# First outbreak of methicillin-resistant *Staphylococcus aureus* on a dairy farm in Poland

Henryk Krukowski[1], Zofia Bakuła[2], Mateusz Iskra[2], Alina Olender[3], Hanna Bis-Wencel[1], and Tomasz Jagielski[2*]

[1]Department of Microbiology and Reproductive Biology, University of Life Sciences in Lublin, Akademicka 13, 20-950 Lublin, Poland
[2]Department of Medical Microbiology, Institute of Microbiology, Faculty of Biology, University of Warsaw, I. Miecznikowa 1, 02-096 Warsaw, Poland
[3]Department of Medical Microbiology, Medical University of Lublin, Chodźki 1, 20-093 Lublin, Poland
Correspondence to: Dr. Tomasz Jagielski – t.jagielski@biol.uw.edu.pl

## BACKGROUND

Methicillin-resistant *Staphylococcus aureus* (MRSA) continue to pose an emerging public health threat globally, being responsible for a wide variety of infections, ranging from mild skin infections to life-endangering invasive diseases. Until quite recently, most of the MRSA isolates have been detected in hospital settings. However, the epidemiology of this pathogen is changing rapidly, with newly established, community-associated reservoirs. To date, only few cases of MRSA transmission between humans and animals have been reported. Here we describe a first putative case of such transmission in Poland, associated with a MRSA outbreak on a dairy farm.

## METHODS

The study was conducted on a dairy farm (herd size 806 cows) located in Lublin Province, from May to August 2018. The milk sampling was performed in accordance with routine laboratory techniques. Oral and nasal swabs were collected from people who had direct contact with the animals on the farm (farm workers and veterinary personnel), and their families. Isolation and identification of *S. aureus* and antimicrobial susceptibility profiling was carried out, as previously described [Jagielski et al., J Dairy Sci;97,6122-8;2014]. Molecular characterization of MRSA isolates was performed with three typing methods, i.e. Multiple-Locus Variable number tandem repeat Analysis (MLVA) [Sabat et al., J Clin Microbiol;41,1801-04;2003], Multilocus Sequence Typing (MLST) [Enright et al., J Clin Microbiol;38,1008-15;2000], and *spa*-typing [Harmsen et al., J Clin Microbiol;41,5442–48;2003].

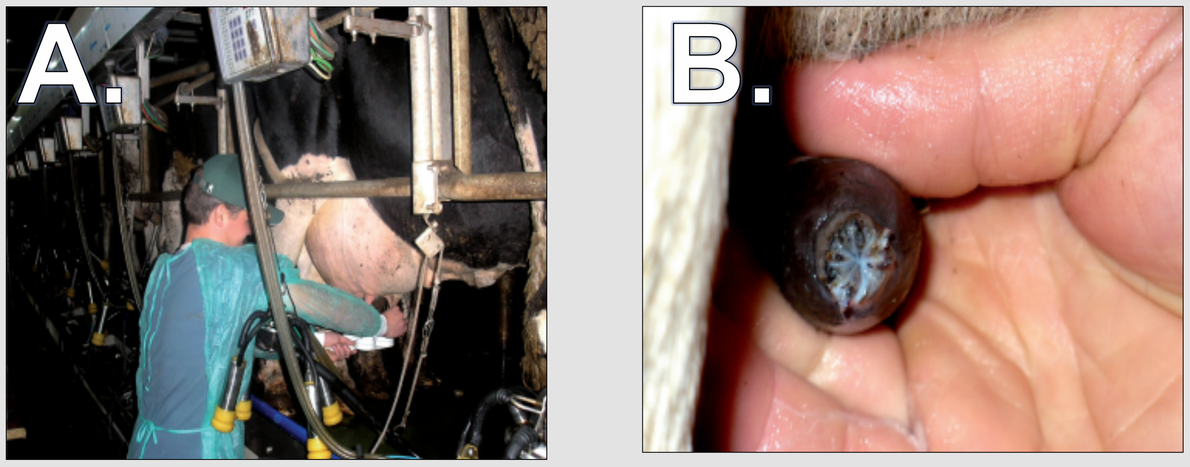


**Figure 1.** Milk sampling (**A.**); Teat inflammation (**B.**)

## RESULTS

A total of 13 MRSA isolates from 9 cases (4 humans, 5 cows) were cultured. Eleven bovine (n=5, 5 cases) and human (n=6, 4 cases) isolates were indistinguishable by MLVA-typing (pattern A) and were of ST398 MLST type and t034 *spa* type. The other two isolates (of human origin, 2 cases) had identical MLVA-pattern (pattern B) and were of ST45 MLST and t2633 *spa* types (**Fig.2; Tab.1**).

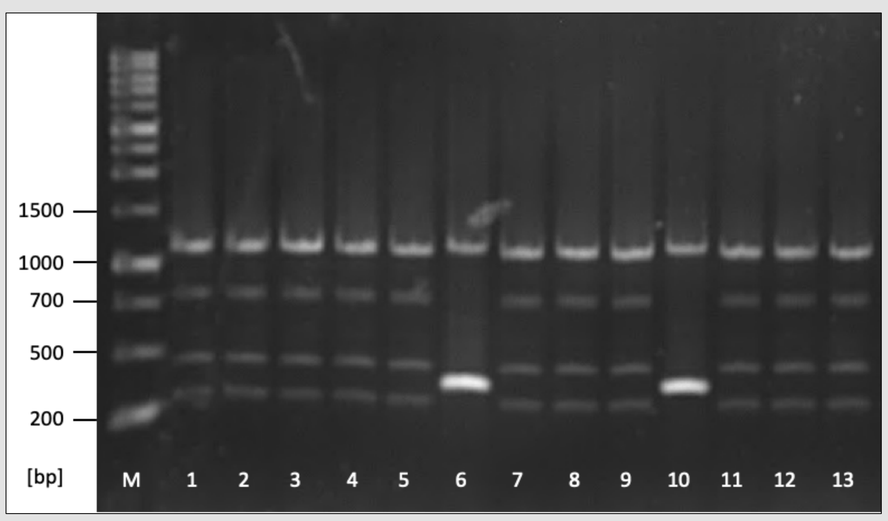


**Figure 2.** MLVA patterns of MRSA isolates under the study. Lane designations (1-13) correspond to isolate numbers (MRSA 1-13; see: **Table 1**); M – size marker (Gene Ruler 1 kB; Thermo Fisher Scientific, USA).

**Table.1** Distribution of MLVA, MLST and *spa* types among MRSA isolates included in this study.

| Isolate ID: | MRSA1 | MRSA2 | MRSA3 | MRSA4 | MRSA5 | MRSA6 | MRSA7 | MRSA8 | MRSA9 | MRSA10 | MRSA11 | MRSA12 | MRSA13 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Isolation source | milk | milk | milk | milk | milk | nasal | nasal | nasal | oral swabs: | nasal | oral | oral | nasal |
| Date of isolation (year 2018) | 10.06 | 17.06 | 02.07 | 06.07 | 06.07 | 27.06 | 27.06 | 19.06 | 19.06 | 27.06 | 27.06 | 27.06 | 27.06 |
| Host* | cow | cow | cow | cow | cow | milker | milker | vet | vet | vet | vet | vet's son | vet's wife |
| MLVAtype | A | A | A | A | A | B | A | A | A | B | A | A | A |
| MLST type** | ST398 | ST398 | ST398 | ST398 | ST398 | ST45 | ST398 | ST398 | ST398 | ST45 | ST398 | ST398 | ST398 |
| spa-type*** | t034 | t034 | t034 | t034 | t034 | t2633 | t034 | t034 | t034 | t2633 | t034 | t034 | t034 |
| Tested drug**** Amikacin | S | S | S | S | S | S | S | S | S | S | S | S | S |
| Chloramphenicol | S | S | S | S | S | S | S | S | S | S | S | S | S |
| Ciprofloxacin | R | R | R | R | R | S | R | R | R | R | R | R | R |
| Clindamycin | R | R | R | R | R | S | R | R | R | R | R | R | R |
| Cotrimoxazole | S | S | S | S | S | S | S | S | S | S | S | S | S |
| Fusidic acid | S | S | S | S | S | S | S | S | S | S | S | S | S |
| Gentamicin | S | S | S | S | S | S | S | S | S | S | S | S | S |
| Mupirocin | S | S | S | S | S | S | S | S | S | S | S | S | S |
| Norfloxacin | R | R | R | R | R | S | R | R | R | R | R | R | R |
| Tetracycline | R | R | R | R | R | S | R | R | R | R | R | R | R |
| Cefoxitin | R | R | R | R | R | R | R | R | R | R | R | R | R |

* The isolates were recovered from 5 bovine and 4 human hosts (i.e. milker, veterinarian, his wife and one of his sons);
** MLST type according to MLST database (http://saureus.beta.mlst.net/); ST398 refers to the following number of repeats: *arc* - 3, *aroe* - 35, *glpf* - 19, *gmk* - 2, *pta* - 20, *tpi* - 26, *yqil* - 39, whereas ST45 to *arc* - 10, *aroe* - 14, *glpf* - 8, *gmk* - 6, *pta* - 10, *tpi* - 3, *yqil* – 2;
***Number of repeats and *spa* type according to spaTyper 1.0 database (Bartels et al., 2014). t034 refers to the 08-16-02-25-02-25-34-24-25 *spa* type, whereas t2633 to the 08-16-02-16-34-13-17-34-13-17-34-16-34 *spa* type.
****Isolates were categorized as either resistant (R) or susceptible (S).

## CONCLUSIONS

This is the first report of a MRSA outbreak in Poland, not associated with hospital setting. It is also the first case of a putative direct transmission of MRSA between human and cows in our country. Noteworthy, the MRSA strain responsible for the outbreak was of MLST type ST398, a highly transmissible clone, with a broad host range.