

The MicrobeSeq project has been underway now for about half a year and the project is already well under way. In June, we could celebrate that all final signatures are in place. This means that over the next 3 years we will receive 3.7 million Euros to improve WGS based surveillance in Denmark.

We now have a homepage <https://microbeseq.ssi.dk> (Danish) and <https://microbeseqen.ssi.dk> (English). While the homepage currently offers limited information, our future plans include incorporating links to lab protocols and computer codes, sharing news updates, and providing an overview of upcoming events, among other features. We also have a leaflet <https://microbeseq.ssi.dk/-/media/arkiv/subsites/microbeseq/microbeseq-brochure.pdf>.

Laboratory development

On the laboratory side we have two main tracks, one optimizing and standardizing current methods and one involving development and implementation of new methods. In the standardization track, initial work has included the preparation of modernized digital protocols to be shared via an online platform. Also, work has been conducted on quality standards related to laboratory processes of whole genome sequencing workflows. Specifically, a set of bacterial strains will be selected that can act as a positive control set. This work has been necessary to prepare for the first meeting in the dialogue group for laboratory protocols and quality standards, which will take place in November. Here, both initiatives will be presented, and the desired outcome of these initiatives will be discussed. The core NGS laboratory for bacterial pathogen surveillance at SSI is in a situation where it is necessary to modernize protocols and workflows related to whole genome sequencing, and the goal is to collaborate and attempt to establish coordinated knowledge sharing.

For the track regarding implementation of new methods, focus has been on exploration and testing of alternative chemistries for Illumina sequencing. This initiative is both important in terms of mitigating supply chain shortages and cost per sample optimization. Secondly, we are validating long read data generated on the Nanopore platform, including development of automated pipelines for assembly and quality control (QC). It is a priority to be able to use Nanopore data and utilize the flexibility that the platform offers in terms of speed, batch size and read lengths, in the national surveillance going forward. Finally, a separate track focusing on rapid diagnostics using RT-PCR approaches is in development.

IT infrastructure

Work is being made on switching SSI's microbial surveillance analysis platform from the local calc system to the new uGerm system which is located on a private cloud space on Computerome. This has been intended for a while due to the transition between IT providers at SSI but has recently been making bigger strides. This was intended to be done before summer originally, but there has been a bottleneck in work with the system administrators. On the positive side, work has been done to rectify this, primarily with the additional hires of [@Hanne Louise Munkholm Kamp](#) and [@Khemindra Maisrikrod](#) as additional system administrators. The expansion of staff is also required due to the transfer

of system monitoring responsibilities from IT to SSI. The new goal is to get initial users onto the system within a month and have most of the transition completed by the end of the year.

The uGerm system will host the new analysis platform which will be responsible for processing national surveillance samples. This is being built on the Irida platform. The pipelines that comprise surveillance will be implemented into this space. The pipelines will be remade so that they are both open-source and can be installed via conda. This should render accessibility to these tools a lot easier. When the code is available on github, references should be accessible from <https://github.com/ssi-dk/MicrobeSeq-Denmark>, (note: currently the page is empty). The intent is that you can collaborate on this code through the associated github issues. After some initial pipeline work is done, this training can be extended to more groups at SSI and to bioinformaticians at the CMDs if they wish to learn, this is optional. This is in fact a substantial change in how our bioinformaticians are approaching their work and we have been training them in collaborative coding. We hope to be able to update you as we progress on these pipelines and let you know which pipelines will be made available and where you can interact to collaborate on them and discuss topics related to the pipeline.

On the visualization side we have been working with the company behind Microreact <https://microreact.org/> in order to get a local install of it (it is open source) and use it as a visualization tool for genomic epidemiology. We have installed it and are looking at pilot cases for how to show these details off.

Data sharing

The first meeting in Dialogue group 1 regarding analysis results and exchange of data between SSI and the regional laboratories was held on 17th August 2023 as an online meeting. All regions were represented by one or more persons. Each region/CMD presented their state of play regarding the use of WGS, including access to sequencing, analysis, bioinformatics as well as which organisms they already have sequenced for various purposes.

SSI presented a short overview of the plans for MicrobeSeq and the possibilities for exchanging data to/from SSI and the regions. Input to MicrobeSeq was given by the representatives from the CMDs.

It was agreed to have a follow-up meeting in 3-4 months.

Training and courses

The first meeting of the Dialogue Group 3, covering training and demonstration projects, was held as an online meeting on 23th August 2023. KMAs in four out of five regions were represented at the meeting. The content, format and style of training sessions were discussed. There was a preference for attending several brief live (and recorded) modules that included knowledge sharing between the KMAs and SSI colleagues. It was proposed to have dialogue meetings on quality parameters and thresholds between the KMAs and SSI as early as possible, in order to align the approaches at local and national levels to allow collaboration and build trust. There was also an interest in receiving bioinformatics training

for non-bioinformatician members of staff in the regions. Moreover, WGS-based outbreak investigations, sample flow and sharing of WGS-data in the public domain were suggested as topics for future training.

Invitations have been sent out to an online knowledge-sharing meeting regarding quality of WGS data. The event will take place on 12th December 2023. If you wish to attend, but have not received an invitation, please contact Camilla Coia (CMWI@ssi.dk).