Emergence of Livestock-Associated Methicillin-Resistant Staphylococcus aureus Bloodstream Infections in Denmark - DTU Orbit (01/01/2019)

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Background: Livestock-associated methicillin-resistant Staphylococcus aureus clonal complex 398 (LA-MRSA CC398) is causing an increasing number of skin and soft tissue infections (SSTIs) in Denmark and other European countries with industrial pig production. Yet, its impact on MRSA bloodstream infections (BSIs) has not been well studied. Methods: We investigated the clinical epidemiology of all human cases of LA-MRSA CC398 BSI during 2010-2015. Cases of LA-MRSA CC398 BSI were compared to cases of BSI caused by other types of MRSA and cases of SSTI caused by LA-MRSA CC398. Whole-genome sequence analysis was used to assess the phylogenetic relationship among LA-MRSA CC398 isolates from Danish pigs and cases of BSI and SSTI. Results: The number of LA-MRSA CC398 BSIs and SSTIs increased over the years, peaking in 2014, when LA-MRSA CC398 accounted for 16% (7/44) and 21% (211/985) of all MRSA BSIs and SSTIs, corresponding to 1.2 and 37.4 cases of BSI and SSTI per 1 000 000 person-years, respectively. Most patients with LA-MRSA CC398 BSI had no contact to livestock, although they tended to live in rural areas. LA-MRSA CC398 caused 24.3 BSIs per 1000 SSTIs among people with no livestock contact, which is similar to the ratio observed for other types of MRSA. Whole-genome sequence analysis showed that most of the BSI and SSTI isolates were closely related to Danish pig isolates. Conclusions: This study demonstrates that the increasing number of LA-MRSA CC398 BSIs occurred in parallel with a much larger wave of LA-MRSA CC398 SSTIs and an expanding pig reservoir.

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