Microflora Danica

Jordens mikroliv: Kortlægning i landbrugjorden

Per Halkjær Nielsen

CENTER FOR MICROBIAL COMMUNITIES

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Vi er gæster i mikrobernes verden!


Biotechnology


Nutrient cycles


Global warming


Human health

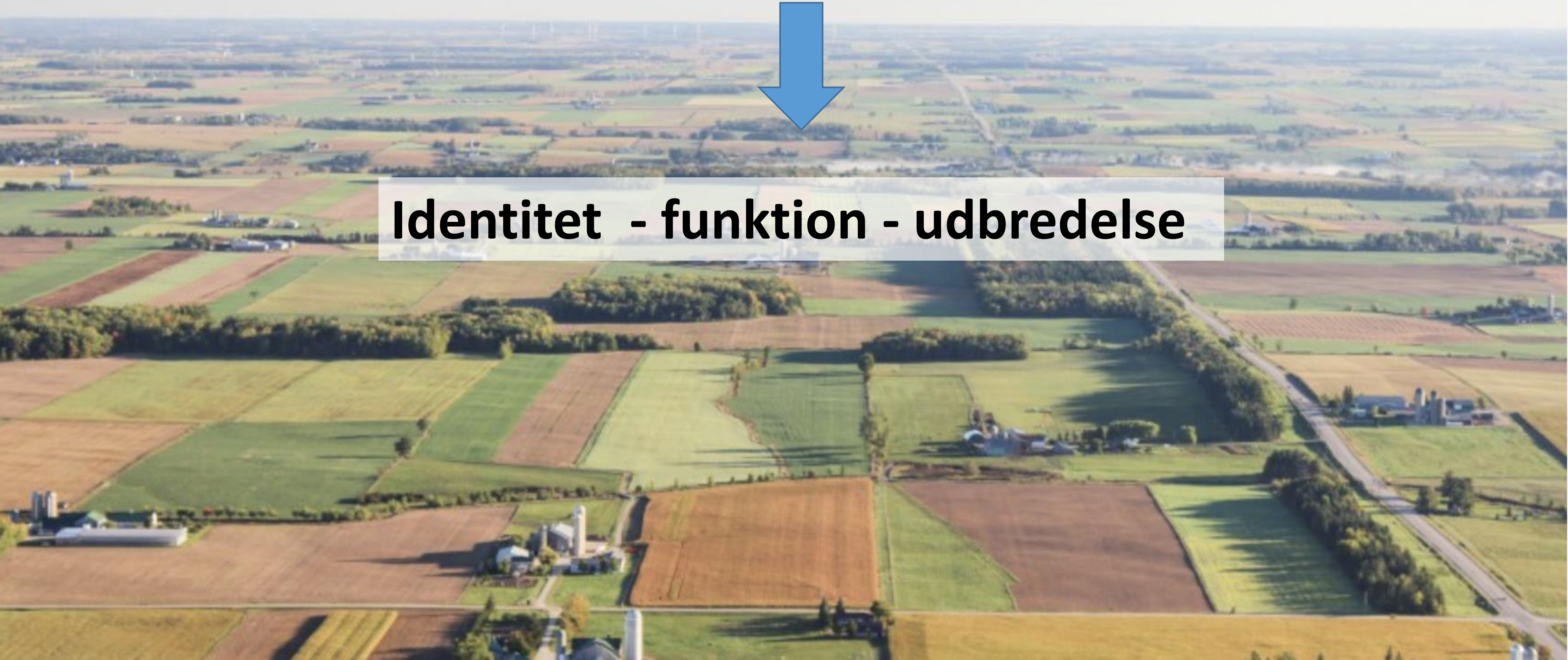

Food


Disease


Symbioses


Sustainability

Forståelse af bakteriers funktion i landbrugsjord, fx klimagasser



Identitet - funktion - udbredelse

Hvor mange bakteriearter findes på jorden?

Bakterier identificeret:

250.000 arter (DNA fingerprints)

80.789 genomer (20 % isoleret)

silva
high quality ribosomal RNA databases

GTDB

Hvor mange bakteriearter findes på jorden?

Bakterier identificeret:

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80.789 genomer (20 % isoleret) GTDB

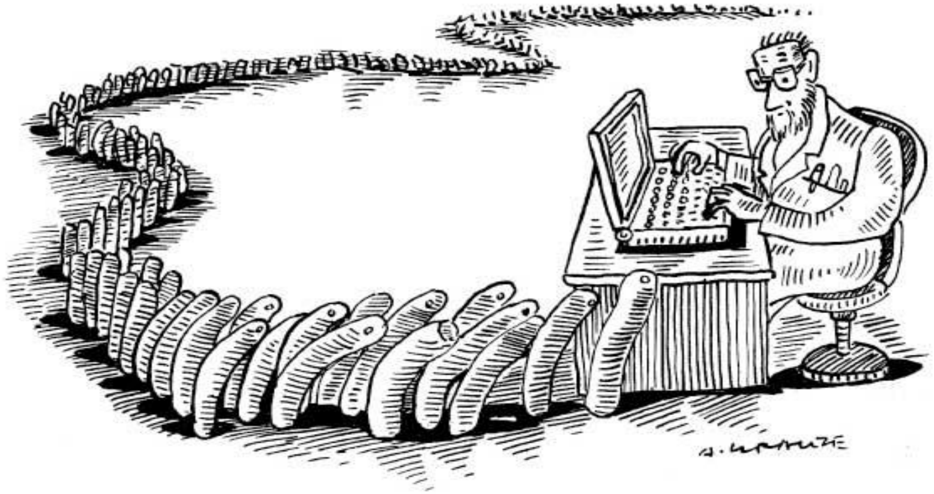
Estimeret:

Tusinder til milliarder

Bedste gæt i dag: nogle millioner… [Louca et al., 2019]

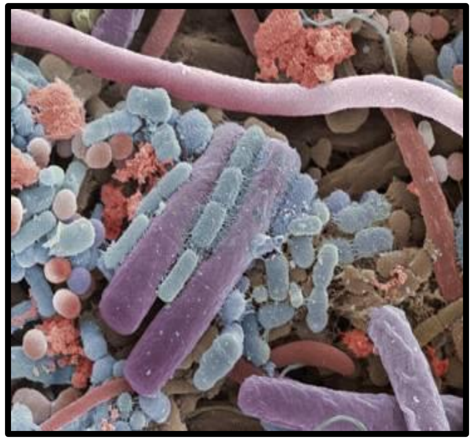
De fleste arter kan
ikke dyrkes med
kendte metoder

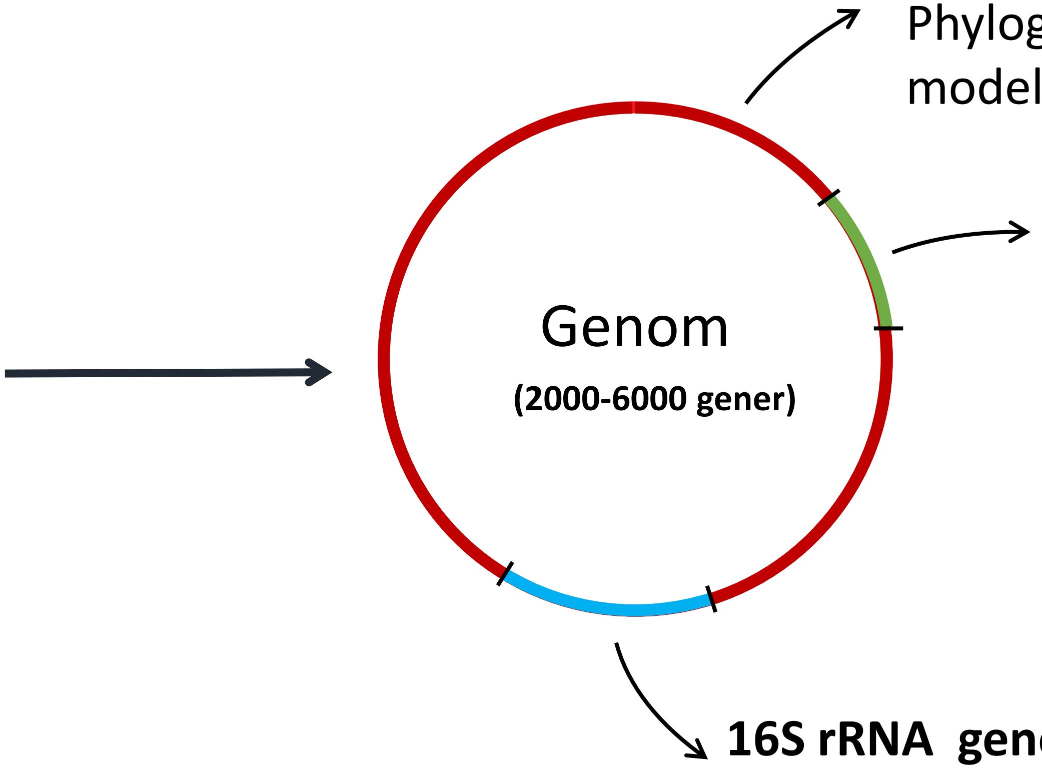
Hvordan identificerer vi millioner af ukendte bakterier?



ANDRZEJ KRAUZE

Vi identificerer mikroorganismerne ved hjælp af DNA analyser





Genom

(2000-6000 gener)

Genom
Phylogenomics + metabolske modeller

Funktionelle gener (fx *amoA*)

16S rRNA gene
(1500 -1600 bp)

Fingerprint

Unik for forskellige organismer

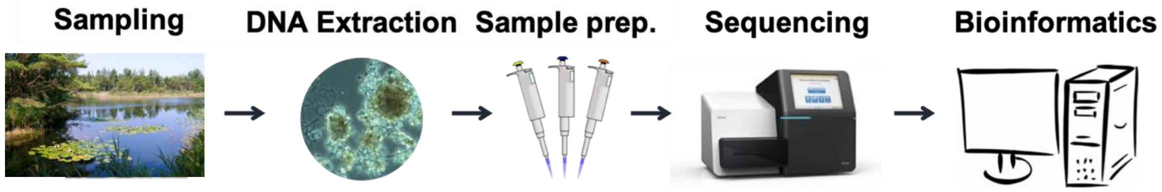
Analyse af mikrobielle samfund (fingerprint)

GREENGENES The 16S rRNA Gene Database and Tools

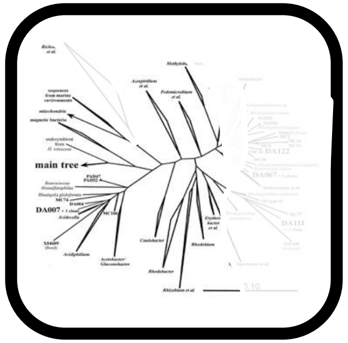
rdp

silva high quality ribosomal RNA databases

GTDB



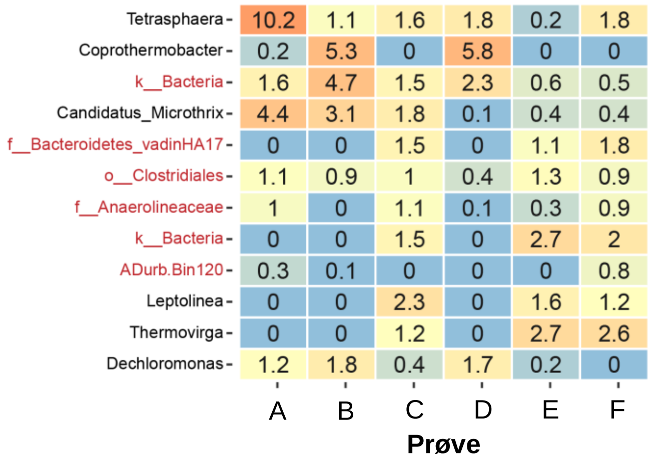
Klassifikation af ASV
med reference database



Manglende
- sekvenser
- taxonomi

Amplicon sequence
variants (ASV) tabel
(relativ hyppighed, %)

Samfundsstruktur



	A	B	C	D	E	F
Tetrasphaera	10.2	1.1	1.6	1.8	0.2	1.8
Coprothermobacter	0.2	5.3	0	5.8	0	0
k__Bacteria	1.6	4.7	1.5	2.3	0.6	0.5
Candidatus_Microthrix	4.4	3.1	1.8	0.1	0.4	0.4
f__Bacteroidetes_vadinHA17	0	0	1.5	0	1.1	1.8
o__Clostridiales	1.1	0.9	1	0.4	1.3	0.9
f__Anaerolineaceae	1	0	1.1	0.1	0.3	0.9
k__Bacteria	0	0	1.5	0	2.7	2
ADurb.Bin120	0.3	0.1	0	0	0	0.8
Leptolinea	0	0	2.3	0	1.6	1.2
Thermovirga	0	0	1.2	0	2.7	2.6
Dechloromonas	1.2	1.8	0.4	1.7	0.2	0

Prøve	A	B	C	D	...
ASV1	8,2	0.8	1.1	0.2	
ASV2	0.8	0	0.3	0.1	
ASV3	0.7	0.6	0.9	0.1	
ASV4	1.3	0.2	0.3	1.4	
ASV5	0	0	1.2	0	
ASV6	0	0	0.9	0	
....					

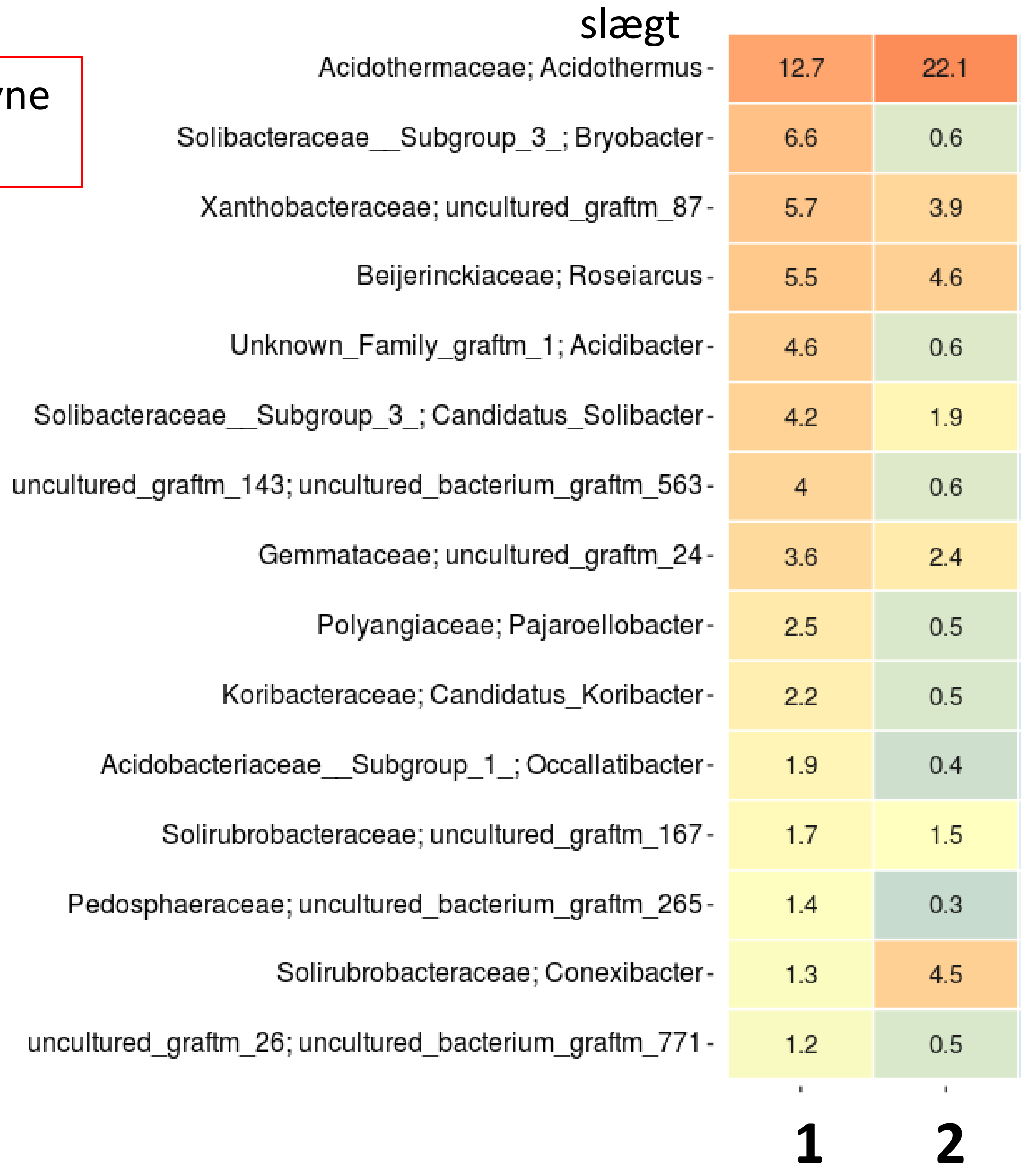
+

ASV1: g_Tetrasphaera
ASV2: f_Anaerolineaceae
ASV3: o_Closteridales
ASV4: g_Tetrasphaera
ASV5: f_Bacteroidetes
ASV6: g_Thermovirga
....

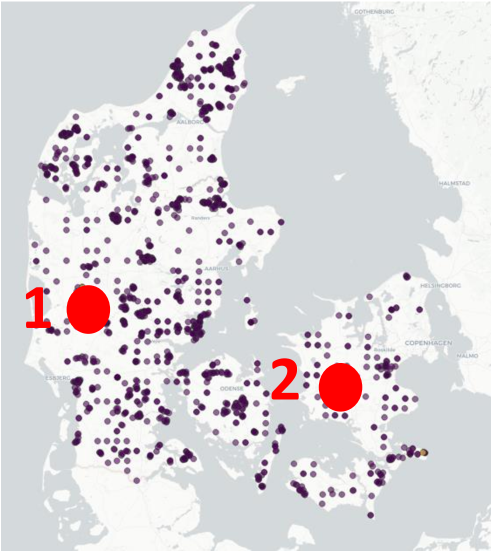
Mange ukendte bakterieslægter i landbrugsjord

Ingen er beskrevet på **artsniveau** – heller ikke blandt de beskrevne slægter!

Ubeskrevne slægter

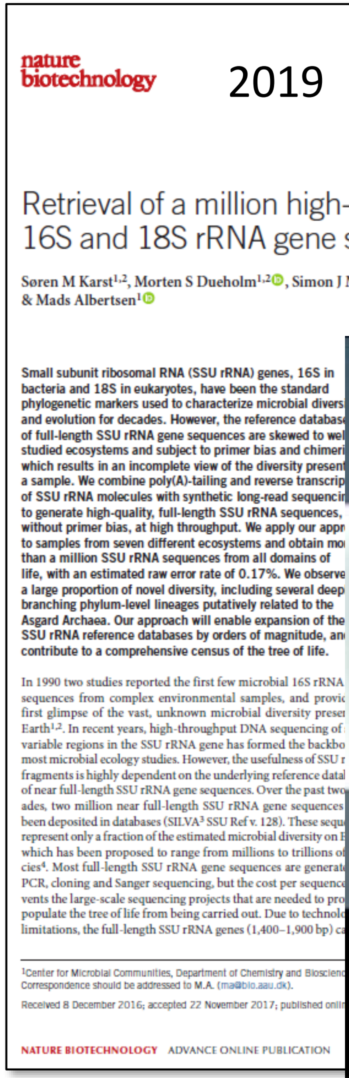


slægt	1	2
Acidothermaceae; Acidothermus	12.7	22.1
Solibacteraceae__Subgroup_3_; Bryobacter	6.6	0.6
Xanthobacteraceae; uncultured_graftm_87	5.7	3.9
Beijerinckiaceae; Roseiarcus	5.5	4.6
Unknown_Family_graftm_1; Acidibacter	4.6	0.6
Solibacteraceae__Subgroup_3_; Candidatus_Solibacter	4.2	1.9
uncultured_graftm_143; uncultured_bacterium_graftm_563	4	0.6
Gemmataceae; uncultured_graftm_24	3.6	2.4
Polyangiaceae; Pajaroellobacter	2.5	0.5
Koribacteraceae; Candidatus_Koribacter	2.2	0.5
Acidobacteriaceae__Subgroup_1_; Occallatibacter	1.9	0.4
Solirubrobacteraceae; uncultured_graftm_167	1.7	1.5
Pedosphaeraceae; uncultured_bacterium_graftm_265	1.4	0.3
Solirubrobacteraceae; Conexibacter	1.3	4.5
uncultured_graftm_26; uncultured_bacterium_graftm_771	1.2	0.5




1


2



LETTERS

nature biotechnology

2019

Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias

Søren M Karst[1,2], Morten S Dueholm[1,2], Simon J McIlroy[1], Rasmus H Kirkegaard[1], Per H Nielsen[1] & Mads Albertsen[1]

Small subunit ribosomal RNA (SSU rRNA) genes, 16S in
bacteria and 18S in eukaryotes, have been the standard
phylogenetic markers used to characterize microbial diversi
and evolution for decades. However, the reference database
of full-length SSU rRNA gene sequences are skewed to wel
studied ecosystems and subject to primer bias and chimeri
which results in an incomplete view of the diversity present
a sample. We combine poly(A)-tailing and reverse transcrip
of SSU rRNA molecules with synthetic long-read sequencin
to generate high-quality, full-length SSU rRNA sequences,
without primer bias, at high throughput. We apply our appr
to samples from seven different ecosystems and obtain mor
than a million SSU rRNA sequences from all domains of
life, with an estimated raw error rate of 0.17%. We observe
a large proportion of novel diversity, including several deep
branching phylum-level lineages putatively related to the
Asgard Archaea. Our approach will enable expansion of the
SSU rRNA reference databases by orders of magnitude, an
contribute to a comprehensive census of the tree of life.

In 1990 two studies reported the first few microbial 16S rRNA
sequences from complex environmental samples, and provic
first glimpse of the vast, unknown microbial diversity preser
Earth[1,2]. In recent years, high-throughput DNA sequencing of
variable regions in the SSU rRNA gene has formed the backbo
most microbial ecology studies. However, the usefulness of SSU r
fragments is highly dependent on the underlying reference datal
of near full-length SSU rRNA gene sequences. Over the past two
ades, two million near full-length SSU rRNA gene sequences
been deposited in databases (SILVA[3] SSU Ref v. 128). These sequ
represent only a fraction of the estimated microbial diversity on E
which has been proposed to range from millions to trillions of
cies[4]. Most full-length SSU rRNA gene sequences are generat
PCR, cloning and Sanger sequencing, but the cost per sequence
vents the large-scale sequencing projects that are needed to pro
populate the tree of life from being carried out. Due to technolo
limitations, the full-length SSU rRNA genes (1,400–1,900 bp) ca

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[1]Center for Microbial Communities, Department of Chemistry and Bioscienc
Correspondence should be addressed to M.A. (ma@bio.aau.dk).

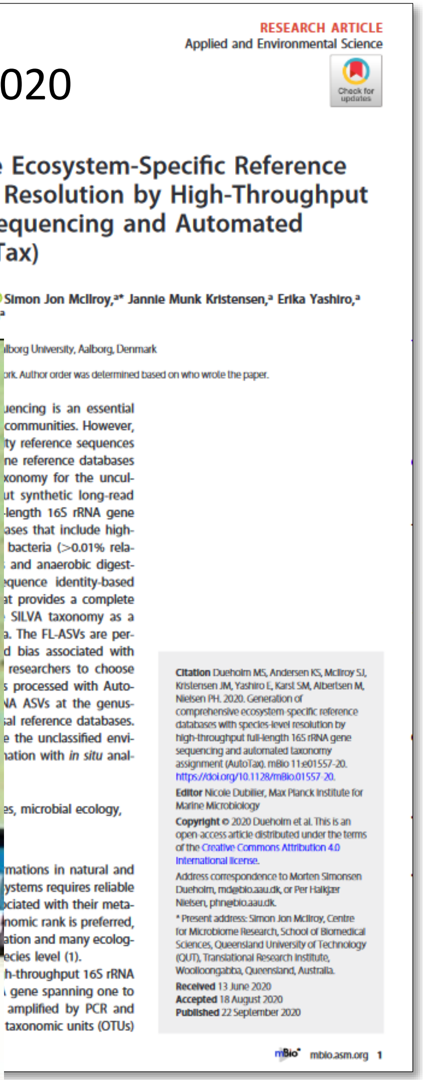
Received 8 December 2016; accepted 22 November 2017; published onlir

NATURE BIOTECHNOLOGY ADVANCE ONLINE PUBLICATION

Mads Albertsen

NY DANSK FORSKNINGSMETODE

Bakterieforskere laver 25 års arbejde på få uger



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RESEARCH ARTICLE
Applied and Environmental Science

2020

Generation of Comprehensive Ecosystem-Specific Reference Databases with Species-Level Resolution by High-Throughput Full-Length 16S rRNA Gene Sequencing and Automated Taxonomy Assignment (AutoTax)

Morten Simonsen Dueholm,[a] Kasper Skytte Andersen,[a] Simon Jon McIlroy,[a*] Jannie Munk Kristensen,[a] Erika Yashiro,[a] Søren Michael Karst,[a] Mads Albertsen,[a] Per Halkjær Nielsen[a]

lborg University, Aalborg, Denmark

ork. Author order was determined based on who wrote the paper.

uencing is an essential
communities. However,
ty reference sequences
ne reference databases
xonomy for the uncul-
ut synthetic long-read
-length 16S rRNA gene
ases that include high-
bacteria (>0.01% rela-
and anaerobic digest-
equence identity-based
at provides a complete
SILVA taxonomy as a
a. The FL-ASVs are per-
d bias associated with
researchers to choose
s processed with Auto-
NA ASVs at the genus-
al reference databases.
e the unclassified envi-
ation with *in situ* anal-

es, microbial ecology,

mations in natural and
ystems requires reliable
ciated with their meta-
nomic rank is preferred,
ation and many ecolog-
ecies level (1).
h-throughput 16S rRNA
gene spanning one to
amplified by PCR and
taxonomic units (OTUs)

Citation Dueholm MS, Andersen KS, McIlroy SJ, Kristensen JM, Yashiro E, Karst SM, Albertsen M, Nielsen PH. 2020. Generation of comprehensive ecosystem-specific reference databases with species-level resolution by high-throughput full-length 16S rRNA gene sequencing and automated taxonomy assignment (AutoTax). mBio 11:e01557-20. https://doi.org/10.1128/mBio.01557-20.

Editor Nicole Dubilier, Max Planck Institute for Marine Microbiology

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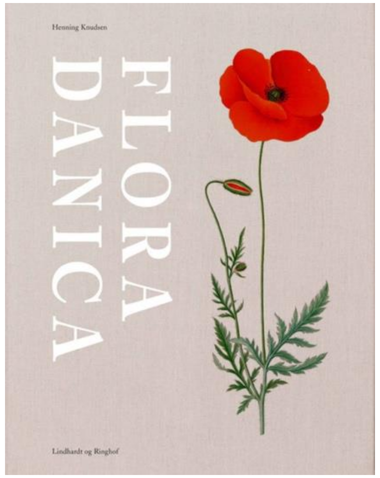
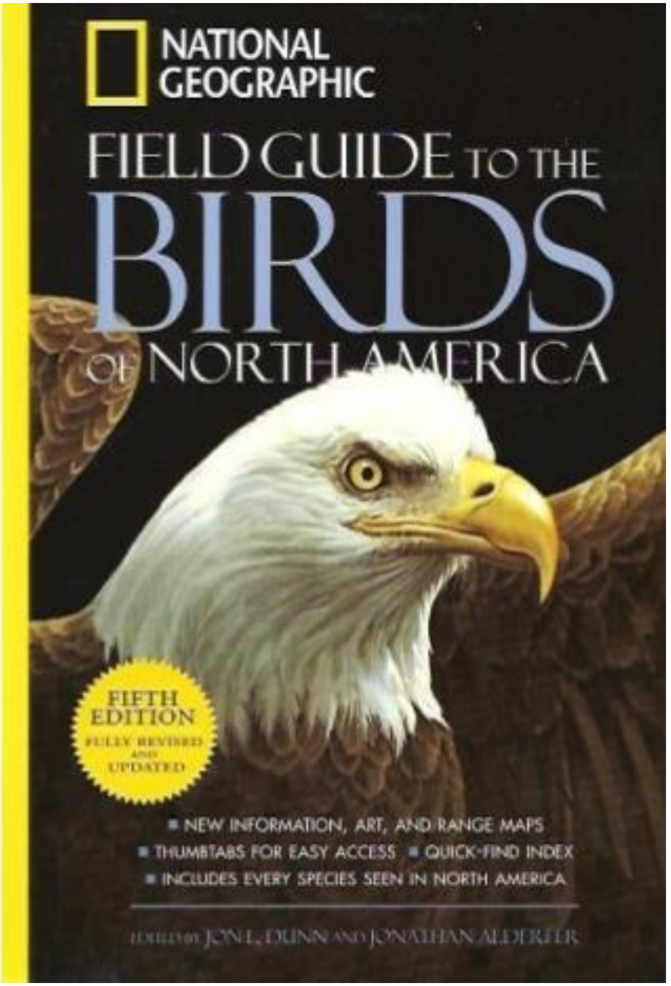
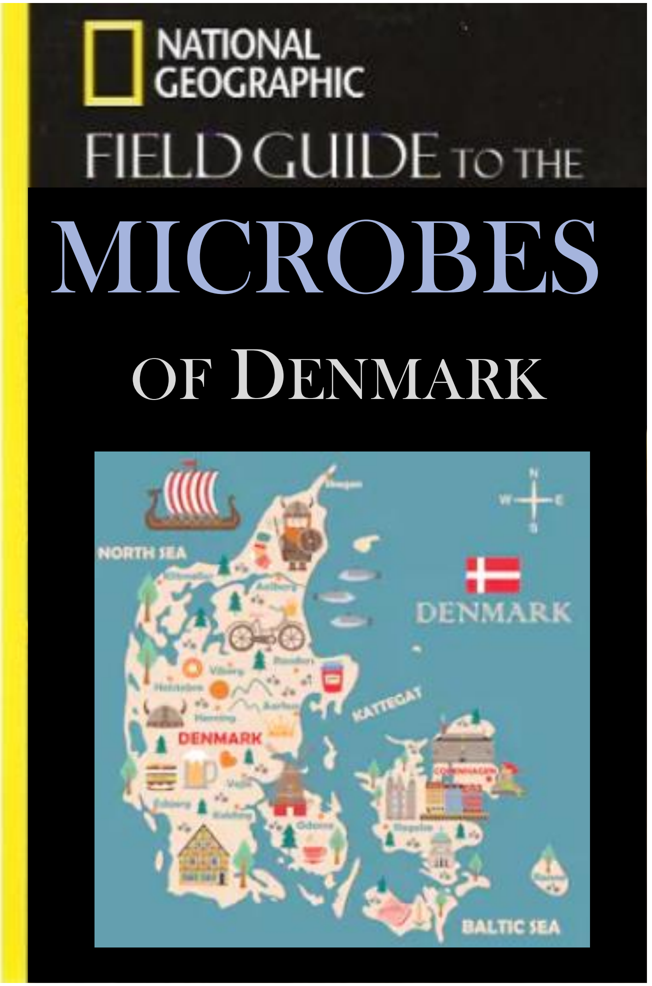
Flora Danica: En omfattende bogserie over Danmarks flora - og porcelæn fra Royal Copenhagen

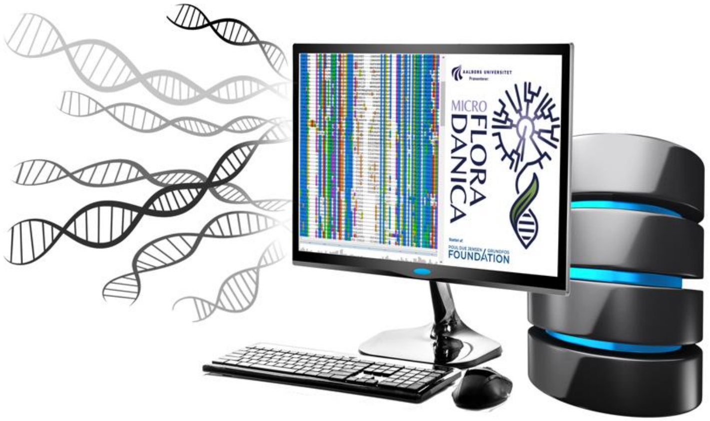


Produceret mellem 1761 og 1883

Microflora Danica – en oversigt over alle bakterier i Danmark







Credit @ Jonathan Eisen

Microflora Danica

- PDJ Fonden ≈ 36 million DKK i perioden 2019-2025
- PIs: Mads Albertsen & Per Halkjær Nielsen
- Vi vil lave **referencedatabasen** over alle mikroorganismer i Danmark. **Det kan kun gøres een gang!**
- Alle områder i Danmark tilstræbes analyseret, ialt ≈ 10.000 prøver
- Sammensætning af arter (biodiversitet) i både naturlige og menneskabte habitater, geografisk fordeling
- En paraply over en masse interne og eksterne samarbejder, fx kvælstofomsætning i landbrugsjord
- Samarbejde med "Earth Microbiome Project"

Hjemmeside: www.microfloradanica.aau.dk

MICRO FLORA DANICA

The microbiome of Denmark

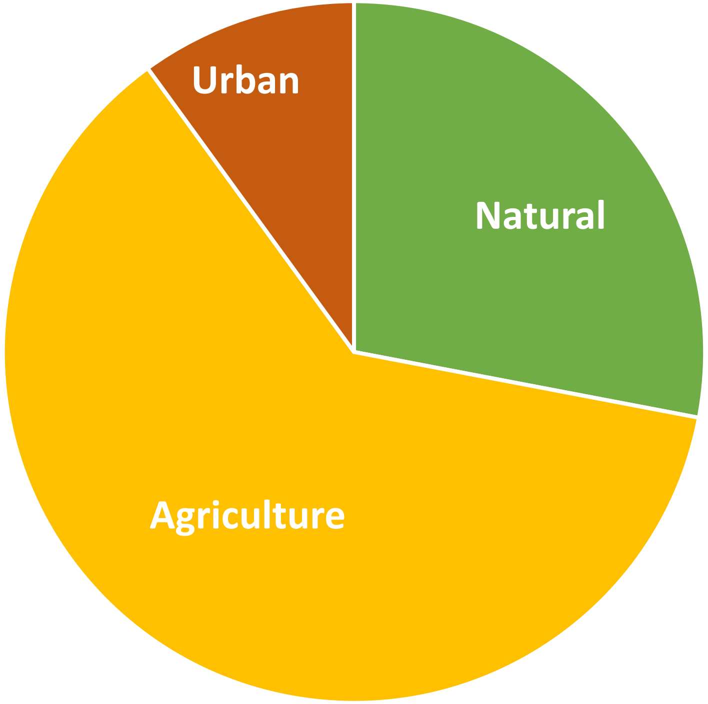
AALBORG UNIVERSITET

POUL DUE JENSEN / GRUNDFOS FOUNDATION

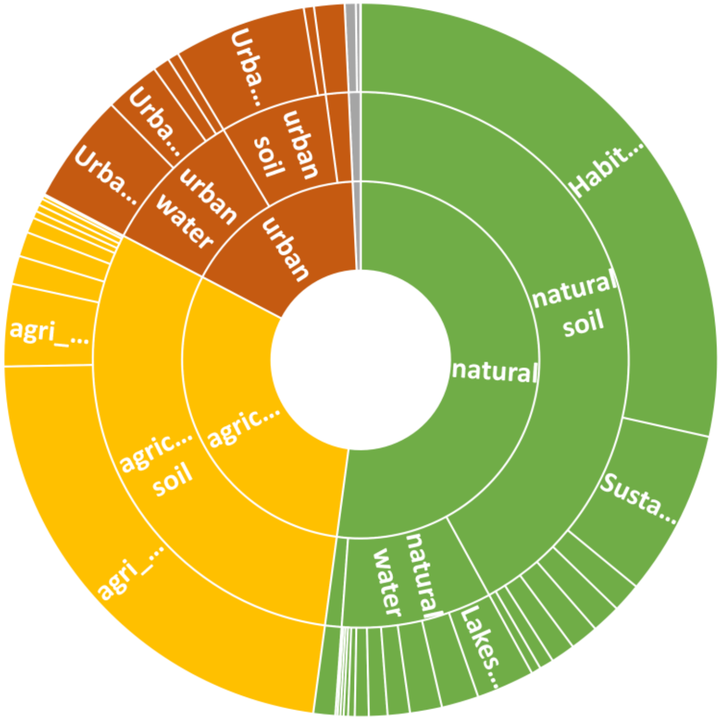
Indsamling af 10.000 prøver i Danmark

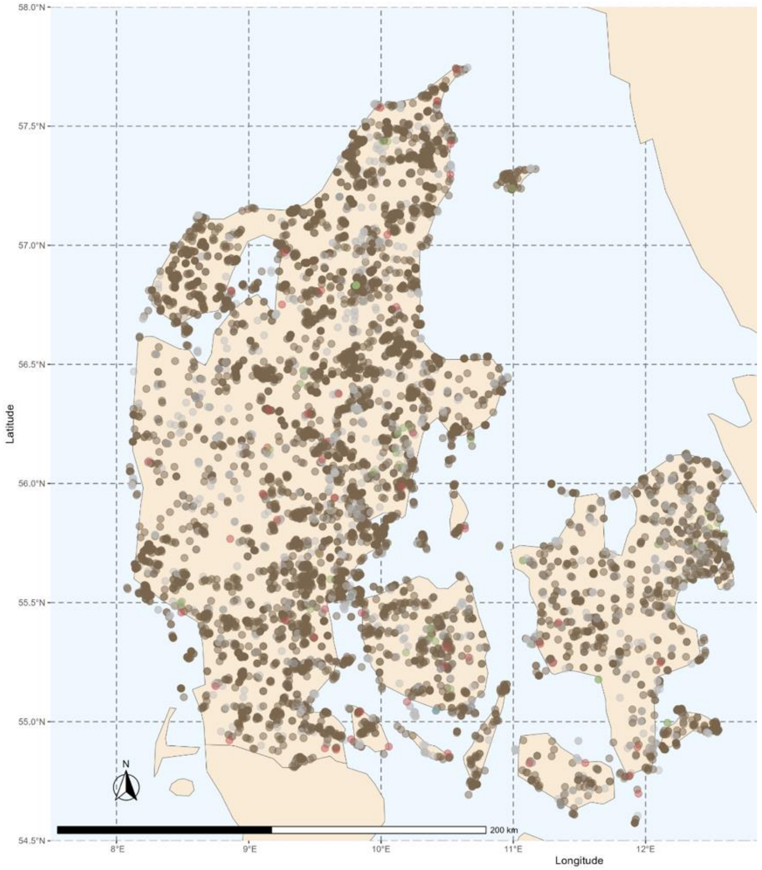
Vibeke Rudkjøbing
Project Co-ordinator

Arealudnyttelse DK



Arealudnyttelse MfD

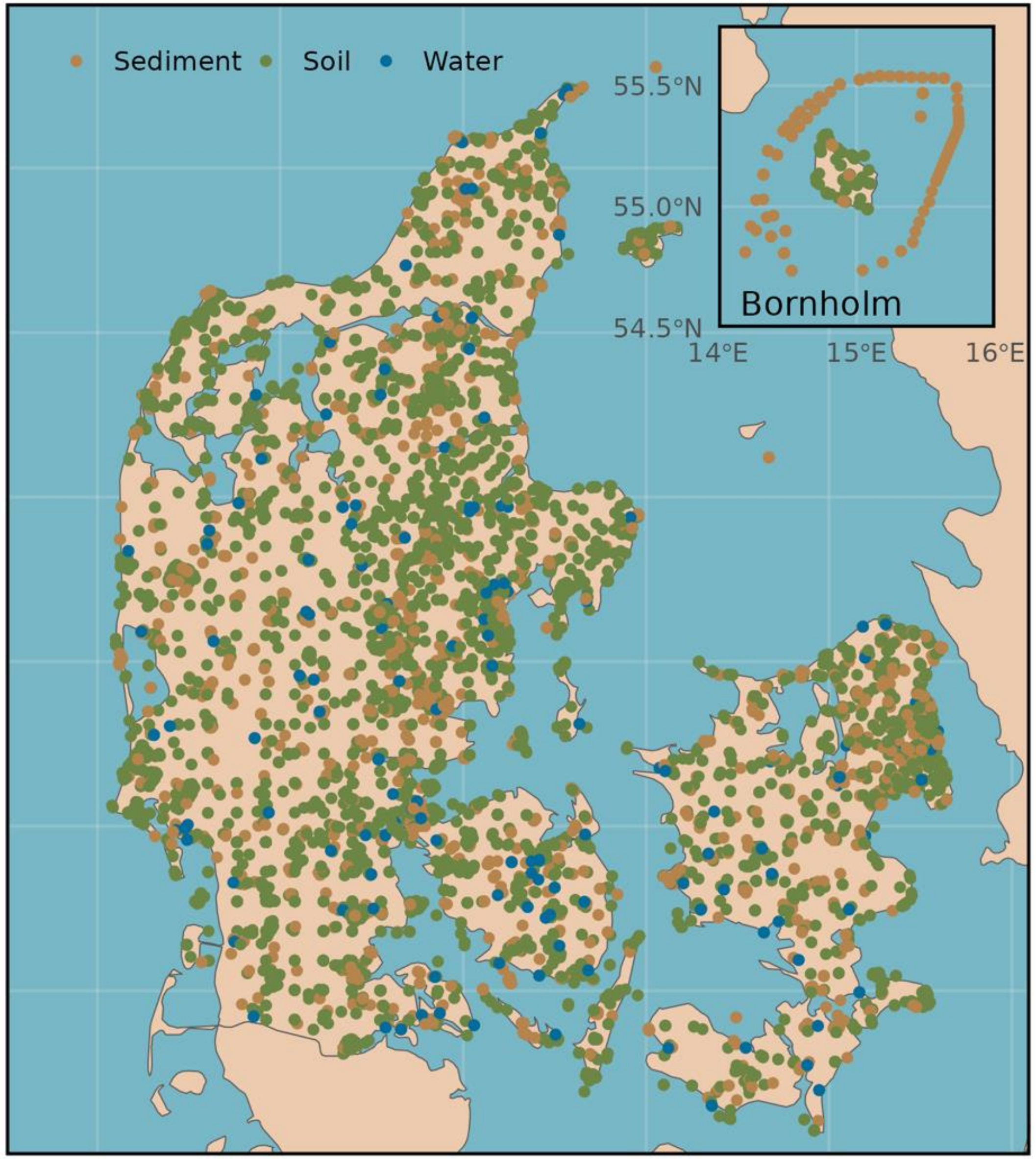




52 indsamlings-projekter

- Geografisk dækning
- Arealudnyttelse
- Fokus på områder med høj forventet diversitet
- Ca. 2500 prøver fra landbrugsområder

Hvor langt er vi nået?



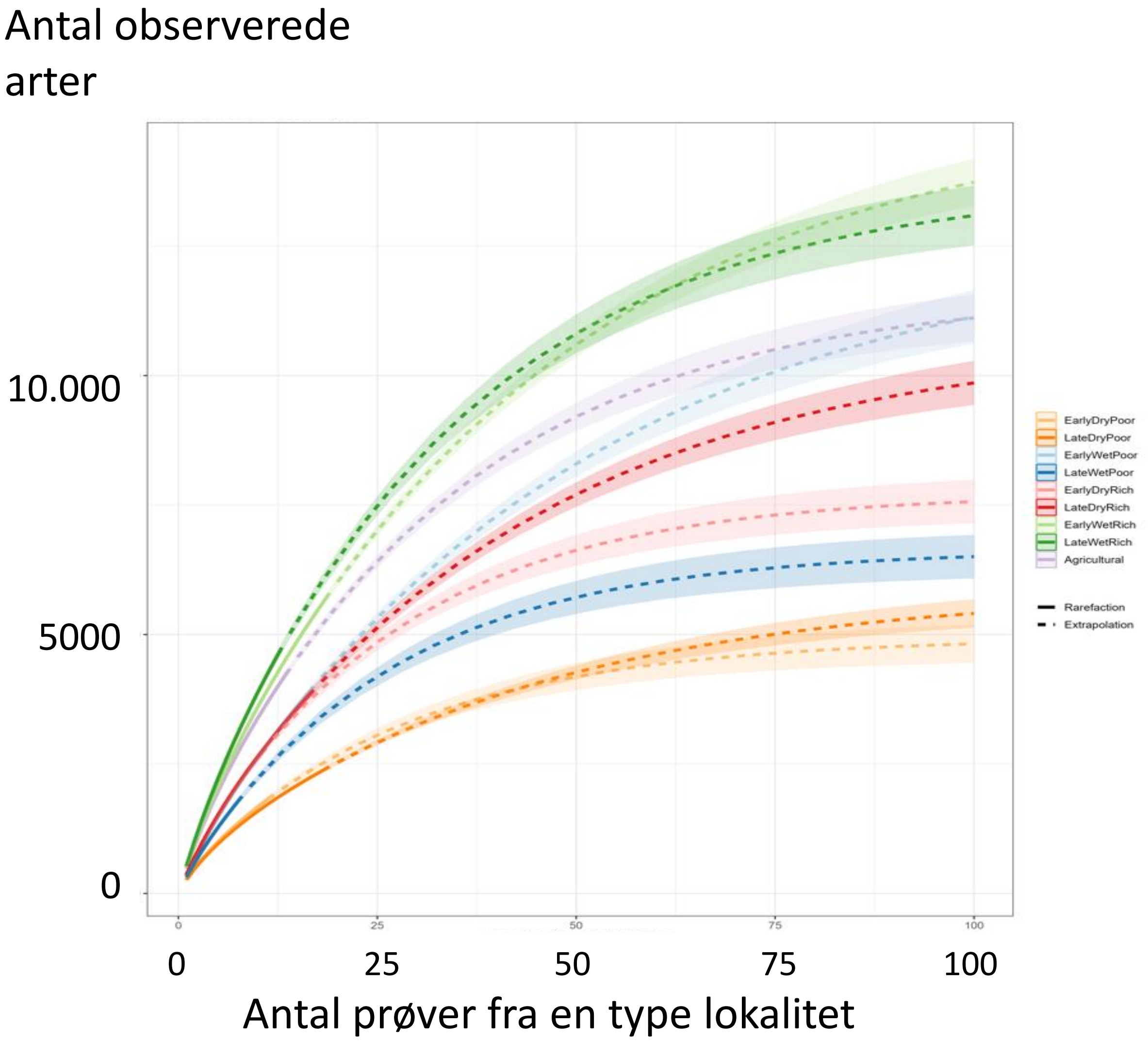
Status

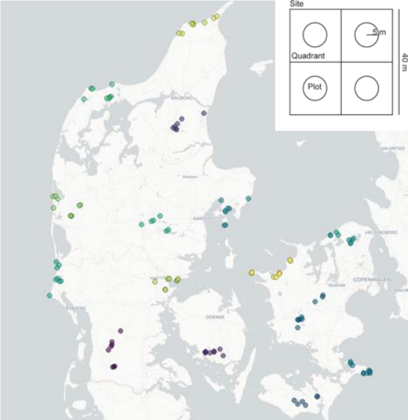
- Vi har indsamlet > 10.000 prøver
- Alle prøver er DNA sekventeret
- Referencedatabase er næsten færdig!
- Vi er i gang med detaljerede analyser.

Eksempler:

- Hvor mange bakteriearter findes Danmark?
- Fordeling af bakterier i forskellige habitattyper (indikatorarter)
- Bakterier involveret i metanomsætning
- Nitrifikanter i jord

Hvor mange bakteriarter findes der i Danmark?





Eksempel:

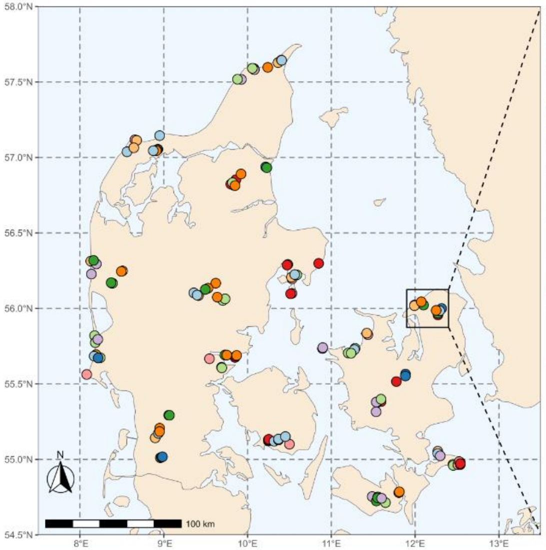
- 8 forskellige habitater.
- Jo flere prøver – jo flere arter.
- Omkring 100 prøver fra et habitat: de fleste arter er detekteret ≈ 5.000 - 15.000 arter pr. habitat.
- Undersøgelser af andre habitater er i gang.
- Vi forventer 0,5-1 million arter ialt – de fleste nye og >99,99% uden et artsnavn.
- Alle vil få et navn/ID.

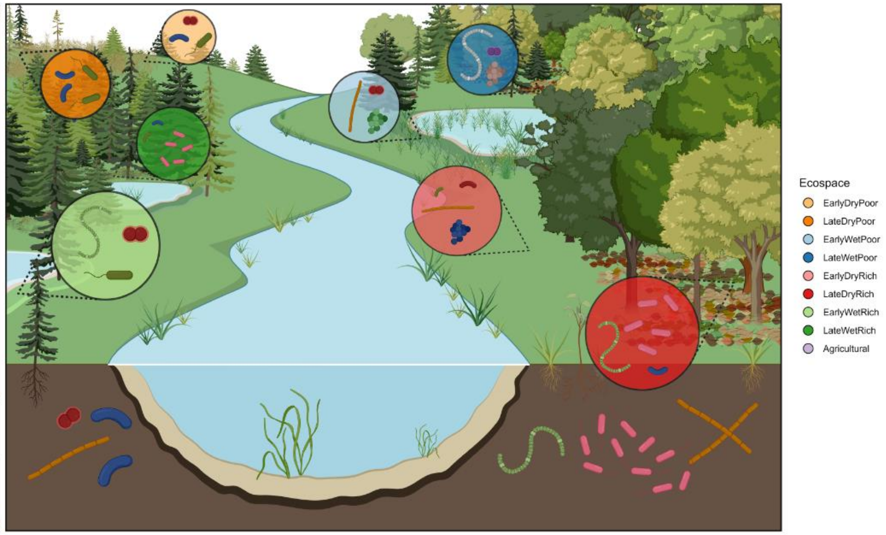
Kan bakterier bruges til at klassificere Natura 2000 habitater (Biowide)?

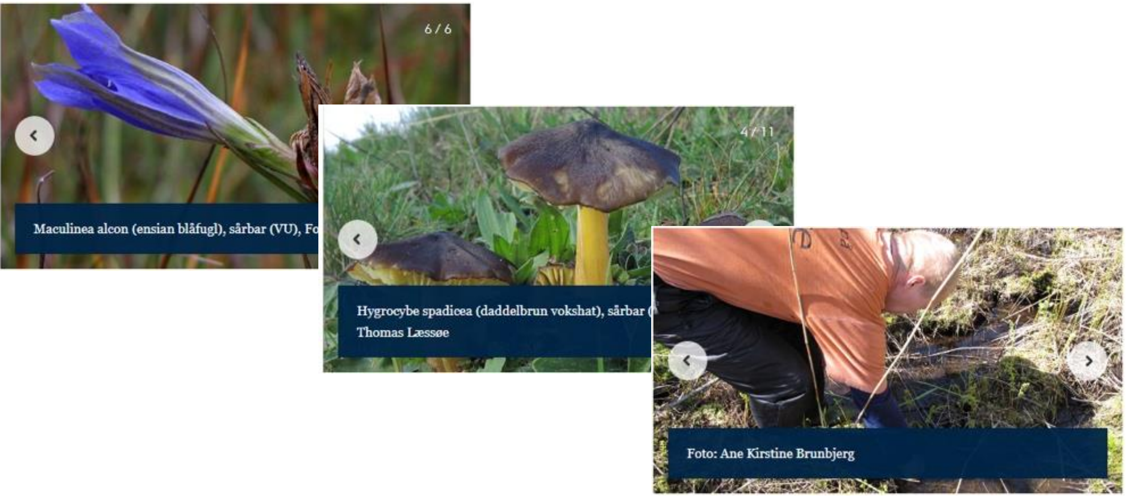
Thomas BN Jensen

Formål

- Overvågning af biodiversitet (makrofauna) er kompliceret
- Nye metoder nødvendige: Kan bakterier i jorden bruges som indikatorer for biodiversitet over jorden?
- Opdagelse af indikatorarter
- Bedre biodiversitet management





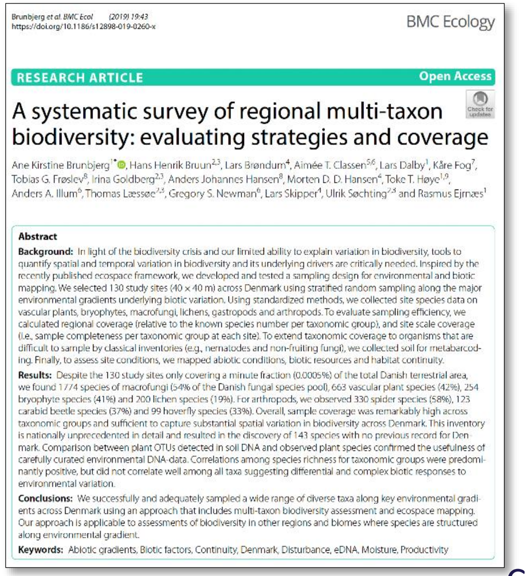


Maculinea alcon (ensian blåfugl), sårbar (VU), Fo

Hygrocybe spadicea (daddelbrun vokshat), sårbar (

Thomas Læssøe

Foto: Ane Kirstine Brunbjerg



Brunbjerg *et al. BMC Ecol* (2019) 19:43
https://doi.org/10.1186/s12898-019-0260-x

BMC Ecology

RESEARCH ARTICLE Open Access

A systematic survey of regional multi-taxon biodiversity: evaluating strategies and coverage

Ane Kirstine Brunbjerg[1*], Hans Henrik Bruun[2,3], Lars Brøndum[4], Aimée T. Classen[5,6], Lars Dalby[1], Kåre Fog[7], Tobias G. Frøslev[8], Irina Goldberg[2,3], Anders Johannes Hansen[8], Morten D. D. Hansen[4], Toke T. Høye[1,9], Anders A. Illum[6], Thomas Læssøe[2,3], Gregory S. Newman[6], Lars Skipper[4], Ulrik Søchting[2,3] and Rasmus Ejrnæs[1]

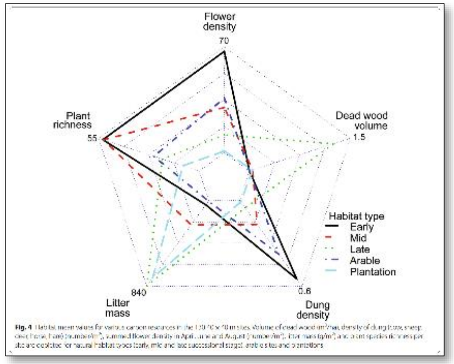
Abstract

Background: In light of the biodiversity crisis and our limited ability to explain variation in biodiversity, tools to quantify spatial and temporal variation in biodiversity and its underlying drivers are critically needed. Inspired by the recently published ecospace framework, we developed and tested a sampling design for environmental and biotic mapping. We selected 130 study sites (40 × 40 m) across Denmark using stratified random sampling along the major environmental gradients underlying biotic variation. Using standardized methods, we collected site species data on vascular plants, bryophytes, macrofungi, lichens, gastropods and arthropods. To evaluate sampling efficiency, we calculated regional coverage (relative to the known species number per taxonomic group), and site scale coverage (i.e., sample completeness per taxonomic group at each site). To extend taxonomic coverage to organisms that are difficult to sample by classical inventories (e.g., nematodes and non-fruiting fungi), we collected soil for metabarcoding. Finally, to assess site conditions, we mapped abiotic conditions, biotic resources and habitat continuity.

Results: Despite the 130 study sites only covering a minute fraction (0.0005%) of the total Danish terrestrial area, we found 1774 species of macrofungi (54% of the Danish fungal species pool), 663 vascular plant species (42%), 254 bryophyte species (41%) and 200 lichen species (19%). For arthropods, we observed 330 spider species (58%), 123 carabid beetle species (37%) and 99 hoverfly species (33%). Overall, sample coverage was remarkably high across taxonomic groups and sufficient to capture substantial spatial variation in biodiversity across Denmark. This inventory is nationally unprecedented in detail and resulted in the discovery of 143 species with no previous record for Denmark. Comparison between plant OTUs detected in soil DNA and observed plant species confirmed the usefulness of carefully curated environmental DNA-data. Correlations among species richness for taxonomic groups were predominantly positive, but did not correlate well among all taxa suggesting differential and complex biotic responses to environmental variation.

Conclusions: We successfully and adequately sampled a wide range of diverse taxa along key environmental gradients across Denmark using an approach that includes multi-taxon biodiversity assessment and ecospace mapping. Our approach is applicable to assessments of biodiversity in other regions and biomes where species are structured along environmental gradient.

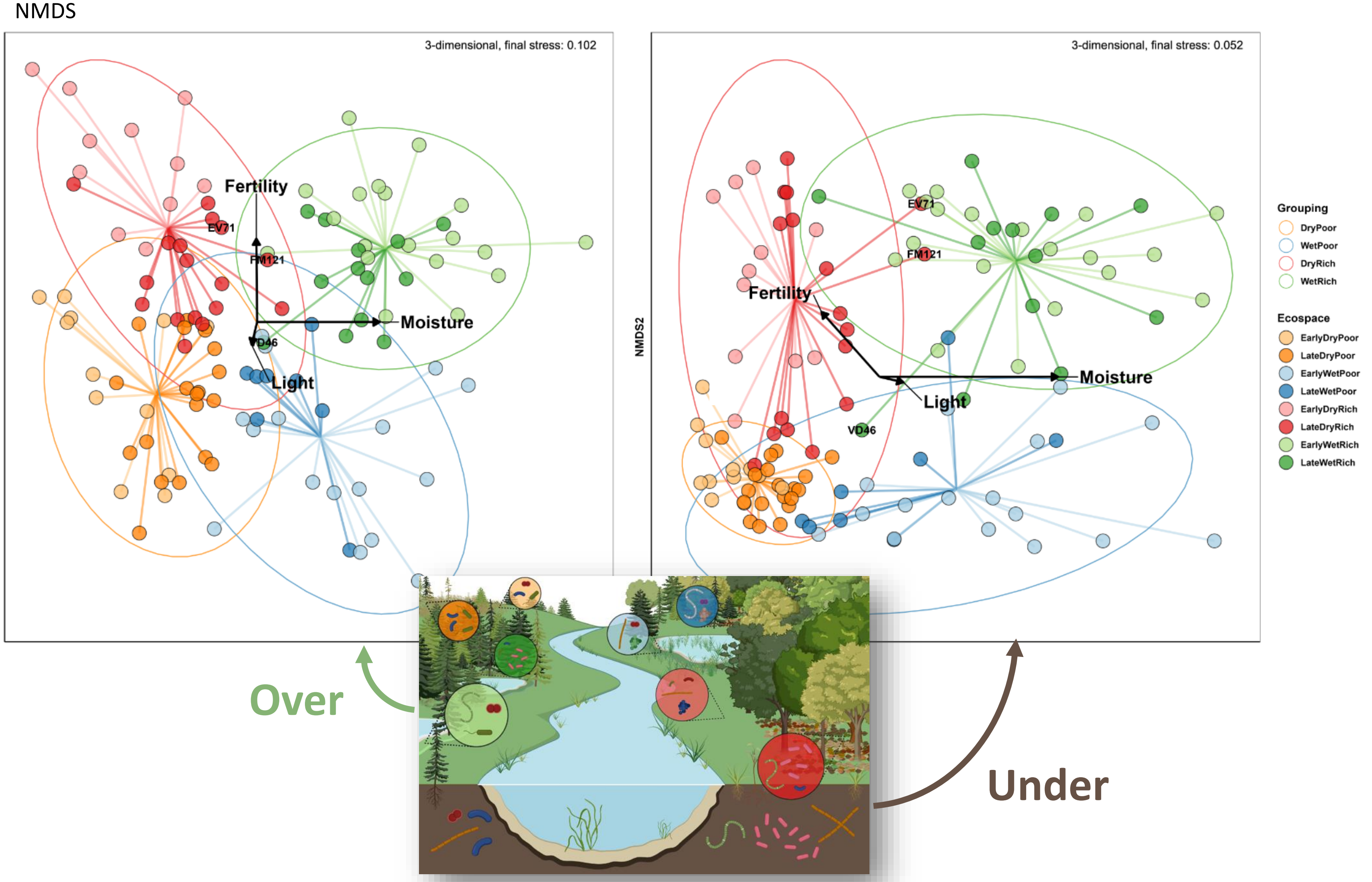
Keywords: Abiotic gradients, Biotic factors, Continuity, Denmark, Disturbance, eDNA, Moisture, Productivity



Tobias Frøslev
Univ. Copenhagen

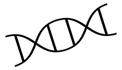
Rasmus Ejrnæs
Aarhus University

Foreløbige resultater: Klar sammenhæng mellem bakterier i jord og biodiversitet over jorden

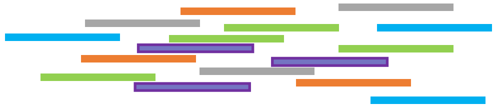


Nu kender vi navne/ID af bakterierne. Hvilken funktion har bakterierne?

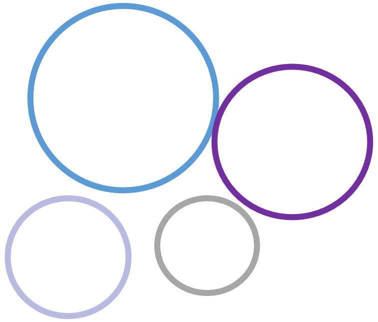
DNA extraktion



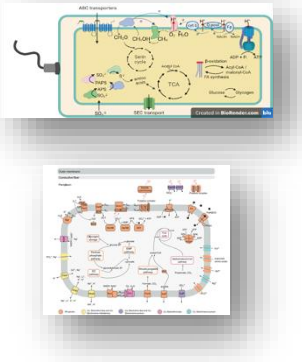
Genom-centric metagenomic



Metagenome assembled genomes (MAGs)



Metabolske modeller



nature methods

BRIEF COMMUNICATION

https://doi.org/10.1038/s41592-022-01539-7

2022

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Oxford Nanopore R10.4 long-read sequencing enables the generation of near-finished bacterial genomes from pure cultures and metagenomes without short-read or reference polishing

Mantas Sereika[1,4], Rasmus Hansen Kirkegaard[1,2,4], Søren Michael Karst[1], Thomas Yssing Michaelsen[1], Emil Aarre Sørensen[1], Rasmus Dam Wollenberg[3] and Mads Albertsen[1]✉

GTDB Genome reference database: ≈ 81.000 genomer

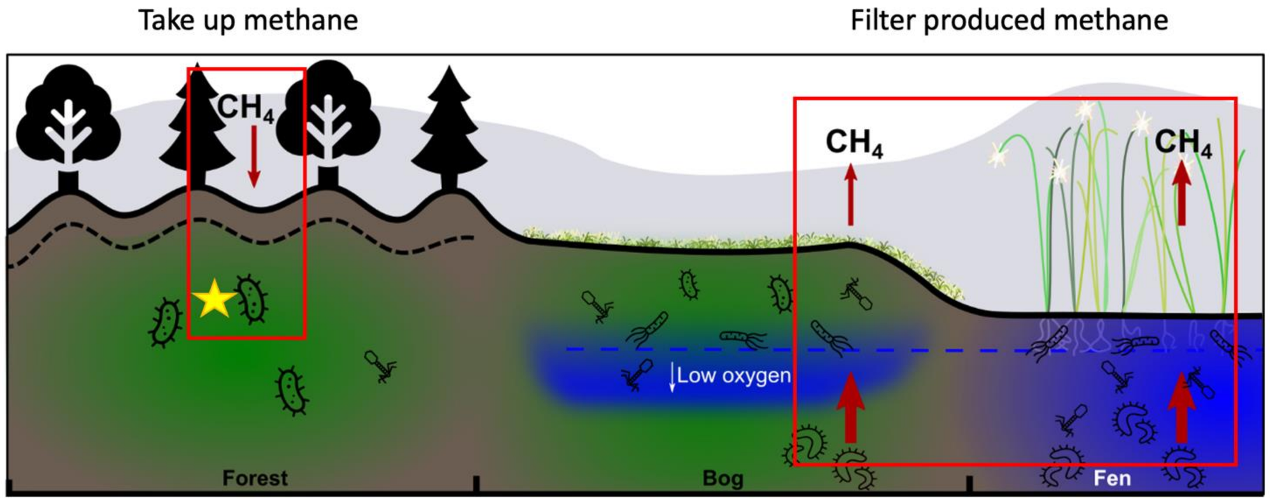
Microflora Danica: ≈ 20.000 nye genomer

Metandannelse og metanfjernelse – vigtig ved udledning af drivhusgasser og gendannelse af vådområder


Kalinka Knudsen


Caitlin Singleton

- Etableret et katalog over metanproducerende og metanoxiderende archaea/bakterier i forskellige miljøer.
- Vi ser mange nye slægter og arter.



Metandannelse og metanfjernelse – vigtig ved udledning af drivhusgasser og gendannelse af vådområder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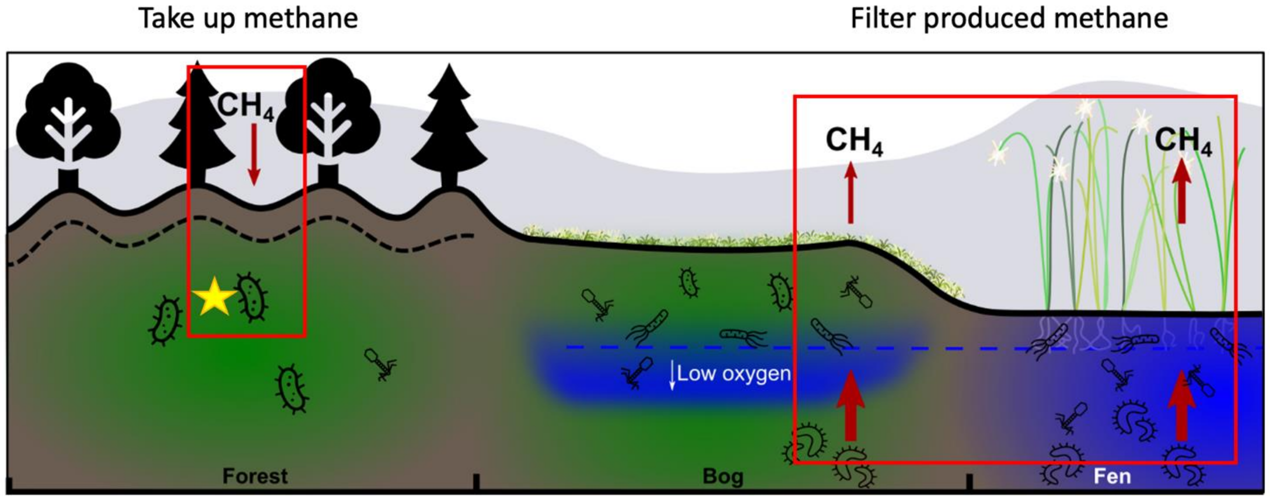
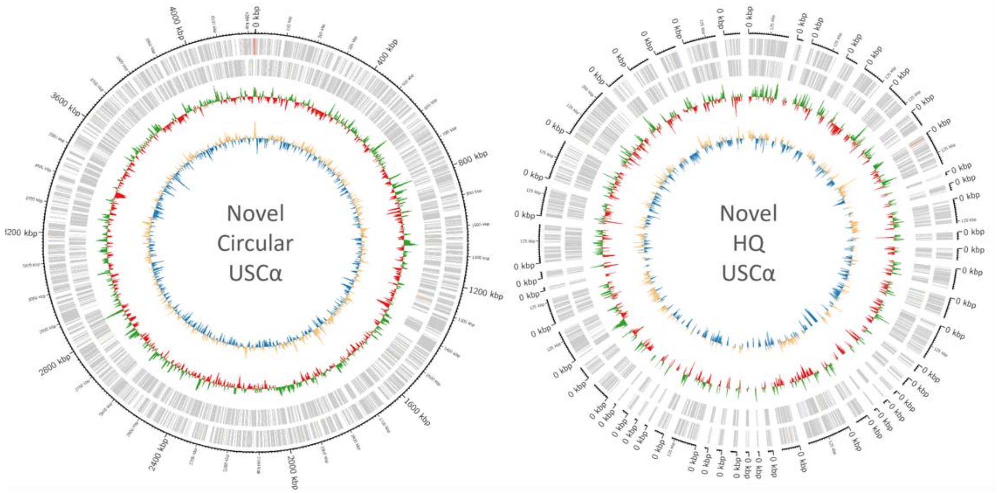
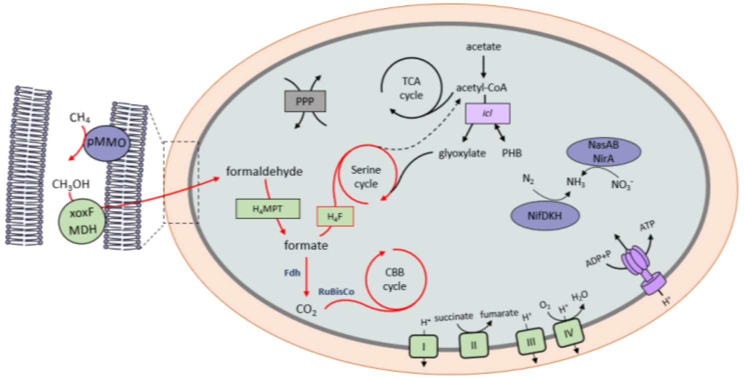
- Etableret et katalog over metanproducerende og metanoxiderende archaea/bakterier i forskellige miljøer.
- Vi ser mange nye slægter og arter.
- Nye genomer af “Upland Soil Clusters, USCα” – kan oxididere metan ved atmosfæriske koncentrationer – etablering af metabolsk model.

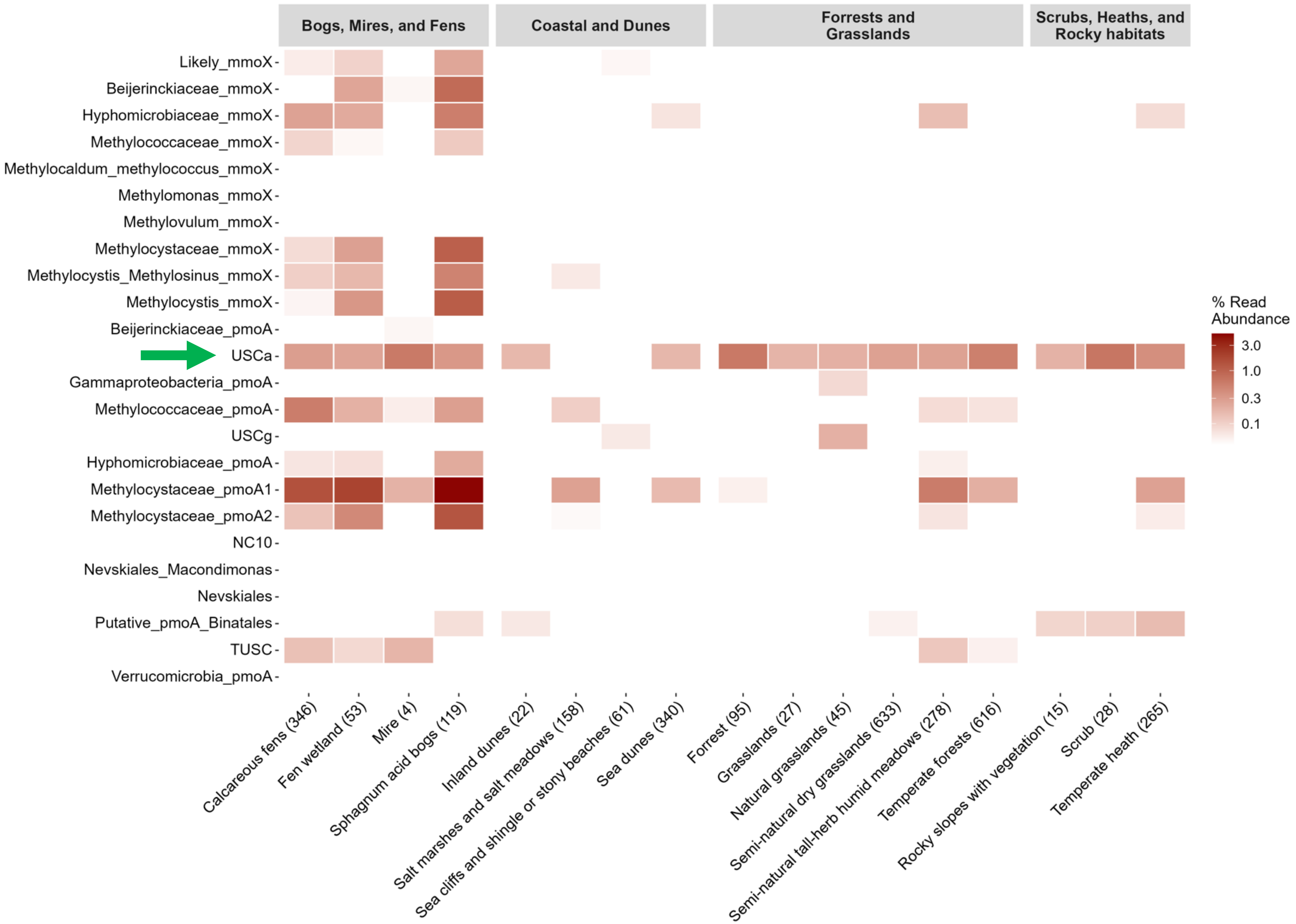


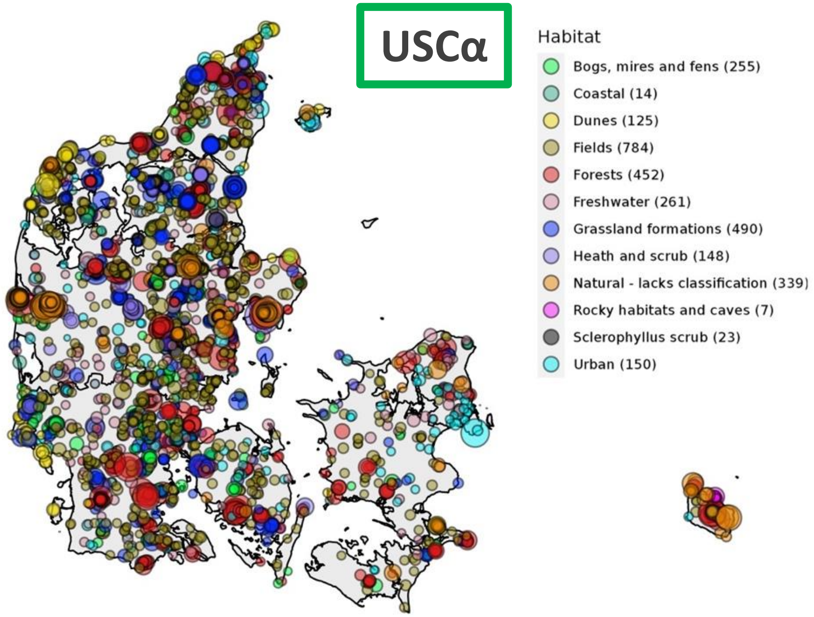


Metabolsk model

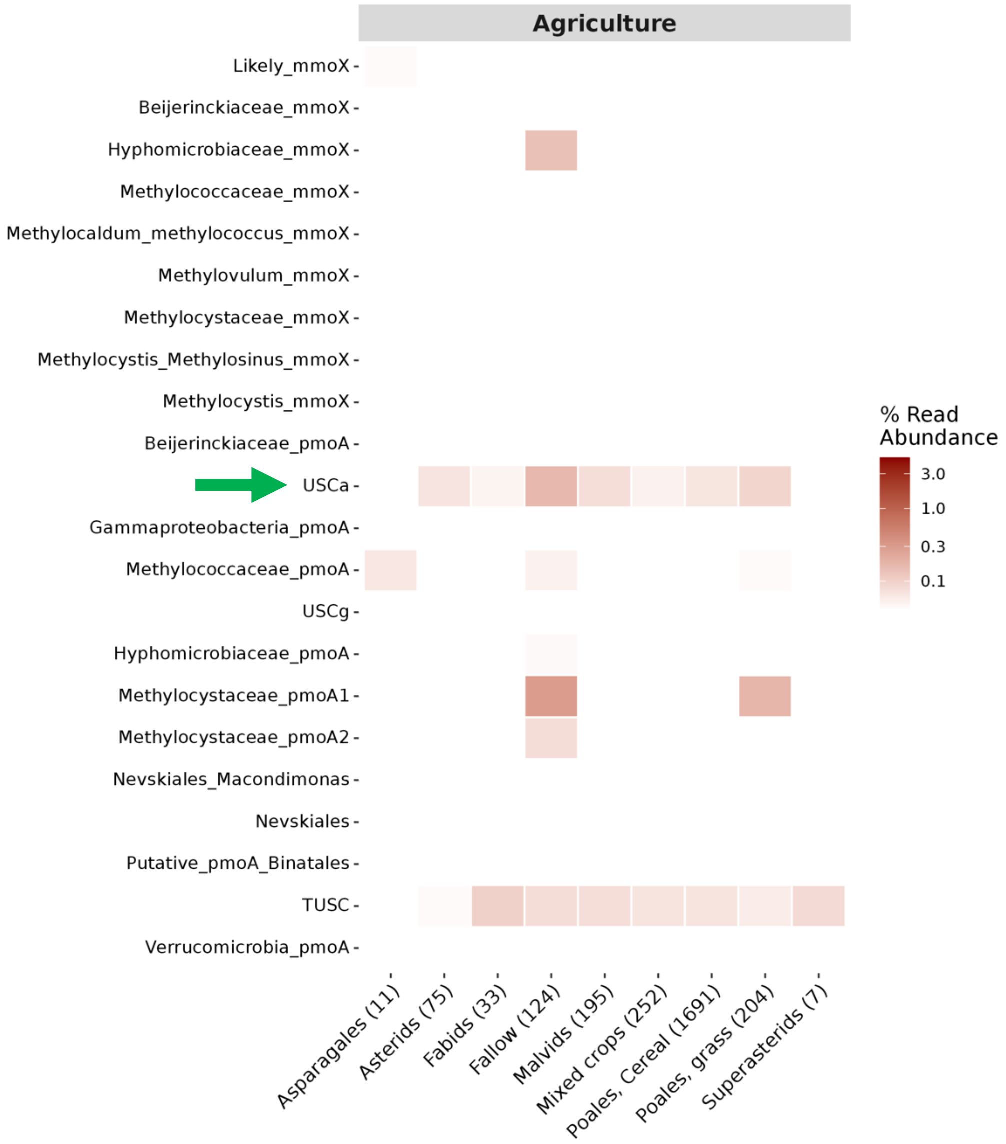


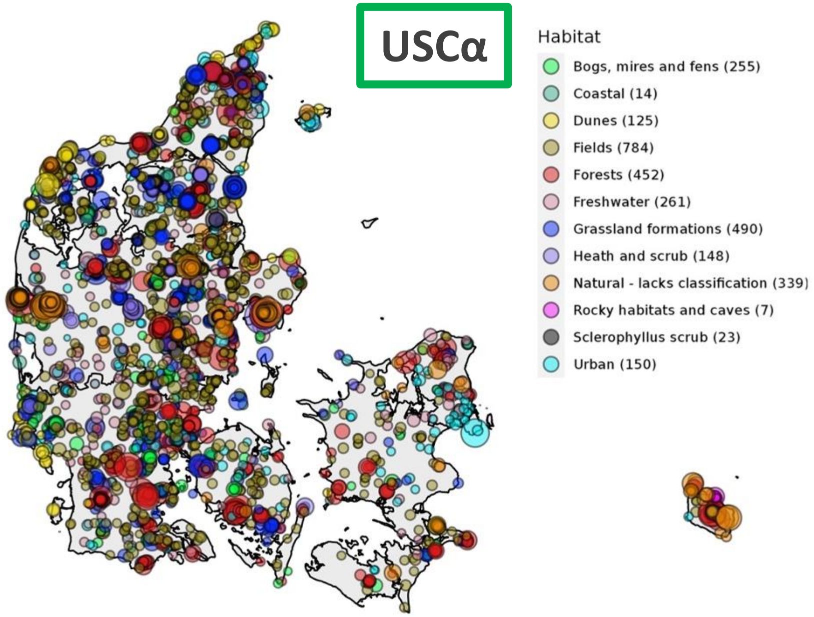
Metanoxiderende bakterier, som kan leve ved atmosfæriske metankoncentrationer, er udbredte i “naturlige” systemer





Metanoxiderende bakterier, som kan leve ved atmosfæriske metankoncentrationer, er også udbredte i landbrugsjord!



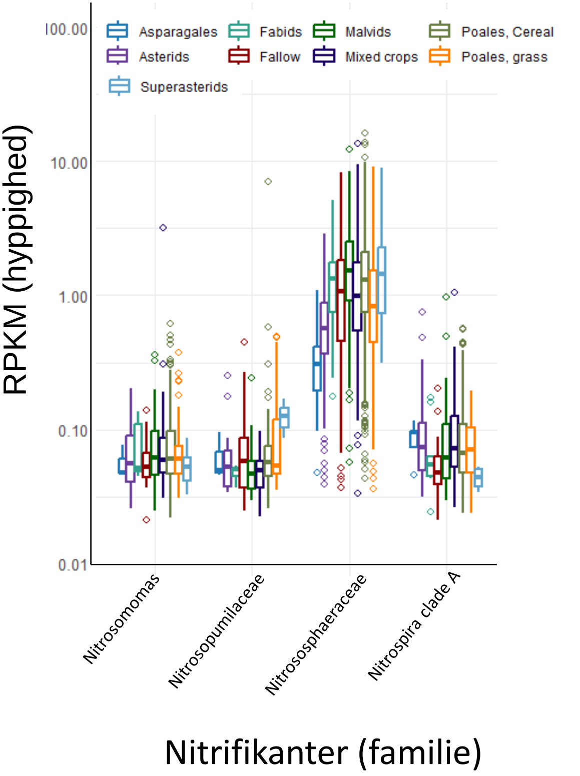


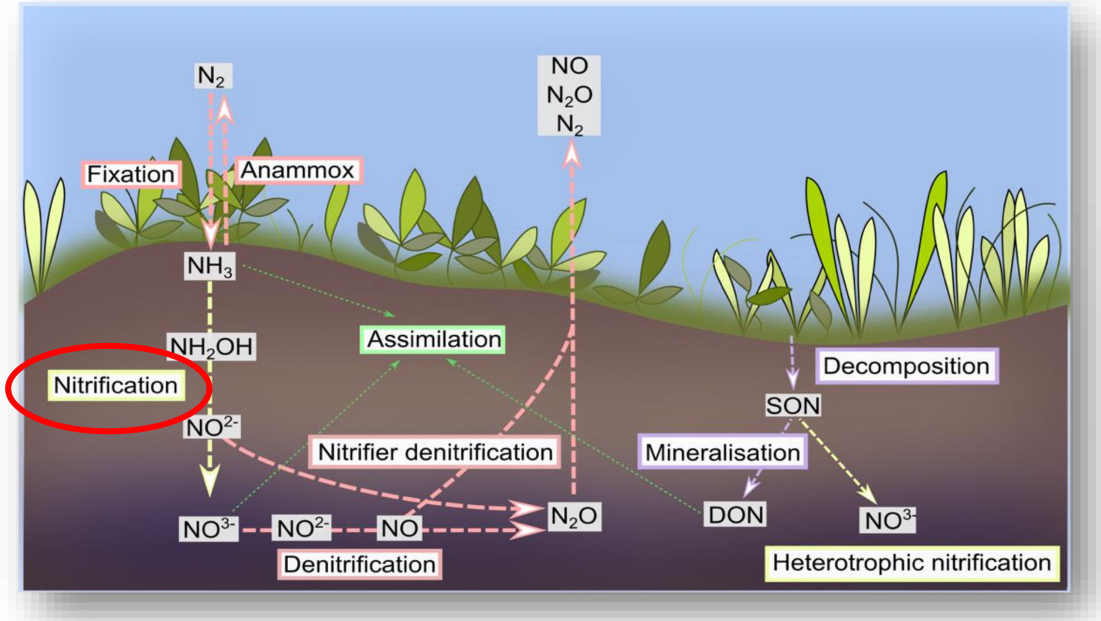
Kvælstofkredsløbet i landbrugsjord

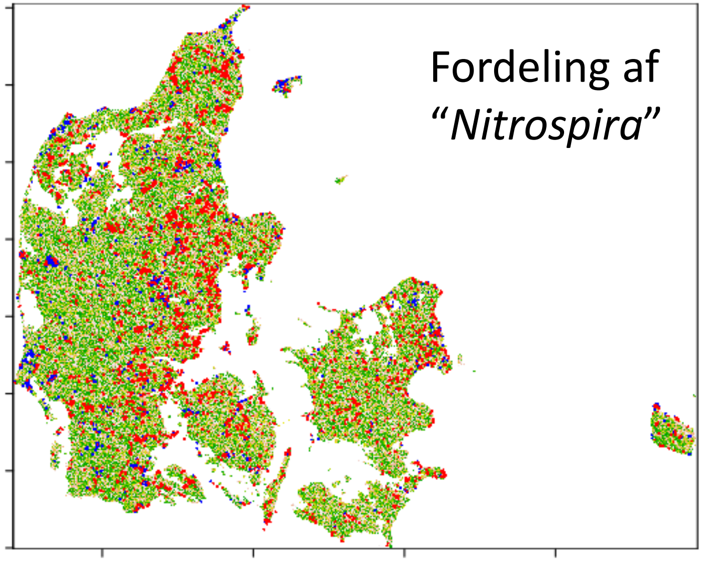
Nitrifikation

- Fordeling af nitrifikanter i Denmark inkl. 2500 prøver i landbrugsjord
- > 600 genomer fra nitrifikanter – det største studie nogensinde
- Mange nye nitrifikanter – både slægter og arter
- Vil danne grundlag for fremtidige studier af nitrifikation i (landbrugs) jord

Relativ hyppighed af de dominerende nitrifikanter i landbrugsjord



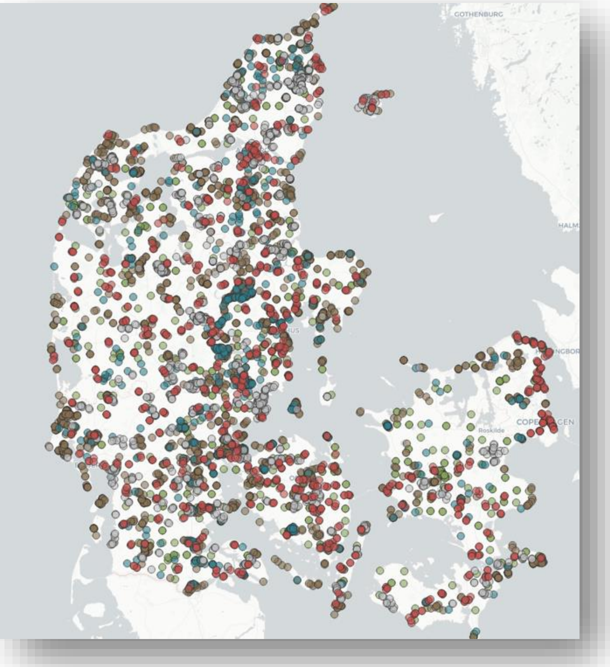



Fordeling af “*Nitrospira*”

Spændende spørgsmål: hvad bestemmer arters udbredelse?

MICRO
FLORA
DANICA

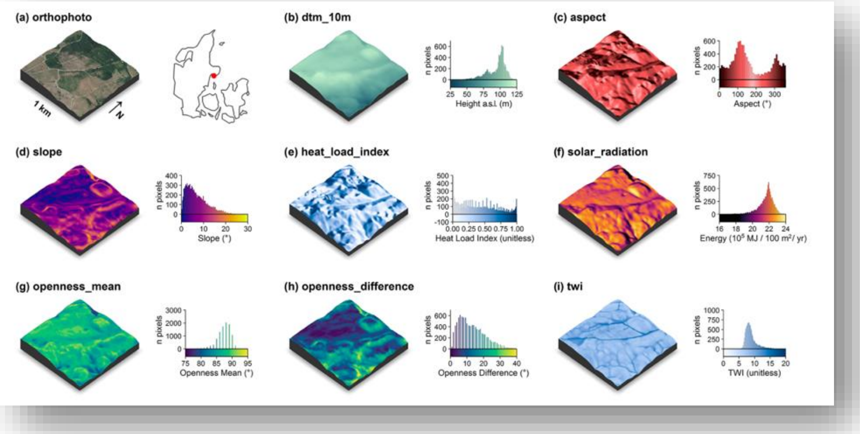
Microflora Danica data



Francesco Delogu

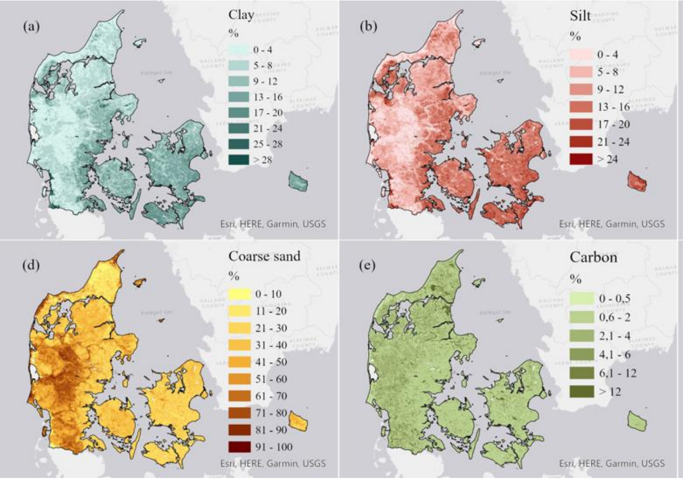
+

Satelite & drone imaging



Prof.
Signe Normand

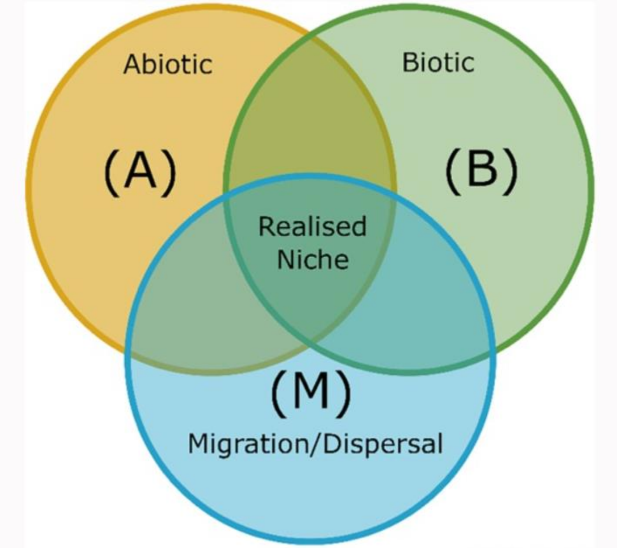
Soil properties



Prof.
Lis W. de Jonge

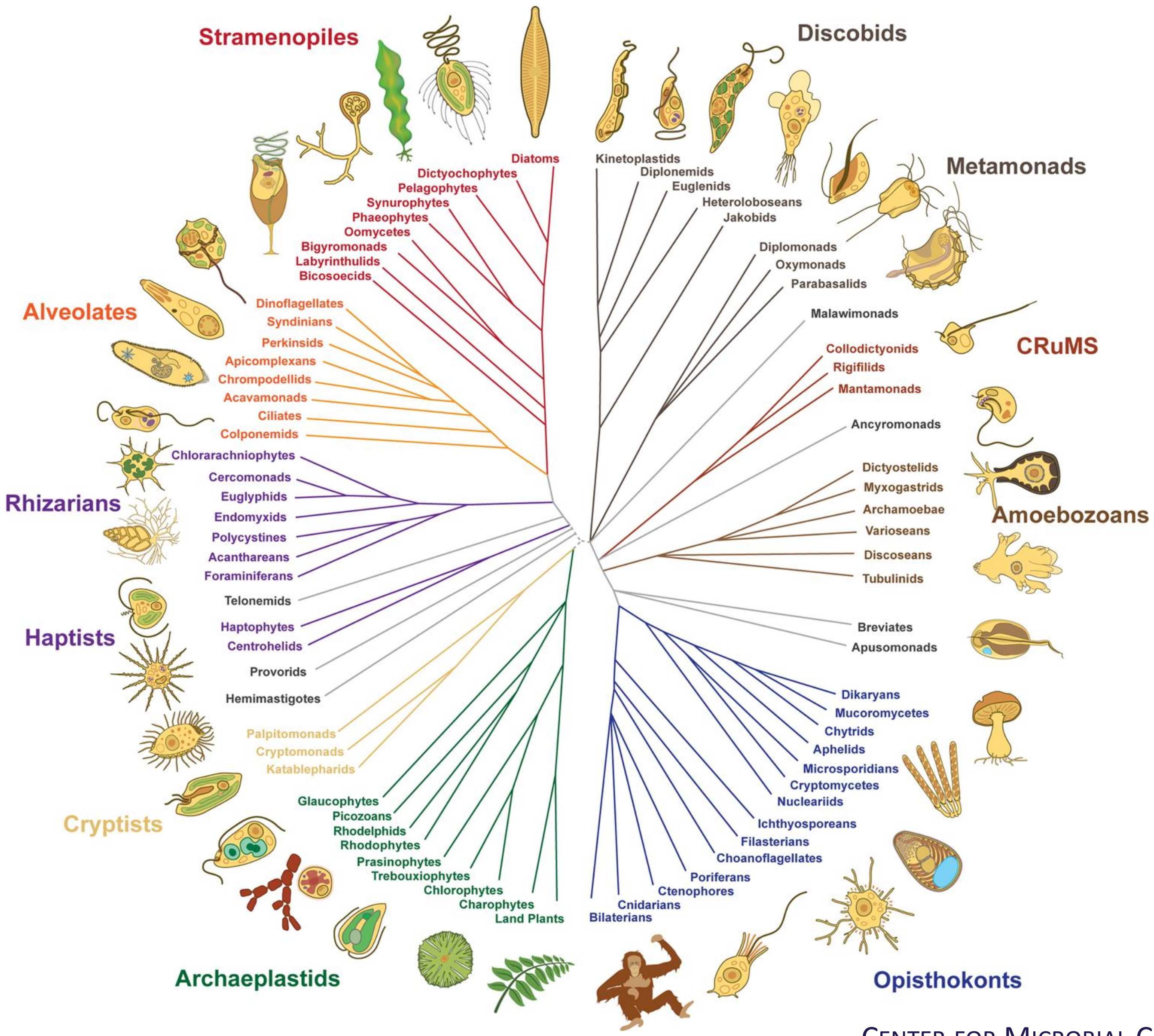
Prof.
Mogens H. Greve

=



BAM framework

Vi er også i gang med at se på de små eukaryoter (svampe, protister,….)



Keeling and Eglit, 2023

Center for Microbial Communities

POUL DUE JENSEN / GRUNDFOS FOUNDATION

VILLUM FONDEN

www.microfloradanica.aau.dk

AALBORG UNIVERSITET

MICROFLORA DANICA

FORSIDE BIO / MICROFLORA DANICA /

HVORDAN DÆKKER VI DANMARK? IDENTIFIKATION AF MIKROORGANISMER BAGGRUND OG METODER MIKROORGANISMER OG DERES BETYDNING TILKNYTNING TIL FLORA DANICA PRESSEARKIV - MICROFLORA DANICA PRESSEARKIV - CORONA DANICA INTERNE SAMARBEJDSPARTNERE EKSTERNE SAMARBEJDSPARTNERE INTERACTIVE MAP

MICRO FLORA DANICA

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– DANMARKS MICROBIOM

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+ OM PROJEKTET

Microflora Danica skal skabe en reference database eller et atlas over alle mikroorganismer, som findes naturligt i Danmark. Projektet udføres på Institut for Kemi og Biovidenskab ved Aalborg Universitet og er støttet af Poul Due Jensen/Grundfos fonden med 30 millioner kroner i perioden 2019-2023

Projektet er finansieret af:

POUL DUE JENSEN / GRUNDFOS FOUNDATION

BAGGRUND OG METODER

Læs mere om Microflora Danicas ideologiske tilknytning til det historiske værk Flora Danica, samt om mikroorganismer og deres betydning, og hvordan mikoorganismer identificeres.

LÆS MERE

"Den videnskabelige og teknologiske betydning af en sådan mikrobiologisk database (et atlas) kan vanskeligt overvurderes. Når de store linjer i atlas'et engang er identificeret, vil det ikke ske igen. Projektet har derfor mulighed for at skabe signifikant impact på både kort og lang tidshorisont."

– Poul Toft Frederiksen, programchef for Forskning, Poul Due Jensen/Grundfos Fonden

HVORDAN DÆKKER VI DANMARK?

Læs mere om, hvordan 10.000 prøver indsamles på tværs af Danmarks geografi og terræn for at dække den mikrobielle diversitet, som findes i jordhøjde, i både terrestriske og akvatiske miljøer.

LÆS MERE

+ SAMARBEJDSPARTNERE

+ MATERIALE TIL PARTNERE

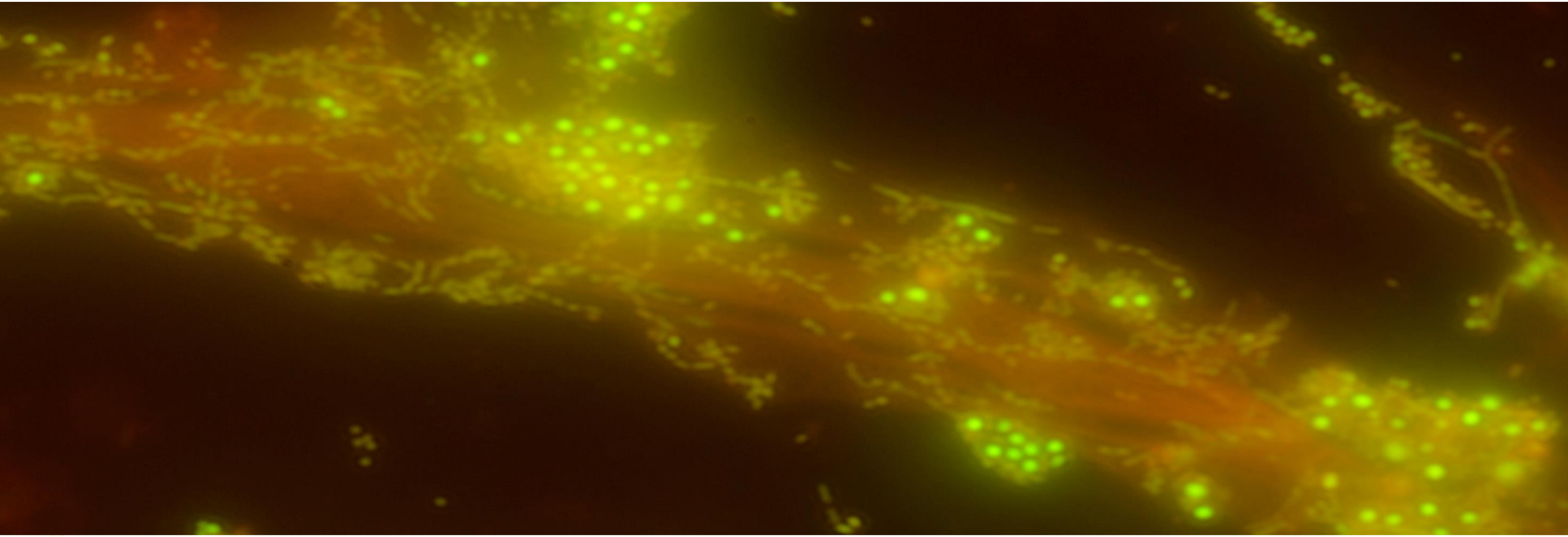
+ PRESSEARKIV

+ MICROFLORA DANICA TEAMET

KORT OVER MICROFLORA DANICA

VERDENSMÅL for bæredygtig udvikling

Mikrodiversitet omkring rødder
- kan vi forædle til et bedre mikrobiom?



INTERACT

novo nordisk fonden

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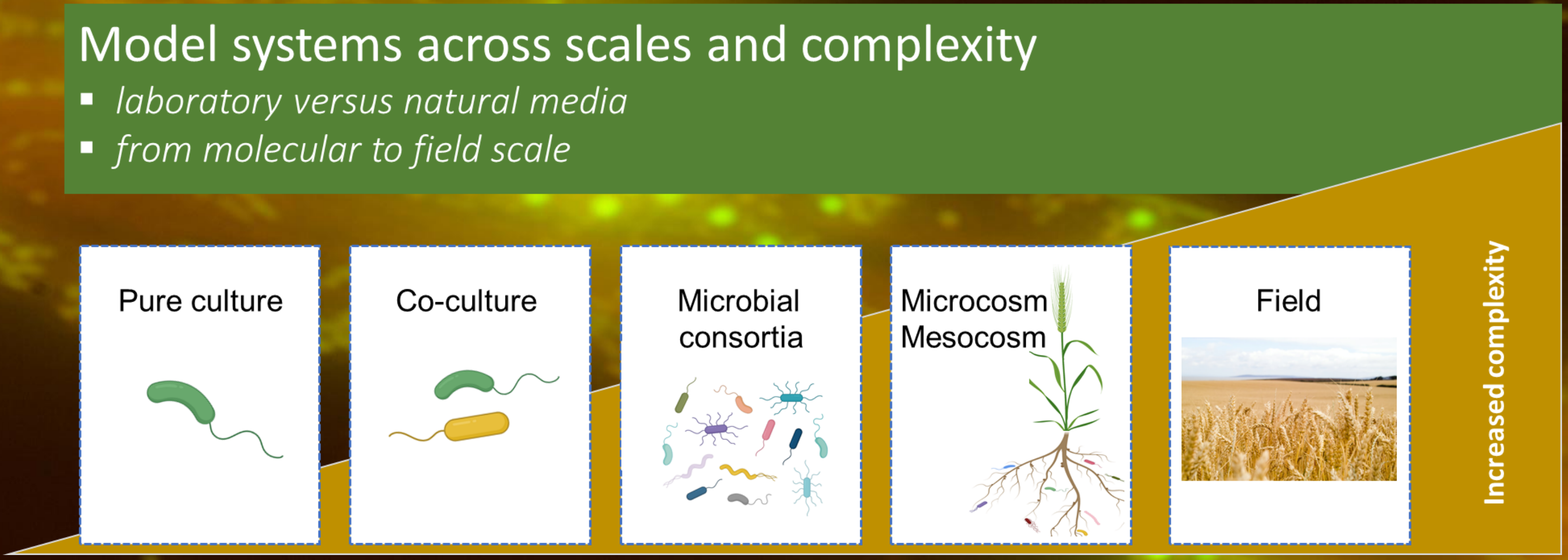
⇨ Green solutions



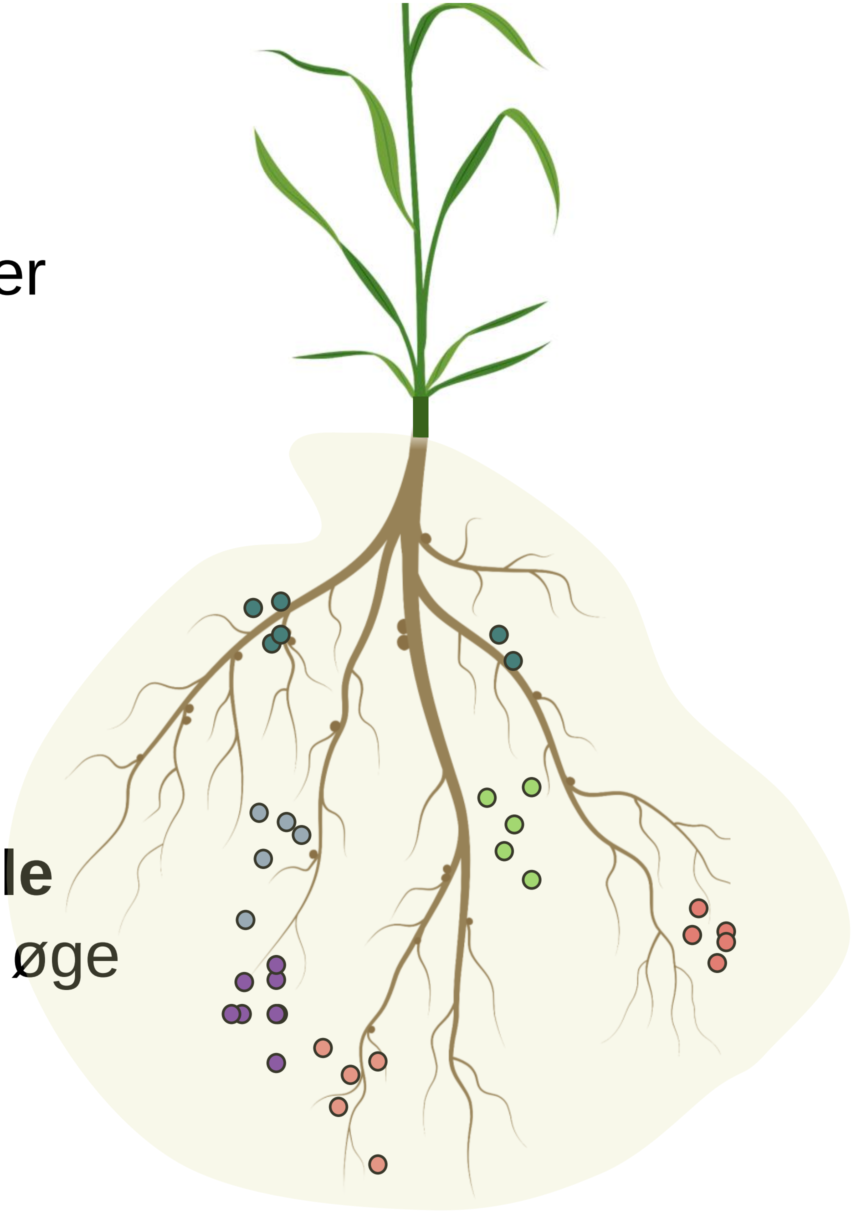
Model systems across scales and complexity

- *laboratory versus natural media*
- *from molecular to field scale*

- **Forstå mikrobiel økologi i jord-plante-microbe systemet**
- **Funktionel forståelse af plante-microbe interaktioner**

Rødder som et forædlings-target?

- Jordens **mikroorganismer** er **diverse**, og lever I samfund med et **komplekst netværk** af interaktioner
- Planterødder – **metabolsk aktivt hotspot**
- **Mikroorganismer** bidrager med mange **vigtige funktioner** der styrker plantevækst



Hvilke parameter er vigtige for hvordan de **mikrobielle samfund etablerer sig** på rødderne – hvordan kan vi øge de positive interaktioner?

1. Er der forskel i den mikrobielle intraspecies diversitet mellem sorter?

- Forskellig resistensprofil i forhold til *Fusarium* infektioner

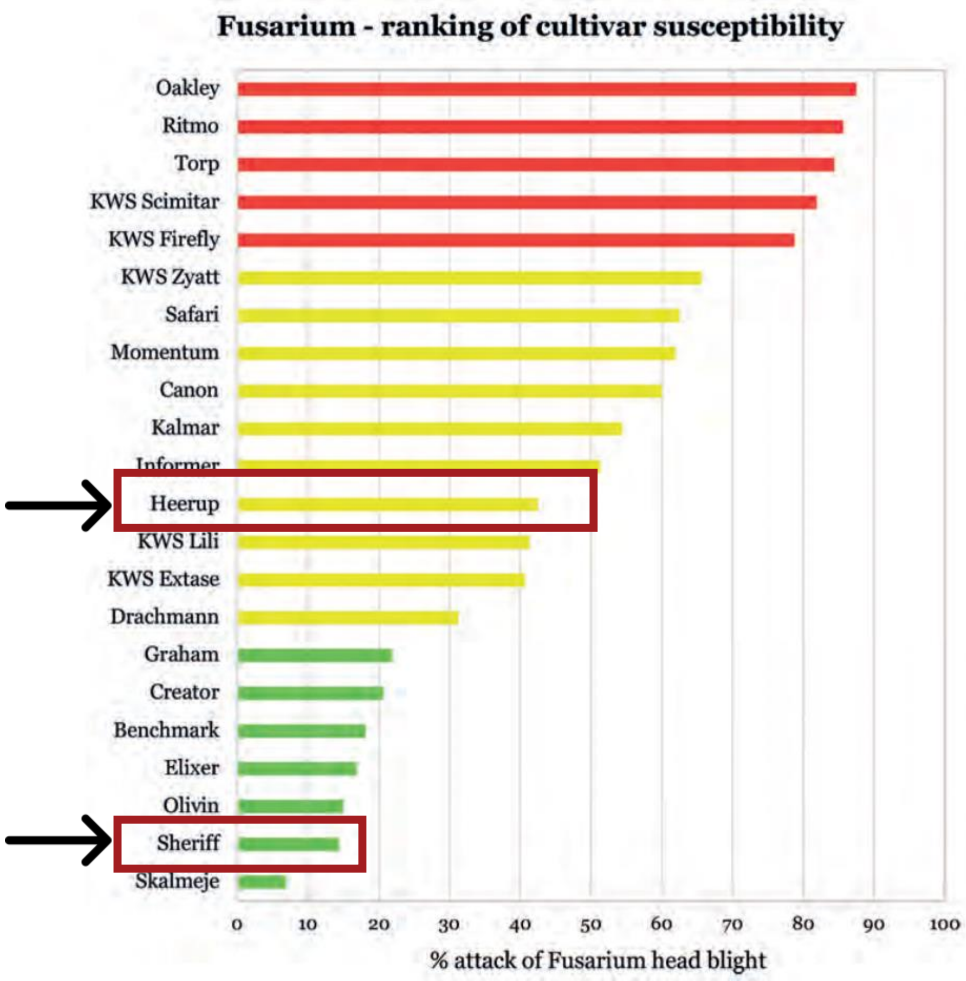


Figure 21. Per cent attack of Fusarium head blight in late July. Average of both trials. The LSD_{95} value = 5.5.

Jørgensen et al., 2020 *Aarhus University*

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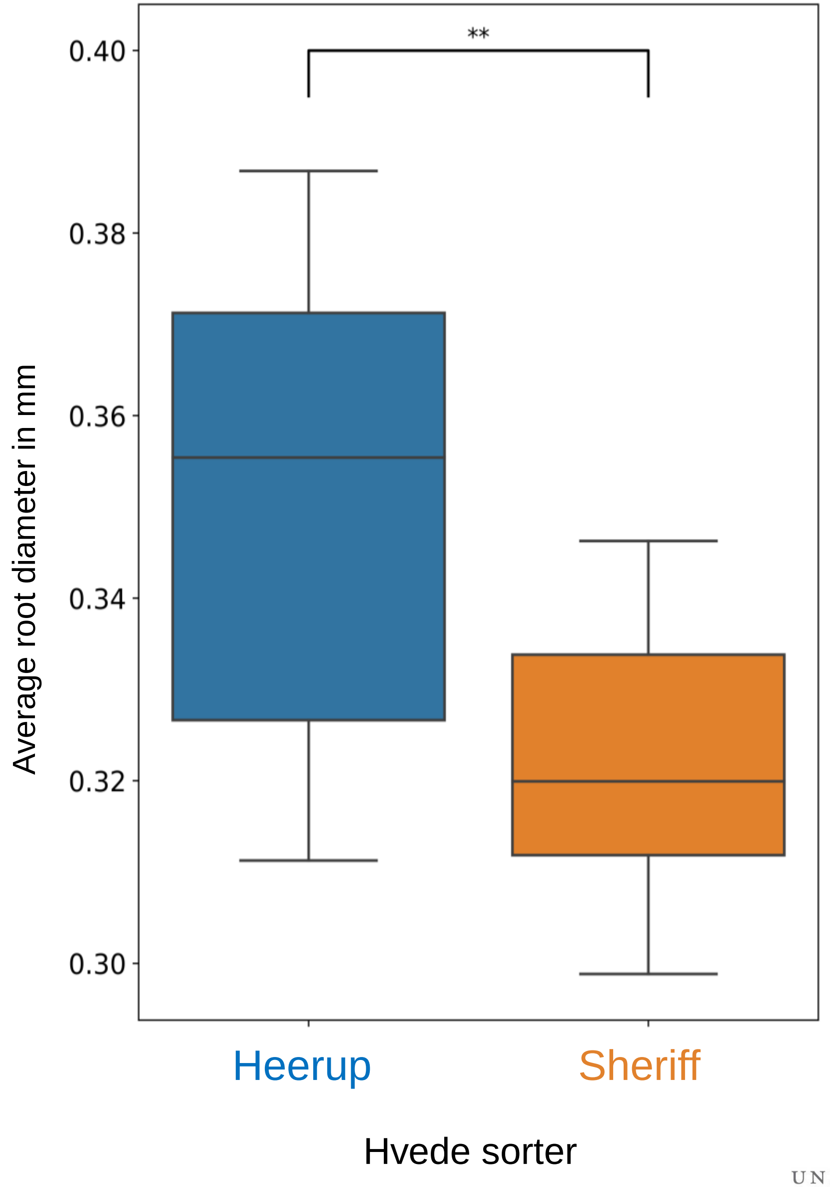
1. Er der forskel i den mikrobielle intraspecies diversitet mellem sorter?

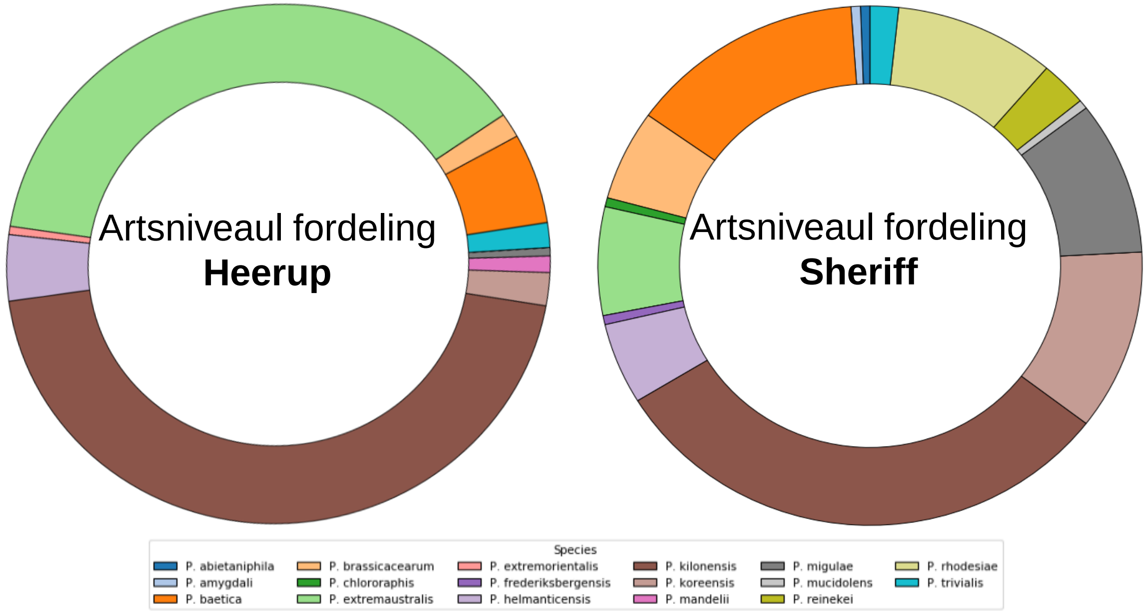
- Forskellig resistensprofil i forhold til *Fusarium* infektioner
- Signifikant forskel i rod-diameter mellem de to sorter



1. Er der forskel i den mikrobielle intraspecies diversitet mellem sorter?

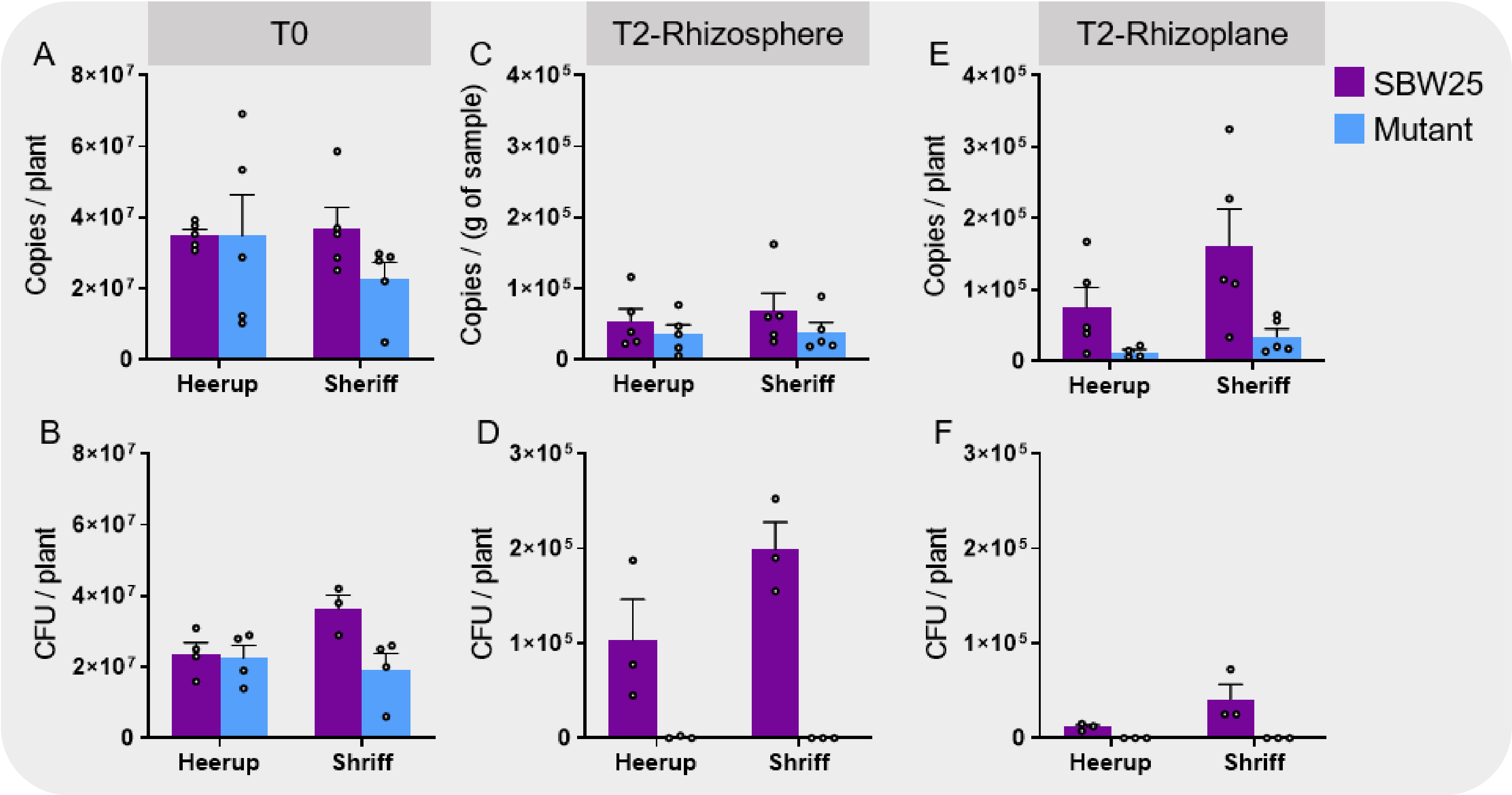
Isolering af 600 Pseudomonas stammer
~300 fra hver sort

16S rRNA **taxonomi**



- Højere diversitet omkring Sheriff rødder
- Samme arter har forskellig gen-sammensætning

2. Er der helt specifikke træk hos mikroberne som er vigtige for at kolonisere rødder?

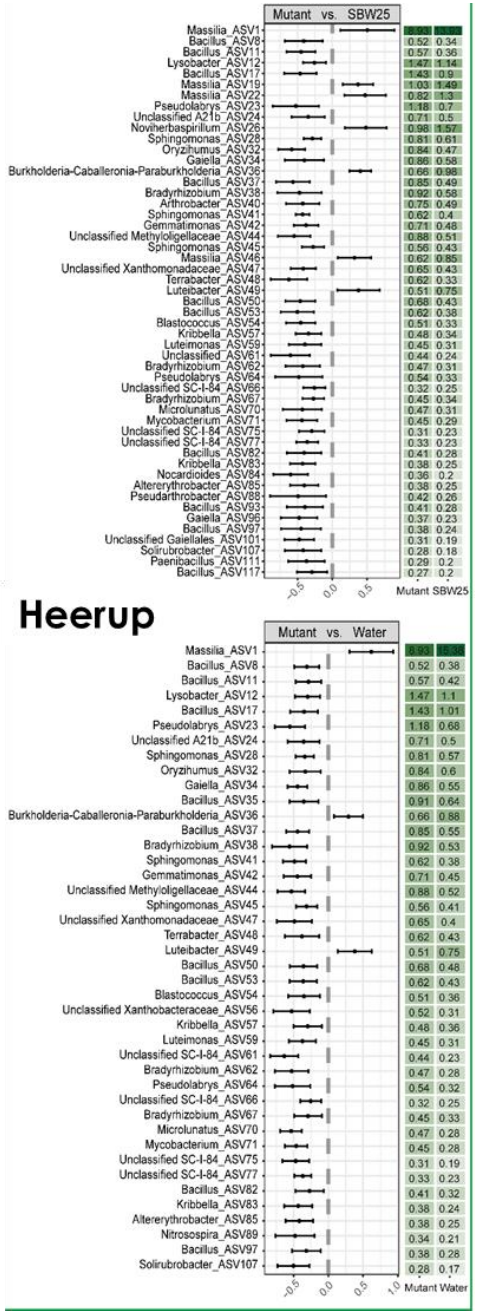


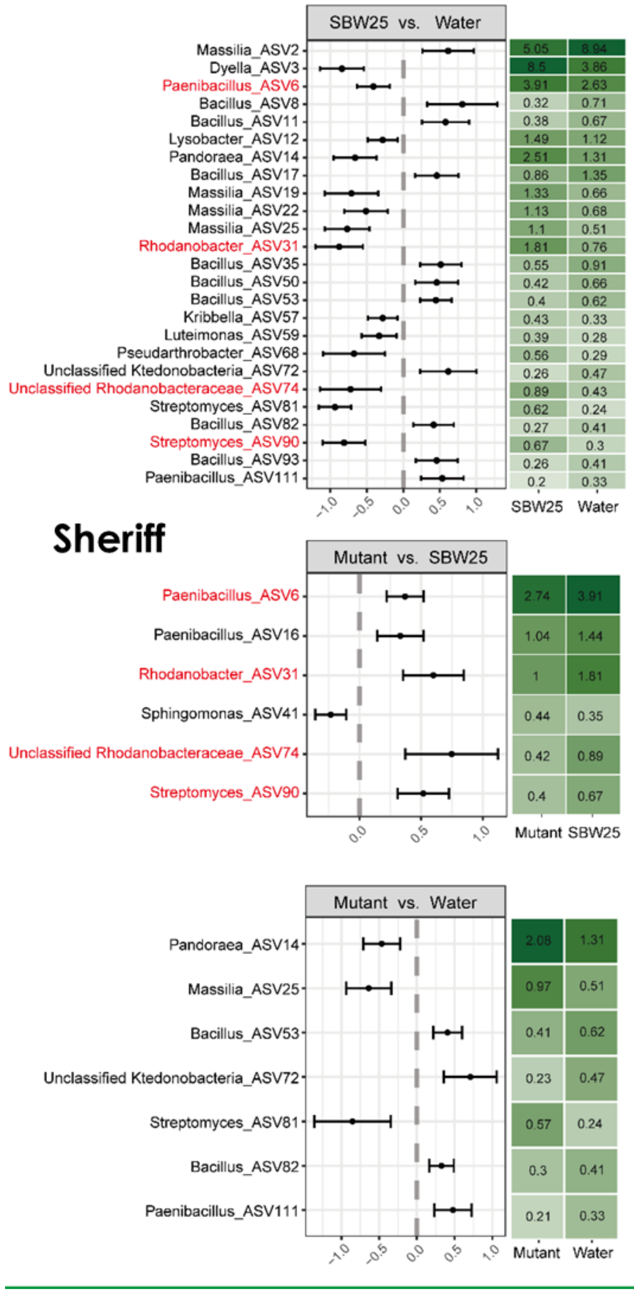
- *Pseudomonas* SBW25, der producerer viscosin, koloniserer hvederødder bedre end den tilsvarende mutant som ikke kan producer viscosin

2. Er der helt specifikke træk hos mikroberne som er vigtige for at kolonisere rødder?

Evnen til at producere viscosin har også en indflydelse på hvilke organismer der ellers koloniserer

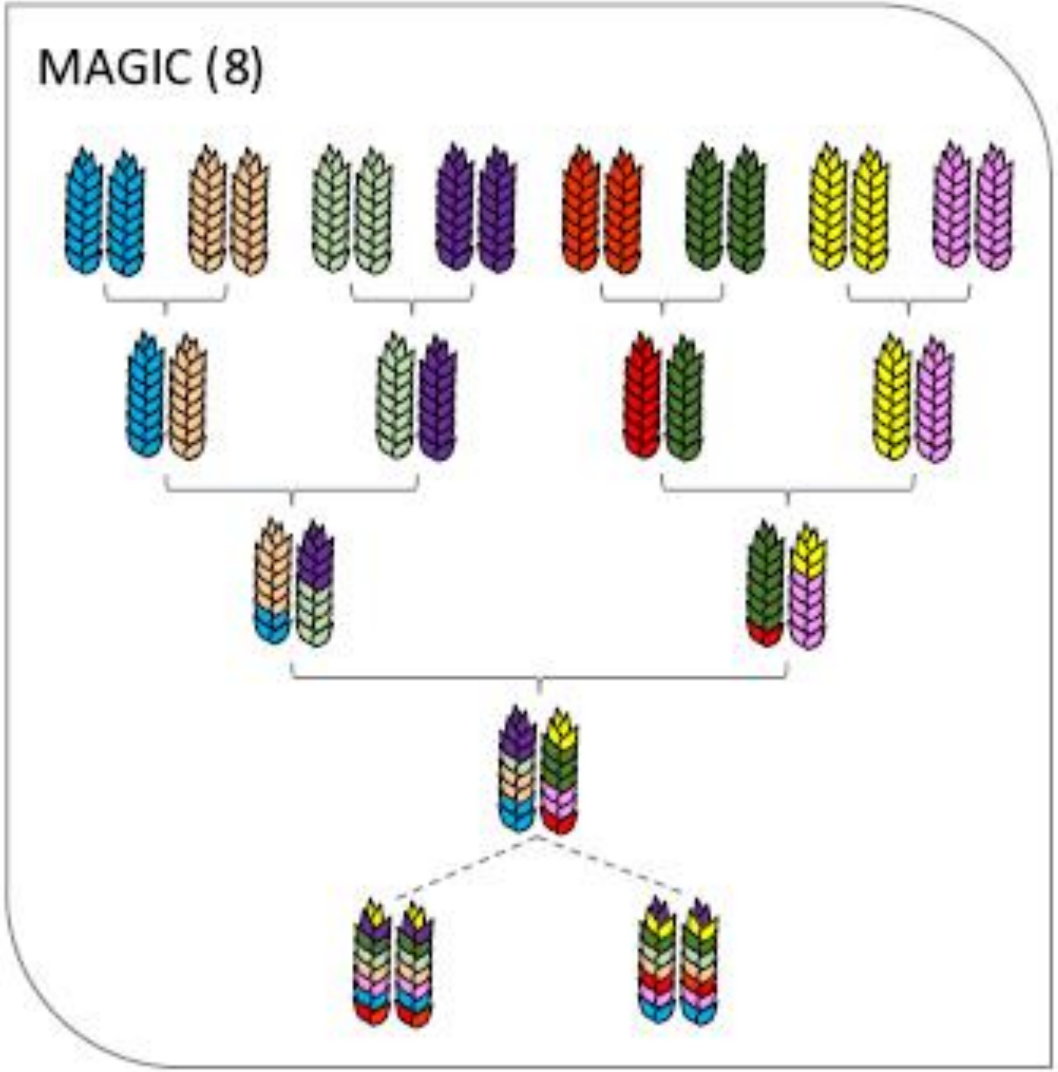
- både bakterier og protozoer





Ved at fokusere ensidet på forædling af udbytte og vækst, har vi så mistet vigtige interaktioner mellem rødder og mikroorganismer?

I samarbejde med hvede genetikere fra NIAB, Cambridge har vi adgang til hvede populationer med forskellig genetisk sammensætning e.g. MAGIC



Cockram J (2023).. Compendium of Plant Genomes. Springer, Cham. Pp 289-320.

Fokus på at forstå kolonisering af rødder, indflydelse på plantevækst samt hvorvidt der er en genetisk komponent der styrer den specifikke kolonisering af mikroorganismer

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