AUTOMATED ELECTROCHEMICALLY ACTIVATED SOLUTION TREATMENT MINIMISES CONTAMINATION OF HOSPITAL WASHBASIN U-BENDS: THE POPULATION STRUCTURE OF *PSEUDOMANAS AERUGINOSA* IN TREATED AND UNTREATED U-BENDS DETERMINED BY WHOLE GENOME SEQUENCING.

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Background: Hospital washbasin U-bends have been increasingly associated with infection outbreaks and the persistence of particular bacterial species in the healthcare environment. *Pseudomonas aeruginosa*, which has a diverse[a] population structure, is predominant in hospital wastewater systems. Previous studies[a] over five months demonstrated the effectiveness of a novel system for automated simultaneous decontamination of multiple washbasin U-bends. This system uses sequential treatments with two electrochemically-activated (ECA) solutions generated from brine; catholyte with detergent properties and anolyte with disinfectant properties.

Objective: The objective of this study was to monitor the long-term effectiveness of ECA decontamination of multiple hospital washbasin U-bends, while investigating the prevalence and population structure of *P. aeruginosa* in treated and untreated washbasin U-bend networks.

Methods: Ten ECA treated U-bends were sampled immediately-, 24 h- and 48 h- post-disinfection for 63 weeks. Concurrently, ten identical untreated U-bends were sampled weekly for 51 weeks. Samples were cultured on Columbian blood agar, *P. aeruginosa* selective agar and Reasoner's 2A agar. Representative *P. aeruginosa* isolates were subjected to whole genome sequencing (WGS) using the Illumina MiSeq platform (Illumina, The Netherlands). Whole genome multilocus typing (wgMLST) was undertaken using BioNumerics software (Applied Maths NV, Belgium).

Results: The average quantitative bacterial densities from treated U-bends showed a >3 log reduction on all media compared with control U-bends and reductions were highly significant (P <0.0001) on all media. *Pseudomonas aeruginosa* was the predominant species recovered from all U-bends. WGS analysis of 21 isolates from treated U-bends identified several sequence types (STs) (ST560, ST179, ST773, ST27, ST308, ST296), whereas WGS analysis of 54 isolates from untreated U-bends yielded four sequence types (ST252, ST560, ST179, ST298). Isolates within individual STs formed closely related clusters, regardless of source (wgMLST allelic difference range of 0-35).

Conclusions: Contamination of ECA-treated U-bends was consistently reduced by 99.9% over a twelve-month period. Unexpectedly, the range of *P. aeruginosa* STs identified in treated and untreated U-bends was very small, indicating adaptation of specific STs to the wastewater networks concerned. Highly related isolates were identified in multiple U-bends, indicating spread via wastewater pipework.

[a]Deasy et al. J Hosp Infect. 2018, 100(3):e98-e104