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### High prevalence of Panton -Valentine leukocidin among methicillin-resistant *Staphylococcus aureus* from refugees in the Netherlands, 2014 - 2015

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#### **Background:**

The presence of the virulence factor Panton-Valentine leukocidin (PVL) is associated with highly-virulent community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA), and several specific genetic backgrounds have been observed among CA-MRSA. In general, the PVL prevalence is still low, but several studies have observed a high PVL prevalence in Africa and the Middle East. Therefore, the increase of MRSA from refugees from Africa and the Middle East to northern Europe with a possible high PVL prevalence is of public health concern. The aim of this study was to investigate the PVL prevalence and the population structure of MRSA isolates obtained from refugees.

#### **Material/methods:**

Between April 2014 and December 2015, 97 MRSA strains were isolated from 965 refugees from Africa and the Middle East, and the presence of PVL and the *spa* type was determined. *Spa* types were clustered into *spa*-CCs using the algorithm based upon repeat pattern (BURP), and the

associated clonal complexes (CCs), as determined with multi-locus sequence typing (MLST), were allocated.

### **Results:**

The MRSA prevalence among refugees was 10.1%. *Spa* typing of MRSA strains revealed 33 different *spa* types, and these were clustered into seven *spa*-CCs. Five strains were classified as singletons, and four *spa* types were excluded from clustering. *Spa*-CCs, singletons and excluded *spa* types were associated with MLST CC1 (23 isolates), CC5 (4 isolates), CC8 (10 isolates), CC15 (1 isolate), CC22 (19 isolates), CC30 (3 isolates), CC80 (7 isolates), CC88 (18 isolates), CC97 (4 isolates), CC121 (4 isolates) and CC361 (1 isolate). *Spa* types t1252 and t1509 could not be associated with a MLST CC.

It was observed that 40 of the 97 isolates (41%) harboured PVL. These 40 PVL-positive MRSA isolates were associated with MLST CC1 (18 isolates), CC30 (two isolates), CC80 (seven isolates), CC88 (nine isolates), and CC121 (four isolates).

Seventy percent of the PVL-positive isolates originated from refugees from Eritrea (14 of 19 isolates) and Syria (14 of 42 isolates). Ten of the 14 PVL-positive MRSA strains from Eritrea were associated with CC1, and nine of them had *spa* type t5100, previously only observed in Denmark, Germany and Sweden. The 14 PVL-positive MRSA strains from Syrian refugees were mainly associated with CC1 (29%) and CC80 (29%).

### **Conclusions:**

We observed a high PVL-prevalence among MRSA isolates with a genetic background common to virulent and epidemic CA-MRSA clones among refugees from Africa and the Middle East seeking asylum in The Netherlands. This finding is of public health concern, especially in a country as The Netherlands with a low prevalence of MRSA. Due to the changing prevalence of PVL-positive MRSA in Europe, it is important to strengthen surveillance on PVL-positive *S. aureus*.