

DNAPROKON: 16S rRNA gene sequencing as a tool for process control in the food industry

Anne Schmidt-Høier (anho@dti.dk), Nanna Bygvraa Svenningsen (nbs@dti.dk), Anette Granly Koch (aglk@dti.dk)

INTRODUCTION

16S rRNA gene sequencing provides faster and much more detailed information compared to traditional microbiological tests, resulting in knowledge on the microbial composition in products and at production sites. This allows the producer to act and ensure optimal shelf life and quality.

Data management is a challenge and providing the producer with user friendly software for assessment of data is the key to ensure easy and appropriate use of the results.

AIM

To demonstrate the use of 16S rRNA gene sequencing as a process control tool in the meat industry and to create a software system that can support the end user in the data analysis.

CONCLUSION

The project has demonstrated that 16S rRNA gene sequencing has the potential for the use as a process control tool in the food industry for:

- fast identification of bacteria causing spoilage
- identification of spoilage bacteria in freshly produced products and production environment

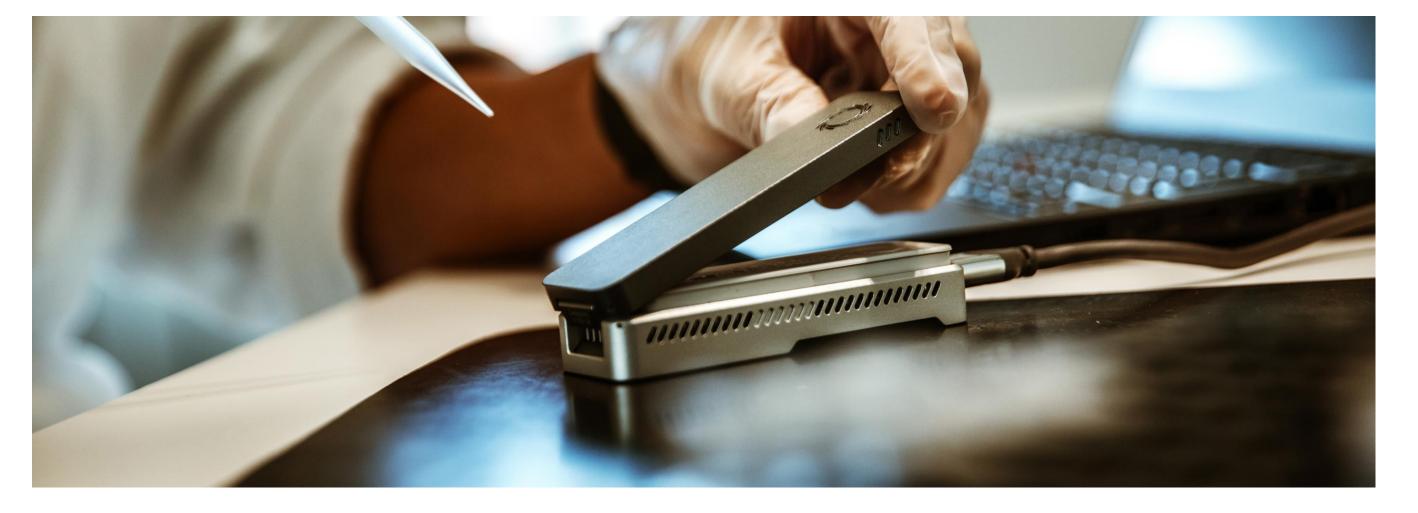


Figure 1: MinION device from Oxford Nanopore Technologies used for sequencing

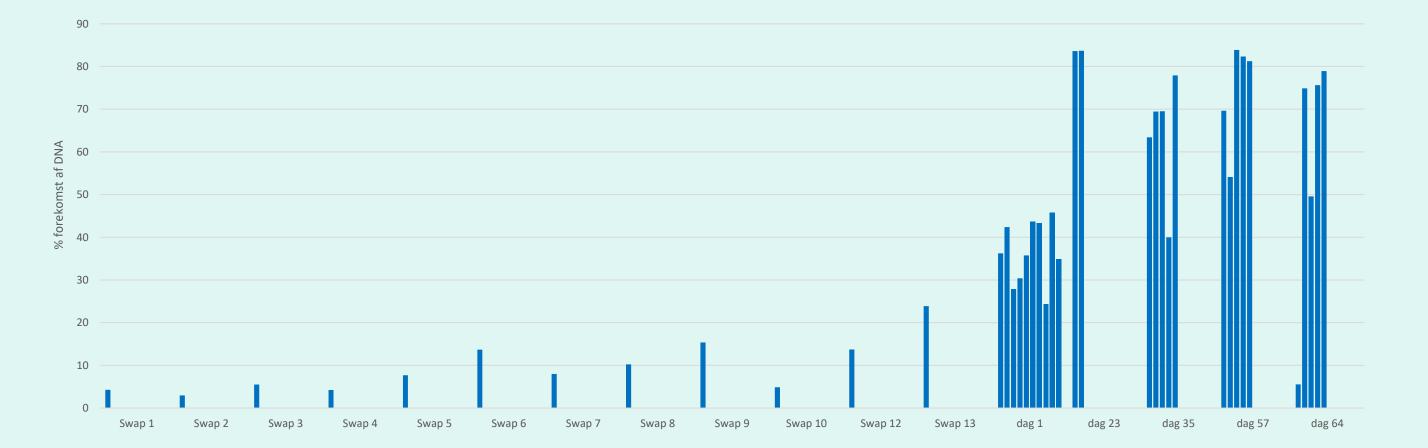
EASY-TO-USE INTERFACE

The interface that end users see should be intuitive and data should be easy to interpret.

celerSe	Data upload & summary		Heatmap and quantification		Process control		L Download							
Heatmap	<unassigned>; <unassigned>-</unassigned></unassigned>	0.2	0.3	83.9	98.4	61.2	99.5	80.8	56.8	0.7	57	100	0.7	5.6
Filter samples:														
Choose your type of filter	Pseudomonadaceae; Pseudomonas	93.3	66.1	0.3	0.1	7.7	0.2	4	2.8	2.6	7.2	0	55.4	3.1
Choose your samples:	Listeriaceae; Brochothrix-	5.5	33.5	1.1	0	1.9	0.1	0.8	0.7	0.1	7.1	0	41.7	71.8
2023_07_10 •	Thermoactinomycetaceae; Laceyella-	o	0	14.5	1.2	23.4	0.1	14.4	35.6	0.6	23.3	D	ū.1	19.2
Sort x-axis according to:	Staphylococcaceae; Staphylococcus-	o	0	٥	0	0	٥	o	0	19	O	D	0	٥
Other variables:	Enterobacteriaceae; Salmonella	0	0	٥	0.2	3.8	٥	0	0	11.8	1.8	0	0	0
Choose variable 1	Listeriaceae; Listeria-	0	0	٥	0	0	0	0	0.7	16.7	0	0	0	0
no plot	Enterococcaceae; Enterococcus-	0	0	0.1	0	0	0.1	0	2.1	12.7	1.8	0	0	0
no plot 🔹	Lactobacillaceae; Limosilactobacillus-	0	ō	٥	0	0	0	0	0.7	13.9	O	o	Ø	0
Adjust heatmap:	Bacillaceae; Bacillus	0	0	•	o	0	0	o	o	14,4	D	D	o	O
Number of top lineages	Remaining taxa (110)-	0.9	0.1	0	0	1.9	0.1	o	0.7	7.5	1.8	D	2	0.3
1 4 7 33 13 38 39 22 28 28 30 Choose Taxonomy levels Level 01		- Ogeb bendrow	- Option dago	-test peat-	-teid_pear_t	-tred_post_it	'uden_peat*	-tree_part_i	- tree _ past-	disorted pare	n Jan daşır.	H. Josef, dagel -	turbir efer-	of tumbles_for-

SAMPLES FROM PRODUCT AND ENVIRONMENT

Spoilers identified in products were found at the same production site during a 2-year study.



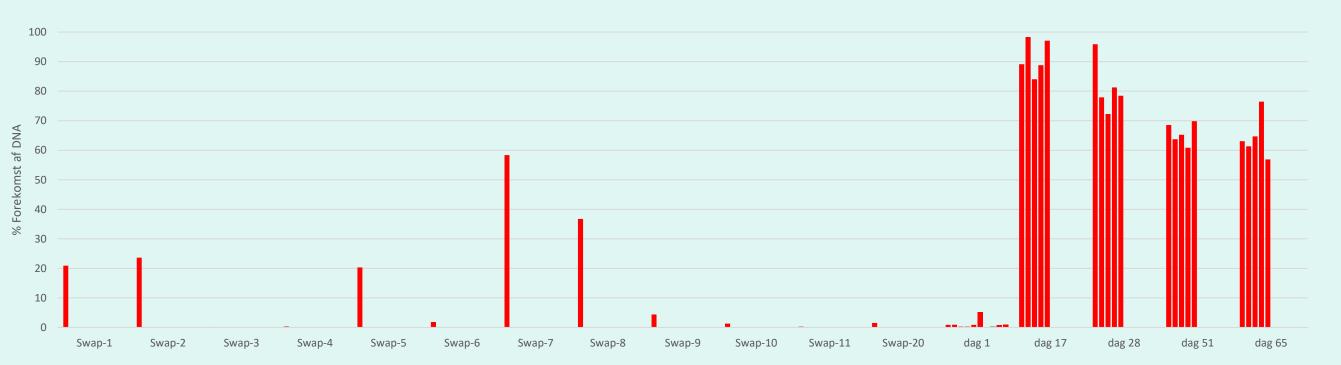




Figure 2: User interface showing the bacterial composition of food samples and environment in a production company

Figure 3: Two examples of bacteria present in a product at different days of storage and the presence of the same bacteria in swaps from the corresponding production sites.

ACKNOWLEDGEMENTS

This work was supported by grants from the Green Development and Demonstration Programme (GUDP), Danish Agricultural Agency in the Ministry of Food, Agriculture and Fisheries; from the Danish Technological Institutes performance contract 2021-2024, entered with the Danish Agency for Higher Education and Science, under The Ministry of Higher Education and Science Denmark and from the Danish Pig Levy Fund, to whom we are grateful.



 Anne Schmidt-Høier
 Gregersensvej 9

 Consultant
 DK-2630 Taastrup

 M anho@teknologisk.dk
 Tel. +45 72 20 20 00

 T +45 7220 1728
 www.DMRI.COM

Food innovation for the future



DANISH TECHNOLOGICAL INSTITUTE