Identification of the *L. monocytogenes* strain serotype permits differentiation between important food-borne strains causing clinical disease and provides a gold standard for comparing isolates analysed in different laboratories and different methods. The objective of the serotyping in this EQA is to assess this capacity in the participating laboratories.

The aim of the cluster analyses part of the EQA is to assess the participant's ability to identify clusters of genetically closely related isolates given the fact that a multitude of different laboratory and analytical methods are used as the primary cluster detection approach in Member States. It assesses the participants' ability to reach the correct conclusion, i.e. correctly categorise cluster test isolates, instead of the ability to follow a specific procedure.

ST 1. Serotyping

Laboratories should use their standard procedure for serotyping and correctness of the typing results shall be evaluated by the contractor independently of the method used (either conventional serotyping with antisera or molecular serogrouping using PCR or predicted with WGS). In addition, the contractor should collect the information on the methods and material used for serotyping by each participant and summarise the results in the EQA report (see DL7 and DL8).

ST 2. Molecular typing -based cluster analyses

Laboratories are expected to use their routinely used methods (PFGE, MLVA or/and derived data from the whole genome sequencing (WGS). Laboratories performing WGS can use their own analysis pipeline for the cluster analysis e.g. single nucleotide polymorphism analysis (SNP-based) or whole genome multi locus sequence typing (cgMLST/wgMLST). The contractor shall:

1. Based on pre-defined categorisation evaluate participants' ability to assess genetic relatedness of the provided test isolates and correct identification of the cluster (see DL4 and DL8);
2. Provide a set of extra genomes and asses laboratories' ability to determine whether these are part of the pre-defined cluster (see DL3);
3. Collect and analyse the raw reads and the quality of sequence data and sequence types of the test isolates uploaded by participants when WGS is performed (see DL7 and DL8);
4. Communicate with participants when identifying problems and offer expert advice and trouble-shooting services to the laboratories not able to achieve acceptable level of performance in the EQA exercise (see DL4);
5. Evaluate the correctness and inter-laboratory comparability of the results of the cluster analysis among the participants (see DL8);
6. Collect information about the analytical approach, tools and methods of the WGS-based cluster analyses in participating laboratories and summarise the results in the EQA report (see DL7 and DL8).

Deliverables (DL) in Lot 3- EQA for *L. monocytogenes*

DL1: A letter of invitation to participate in the EQA scheme within one month after the agreed start of the EQA. The letter should include information about the EQA timetable, methods to be used and how the results will be reported.