

O0860 **Five-year clinical, environmental and genomic epidemiology follow-up of a multifaceted response to an outbreak of Legionnaires Disease (LD) at a Veterans Affairs (VA) healthcare system**

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Background: A 2011-12 LD outbreak at the VA Pittsburgh Healthcare System (VAPHS) involved 22 patients (pts) and caused 6 deaths. Multiple factors contributing to a control-system failure were identified. A multifaceted response was initiated in Nov 2012. Our objective is to report 5-year clinical, environmental and genomic epidemiology follow-up data.

Materials/methods: We retrospectively reviewed clinical, epidemiologic, and water system (WS) surveillance data from Nov 2012-present. MiSeq whole genome sequencing (WGS) was performed on 72 *Legionella* isolates recovered from pts, pts' homes, VAPHS WS, and the Pittsburgh region in 1982-2016. Phylogenetic trees were constructed based on core genome single nucleotide polymorphisms.

Results: VAPHS switched from copper-silver to hyperchlorination WS treatment, and instituted analyzer-chlorination units, daily random biocide level sampling, active monthly WS *Legionella* surveillance, zero-tolerance WS remediation, mandatory ID consults and *Legionella* testing for all pts with pneumonia, and a rigorous genomic epidemiology program. WGS revealed that the outbreak was caused by *L. pneumophila* (Lp) subsp. *pascullei* that evolved through 3 recombinations from an endemic 1982 WS strain. Post-outbreak, 21 cases of LD have been diagnosed, including 12 community and 9 possible healthcare-associated. Etiologies included *L. pneumophila* (Lp) serogroups 1 (n=17) and 2-14 (n=4). WS *Legionella* positivity has decreased from 15.5% during the outbreak, to 1.8% post-outbreak. Pt and WS isolates included Lp subsp. *pneumophila* (5 clades), *pascullei* (2 clades), and *fraseri*. WS *L. longbeachae* were also recovered. VAPHS clades were distinct from publically-available genomes. Outbreak and 1982 Lp *pascullei* strains have not been detected since Nov. 2012. A Dec. 2012 Lp *pascullei* pt isolate was distinct from outbreak isolates, but identical to an isolate from the pt's home. Classical and genomic epidemiology verified that no cases of nosocomial LD have occurred since 2012.

Conclusions: A *Legionella* surveillance and prevention program at a VA healthcare system ended an LD outbreak due to endemic Lp subsp. *pascullei*, eliminated subsequent nosocomial cases, and significantly reduced WS *Legionella* positivity. Results have been sustained for 5 years.