

Bathroom Bioterror: How *Pluralibacter gergoviae* Travels from Products to Prostheses

Wong T H N¹, Teh B T², Koh T H¹, Lai C M D¹, Ko K K K¹, Chung S J³, Pang H N⁴

- ¹ Department of Microbiology, Singapore General Hospital
- ² Singhealth Duke-NUS Institute of Biodiversity Medicine
- ³ Department of Infectious Diseases, Singapore General Hospital
- ⁴ Department of Orthopedics, Singapore General Hospital

Background: *Pluralibacter gergoviae*, a rare opportunistic pathogen within the former *Enterobacter* group, is notable for its resistance to preservatives found in cosmetic and cleaning products^{1,2,3}. PJI caused by this organism are uncommon, and its routes of transmission remain poorly understood. We present a case of PJI following total knee replacement (TKR) and utilize whole-genome sequencing (WGS) to investigate the potential source of infection.

Methods: A 59-year-old male underwent an elective TKR surgery with rapid post-op recovery and return to function. His surgical wound was healing well and dressings were removed on post operative day 7 (figure 1). However, he developed erythema and pus discharge 3 weeks post-TKR (figure 2), leading to a single-stage revision. *P. gergoviae* was isolated from 6 of 7 intraoperative tissue and fluid specimens. To identify a potential reservoir, epidemiological samples were collected from the patient's home, including showerheads, sinks, drains, and toiletries. Isolates from these environmental sources were cultured, and all *P. gergoviae* isolates underwent WGS to determine single nucleotide polymorphism (SNP) similarity to the clinical isolates.



Figures 1 and 2. Patient's right knee 9 days (left) and 21 days post op (right)

Results: A total of 14 *P. gergoviae* isolates were whole genome sequenced. Coverage to full reference genome was between 83-88%. Two of the isolates were unlinked archival environmental samples for comparison (see figure 3). Eight isolates exhibited near-identical genomes: this group comprised of 3 out of the 6 clinical isolates from the patient's knee and 5 isolates obtained from shower gel used in the patient's main and second bathrooms. In contrast, 3 isolates from a different shower gel, which the patient did not use, formed a phylogenetically distinct cluster. A single isolate from the patient's own shower gel was genomically unique and unrelated to the other groups. In addition, unopened bottles of the patient's shower gel were also cultured for sequencing, though none yielded bacterial growth.

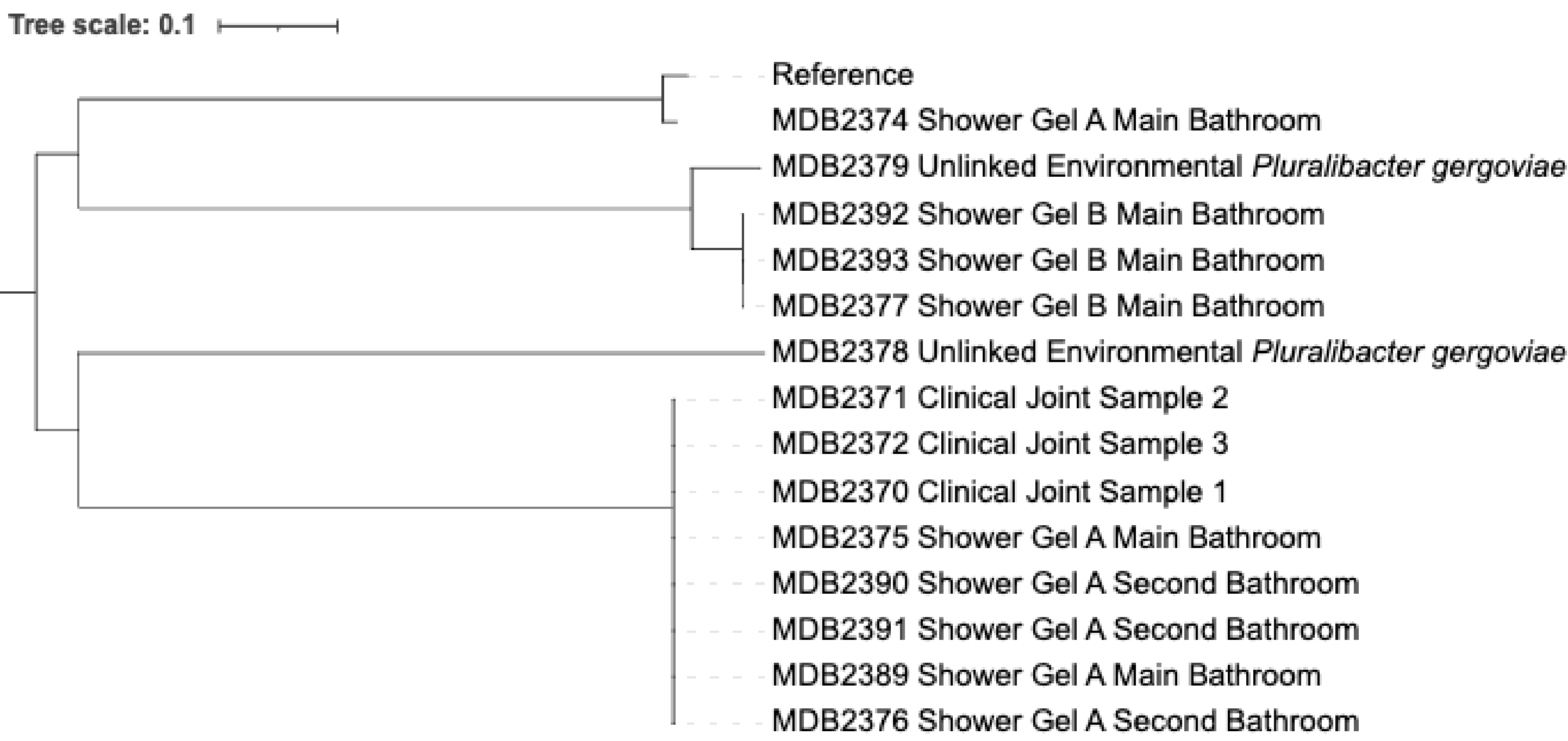


Figure 3. Phylogenetic tree displaying the relatedness of all *P. gergoviae* that were sequenced.

Conclusion: WGS revealed near-identical *P. gergoviae* strains in the patient's infected prosthetic joint and in a shower gel he was actively using. Although we cannot confer the directionality of transmission, the identification of genomically distinct *P. gergoviae* strains in other household toiletries further highlights the organism's capacity to persist in common consumer products. This investigation underscores the utility of WGS in tracing routes of transmission for rare healthcare-associated pathogens and raises important considerations regarding the safety of preservative-resistant bacteria in everyday personal care products. Enhanced infection prevention measures pertaining to post-operative wound care management may avoid rare causes of PJIs caused by environmental pathogens.