Supplementary Material (for online publishing only)

Supplementary Methods

*Environmental colonization sampling:* The swabs were inserted 2.5 cm below the drain plate for sampling.1 Approximately 50 mL of drain water was collected from P-traps either by disconnecting the P-trap (MSP and BSP) or by inserting a Salem sump™ dual-lumen tube with a Luer-Lok™ General Purpose 60 mL syringe (SDP). For the post-intervention survey, only 3 swabs were obtained from each room: main sink drain, bathroom sink drain, and toilet rim. OHSU was on COVID-19 restrictions for research activity at the time of post-intervention sampling; our IRB granted permission for a single entrant to obtain main sink drain, bathroom sink drain and toilet rim swabs, but not shower drain or P-trap samples because those required facilities staff support.

*Isolate cultivation technique:* Environmental swabs and patient pooled axillary and rectal swabs were cultivated with 5 mL of Tryptic Soy Broth (TSB) followed by incubation and centrifugation at 40 C and 200 rpm. For the effluent from the P-traps: 50 mL of P-trap effluent was placed in 50 mL conical tubes and centrifuged at 3000 rpm for 15 minutes, after which time the supernatant was removed and 1 mL of pelleted debris was inoculated into 5 mL of TSB. TSB was inoculated onto Cetrimide agar (Millipore Sigma-Aldrich, Germany), a *Pseudomonas*-selective agar.2,3 Colonies that were green or yellow in color, suggestive of growth of *Pseudomonas*, were isolated onto Mueller Hinton agar, after which isolates were prepared in Luria-Bertani (LB) broth for freezing at -80° Fahrenheit for future antibiotic susceptibility testing and whole genome sequencing.

*Phylogenetic analysis:* Separate reference genome sequences for each of the three predominant STs were obtained from NCBI GenBank. The reference genome sequences selected were FRD1 (ST-111, NCBI accession NZ\_CP010555.1), Pa58 (ST308, CP021775.1), and S04 90 (ST446, CP011369.1). These reference sequences were selected as they were complete single-contig circularized chromosome assemblies with the same ST as the newly-sequenced isolates. Sequence reads were analyzed using core genome alignment to the ST-respective reference genome sequence using bwa v 0.7.15.4 SNVs relative to the reference were identified using bcftools v1.9 skipping bases with base quality lower than 25, alignment quality less than 30, and using a haploid model. Variants were further filtered as previously described5 using the bcftools\_filter software6 to remove variants with single nucleotide variant (SNV) quality scores less than 200, read consensuses less than 75%, read depths less than five, read numbers in each direction less than one, or locations within repetitive regions (as defined by blast alignment of the reference genome sequence against itself). Maximum likelihood phylogenetic trees were created from consensus genome alignments with IQ-TREE v2.0.7.7,8 Phylogenetic tree visualization and annotation was performed using R and the ggtree package.9,10 SNVs between pairwise isolates within each ST groups were analyzed.

References

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