

# Investigation of a legionellosis outbreak in Sydney CBD – a brief report

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## Abstract

**Objective:** To identify and control a source of *Legionella* in Sydney CBD.

**Methods:** Clinical, epidemiological, environmental and genomic techniques were employed to identify cases and the source of *Legionella*.

**Results:** Eleven legionellosis cases were linked to Sydney CBD with a median age of 69 years. All were hospitalised and had risk factors for *Legionella* infection. Eight of 11 cases identified as male. Genomic analysis linked three cases to a contaminated cooling water source in Sydney CBD, with a further case infected with a similar strain to that found in Sydney CBD. Another case, although epidemiologically linked to Sydney CBD, was infected with a genomically different strain to that found in Sydney CBD. Six other cases had no viable sample for genomic analysis.

**Conclusion/Implications for Public Health:** An outbreak of legionellosis is a serious public health threat that requires rapid investigation and environmental control. We were able to identify a source in Sydney CBD through the application of clinical, epidemiological, environmental and genomic techniques. Genomic analysis is a powerful tool that can be used to confirm the source location but requires close collaboration between clinicians, public health units and microbiologists to recover viable sputum cultures from cases diagnosed with legionellosis.

**Key words:** legionnaires disease, legionellosis, outbreak, genomic, environmental

Legionellosis is an infection of the lungs (pneumonia), which in its severest form also affects other organs. It is caused by one of a number of bacteria of the genus *Legionella* although the main cause of disease is from *Legionella pneumophila*.<sup>1</sup> *Legionella pneumophila* can colonise air conditioning cooling towers, whirlpool spas, shower heads, and other bodies of water and may cause legionellosis when these contaminated water droplets are breathed in.

For those who develop legionellosis, symptoms occur between 2 and 10 days after exposure to the bacteria (exposure period) and may include fever, headache, cough, shortness of breath, and muscle aches. People with significant underlying health conditions such as diabetes and chronic obstructive pulmonary disease, those over 50 years old, male, and people who smoke are more likely to develop symptomatic or severe legionellosis after exposure to the bacteria.

In Australia, all cases of legionellosis are notified to the relevant state and territory public health authority by law. If two or more cases are identified as occurring within a limited geographical and time period,

a *Legionella* outbreak may be declared and outbreak investigation undertaken.

An outbreak investigation may draw on several lines of evidence. These include clinical, epidemiological, environmental, and genomic evidence. However, it is noted that many legionellosis outbreaks remain unsolved due to a lack of this evidence.<sup>2</sup> The application of genomic techniques is a more recent phenomenon that has been used to confirm the source of infection in several outbreaks<sup>3,4</sup> although there are limited peer reviewed publications of its successful use in Australia.<sup>5,6</sup>

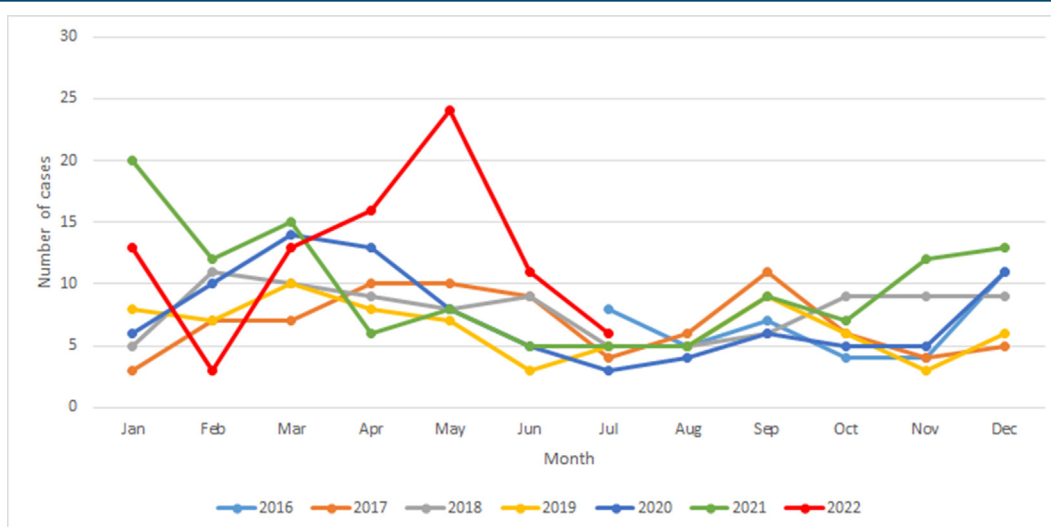
During April and May, 2022 there was a notable increase in notifications of *Legionella pneumophila* in New South Wales with the third largest and largest monthly case counts over the previous 6 years. Eleven of these cases reported attending the Sydney CBD during their exposure period prompting an investigation by the South Eastern Sydney Public Health Unit (SESPHU) (Figure 1). This investigation's objective was to collect and analyse clinical, epidemiological, environmental, and genomic evidence in order to identify and control the source of *Legionella*.

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Figure 1: Legionellosis (*Legionella pneumophila*) notifications in NSW residents, by month of disease onset. July 2016 to July 2022\*.

\*Source - NSW Health Notifiable Conditions Information Management System (NCIMS), Communicable Diseases Branch and Centre for Epidemiology and Evidence, NSW Health.

## Methods

### Case attainment—clinical and epidemiological investigation

A legionellosis case is identified if they test positive to a *Legionella* urinary antigen test. In some circumstances, these cases may also undertake a sputum sample to determine whether any *Legionella* bacteria can be isolated. Once identified, these cases are interviewed using the Communicable Disease Network of Australia *Legionellosis Investigation Form*. This form includes questions around clinical symptoms experienced, risk factors, and environmental exposures 2–10 days prior to symptom onset.

All legionellosis cases who identified visiting the Sydney CBD during their exposure period were notified to SESPBU. SESPBU on identifying this outbreak released a media statement to the general public regarding the outbreak and notified other public health units, hospitals, and general practitioners. Case movements through the CBD were mapped using QGIS v3.24.0, with a 500 m buffer created around these movement locations. Buffers from each case movement were overlaid to refine a likely *Legionella* source area.

### Environmental investigation

An initial environmental investigation area was defined by a 500 m radius around the CBD work location of one of the first legionellosis cases. This investigation area was latter modified as further case location movements were identified.

With 332 cooling water systems identified in the initial investigation area, a desktop review of these cooling water systems was undertaken to identify those systems at greatest risk of *Legionella* contamination. Cooling water systems were classified as high, medium, or low risk based on a review of the cooling water system's current risk management plan (as required under *NSW Public Health Regulation* [2022]); its current audit report; and cleaning, maintenance, and microbial sampling results from the previous 3–6 months.

Physical inspections with water sampling were undertaken on all identified high-risk cooling water systems, cooling water systems at a

case's work location, and medium and low risk cooling water systems that either failed or did not have an audit report. All water samples were analysed for *Legionella*.

Where *Legionella* or other significant bacterial contamination was found in water samples, the person responsible for the cooling water system was ordered to undertake immediate disinfection of the system.

### Genomic investigation

Positive sputum and water samples underwent confirmatory typing and genome sequencing. Sequencing was performed on an Illumina NextSeq, and assembled sequences were genotyped using the *Legionella* sequence-based typing (SBT) scheme.<sup>7</sup> Sequence relatedness and phylogeny was determined using core sequence nucleotide polymorphisms (core SNPs) using snippy<sup>8</sup> and a curated recombination-masked LP1 SBT ST211 reference genome. Available historical ST211 sequences from clinical and environmental isolates were included in the cohort analysis for context.<sup>6</sup>

## Results

### Clinical and epidemiological investigation

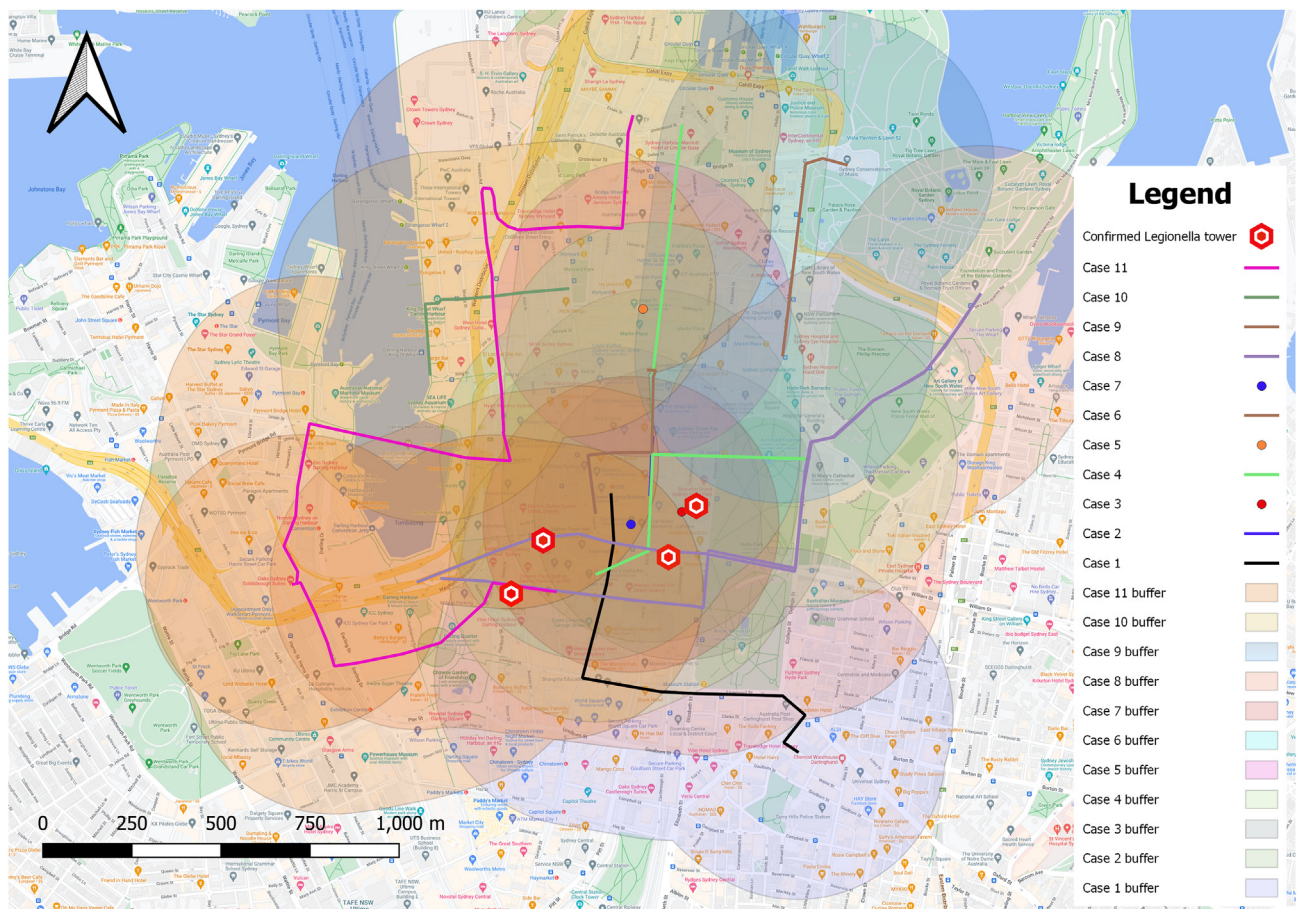
Eleven cases were identified as epidemiologically linked to the Sydney CBD as they had visited or passed through Sydney CBD 2–10 days prior to their onset of symptoms. **Figure 2** shows each case's movements through Sydney CDB, with 500 m buffer zones around these movements.

All eleven cases were positive for *Legionella pneumophila* serogroup 1 urinary antigen. Six cases had a sputum sample collected, of which five were successfully cultured to grow *Legionella* colonies.

**Table 1** displays case demographic, hospitalisation, and prevalence of legionellosis risk factors among cases, with all cases having at least one risk factor.

### Environmental investigation

One hundred and twenty-three cooling water systems were inspected that included all those which were identified as high risk in the

Figure 2: Case movements and 500m buffers in the Sydney CBD, along with *Legionella* positive cooling towers.


investigation area (69), plus 54 medium to low risk cooling water systems that were selected because they were a building visited by a case, had a failed or no risk management plan audit on record, or had a past history of *Legionella* contamination.

One hundred and fifty samples were collected from the 123 cooling water systems inspected. Five samples from four cooling water systems were found to be positive for *Legionella*.

### Genomic investigation

Five clinical isolates and five environmental isolates of *Legionella* were available for genome sequencing and analysis. Three case isolates

Table 1: Case demographic, hospitalisation, and prevalence of legionellosis risk factors.

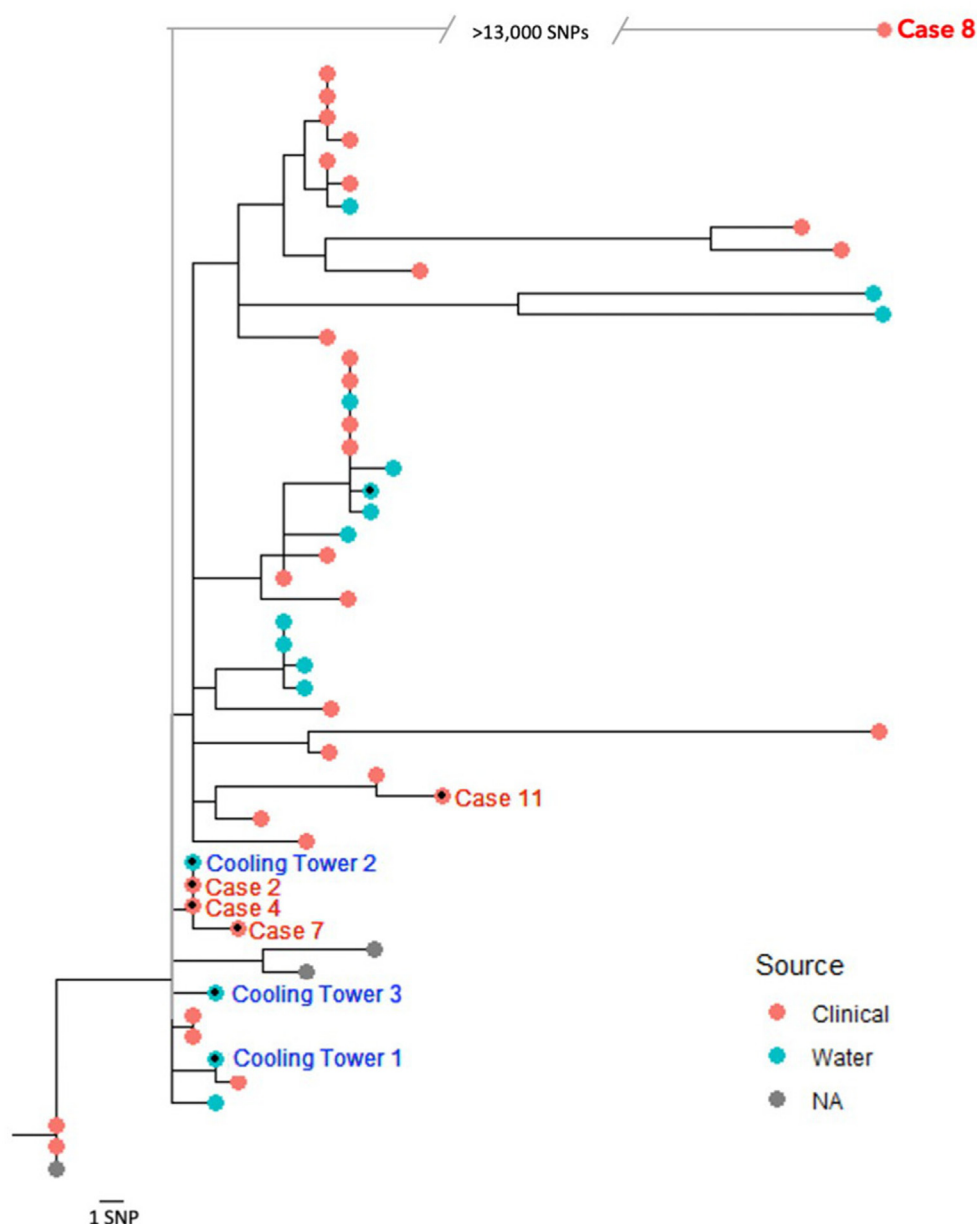
Gender [Male] (N; %)	8	73%
Age [years] (median; Range)	69	46–79
Hospitalisation (N; %)	11	100%
Hospital stay [days] (median; Range)	14	3–56
<b>Risk Factor</b>		
Greater than 50 years old (N; %)	9	82%
Smoker or Ex-smoker (N; %)	6	55%
Chronic disease – respiratory (N; %)	3	27%
Chronic disease – cardiac (N; %)	5	45%
Other chronic disease (diabetes, obesity, hypothyroidism, spina bifida, immunocompromised) (N; %)	7	64%

(from cases 2, 4, and 7) were genomically clustered (being indistinguishable or differing by one SNP) with the *Legionella* isolate recovered from one cooling water system. Another case (Case 11) was infected with a *Legionella* strain similar to that found in cooling water systems in the Sydney CBD over many years<sup>6</sup> but was genetically distinct (more than 12 SNPs) from the cluster (Figure 3). Genomic analysis also revealed that one case (Case 8), although epidemiologically linked to the CBD, was infected with *Legionella* that was genomically different from the Sydney CBD strain.

### Discussion

Through the intersection of clinical, epidemiological, environmental, and genomic evidence, we were able to successfully link three cases in this outbreak to a cooling water system source in Sydney CBD. Further, genomic analysis was able to provide a strong argument for another case's source being in Sydney CBD, owing to a similar strain of *Legionella* to that identified in current and historical samples of *Legionella* from Sydney CBD. Interestingly, it appears one case assigned to this cluster may actually be misclassified. Although the epidemiological evidence aligns with a Sydney CBD exposure, the genomic evidence points to an exposure elsewhere, due to a genomically different isolate from the Sydney CBD strains. Unfortunately, the other six cases in this investigation had no viable sputum culture available for analysis so were unable to be conclusively linked to the cluster. With genomic analysis becoming an

Figure 3: Genome phylogenetic analysis of isolates.



important tool to investigate the sources of legionellosis outbreaks around the world<sup>4,9</sup>, our inability to link these six cases is an important reminder that clinicians, public health units, and microbiologists need to collaborate to recover positive sputum cultures from all patients diagnosed with legionellosis.

We were confident that our investigation met its objectives and the source or sources were contained. Following our investigation, no further cases of legionellosis with exposures in the CBD were reported to SESPHEU.

This investigation has some limitations. Environmental sampling of the cooling water systems occurred after a media release regarding a cluster of legionellosis cases in Sydney CBD. We had evidence that some cooling water systems had been disinfected prior to sampling, meaning these systems would no longer contain *Legionella*, if *Legionella* was present prior to disinfection. This limits the ability to identify all cooling water systems that may have contributed to the

outbreak and the ability to genomically link these water systems samples to cases' samples. However, as the main aim of a public health response is to stop the outbreak by ensuring that all sources of *Legionella* are controlled as quickly as possible, this is an acceptable limitation. Further, for the six cases who did not have sputum samples to allow for genomic analysis, although the epidemiological investigation has linked these six cases to the Sydney CBD it is possible that their *Legionella* source could have been from a number of other places they visited outside the Sydney CBD during their exposure period.

### Implications for public health

This investigation highlights the value of genomic analysis to legionellosis investigations. Obtaining viable sputum cultures from cases diagnosed with legionellosis requires close collaboration between clinicians, public health units and microbiologists.

## Acknowledgements

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