 isolates) and CC5 (1 isolate). None of the MRSA strains contained genes for Panton-Valentine Leukocidin (PVL) and all LA-MRSA CC398 strains were resistant to tetracyclines.

36. In terms of cases of infection, only one (5%) of 20 CA-MRSA isolates collected in the same hospital between March 2010 and February 2011 was characterised as LA-MRSA. This was from an otitis externa infection.

37. In summary, although LA-MRSA CC398 was the most prevalent MRSA lineage in terms of colonisation among individuals entering the hospital, CA-MRSA was the predominant MRSA in terms of MRSA associated infections within the hospital. The percentage of LA-MRSA out of all MRSA colonising strains (56%) was similar to that found in patients admitted to hospital in Germany in a region with high density of animal farming.[37]

6.2.4 The Netherlands

38. The first outbreak of MRSA with a potential link to the consumption of food occurred in a Dutch hospital between November 1992 and April 1993. A total of 27 patients and 14 healthcare workers were found to be colonised with MRSA, of which 21 patients (77.8%) developed clinical disease (one case of septicaemia and 20 wound infections) and five died.

39. The first patient involved in the outbreak, who died from MRSA septicaemia, was identified in a private room in the haematology unit. Surveillance samples from all other patients and healthcare workers on this unit were negative, and no environmental source was identified. Ten days after this patient was identified, 26 additional patients and 13 healthcare workers colonised with MRSA were identified in the surgical unit, located some distance from the haematology unit. Of the 26 patients colonised, 20 (77%) went on to develop a clinical infection with MRSA. The outbreak in the surgical unit was thought to be transmitted by a healthcare worker, who was subsequently found to carry the outbreak strain, and had been transferred from the haematology unit shortly after the first patient was identified.

40. Twenty-two weeks after the outbreak began, routine bacterial cultures of food prepared for patients on the haematology unit identified MRSA on a piece of banana. Investigation into the source of the contamination detected MRSA in the throat of a dietary worker who had been working in the haematology unit when the first patient (index case) was detected. No direct contact with patients occurred. Isolates from the banana and the dietary worker were indistinguishable from the outbreak strain, suggesting that the most likely source of this outbreak was the dietary worker preparing patient's food on the haematology unit, and that food contaminated by the dietary worker probably caused the first case of MRSA septicaemia. It is thought that airborne transmission of MRSA played an important role in disseminating the organism as swabs of the surgical unit found extensive environmental contamination. Although ingestion of MRSA does not normally lead to subsequent infection, in the case of this index patient it was assumed that the patient became infected because they were severely immunocompromised and taking antacids which neutralised the gastric acid, which would normally provide some protection against colonisation by this organism. Characterisation of the outbreak strain identified it to be MRSA phage type III29; there is no indication that the outbreak strain was LA-MRSA.[38]

41. The first outbreak of LA-MRSA CC398 in the Netherlands occurred in a hospital in June 2007. In total, ten cases of infection and/or colonisation were identified among patients (n=5) and healthcare workers (n=5). All strains displayed resistance to tetracyclines and were classified as CC398. None of the patients had contact with pigs or veal calves; one of the healthcare workers lived on a pig farm but neither she nor her partner came into contact with pigs. This healthcare worker was presumed to be the source of the outbreak, but this was never proven.[39] There was no indication that food was the source of this outbreak.

42. A study carried out between March and July 2008 in the Netherlands, looked at the prevalence of MRSA among employees who work in the cold meat processing industry and in institutional kitchens. The aim was to assess the risk of colonisation with both MRSA and MSSA of professionals who work intensively with raw meat products. The study collected hand and nasal swabs from 95 professionals working with raw meat on a daily basis, but were not in contact with live farm animals. Swabs were analysed for MRSA and MSSA. In addition, samples of meat handled by those participants were taken for analysis (See Paragraph 131 under section '6.12 Exposure to contaminated food in other European countries'). The study found that 31/95 (32.6%) participants were colonised with MSSA, but all nasal and hand swabs were negative for MRSA, suggesting that the prevalence of MRSA colonisation among this group of professional meat handlers was less than 3%. This study showed that high-frequency exposure does not necessarily result in a measurable risk of colonisation with MRSA. These findings also imply that the risk of colonisation of the general Dutch population by contact with raw meat should be even lower.[40]

43. A study in the Netherlands during June-December 2008 investigated the persistence of LA-MRSA CC398 carriage and the role of intensity of contact with livestock. A total of 155 people living or working on veal farms were selected and followed for approximately 2 months during periods of both high (veal calves present on farm) and low (veal calves absent in-between production cycles) or no (participants on holiday) exposure.

44. Nasal and throat swabs were taken in the morning (before animal contact) and evening (after animal contact) each day. In total, 2,864 nasal and 2,865 throat swabs were taken throughout the study period. The mean MRSA prevalence was reported as 38% in farmers and 16% in family members. MRSA prevalence was strongly reduced (-24%) during low exposure periods and even more strongly reduced (-58%) during no exposure periods. MRSA carriage was more common in nasal than throat samples. As MRSA carriage was strongly associated with the duration of animal contact, large fluctuations were observed in carrier status over time. Persistent carriers (who were positive throughout the study period) were identified for 11 participants (7%), of which 9 were farmers. All persistent carriers, except for one, were either nasal or nasal and throat carriers. The majority of participants i.e. 93 out of 155 (58%) were deemed intermittent carriers (those positive for a duration of 1-10 days), and 54 (35%) were non-carriers, that is consistently negative for MRSA.

45. In conclusion, persistence of human LA-MRSA colonisation seems to depend upon the frequency and intensity of animal contacts and duration of exposure. Results indicate that carriage of MRSA in a highly-exposed population is mainly transient, and that LA-MRSA is a poor persistent coloniser of humans.[41,42]

46. A study in The Netherlands between January 2009 and December 2010 aimed to identify the proportion of LA-MRSA CC398 in individuals with no known contact with pigs/veal calves or other known risk factors. In total, 1,020 patients were found to be MRSA-positive from 17 participating hospitals, of which 649 (63.6%) were identified as LA-MRSA CC398. In addition, 271 (26.6%) of all newly identified carriers of MRSA were

reported as not having been in contact with animals and 56 (20.7%) of these new carriers had LA-MRSA CC398. All 56 LA-MRSA CC398 isolates were resistant to tetracycline. Thirty-five of these 56 (62.5%) individuals had LA-MRSA CC398 infection. In hospitals in high pig-density areas, the proportion of LA-MRSA CC398 of all MRSA of unknown origin (MOU) was higher than the proportion in low pig-density areas. This indicates that LA-MRSA may be spreading through other sources than direct exposure to livestock. In conclusion, one fifth of the individuals carrying MOU carried LA-MRSA CC398, and therefore LA-MRSA CC398 was found in individuals without contact to pigs or veal calves. The mode of transmission from the animal reservoir to these individuals is unclear, but it is likely to be person-to-person transmission or by exposure to the environment.[43]

47. Increasing numbers of cases of CA-MRSA of unknown aetiology within the Netherlands prompted a hospital-based case-control study, involving 16 hospitals between July 2009 and July 2011, which aimed to identify additional risk factors for MRSA carriage in patients not belonging to established risk groups. The study targeted patients with a MRSA-positive culture from any site, who had no previous history of MRSA colonisation or infection, were not known to have acquired their MRSA through nosocomial transmission, and had no known healthcare- or livestock-associated risk factors. In total, 96 patients and controls participated in the study. Data on risk factors was collected via a standardised questionnaire.

48. Univariate analysis identified that the consumption of poultry at least once a week, was more common among the cases than the controls (OR 2.33; 95% CI 1.09-5.00). No statistically significant differences were observed in relation to the consumption of pork (OR 1.56; 95% CI 0.87-2.82) or beef (OR 0.65; 95% CI 0.30-0.94). Cases had shared scuba diving equipment more often than controls (OR 2.26; 95% CI 1.00-5.14). No statistically significant differences between cases and controls were found for the remaining examined potential risk factors, i.e. country of origin, day care centre attendance, professional contact with children, practicing contact sports, visiting a sauna, foreign travel and livestock density.

49. Multivariate analysis identified consumption of poultry at least once a week (OR 2.40; 95% CI 1.08-5.33), cattle density per municipality (OR 1.30; 95% CI 1.00-1.70), and sharing of scuba diving equipment (OR 2.93; 95% CI 1.19-7.21) as independently associated with CA-MRSA carriage. Of the 96 MRSA-positive cases, 29 (30%) were characterised as CC398. Multivariate analyses were performed separately for MRSA CC398 cases (n=29) and non-CC398 cases (67). Cattle density per municipality was found to be independently associated with MRSA CC398 carriage, but not with MRSA non-CC398 carriage. Sharing of scuba diving equipment was independently associated with MRSA non-CC398 carriage, but not with MRSA CC398 carriage. The association between consumption of poultry and CA-MRSA carriage was comparable for MRSA CC398 and non-CC398 carriage, but was not statistically significant. This is the first study to identify an association between the consumption of poultry and MRSA carriage in humans, which suggests that MRSA in the food chain may be a source for MRSA carriage in humans. The risk for MRSA CC398 carriage in areas with a high cattle density may be

due to environmental contamination with MRSA CC398 or human-to-human transmission.[44]

6.2.5 Spain

50. A study in Spain looked at 98 strains of tetracycline-resistant MRSA, isolated during 2011-2012 from patients in a Spanish hospital. The aim was to determine the *spa*-types and clonal complexes of these strains, as well as any correlation with livestock contact, as tetracycline resistance is thought to be a putative marker for potential LA-MRSA CC398. Of the 98 strains analysed, 60.2% were identified as LA-MRSA CC398 and out of those patients who had contact with livestock (n=25), 17 (76%) were infected with the CC398 strain. Of the patients who reported no contact with livestock (n=42), 21 (50%) were infected with CC398 and of those providing no information about livestock contact (n=31), 61.3% were infected with the CC398 strain. All of the LA-MRSA CC398 strains were found to lack the genes of the immune-evasion-cluster. In conclusion, a significantly higher proportion of the clinical CC398 strains were associated with livestock-contact.[45]

6.3 Surveillance data on carriage and infection in humans outside of Europe

6.3.1 Hong Kong

51. A study in Hong Kong between June 2011 and June 2012 aimed to determine if food handlers employed in large scale catering establishments who were regularly in contact with raw meats, exhibit an increased risk for carriage of *S. aureus* and whether or not LA-MRSA is more common in these food handlers. In total, 434 food handlers (288 male (66%), 146 female (34%)) from six catering establishments participated in the study. Overall, 99 (22.8%) were nasally colonised with *S. aureus*, of whom 74 were meat handlers. The types of raw meat handled were predominantly pork, beef and chicken. Colonisation rates were considerably higher in workers handling raw meats (30%) than in non-exposed workers (13.4%). In addition there was a positive trend of increased colonisation among workers who never, sometimes (one to two days per week) or always handled raw meat. When compared to food handlers who were never exposed, those sometimes handling raw meat had a two-fold higher colonisation risk, which increased to almost four-fold for regular handlers. Five of the *S. aureus* isolates were characterised as MRSA and all of these MRSA were isolated from raw meat handlers. None of the MRSA strains were LA-MRSA or carried enterotoxin genes. In conclusion, this study showed that contact with raw meat is a significant risk factor for nasal colonisation of *S. aureus*. In spite of this, the nasal colonisation rate of *S. aureus* in the food handlers (22.8%) was similar to that of the general public (24%) in Hong Kong.[46]

6.3.2 New Zealand

52. Between August 2011 and May 2013, nine patients from the South Island of New Zealand were found to be positive for LA-MRSA CC398, of whom three were reported to reside on a pig farm or had recently handled swine carcasses. The mode of transmission

for the other six cases remains unclear. All isolates exhibited resistance to tetracyclines and none contained the genes encoding for enterotoxins. Prior to this study, there had been no reports of LA-MRSA CC398 from New Zealand and these cases represent the first known human isolations of LA-MRSA CC398.[47]

6.3.3 USA

53. In the USA, the first foodborne outbreak of CA-MRSA occurred in 2001. It involved three adult family members consuming barbequed shredded pork and coleslaw purchased from a market delicatessen. The pork was reheated in a microwave at the family's home 30 minutes after purchase. Approximately 3-4 hours after the meal, all three adults became ill with symptoms of nausea, vomiting and stomach cramps. Two children who were at the dinner who did not eat the pork or the coleslaw did not become ill. Stool samples from the three adults were taken, and environmental investigations were carried out at the market whereby three samples of the pork, one sample of the coleslaw as well as five nasal swabs from three food handlers were taken. The results revealed the presence of *S. aureus* in all twelve samples. Five (41.7%) of the samples, including those from the three family members, the coleslaw and a nasal swab from one of the food handlers were characterised as indistinguishable CA-MRSA strains. The positive food handler was found to perform various tasks at the market, including preparing foods and handling barbequed pork and coleslaw. An inspection at the market revealed no apparent lapses in hygiene practices. In conclusion, it appears that MRSA-contaminated food was the vehicle in this outbreak, affecting low-risk persons within the community and that this food was likely to have been contaminated by an asymptomatic carrier.[48]

54. Between May and November 2010, a study in Iowa in the USA aimed to assess the rate of MRSA acquisition and longevity of carriage in un-colonised students exposed to pig farms during a two week clinical swine medical course. A total of 30 students participated in the study and were sampled: 1) at the beginning of the course, before any visits to pig farms, 2) before entry into a pig farm, 3) immediately after leaving a pig farm, 4) on weekends or non-visit weekdays during the course, and 5) daily for four consecutive days after the end of the course. Nasal samples were also collected from pigs as part of routine diagnostic investigations, and 3-5 swabs of these were submitted for MRSA testing. Environmental samples were also collected from the same farms visited by the students during the time of the visit. A total of 40 farms were visited during the study period and no farm was visited more than once. A total of 362 samples were collected from the farms, including 194 from pigs and 168 from the farm environment.

55. This study reported that 30% (12/40) of the farms visited were MRSA-positive from the pigs or their environment. Overall, MRSA was detected in 63/362 (17.4%) of the samples, which includes 17.5% (34/194) of the pig samples and 17.3% (29/168) of the environmental samples. Student nasal swabs taken at the beginning of the study period were negative for MRSA. Throughout the rest of the study a total of 604 student samples were collected, of which 8 (1.3%) were positive for MRSA. Twenty one (70%, 21/30) students visited MRSA-positive pig farms at least once and six students visited

these farms on two separate occasions. Therefore, there were 27 student exposure events and MRSA was detected six times in separate students (22.2%, 6/27). MRSA was detected in five out of these six students from the first nasal sample following the visit to a MRSA-positive farm. In one student, MRSA was not detected until five days after a visit to a MRSA-positive farm. MRSA was not detected in any student for more than 24 hours. MRSA was not detected in any student following visits to pig farms which were negative for MRSA. Further characterisation of the MRSA isolates identified all the pig and environmental isolates as CC5 and, all but two of the student isolates were also CC5. In conclusion, this study found that following short-term exposure (3-4 hours) to MRSA-positive pig farms, MRSA was detected in students approximately 22% of the time. However, MRSA was not observed to persist in any student for more than 24 hours, suggesting that MRSA from the pig farms did not become established in the students.[49] The findings of this study are consistent with the findings from other LA-MRSA studies, which have shown that short-term exposure to production farm animals does not lead to colonisation, or that carriage rapidly decreases when exposure is removed.[50,51]

56. In the USA, there have been no reported outbreaks of human LA-MRSA CC398 infections, as well as no single reported cases of clinical infection.[52]

6.4 Key points from human surveillance data

- Current data suggest that LA-MRSA infection is rare in humans in England.
- Evidence suggests that LA-MRSA is not readily transmitted from person-to-person.
- There have been no reported foodborne outbreaks of LA-MRSA in humans in either the UK or worldwide.
- The prevalence of MRSA in people in contact with livestock is higher than that of the general population.
- Persistence of LA-MRSA colonisation for people in contact with livestock seems to depend upon the frequency and intensity of animal contacts, and duration of exposure.
- Evidence suggests that carriage of MRSA in a highly-exposed population (i.e. people in contact with livestock) is mainly transient, and that LA-MRSA is a poor persistent coloniser of humans.
- MRSA in the food chain may be a source for MRSA carriage in humans.

6.5 Surveillance data on carriage and infection in animals in the UK

57. In 2008, a survey was undertaken to determine the prevalence of LA-MRSA positive pig herds in EU Member States. The prevalence in EU Member States ranged from 0-46% in

breeding herds and 0-51% in production (fattening herds). In total, 258 pig holdings were tested in the UK and none were found to be positive for LA-MRSA CC398.[53]

58. In 2009, LA-MRSA CC398 was isolated from two horses in South-Eastern England. One horse had never been outside of the UK and the second horse was imported from Spain via France. At the time, LA-MRSA CC398 had been reported from France, but not Spain. Analysis of the two equine strains found that the phenotypic and genotypic characteristics matched those reported from horses in Belgium, Austria and Germany. However, for the first horse an epidemiological link to countries where LA-MRSA CC398 is prevalent could not be established.[54]

59. Since the isolation of LA-MRSA in UK horses in 2009, the Animal and Plant Health Agency (APHA) reported the isolation of LA-MRSA CC398 from a poultry farm in East Anglia in November 2013.[55]

60. In May 2014, LA-MRSA CC398 was isolated from a post-weaning piglet in Northern Ireland. The piglet was one of a group of five piglets submitted to Agri-Food and Biosciences Institute (AFBI) with a history of pneumonia and wasting. This was the first reported isolation of LA-MRSA from a pig in the UK.[56]

61. In December 2014, two piglets with skin lesions from a breeder-finishing farm in Eastern England were submitted to the APHA and LA-MRSA CC398 was isolated. In total, 11 litters were affected and, of 60 piglets with the condition, six died.[57]

62. In February 2015, three pigs from a farm in Northern Ireland were submitted for post-mortem investigation due to signs of ill-thrift (low growth rate). Microbiological examination of various tissues identified the presence of *S. aureus* in nine different tissues from the three pigs, of which eight were confirmed as MRSA. All isolates were resistant to tetracycline, contained the enterotoxin gene cluster and encoded the lukM and lukF-P83 genes, a marker of virulence restricted to animal lineages. All isolates lacked the immune evasion cluster, a recognised marker of human adaptation. Further characterisation identified the isolates as CC30, and were confirmed as genetically distinct from CA-MRSA CC30. MSSA CC30 is known to be common among pigs, but MRSA CC30 has only been identified on rare occasions from pigs in Portugal (n=3), Denmark (n=4) and Germany (n=2). In these studies the strains of MRSA CC30 have different but related spa types and sequence types to the pigs in Northern Ireland. In conclusion, the results from this study suggest that the eight isolates of MRSA belong to a novel LA-MRSA CC30 clone. This is the first report of LA-MRSA CC30 being isolated from livestock in the UK, and also the first report of a lukM-positive LA-MRSA clone.[58]

63. In February/March 2015, milk samples taken from two mastitic cows from a dairy herd in Northern Ireland were found positive for LA-MRSA CC398.[59]

64. In March 2015, LA-MRSA CC398 was isolated from the lung of a pig in Northern Ireland submitted for post-mortem examination.[60]

65. In October 2015, two isolations of LA-MRSA CC398 in pigs were reported in the UK. One of the findings was isolated from a pooled caecal sample of healthy pigs at slaughter in England and Wales, collected as part of a research project. The second finding of LA-MRSA CC398 was isolated from the brain, lung and joint tissues of a pig submitted for post-mortem examination, from a farm in Northern Ireland.[61,62]

66. In February 2016, LA-MRSA was identified in a turkey from a fattening turkey farm in England during an investigation into upper respiratory tract (URT) disease. The strain was confirmed as CC398 and *spa*-type t899. The presence of the *mecA* gene was confirmed by PCR and the strain is phenotypically resistant to multiple antimicrobials, including tetracyclines. This isolate, as has been described for some other t899 strains, harbours the immune evasion cluster genes. While this is not a virulence factor per se, it may represent a development that would result in potentially increased human adaptation. The risk from such strains should therefore be reviewed on an ongoing basis. Isolation of the *S. aureus* isolate was considered to be incidental and not related to the clinical disease being investigated.[63]

67. In April 2016, LA-MRSA CC398 *spa*-type t011 was isolated from the foetal stomach contents and placenta of an aborted calf from a beef herd in England. The abortion occurred 4-5 months into gestation and was considered to be a spontaneous abortion.[64]

68. In recent years, there has been an increase in the number of LA-MRSA CC398 isolates from farm animals in the UK. This increase in the number of cases suggests the gradual emergence and change in epidemiology of LA-MRSA among UK livestock. One study therefore aimed to establish the phylogenetic relationship between LA-MRSA CC398 recovered in the UK and those circulating in other countries, and to identify similarities/differences in the carriage of antimicrobial resistance, heavy metal resistance, disinfectant resistance and virulence genes, to provide insight into the emergence, evolution and possible adaptation of LA-MRSA in livestock in the UK.

69. In this study, whole genome sequences (WGS) of UK LA-MRSA CC398 animal isolates collected between 2013 and 2015 were compared to isolates from European and non-European countries. The UK LA-MRSA isolates selected for WGS were identified from a panel of more than 1,000 *S. aureus* strains recovered from pig caeca collected from abattoir and from samples submitted for routine diagnostic testing during this period. In total 89 isolates were investigated (88 from various animal species & 1 reference strain), of which twelve were from UK livestock (horses, poultry and pigs) and 76 were from European and non-European livestock.

70. Profiling of the 89 CC398 isolates using WGS identified nine different *spa*-types (t011, t034, t108, t567, t571, t1451, t1793, t2370 and t4872). The most frequently observed *spa*-types were t034 and t011 (84%). All 89 isolates carried genes encoding tetracycline resistance and approximately 98% encoded resistance to Beta-lactams and 74% of isolates harboured genes encoding resistance to ≥3 antimicrobial classes. Nine percent of isolates harboured genes which have been associated with resistance to quaternary ammonium compounds and 64% carried genes conferring resistance to ≥1 heavy metals. None of the isolates carried any human-associated virulence genes. There was some

evidence of phylogeographic patterns with a majority of European isolates clustering together forming a separate lineage to the non-European isolates. The European lineage divided into two main sub-lineages, based on *spa*-type, EU t011 and t034. EU t011 included the majority of European *spa*-type t011 isolates present in the panel which were from a variety of animal host species, including turkeys, pigs, rats and horses. All seven UK *spa*-type t011 isolates from pig, turkey and horse were within this host generalist lineage. The second European lineage (EU t034) predominantly included *spa*-type t034 isolates from pigs; which was distinct from the non-European t034 isolates that included isolates from pigs but also from turkeys, which indicates radiation and adaptation of *spa*-type t034 in different host species. The five remaining UK LA-MRSA CC398 isolates clustered within the EU t034 lineage, and included several isolates from pigs and one from a cow.

71. The results from this study show most LA-MRSA isolates, including several from the UK, harboured multiple antimicrobial resistance (AMR) genes. All twelve UK isolates were found to belong to European lineages. The occurrence of UK MRSA isolates of both *spa*-type t011 and t034 in different sub-lineages indicates that there have been multiple independent incursions of LA-MRSA CC398 into the UK, rather than clonal expansion following a single introduction.[65]

72. Other possible routes by which LA-MRSA may enter the UK food chain include wild and migratory birds. However, there is insufficient data in this area to draw meaningful conclusions.

73. As far as we are aware, no enumeration data has been reported for LA-MRSA in live animals in the UK or worldwide.[66] Such data would help assess the risk of cross-contamination and acquisition of LA-MRSA by people in contact with live animals and food.

6.6 Surveillance data on carriage and infection in animals in other European countries

74. The primary reservoirs of LA-MRSA CC398 in affected countries are pigs, veal calves and broilers. LA-MRSA CC398 has also been found in companion animals and horses on farms with colonised livestock.[67]

75. In 2008, a European study conducted and funded by the European Food Safety Authority (EFSA) looked at the prevalence of LA-MRSA CC398 in pig holdings in 17 countries. Of these holdings, 1-50% were positive for LA-MRSA which was detected in the dust as an indicator for colonisation of the animals.[68,69]

6.6.1 Denmark

76. In 2007, the first case of LA MRSA CC398 in pigs in Denmark was identified. At that time, the prevalence of this strain in Denmark was considered to be relatively modest in comparison with the Netherlands, where 60-80% of herds were known to be LA-MRSA CC398 positive.

77. In 2010, sampling of Danish pig herds (n=99) for LA-MRSA CC398 indicated a prevalence of 16% (16/99) and a subsequent study in 2014 indicated an increase in prevalence to 63-70% (Table 3). The sampling protocol in both these studies involved sampling five pigs from each of five pens in each herd. Nasal swabs from five slaughter pigs from each sampled pen (n=5) were pooled and analysed for the presence of MRSA.[70,71] Additionally, in 2013 LA-MRSA CC398 was identified in two mink fed with offal from pigs and poultry waste.[72]

Table 3. LA-MRSA CC398 results for 2014 in 70 breeding herds and 205 finisher herds

	Number of Herds Studied	Prevalence (%)
Breeding Herds	**70**	**63**
Finishers – Jutland	147	70
Finishers – Funen	39	69
Finishers - Zealand	19	53
Finishers – Denmark (Total)	**205**	**68**

6.6.2 Finland

78. A study carried out from June to July 2015 aimed to determine the clonal complexes and *spa*-types, as well as the resistance phenotypes, virulence and resistance gene profiles of LA-MRSA isolated from Finnish fattening pigs at slaughter.

79. A total of 29 pig herds from 29 different farms from the most dense pig production area of Finland, Western Finland, were included in the study. Samples from the anterior nares of pigs at slaughter and from pig carcasses were obtained. For each herd, 20 nasal swabs from pigs and 10 swabs from carcasses were taken. Five swabs each were pooled, resulting in four pooled pig nasal swabs and two pooled carcass swabs per herd.

80. Fifty MRSA isolates were identified from nasal swabs of fattening pigs (n=49) and a pig carcass (n=1), originating from 18 different herds/farms. Further characterization assigned the 50 MRSA isolates to clonal complexes CC1 (n=4) and CC398 (n=46). One dominant *spa*-type, t2741, was identified in 33 out of 50 isolates, originating from 15 out of 18 farms. The remaining isolates were assigned to *spa*-types t034 (n=7), t108 (n=5) and t011 (n=1). Although each herd harbored only isolates assigned to one clonal complex, two or three different *spa*-types were identified in five of the herds. Most of the isolates lacked several important virulence genes, including enterotoxin genes. All isolates were resistant to tetracyclines.

81. In conclusion, LA-MRSA CC398 *spa*-type t2741 was the most dominant isolate identified during this study. To date, few individual isolates of this type have been reported in association with human hosts. This is the first study identifying t2741 as a common *spa*-type in LA-MRSA in pigs.[73]

6.6.3 Germany

82. A study carried out from June to October 2009 aimed to investigate the prevalence of LA-MRSA in fattening turkeys and the risk of colonisation for people working on the farms. A total of 500 swabs were taken in a random sample of 20/90 meat turkey farms located in three districts in Baden-Württemberg in the southwest of Germany. One tracheal and one cloacal swab from each of ten turkeys per flock (n=400) and five dust samples per turkey house (n=100) were collected one day to two weeks prior to slaughter. Dust samples were taken from different locations in the turkey houses, including the windowsills of the right and left side of the house, the surface of a feed trough, the surface of a food distribution system and the wall of the separation area for sick animals. Nasal swabs were taken from three persons per farm, except for one farm where only two could be included in the study (n=59). Two groups of people were tested; one consisted of those who had been in the turkey houses at least once a week (n=39, two persons per farm, one person missing) and the other group consisted of those who had been in the turkey houses never or less than once per week (n=20, one person per farm).

83. MRSA was detected in 18/20 (90%) turkey flocks investigated. Two flocks were MRSA-negative in all animal and environmental samples taken. In 16/18 (89%) positive flocks, MRSA could be found in all types of samples (tracheal, cloacal and dust). Of the total 200 turkeys examined 143 (71.5%) were MRSA-positive, and of these MRSA was isolated from 84 (58.7%) tracheal and cloacal swabs, 45 (31.5%) tracheal swabs only and 14 (9.8%) cloacal swabs only. MRSA was detected in 22/59 (37.3%) nasal swabs taken from people working on the turkey farms and none showed clinical symptoms indicative of MRSA infection. People in contact with turkeys daily or at least once per week were more likely to be a carrier of MRSA (18/39, 46.2%) than those with rare (less than once per week) or no contact (4/20, 20%). Further characterisation of the MRSA isolates identified that the most common *spa*-types were t011 (83.2% of turkeys, 90.2% of humans) followed by t002, t1456, t034 and t2330, of which the majority were attributed to CC398. To conclude, the prevalence of MRSA in this study was high with the predominant type being LA-MRSA CC398. People working on turkey farms, especially those with regular contact, have an increased risk of being colonised with MRSA compared to the general public and should therefore be considered risk patients with respect to introduction of LA-MRSA into healthcare facilities.[74]

84. A German study carried out between 2009 and 2012 aimed to estimate the prevalence of MRSA in different cattle food chains (milk, beef and veal) and to analyse the MRSA diversity along each food chain. Samples were collected from dairy herds (bulk tank milk), veal herds (dust from the stables), veal calves, beef cattle at slaughter (nasal swabs), carcasses of veal calves (surface cuts) and beef and veal meat at retail. Sampling was proportionally distributed over the country according to the cattle population (on-farm sampling), slaughterhouse capacity (abattoir samples) and the human population (meat at retail).

85. MRSA was detected in all types of samples taken, with the highest proportion of positive samples found in nasal swabs from veal calves at slaughter in 2012 (144/320, 45%). This

had increased from 35.1% in 2009 and was substantially higher when compared to nasal swabs from beef cattle at slaughter (25/288, 8.7%). The lowest rate of MRSA was found in bulk tank milk in 2009 (14/388, 4.1%) and this was similar in 2010 at 4.7%. MRSA-positive veal meat at retail was higher than beef meat with a prevalence of 19.4% (6/31) compared to 8.1% (41/509). A total of 632 isolates were confirmed as MRSA and 28 different *spa*-types were identified among these isolates. The most common *spa*-types were t011 (58.1%) and t034 (32%), which are attributed to LA-MRSA CC398. Diversity of MRSA tended to be minimal in bulk tank milk samples, with only three different *spa*-types identified. In contrast, eleven different *spa*-types were isolated from dust samples from veal farms, veal calves at slaughter and veal meat at retail. Overall, s*pa*-type patterns were similar along individual food chains but differed between food chains. Antimicrobial resistance patterns also differed between isolates from the different food chains and *spa*-types. Isolates from the veal food chain displayed the highest resistance rates. In summary, there is substantial diversity in MRSA prevalence across the different cattle production sectors, with the highest rate of prevalence in the veal food chain. The MRSA strains found in veal and beef meat at retail were very similar to those for primary production, indicating transmission along the food chain.[75]

86. In 2012, a study carried out in the north, east and southwest of Germany reported the prevalence of MRSA on poultry farms and the distribution of MRSA on positive farms inside and outside the barns. A longitudinal study conducted on five turkey and two broiler farms were investigated four and three times respectively, during one fattening period. Samples were taken from the animals, the animals' environment inside the barn, including the air and the barns' surroundings, such as ambient air and boot swabs of ground surfaces at different distances from the barn. A cross-sectional study was also carried out inside the barns on five turkey and four broiler farms during the last third of a fattening period. In the cross-sectional study, LA-MRSA was detected in the air of most barns (7/9, 77.8%), of which four were from turkey and three were from broiler barns. LA-MRSA was also detected in animal samples on eight of the nine farms (88.9%), with detection levels of 50-54% in broiler and 62-77% in turkey farms. In the longitudinal study, LA-MRSA was found in the ambient air from the downwind side of two turkey barns compared to no positive air samples from the upwind side of any barn. LA-MRSA was also detected on the ground surface on the downwind side of 44.4% (36/81) of turkey and broiler farms, compared to 26.9% (7/26) on the upwind side. Further characterisation of the MRSA isolates found ten different *spa*-types, the majority being *spa*-type t011 (31/80, 38.8%) and clonal complex CC398 (62/78, 79.5%). At five barns, the same *spa*-types were observed both inside and outside of the buildings. In conclusion, transmission of MRSA within poultry farms, as well as emission via the airborne route, seems to be possible.[76]

87. In 2013, a German study reported a high prevalence of LA-MRSA CC398 (39.4%, 84/213) on skin swabs taken from broilers at the slaughterhouse, and a lower prevalence of LA-MRSA CC398 (1.3%, 2/157 flocks) in environmental dust samples taken on farm (before slaughter) from the same animal population. The prevalence of LA-MRSA CC398 in the nares of cattle at the same slaughterhouse was low (8.2%).[77]

6.6.4 Ireland

88. A study in Ireland between July and October 2007, and February and April 2009 aimed to evaluate the prevalence of MRSA in the Irish pig population. In total, 440 pigs from 41 geographically distributed farms were swabbed nasally in three major abattoirs, located in Southern, Central and Eastern Ireland. In addition, 100 individuals who work in the pig industry were nasally screened. The results showed that none of the pigs were positive for MRSA and only two (2%) of the workers were identified as MRSA carriers. Importantly, MRSA was not obtained from pig producers, veterinarians or abattoir employees and the two positive individuals worked in the wider pig industry. Further characterisation of the two MRSA isolates identified them as CC22 and CC1307; the latter being a previously unreported single locus variant of CC5. Dust samples taken from the lairage pens and stunning area in each of the three abattoirs were also negative for MRSA. In conclusion, these results indicate that MRSA colonisation in pigs, and in particular LA-MRSA CC398, was not common in the Ireland during the period of study. A possible explanation for the low prevalence of LA-MRSA in Ireland may be that Ireland does not import a considerable number of pigs, which limits opportunities for the import and transmission of LA-MRSA CC398. Other explanations may include differences in pig husbandry practices and antimicrobial usage.[78]

6.6.5 Italy

89. A study undertaken between January and June 2008 aimed to estimate the herd prevalence of MRSA colonisation in finishing pig holdings in Italy. A total of 118 holdings from 29 provinces and 10 different regions (Northern Central and Southern Italy, accounting for >90% of the Italian pig population) participated in the survey. Sixty nasal swabs were taken from each holding and pooled cultures of 10 nasal swabs (6 pools from each holding) were examined. The results showed that 45/118 (38.1%) holdings had at least one MRSA-positive pool. A total of 98/701 (14%) positive pools were detected. Nearly 50% (22/45) of positive holdings had only one positive pool. Two, three and four positive pools were found in 18%, 13% and 11% of positive holdings respectively, while five and six positive pools were found in 4% of positive holdings. Further characterisation identified five different lineages; CC398, CC1, CC9, CC97 and CC1476. An estimated 7.6% (9/118) of the holdings were positive for 2, 3 or 4 lineages belonging to CC1, CC97, CC1476 and CC398 in different combinations. Four holdings (3.4%) were positive for both human- and animal-associated MRSA. An estimated 28% (33/118) of holdings were positive for LA-MRSA CC398 and an estimated 5.9% (7/118) were positive for human-associated MRSA (CC1). None of the isolates carried the Panton-Valentine Leukocidin (PVL) genes. Isolates were not screened for enterotoxin genes. This study is the first description of MRSA among the pig population in Italy; the first report of MRSA CC1, CC1476 and CC97 lineages among pigs, and the first report of MRSA CC9 in Europe.[79]

6.6.6 The Netherlands

90. In 2004, the first isolation of LA-MRSA CC398 was identified in a pig reservoir in the Netherlands.[80]

91. In 2007-2008, a study was undertaken in the Netherlands to determine the prevalence of LA-MRSA in pig herds. In total, 202 pig herds were analysed and 67% of breeding herds and 71% of finishing herds were found to be positive for LA-MRSA. During the study period, the number of herds positive for LA-MRSA increased from approximately 30% to approximately 75%. This increase was thought to have most likely been caused by transmission between herds.[81]

92. In 2013, a study of nasal swabs taken from fattening pigs at the slaughterhouse reported an extremely high prevalence of LA-MRSA CC398 positive herds (97.8%, 91/93). This study also reported 71.9% (69/96 herds) prevalence of LA-MRSA CC398 from nasal swabs from cattle at the slaughterhouse.[82]

6.6.7 Spain

93. Between September 2008 and March 2009, a study in Spain aimed to investigate the carriage rates of MRSA in pigs of two distinct age groups at slaughter. Individual nasal swabs were collected from 106 healthy pigs, which included 53 finishing pigs and 53 suckling pigs, in La Rioja (Northern Spain). Samples were collected on four different occasions (two each for finishing and suckling pigs) at two abattoirs, one for each age group. Tested animals came from six different farrow-finish holdings. The results showed that of 53 finishing pigs and 53 suckling pigs, 11 (21%) and 26 (49%) respectively were positive for MRSA. This corresponds to five of the six production holdings. Forty-four MRSA isolates (14 from finishing pigs, 30 from suckling pigs) were recovered and further characterised. Of the 14 MRSA isolates from finishing pigs, 10 (71.4%) were CC398 and 4 (28.6%) were CC97. In this regard, 7/11 (63.6%) MRSA-positive finishing pigs were colonised by LA-MRSA CC398. All 30 MRSA isolates from suckling pigs were CC398. All MRSA isolates were resistant to tetracyclines and all were negative for the PVL and enterotoxin genes. In conclusion, the study observed a high rate of MRSA among the production holdings and a high incidence of MRSA carriage within pigs at slaughter. LA-MRSA CC398 was the most prevalent lineage detected.[83]

6.7 Surveillance data on carriage and infection in animals outside of Europe

6.7.1 Australia

94. Between January 2009 and October 2010, a study in Australia aimed to determine the prevalence of MRSA in food producing animals. In total, 324 nasal swabs were collected from pigs from five commercial herds (one in Queensland, one in Victoria, three in New South Wales) and one feral herd (Western Australia). The results revealed that 3/324 (0.9%) nasal swabs were positive for MRSA and originated from one herd in New South Wales. All isolates were characterised as LA-MRSA CC398 and were resistant to tetracyclines. This study confirms that LA-MRSA CC398 is established within pigs in Australia. Although it is possible that LA-MRSA CC398 may have independently evolved in Australia, the findings from this study suggest that isolates have a common ancestry with European isolates. However, it is unlikely that imported pigs or poultry were the

source of LA-MRSA CC398 in the Australian pig herd, as live importation into Australia is banned. It is more likely that human carriers are the source as millions of international visitors and returning residents enter Australia each year. The movement of horses into Australia is also a potential risk and the importation of ruminants cannot be excluded as a source. Until this study, MRSA had not been reported in food producing animals in Australia and this study is the first detection of LA-MRSA CC398 in Australian pigs.[84]

6.7.2 China

95. From September 2008 to August 2011, a study in China aimed to investigate the prevalence of MRSA and MSSA among various animals. Nasal or tracheal swabs were obtained from animals in a central slaughterhouse (cattle and pigs), wet markets (chickens) and urban areas (stray dogs, stray cats and wild rodents). In total, samples from 3,081 animals, including 609 cats, 660 chickens, 589 dogs, 310 cattle, 305 pigs and 608 rodents, were examined. Overall, 24.9% of pigs, 4.7% of chickens, 6.3% of dogs, 10.5% of cats and 7.1% of rodents were positive for *S. aureus*. A total of 254 *S. aureus* isolates, including 188 MSSA and 66 MRSA (65 pig, 1 chicken), were recovered from 252 animals. All but one of the isolates from chickens and pigs were resistant to three or more non-beta lactam drugs. In contrast, most of the isolates from dogs, cats and rodents were fully susceptible. Further characterisation identified all MRSA isolates as LA-MRSA CC9. This study demonstrates that CC9 is the major LA-MRSA strain in pigs in China. No infections caused by LA-MRSA CC9 in animals and humans in China were identified in the literature. Although all *S. aureus* isolates from rodents were identified as MSSA, the predominant strain was CC398. This suggests that urban rodents could be an important reservoir of CC398.[85]

6.7.3 Korea

96. Between February 2008 and May 2009, a nationwide study in Korea aimed to determine the presence of MRSA in pigs by examining slaughtered pigs originating from pig farms throughout the country. In total, 657 nasal swabs of pigs originating from 66 different randomly chosen pig farms were collected from eight slaughter houses. About ten swabs were collected from each of the 66 farms, which were located in nine provinces in Korea. The results identified 21/657 (3.2%) MRSA-positive swabs, and the percentage of MRSA-positive pig farms was 22.7% (15/66) during the study period. The prevalence of MRSA among the nine provinces in Korea varied from 0-7.8% in pigs, and 0-50% in farms. No MRSA was detected in 4 of 9 provinces. Further characterisation of the 21 MRSA isolates identified three different lineages; CC398 (n=12), CC541 (n=5) and CC72 (n=4). Both CC398 and CC541 (a single locus variant of CC398) are livestock-associated strains while CC72 is human-associated. None of the isolates carried the genes encoding for PVL toxin or enterotoxins. In conclusion, the prevalence (3.2%) of MRSA in pigs was higher than those reported from other Asian countries such as Malaysia (1.38%) and Japan (0.9%), but not China (11.4%). However, prevalence is markedly lower than in European countries and North America, e.g. 49% in Germany, 39% in the Netherlands, 21% in Spain, 36% in the USA and 26% in Canada. This study suggests that MRSA prevalence among pigs may not be a major issue in Korea, and is the first report of LA-MRSA CC398 in commercial pigs in Asian countries.[86]

6.7.4 Taiwan

97. Between June and October 2012, a study in Taiwan aimed to investigate the prevalence of nasal colonisation of MRSA among pigs and related workers. Twenty two pig farms from six counties with different cultivation scales ranging from 1,000-30,000 pigs, and two pig auction markets in two different counties, were selected for this study. In total, 641 and 100 nasal swabs were collected from live pigs (536 from pig farms, 105 from auction markets) and workers (52 pig farm workers, 32 auction market employees and 16 regular visitors e.g. suppliers) respectively. MRSA positive isolates were identified from 89/641 (14.4%) pigs, which includes two (1.9%) from one of the auction markets. The percentage of MRSA positive pig farms was 59.1% (13/22). The carriage rate for pigs in large-scale herds (≥10,000 pigs) was significantly higher than that in small-scale herds (34.3% versus 7%) and that in auction markets (1.9%). Among the workers, 13/100 (13%) nasal swabs were positive for MRSA. The carriage rate for the pig farm workers was 19.2% (10/52), 0% (0/32) for the auction market employees and 18.8% (3/16) for regular visitors. The carriage rate for workers in large-scale farms was also significantly higher than that in small-scale farms (36.8% versus 9.1%). Further characterisation of the MRSA isolates identified all but three (from humans) to be LA-MRSA CC9. In conclusion, the prevalence of MRSA among pigs in Taiwan was 14.4%, which was lower than that for Western countries but higher for Asian countries such as China (11.4%), Korea (3.2%), Malaysia (1.4%) and Japan (0.9%), with the exception of Hong Kong (16-21.3%). All MRSA isolates from pigs in this study were LA-MRS CC9. In Asia, LA-MRSA CC9 has also been reported predominantly in swine-associated environments in countries such as China, Hong Kong, Japan, Thailand and Malaysia. Despite this prevalence of LA-MRSA CC9 among pigs in Asia, infections caused by this clone in animals and humans have not been reported in the literature.[87]

6.7.5 USA

98. A study in the USA in 2008 aimed to investigate the carriage of MRSA among pigs and pig farmers. Two production systems in Iowa and Illinois, comprising approximately 87,000 animals were included in the study and in total nasal swabs were taken from 299 pigs and 20 workers. Production system A (PSA) is a conventional commercial confinement operation consisting of a 5,200 head breed-to-wean sow farm with multiple age-segregated nurseries, finishing, and wean-to-finish sites scattered throughout northern Illinois and eastern Iowa. Collectively, approximately 60,000 swine are present at any one time. Production system B (PSB) is also a relatively young sow herd comprising approximately 2,600 sows at the single sow farm location and 27,000 total animals housed at multiple, age-segregated nursery, finisher and wean-to-finish sites throughout eastern Iowa.

99. The results showed that the overall prevalence of MRSA in pigs was 49% (147/299) and in workers was 45% (9/20). The prevalence of MRSA carriage among production system A's pigs varied by age, ranging from 36% (11/30) in adult pigs to 100% (60/60) in pigs aged 9 and 12 weeks. The prevalence among workers from production system A was 64% (9/14). LA-MRSA CC398 was the only lineage isolated from this farm. MRSA was

not isolated from pigs or workers in production system B. Suggested reasons for the differing results between production system A and B include different breeds of pigs, production system A was older and more established with roughly twice the number of pigs. Also, a portion of the pigs at production system A were imported from Canada compared to production system B, whose pigs originated in Michigan.[88]

100. In the USA in 2010, a study was carried out to determine the prevalence of MRSA, particularly LA-MRSA in pigs on farm, at lairage, on carcasses and in retail pork. A serial cross-sectional sampling design was used on market-age pigs on 10 farms in Ohio. Both nasal and perianal swabs were taken from selected pigs (24 pigs from different pens on each farm) from a total of 10 farms (n=480). Carcass swabs (24 per farm) were then collected from the same batch of slaughtered pigs at the post-evisceration stage and before chilling (n=235; 5 were missed for various reasons). After processing, a total of 135 retail pork samples (n=12-15 per batch) from the same batch of pigs were collected from retail stores within 24 hours of processing on the day of product arrival.

101. The study found that out of ten farms three (30%) had one or more pigs positive for MRSA on the farm, and pigs from five (50%) of the farms tested positive for MRSA at lairage. Of all the pigs examined on farm, 3% (7/240) were positive for MRSA and prevalence at lairage was higher at 11% (27/240). The carcass swabs results identified 4/235 (2%) as positive for MRSA, of which three were from the same farm. Additionally, three of the farms which were positive for MRSA on farm and at lairage had no MRSA-positive carcass swabs. Of the retail pork samples (n=135), five (4%) tested positive for MRSA and originated from three of the farms. One of these farms had MRSA-positive results on farm, at lairage and at retail pork, but no positive carcass swabs. The second farm had MRSA-positive results at all sampling stages, and the third farm had one pig positive for MRSA at lairage. Further characterisation of 50 of the MRSA isolates showed that they belonged to six different clonal complexes; CC5 (n=32), CC398 (n=12), CC9 (n=2), CC39 (n=2), CC72 (n=1) and CC1340 (n=1). In conclusion, the higher proportion of MRSA-positive pigs at lairage compared to on farm suggests that other risk factors contributed to the increased proportion of contaminated or colonised pigs during transportation or lairage. These findings support the results of a study in The Netherlands, which reported that pigs can become colonised with MRSA in the short period of time during transportation from the farm to the slaughterhouse. The findings from one of the farms showing MRSA-positive pigs on farm, lairage, from carcasses and in retail pork illustrates the potential for the occurrence and persistence of MRSA at all stages of the pork production chain.[89]

6.8 Key points from animal surveillance data

- The first isolation of LA-MRSA in food-producing animals in the UK was from a poultry farm in East Anglia in November 2013.

- The first reported isolation of LA-MRSA from a pig in the UK was in May 2014. Following this, a further five (one in 2014, four in 2015) separate geographical incidents of LA-MRSA in pigs in the UK have been reported.

- The prevalence of LA-MRSA in animals in European countries appears to be significantly higher compared to animals in the UK.

- Current data suggests that LA-MRSA CC398 is the most predominant lineage in animals in the UK and other European countries. LA-MRSA CC9 appears to be the most predominant lineage in animals in Asia.

- LA-MRSA CC398 isolates found in UK livestock may originate from European lineages.

6.9 Other lineages of LA-MRSA

102. Since the presence of LA-MRSA CC398 was first described in the Netherlands and France in both pigs and humans who work with pigs, MRSA CC398 has spread to animals in most parts of the world. This includes most of Europe, South and North America, Canada, Australia and Asia.

103. In Asia, the epidemiology of MRSA in animals is dominated by another lineage, LA-MRSA CC9. In addition to CC398 and CC9, other CC types in pigs have been described in Europe (such as Italy) and in the US and Canada, i.e. CC5. Human cases in Demark have been associated with these CC types, but do not seem to originate from livestock to a significant degree.[90]

104. In the US, the diversity of LA-MRSA appears to be greater than in Europe or Asia, with reports of both CC398 as well as a variety of other types in live animals, including CC5 and CC8.[91]

6.10 Seasonality of LA-MRSA carriage

105. To our knowledge, there are no data available regarding seasonal variation in carriage of LA-MRSA in food production animals.[92]

6.11 MRSA in Food in the UK

6.11.1 Exposure via raw milk

106. The first isolation of LA-MRSA CC398 from dairy cattle in the UK was described in a study undertaken from January 2012 to July 2012. This study involved the collection of 1,500 bulk tank milk samples from 1,500 dairy farms in the UK. Following analysis, seven LA-MRSA CC398 isolates were identified from five geographically dispersed dairy farms which were located in Dumfries and Galloway (Scotland), Worcestershire, Berkshire, Warwickshire and Wrexham (Wales). Three isolates were from the same farm (Dumfries and Galloway).[93] It is unclear whether any of these farms were producing raw drinking milk or only milk for pasteurisation.

107. LA-MRSA CC398 in milk should be destroyed by pasteurisation, assuming that MRSA is similar to other *Staphylococcus aureus* with respect to heat sensitivity. The likelihood of LA-MRSA entering the food chain via this route is therefore likely to be very low. There is potential for exposure to consumers if the raw milk is used for drinking or used for the manufacture of raw milk products where no heat treatment is applied. Furthermore, the application of good hygiene practices should minimise the potential for raw milk to become contaminated with LA-MRSA as well as other pathogens, and the results from 1,500 milk samples indicate that contamination at the time of the survey was low. No indication was given on the exact levels of LA-MRSA present.

108. The observation that only five of 1,500 (0.3%) farms within the study had positive milk samples indicates that the prevalence of LA-MRSA CC398 in dairy cattle is low, but that LA-MRSA CC398 is present in UK cattle. Therefore the risk of colonisation or infection with LA-MRSA of dairy farm workers or individuals with regular contact with dairy cows is likely to be higher compared to the general UK population.[94]

6.11.2 Exposure via raw meat

109. The Food Standards Agency (FSA) carried out a UK wide microbiological survey over a period of 15 months, from March 2006 to June 2007, to collect information on the microbiological contamination of the surface of whole cuts of fresh red meat on retail sale in the UK. Samples were tested for a range of foodborne pathogens and indicator organisms, which included *S. aureus*. In total, 5,998 red meat samples (beef, n=3,249; pork, n=1,693; lamb, n=1,056) were tested, of which 423 (7.2%) were positive for *S. aureus*. Among the individual red meat types, *S. aureus* was found in 181/3,249 (5.6%) beef samples, 191/1,693 (11.3%) pork samples, and 51/1,056 (5.6%) lamb samples. The levels of *S. aureus* on red meat were also investigated (Table 4),[95] although the levels of *S. aureus* according to specific meat types were not analysed. These data provide an indication as to the levels of *S. aureus* present in raw meat in 2006/2007; no data were collected on MRSA.

Table 4. *S. aureus* levels detected on retail red meat in the UK, 2006-2007

	Levels (cfu/meat sample)						Total
	<10	**10-100**	**100-1,000**	**1,000-10,000**	**10,000-100,000**	**>100,000**	
S. aureus	36.2% (156)	37.2% (157)	19.6% (83)	5.0% (21)	1.4% (6)	0.0% (0)	100.0% (423)

110. During 2011 the University of Salford, in collaboration with PHE, undertook a survey in Greater Manchester which looked at 30 samples each of frozen raw chicken (various cuts, including whole chicken, drumsticks and breast fillets), pork and beef (various cuts of both meat types, including minced meat, slices and meat pieces) collected from supermarkets and retail butchers shops. MRSA was isolated from five of the 90 (5.6%) meat samples, and the highest prevalence of MRSA was identified in 10% (n=3) chicken samples, 3.3% (n=1) pork and 3.3% (n=1) beef samples. All five MRSA isolates were

identified from pre-packaged supermarket meat. Four of the MRSA were identified as representatives of the most common human HA-MRSA clone in the UK (CC22), suggesting contamination from human source(s) during meat processing. The fifth isolate (from chicken) was multiply-resistant (including oxacillin, ciprofloxacin, erythromycin, clindamycin and tetracycline), identified as CC9 and lacked the immune evasion cluster, a characteristic of livestock-associated strains. This lineage has been identified previously from animals and meat products in Asia and mainland Europe but not the UK. It is unclear if the chicken sample with the CC9 lineage was derived from animals raised in the UK or imported from abroad. This is the first study in the UK to report the recovery of MRSA from raw chicken, beef and pork.[96]

111. Following this, the PHE Food, Water and Environmental (FW&E) Microbiology Service commenced a survey on the detection of LA-MRSA in raw meat (poultry and pork) on retail sale in North West England between March and July 2015. Local authorities in the North West as part of the North West Survey Sampling Programme were requested to submit samples of raw poultry and pork, including minced and diced products either loose or pre-packed from retail premises (including butchers, supermarkets and convenience stores) for testing for LA-MRSA. A total of 124 samples of pork (n=63), chicken (n=50) and turkey (n=11) were obtained from supermarkets (n=38), butchers (n=56) and convenience stores (n=30).

112. The results have shown that nine of 124 (7.3%) samples were positive for LA-MRSA CC398 and all were resistant to tetracycline. This includes chicken [n=4; thighs (1), whole breasts (2) and diced breast (1)], turkey [n=2; turkey steaks (1) and turkey mince (1)] and pork [n=3; pork mince (2) and pork valentine (1)]. These positive samples were obtained from nine different outlets geographically dispersed throughout the North West. Enumeration was carried out on four of the raw meat samples; all showed a level of <20 cfu/g for LA-MRSA CC398, which indicates a very low level of contamination.[97]

113. Traceability investigations were carried out by the FSA for five (minced pork; n=1, pork valentine; n=1, whole chicken breast; n=2, diced chicken breast; n=1) of the nine positive samples, where sufficient product details were provided, to identify the origin of the raw meat. Two of the samples (minced pork and diced chicken breast) were identified as UK origin. The remaining three samples were identified as originating from different European countries, with the pork valentine from Belgium, one chicken breast from Romania and one chicken breast from Holland (meat processed) and France (chickens born and raised). These results may suggest that contamination of raw meat with LA-MRSA CC398 is widespread in Europe.

114. A survey carried out by the University of Cambridge in February 2015 aimed to detect the presence of MRSA in retail meat products obtained from supermarkets in the UK. In total, 103 samples (52 pork and 51 chicken) of pre-packaged fresh meat products, labelled as being of UK farm origin, were taken from supermarkets in five different locations in the UK. This resulted in the detection of three (2.9%) MRSA isolates from processed pork (2 pork sausage, 1 pork mince), of which all were identified as LA-MRSA CC398. All chicken samples were negative for MRSA. All three isolates were resistant to tetracycline and lacked the human virulence phage. No information was available on

the levels of LA-MRSA present on the meat as enumeration was not carried out, however it was hypothesised that as a highly sensitive method of detection of bacterial contamination was used, the numbers present may be low. Although these products were labelled as being of UK origin, processed pork is likely to comprise meat from multiple carcases and it is possible that the meat packing plants from which these products originated also handle imported meat such that cross-contamination could have occurred between non-UK and UK sourced meat.[98]

115. The findings of these surveys show that LA-MRSA CC398 can enter the food chain and survive on raw meat up to the point of retail. There are only limited data to indicate the prevalence of LA-MRSA CC398 in raw retail meat or the numbers of these bacteria in positive samples. There is also uncertainty about whether the meat originates from animals reared in the UK or whether the meat was sourced from outside the UK. Nevertheless, thorough heat treatment of raw meat is sufficient to destroy the presence of bacteria, including LA-MRSA. Advice to ensure that meat is stored appropriately, handled hygienically and cooked thoroughly remains and will reduce the likelihood of exposure which is likely to be low. [99,100] In addition, LA-MRSA CC398 has distinct genotypic and phenotypic features that separate it from other MRSA variants[101] such as it lacks the genes encoding for classical enterotoxins, so is unlikely to be associated with cases of staphylococcal food poisoning/intoxication. To our knowledge there are no reported cases of LA-MRSA being contracted through ingestion of contaminated meat.[102] The risk of colonisation or infection from handling and cross-contamination of contaminated meat in the kitchen is not known, but has been identified as a potential source in professional food handlers.[103,104]

6.12 Exposure to contaminated food in other European countries

116. In addition to the data obtained in the UK, studies from Europe, North America and Asia have demonstrated that LA-MRSA can be found in food, in particular raw meat and milk.

6.12.1 Belgium

117. A Belgian study carried out between February and April 2012, aimed to determine the prevalence of LA-MRSA in Belgian pork and to determine the role of the pork production chain and butcheries in the transmission of LA-MRSA to the human population.

118. Various pork meat samples (pork chop, bacon, minced pork, rib, forelimb and ear) were collected from two local butcheries (A and B) and two supermarket butcheries (C and D) in the region of Ghent, Belgium. These six pork samples were collected every week from each butchery for six successive weeks, however no minced pork was available at butchery D, and on one occasion no ear sample was available at butchery B. A total of 137 samples were collected (bacon, n=24; forelimb, n=24; rib, n=24; chop, n=24; ear, n=23; minced meat, n=18). Each sample was homogenised and a 10-fold dilution series made to be plated on to Chrom-ID MRSA both before and after overnight

enrichment. However, because the rib, forelimb and ear could not be homogenised mechanically, these samples were measured to determine the area (in square centimetres) per sample, weighed and diluted two-fold. After homogenising manually, the samples were removed and a 10-fold dilution series was made.

119. After direct plating of the samples, MRSA was detected in 11 (8%) of the 137 meat samples (bacon = 1 [butchery A], rib = 1 [butchery B], chop = 2 [butcheries A & D], forelimb = 3 [butcheries A, B & C], ear = 4 [butcheries A, B & C]). The level of MRSA found varied between 200 – 80,000 cfu/g or 6 – 14,776 cfu/cm^2 depending on the sample type. After enrichment, MRSA was isolated from 98 (72%) of the 137 samples (ear [n=23, 100%], forelimb [n=21, 88%], rib [n=20, 83%], minced meat [n=11, 61%], bacon [n=12, 50%], chop [n=11, 46%]). MRSA-contaminated ears, forelimbs and ribs were found in all four butcheries and on all six sampling occasions. For 8 of the 11 samples from which MRSA was isolated after direct plating, MRSA was also detected after enrichment. The level of MRSA found after enrichment is shown in Table 5. No clear link was identified between the high MRSA levels and meat type or butchery.

Table 5. Number of samples identified with varying levels of MRSA on different pork meat types from four butcheries in Ghent, Belgium. February – April 2012

MRSA Levels (cfu/ml)	Total Number of Samples (%)
<10	70 (51)
<100	14 (10)
<1,000	5 (3.6)
<10,000	1 (0.7)
<100,000	2 (1.5)
<1,000,000	6 (4.4)

120. In total, 147 MRSA isolates were obtained (butchery A; n=48, butchery B; n=40, butchery C; n=30, butchery D; n=29). Further characterisation of these isolates identified 143 (97%) as belonging to CC398 and combined typing results revealed that one overall MRSA genotype (MLVA cluster I, SCCmec V, spa type t011, pulsotype VIII) was found on meat from all butcheries, whereas other MRSA genotypes occurred more sporadically. In most cases, isolates originating from the same meat type collected at various sampling events in one butchery did not belong to the same MRSA genotype, and isolates retrieved from different meat types collected at the same sampling event in one butchery had different MRSA genotypes.

121. In summary, a considerably higher prevalence of MRSA after enrichment (72%) was observed on Belgian pork compared with similar studies in other countries; Switzerland (0%), the Netherlands (11%) and in the US and Canada (<10%).[105,106,107] These differences may be explained by the MRSA isolation protocols, such as the choice of enrichment medium and chromogenic medium. Alternatively, it could be an accurate reflection of the high prevalence in Belgian pork compared with pork in other countries, but more research is needed. **I**nvestigation into the genetic diversity of the MRSA isolates from Belgian pork products, identified that the majority of the isolates belonged to CC398. A genetically diverse population of isolates was obtained from the butcheries,

but these isolates had only a few apparent overall genotypes. Comparisons with isolates from the pork production chain supports the hypothesis that some genotypes are maintained and spread throughout the chain, resulting in contaminated pork at butchery level, which can allow MRSA transmission to the general human population. This is the first report of the presence of MRSA and specifically LA-MRSA CC398 in Belgian pork.[108]

6.12.2 Denmark

122. A survey in Denmark between February and November 2009 aimed to investigate the prevalence of MRSA in pigs at slaughter and in Danish and imported retail meat. Nasal swabs were taken from pigs at eleven slaughter plants representing 90-95% of the total number of pigs slaughtered in Denmark. Raw meat samples (frozen or refrigerated) were collected randomly at retail and at outlets in all regions of Denmark. For the slaughter pigs, a total of 789 nasal swabs were taken and 101 (12.8%) were positive for MRSA, representing 100 farms. Further characterisation found the most common lineage to be LA-MRSA CC398 (94/101; 93.1%). Four (4%) isolates belonged to CC30, one (1%) belonged to CC1, and two were a novel type. For the retail meat, a total of 865 samples (Danish: pork (153), chicken (121), beef (143) and imported: pork (173), chicken (191), and beef (84)) were taken. The highest prevalence of MRSA was found in imported chicken (34/191; 18%) followed by pork (13/173; 7.5%) and beef (0/84; 0%). The majority of the imported chicken meat was from Germany (149/191; 78%) and France (33/191; 17.3%). Most of the imported pork meat was from Germany (142/173; 82%), but MRSA positive samples could be found in pork meat that came from all European countries tested. Further characterisation of the MRSA isolates found all pork meat (Danish and imported) to be contaminated with LA-MRSA CC398; only Danish beef was contaminated with LA-MRSA CC398 (2/143; 1.4%) and chicken was contaminated with a number of different MRSA variants; CC398, CC9, CC5 and CC45. In conclusion, imported chicken meat was the most important source of exposure of MRSA to Danish consumers during the study period. LA-MRSA CC398 was found in Danish beef for the first time, which had not previously been reported from Danish cattle or cattle farmers in Denmark.[109]

123. Between September 2012 and January 2013, an investigation into the presence of MRSA in bulk tank milk was carried out in Denmark. In total, 219 bulk tank milk samples were collected from 219 different farms. *S. aureus* was detected in 153/219 (70%) samples, of which four (2.6%) were identified as MRSA. Follow-up sampling of bulk tank milk samples from the four farms testing positive for MRSA, found two of the farms testing positive for MRSA a second time and the other two were negative. This could be due to the farms being transiently contaminated with MRSA or that MRSA is present at a concentration close to the detection level. Further characterisation of the MRSA isolates identified them as CC398 and CC1, which have previously been detected in pigs, and may indicate transmission of MRSA from pig production to dairy cattle. This is the first finding of MRSA from bulk tank milk in Denmark.[110]

6.12.3 Germany

124. In Germany, a national surveillance program of MRSA in food in 2009 has shown that chicken, veal, turkey and pork meat at retail were contaminated with MRSA in 23.1% of samples (Table 6), and LA-MRSA CC398 was the most prevalent genotype. However, MRSA other than CC398 accounted for 26.6%, 3.0%, 14.5% and 9.1% of all MRSA isolated from chicken, veal, turkey and pork meat respectively.[111,112]

Table 6. MRSA-positive retail meat samples in Germany, 2009

Meat Type	Total Number of Samples	Number of MRSA-Positive Samples (%)
Broiler meat - Total	**629**	**140 (22.3)**
- Fresh meat	439	104 (23.7)
- Meat preparations	190	36 (18.9)
Veal – Total	**418**	**54 (12.9)**
- Fresh meat	387	48 (12.4)
- Meat preparations	31	6 (19.4)
Turkey meat – Total	**612**	**258 (42.2)**
- Fresh meat	424	184 (43.4)
- Meat preparations	188	74 (39.4)
Pork meat - Total	**925**	**146 (15.8)**
- Fresh meat	409	48 (11.7)
- Meat preparations	220	26 (11.8)
- Minced meat	296	72 (24.3)
All Origins	**2584**	**598 (23.1)**
- Fresh meat	1659	384 (23.1)
- Meat preparations	629	142 (22.6)

125. A German survey carried out between May and December 2009 in the federal state Rhineland-Palatinate, aimed to determine the MRSA types present in raw poultry meat and poultry meat products at retail. Eighty six samples from food and food products of poultry origin were obtained from individual retail stores, which included fresh chicken meat (n=24), chicken meat products (n=19), fresh turkey meat (n=22) and turkey meat products (n=21). The results found that 37.2% (32/86) of samples were positive for MRSA. This included 25% (6/24) of samples from fresh chicken meat, 21.1% (4/19) of samples from chicken meat products, 50% (11/22) of samples from fresh turkey meat and 52.4% (11/21) of samples from turkey meat products. Further characterisation revealed that 87.5% (28/32) of the MRSA isolates belonged to LA-MRSA CC398. Of the remaining four MRSA isolates, two belonged to CC9 and two belonged to CC5. Testing for the presence of enterotoxin genes found that the CC9 and CC5 isolates were positive whereas the CC398 isolates were negative. In conclusion, the vast majority of the MRSA isolates from fresh poultry meat and poultry meat products were identified as LA-MRSA CC398. None of CC398 isolates were positive for enterotoxin genes, which is consistent with other currently available data. The presence of the enterotoxin genes in the CC9 and CC5 isolates however is considered a common feature for these strains. This study presented only a limited snapshot of the presence of MRSA in fresh poultry meat and

poultry meat products sold in the federal state Rhineland-Palatinate in Germany. It is uncertain how far these results can be extrapolated to Germany in general and further investigation is needed.[113]

126. Another study in Germany during 2009-2010 aimed to investigate the prevalence of MRSA in bulk tank milk from dairy herds. In total, 635 samples of bulk tank milk were taken across the different federal states in Germany over the two year period, of which 28 (4.4%) were positive for MRSA. The prevalence of MRSA was similar in 2009 (4.1%; n=14/338) and 2010 (4.7%; n=14/297). All isolates were characterised as LA-MRSA CC398 and exhibited resistance to tetracyclines. This study demonstrates that LA-MRSA CC398 does occur in German dairy herds.[114] In addition to this German study on MRSA in bulk tank milk, regional studies performed in Southern Germany reported a comparable, while slightly lower, prevalence of 2.2%.[115,116] There is no indication from either of these two studies as to whether the bulk tank milk samples were to be consumed raw.

6.12.4 Italy

127. An Italian study carried out between January and December 2008 aimed to investigate the occurrence of MRSA isolated from food and wild animal carcasses. A total of 2,162 food samples (Table 7) were collected in accordance with national official control programs and regional monitoring activities. Also, samples from 1,365 wild animals (697 wild boars, 242 alpine wild ruminants, 276 foxes, 134 mustelids, 16 rodents) collected by the National Reference Center for Wild Animal Diseases in 2003-2009 were examined.

Table 7. Total number and type of food samples collected, January-December 2008

Food Type	Number of Samples (%)	Food Type	Number of Samples (%)
Cow's cheese	476 (22.0)	Pasta, rice	38 (1.8)
Raw cow's milk for vending machine	453 (21.0)	Meat products	32 (1.5)
Organs – slaughter activities – no lesions	363 (16.8)	Fruit and vegetables	16 (0.7)
- *Bovine*	*342*	Sauces and flavourings	13 (0.6)
- *Equine*	*6*	Poultry fresh meat	12 (0.6)
- *Wild boar*	*6*	Ready to eat – not meat	11 (0.5)
- *Swine*	*3*	Butter and animal fat	7 (0.3)
- *Rabbit*	*3*	Ice cream	5 (0.2)
- *Caprine*	*3*	Egg products	4 (0.2)
Goat's and sheep's milk	283 (13.1)	Crustaceans and molluscs	4 (0.2)
Bulk tank milk	261 (12.1)	Fish threads and slices	3 (0.1)
Meat preparations	100 (4.6)	Canned fish	3 (0.1)
Fresh meat (not poultry)	76 (3.5)	Pastry	2 (0.1)
Total			2,162 (100)

128. The prevalence of *S. aureus* in food was 17.1% (370/2,162) and the food types with the greatest association for presence of *S. aureus* were cow's cheese (155/370; 41.9%) and bulk tank milk (n=107/370; 28.9%). Further characterisation identified nine strains as MRSA, of which two (both from bulk tank milk) were resistant to tetracycline and were spa-type t899 which is generally associated with LA-MRSA CC398. The prevalence of *S. aureus* in wild animals was 2.6% (35/1,365) and further characterisation revealed none as MRSA. In summary, a low prevalence of MRSA in food was observed in this study, which suggests that there is a limited risk of MRSA transmission to humans via food. However, the detection of LA-MRSA in bulk tank milk suggests that the cattle food chain could play a role in the spread of MRSA among animals, workers and the farm environment.[117]

129. A study in Italy aimed to investigate the prevalence and characteristics of MRSA isolates from slaughtered pigs intended for human consumption and from abattoir workers, in order to create the basis for further study on defining the risks of occupational and foodborne transmission linked to the handling or consumption of pork products in Italy. In one year, a total of 328 samples were taken from two industrial abattoirs in Southern Italy; 215 from pigs and 113 from abattoir workers. The pigs examined originated from Italy, and were also imported from Belgium and Spain. The results for the slaughtered pigs identified a total of 81 (37.6%) MRSA isolates, from which 37 were selected for further characterisation which identified eight different CC-types. The most frequently recovered CC-types were CC398 (16 isolates, 43.2%) followed by CC8 (9 isolates, 24.3%) and CC1 (4 isolates, 10.8%). All MRSA isolates from pigs did not have the genes for enterotoxin production, and were resistant to tetracycline. The results for the abattoir workers identified a total of nine (7.9%) MRSA isolates, and all were further characterised which identified five different CC-types. The most frequently recovered CC-types were CC1 (4 isolates, 44.4%) and CC398 (3 isolates, 33.3%), followed by CC8 (1 isolate, 11.1%) and CC15 (1 isolate, 11.1%). All isolates did not have the genes for enterotoxin production, and were resistant to tetracyclines. In conclusion, the most frequently isolated MRSA strain was LA-MRSA CC398. The isolates identified in the abattoir workers were indistinguishable to those isolated from pigs demonstrating that transmission via handling of contaminated meat may be possible. The absence of enterotoxin genes indicates that foodborne intoxication linked to consumption of MRSA-contaminated meat is quite limited.[118]

6.12.5 The Netherlands

130. In the Netherlands, the Dutch Food Safety Agency undertook a survey from June 2007-May 2008 to estimate the prevalence of MRSA in raw retail meats. Out of a total of 2,217 samples, MRSA was isolated from 264 (11.9%) and this includes beef (10.6%), veal (15.2%), lamb and mutton (6.2%), pork (10.7%), chicken (16%), turkey (35.3%), fowl (3.4%) and game (2.2%). The majority (85%) of the isolates belonged to genotype CC398. A limited number of 75 samples of meat were also enumerated and colony counts of MRSA were all found to be below 10 cfu/g. The results of this study showed a high prevalence of MRSA in low numbers in meat of different animals.[119] This appears to be the first study reporting enumeration data of MRSA in raw retail meat.

131. A study in the Netherlands between March and July 2008 looked at the prevalence of MRSA among employees who work in the cold meat processing industry and in institutional kitchens, and also the presence of MRSA on meat handled by those professionals. In total 35 meats samples were taken from a single randomly chosen piece of meat that was being prepared by participants. The results identified five (14%) samples positive for MRSA (Table 8) and further analysis revealed that four out of five (one veal, two pork, one chicken) were CC398. The remaining chicken sample was CC9. In addition, enumeration studies on the samples indicated that the Mean Probable Number (MPN) varied between 0.06 and more than 10 bacteria per gram of meat. The results from the professionals who handled the raw meat showed that 31/95 (32.6%) were colonised with MSSA, but none were positive for MRSA.[120] Full details of the human data from this study can be found in Paragraph 42 under section '6.2 Surveillance data on carriage and infection in humans in other European countries'.

Table 8. MRSA-positive meat samples prepared by food handlers in the Netherlands, March-July 2008

Origin	MRSA Present		Total
	Yes	No	
Veal	1	15	16
Pork	2	8	10
Chicken	2	4	6
Turkey	0	2	2
Fish	0	1	1
Total	**5**	**30**	**35**

132. Another survey in the Netherlands from February-May 2006 found that out of 79 samples of raw retail meats (pork, n=64; beef, n=15) 36 (46%) were contaminated with *Staphylococcus aureus*. Two of those isolates (2.5%) were meticillin-resistant, of which one was typed as CC398.[121,122]

6.13 Exposure to contaminated food outside of Europe

6.13.1 Canada

133. A Canadian study carried out between September 2010 and August 2011 aimed to investigate the prevalence of MRSA at various steps during commercial pork production from three processing plants.

134. Two of the pork processing plants (A & B) slaughtered 500-1,200 pigs per day and performed skinning of the carcasses after bleeding. The third plant (C) slaughtered about 8,000 pigs per day and performed scalding after bleeding and was the only plant that pasteurised carcasses with hot water (80°C). Sampling at each plant was performed every three weeks and about 10 samples were obtained from each of the following sampling points: nasal swabs after bleeding (NSAB); nasal swabs after scalding or skinning (NSASc or NSASk), depending on the operation; carcass samples after pasteurisation or washing (CSAP or CSAW), depending on the operation. Two of the

processing plants (A & B) provided pork loin/chops for retail pork sampling, whereas retail pork samples for plant C were purchased from the supermarket. A total of 2,640 samples were obtained over the study period (800-880 samples per plant) from all sampling points during slaughter and processing, and from retail pork.

135. MRSA was found in 24.8% (655/2,640) of all samples and the overall prevalence by plant was 37.5% for Plant A, 12.7% for Plant B and 24.2% for Plant C. The overall MRSA prevalence by sampling points was 61.9% (410/662) for NSAB, 28.4% (187/658) for NSASc/Sk, 7.6% (50/660) for CSAP/W and only 1.2% (8/660) for retail pork samples. All MRSA isolates carried the mecA gene and were negative for the PVL gene. Further characterisation identified twelve different spa-types, with spa-type t034 being the most prevalent (71.6%), followed by t002 (19.5%) and t011 (4.3%). Spa-types t034 and t011 are associated with LA-MRSA CC398. All MRSA-positive retail pork samples were spa-type t034 and all tested MRSA isolates were resistant to tetracyclines.

136. In summary, this study showed a high prevalence of MRSA in the nasal cavities (61.9%) of incoming pigs and a low prevalence of MRSA in retail pork samples (1.2%). The various processing steps applied at slaughter (scalding/skinning and pasteurisation/washing) contributed to a substantial reduction in MRSA contamination, which suggests that the sanitation practices applied at the individual plants may have more effect on MRSA prevalence in the final product than the initial MRSA carriage rate in the animals.[123]

6.13.2 Korea

137. A study in Korea during 2010-2013 investigated the prevalence of MRSA in animal carcasses and slaughterhouse workers. In total 9,669 carcass samples (3,396 cattle, 3,613 pigs, 2,660 chickens) were taken from 30, 35 and 28 cattle, pig and chicken slaughterhouses respectively. Of these, *S. aureus* was isolated from 830 samples comprised of 175 from cattle carcasses, 269 from pig carcasses and 386 from chicken carcasses. MRSA was isolated from 65 samples comprised of nine from cattle carcasses, 23 from pig carcasses and 33 from chicken carcasses. MRSA was more frequently isolated from chicken carcasses than in cattle and pig carcasses. The prevalence of MRSA in workers was 6.9% (4/58) in chicken slaughterhouse workers, but no MRSA was detected in pig and cattle slaughterhouse workers (0/41). Two different lineages of MRSA were identified in the carcase samples; HA-MRSA CC5, CC59 and CC72, and LA-MRSA CC398, CC541 and CC692. Only LA-MRSA (CC692) was observed in the chicken carcasses, whereas both types (HA and LA-MRSA) were found in cattle and pig carcasses (CC5, CC59, CC72, CC398, CC541) and workers (CC72, CC692). All HA-MRSA isolates carried the enterotoxin and/or leukotoxin genes, whereas the LA-MRSA isolates did not carry these genes, except for variant CC692.[124] The presence of HA-MRSA variants on animal carcasses suggests that cross-contamination from workers or the environment may have occurred. In addition, as LA-MRSA CC692 was uniquely found in chicken carcasses, the finding of this strain in chicken slaughterhouse workers suggests human acquisition of LA-MRSA via handling of contaminated animal products is possible.

6.13.3 USA

138. In 2007, the USA Department of Agriculture (USDA) National Animal Health Monitoring System (NAHMS) conducted a study in 17 of the major dairy States representing 79.5% of US dairy operations and 82.5% of US dairy cows. One aim of the study was to investigate the prevalence of MRSA in bulk tank milk from dairy operations. Of a total of 542 samples, 218 (40.2%) were positive for the presence of *S. aureus*, but MRSA could not be detected in any of the samples for which both phenotypic and genotypic methods were used. These results suggest that, in 2007, bulk tank milk in the USA was not a common source of MRSA.[125]

139. In the USA, a survey on MRSA in retail meats in 2008 found that out of 120 samples (pork, n=90; beef, n=30), 47 (39.2%) were contaminated with *S. aureus*, of which 6 (5%) tested positive for MRSA (pork, n=5 (5.6%); beef, n=1 (3.3%). No strains of CC398 were found and instead types CC5 and CC8 were identified.[126] In 2008, a survey of MRSA in retail meats carried out in Canada involved taking samples of pork chops, ground pork, and pork shoulders from retail outlets in four Canadian provinces. Of a total of 402 samples, 31 (7.7%) were contaminated with MRSA. There was no significant difference between different products, with MRSA isolated from 23/296 (7.8%) pork chops, 7/94 (7.4%) ground pork and 1/12 (8.3%) pork shoulders. Genotyping identified three main types, of which CC398 comprised 32% of the isolates identified and CC8 and CC5 comprised 39% and 29% respectively.[127,128]

140. A study carried out in the US aimed to investigate the prevalence of MRSA in conventional and alternative (labelled and/or marketed as raised without antibiotics or raised without growth promoters) retail pork products. In total, 395 raw pork samples were collected from 36 retail food stores in Iowa, Minnesota and New Jersey in four rounds of sampling carried out at weekly intervals in September and October 2010. A range of fresh raw pork products, both pre-packaged and individually wrapped at point of sale from the meat counter were tested. Pork cuts collected included pork chop, ground pork, riblets, ribs, sausages, blade steak, cube steaks, pork loin, pork roast, and pork cutlet. The results identified *S. aureus* in 256 (64.8%) samples, which consisted of 74/124 (59.7%) in Iowa, 102/141 (72.3%) in Minnesota and 80/130 (61.5%) in New Jersey. The differences among states were not statistically significant. Likewise, no significant difference was observed for *S. aureus* prevalence between conventional and alternative pork samples. Of 300 conventional pork samples, *S. aureus* was isolated from 202 (67.3%) samples compared to 54/95 (56.8%) alternative pork samples. For MRSA, 26 (6.6%) positive samples were identified, which consisted of 10/124 (8.1%) in Iowa, 10/141 (7.1%) in Minnesota and 6/130 (4.6%) in New Jersey. MRSA prevalence in conventional and alternative pork samples were similar; 19/300 (6.3%) and 7/95 (7.4%) respectively. Out of all 26 MRSA isolates, further characterisation identified 7 (26.9%) as CC398, 6 (23.1%) as CC5 and 6 (23.1%) as CC8. A similar percentage prevalence of CC398 was observed in both conventional and alternative pork products, i.e. 5/19 (26.3%) and 2/7 (28.6%) respectively. No statistically significant differences in the prevalence of *S. aureus* or MRSA were observed between the different cuts of pork. This study concludes that there is no significant difference in the prevalence of MRSA on conventional and alternative pork products, which is in contrast to the findings from a

study carried out in The Netherlands. In the Netherlands a lower prevalence of MRSA in meat from chickens, wild fowl and game raised with no growth promoters, was found in comparison to conventionally reared poultry. The US study results may be explained by the possibility of cross-contamination at the processing plant, either from contaminated products processed on the same equipment or by colonised workers.[129]

141. Between March 2010 and April 2011, a survey was carried out to determine the prevalence of *S. aureus* and MRSA in retail beef, chicken, pork and turkey from eight states in the US. A total of 3,520 retail meat samples (880 each of ground beef, chicken breast, pork chop, ground turkey) were collected from 345 local grocery stores in Colorado, Connecticut, Maryland, New Mexico, New York, Oregon, Pennsylvania and Tennessee. The results show 982 out of 3,520 (27.9%) retail meats yielded *S. aureus* and 66 (1.9%) tested positive for MRSA. The prevalence of *S. aureus* was highest in turkey (50.9%) followed by beef (24.5%), pork (22.6%) and chicken (13.5%). MRSA prevalence, ranging from 0.3% in chicken to 3.5% in turkey, also differed significantly among meat types. Among the MRSA isolates, further characterisation identified five MLST types and eleven *spa*-types. The predominant MLST types were CC8 (72.7%) and CC5 (22.7%) and others included CC39, CC398 and CC840. All three chicken isolates belonged to CC8, as well as 96.8% of those from turkey, 60% from beef and 35.3% from pork. CC5 was identified in 52.9% of pork, 33.3% of beef and 3.2% of turkey isolates. CC39, CC398 and CC840 were each found in one beef, turkey and pork, respectively. Major *spa*-types were t008 (43.9%), t2031 (22.7%), t002 (9.1%) and t548 (9.1%). All four types of meat harboured t008, whereas t2031 was recovered from turkey only. In summary, this is one of the largest surveys examining MRSA prevalence in retail meats in the US.[130]

6.14 Key points from food surveillance data

- Evidence suggests that the prevalence of LA-MRSA contaminated food is low in the UK.

- Evidence suggests that LA-MRSA is present in UK dairy cattle, although the prevalence of LA-MRSA appears to be low.

- The risk of colonisation or infection with LA-MRSA of dairy farm workers or individuals with regular contact with dairy cows is likely to be higher than in the general UK population.

- Findings show that LA-MRSA can enter the food chain and survive on raw meat up to the point of retail.

- LA-MRSA CC398 has distinct genotypic and phenotypic features that separate it from other MRSA variants such as it lacks the genes encoding classical enterotoxins, so is unlikely to be associated with cases of staphylococcal food poisoning/intoxication.

- Transmission of LA-MRSA via handling of contaminated meat may be possible.

- Thorough heat treatment of raw meat is sufficient to destroy the presence of bacteria, including LA-MRSA and advice to ensure that meat is stored appropriately, handled hygienically and cooked thoroughly remains and will reduce the likelihood of exposure which is likely to be low.

- To our knowledge, there are no reported cases of LA-MRSA being contracted through ingestion of contaminated meat or milk, in the UK.

6.15 Contamination with MRSA in food handling environments

142. Studies investigating the prevalence of environmental contamination of MRSA in the home are rare in comparison to those investigating the prevalence of environmental contamination in hospitals or nursing homes.[131] Given the lack of data, a pilot study in the USA between January-April 2006 aimed to identify the occurrence of MRSA on surfaces in healthy homes. In total, 35 homes of healthcare and non-healthcare workers were included, and each home had a young child and either a cat or a dog. In each home, a total of 32 surfaces were sampled in kitchens, bathrooms and living areas. The results found MRSA to be present in nine (26%) of the homes and was found on a variety of surfaces. In addition, a positive correlation was identified between the presence of a cat and the isolation of MRSA from household surfaces. This study has shown the presence of MRSA at hand-contact surfaces in healthy homes, and emphasises the need for good hygiene practice in the home.[132] There are no published data available on the prevalence of MRSA in the environment of abattoirs and food production premises.[133] No studies have been identified with regards to LA-MRSA CC398 in food handling environments.

6.16 Transmissibility of LA-MRSA versus other MRSA variants

143. There are reports indicating that the transmission of LA-MRSA between humans is less likely to occur compared with other MRSA variants, particularly in the nosocomial setting.[134]

144. A study in The Netherlands from July 2006 to January 2007 investigated the nosocomial transmission rates of LA-MRSA CC398 and other HA-MRSA isolates (non-CC398 MRSA). The study was carried out by calculating the number of secondary cases following the detection of MRSA index patients who were hospitalised without MRSA-specific infection control measures. In total, 51 Dutch hospitals (52% of all general and academic hospitals in The Netherlands) participated in the study. There were 174 MRSA-positive index patients, and post-exposure screenings were performed in 139 cases in 38 hospitals (with 9,925 individuals being screened for MRSA). MRSA carriage was documented in 24 of 139 (17%) contact screenings, in most cases (75%) in a single person only. Secondary cases were documented in three of 964 (0.3%) healthcare workers and none of 183 patients screened (0.3% of all individuals screened) for LA-MRSA CC398, and in 29 of 4,794 (0.6%) healthcare workers and 33 of 1,951 (1.7%) patients screened (0.9% of all individuals screened) for non-CC398 MRSA. The relative

risk of transmission of LA-MRSA CC398, as compared with non-CC398 MRSA, was 0.28. In conclusion, LA-MRSA CC398 is 72% less transmissible than other MRSA variants in Dutch hospitals.[135] Another study in The Netherlands also investigating the nosocomial transmission rates for LA-MRSA CC398 and other MRSA variants in Dutch hospitals, confirmed that LA-MRSA CC398 is less transmissible (5.9 times) than non-CC398 MRSA.[136]

7.0 Risk Characterisation

7.1 Risk to human health from food poisoning

145. Based on current knowledge, the risk to human health from food poisoning with LA-MRSA is likely to be very low, as the likelihood of LA-MRSA CC398 possessing the genes for enterotoxin production is considered to be rare, but cannot be excluded. In the event of the presence of enterotoxin genes (more likely for other MRSA variants i.e. HA- and CA-MRSA) the risk of enterotoxin production is low, as high numbers of bacteria would be required to produce enterotoxin leading to illness and this risk can be mitigated by appropriate temperature control. This suggestion is supported by the low general incidence of staphylococcal food poisoning. In addition, LA-MRSA CC398 has so far not been associated with staphylococcal foodborne intoxication.[137]

7.2 Risk to human health from the development of invasive disease

146. The risk to human health from the development of invasive disease following consumption of contaminated food with LA-MRSA is considered negligible, and the risks associated with other MRSA variants (HA- and CA-MRSA) are considered very low. This conclusion is based on there being only one report in the literature of such a case occurring caused by MRSA. This isolate was not LA-MRSA. If infection were to occur, then vulnerable consumers would be at greatest risk.

7.3 Risk of being colonised through handling and consumption

147. The risk of becoming colonised with LA-MRSA and/or other MRSA variants through handling and/or consumption of contaminated food or during food processing is likely to be dependent on a number of factors. These include the food processing treatment applied, the effectiveness of the hygienic practices observed, the level of contamination of the food with LA-MRSA and other MRSA variants and the susceptibility of the individual. [138]

148. The risk of colonisation from consumption of contaminated food is considered to be very low, as the heat treatment applied to cook food thoroughly would destroy the organism. The likelihood that an appropriate heat treatment is not applied is considered low, but cannot be excluded.

149. The risk of becoming colonised with LA-MRSA and/or other MRSA variants through handling and/or food processing of contaminated food in the kitchen is considered to be

very low based on current evidence, which suggests low prevalence of contamination. In addition, a study in the Netherlands has suggested that regular exposure of food handlers to MRSA contaminated meat did not result in a measurable increased risk of colonisation with MRSA. This result may also imply that the risk of colonisation by contact with contaminated food is lower for the general population.[139] Other routes of transmission present a higher risk of becoming colonised, for example the major risk factor for acquiring LA-MRSA is having contact with livestock.[140]

150. In the event that colonisation from handling contaminated food did occur, there is a risk of subsequent infection, although this risk is considered to be low. This is based on the very low risk of becoming colonised following handling of contaminated food. In addition, *S. aureus* is an opportunistic pathogen and therefore subsequent infection would be dependent on the susceptibility of the individual (e.g. if the person becomes immunocompromised). The majority of the population is unlikely to be affected.

151. Food businesses are required to have appropriate hygiene controls in place and consumers are reminded about good practice in handling and preparing foods, although there is a degree of uncertainty regarding compliance with this advice for food prepared in the home. There is a lack of data available on the level of LA-MRSA/MRSA contaminated food, but the limited data that are available do suggest that contamination may be low, with a high level of uncertainty. EFSA's Panel on Biological Hazards in 2009 concluded that "there is currently no evidence for increased risk of human colonisation or infection following contact or consumption of food contaminated with CC398 both in the community and in hospital".[141] We are not aware of any additional studies that imply the situation has changed.

7.4 Risk to human health from skin and soft tissue infections

152. The risk to human health from skin and soft tissue infections through handling and preparation of food contaminated with LA-MRSA and/or other MRSA variants is dependent on a number of factors. These include the prevalence of LA-MRSA and other MRSA variants on food and the level of contamination likely to be present (i.e. the higher the level, the higher the risk). Other factors include the likelihood of a person having a cut/open wound on their body to allow entry of the bacteria to cause infection. The site of the open wound is also important as a wound on the hand, when handling contaminated food, would be associated with a higher risk of infection.

153. Based on current knowledge, the risk to human health from skin and soft tissue infections through handling and preparation of food contaminated with LA-MRSA is likely to be very low. This is because the likelihood of food being contaminated with LA-MRSA is low and based on current evidence, the levels present on food are likely to be very low.[142]

154. Based on current knowledge, the risk to human health from skin and soft tissue infections through handling and preparation of food contaminated with other MRSA variants is likely to be low. The risk is slightly higher compared to LA-MRSA as the likelihood of food being contaminated with other MRSA variants is higher. This is

because food can become contaminated via other transmission routes, such as via food handlers.

8.0 Uncertainty

155. This risk assessment contains uncertainties (see Annex 2b) as there is a lack of data for LA-MRSA and other MRSA variants in humans, animals and food in the UK. Further data from other European countries and outside of Europe has been provided, although this is also quite limited and is not an exhaustive collection of international data on MRSA.

156. The main uncertainty surrounding the risk that MRSA, and in particular LA-MRSA, presents to UK consumers from food is the lack of data on the prevalence and levels of MRSA in food, and the ability to link the source of human cases of LA-MRSA and other MRSA variants to the handling and/or consumption of food.

9.0 Conclusions

- **The risk to human health in the UK from the consumption of foodstuffs contaminated with LA-MRSA is likely to be very low, especially when compared to other routes of transmission. There are uncertainties surrounding the prevalence of LA-MRSA in food and food animals. Some of these uncertainties are reduced if data from the continent is extrapolated (see Annex 2b).**

- **The risk to human health in the UK from the handling and/or preparation of foodstuffs contaminated with LA-MRSA is likely to be very low, especially when compared to other routes of transmission. There are uncertainties surrounding the prevalence of LA-MRSA in food and food animals. Some of these uncertainties are reduced if data from the continent is extrapolated (see Annex 2b).**

- **The risk to human health in the UK from the consumption of foodstuffs contaminated with MRSA is likely to be very low, especially when compared to other routes of transmission. There are uncertainties surrounding the prevalence of MRSA in food and food animals. Some of these uncertainties are reduced if data from the continent is extrapolated (see Annex 2b).**

- **The risk to human health in the UK from the handling and/or preparation of foodstuffs contaminated with MRSA is likely to be very low, especially when compared to other routes of transmission. There are uncertainties surrounding the prevalence of MRSA in food and food animals. Some of these uncertainties are reduced if data from the continent is extrapolated (see Annex 2b).**

- **This risk assessment is based on the best available evidence. It is recognised that there is a lack of data in this area, some of which is based on research carried out more than 10 years ago.**

- **FSA advice remains unchanged - i.e. that raw food should be stored appropriately, handled hygienically and cooked thoroughly. In combination, these measures should be sufficient to ensure that any harmful bacteria present are destroyed.**

Annex 1

Search Strategy

157. When developing this risk assessment it was not intended to be a systematic literature review or rapid evidence assessment. Scientific papers were obtained from various sources, including Government Departments, Members of the Advisory Committee for the Microbiological Safety of Food (ACMSF) Sub-Group on Antimicrobial Resistance (AMR), and from websites such as ScienceDirect. In consultation with the ACMSF Sub-Group on AMR, it was considered beneficial to aid the evidence gathering for the risk assessment by using specific search terms in PubMed. This was done at the end of the risk assessment as a sense-check to ensure that important and relevant papers had been included to provide reassurance that the risk from LA-MRSA had been adequately assessed.

Search Terms Used:

- LA-MRSA and Food
- LA-MRSA and Food and Risk
- LA-MRSA and Poultry
- LA-MRSA and Turkey
- LA-MRSA and Chicken
- LA-MRSA and Beef
- LA-MRSA and Cattle
- LA-MRSA and Bovine
- LA-MRSA and Pork
- LA-MRSA and Pigs
- LA-MRSA and Lamb
- LA-MRSA and Sheep
- LA-MRSA and Ovine
- LA-MRSA and Milk
- LA-MRSA and Milk and Risk
- LA-MRSA and Food Poisoning
- LA-MRSA and Food Handlers
- LA-MRSA and Environment
- MRSA and Livestock-Associated
- MRSA and Livestock-Associated and Food
- MRSA and Livestock-Associated and Food and Risk

Annex 2a

Qualitative categories for expressing uncertainty in relation to qualitative risk estimates[143]

Uncertainty Category	Interpretation
Low	There are solid and complete data available; strong evidence is provided in multiple references; authors report similar conclusions
Medium	There are some but no complete data available; evidence is provided in small number of references; authors report conclusions that vary from one another
High	There are scarce or no data available; evidence is not provided in references but rather in unpublished reports or based on observations, or personal communication; authors report conclusions that vary considerably between them

Table from EFSA (2006)

Annex 2b

Key Uncertainties

High Uncertainty

- The source of the UK's human clinical cases of LA-MRSA is unclear as none of the cases reported agricultural links. The role of food is therefore unclear.

- The role of food as a source of clinical cases in other European and non-European countries is unproven. Many cases report agricultural links but, there are no documented reports providing definitive links to colonisation or infection with LA-MRSA arising from the consumption or handling of contaminated food.

- The level of *S. aureus* and/or MRSA required for human colonisation following exposure is not known.

- There is a lack of surveillance data on the prevalence and levels of LA-MRSA in food production animals in the UK.

- There are no data on how LA-MRSA and other MRSA variants from food production animals may contribute to the presence of such organisms in food.

- There is a lack of data on seasonal variation (if any) of LA-MRSA carriage in animals.

- There is a lack of data available on the prevalence of LA-MRSA and other MRSA variants in food handling environments, such as abattoirs and food production premises.

Medium Uncertainty

- The relative contribution of different transmission routes of LA-MRSA is unclear.

- There is uncertainty over the difference between being persistently colonised and transiently colonised with LA-MRSA, as there are no widely accepted definitions in the literature. These terms are used differently and are dependent on the studies.

- There is a lack of surveillance data for the prevalence of food contaminated with LA-MRSA and other MRSA variants, and of the levels present. There is uncertainty over the source of LA-MRSA and other variants found i.e. from animals or food handlers.

- There is uncertainty as to how the risk of LA-MRSA and other MRSA variants in UK food relates to domestically-produced and imported food.

- There is uncertainty over whether MRSA displays any differences to MSSA in growth and survival characteristics in food.

- There is uncertainty regarding compliance with good hygiene advice to help prevent colonisation with LA-MRSA and other MRSA variants.

Low Uncertainty

- There is uncertainty regarding the virulence of LA-MRSA CC398; most data show that this lineage lacks the genes for enterotoxin production. As toxin genes may be present on mobile elements such as bacteriophage or plasmids, it is possible that strains of CC398 may acquire such genes.

Annex 3

Risk Level Classification[144]

Probability Category	Interpretation
Negligible	So rare that it does not merit to be considered
Very Low	Very rare but cannot be excluded
Low	Rare, but does occur
Medium	Occurs regularly
High	Occurs very often
Very High	Events occur almost certainly

Table from EFSA (2006) modified from OIE (2004)

Glossary

Asymptomatic – Carrier of organism/disease/infection, but exhibits no symptoms.

Bacteraemia – Presence of bacteria in the blood.

Broiler – Chicken/poultry bred for meat production.

CA-MRSA – Community-associated meticillin-resistant *Staphylococcus aureus*. This type of MRSA is most commonly acquired in the community.

Carrier – Someone who is asymptomatically colonised with MRSA.

Cloacal – Opening to the intestinal, reproductive and urinary tracts of certain animal species.

Colonisation – Carriage of micro-organisms that may be present without causing signs or symptoms of infection. Colonisation may be transient or persistent. There are no internationally agreed definitions, but in this risk assessment transient MRSA colonisation is considered to constitute colonisation for less than 24 hours following exposure, whereas persistent colonisation is colonisation for a prolonged period of weeks following exposure.

Confidence Interval (CI) – A type of interval estimate of a population parameter.

Cross-contamination – Spread of micro-organisms between humans, animals and/or the environment.

Enterotoxin – A toxin produced by bacteria that targets the intestines and causes gastrointestinal symptoms.

Enumeration – Method of determining the levels of micro-organisms present.

Epidemiology – The science that studies the patterns, causes, and effects of health and disease conditions in defined populations.

HA-MRSA – Healthcare-associated meticillin-resistant *Staphylococcus aureus*. This type of MRSA is most commonly acquired in hospital settings.

Immunocompromised – Having an impaired immune system.

LA-MRSA – Livestock-associated meticillin-resistant *Staphylococcus aureus*. This type of MRSA is most commonly acquired from livestock.

MRSA - Meticillin-resistant *Staphylococcus aureus*.

MSSA – Meticillin-sensitive *Staphylococcus aureus*.

Multivariate Analysis – A statistical approach involving the observation and analysis of more than one statistical outcome variable at a time.

Nosocomial – Disease originating in a healthcare setting.

Odds Ratio (OR) – A measure of association between an exposure and an outcome. The OR represents the odds that an outcome will occur given a particular exposure, compared to the odds of the outcome occurring in the absence of that exposure.

Opportunistic – A micro-organism or infection that only affects patients (causes symptoms) when the immune system is weakened.

Panton-Valentine Leukocidin (PVL) – A toxin produced by *Staphylococcus aureus* that affects the skin/mucosa.

Pasteurisation – Heat treatment used in food to destroy harmful micro-organisms and increase shelf-life.

Pathogen – A harmful micro-organism i.e. causes disease.

pH – The acidity/alkalinity of a particular substance.

Prevalence – The proportion of a population who have (or had) a specific characteristic in a given time period.

Self-limiting disease – A disease that usually clears by itself without treatment.

Staphylococcus aureus – Gram-positive opportunistic bacterium.

Superficial – Existing or occurring at or on the surface.

Systemic – Affects the entire body rather than a single organ or body part.

Univariate Analysis – A statistical approach involving the observation and analysis of only one variable. Each variable in a data set is explored separately.

Water activity (a_w) – The amount of water available for the growth of bacteria.

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