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P2600 All is not what it seems: *Klebsiella oxytoca* on a neonatal intensive care unit

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Background: Premature neonates are at an increased risk of bacterial infections, and are thus routinely monitored closely for colonizing pathogens. Most notorious is *Serratia marcescens*, but due to the vulnerable patient population even other non-antimicrobial-resistant species pose a threat. Whole genome sequencing is now often used in our hospital to sequence suspicious clusters of same species isolates to resolve putative transmission chains. Here we report on several clusters of *Klebsiella oxytoca* isolates over 5 months' time.

Materials/methods: Isolates were collected as part of weekly routine screening procedure on the ward. Whole genome sequencing was carried out using Illumina Nextera XT kits. A total of 21 samples were sequenced. Sequence reads were mapped to reference genome NCTC11696, as well as within-cluster references. Single nucleotide polymorphisms were identified and used to reconstruct phylogenetic relationships.

Results: On average we identify 1-2 *K. oxytoca* a month on the neonatal intensive care unit in our hospital. When we identified 7 positive patients within two weeks, we undertook whole genome sequencing of these isolates. We also added previous and subsequent isolates from the same ward. Sequencing revealed that there were three co-occurring transmission chains, each involving between 3-6 patients, plus additional unrelated, distinct strains. Two of the transmission chains overlapped temporally and included the initial event that prompted the investigation. Also, one of the patients had been treated for a prolonged period on the ward and could theoretically have been involved in any of the three transmission chains.

Conclusions: Despite an apparent increase in *K. oxytoca* incidence on our neonatal intensive care unit, there was no single, protracted outbreak but in fact three separate transmission clusters involving between 5 and 6 patients each and additionally independent isolates.