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P2741 Surveillance-embedded genomic outbreak resolution of methicillin-susceptible *Staphylococcus aureus* in a neonatal intensive care unit

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Background: We observed an increase in methicillin-susceptible *Staphylococcus aureus* (MSSA) infections among neonates at a Dutch third level neonatal intensive care unit. Weekly surveillance data of MSSA carriage among neonates and cross-sectional screenings of health care workers (HCWs) were available for outbreak tracing. While traditional typing of MSSA isolates by staphylococcal protein A gene (*spa* typing) and Multiple-Locus Variable number tandem repeat Analysis (MLVA) suggested that nosocomial transmission had contributed to the infections, here they lacked the resolution to draw solid conclusions.

Materials/methods: MSSA isolates were subjected to whole-genome sequencing and compared by a series of automated tools including *de novo* assembly, identification and localization of high-quality single nucleotide polymorphisms, and in-depth analysis of subsets of isolates. Outbreaks were defined as isolates that were more closely related than was to be expected from the genetic diversity in background surveillance.

Results: Genomic analysis identified isolates that had been unjustly assigned to clusters based on MLVA typing, while *spa* typing was concordant but of insufficient resolution. Detailing particular subsets of isolates further improved resolution and although it provided evidence that HCWs were involved in multiple outbreaks, it alleviated heavy concerns about one particular HCW. Genomic clustering of isolates based on deviations from background surveillance matched epidemiological patient linkage. Compared to MLVA typing, the genomic analysis demonstrated more, shorter, and re-assorted nosocomial transmission chains during this outbreak.

Conclusions: In this study the improved resolution and accuracy of genomic outbreak analyses compared to *spa* typing and MVLA substantially altered the view on outbreaks, along with apposite outbreak measures. Inclusion of the circulating background population has the potential to overcome current issues in genomic outbreak inference.