Listeria EQA-11 2024-2025

Dear Participant
Welcome to the Eleventh External Quality Assessment (EQA-11) scheme for typing of Listeria in 2024-2025.
Please note that most of the fields are required to be filled in before the submission can be completed.
Any comments can be written at the end of the form.
You are always welcome to contact us at list.eqa@ssi.dk.

Please start by filling in your country, your Laboratory name and your LAB_ID.

Available options in this participation form include:

- Fill in your email to receive a link with your answers. The email with the link will be sent after pressing "Finish" in the last slide in the survey.
- If the survey is shut down before finish, the answers are saved and possible return to the survey through the same link.

Note: After pressing "Finish" you will not be able to review your results.

1. Country

(1) □ Austria

(2) □ Australia

(3) □ Belgium

(4) □ Croatia

(4) □ Czech Republic

(5) □ Denmark

(6) □ Finland

(7) □ France

(8) □ Germany

(9) □ Greece

(10) □ Hungary

(11) □ Iceland

(11) □ Ireland

(12) □ Italy

(13) □ Israel

(14) □ Latvia

(15) □ Lithuania

(16) □ Luxembourg

(17) □ Malta

(18) □ New Zealand

(19) □ Norway

(20) □ Portugal

(21) □ Scotland

(22) □ Slovakia

(23) □ Slovenija

(24) □ Spain

(25) □ Sweden

(23) □ The Netherlands

(24) □ Turkey

(25) □ United Kingdom

(26) □ United States

2. Institute name _____
_____

3. Laboratory name _____
_____

4. Laboratory ID: _____
_____

Consisting of country code (two letters) Lab ID on the vial e.g DK_SSI

5. E-mail	_____ _____

6. Listeria EQA-11 Strain ID´s
Please enter the isolate ID(4 digits)

Strain number	Isolate ID
Strain1	_____ _____
Strain2	_____ _____
Strain3	_____ _____
Strain4	_____ _____
Strain5	_____ _____
Strain6	_____ _____
Strain7	_____ _____

Serotyping/grouping of Listeria

7. Would you like to submit serotyping/grouping results?

(1) □ Yes

(2) □ Did not participate in the serotyping/grouping part - Go to 12

8. Submitting results - Serotyping/grouping of Listeria

(1) □ Both molecular and conventional serogrouping/serotyping - Go to 9

(2) □ Molecular serogrouping - Go to 9

(3) □ Conventional serotyping - Go to 11

9. Method used for molecular serogrouping of Listeria

(1) □ PCR based

(2) □ WGS based

10. Results for serotyping/grouping Listeria - Molecular serogrouping please select the serogroup

	IIa	IIb	IIc	IVb	L	Un-typable
Strain1	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐
Strain2	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐
Strain3	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐

Strain4	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐
Strain5	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐
Strain6	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐
Strain7	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐

11. Results for serotyping Listeria - Conventional serotyping please select the serotype

	1/2a	1/2b	1/2c	3a	3b	3c	4a	4ab	4b	4c	4d	4e	7	Autoagglutinable	Un-typeable
Strain1	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐	(9) ☐	(10) ☐	(11) ☐	(12) ☐	(13) ☐	(14) ☐	(15) ☐
Strain2	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐	(9) ☐	(10) ☐	(11) ☐	(12) ☐	(13) ☐	(14) ☐	(15) ☐
Strain3	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐	(9) ☐	(10) ☐	(11) ☐	(12) ☐	(13) ☐	(14) ☐	(15) ☐
Strain4	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐	(9) ☐	(10) ☐	(11) ☐	(12) ☐	(13) ☐	(14) ☐	(15) ☐
Strain5	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐	(9) ☐	(10) ☐	(11) ☐	(12) ☐	(13) ☐	(14) ☐	(15) ☐
Strain6	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐	(9) ☐	(10) ☐	(11) ☐	(12) ☐	(13) ☐	(14) ☐	(15) ☐

Strain7	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐	(9) ☐	(10) ☐	(11) ☐	(12) ☐	(13) ☐	(14) ☐	(15) ☐	

12. Submitting Cluster results

(1) □ Cluster analyses based on PFGE and/or WGS

(2) □ Did not participate in the Cluster part - Go to 103

13. Submitting Cluster results

(1) □ Cluster analysis based on PFGE - Go to 14

(2) □ Do not wish to submit any cluster results based on PFGE analysis - Go to 17

Cluster analysis based on PFGE data

14. Please list the ID for the isolates included in the cluster of closely related isolates detected by PFGE combining ApaI- and AscI-results: please use semicolon (;) to separate the ID´s

_____

15. ApaI - Total number of bands (>33kb) in a cluster strain (use 9999 if not analysed)

_____

16. AscI - Total number of bands (>33kb) in a cluster strain (use 9999 if not analysed)

_____

17. Submitting Cluster results

(1) □ Cluster analysis based on WGS data - Go to 18

(2) □ Do not wish to submit any cluster results based on WGS data - Go to 103

Cluster analysis based on WGS data

18. Please select the analysis used to detect the cluster using WGS
The results of the cluster detection can only be reported once (main analysis). If more than one analysis is performed please report later in this submission

(1) □ SNP based - Go to 20

(2) □ Allele based - Go to 27

(3) □ Other - Go to 19

19. If another analysis is used please describe in detail your approach (including: assembler, number of loci, variant caller, read mapper or reference ID ect.)

_____
_____
_____
_____
_____
_____

20. Please report the used SNP-pipeline
(reference if publicly available or in-house pipeline)

_____

21. Please select the approach used for the SNP analysis

(1) □ Reference based - Go to 22

(2) □ Assembly based - Go to 25

22. Reference genome used:
Preferable use EQA strain0013 (downloaded sequences) as reference. Otherwise indicate Multi-locus Sequence Type (e.g. ST8) and identification of the used reference.

_____

23. Please indicate the read mapper used (e.g. BWA, Bowtie2)

_____

24. Please indicate the variant caller used (e.g. SAMtools, GATK)

_____

25. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

26. Please specify the variant caller used (e.g. NUCMER)

_____

27. Please select tools used for the allele analysis

(1) □ BioNumerics - Go to 29

(2) □ SeqSphere - Go to 29

(3) □ BIGSdb-*Lm* - Go to 29

(4) □ Other - Go to 28

28. If another tool is used please enter here:

_____

29. Please indicate allele calling method:

(1) □ Assembly based and mapping based - Go to 30

(2) □ Only assembly based - Go to 30

(3) □ Only mapping based - Go to 31

30. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

31. Please select scheme used for the allele analysis

(1) □ Applied Maths (wgMLST) - Go to 33

(2) □ Applied Maths (cgMLST/Pasteur) - Go to 33

(3) □ Pasteur (cgMLST) - Go to 33

(4) □ Ruppitsch (cgMLST) - Go to 33

(5) □ Other - Go to 32

32. If another scheme (e.g. in-house) is used, please give a short description

_____
_____
_____
_____
_____
_____

33. Please report the number of loci in the used allelic scheme

_____
_____
_____
_____

_____
_____

Cluster detected by analysis on data derived from WGS

On this page you have to report the results for the cluster detected by the selected analysis (e.g. SNP based). If another additional analysis (e.g. allele based or another SNP based analysis) is performed please report results later, but you will not be asked to submit the ID´s for isolates in the cluster detected with the additional analysis.

34. Please list the ID for the strains included in the cluster of closely related strains detected by WGS: please use semicolon (;) to separate the ID´s

This includes the 7 test strains and the 10 provided sequences (17 in total). For the provided sequences write the numbers like: 0008, 0009, 0010, 0011 ect.

_____
_____
_____
_____
_____
_____

35. Report the strain ID, part of the cluster (yes/no), and SNP distance/allele difference to the strain0013 (reference)

Please use 9999 for not analyzed

	ID	Cluster (Yes/No)	AD/SNP
Strain1	_____	❍ (Yes) ❍ (No)	_____

Strain2	_____	❍ (Yes) ❍ (No)	_____
Strain3	_____	❍ (Yes) ❍ (No)	_____
Strain4	_____	❍ (Yes) ❍ (No)	_____
Strain5	_____	❍ (Yes) ❍ (No)	_____
Strain6	_____	❍ (Yes) ❍ (No)	_____
Strain7	_____	❍ (Yes) ❍ (No)	_____

36. For each ID report: part of the cluster (yes/no), QC status (A/B/C), QC comment and SNP distance /allele difference to the strain0013 (reference)

QC status:
Please select the QC status that fits with your assessment of the strain
A = Acceptable quality, B = Quality only acceptable for outbreak situations (less good quality), C = Not acceptable quality - strain not analyzed

Distance:
Please use 9999 for not analyzed

	Cluster (Yes/No)	QC (A/B/C)	QC comment	AD/SNP
Strain0008	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____

Strain0009	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0010	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0011	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0012	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0013	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0014	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0015	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0016	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0017	❍ (Yes)	❍ (A)	_____	_____

❍ (No) ❍ (B)

❍ (C)

37. (Optional) Would you like to add additional information for the strains? e.g. serotype or sequence type (ST)

(1) ❍ Yes

(2) ❍ No – Go to 38

	Serotype	**Sequence type (ST)**
Strain1	_____	_____
Strain2	_____	_____
Strain3	_____	_____
Strain4	_____	_____
Strain5	_____	_____
Strain6	_____	_____
Strain7	_____	_____
Strain0008	_____	_____

Strain0009	_____	_____
Strain0010	_____	_____
Strain0011	_____	_____
Strain0012	_____	_____
Strain0013	_____	_____
Strain0014	_____	_____
Strain0015	_____	_____
Strain0016	_____	_____
Strain0017	_____	_____

38. Would you like to add results performed with another additional analysis on the data derived from the WGS?
e.g. if SNP based results are submitted you can also report allele based results or results from a second SNP analysis

(1) □ Yes - Go to 39

(2) □ No - Go to 74

39. Please select the additional analysis used on data derived from WGS

(1) □ SNP based - Go to 41

(2) □ Allele based - Go to 48

(3) □ Other - Go to 40

40. If another analysis is used please describe in detail your approach (including: assembler, number of loci, variant caller, read mapper or reference ID ect.)

_____

41. Please report the used SNP-pipeline
(reference if publicly available or in-house pipeline)

_____

42. Please select the approach used for the SNP analysis

(1) □ Reference based - Go to 43

(2) □ Assembly based - Go to 46

43. Reference genome used: (preferable use EQA strain0013, downloaded sequences as reference). Otherwise indicate Multi-locus Sequence Type (e.g. ST8) and isolate ID

_____

44. Please indicate the read mapper used (e.g. BWA, Bowtie2)

_____

45. Please indicate the variant caller used (e.g. SAMtools, GATK)

_____

46. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

47. Please specify the variant caller used (e.g. NUCMER)

_____

48. Please select tool used for the allele analysis

(1) □ BioNumerics - Go to 50

(2) □ SeqSphere - Go to 50

(3) □ BIGSdb-*Lm* - Go to 50

(4) □ Other - Go to 49

49. If another tool is used please list here:

_____

50. Please indicate allele calling method:

(1) □ Assembly based and mapping based - Go to 51

(2) □ Only assembly based - Go to 51

(3) □ Only mapping based - Go to 52

51. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

52. Please select scheme used for the allele analysis

(1) □ Applied Maths (wgMLST) - Go to 54

(2) □ Applied Maths (cgMLST/Pasteur) - Go to 54

(3) □ Pasteur (cgMLST) - Go to 54

(4) □ Ruppitsch (cgMLST) - Go to 54

(5) □ Other - Go to 53

53. If another scheme (e.g. in-house) is used, please give a short description

_____

54. Please report the number of loci in the used allelic scheme

_____

55. Additional analysis on data derived from WGS

Results for an additional cluster analysis.
Reporting allele differences /SNP distances to strain 0016 (as downloaded sequence) (e.g. SNP or Allele based)
Please use 9999 for not analysed

Strain number	Allele differences /SNP distances
Strain1	_____ _____
Strain2	_____ _____

Strain3	_____ _____
Strain4	_____ _____
Strain5	_____ _____
Strain6	_____ _____
Strain7	_____ _____
Strain0008 (as downloaded sequence)	_____ _____
Strain0009 (as downloaded sequence)	_____ _____
Strain0010 (as downloaded sequence)	_____ _____
Strain0011 (as downloaded sequence)	_____ _____
Strain0012 (as downloaded sequence)	_____ _____
Strain0013 (as downloaded sequence)	_____ _____
Strain0014 (as downloaded sequence)	_____ _____

Strain0015 (as downloaded sequence)	_____ _____
Strain0016 (as downloaded sequence)	_____ _____
Strain0017 (as downloaded sequence)	_____ _____

56. Would you like to add results performed with a third analysis on the data derived from the WGS?
e.g. if SNP based results are submitted you can also report allele based results or results from a second SNP analysis

(1) □ Yes - Go to 57

(2) □ No - Go to 74

57. Please select the third analysis used on data derived from WGS

(1) □ SNP based - Go to 59

(2) □ Allele based - Go to 66

(3) □ Other - Go to 58

58. If another analysis is used please describe in detail your approach (including: assembler, number of loci, variant caller, read mapper or reference ID ect.)

_____

59. Please report the used SNP-pipeline
(reference if publicly available or in-house pipeline)

_____

60. Please select the approach used for the SNP analysis

(1) □ Reference based - Go to 61

(2) □ Assembly based - Go to 64

61. Reference genome used:(preferable use EQA strain0013, downloaded sequences as reference) Otherwise indicate Multi-locus Sequence Type (e.g. ST8) and isolate ID

_____

62. Please indicate the read mapper used (e.g. BWA, Bowtie2)

_____

63. Please indicate the variant caller used (e.g. SAMtools, GATK)

_____

64. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

65. Please specify the variant caller used (e.g. NUCMER)

_____

66. Please select tool used for the allele analysis

(1) □ BioNumerics - Go to 68

(2) □ SeqSphere - Go to 68

(3) □ BIGSdb-*Lm* - Go to 68

(4) □ Other - Go to 67

67. If another tool is used please enter here:

_____

68. Please indicate allele calling method:

(1) □ Assembly based and mapping based - Go to 69

(2) □ Only assembly based - Go to 69

(3) □ Only mapping based - Go to 70

69. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

70. Please select scheme used for the allele analysis

(1) □ Applied Maths (wgMLST) - Go to 72

(2) □ Applied Maths (cgMLST/Pasteur) - Go to 72

(3) □ Pasteur (cgMLST) - Go to 72

(4) □ Ruppitsch (cgMLST) - Go to 72

(5) □ Other - Go to 71

71. If another scheme (e.g. in-house) is used, please give a short description

_____

72. Please report the number of loci in the used allelic scheme

_____

73. Third analysis on data derived from WGS

Results for the third cluster analysis. Reporting allele differences /SNP distances to strain0013 (as downloaded sequence) (e.g. SNP or Allele based)
Please use 9999 for not analysed

Strain number	Allele differences /SNP distances
Strain1	_____ _____
Strain2	_____ _____
Strain3	_____ _____
Strain4	_____ _____
Strain5	_____ _____
Strain6	_____ _____
Strain7	_____ _____
Strain0008 (as downloaded sequence)	_____ _____
Strain0009 (as downloaded sequence)	_____ _____
Strain0010 (as downloaded sequence)	_____ _____
Strain0011 (as downloaded sequence)	_____ _____

Strain0012 (as downloaded sequence)	_____ _____
Strain0013 (as downloaded sequence)	_____ _____
Strain0014 (as downloaded sequence)	_____ _____
Strain 0015 (as downloaded sequence)	_____ _____
Strain 0016 (as downloaded sequence)	_____ _____
Strain 0017 (as downloaded sequence)	_____ _____

74. Additional questions to the WGS part

Where was the sequencing performed

(1) □ In own laboratory

(2) □ Externally

75. Protocol used to prepare the library for sequencing:

(1) □ Commercial kits - Go to 76

(2) □ Non-commercial kits - Go to 78

76. Please indicate name of commercial kit:

_____

77. If relevant please list deviation from commercial kit shortly in few bullets:

_____
_____
_____
_____
_____
_____

78. For non-commercial kit please indicate a short summary of the protocol:

_____
_____
_____
_____
_____
_____

79. The sequencing platform used

(1) □ Ion Torrent PGM - Go to 81

(2) □ Ion Torrent Proton - Go to 81

(3) □ Ion S5 XL system - Go to 81

(4) □ Genome Sequencer Junior System (454) - Go to 81

(5) □ Genome Sequencer FLX System (454) - Go to 81

(6) □ Genome Sequencer FLX+ System (454) - Go to 81

(7) □ PacBio RS II - Go to 81

(8) □ PacBio RS - Go to 81

(9) □ HiScanSQ - Go to 81

(10) □ HiSeq 1000 - Go to 81

(11) □ HiSeq 1500 - Go to 81

(12) □ HiSeq 2000 - Go to 81

(13) □ HiSeq 2500 - Go to 81

(14) □ HiSeq 4000 - Go to 81

(15) □ Genome Analyzer Iix - Go to 81

(16) □ MiSeq - Go to 81

(17) □ MiSeq Dx - Go to 81

(18) □ MiSeq FGx - Go to 81

(19) □ MiniSeq - Go to 81

(20) □ ABI SOLiD - Go to 81

(21) □ NextSeq - Go to 81

(22) □ NovaSeq - Go to 81

(23) □ MinION (ONT) - Go to 81

(24) □ Other - Go to 80

80. If another platform is used please list here:

_____

81. Criteria used to evaluate the quality of sequence data.

In this section you can report criteria used to evaluate the quality of sequence data.
Please first reply on the use of 5 selected criteria, which were the most frequently reported by in previous EQAs.
Next you will be asked to report 5 **additional** criteria of your own choice.
For each criteria please also report the threshold or procedure used to evaluated the current criteria.

82. Did you use confirmation of species to evaluate the quality of sequence data?

(1) □ Yes

(2) □ No - Go to 84

83. Procedure used to evaluate confirmation of genus:

_____

84. Did you use coverage to evaluate the quality of sequence data?

(1) □ Yes

(2) □ No - Go to 86

85. Procedure or threshold used for coverage:

_____

86. Did you use Q score (Phred) to evaluate quality of sequence data?

(1) □ Yes

(2) □ No - Go to 88

87. Threshold or procedure used to evaluate Q score (Phred):

_____

88. Did you use genome size to evaluate the quality of sequence data?

(1) □ Yes

(2) □ No - Go to 90

89. Procedure or threshold used for genome size:

_____

90. Did you evaluate the number of good cgMLST loci?

(1) □ Yes

(2) □ No - Go to 92

91. Threshold or procedure used to evaluate the number of good cgMLST loci:

_____

92. ONLY list additional information related to other criteria used to evaluate the quality of sequence data.

Please list up to 5 additional criteria (e.g. N50, read length, contamination)

93. Other criteria used to evaluate the quality of sequence data - additional criteria 1:

_____

94. Threshold or procedure used to evaluate the additional criteria 1:

_____

95. Other criteria used to evaluate the quality of sequence data - additional criteria 2:

_____

96. Threshold or procedure used to evaluate the additional criteria 2:

_____

97. Other criteria used to evaluate the quality of sequence data - additional criteria 3:

_____

98. Threshold or procedure used to evaluate the additional criteria 3:

_____

99. Other criteria used to evaluate the quality of sequence data - additional criteria 4:

_____

100. Threshold or procedure used to evaluate the additional criteria 4:

_____

101. Other criteria used to evaluate the quality of sequence data - additional criteria 5:

_____

102. Threshold or procedure used to evaluate the additional criteria 5:

_____

103.Comment(s):
e.g. remarks to the submission, the data analyses or the laboratory methods

_____
_____
_____
_____
_____
_____

104. Please remember to upload your raw reads to the sFPT site:

https://sit-ftp.statens-it.dk/
Password: EQA_List11_upload

Have you remembered to upload your raw reads?

(1) ❍ Yes

105.You have reached the end of the reporting scheme.
Please note that when you select "Yes" and "Next", your results will be automatically submitted and the reporting form will be locked.
If you wish to change your answers, use "Previous" to navigate backwards.
Upon completion, you will receive a link with your answers.

(1) □ Yes

Thank you for your participation

Thank you for filling out the Submission form for the Listeria EQA-11.

For questions, please contact list.eqa@ssi.dk or phone +45 3268 8341

Remember to press "Finish" to complete submission.

After submission you will recieve a confirmation email with a link to the answers. We highly recommend to save this email.

Important: After pressing "Finish" you will no longer be able to edit or print your information.