

Outbreak of a rare type of Methicillin-resistant *Staphylococcus aureus* (MRSA) among teenagers and their families in a community in Norway, 2016-2017

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Background

MRSA is a notifiable disease in Norway with 2,338 cases notified in 2016, whereof 835 were clinical infections. The majority of cases were found in primary care.

As the focus of MRSA guidelines in Norway is the prevention of spread in healthcare institutions, although outbreaks in the community are sometimes reported they are rarely investigated. Furthermore, while FHI has standard questionnaires for foodborne outbreaks none such exists for MRSA outbreaks in the community.

Methods

Case definitions

- Probable case: a person from the municipality reported to the Norwegian Surveillance for Communicable Diseases (MSIS) in 2016 to 2017, with an isolate of PVL-positive MRSA CC398, spa type t034
- Confirmed case: a probable case with WGS confirmed genetic relatedness between isolates. In this outbreak, ≤ 6 single nucleotide polymorphisms

Results

Epidemiological results

- 12 confirmed cases from 5 families, all from the same village (Fig. 1)
- 3 children (2 males), 5 male teenagers, and 4 adults (2 males)
- 9 of the confirmed cases presented with superficial wounds or skin abscesses, 3 were asymptomatic

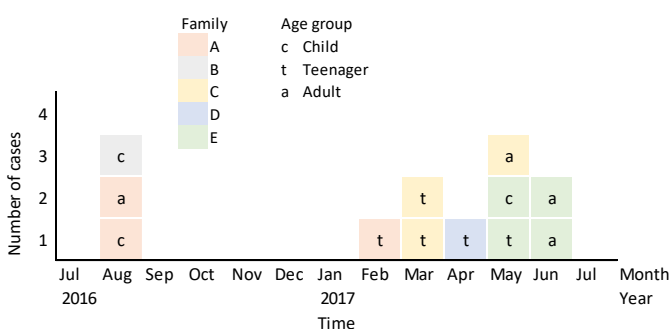


Figure 1. Sampling date for confirmed cases in a community outbreak of MRSA, Norway.

Conclusions and recommendations

- Transmission of MRSA could be explained through close social contacts
- The interview tool was useful to investigate the outbreak
- Because the outbreak did not extend with further symptomatic cases in the community, local authorities and the NIPH agreed that no community-focused control actions were needed

The alert

- In May 2017, the reference laboratory noted a cluster of 7 isolates of PVL-positive MRSA CC398, spa type t034, ongoing since February 2017
- Unusual for Norway, all cases were without travel history, from one municipality, and 6 were adolescents
- At the time no known epidemiological link outside family members

Aim

To investigate the outbreak in order to generate hypothesis on the transmission route, and to develop an interview tool for investigating community outbreaks of resistant bacteria.

Approach

1. Surveillance data: all cases in Norway with PVL-positive MRSA CC398, spa-type t034, reported to MSIS between 2016 to 2017 were identified.
2. Whole genome sequencing (WGS): of all probable case isolates from 2016 and 2017.
3. Interview tool: we developed a questionnaire and interviewed probable cases about school, employment, organised and non-organised activities they participated in (what, where, and when), and their social network, for the year before they were tested for MRSA.

Interview results

- Interviews covered 8 cases from 4 families
- Epidemiological links between all 5 families through at least one member (Fig. 2)
- The interview tool worked well

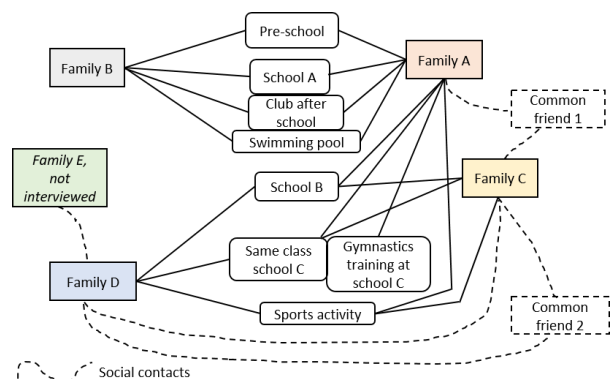


Figure 2. Epidemiological links between families with cases in a community outbreak of MRSA, Norway 2016-2017.

- The approach of combining surveillance information, WGS and case interviews has previously not been used by the NIPH to investigate epidemiological links in MRSA community outbreaks
- We recommend this approach for future community outbreaks of drug resistant bacteria known to be transmitted via person-to-person contacts