Abstract:
Whole genome sequencing (WGS), due to its high discriminatory power, is routinely being used for source tracking, pathogen surveillance and outbreak investigation. In the food industry, WGS used for source tracking is beneficial to support contamination investigations. Despite its increased use worldwide, no standards or guidelines are available today for its use in outbreak and/or trace-back investigations. The differences between genomes identified by WGS need to be trusted and a validation of all steps of the WGS workflow is therefore recommended. Here we present a validation of an end-to-end WGS workflow for *Listeria monocytogenes* and *Salmonella enterica*, including isolates sub-culturing, DNA extraction, sequencing and bioinformatics analysis. The following performance criteria were assessed: stability, repeatability, reproducibility, discriminatory power and epidemiological concordance. Few SNPs were observed for *L. monocytogenes* and *S. enterica* when comparing isolate sequences derived from the same subculture and between isolates after 10 subcultures. Consequently, the stability of the WGS workflow for *L. monocytogenes* and *S. enterica* was demonstrated despite the few genomic variations that can occur during sub-culturing steps. Repeatability and reproducibility were confirmed. The WGS workflow has a high discriminatory power and confirms genetic relatedness. Additionally, the WGS workflow was able to reproduce published outbreak results, illustrating the epidemiological concordance. The current study proposes a validation approach comprising all steps of a WGS workflow and demonstrates that the workflow can be applied to *L. monocytogenes* or *S. enterica*. This work is one of the first steps to the harmonization of WGS methodologies for source tracking.