

Cystic Fibrosis Research News

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Title:

Emergence of livestock-associated MRSA isolated from cystic fibrosis patients: result of a Belgian national survey

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What was your research question?

The aim of this study was to characterise *Staphylococcus aureus* strains isolated from Belgian individuals with cystic fibrosis (CF) based on their antibiotic resistance (methicillin susceptible -MSSA- or resistant -MRSA-) and virulence profile (toxin presence). We were also interested in determining the type of *S. aureus* clones recovered from people with CF in Belgium.

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Why is this important?

S. aureus is one of the first bacteria to colonize and infect the airways of children with CF. Sometimes, *S. aureus* acquires resistance to most antibiotics used to treat staphylococcus infections and is then called MRSA. MRSA in people with CF has been associated with more severe pulmonary disease and poorer clinical outcomes.

There are three main MRSA reservoirs and hence sources of spread and infection: hospital (hospital-associated MRSA; HA-MRSA), community (community-associated MRSA; CA-MRSA) and livestock (livestock-associated MRSA; LA-MRSA) The LA-MRSA are rarely reported as a source of infection for people with CF. Knowing about *S. aureus* epidemiology in this population allows for identification of risk factors for acquisition of MRSA and revision of recommendations on how to protect children with CF from acquiring MRSA.

What did you do?

S. aureus isolated from respiratory samples of 340 patients with CF (out of a total of 510 patients attending four CF-centres and one rehabilitation CF-centre) were analysed for their methicillin susceptibility at the DNA level by using technique called polymerase chain reaction (PCR). This enabled detection of two target genes, *mecA* and *mecC*, that confer resistance to methicillin and indicate MRSA. The toxin profile was also characterized by PCR for genes encoding the toxic shock syndrome toxin (TSST-1) and Panton-Valentine leucocidin (PVL). The study of *S. aureus* clones was performed using diverse molecular typing methods (*spa*-typing, MLST, SCC*mec* typing) that show how *S. aureus* is related at the genetic level.

What did you find?

Among the 340 patients (mean age: 20 years), 25 were colonized with MRSA (29 strains, 4.9% of patients MRSA positive). We found that 90% MRSA in this study belonged to one of the HA-MRSA clones spread in Belgian hospitals, suggesting that the health-care system was the main source of contamination. Contrary to the observation made in people with CF in America, the prevalence of infections caused by CA-MRSA was very low in Belgium. Indeed, no PVL-positive MRSA, and thus no suspected CA-MRSA, was isolated in Belgian CF individuals. Surprisingly, 12% of MRSA carriers were colonized by LA-MRSA, suggesting that contact with farming animals and farmworkers could represent new risk factors for people with CF.

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What does this mean and reasons for caution?

The emergence of LA-MRSA in the CF-population is alarming, and represents a new source of MRSA acquisition for people with CF. Private farm visits or contact with persons directly exposed to livestock may increase the risk for LA-MRSA acquisition. This is particularly worrisome for countries with high levels of LA-MRSA. However, this observation should be confirmed by other studies on CF-populations from different countries.

What's next?

Careful surveillance is essential for monitoring trend in the evolving epidemiology and the management of S. aureus including MRSA in the CF-population.

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