



Aalborg Universitet

AALBORG UNIVERSITY
DENMARK

From days to hours

Development and implementation of metagenomic DNA- sequencing in clinical microbiology diagnostics

Nielsen, Morten Eneberg; Søgaard, Kirstine Kobberøe; Nielsen, Hans Linde; Albertsen, Mads

Publication date:
2021

[Link to publication from Aalborg University](#)

Citation for published version (APA):

Nielsen, M. E., Søgaard, K. K., Nielsen, H. L., & Albertsen, M. (2021). *From days to hours: Development and implementation of metagenomic DNA- sequencing in clinical microbiology diagnostics*. Abstract from Danish Microbiological Society congress 2021, Copenhagen, Denmark.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal -

Take down policy

If you believe that this document breaches copyright please contact us at vbn@aub.aau.dk providing details, and we will remove access to the work immediately and investigate your claim.

From days to hours: Development and implementation of metagenomic DNA-sequencing in clinical microbiology diagnostics

Morten Eneberg Nielsen¹, Kirstine Kobberøe Søgaaard², Hans Linde Nielsen², Mads Albertsen¹

¹*Aalborg University, Center for Microbial Communities, Dept. of Chemistry and Bioscience, Aalborg, Denmark*

²*Aalborg University Hospital, Dept. of Clinical Microbiology, Aalborg, Denmark*

The gold standard of clinical microbiology diagnostics is to culture the pathogen, which takes 1-3 days and has poor sensitivity. Due to the long turnaround time, critically ill patients are administered empiric broad-spectrum antibiotics prior to pathogen identification and an estimated ~20% of patients receive ineffective treatment causing excess mortality. The wide deployment of broad-spectrum antibiotics is also the main reason for the development of multi resistant bacteria, a health crisis predicted by WHO to cause 20% of all deaths in 2050 if there is no change in our use of antibiotics.

To overcome the limitations of current methods, we are exploring the use of DNA sequencing on the MinION platform for pathogen identification in critically ill hospitalised patients. This has the potential to revolutionise clinical microbiology diagnostics by lowering turnaround times from multiple days to <6 hours, providing medical doctors with the basis for a more informed choice of treatment. We will utilise methods developed for archaeogenetics (the study of ancient DNA) to enrich microbial DNA with the aim of obtaining higher sensitivity at a reduced cost. Furthermore, we will use methods from machine learning to separate DNA profiles of diseased from that of healthy individuals to increase analysis specificity.