

Tue Kjærsgaard Nielsen
Tenure Track Adjunkt
Microbial Ecology and Biotechnology
Postadresse:
Thorvaldsensvej 40
1871
Frederiksberg C
E-mail: tkn@plen.ku.dk
Telefon: +4535324188
Hjemmeside: <https://plen.ku.dk/forskning/mikrobiel-oekologi-og-bioteknologi/>

Kort præsentation

About me:

I am a molecular microbiologist with a special interest in 3rd generation sequencing (Nanopore) and bioinformatics. I apply these methods to study how mobile genetic elements (MGEs) affect microbial evolution. This includes important traits such as resistance to antibiotics, degradation of xenobiotics, and virulence traits. I enjoy devising new ways of utilizing state-of-the-art technologies and methods.

Current research topics:

Improving the accuracy of antibiotic resistance prediction by analyzing the genetic context of antibiotic resistance genes.

Investigating how non-resistance genes become resistance determinants by interactions with MGEs.

Detecting and analyzing exotic DNA modifications of bacteriophages using Nanopore sequencing.

Virulence traits of plant pathogens associated with MGEs.

Detection and quantification of the activity of MGEs in single bacterial genomes using new lab and bioinformatics techniques.

Teaching and supervision:

Lecturer and co-organizer on MSc course "Applied Microbiology" LBIK10180U

Lecturer on courses "Synthetic Biology" LBIK10207U and "Microbiology" NPLB14012U

Organizer and teacher on courses on DNA/RNA extraction, sequencing, qPCR, and bioinformatics at Zealand Academy of Technologies and Business.

Supervisor of MSc, BSc, and project students.

Previous organizer and main teacher on PhD courses in microbial bioinformatics.

Key words:

bioinformatics, antibiotic resistance genes, mobile genetic elements, 3rd generation sequencing, Nanopore, Illumina, bacteriophages, plasmids, xenobiotics, antibiotics.

If you are interested in working with me on your BSc or MSc thesis project or wish to collaborate on future projects please feel free to contact me at tkn@plen.ku.dk.

Uddannelse

Miljøvidenskab, PhD, Department of Environmental Science, Aarhus University

Dimissionsdato: 16 jun. 2017

Biologi, Kandidatgrad, Institute of Biology, University of Copenhagen, Copenhagen

Dimissionsdato: 14 maj 2013

Biologi, Bachelorgrad, Institute of Biology, University of Copenhagen, Copenhagen

Dimissionsdato: 2 sep. 2010

Ansættelse

Tenure Track Adjunkt

Microbial Ecology and Biotechnology

Københavns Universitet

Frederiksberg C

1 maj 2019 → nu

Publikationer

A novel *Queuovirinae* lineage of *Pseudomonas aeruginosa* phages encode dPreQ₀ DNA modifications with a single GA motif that provide restriction and CRISPR Cas₉ protection *in vitro*

Olsen, Nikoline S., Nielsen, Tue Kjærgaard, Cui, L., Dedon, P., Neve, H., Hansen, Lars Hestbjerg & Kot, Witold, 2023, I: Nucleic Acids Research. 51, 16, 14 s.

Complete Genome Sequence of *Sphingopyxis* sp. Strain PET50, a Potential Polyethylene Terephthalate (PET)-Degrading Bacterium Isolated from Compost

Lago-Maciel, A., Nielsen, Tue Kjærgaard, Jensen, K., Nicolaisen, Mette Haubjerg & Hennessy, Rosanna Catherine, 2023, I: Microbiology Resource Announcements. 12, 1, 2 s., e0097022.

Detection of nucleotide modifications in bacteria and bacteriophages: Strengths and limitations of current technologies and software

Nielsen, Tue Kjærgaard, Forero Junco, Laura Milena, Kot, Witold, Moineau, S., Hansen, Lars Hestbjerg & Riber, Leise, 2023, I: Molecular Ecology. 32, 6, s. 1236-1247 12 s.

Draft Genome Sequences of Phytase Active Endophytic and Epiphytic *Erwinia gerundensis* Isolated from Wheat (*Triticum aestivum*) Seeds

Sølvé, Jonathan, Nielsen, Tue Kjærgaard, Nicolaisen, Mette Haubjerg & Bak, Frederik, 2023, I: Microbiology Resource Announcements. 12, 1, 3 s., e0107322.

Four novel *Curtobacterium* phages isolated from environmental samples

Alanin, K. W. S., Olsen, Nikoline S., Djurhuus, Amaru Miranda, Carstens, Alexander Byth, Nielsen, Tue Kjærgaard, Rothgardt, M. M., Russel, A. M., Wagner, N., Lametsch, Rene, Bak, Frederik, Hennessy, Rosanna Catherine, Nicolaisen, Mette Haubjerg, Hansen, Lars Hestbjerg & Kot, Witold, 2023, I: Archives of Virology. 168, 3

Genetic rearrangements in *Pseudomonas amygdali* pathovar *aesculi* shape coronatine plasmids

Nielsen, Tue Kjærgaard, Winther-Have, Caroline Sophie W, Thomsen, Iben Margrete, Jackson, R. W., Rabiey, M., Hennessy, Rosanna Catherine, Bak, Frederik, Kot, Witold, Nicolaisen, Mette Haubjerg, Carstens, Alexander Byth & Hansen, Lars Hestbjerg, 2023, I: Infection, Genetics and Evolution. 113, 10 s., 105486.

Intestinal epigenotype of Atlantic salmon (*Salmo salar*) associates with tenacibaculosis and gut microbiota composition

Hansen, Søren Blikdal, Bozzi, D., Mak, Sarah Siu Tze, Clausen, C. G., Nielsen, Tue Kjærgaard, Kodama, M., Hansen, Lars Hestbjerg, Gilbert, M Thomas P & Limborg, Morten Tønberg, 2023, I: Genomics. 115, 3, 9 s., 110629.

Three novel *Erwinia billingiae* phages isolated from organic waste represent three new genera

Alanin, K. W. S., Olsen, Nikoline S., Djurhuus, Amaru Miranda, Carstens, Alexander Byth, Nielsen, Tue Kjærgaard, Wagner, N., Lametsch, Rene, Bak, Frederik, Hennessy, Rosanna Catherine, Nicolaisen, Mette Haubjerg, Kot, Witold & Hansen, Lars Hestbjerg, 2023, I: Archives of Virology. 168, 7 s., 71.

Widespread and largely unknown prophage activity, diversity, and function in two genera of wheat phyllosphere bacteria

Dougherty, Peter Erdmann, Nielsen, Tue Kjærgaard, Riber, Leise, Lading, H. H., Forero Junco, Laura Milena, Kot, Witold, Raaijmakers, J. M. & Hansen, Lars Hestbjerg, 2023, I: ISME Journal. 17, 12, s. 2415-2425

Antibiotic resistance genes are differentially mobilized according to resistance mechanism

Nielsen, Tue Kjærgaard, Browne, Patrick Denis & Hansen, Lars Hestbjerg, 2022, I: GigaScience. 11, 17 s., giac072.

Complete Genome Sequence and Benzophenone-3 Mineralisation Potential of *Rhodococcus* sp. USK10, A Bacterium Isolated from Riverbank Sediment

Martin, J. D., Krüger, U. S., Zervas, A., Schostag, M., Nielsen, Tue Kjærgaard, Aamand, J., Hansen, Lars Hestbjerg & Ellegaard-Jensen, L., 2022, I: Applied Microbiology. 2, s. 104-112 9 s.

Muskoxen homogenise soil microbial communities and affect the abundance of methanogens and methanotrophs

Aggerbeck, M. R., Nielsen, Tue Kjærgaard, Mosbacher, J. B., Schmidt, N. M. & Hansen, Lars Hestbjerg, 2022, I: Science of the Total Environment. 827, 9 s., 153877.

The *Bacillus cereus* Strain EC9 Primes the Plant Immune System for Superior Biocontrol of *Fusarium oxysporum*
Madriz Ordenana, Kenneth, Pazarlar, S., Jørgensen, Hans Jørgen Lyngs, Nielsen, Tue Kjærgaard, Zhang, Y., Nielsen, K. L., Hansen, Lars Hestbjerg & Thordal-Christensen, Hans, 2022, I: *Plants*. 11, 5, 19 s., 687.

A non-antifungal rhizobacterium stimulates plant immunity to protect tomato and Kalanchoe against *Fusarium oxysporum* and wheat against *Zymoseptoria tritici*

Madriz Ordenana, Kenneth, Pazarlar, Sercan, Jørgensen, Hans Jørgen Lyngs, Nielsen, Tue Kjærgaard, Nielsen, K. L., Zhang, Y. & Thordal-Christensen, Hans, 2021. 1 s.

Complete Genome Sequence of *Paenibacillus* sp. Strain 37, a Plant Growth-Promoting Bacterium Isolated from the Rhizosphere of *Abies nordmanniana* (Nordmann Fir)

Garcia-Lemos, A. M., Hennessy, Rosanna Catherine, Nielsen, Tue Kjærgaard, Hansen, Lars Hestbjerg & Nicolaisen, Mette Haubjerg, 2021, I: *Microbiology Resource Announcements*. 10, 8, 2 s.

Complete Genome Sequence of a Novel *Dyadobacter* sp. Strain, NIV53, Isolated from 2-Meter Deep Subsurface Sediment

Bak, Frederik, Henriksen, Alexander Pil, Nielsen, Tue Kjærgaard & Nicolaisen, Mette Haubjerg, 2021, I: *Microbiology resource announcements*. 10, 44, 2 s., e0075421.

Complete Genome Sequence of the Cytokinin-Producing Biocontrol Strain *Pseudomonas fluorescens* G20-18

Nielsen, Tue Kjærgaard, Mekureyaw, M. F., Hansen, Lars Hestbjerg, Nicolaisen, Mette Haubjerg, Roitsch, Thomas Georg & Hennessy, Rosanna Catherine, 2021, I: *Microbiology Resource Announcements*. 10, 30, 2 s.

Metaviromes Reveal the Dynamics of *Pseudomonas* Host-Specific Phages Cultured and Uncultured by Plaque Assay

Alanin, K. W. S., Forero Junco, Laura Milena, Jørgensen, J. B., Nielsen, Tue Kjærgaard, Rasmussen, Morten Arendt, Kot, Witold & Hansen, Lars Hestbjerg, 2021, I: *Viruses*. 13, 6, 21 s.

The complete genome of 2,6-dichlorobenzamide (BAM) degrader *Aminobacter* sp. MSH1 suggests a polyploid chromosome, phylogenetic reassignment, and functions of plasmids

Nielsen, Tue Kjærgaard, Horemans, B., Lood, C., T'Syen, J., van Noort, V., Lavigne, R., Ellegaard-Jensen, L., Hylling, Ole, Aamand, J., Springael, D. & Hansen, Lars Hestbjerg, 2021, I: *Scientific Reports*. 11, 12 s., 18943.

Bone biodeterioration - The effect of marine and terrestrial depositional environments on early diagenesis and bone bacterial community

Eriksen, A. M. H., Nielsen, Tue Kjærgaard, Matthiesen, H., Carøe, C., Hansen, Lars Hestbjerg, Gregory, D. J., Turner-Walker, G., Collins, Matthew James & Gilbert, M Thomas P, 2020, I: *PLoS ONE*. 15, 10 October, 24 s., e0240512.

Detection of preQ₀ deazaguanine modifications in bacteriophage CAjan DNA using Nanopore sequencing reveals same hypermodification at two distinct DNA motifs

Kot, Witold, Olsen, Nikoline S., Nielsen, Tue Kjærgaard, Hutinet, G., de Crecy-Lagard, V., Cui, L., Dedon, P. C., Carstens, Alexander Byth, Moineau, S., Swairjo, M. A. & Hansen, Lars Hestbjerg, 2020, I: *Nucleic Acids Symposium Series*. 48, 18, s. 10383-10396 14 s.

GC bias affects genomic and metagenomic reconstructions, underrepresenting GC-poor organisms

Browne, Patrick Denis, Nielsen, Tue Kjærgaard, Kot, Witold, Aggerholm, A., Gilbert, M Thomas P, Puetz, Lara Christine, Rasmussen, M., Zervas, A. & Hansen, Lars Hestbjerg, 2020, I: *GigaScience*. 9, 2, 14 s.

Land use as a driver for protist community structure in soils under agricultural use across Europe

Santos, S. S., Schöler, A., Nielsen, Tue Kjærgaard, Hansen, Lars Hestbjerg, Schloter, M. & Winding, A., 2020, I: *Science of the Total Environment*. 717, 137228.

Metagenomic analysis of planktonic riverine microbial consortia using nanopore sequencing reveals insight into river microbe taxonomy and function: [incl. Erratum]

Reddington, K., Eccles, D., O'Grady, J., Drown, D. M., Hansen, L. H., Nielsen, T. K., Ducluzeau, A-L., Leggett, R. M., Heavens, D., Peel, N., Snutch, T. P., Bayega, A., Oikonomopoulos, S., Ragoussis, J., Barry, T., van der Helm, E., Jolic, D., Richardson, H., Jansen, H., Tyson, J. R. & 2 flere, Jain, M. & Brown, B. L., 2020, I: *GigaScience*. 9, 6, 12 s., 053.

Potential Rhodopsin- and Bacteriochlorophyll-Based Dual Phototrophy in a High Arctic Glacier

Zeng, Y., Chen, X., Madsen, A. M., Zervas, A., Nielsen, Tue Kjærgaard, Andrei, A., Lund-Hansen, L. C., Liu, Y. & Hansen, Lars Hestbjerg, 2020, I: *mBio*. 11, 6, 22 s., e02641-20.

Releasing the microbes from old bones: the effect of different DNA extraction protocols on microbial community profiling

Eriksen, A. M. H., Puetz, Lara Christine, Rocha, C., Nielsen, Tue Kjærgaard, Hansen, Lars Hestbjerg & Gilbert, M Thomas P, 2020, I: *STAR: Science & Technology of Archaeological Research*. 6, 1, s. 1-15 15 s.

Complete Genome Sequences of Highly Arsenite-Resistant Bacteria *Brevibacterium* sp. Strain CS2 and *Micrococcus luteus* AS2

Sher, S., Rehman, A., Hansen, Lars Hestbjerg & Nielsen, Tue Kjærgaard, 2019, I: *Microbiology Resource Announcements*. 8, 31, 2 s., e00531-19.

Expanding the biodiversity of *Oenococcus oeni* through comparative genomics of apple cider and kombucha strains

Lorentzen, M. P., Campbell-Sills, H., Jorgensen, T. S., Nielsen, Tue Kjærgaard, Coton, M., Coton, E., Hansen, L. & Lucas, P. M., 2019, I: *BMC Genomics*. 20, 330.

Inter-laboratory testing of the effect of DNA blocking reagent G2 on DNA extraction from low-biomass clay samples

Jacobsen, C. S., Nielsen, T. K., Vester, J. K., Stougaard, P., Nielsen, J. L., Voriskova, J., Winding, A., Baldrian, P., Liu, B., Frostegard, A., Pedersen, D., Tveit, A. T., Svenning, M. M., Tebbe, C. C., Ovreas, L., Jakobsen, P. B., Blazewicz, S. J., Hubablek, V., Bertilsson, S., Hansen, L. H. & 4 flere, Cary, S. C., Holben, W. E., Ekelund, Flemming & Bælum, J., 2018, I: *Scientific Reports*. 8, s. 1-6 6 s., 5711.

Mind the gut: genomic insights to population divergence and gut microbial composition of two marine keystone species

Fietz, K., Hintze, C. O. R., Skovrind, Mikkel, Nielsen, Tue Kjærgaard, Limborg, Morten Tønsberg, Krag, M. A., Palsboll, P. J., Hansen, L. H., Møller, Peter Rask & Gilbert, M Thomas P, 2018, I: *Microbiome*. 6, 16 s., 82.

The Genome of BAM-degrading *Aminobacter* sp. MSH1 with Several Low Copy Plasmids

Nielsen, Tue Kjærgaard, Hylling, Ole & Ellegaard-Jensen, L., 2018, 12 s.

Soil DNA extraction procedure influences protist 18S rRNA gene community profiling outcome

Santos, S. S., Nunes, I. M., Nielsen, Tue Kjærgaard, Jacquioid, S. J. A., Hansen, L. H. & Winding, A., jul. 2017, I: *Protist*. 168, 3, s. 283-293 11 s.

Degradation of mecoprop in polluted landfill leachate and waste water in a moving bed biofilm reactor

Escolà Casas, M., Nielsen, Tue Kjærgaard, Kot, Witold, Hansen, Lars Hestbjerg, Johansen, A. & Bester, K., 2017, I: *Water Research*. 121, s. 213-220

Evolution of Sphingomonad Gene Clusters Related to Pesticide Catabolism Revealed by Genome Sequence and Mobilomics of *Sphingobium herbicidovorans* MH

Nielsen, Tue Kjærgaard, Rasmussen, M., Demanèche, S., Cecillon, S., Vogel, T. M. & Hansen, Lars Hestbjerg, 2017, I: *Genome Biology and Evolution*. 9, 9, s. 2477-2490

The first characterized phage against a member of the ecologically important sphingomonads reveals high dissimilarity against all other known phages

Nielsen, Tue Kjærgaard, Carstens, A. B., Browne, P., Lametsch, Rene, Neve, H., Kot, Witold & Hansen, Lars Hestbjerg, 2017, I: *Scientific Reports*. 7, 10 s., 13566.

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Long, M., Nielsen, Tue Kjærgaard, Leisner, Jørgen, Hansen, L. H., Shen, Z. X., Zhang, Q. Q. & Li, A., sep. 2016, I: F E M S Microbiology Letters. 363, 17, 8 s., 190.

Establishment of Bacterial Herbicide Degraders in a Rapid Sand Filter for Bioremediation of Phenoxypropionate-Polluted Groundwater

Feld, L., Nielsen, Tue Kjærgaard, Hansen, Lars Hestbjerg, Aamand, J. & Albers, C. N., 2016, I: Applied and Environmental Microbiology. 82, 3, s. 878-887

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Comparison of three DNA extraction methods for recovery of soil protist DNA

Santos, S. S., Nielsen, Tue Kjærgaard, Hansen, L. H. & Winding, A., 2015, I: Journal of Microbiological Methods. 115, s. 13-19 7 s.

Draft Genome Sequence of Isoproturon-Mineralizing *Sphingomonas* sp. SRS2, Isolated from an Agricultural Field in the United Kingdom

Nielsen, Tue Kjærgaard, Sørensen, S. R. & Hansen, Lars Hestbjerg, 2015, I: Genome Announcements. 3, 3, 2 s.

Draft genome sequence of MCPA-degrading *Sphingomonas* sp. strain ERG5, isolated from a groundwater aquifer in Denmark

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