

**ESGLI & ESGPHM: The European Reference laboratory in Public Health on  
*Legionella*: Promoting harmonized Legionnaires' disease diagnostic and  
detection in the EU/EEA**

Remaining questions after the webinar:

- **Are there any updates upcoming for standardised protocols for legionella testing in healthcare facilities and the water distribution infrastructure?**

Lara Payne Hallstrom: No such protocols are produced or published by ECDC.

Camille Jacqueline: If the question is whether there is an SOP for sampling in healthcare facilities, it falls outside of the scope of the EURL-PH-LEGI as it is water management, maybe something like this [document](#) from UK might answer the question (There might be also new [Australian standards](#) of interest).

However, for laboratory testing of water, sludge, and swab samples, the standard is ISO 11731:2017 (Water quality – Enumeration of Legionella). That should also apply to healthcare facilities but countries should apply national norms if they exist.

- **Is the goal standard still the phenotypic approach or are there any countries using molecular approaches or hybrid approaches?**

Lara Payne Hallstrom: EU surveillance data show that phenotypic information is used and reported. Use of molecular approaches is reliant on available materials and methods.

- **How is your new typing scheme compare with the old? Did you face any challenges?**

Camille Jacqueline: The new scheme provides an increased resolution, results in less sample and loci exclusion. There were many challenges, I would defer to the manuscript soon in pre-print (around 20 February 2026) to better describe them.

- **Very interesting but a question of resources to type/sequence 5-10 isolates, so maybe most relevant for outbreak situations?**

Camille Jacqueline: Of course, resources are limited and there are not strong evidences to support systematic sequencing of 5 or more colonies. However in context of outbreak or when discrepancies are observed in the results, it is beneficial to be able to sequence more sequences. However, typing (Oxid, Mabs or Maldi-TOFF) could be done on multiple colonies systematically to identify co-infection with different species or serogroups.