ESGMD and ESGEM Survey on a new genome sequencing-reporting form for bacteria

Purpose: The COVID19 pandemic has pushed sequencing capacities across Europe, but also showcased the importance and challenges associated with communicating complex data. A clear, concise, harmonized, and interoperable laboratory report standard for bacterial and viral genomic data will support and facilitate the communication across diagnostic microbiology laboratories, thereby helping clinicians, epidemiologists, public health experts, and microbiologists to better understand complex genomic information.
Together with the **ESCMID study groups** on Genomics and Molecular Diagnostics (**ESGMD**) and Epidemiological Markers (**ESGEM**), we aim to (i) design, (ii) standardize, and (iii) integrate the final reporting recommendations into online data sharing platforms such as the Swiss Pathogen Surveillance Platform (www.spsp.ch). (iv) We aim to publish the results of this survey as a guideline document from ESGMD and ESGEM and a suggestion for a harmonization of bacterial genomic data reporting.
For more information about ESGMD and ESGEM, please visit the following links:
ESGMD: www.escmid.org/research_projects/study_groups/study_groups_g_n/genomic_molecular_diagnostics/
ESGEM: www.escmid.org/research_projects/study_groups/study_groups_a_f/epidemiological_markers/

The following online survey will take an estimated completion time of maximum 10 minutes. The results of this survey will serve as preliminary work to a content-definition workshop, where the reports and content of blocks therein will be defined in more detail. If you provide your contact details, we can inform you about future activities. Ultimately, the results and final report designs will be shared with the research community through an open-access publication and implemented into online platforms such as the Swiss Pathogen Surveillance Platform and beyond.

Please support us with your feedback in this 10-min survey! Press "Next" on the bottom of the page to start the survey.

Detailed background: Many institutions use bacterial whole genome sequencing as a tool for outbreak investigations, pathogen identification, and prediction of antibiotic drug resistance. Microbial genome sequencing generates a lot of information, only some of which is actually used for patient and epidemiological management and thereby it remains unclear (i) which information should be reported, (ii) how this should be reported (e.g. standards), and (iii) in what degree of detail. We have developed the “Swiss Pathogen Surveillance Platform (www.spsp.ch)”, which aims to support this process by standardizing pathogen genomic analysis and reporting across Switzerland. . Clearly, other incentives are developed across many European countries. A more detailed understanding on current laboratory needs and daily practice of data reporting is needed, also in order to rapidly adapt towards changes in epidemiology and technology, reflecting diverse stakeholder requirements.

Methods: Complex data can be presented and visualized in various ways. There is research ongoing in this field and we will apply such principles in designing a new report format, generic for the field of bacterial whole genome sequencing analyses, and which will be shared with public health and diagnostic laboratories to initiate a discussion and harmonization process.
During the survey you will provide helpful information to better understand how you use sequencing data in your daily routine, what is important to you and what is not important to you. Based on these answers, we will organise a workshop to further discuss the content of the blocks and design together a series of pilot reports for further validation.

Survey: Our survey is divided into several parts:
Part I: Professional background, familiarity with reporting concepts and data types.
Part II: Focus on impact of reporting on clinical management (only asked to physicians/clinicians).
Part III: Focus on surveillance (only to epidemiologists, surveillance analysts, and researchers).
Part IV: Design your own short ideal report (through drag and drop with specific blocks)
Part V: Optional: share contact information for more interaction.

Measures to maintain confidentiality:
Data collection from this study will be coded and we would like to collect your email to contact you in case of further questions. The responses will be aggregated for a publication.

Contact for additional feedback on the survey:
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The survey is supported by ESGMD and ESGEM.

ESGMD: www.escmid.org/research_projects/study_groups/study_groups_g_n/genomic_molecular_diagnostics/
ESGEM: www.escmid.org/research_projects/study_groups/study_groups_a_f/epidemiological_markers/

IN01

1. What is your role in diagnosis, treatment, management, and/or surveillance of patients/outbreaks?

(You may select more than one role)

- [ ] Clinical management – I work directly with patients, providing care and/or case management
- [ ] Laboratory work – I work in a laboratory setting where I am involved with lab testing
- [ ] Public surveillance/epidemiology – I work with data to understand patterns in disease occurrence
- [ ] Infection prevention and control (hospital hygiene)
- [ ] Academic Research
- [ ] Other, please specify:

IN04

2. Who is your primary employer?

- [ ] Public Health Organization
- [ ] Private Clinic/Primary Care – e.g. a doctor's office
- [ ] Hospital
- [ ] Academic/research institution
- [ ] Reference laboratory
- [ ] Other, please specify:

IN02

3. Please indicate the highest level of training (if any) you have in the following subject areas:

* By professional experience, we mean collaborating with others on a project

** By continuing education, we mean attending workshops, training sessions, or self-directed learning

	None	Undergrad.	Graduate (MSc and/or PhD)	Professional experience*	Continuing Education**
Molecular Biology, Biochemistry	○	○	○	○	○
Epidemiology	○	○	○	○	○
Biostatistics	○	○	○	○	○
Bioinformatics	○	○	○	○	○
Genomics	○	○	○	○	○
Infectious Diseases	○	○	○	○	○
Clinical Microbiology	○	○	○	○	○

Page 03

FilterClinician

IN03

4. What is your clinical role?

- ○ Physician/Clinician
- ○ Nurse
- ○ Other, please specify:

DT02

5. When you are using laboratory data to diagnose a patient with the help of NGS, you encounter the following challenges:

- [ ] No challenges – the lab data I currently receive is sufficient
- [ ] The lab data I currently receive does not help me to make a diagnosis
- [ ] I would like to receive data faster to make a more timely diagnosis
- [ ] Important results come at different times and/or in different documents
- [ ] I find it difficult to interpret the lab results I receive
- [ ] I am not regular receiving data that would help me to make a diagnosis
- [ ] The lab data I receive is not routinely linked to patient data
- [ ] Other, please specify:

DT01

6. What are the main barriers for improving the efficiency of treatment through the use of molecular laboratory data?

- [ ] I do not encounter any issues
- [ ] Need for additional data
- [ ] Timeliness of results
- [ ] Results provided over multiple unconnected documents
- [ ] Difficultly interpreting lab results
- [ ] Lab data is not routinely provided
- [ ] Lab data is not linked to patient data
- [ ] Other, please specify:

DT03

7. Do you want to know any laboratory or bioinformatics quality metrics that may be associated with that data being reported to you?

- ○ Yes – I always want to have data quality metrics
- ○ No – Data quality results are not relevant, the lab would not release low quality data and I trust their processes
- ○ I don’t know
- ○ Other, please specify:

DT04

8. Do you have any additional comments you wish to make on the use of genomic and molecular data for diagnosis and treatment?

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Surveillance

SU01

9. What data does your institution currently use as part of its surveillance practices?

Items marked with a * are needed for the accreditation of the report.

- [ ] Patient identifiers (Name, age, location)
- [ ] Requester identifiers (Name, contact, copy to etc.)
- [ ] Reviewer identifiers (Name, position etc.)*
- [ ] Type of sample (urine and blood, etc.)
- [ ] Sample collection site (lymph node, peripheral blood draw etc.)
- [ ] Sample collection date
- [ ] Report release date*
- [ ] Interpretation or comments from reviewer
- [ ] Methods used*
- [ ] Laboratory performance measures (Sequence quality, coverage etc.)
- [ ] Culture results
- [ ] Species identification
- [ ] Phenotypic drug susceptibility testing
- [ ] Predicted (in silico) drug susceptibility testing
- [ ] Presence/absence of acquired resistance genes
- [ ] Detection of chromosomal mutations conferring antibiotic resistance
- [ ] Presence / absence of virulence genes
- [ ] Virulence gene profile
- [ ] NGS based cluster assignment
- [ ] Phylogenetic tree
- [ ] cgMLST result
- [ ] other Typing (ribotype, spa-Type, RFLP, MLST)
- [ ] Single Nucleotide Polymorphism/Variant distance from other isolates
- [ ] Other (eg. Species-specific results such as “Tuberculin Skin Test Results”, “Chest X-ray results”, “Acid Fast Bacilli Smear results”, “Interferon Gamma Release Assay (IGRA) results”, etc.). Please specify:

SU02

10. What is the main barrier of using genomic data more routinely as part of surveillance?

- [ ] Data is not consistently accessible
- [ ] Data are not consistently linked to relative patient data
- [ ] It is not clear how this data is useful for surveillance
- [ ] It is not clear how to interpret this data for surveillance purposes
- [ ] Difficulty interpreting lab results
- [ ] Costs
- [ ] Other, please specify:

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Blocks

BL01

11. Please rank the presented sections of a possible NGS-report, assuming all these sections had to be present in the report (note: in the next question, you will have the possibility to indicate how much/little detailed information would actually be needed in each block). Hence, your ranking here only represents your wished order/placement of the sections on a future report.

Please move the sections on the left side to the right side in that order, in which you wished a future NGS-report was organized. Rank n°1 represents the top of the report, n°9 the bottom of the report.

Drug susceptibility/Resistance prediction of the organism	Disclaimer regarding limitations of the analysis	1
	Lineage/Organism (eg. “M. tuberculosis”)	2
Sample Details (eg. patient information, sample type, laboratory technician, etc)	Assay Details (eg. sequencer, method)	3
	Short summary of final results	4
Depth and coverage details (eg. N° of reads mapped, proportion covered, mutation frequency)	Authorization of the analysis/Signature	5
	NGS based Cluster detection (eg. cgMLST or SNPs)	6
		7
		8
		9

BL05

12. Are there any comments, explanations, remarks or inputs you would like to give regarding the report you suggested? Please tell us below:

BL02

13. Below, we present you the same hypothetic blocks again. Please choose how detailed the information should be in each block, so that it suits your everyday work best.

	Block is not needed	Basic information is required	Detailed information is required
Authorization of the analysis	○	○	○
Sample Details (eg. patient information, sample type, laboratory technician, etc)	○	○	○
Lineage/Organism	○	○	○
Short summary of final results	○	○	○
Disclaimer regarding limitations of the analysis	○	○	○
NGS based Cluster detection (eg. cgMLST or SNPs)	○	○	○
Depth and coverage details (eg. N° of reads mapped, proportion covered, mutation frequency)	○	○	○
Drug susceptibility/Resistance prediction	○	○	○
Assay Details (eg. sequencer, method)	○	○	○

14. We presented you various possible blocks for a NGS-report. Are there some more blocks we have not mentioned yet but seem crucial to you that they are included, as well? If yes, please tell us below: BL04

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Contact

EN06

15. Personal information and contact details

You almost made it to the end, thank you very much!

Below you will be asked to provide us some information about yourself and to tell us your email-address. We would be very happy if you did so, in order to contact you on a later stage of our research to discuss the different blocks of the report. This would also make it possible to form working groups based on your answers in the questionnaire. So we could focus on the specific needs you have regarding the report.

EN02

16. Please indicate the geographic location of your working place (eg. city, region, country):

EN03

17. Please indicate how many years of professional experience you have in your field:

- ○ 0-5 years
- ○ 6-10 years
- ○ 11-20 years
- ○ 20+ years

EN08

If you would like to be further updated on our activities and news, please share your contact details with us.

EN07

18. Please tell us your full name:

EN05

19. Please tell us your email-address:

Your email will be handled confidentially and will not be used outside of this questionnaire.

Last Page

Thank you for completing this questionnaire!

We would like to thank you very much for helping us.

Your answers were transmitted, you may close the browser window or tab now.

Eugenio Mutschler, Universität Basel – 2021