42nd Annual Meeting of NSCMID

ABSTRACT BOOK

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Oral Presentations

O1 The Effects of Infant Antibiotic Exposure on Microbiome Composition and Vaccine Responses

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Background: Antibiotics are essential and effective in the treatment of serious infections in infants. Disruption of the gut microbiome following antibiotic treatment may however have adverse effects on normal development of the immune system.

Methods: This prospective, cohort study included 199 term infants born in Iceland with follow-up for 13 months. The cohort had four equal groups according to early antibiotic exposure; G1: Elective caesarean section with maternal intra-operative antibiotics, G2: Vaginal birth and maternal intra-partum antibiotics, G3: Infants treated with systemic antibiotics during the first week of life for ≥48 hours, and G4: Vaginal birth infants without antibiotic exposure. Blood and stool samples were collected. Microbiome composition and antibody responses to pneumococcal vaccinations were measured and compared.

Results: In total, 187 children completed the study. The microbiome composition was significantly different between the study groups where mode of delivery was the strongest driving factor ($p<0.05$). The microbiome was more diverse in the control group compared with other groups ($p<0.1$) and this was correlated with higher serum antibodies against pneumococcus, serotype 19F, at 13 months ($p<0.05$). Cluster analysis revealed four different clusters where children in the control group had the highest proportion of the BACT/BIFI cluster and lowest proportion of the CLOS cluster (Figure 1). The microbiome of infants in the control group was richer in Bacteroides species whereas children treated with antibiotics had lower amount of Lactobacillus species. The amount of Clostridium sensu stricto species increased with longer duration of antibiotic treatment.

Conclusions: The microbiome of infants born vaginally without antibiotic exposure was more diverse and richer in Bacteroides compared with antibiotic exposure groups. Greater microbiome diversity in the control group was associated with stronger pneumococcal vaccine responses. These results should support a more conservative approach to antibiotic treatment during delivery and in early infancy.

O2 Risk of acute kidney injury after empirical gentamicin treatment in patients with suspected sepsis

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Objective
Aminoglycosides are important in treatment of sepsis, but their use is debated, and there is a concern for aminoglycoside nephrotoxicity. This study assesses the presence of acute kidney injury (AKI) after admission in patients admitted to hospital with suspected sepsis receiving either empirical gentamicin-combination therapy or non-gentamicin regimens.
Methods
We conducted a retrospective cohort study at Oslo University Hospital Ullevål from 2017 to 2024. Patients without known chronic kidney disease admitted with suspected sepsis were included. The two treatment groups (gentamicin and non-gentamicin) were matched using 1:1 nearest neighbor propensity score matching. The primary outcome was presence of AKI at any time between day 2 and 10 after admission. Secondary outcomes were new or worsened stages of AKI after admission, 30-days mortality and total burden of broad-spectrum antibiotics.
Results
The propensity score matching yielded two balanced groups comprising a total of 2,086 patients, including 1,043 receiving a gentamicin-based empirical regimen and 1,043 receiving other, mostly broad-spectrum antibiotic regimes. No significant difference in presence of AKI between day 2 and 10 was detected between the gentamicin group and non-gentamicin group (259/1,043 (24.8%) versus 281/1,043 (26.9%), odds ratio (OR) 0.90 [95% CI 0.74; 1.08]). Similarly, no significant differences were observed in secondary outcomes; new or worsened stage of AKI after admission (133/1,043 (12.8%) versus 122/1,043 (11.7%), OR 1.10 [95% CI 0.85; 1.44] or 30-days mortality (95/1,043 (9.1%) versus 116/1,043 (11.1%) hazard ratio 0.81 [95% CI 0.63; 1.05]). Patients in the gentamicin group had significantly lower probability of receiving broad-spectrum antibiotics such as beta-lactam/beta-lactamase-inhibitor combinations (ATC code J01CR) (OR 0.52 [95% CI, 0.41-0.66]) and third generation cephalosporins (ATC code JO1DD) (OR 0.26 [95% CI 0.21-0.32]) during the hospital stay.
Conclusions
Empirical treatment with gentamicin was not associated with increased presence of AKI between days 2-10 after admission in patients with suspected sepsis.

O3 Plasma level of soluble urokinase-type plasminogen activator receptor (suPAR) predicts severe disease in Streptococcus dysgalactiae subsp. equisimilis bacteremia

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Background: Streptococcus dysgalactiae subspecies equisimilis (SDSE) is increasingly recognized as a cause of severe systemic and bacteremic infections [1,2]. Elevated soluble form of urokinase-type plasminogen activator receptor (suPAR) concentration predicts disease severity and outcome in bacteremic infections [3,4]. The aim of this study is to evaluate the association between elevated suPAR levels and underlying diseases, clinical manifestations, and disease severity in SDSE bacteremia.
Methods: Adult patients with a positive blood culture for SDSE treated at Tampere University Hospital or Hatanpää City Hospital in Tampere, Finland, between November 2015 and November 2019 were recruited into this prospective study (N = 159). Severe disease was defined as requiring intensive care unit treatment or death within 30 days of hospital admission. Plasma suPAR analyses were performed using enzyme-linked immunosorbent assay (ELISA) (suPARnostic®, ViroGates A/S, Birkerød, Denmark).
Results: Plasma suPAR levels were quantified in 153 samples. The median first suPAR concentration (0 to 2 days after admission) was 4.81 ng/mL (interquartile range [IQR], 3.53-7.19 ng/mL). SuPAR concentrations were significantly higher in severe disease compared with non-severe disease (medians 8.03 ng/mL vs. 4.54 ng/mL, $p < 0.001$). Patients with chronic liver disease (10.7 ng/mL [7.54-17.1 ng/mL], $p < 0.001$), cardiovascular disease (5.80 ng/mL [4.26-7.84 ng/mL], $p = 0.001$), kidney disease (6.89 ng/mL [4.99-8.22 ng/mL], $p = 0.003$), and alcohol abuse (7.54 ng/mL [5.07-11.2 ng/mL], $p = 0.009$) had elevated suPAR levels. Elevated suPAR levels were associated with pneumonia (6.15 ng/mL [IQR 5.07-8.63 ng/mL], $p = 0.002$) and abscesses (7.43 ng/mL [4.76-8.73 ng/mL], $p = 0.010$). Notably, the association between high suPAR levels and severe disease remained significant also in multivariable-adjusted logistic regression models when adjusted for confounding factors.
Conclusions: High suPAR levels predict severe disease in SDSE bacteremia. Assessing suPAR levels in the emergency department could help identify patients at increased risk of severe outcomes.

O4 Host-pathogen interactions shape persistence in Staphylococcus aureus bacteremia: a machine learning approach in a population-based cohort

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Background:
Persistent Staphylococcus aureus bacteremia (SAB) is associated with adverse outcomes and reflects complex host–pathogen interactions. The contribution of bacterial genomic variation to persistence remains incompletely defined. We evaluated whether integration of bacterial genomic features and clinical data improves prediction of persistent SAB in a population-based cohort.
Methods:
All adult patients with SAB in two Swedish regions were included. Whole-genome sequencing was performed for all available isolates. Persistent bacteremia was defined based on follow-up blood cultures. Machine learning models were developed using five feature sets comprising clinical variables, infection focus, and bacterial pangenome data. Model performance was assessed using the area under the receiver operating characteristic curve (ROC-AUC), with final evaluation on a held-out test set. Genome-wide association and phylogenetic analyses were conducted to identify bacterial genomic features associated with persistence.
Results:
Among 303 SAB episodes, persistent bacteremia occurred in 36%. Models incorporating bacterial genomic features outperformed those based solely on clinical variables. The combined model including pangenome, patient characteristics, and infection focus achieved the highest performance on the test set (sensitivity 0.83, specificity 0.81). Genomic features associated with persistence included loci linked to mobile genetic elements and virulence-associated genes, including components of the type VII secretion system and oxidative stress response pathways. Sequence type 45 was significantly associated with persistent bacteremia (odds ratio 1.87; 95% confidence interval, 1.03–3.38).
Conclusions:
Integration of bacterial genomic features with clinical variables improved prediction of persistent SAB compared with either domain alone. These findings support the concept that persistent SAB reflects dynamic host–pathogen interactions rather than a single determinant.

O5 Faecal microbiota transplantation for decolonisation of multidrug-resistant organisms in adult gastrointestinal carriers – a randomised clinical trial

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Background
The aim of the study was to investigate the effect of faecal microbiota transplantation (FMT) on decolonisation of gastrointestinal multidrug resistant organisms (MRO) defined as vancomycin resistant Enterococcus faecium (VREfm), carbapenemase-producing Enterobacterales (CPE), and extended-spectrum beta-lactamase-producing/AmpC-carrying Enterobacterales (ESBL/AmpC-E).

Methods
We conducted a multicentre, randomised, placebo-controlled, and double-blinded clinical study. We routinely sent invitations by secure digital mail to individuals with an MRO positive sample. Participants were randomised 1:1 to FMT or placebo. The intervention consisted of one portion of 20-36 capsules with FMT/placebo consumed once. The capsules were produced at Copenhagen University Hospital Hvidovre.
Two rectal swabs were collected at baseline and at the follow-up visits after eight weeks, 16 weeks and one year for MRO detection and microbiome analysis.
Inclusion criteria were minimum 18 years of age, capable of swallowing capsules, able to speak and understand Danish or English, and a positive rectal screening for MRO at baseline.
The study was approved by the Independent Ethics Committee with reference number H-22040517 and registered at clinicaltrials.gov (NCT05742074) before inclusion of the first participant.
We are currently working on the microbiome analysis.

Results
We included 83 participants (3 CPE, 78 ESBL/AmpC-E, 1 VREfm, and 1 VREfm and ESBL/AmpC-E). After 8 weeks 30% (12/40) decolonised in the FMT-group vs. 25% (10/40) in the placebo-group (OR 1.42 95% confidence interval [0.51:4.05], and p = 0.503). At 16 weeks 51.3% (20/39) decolonised in the FMT-group vs. 22.5% (9/40) in the placebo-group (OR 4.07 95% confidence interval [1.43:12.52], and p = 0.011). After 1 year 63.6% (21/33) decolonised in the FMT-group vs. 40% (14/35) in the placebo-group (OR 5.95 95% CI [1.68:26.08], and p = 0.010).

Conclusion
In our study population an effect of FMT on decolonisation of MRO was shown after 16 weeks and sustained at 1 year.

Poster presentations

Total poster walk and theme overview

Poster walk number	Poster walk day	Poster number	Themes
1	Friday	P01-P06	Antimicrobial Resistance (AMR) Antimicrobial Stewardship (AMS)
2	Friday	P07-P12	Basic research Microbiome
3	Friday	P13-P18	Diagnostic microbiology
4	Friday	P19-P23	Bacterial, fungal and viral infections
5	Saturday	P24-P29	Bacterial, fungal and viral infections
6	Saturday	P30-P35	Antimicrobial Resistance (AMR)
7	Saturday	P36-P41	Infection prevention and Infection control
8	Saturday	P42-P46	Diagnostic microbiology

See more detailed poster walk overview under each poster theme below

Antimicrobial Resistance (AMR) posters

Poster walk overview

Poster number	Abstract title	Poster walk number	Poster walk day
P01	AI-based prediction of antibiotic susceptibility in Escherichia coli using partial phenotypic data	1	Friday
P02	Penicillin susceptibility and resistance in Staphylococcus aureus from blood isolates– a multicenter surveillance study in Denmark, Iceland, Norway and Sweden	1	Friday
P03	Surveillance of Antibiotic Treatment and Resistance in Urinary Tract Infections Among the Older Population in Denmark	1	Friday
P04	Real-world cefiderocol outcomes in the treatment of Stenotrophomonas spp. infections: data from the PROVE study	1	Friday
P30	Activity of cefiderocol against Stenotrophomonas maltophilia collected in multinational surveillance studies SIDERO-WT (2014-19) and SENTRY (2020-24)	6	Saturday
P31	Detection of Carbapenemase producing Gram-negative bacteria in wastewater from the Reykjavík Capital area	6	Saturday
P32	Antimicrobial Resistance Profiles and Resveratrol Activity Against Clinical Aeromonas Species Isolates	6	Saturday
P33	Contrasting pH optima of beta-lactamases CTX-M and CMY influences Escherichia coli fitness and resistance ecology	6	Saturday
P34	Penicillin susceptibility in Enterococcus faecalis: An indel n.1216129delT is a necessary but not sufficient genetic determinant of decreased susceptibility.	6	Saturday
P35	Clindamycin's role in MRSA decolonization treatment; A randomized, placebo-controlled, double-blinded trial	6	Saturday

P01 AI-based prediction of antibiotic susceptibility in Escherichia coli using partial phenotypic data

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Background:
Rapid antimicrobial susceptibility results are important for treatment decisions and antimicrobial stewardship. Artificial intelligence (AI) models trained on large datasets may enable prediction of resistance to untested antibiotics using partial routine diagnostic data. Such approaches could support clinical decision-making before full results are available. This study evaluated an AI model trained on European surveillance data from clinical blood isolates, including 1,161,303 Escherichia coli.

Materials/Methods:
Ninety-nine E. coli isolates from clinical urine cultures were selected to maximize phenotypic diversity. Disk diffusion susceptibility testing followed EUCAST methodology. The AI model predicted susceptibility to 14 antibiotics using 4–8 known results as input. An optional uncertainty layer allowed the model to refrain from predictions when the estimated error risk exceeded a predefined threshold. Performance was evaluated using major error (ME; false resistant prediction) and very major error (VME; false susceptible prediction) rates across combinations of input antibiotics.

Results:
The overall ME rate was 15% and the VME rate 9.5% when six input antibiotics were used to predict eight additional antibiotics, restricted to combinations including ≥1 antibiotic from each class. Applying a 10% uncertainty threshold reduced errors to 8% and 2.5%, respectively, but also reduced predictions as the model abstained in uncertain cases. Major errors were more frequent than very major errors, and this pattern was reinforced with the uncertainty threshold. Error rates varied substantially between antibiotics, with highest ME for amoxicillin/clavulanic acid and highest VME for piperacillin/tazobactam. This skew toward major errors was not observed during model development.

Conclusions:
AI-assisted susceptibility prediction from partial phenotypic data is feasible and improves with additional input antibiotics. Incorporating uncertainty thresholds reduced prediction errors, particularly very major errors. Remaining antibiotic-specific errors likely reflect limitations of available input information, highlighting the need for more informative data such as zone diameters or genomic information before clinical implementation.

P02 Penicillin susceptibility and resistance in Staphylococcus aureus from blood isolates– a multicenter surveillance study in Denmark, Iceland, Norway and Sweden

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Background

Staphylococcus aureus bloodstream infection remains a major clinical concern, with high incidence and substantial mortality. Although wild type S. aureus is susceptible to benzylpenicillin, resistance emerged rapidly after the introduction of benzylpenicillin, driven by blaZ-encoded penicillinase. Recently there has been renewed interest in the potential benefits of using benzylpenicillin to treat infections caused by penicillin susceptible S. aureus (PSSA). Accurate local prevalence data and reliable susceptibility testing are essential. This study aimed to determine the prevalence of PSSA in Denmark, Iceland, Norway, and Sweden and to examine susceptibility patterns to non-beta lactam antibiotics for S. aureus in positive blood cultures.

Methods

Clinical microbiology laboratories in Sweden, Denmark, Norway, and Iceland contributed antibiotic susceptibility testing (AST) results for S. aureus blood culture isolates collected during a consecutive six month period in 2024-2025. Only the first isolate per patient was included. Susceptibility to non-beta lactam antibiotics was also recorded.

Results

A total of 2,260 isolates were included. The incidence of SAB ranged from approximately 40 to over 60 cases per 100,000 inhabitants annually. Overall, 32% of isolates were PSSA, with similar proportions across countries except for Iceland (where 17.5% of isolates were PSSA). MRSA isolates showed significantly higher resistance to clindamycin, fluoroquinolones, trimethoprim sulfamethoxazole, and erythromycin compared with MSSA and PSSA isolates (see table).

Conclusions

PSSA constitutes a substantial proportion of S. aureus isolated from blood cultures in Nordic countries. Implementing and reporting penicillin susceptibility testing more widely would support its role in treatment strategies and enable more targeted therapy with benzylpenicillin, with potential benefit for many patients with Staphylococcus aureus bloodstream infection.

P03 Surveillance of Antibiotic Treatment and Resistance in Urinary Tract Infections Among the Older Population in Denmark

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Background: Antimicrobial resistance is highly correlated with inappropriate use of antimicrobials. Urinary tract infections (UTIs) are the main infections in the older population treated with antibiotics.

Aim: The aim of this study is to investigate antibiotic prescription patterns for UTI among older Danish inhabitants as well as resistance trends to assess the impact of antibiotic stewardship interventions and quality improvement strategies.

Methods: This national register-based surveillance study covers older inhabitants (≥ 70 years) in Danish primary healthcare and explores the following:
- Consumption of pivmecillinam, trimethoprim, nitrofurantoin, and sulfamethizole, 1999-2023 (Register of Medicinal Product Statistics)
- Resistance towards pivmecillinam, trimethoprim, nitrofurantoin, and sulfamethizole in E. coli and K. pneumoniae from UTIs, 2018-2023 (Danish Microbiology Database)
- Quality improvement strategies and antibiotic stewardship programs as context for the study, 2005-2020

Results: The highest level of antibiotic consumption for UTI in older inhabitants was registered in 2014 (447 prescriptions/1,000 elderly inhabitants), which decreased by 28.4% in 2023. Resistance towards pivmecillinam, trimethoprim, sulfamethizole, and nitrofurantoin in E. coli and K. pneumoniae decreased significantly from 2018 to 2023 correlating with the simultaneous decline in consumption. Focus on antibiotic stewardship was intensified after 2013, with several quality improvement initiatives (Quality Clusters in general practice, National Antibiotic Council, National Action Plan, national campaigns) and updated treatment guidelines aiming at improving diagnostic and treatment with antibiotics (Figure 1).

Conclusion: Antibiotic consumption for UTI in the older population decreased notably with a simultaneous decrease in resistance levels, reflecting a positive impact of antibiotic stewardship programs to improve diagnostics and treatment. However, the older population increased over the study period, resulting in a higher number of individuals at risk of UTI. This indicates that while AMR in UTI may not pose an acute threat at the moment, it could strain healthcare resources in near future.

P04 Real-world cefiderocol outcomes in the treatment of Stenotrophomonas spp. infections: data from the PROVE study

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Stenotrophomonas spp. have emerged as significant opportunistic pathogens owing to their intrinsic resistance, which limits treatment options.1 This subgroup analysis of the PROVE study examined clinical outcomes of individuals with infections caused by Stenotrophomonas spp. who received treatment with cefiderocol.
PROVE was an international, observational chart review study of real-world cefiderocol use (≥72 hours) in hospitalized patients with confirmed Gram-negative bacterial infections (November 2020-July 2024). We evaluated baseline demographics, clinical characteristics, clinical cure, clinical response and all-cause mortality (ACM) rates from patients treated with cefiderocol for infections caused by Stenotrophomonas spp.
A total of 119 patients had infections caused by Stenotrophomonas spp. Patients had a median (interquartile range [IQR]) age of 60.0 (49.0-67.0) years, and 66.4% were male. In total, 73.9% of patients required an intensive care unit stay at the time of cefiderocol initiation, while 63.0% and 49.6% received mechanical ventilation and vasopressors, respectively. Overall, 9.2% of patients had sepsis at admission, with 7.6% having septic shock; 31.1% of patients were immunocompromised. Median (IQR) time from culture to first cefiderocol dose was 5.0 (3.0-8.0) days and duration of cefiderocol use was 11.0 (7.0-15.0 days). Respiratory tract was the main primary site of infection. Approximately two-thirds of patients with Stenotrophomonas spp. infection attained clinical cure (Table 1), including 67.4% of those who received cefiderocol monotherapy (vs 50.0% receiving combination therapy). Clinical response to cefiderocol at end of treatment occurred in 72.3% of patients overall (74.7% and 62.5% of patients given monotherapy vs combination therapy, respectively). Day 14 and Day 30 ACM rates were 20.0% and 29.5%, respectively, with cefiderocol monotherapy and 12.5% and 33.3%, respectively, with combination therapy.
Results from the PROVE study suggest that cefiderocol is an effective treatment for patients with Stenotrophomonas spp. infections, with no obvious differences in outcomes between monotherapy and combination therapy.

P30 Activity of cefiderocol against Stenotrophomonas maltophilia collected in multinational surveillance studies SIDERO-WT (2014-19) and SENTRY (2020-24)

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Stenotrophomonas maltophilia is an opportunistic life-threatening pathogen which shows high intrinsic resistance to a variety of antimicrobials, resulting in limited treatment options. In this study, the activity of cefiderocol, a siderophore-conjugated cephalosporin, was analyzed against clinical isolates collected in two antimicrobial surveillance studies from 2014 to 2024, including the pre-marketing surveillance SIDERO-WT and the post-marketing surveillance SENTRY study.
A total of 4,202 non-duplicate clinical isolates of S. maltophilia collected in the US and Europe from SIDERO-WT (788 isolates from the US and 1,068 isolates from Europe) and SENTRY (1,291 isolates from the US and 1,055 isolates from Europe) were used for analysis. Minimum inhibitory concentrations (MICs) were determined according to CLSI methods using broth microdilution with cation-adjusted Mueller-Hinton broth (CAMHB) for comparator agents and iron-depleted CAMHB for cefiderocol. Susceptibility for cefiderocol and comparator agents was interpreted based on CLSI breakpoints (2025). Cefiderocol susceptibility trends in each region (US and Europe) across ten years were assessed.
Isolates collected in this study were mainly from respiratory infections (64.3%). Against a total of 4,202 isolates, cefiderocol showed potent antimicrobial activity with an MIC50 value of 0.06 mg/L and MIC90 value of 0.25 mg/L (Figure 1). Overall consistent high activity with %S ranging from 95.5% to 100% irrespective of region was observed over time (Figure 1). In comparison to comparator agents (trimethoprim/sulfamethoxazole, levofloxacin, minocycline and aztreonam-avibactam, only analyzed for isolates from the SENTRY study) cefiderocol showed the highest %S (97.9-100%) and lowest MIC90 (0.25-0.5 mg/L) study.
Cefiderocol consistently demonstrated high activity against S. maltophilia over a ten-year period, with no significant change in susceptibility before or after its market introduction. Continued monitoring of cefiderocol susceptibility is warranted to assure its activity is maintained over time.

P31 Detection of Carbapenemase producing Gram-negative bacteria in wastewater from the Reykjavík Capital area

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Antimicrobial resistance is a growing One-Health challenge. Carbapenem-resistant Gram-negative bacteria pose a global health threat due to limited treatment options and widespread burden. Among these, Pseudomonas, and members of the Enterobacterales are priority antimicrobial-resistant pathogens, as identified by the WHO. Wastewater surveillance provides insight into the distribution of resistance genes within communities, and Iceland's national action plan on antimicrobial resistance (2025–2029) highlights the need for increased environmental monitoring. This study aimed to screen wastewater from the Reykjavík capital area for carbapenemase-producing Gram-negative bacteria and to characterise recovered Enterobacterales and Pseudomonas aeruginosa isolates to support future surveillance efforts.
Wastewater samples, collected the winter of 2025-2026, were cultured on antibiotic-supplemented MacConkey agar containing ertapenem and meropenem. Isolates were identified to species level, characterised by antimicrobial susceptibility testing, and screened for carbapenemase activity using the β-CARBA test. In parallel, DNA from wastewater, isolates, and cultured biomass was analysed by qPCR targeting five major carbapenemase families (IMP, NDM, VIM, KPC, and OXA-48-like).
Of 590 isolates recovered, most were non-fermenting Gram-negative bacteria (86.9%), predominantly Pseudomonas spp. (56.3%) and Acinetobacter spp. (22.4%). Only 11 isolates (1.9%) were target organisms (5 Enterobacterales, 6 P. aeruginosa). Among the Enterobacterales isolates, 4/5 were resistant to ertapenem and 1/5 to meropenem. All P. aeruginosa isolates were susceptible to meropenem and showed reduced susceptibility to other antibiotics. One Klebsiella oxytoca isolate tested positive for carbapenemase activity.
Carbapenemase genes were detected, by direct qPCR in, 5/10 wastewater samples. In cultured biomass, genes were detected in all samples, most frequently IMP and VIM, followed by OXA-48-like. KPC was detected in the Klebsiella oxytoca isolate, carbapenemase genes were not detected in other isolates.
These findings demonstrate the repeated presence of carbapenemase genes in wastewater. Combining culture-based methods with qPCR provided a more comprehensive assessment of antimicrobial resistance and supports ongoing wastewater surveillance.

P32 Antimicrobial Resistance Profiles and Resveratrol Activity Against Clinical Aeromonas Species Isolates

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Aeromonas species are opportunistic Gram-negative pathogens associated with gastroenteritis, bacteremia, and soft tissue infections. Increasing multidrug resistance (MDR) among Aeromonas isolates has become an emerging clinical concern. This study investigated the epidemiological characteristics, antimicrobial resistance mechanisms, and potential alternative antimicrobial strategies against clinical Aeromonas isolates.

A total of 100 clinical Aeromonas isolates were identified using matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS). Genotyping was performed using randomly amplified polymorphic DNA polymerase chain reaction (RAPD-PCR) and pulsed-field gel electrophoresis (PFGE). Antimicrobial susceptibility testing was conducted according to Clinical and Laboratory Standards Institute (CLSI) guidelines, while resistance-associated genes including MOX, AQU-1, cphA, CTX-M, qnrA, and sul were detected by polymerase chain reaction. The antimicrobial activity of resveratrol (RSV) was evaluated by minimum inhibitory concentration (MIC) testing.

Most isolates remained highly susceptible to third-generation cephalosporins and aminoglycosides. However, reduced susceptibility to cefoxitin and imipenem was observed, particularly among Aeromonas hydrophila isolates. The presence of MOX and AQU-1 genes was strongly associated with cefoxitin resistance, whereas cphA correlated with carbapenem resistance. Resveratrol demonstrated inhibitory activity against all isolates, with MIC values ranging from 16–256 μg/mL, and most isolates inhibited below 128 μg/mL.

In conclusion, AmpC β-lactamases and cphA are major contributors to antimicrobial resistance in clinical Aeromonas isolates. Resveratrol demonstrated promising antimicrobial activity and acceptable safety profiles, suggesting its potential as an adjunct antimicrobial agent against MDR Aeromonas infections.

P33 Contrasting pH optima of beta-lactamases CTX-M and CMY influences Escherichia coli fitness and resistance ecology

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Antimicrobial resistance (AMR) is a pressing threat on global health, agriculture, and economy and new strategies are needed to avoid resistance and improve treatment. Clinical microbiology and AMR research have long prioritized standardization in antimicrobial susceptibility testing; using one growth medium, CAMHB; one pH, 7.2-7.4; and one temperature, 35C. For practical reasons however, sites of infection rarely conform to just one environmental condition, and wide pH variations and gradients can be found within the human body, with direct effects on any infecting pathogen. Focusing on pH, we determined the MIC of a panel of isogenic strains expressing CTX-M-15 and CMY-2 β-lactamases at different pHs, resulting in distinct and contrasting pH optima. CTX-M-15 favoring the acidic (pH<7), and CMY-2 the basic (pH >7). In exploring the effects of temperature, we also saw a diversifying effect between avian (42 C) and mammalian (37 C) body temperature. Finally, we verified these findings using enzyme kinetics, co-cultures, and growth experiments, showing that AMR is not only influenced by the choice of antibiotic but also the environment. This knowledge might be used to renew and extend the use of old antibiotics, for certain resistant infections where it is possible to modify the environment.

P34 Penicillin susceptibility in Enterococcus faecalis: An indel n.1216129delT is a necessary but not sufficient genetic determinant of decreased susceptibility.

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Background:
In E. faecalis PBP4 is the principal binding target for penicillins. A deletion in the promotor for PBP4 (n.1216129delT) has been associated with increased expression of PBP4 and decreased susceptibility to ampicillin.

Study samples and methods:
We queried a sequence database of 4920 E. faecalis clinical isolates from Rigshospitalet between 2022 and 2026 for the presence of n.1216129delT. n.1216129delT was present in 261 (0.053) sequences. The presence of the deletion was linked to specific sequence types with ST6 being the most prevalent. In all 20 isolates belonging to ST28, half of the isolates carried n.1216129delT. ST179 was the most prevalent serotypes with 748 (0.152) isolates of which only two isolates carried n.1216129delT. SNP analyses within the three STs were done and 10 genetically distinct isolates belonging to ST6, ST179 and 9 genetically distinct isolates belonging to ST28 were selected for disc susceptibility testing of which 14 carried n.1216129delT. Disc diffusion susceptibility testing was done using the amp10 and tzp30/6 discs.
Results: For isolates not carrying n.1216129delT (N=15) amp(10) inhibition zones varied between 22 and 28 mm and tzp(30/6) between 24 and 27 mm. In contrast, isolates carrying n.1216129delT (N=12) showed a bimodal zone diameter distribution with 6 isolates displaying inhibition zones <22 mm (average: 19.3 mm) for amp(10) and 8 isolates displaying inhibition zones <24 mm (average: 19.6 mm) for TZP(30/6).

Interpretation:
The results are consistent with n.1216129delT being a prerequisite for decreased susceptibility for penicilins, however, it is not sufficient to alone convey resistance. The fact that genetic determinants for decreased susceptibility to penicillins have been identified arguments in favor of revising antibiotic wildtype distributions of E. faecalis and consider the introduction of a susceptible by increased exposure (I) category.

P35 Clindamycin's role in MRSA decolonization treatment; A randomized, placebo-controlled, double-blinded trial

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Background: When methicillin-resistant Staphylococcus aureus (MRSA) colonizes the throat, topical decolonization with mupirocin nasal ointment and chlorhexidine body wash often fails. Systemic antibiotics are sometimes added, but evidence is limited. We conducted a randomized, placebo-controlled, double-blinded trial to evaluate whether adding oral clindamycin improves MRSA throat decolonization.
Methods: Adults with MRSA throat carriage after one prior topical decolonization treatment received standard topical therapy for 5 days plus oral clindamycin or placebo for 10 days. MRSA screening (nose, throat, perineum) was performed at 1 and 6 months. Only participants MRSA-negative at 1 month were included in the 6-month analysis.
Results: Of 53 randomized participants, 43 had 1-month MRSA swab results available and were included in the complete-case analysis. At 1 month, MRSA-negative status was observed in 17 of 21 (81.0%) in the clindamycin group and 8 of 22 (36.4%) in the placebo group. Clindamycin was favored in unadjusted
analysis (RR, 2.2; 95% CI, 1.2–4.0; one-sided p=0.004) and after adjustment for age, sex, and number of household members using logistic regression (OR, 7.23; 95% CI, 1.85–34.03; one-sided p=0.002). Among the 25 participants who were MRSA-negative at 1 month, sustained MRSA negativity at 6 months occurred in 13 of 17 participants (76.5%) in the clindamycin group and 4 of 8 (50.0%) in the placebo group. Estimates favored clindamycin but were not statistically significant in either the unadjusted (RR, 1.5; 95% CI, 0.7–3.2; one-sided p=0.193) or adjusted logistic regression analysis (OR, 2.81; 95% CI, 0.42–19.61; one-sided p=0.141).
Conclusion: Oral clindamycin was associated with improved MRSA eradication at one-month. No significant difference was observed at 6 months, possibly due to limited power following early termination. Findings suggest that clindamycin may help rapidly clear MRSA from the throat and may have a role in treating selected patients with persistent throat carriage.

Antimicrobial Stewardship (AMS) posters

Poster walk overview

Poster number	Abstract title	Poster walk number	Poster walk day
P05	Gaps in sepsis recognition and early management in two University hospital Emergency departments without electronic decision support: opportunities for improvement through targeted interventions	1	Friday
P06	Impact of introducing a regional antibiotic guide on in-hospital acute care – a population-based cohort study from a country with a restrictive antibiotic policy	1	Friday

P05 Gaps in sepsis recognition and early management in two University hospital Emergency departments without electronic decision support: opportunities for improvement through targeted interventions

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Background
Sepsis remains a leading cause of in-hospital mortality, yet up to 40% of cases are not recognised in time. This study evaluated approaches for assessing sepsis recognition in emergency departments (Eds) operating without electronic medical records (EMRs) and identified targets to improve early identification and management.

Methods
Prevalence audits were undertaken in two university hospital EDs. Hospital 1 conducted a 7 day audit followed by two 24 hour audits; Hospital 2 subsequently completed two 24 hour audits using the same standardised protocol. Illness severity was assessed using the NEWS2. Findings were disseminated through structured feedback sessions and Microsoft Teams meetings. Binomial analysis estimated the number of ED visits and hospitalisations required to detect one sepsis case. In Hospital 1, blood-culture sampling rates per 1,000 hospitalisations werewere calculated.

Results
Among 516 hospitalised patients, 133 (25.8%) had suspected infection and 20 (3.9%) met sepsis criteria; only 25% were documented. Adherence to early management was limited, including timely antibiotics, adequate fluid resuscitation, and collection of two blood culture sets. Approximately 250 ED visits or 82 hospitalisations were required to detect one sepsis case, supporting the feasibility of a 48-hour audit.
In Hospital 1, blood-culture sampling improved to 606 sets per 1,000 hospitalisations in 2025 vs 517 in 2024. The proportion of single sets decreased from 86% to 63%, and true pathogens accounted for 19% of positive results.

Conclusions
Sepsis was frequently underrecognised, contributing to delayed treatment and suboptimal diagnostics. Workflow variability and lack of decision support contributed to missed cases. However, improved blood-culture practices indicate a positive trend. Targeted improvements in triage, diagnostics, and early management are needed. A 48-hour audit is feasible for surveillance, while electronic NEWS2 alerts may enhance timely, life-saving recognition.

Figure 1. Timline in the university hospital emergency departments, highlighting key data collection parameters and interventions.

P06 Impact of introducing a regional antibiotic guide on in-hospital acute care – a population-based cohort study from a country with a restrictive antibiotic policy

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Introduction: WHO regards increasing antimicrobial resistance as a great threat to human health. An antibiotic guide is essential for reducing overall antibiotic use and increasing use of narrow-spectrum antibiotics. In this study, we assessed the impact of introducing a regional antibiotic guide in Denmark, a country with a restrictive antibiotic use.

Methods: We performed a retrospective, multicenter cohort study of all acute adult contacts in the Region of Southern Denmark from 1 January 2016 to 20 March 2018. The antibiotic guide was implemented from January 2017, so we defined a pre-period before January 2017 and post-period afterwards. The primary outcome was the proportion of patients treated with antibiotics within the first 48 hours after arrival at the hospital, stratified by antibiotic groups. To examine how a regional antibiotic guide impacts the choice of antibiotics, we used random forest models to predict the counterfactual outcome in a time series design (i.e. as if the regional antibiotic guide was not implemented).

Results: We identified 432,882 acute contacts. The most frequently used antibiotics were penicillins including beta-lactamase inhibitors (35.7%), cephalosporins (22.6%), beta-lactamase sensitive penicillins (19.1%), penicillins with extended spectrum (16.9%), and beta-lactamase resistant penicillins (12.9%).
When comparing the pre- to the postperiod, we found an increased use of beta-lactamase sensitive penicillins (16.4% vs 20.7%), and penicillins with extended spectrum (14.4% vs 18.4%). The use of the broader spectrum antibiotics increased for cephalosporins (19.1% vs 24.7%) and decreased for penicillins including beta-lactamase inhibitors (43.1% vs 31.4%). No difference was found for beta-lactamase resistant penicillins (14.1% vs 12.2%). The results of this study were influenced by the global shortage of piperacillin/tazobactam in 2017.

Discussion: The introduction of a regional antibiotic guide led to increased use of antibiotics .

Basic research posters

Poster walk overview

Poster number	Abstract title	Poster walk number	Poster walk day
P07	Differential nutrient utilization between uropathogenic and commensal Escherichia coli revealed by phenotype microarray screening	2	Friday
P08	Fluorescent anti-PNAG demonstrate superior accumulation at the infection site in a murine model of S. aureus Implant-Associated Osteomyelitis	2	Friday
P09	Non-specific IgY as possible prophylaxis against catheter-associated urinary tract infections	2	Friday

P07 Differential nutrient utilization between uropathogenic and commensal Escherichia coli revealed by phenotype microarray screening

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Urinary tract infections (UTIs) are among the most common bacterial infections worldwide, placing a high burden on public health and the economy. Uropathogenic Escherichia coli (UPEC) are the leading causative agent of UTIs. A key factor in UPEC virulence is metabolic flexibility, enabling colonization of diverse host environments. While genomic characterization of UPEC virulence traits is well established, less is known about functional metabolic differences between commensal and pathogenic E. coli.

This study employed high throughput phenotypic profiling to compare a commensal control strain (Nissle 1917) with two reference UPEC strains from distinct phylogroups (CFT073, B2; UMN026, D). Screening was performed using the OmniLog Phenotype MicroArray system, which quantifies cellular respiration across approximately 1,000 conditions on the PM1–PM10 panels. Results were expressed as area under the curve and substrates ranked by the magnitude of the difference between UPEC and control. Top-ranking substrates were taken forward to a custom validation assay using M9 minimal medium supplemented with the substrate of interest and quantified with OmniLog redox dye A.

The screening revealed multiple differences in metabolic capacity between the UPECs and the control. The most pronounced contrasts were in carbon source utilization (PM1–PM2), where several substrates were exclusively or preferentially metabolized by one or both UPEC strains. For example, sucrose was exclusively metabolized by UMN026. Additional differences were observed in the nitrogen sources or response to chemical stress. The custom validation assay confirmed the top hits from the initial screening.

Planned work will extend this approach to a panel of clinical UPEC isolates to assess the prevalence of these traits. Identifying metabolic traits that distinguish UPEC from commensal E. coli may reveal vulnerabilities as targets for adjunct therapies amid rising antibiotic resistance.

P08 Fluorescent anti-PNAG demonstrate superior accumulation at the infection site in a murine model of S. aureus Implant-Associated Osteomyelitis

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Introduction:
Implant-associated osteomyelitis (IAOM) is difficult to treat due to biofilm formation, which reduces bacterial metabolic activity and promotes antibiotic tolerance and immune evasion. Targeted delivery of cytotoxic compounds to bacterial surfaces may improve treatment while limiting off-target effects. We investigated the targeting potential of antibodies against biofilm-associated molecules antibiotics in a murine model of S. aureus IAOM.

Methods:
Antibodies against biofilm-derived molecules anti-ZD11, anti-Z22, anti-PNAG and anti-dPNAG were conjugated to sulfo-Cyanine5 (sCy5). Controls included polyclonal S. aureus-IgG and anti-FITCS. Likewise, Dalbavancin(0.01 mg/kg) and Vancomycin(0.01 mg/kg) were conjugated to sCy5.
A murine model of S. aureus IAOM was used. 7 days post-inoculation, mice(n=4) were injected with the fluorescent targeting agents. For each agent, sterile implant controls(n=4) were included. At 1, 6, 24 and 48 hours post-injection, mice were scanned using an IVIS Newton(7.0) imaging system, and total radiance(ph/s/sr) was quantified. 48 hours post-injection,mice were euthanized and the tibia and implant were removed for microbiological or histological analysis.

Results:
All infected mice(n=72) had comparable mean(SD) CFU levels from either implant(4.71(0.83) log CFU/implant) or bone(6.89(0.61) log CFU/bone). All sterile mice(n=72) were sterile. Anti-PNAG demonstrated significant accumulation in infected(n=8) vs sterile mice(n=8) at 24h and 48h post-injection(p=0.021 and p=0.012, respectively).
Both vancomycin and dalbavancin accumulated significantly at the site of infection 24h after injection, independent of administration route. Radiance was comparable, with a trend toward higher signal for dalbavancin administered SC compared to vancomycin(p=0.057).
Histology demonstrated tissue damage, intracellular staphylococci and OLCN invasion.

Conclusion:
Among the investigated antibodies, only anti-PNAG demonstrated significant accumulation at 24h and 48h following injection. As PNAG is an important constituent of S. aureus biofilm matrices anti-PNAG holds promise as a targeting molecule. Further, dalbavancin demonstrated targeting properties in a setting in which both intracellular staphylococci and invasion of the OLCN were observed, highlighting its potential in novel applications.

P09 Non-specific IgY as possible prophylaxis against catheter-associated urinary tract infections

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Catheter-associated urinary tract infections (CAUTIs) represent a significant challenge in healthcare settings. CAUTIs are frequently characterized by recurrent infections and increased antimicrobial resistance, contributing to elevated antibiotic consumption. Biofilm formation on catheter surfaces is considered a key factor in the pathogenesis of CAUTIs. This study aimed to evaluate the potential of non-specific immunoglobulin Y (IgY) as a prophylactic agent against bacterial biofilm formation. Biofilms were cultivated on peg lids for 24 hours submerged in 96-well microplates using Escherichia coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa, in dilutions adjusted to OD600 nm 0.1, and treated with non-specific IgY at concentrations of 2, 4, 8, and 16 mg/mL. Biofilm biomass was quantified via crystal violet staining, with optical density measured at 585 nm using a microplate reader. No significant reduction in biofilm formation was observed for E. coli (mean OD and 95% CI at 0 and 8 mg/mL 0.11 (0.037, 0.18) and 0.21 (0.059, 0.35), respectively). P. aeruginosa exhibited robust biofilm formation (mean OD and 95% CI at 0 mg/mL 0.75 (0.63, 0.88)), with no significant inhibition following IgY treatment (mean OD and 95% CI at 16 mg/mL 0.81 (0.47, 1.15)). In contrast, K. pneumoniae demonstrated a significant reduction in biofilm formation when treated with 16 mg/mL non-specific IgY (mean OD and 95% CI at 0 and 16 mg/mL 0.48 (0.37, 0.60) and 0.10 (0.047, 0.16), respectively). These findings suggest that non-specific IgY may hold prophylactic potential against biofilm formation of select bacterial species on urinary catheters, and thereby an antibiotic saving strategy. Assay optimization and evaluation of higher IgY concentrations, to clarify species-specific effects and clinical applicability is ongoing.

Bacterial, fungal and viral infections posters

Poster walk overview

Poster number	Abstract title	Poster walk number	Poster walk day
P19	Dramatic increase of invasive pneumococcal disease caused by vaccine types 19A and 3 following the COVID-19 pandemic in Sweden.	4	Friday
P20	Children with tularemia at Hvidovre Hospital. A forgotten disease.	4	Friday
P21	Invasive Disease Caused by Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus agalactiae, Haemophilus influenzae and Neisseria meningitidis in the Faroe Islands: National Surveillance, 2013–2023	4	Friday
P22	Computer assisted detection of TB on chest x-rays from initial microbiological negative cases can improve Tuberculosis case detection.	4	Friday
P23	Sexually Transmitted Infections Before and After Initiation of HIV Pre-Exposure Prophylaxis in the North Denmark Region	4	Friday
P24	Improved case detection of Tuberculosis by clinical follow up and CAD CXR investigation of initially Xpert negative but persistently symptomatic patients at one week.	5	Saturday
P25	Acute Kidney Injury Following Dicloxacillin or Cloxacillin for Staphylococcus aureus Bacteraemia: Does Dose Matter?	5	Saturday
P26	Community-acquired bacterial meningitis in adults in Iceland, 2011-2025: A long-term, population-based study	5	Saturday
P27	Brain abscess with Nocardia paucivorans in a male with T-cell depletion	5	Saturday
P28	Risk of Invasive Aspergillosis in Lung Transplant Recipients Randomized to Tacrolimus versus Ciclosporin in the ScanCLAD study	5	Saturday
P29	Longitudinal metabolomic changes following nucleoside analogue initiation in chronic hepatitis B	5	Saturday

P19 Dramatic increase of invasive pneumococcal disease caused by vaccine types 19A and 3 following the COVID-19 pandemic in Sweden.

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Background: Introduction of pneumococcal conjugate vaccines (PCVs) in the childhood immunization programs has successfully reduced the number of invasive pneumococcal disease (IPD) cases in young children. In Sweden PCVs were introduced in 2009, first only PCV7, then PCV10 or PCV13 in 2010 and from 2018 only PCV10 was used. In this study we have analyzed the incidence and studied the serotype and clonal distribution of IPD from 2007 until 2022.
Methods: In this population-based national cohort study of the IPD incidence in Sweden, the yearly incidences of IPD during 2007–2022 were estimated for the age groups 0–4, 5–64, ≥65 years and in total, as well as by age group and by serotype. Serotyping was performed (Quellung) and selected isolates from densely populated areas in Sweden were whole genome sequenced (Illumina NovaSeq X Plus and MiSeq).
Results: A significant decrease of the IPD incidence was observed from 2007 to 2019 in children 0-4 years of age (but also in elderly ≥65 years) that declined even more during COVID-19 pandemic. However post-pandemic, the incidence increased dramatically in all age groups, especially among children 0-4 years of age, approaching the pre-PCV introduction levels. This increase was mainly attributed to the expansion of PCV13 vaccine serotypes 19A and 3. For 19A, two clonal types expanded, whereas for serotype 3, the same two clonal typesdominated before and after the pandemic.
Conclusions: The effect of PCV introduction has been hampered post-pandemic due to the expansion of serotypes 19A and 3 among IPD cases in Sweden. This issue needs to be monitored closely.

P20 Children with tularemia at Hvidovre Hospital. A forgotten disease.

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Tularemia is a zoonotic infection caused by Francisella tularensis (F. tularensis). Although traditionally considered rare in Denmark, recent epidemiological data suggest increasing incidence and wider geographic distribution. In children, tularemia may be overlooked due to nonspecific symptoms and resemblance to common bacterial infections.
We report two pediatric cases of ulceroglandular tularemia in patients presenting with fever, unilateral inguinal lymphadenitis, and adjacent punched-out skin ulcers (eschars) following presumed insect bites. Both patients were initially treated for suspected bacterial soft tissue infection with beta-lactam antibiotics without clinical response. Persistent fever, progressive lymphadenitis, and the characteristic inoculation lesions raised suspicion of tularemia, which was confirmed by serology and PCR. Following targeted antimicrobial therapy with doxycycline and ciprofloxacin respectively, both patients recovered clinically.
These cases illustrate the diagnostic challenges of pediatric tularemia in a low-incidence setting and emphasize the importance of reconsidering the diagnosis in children with persistent lymphadenitis and failure to respond to first-line antibiotic therapy.
Increasing numbers of reported Danish cases, together with the recent detection of F. tularensis in a wild hare in Denmark, suggest broader environmental circulation of the pathogen and highlight the need for increased clinical awareness of tularemia in Danish children.

P21 Invasive Disease Caused by Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus agalactiae, Haemophilus influenzae and Neisseria meningitidis in the Faroe Islands: National Surveillance, 2013–2023

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Background: Comprehensive multi-pathogen invasive bacterial disease (IBD) surveillance in small island populations provides a unique closed-denominator baseline and can reveal trends invisible in larger national datasets. The Faroe Islands, with a centralised microbiological laboratory and near-complete case ascertainment, offer an ideal natural sentinel for IBD epidemiology.
Methods: We conducted a nationwide retrospective cohort study of all laboratory-confirmed invasive disease caused by five key bacterial pathogens — Streptococcus pneumoniae (IPD), S. pyogenes (iGAS), S. agalactiae (iGBS), Haemophilus influenzae (iHi) and Neisseria meningitidis (IMD) — in the Faroe Islands from 2013 to 2023. Isolates were retrieved from the national microbiology laboratory. Annual incidence was calculated using mid-year population estimates from Statistics Faroe Islands. MLST was performed for iGAS isolates from 2022 to 2023. Statistical analyses included linear regression, Fisher's exact test, Kruskal–Wallis rank-sum test, and Wilson 95% confidence intervals.
Results: Eighty-two cases were identified (overall incidence 14.7 per 100 000 person-years). Annual total incidence increased significantly over the eleven-year period (+1.54/100 000·year; $R^2 = 0.65$; $p = 0.003$). IPD accounted for 45 cases (54.9%) and iGAS for 16 (19.5%). A striking surge in iGAS occurred in 2023, with seven cases compared with ≤2 in all preceding years (Fisher's exact $p < 0.001$). MLST revealed that six of seven isolates from 2022–2023 were sequence type 28 (ST28), associated with the global emm1/M1 lineage. Age at onset differed significantly across pathogens (Kruskal–Wallis $H = 10.2$; $p = 0.037$). Detailed serotype, vaccine-impact, and antimicrobial resistance analyses for IPD and iGBS are reported in companion studies.
Conclusions: The Faroe Islands experienced a sustained rise in IBD incidence between 2013 and 2023, culminating in a 2023 iGAS cluster dominated by the internationally circulating ST28/M1 clone. These findings corroborate European surveillance signals and underscore the value of small-nation sentinel surveillance for detecting emerging threats.

P22 Computer assisted detection of TB on chest x-rays from initial microbiological negative cases can improve Tuberculosis case detection.

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Background: Tuberculosis (TB) case detection remains inadequate, with a large gap between estimated and reported cases. Although the use of WHO-recommended rapid diagnostic tests (WRDs) is increasing, additional strategies are needed. We aimed to assess if simple, easily applicable methods can improve case detection.
Methods: A stepped wedge cluster randomized trial (June 2024–September 2026) was conducted at health care centers (HCs) in Guinea-Bissau and Ethiopia. At baseline, HCs used standard procedures applying the TBscore to guide the choice for diagnostic modality. At one-week follow-up (FU) all were assessed for per-sisting symptoms, results, and, if TB detected, treatment initiation. The intervention included guided spu-tum collection, CAD for TB on chest X-ray (CXR) (Qure.ai), and additional fecal, saliva, tongue swab, and sputum samples for GenXpert (GX) in initially negative patients with persistent symptoms. The primary outcome was increased case detection by GX and CAD CXR.
Results: Of the 3090 patients included 51% were female. The mean age was 39 years (95%CI 38 – 40) and the HIV prevalence 5% (n=125). One hundred and six (3%) patients were diagnosed with TB at inclusion, 35 (33%) females. The FU rate was 96% (n=2876) and 86 additional TB patients were diagnosed at clinical FU. The rate of up-front detected cases was slightly higher at baseline than intervention (56 vs 50) while the number of cases diagnosed at FU remained the same (45 vs 42). Using CAD CXR increased clinically di-agnosed cases from 29 (64% of diagnosed cases at baseline FU) to 37 (88% of cases diagnosed at interven-tion FU). Three additional cases were detected by fecal or swab sample.
Conclusion: A follow up CAD CXR for initially sputum negative but still symptomatic patients can improve case detection and is easily implementable. The gain of using fecal samples and spit/swaps is negligible.

P23 Sexually Transmitted Infections Before and After Initiation of HIV Pre-Exposure Prophylaxis in the North Denmark Region

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Background: HIV pre-exposure prophylaxis (PrEP) is efficient to prevent HIV infection among high-risk men who have sex with men (MSM) and transgender persons (TP). Consequently, the incidence of sexually transmitted infections (STIs) may increase, a phenomenon known as risk compensation.

Aim: To address changes in incidences of STIs representing sexual risk compensation associated with PrEP initiation in the North Denmark Region.

Methods: This longitudinal observational study with a self-controlled case series design on MSM and TP PrEP users in the North Denmark Region ran from January 1st, 2014, to October 1st, 2024. Data on STIs were collected before and after PrEP initiation. Chlamydia and gonorrhea were tested at three anatomic sites: urethra, rectum and oropharynx. Syphilis was tested by serology for Treponema pallidum. Incidence rates per 100 person-years (PY) were calculated and incidence rate ratios (IRR) were calculated using mixed-effects negative binomial regression and afterwards adjusted for individual testing rate (aIRR) to minimize detection bias.

Results: 106 PrEP users were included. Statistically significant increases were observed for any STI (IRR 1.62 [95% CI 1.21-2.16]) and chlamydia at any site (IRR 1.49 [95% CI 1.01-2.19]), however, the results were not significant after adjusting for test frequency (any STI aIRR 1.32 [95% CI 0.98-1.76]; any site chlamydia aIRR 1.37 [95% CI 0.95-1.98]). Statistically significant increases were observed for gonorrhea at any site (IRR 2.18 [95% CI 1.29-3.67]; aIRR 1.98 [95% CI 1.17-3.36]), rectal (IRR 5.10 [95% CI 2.20-11.80]; aIRR 4.60 [95% CI 1.98-10.68]) and oropharyngeal (IRR 3.54 [95% CI 1.54-8.15]; aIRR 3.17 [95% CI 1.37-7.31]). No significant increase in syphilis was found (IRR 1.53 [95% CI 0.89-2.64]; aIRR 1.39 [95% CI 0.81-2.38]).

Conclusion: Overall, no increase in STIs was found and increased gonorrhea infection alone was insufficient evidence of clear risk compensation after PrEP initiation in the North Denmark Region.

P24 Improved case detection of Tuberculosis by clinical follow up and CAD CXR investigation of initially Xpert negative but persistently symptomatic patients at one week.

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Background: Despite recent improvements, Tuberculosis (TB) case finding is insufficient. We have recently shown that a follow-up (FU) of initially smear-negative cases increases detection rates. We aimed to strengthen the diagnostic pathway for TB for patients presenting with cough, sputum production and/or weight loss combining a clinical follow up with CAD CXR and GenXpert (GX) examination of feces, sputum and saliva.
Methods: A stepped wedge cluster randomized trial (June 2024–September 2026) was conducted at prima-ry health care centers (HCs) in Guinea-Bissau and Ethiopia. At baseline, HCs followed standard TB diag-nostic procedures, using the TBscore to guide test modality. All patients were assessed after one week for persisting symptoms, test results, and, if diagnosed with TB, treatment initiation. During intervention, ini-tial sputum collection was optimized by visual instructions. Patients with persistent symptoms and no ini-tial diagnosis provided additional fecal, saliva, tongue swab, and sputum samples for GX testing. Computer assisted detection (CAD) for chest x-ray (CXR) at FU combined with clinical symptoms was used by an ex-perienced clinician to decide on treatment initiation.
Results: Of 3090 adult patients included 51% were female and the mean age was 39 years (95%CI 38 – 40). The HIV prevalence was 5% (n=125) overall. One hundred and six (3%) patients were diagnosed with TB at baseline, mainly by GX. The FU rate was 96% (n=2876) and among these, 573 (20%) fulfilled the criteria for clinical FU. Among the 488 (85%) who were re-evaluated clinically 87 patients were diagnosed with TB; patients which would otherwise have been missed. The number of GX detected cases at FU was 21 (21%), 16 of those tested negative at inclusion and five not tested initially.
Conclusion: A clinical FU of initially negative but persistently symptomatic patients will increase the num-ber of diagnosed cases two-fold.

P25 Acute Kidney Injury Following Dicloxacillin or Cloxacillin for Staphylococcus aureus Bacteraemia: Does Dose Matter?

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Background: Antistaphylococcal penicillins (ASPs) such as cloxacillin (CLX) and dicloxacillin (DCLX) are standard treatment for methicillin-susceptible Staphylococcus aureus bacteraemia (MSSA-SAB) in Denmark, whereas cefuroxime is the primary alternative in cases of allergy or when central nervous system coverage is required. During 2020, standard MSSA-SAB treatment in the North Denmark Region changed from DCLX 4 g daily to CLX 8 g daily. We investigated incidence, timing, and severity of acute kidney injury (AKI) associated with CLX, DCLX, and cephalosporins (CF).
Methods: We conducted a cohort study of first-episode SAB in the North Denmark Region (2015–2025). AKI was defined using modified KDIGO criteria. Primary analyses used time-varying antibiotic exposure attributing person-time and AKI events to the antibiotics received during follow-up. Secondary outcomes were analysed according to day-3 targeted therapy. Incidence rates (IR), cumulative incidence functions (CIF) with competing risk of death, restricted mean survival time (RMST), and multivariable Cox regression were applied.
Results: Among 1,783 AKI-eligible patients, 517 (29%) developed AKI. AKI IRs were 7.63 (95% CI 5.47–9.95), 6.06 (95% CI 4.20–8.08), and 8.76 (95% CI 6.70–10.95) per 1,000 person-days for CLX, DCLX, and CF, respectively. Both ASPs showed a median AKI onset of 4-5 days after SAB diagnosis, with cumulative incidence of 1.6–1.9% at day 7 (Fig. 1). No significant difference in AKI-free days at day 30 was observed between CLX and DCLX (RMST difference 0.49, 95% CI −0.31 to 1.30, p=0.231). CF was associated with fewer AKI-free days compared with CLX (RMST difference −1.65, 95% CI −2.86 to −0.45, p<0.01). 30-day mortality was 18.2%, 13.8%, and 17.1% for CLX, DCLX and CF, respectively.
Conclusion: AKI incidence increased during the study period following the regional transition from DCLX to higher-dose CLX. However, CLX and DCLX demonstrated comparable renal outcomes, suggesting no clinically significant excess nephrotoxicity with higher-dose CLX.

P26 Community-acquired bacterial meningitis in adults in Iceland, 2011-2025: A long-term, population-based study

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Background: Bacterial meningitis is a life-threatening infection with potentially severe long-term sequelae. Ageing population, changes in vaccination practices and new diagnostic approaches have influenced the epidemiology of bacterial meningitis in many countries in recent years. The aim of this study was to determine trends in incidence rates and aetiology of community-acquired bacterial meningitis (CABM) among adults in Iceland during 2011-2025, as well as clinical characteristics, predisposing conditions, treatment and mortality trends.
Methods: Data on all cases of CABM among adults (≥18 years) in Iceland during 2011-2025 were analysed. Cases were identified based on a clinical picture compatible with meningitis combined with a positive test (culture, PCR or antigen tests) on cerebrospinal fluid and/or ICD-10 code indicative of meningitis. Disease severity and comorbid conditions were assessed with APACHE II and Charlson Comorbidity Index scoring systems. Age-standardised incidence rates (ASRs) were calculated, standardised to the 2025 Icelandic population.
Results: Overall, 66 episodes of CABM in 66 patients were identified. Most patients were females (67%). The average ASR was 1.7 cases/100.000 population and there was a trend towards decreased ASR from 2011 to 2025 (incidence rate ratio [IRR] 0.95, p=0.058). Incidence was higher among females than males (p=005). The highest age-specific incidence rate was seen among ≥80-year-olds (4.8/100,000). A pathogen was identified in 89% of cases. The most common pathogens were Streptococcus pneumoniae (47%) and Listeria monocytogenes (9.1%). The ASR for S. pneumoniae meningitis decreased significantly from 2011 to 2025 (IRR 0.90, p=0.013). Overall, 72% of pneumococcal cases were caused by serotypes included in current vaccines.
Conclusion: During the past 15 years there has been a trend towards decreased incidence of CABM in Iceland, mainly driven by decreased incidence of pneumococcal meningitis, which probably reflects the effects of vaccination. High incidence among females and the elderly warrants further study and potentially targeted interventions.

P27 Brain abscess with Nocardia paucivorans in a male with T-cell depletion

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Background:
Nocardia species can cause opportunistic infections, predominantly among immunocompromised individuals. Clinical manifestations range from localized infection to severe, disseminated disease.
Case:
The case is an 85-year-old male, with previous splenic marginal zone lymphoma in remission. He had been treated with Rituximab and Bendamustine, known to cause prolonged B-cell and T-cell depletion, respectively.
He presented with a 4-week history of progressive headache, diplopia, left-sided imbalance, and multiple falls. He presented no fever, nausea, or vomiting; white blood cell and C-reactive protein levels were within normal range. He demonstrated left-sided incoordination, dysarthria, and nystagmus. Magnetic resonance imaging of the cerebrum revealed a centrally necrotic process in the left cerebellar hemisphere. Neurosurgical intervention was performed, and 12 mL of purulent fluid was aspirated. Culture grew Nocardia paucivorans, susceptible to ceftriaxone, trimethoprim sulfamethoxazole (TMP-SMX), linezolid and moxifloxacin.
Empiric treatment was ceftriaxone (4g x 1 daily) and metronidazole (500mg x 3 daily). After microbiological diagnosis was obtained, ceftriaxone was continued in combination with TMP-SMX (15mg/kg/day of the trimethoprim component); metronidazole was discontinued.
However, TMP-SMX was discontinued on day 19, since the patient developed thrombocytopenia, hyponatremia, hyperkalemia, and kidney failure. Ceftriaxone was continued, and oral treatment was switched to linezolid (600mg x 2 daily) for 3 weeks, after which TMP-SMX was reinstituted in reduced dosing of 10mg/kg/day. After six weeks, ceftriaxone was discontinued. He tolerated reinstitution of TMP-SMX well with a transient rise in potassium and creatinine levels.
Conclusion:
The evidence on optimal treatment regimens in brain abscesses caused by Nocardia species is sparse; treatment duration is typically prolonged, and the available antimicrobial agents have considerable toxicity, frequently leading to modifications in treatment strategy. Microbiological identification of the causative pathogen and determination of antimicrobial susceptibility are therefore essential for guiding appropriate therapy. It is therefore of paramount importance to obtain abscess material for microbiological examination.

P28 Risk of Invasive Aspergillosis in Lung Transplant Recipients Randomized to Tacrolimus versus Ciclosporin in the ScanCLAD study

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Purpose: The incidence of invasive aspergillosis (IA) is high in lung transplant (LTx) recipients and is associated with significant morbidity and mortality. The purpose of this study is to compare the risk of IA in LTx recipients randomized to tacrolimus versus ciclosporin in the ScanCLAD trial.

Methods: ScanCLAD is a Scandinavian, multicenter randomized controlled trial comparing the risk of chronic allograft dysfunction (CLAD) in patients randomized to tacrolimus versus ciclosporin. In this substudy with a three-year follow-up period, we reviewed medical records and classified invasive aspergillosis (IA) according to ISHLT criteria. We analyzed the cumulative incidence of IA, treating death as a competing event.

Results: 249 patients underwent double LTx and were included in the ScanCLAD study: 125 (50%) in the ciclosporin group and 124 (50%) in the tacrolimus group. The mean age was 55 years in both groups. Males accounted for 70 participants (56%) in the ciclosporin group and 68 (55%) in the tacrolimus group. After a median of 3.1 months (IQR 0.4 – 6.4) 43 patients developed IA. The cumulative incidence for IA after 3 years of follow-up was 18% (95% CI 0.12 – 0.26) in the ciclosporin group and 19% (95% CI 0.13 – 0.28) in the tacrolimus group (Figure 1). The incidence of IA varied across centers. The Finish center had the lowest incidence, with 8% of developing IA (95% CI 0.03 – 0.19) and the Swedish center in Lund reported the highest incidence at 30% (95% CI 0.14 – 0.52).

Conclusion: In this substudy of the randomized ScanCLAD trial we found that the incidence of IA differed between centers, but the risk of IA was similar for lung transplant recipients treated with ciclosporin versus tacrolimus.

P29 Longitudinal metabolomic changes following nucleoside analogue initiation in chronic hepatitis B

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Background: Chronic Hepatitis B (CHB) triggers continuous stimulation of the host's inflammatory response, which can lead to liver damage, procarcinogenic processes and metabolic dysregulation. The persistence of chronic inflammation states, even if low-grade, has been linked to increased risk and acceleration of cardiometabolic conditions (CMD), which can independently increase disease burden and mortality risk. The direct relationship between CHB and CMD and its underlying mechanisms nonetheless remain unclear.

Methods: This longitudinal study aims to investigate changes in blood metabolic profiles following antiviral treatment with nucleos(t)ide analogues (NA) for CHB. We collected blood plasma samples from 16 individuals with CHB at multiple time points before and after the initiation of NA treatment. Participants receiving treatment will be matched by age (±5 years) and sex with another group of 16 individuals with CHB who remained treatment-naïve throughout the entire study period. The obtained data from the different timepoints will be cross-referenced both at individual level and between the two subgroups to investigate differences in the metabolomic profile that accompany antiviral treatment initiation. Analysis of the samples will be performed using mass spectrometry-based platforms.

Expected results: We hypothesize that distinct metabolomic profiles before and after NA treatment initiation could accurately reflect different phases of infection. By correlating the obtained results from participants that have started treatment, against treatment- naïve, it may be possible to identify metabolite expression patterns associated with therapeutic response. It may likewise elucidate the relationship between CHB and CMD by distinguishing metabolic patterns that are typically associated with certain cardiovascular events and metabolic conditions. Thus, serum metabolomics may offer a noninvasive approach to detect liver specific biomarkers that together reflect disease status and metabolic risk. These findings can have implications concerning antiviral treatment, possibly extending it to a wider group of individuals with CHB to mitigate CMD risk.

Diagnostic microbiology posters

Poster walk overview

Poster number	Abstract title	Poster walk number	Poster walk day
P13	metaPreD: Workflow Optimization for RNA Virus Detection in Cerebrospinal Fluid by Metagenomic Sequencing	3	Friday
P14	Organization of Clinical Microbiology Emergency Services in Norway	3	Friday
P15	An outbreak of Dermatophilus congolensis in Norway.	3	Friday
P16	Microbiological diagnostic practice and antibiotic treatment in management of acute exacerbations of chronic obstructive pulmonary disease.	3	Friday
P17	RAPD-Based Strain Typing Reveals Ward-Associated Clusters and Resistance Features of Burkholderia cepacia Complex in a Medical Center	3	Friday
P18	Risk factors for cryptosporidiosis in Denmark: preliminary results from an 18-month nationwide case-control study	3	Friday
P42	Utility of metagenomic sequencing of microbial cell-free DNA as a diagnostic tool in vascular graft and endograft infections: a cross-sectional analysis	8	Saturday
P43	Multiplex PCR Diagnostics of Enteric Pathogens in a Nationwide Study: Experience from Centralized Diagnostics in the Faroe Islands in a 3-Year Period	8	Saturday
P44	Evaluation of cefoxitin disk diffusion to determine methicillin susceptibility in Staphylococcus epidermidis	8	Saturday
P45	Validation of a Novel Commercial Multiplex PCR Platform for the Diagnosis of Acute Gastroenteritis in a Hospital Laboratory Setting	8	Saturday
P46	Categorization of cefiderocol susceptibility by EUCAST disk breakpoints has low predictability of clinical outcome for MBL-producing Enterobacterales	8	Saturday

P13 metaPreD: Workflow Optimization for RNA Virus Detection in Cerebrospinal Fluid by Metagenomic Sequencing

MD Phd Maria Schei Haugan[1,2], Anna Matilde Toftemo[1], Torunn Gresdal Rønning[1,2], Tirill Sofie Eriksen[2], Christina Gabrielsen Ås[1,2], Erling Høyer[1], Andreas Christensen[1,2], Jan Egil Afset[1,2], Janne Malmring Fossum[1], Anette Skjærvik[1], Sofie Sagvaag Kristensen[1], Kjersti Haugum[1,2], Hans-Johnny Schjelderup Nilsen[1,3], Lene Christin Olsen[1,2]
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Introduction:
Viral infections of the central nervous system (CNS) cause substantial neurological morbidity. Despite advances in molecular diagnostics, etiology remains undetermined in many cases. Metagenomic sequencing of cerebrospinal fluid (CSF) enables hypothesis-free detection of viral pathogens but is limited by low nucleic acid input and high host background. We aimed to optimize a diagnostic workflow for viral metagenomics of frozen CSF, focusing on RNA viruses.

Methods:
Workflow optimization encompassed pre-analytical and analytical steps, including nucleic acid extraction, DNase treatment, cDNA synthesis, library preparation, host rRNA depletion, target enrichment and sequencing. Different protocols were tested for sensitivity and robustness in detection of viruses in low-input, frozen samples, evaluating preservation of RNA integrity, reduction of host genomic DNA, and viral recovery.
Three library preparation strategies—Illumina DNA Prep, QIAseq Ultralow Input Library Kit, and SMART-Seq Total RNA Pico Input (ZapR Mammalian) —were compared using CSF samples spiked with a virus standard. The sensitivity of the SMART-Seq workflow was evaluated with and without viral enrichment (Twist Comprehensive Viral Research Panel (CVRP)) on spiked and virus-positive CSF samples. Libraries were sequenced on an Illumina MiSeq platform (300 bp paired-end reads). Bioinformatic analysis included quality filtering, host read depletion, and viral taxonomic classification.

Results:
Automated extraction outperformed the manual approach tested for low-input samples. Optimization of DNase treatment revealed a trade-off between DNA removal efficiency and RNA preservation, with ezDNase selected for subsequent analyses. The SMART-Seq workflow combined with Twist CVRP target enrichment achieved the greatest analytical sensitivity and viral recovery (Figure 1).

Conclusion:
An optimized metagenomics workflow was established for detection of RNA viruses in frozen CSF. The SMART-Seq Total RNA Pico Input (ZapR Mammalian) workflow, especially when combined with Twist CVRP enrichment, delivered the highest sensitivity for RNA virus detection in low-input samples and represents a robust approach for agnostic diagnosis of CNS infections.

P14 Organization of Clinical Microbiology Emergency Services in Norway

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Background
Norway is a geographically large country with a dispersed population, and acutely ill patients with infectious diseases are admitted to hospitals nationwide. The organization of clinical microbiology emergency services, including access to clinical microbiology expertise, varies. Timely access to microbiological diagnostics and clinical microbiology expertise is essential for appropriate antimicrobial therapy and outcomes in severe infections. A national overview of these services has been lacking.
Methods
The Quality Committee of the Norwegian Society for Medical Microbiology conducted a nationwide cross-sectional survey in 2025 among Norwegian laboratories providing microbiological emergency services. A structured questionnaire assessed opening hours, diagnostic service availability, and access to clinical microbiology expertise outside regular hours.
Results
All 18 laboratories responded (seven university hospitals, eleven non-university hospitals). Catchment populations ranged from 110,000 to 725,000 inhabitants. Opening hours varied substantially, from 7.5 to 24 hours per day, only one laboratory operated 24/7. Most had limited daytime opening hours on weekends and public holidays. Eleven laboratories processed positive blood cultures in the evening on weekdays, with similar patterns for urgent cerebrospinal fluid diagnostics.
Eleven laboratories had an on call system for clinical microbiologists. On call structures varied: nine laboratories had scheduled physician presence during daytime on weekends, seven on public holidays, but only one in the evening. Four laboratories reported physician availability not extending beyond regular daytime presence. Two laboratories with on-call systems had no scheduled physician presence during on call hours. Continuous 24/7 telephone access to a clinical microbiologist was available at two hospitals.
Conclusion
Norwegian hospitals differ substantially in their organization of clinical microbiology emergency services, including opening hours, diagnostic availability outside regular hours, and access to on call clinical microbiologists. These disparities may contribute to geographic inequities in the management of patients with severe infections and warrant discussion of national minimum standards.

P15 An outbreak of Dermatophilus congolensis in Norway.

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Introduction: Dermatophilosis is an acute to chronic skin disease caused by Dermatophilus congolensis. Primarily an animal pathogen, zoonotic infection in humans has been described after contact with infected animals. To our knowledge, this is the first report of a large-scale human outbreak of D.congolensis.

Aim: Microbiological identification, genomic profiling and antibiotic susceptibility testing of D.congolensis in a Norwegian outbreak.

Material and methods: Skin swab samples from patients (n=10) with pustulosis were submitted on Amies liquid medium and inoculated on blood agar with 5% sheep blood, MacConkey agar and chocolate agar and incubated at 37°C in 5% CO2 for 24-48h.

Identification was based on phenotypical appearance on blood agar and Gram stain in addition to MALDI-ToF MS (MALDI Biotyper® Sirius, Bruker Daltonics V13.0.0.2_11897-12438) (n=10). Identification of 9 isolates were confirmed with whole genome sequencing (WGS) with Illumina MiSeq.

Antimicrobial susceptibility testing was performed by broth microdilution (Sensititre™ EUSTAPH and STP6F, Thermo Scientific).

Results: All samples grew pure culture of typical adherent, white, wrinkled colonies with beta haemolysis and characteristic Gram stain displaying filamentous forms with transverse and longitudinal segmentation as well as coccoid forms within 2 days.

Maldi-ToF MS yielded low score values ranging from 1.47 to 1.66 with simple extraction. Full extraction yielded no extra benefit. WGS confirmed all isolates as D.congolensis, differing with 0-3 singule nucleotide polymorphisms, confirming close genetic relatedness.

All samples showed low MICs for most clinically relevant antibiotics including penicillin, clindamycin and tetracycline. For tetracycline all samples were tested to MIC <0,5µg/mL and the tetZ gene was not detected by WGS.

Conclusions: Identification of D.congolensis using MALDI-ToF MS alone may be inadequate with current extraction methods and databases. There are no established methods, nor clinical breakpoints for susceptibility testing of D.congolensis and further work is needed to establish clinical relevance of tested MIC values.

P16 Microbiological diagnostic practice and antibiotic treatment in management of acute exacerbations of chronic obstructive pulmonary disease.

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Introduction
Chronic obstructive pulmonary disease (COPD) is characterised by chronic respiratory symptoms, and episodes with acute worsening of symptoms is common [1,2]. Although only around half of acute exacerbation of COPD (AECOPD) are caused by bacteria, and evidence for benefit of antibiotic treatment is limited, a majority of patients admitted to hospital receive antibiotics [3-6]. To provide targeted antimicrobial treatment of AECOPD, diagnostic microbiological sampling is necessary, and judicious use of antibiotics is warranted.

Material and methods
We conducted a retrospective quality study analysing all admissions at Drammen Hospital with AECOPD in 2019, as part of an evaluation on management of AECOPD in Vestre Viken Hospital Trust. Microbiological sampling and findings, and use of antimicrobial therapy was registered. We present preliminary results from our study.

Results
260 patients accounted for 417 admissions. Nasopharyngeal specimens for polymerase chain reaction (PCR) and/or culture were obtained in 84.4% of admissions. Sputum was collected in 15 admissions. PCR was positive in 23.6% of the nasopharyngeal specimens, while culture positivity was 18.8%. 33.3% of the sputum specimens were culture positive (figure 1).
Clinicians classified 52.0% of cases as bacterial, 14.2% as mixed viral/bacterial and 4.8% as pure viral. Antibiotic treatment was started in 72.4% of admissions. Narrow-spectrum penicillins were most frequently prescribed. We found no connection between COPD stage and antibiotic prescription. Antibiotic use was higher in patients receiving mechanical respiratory support (81.4% vs 71.5%, p=0.04), and those with positive culture results (87.9% vs 74.5%, p=0.02).
Mean treatment duration was 8.3 days, with no significant difference between the aforementioned groups.

Discussion
Although most patients received antibiotics, lower respiratory tract samples were rarely collected. Also, treatment duration exceeded national and international recommendations. Strengthening sampling practices is essential to support targeted therapy and reduce unnecessary antibiotic exposure in AECOPD.

P17 RAPD-Based Strain Typing Reveals Ward-Associated Clusters and Resistance Features of Burkholderia cepacia Complex in a Medical Center

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Background:
The Burkholderia cepacia complex (BCC) comprises genetically diverse, intrinsically drug-resistant non-fermenting Gram-negative bacteria associated with healthcare-associated infections. This study characterized clinical BCC isolates using RAPD-based typing, antimicrobial resistance profiling, and molecular detection of resistance determinants to provide a strain-level epidemiological overview in a medical center in northern Taiwan.

Methods:
A total of 186 clinical BCC isolates (2023–2024) were identified using MALDI-TOF mass spectrometry. Molecular typing was performed by RAPD-PCR, and genetic relatedness was evaluated using UPGMA clustering. Antimicrobial susceptibility testing included ceftazidime (CAZ), cefoperazone/sulbactam (SFP), levofloxacin (LVX), trimethoprim–sulfamethoxazole (SXT), and tigecycline (TGC). PCR assays targeting selected resistance determinants—including sul-family genes, fluoroquinolone-associated resistance genes, and ESBL-related β-lactamases—were conducted to complement phenotypic profiles. Clinical metadata such as ward distribution and specimen source were integrated for epidemiological analysis. Environmental water samples were additionally screened for BCC-infecting bacteriophages, with positive isolates confirmed by plaque assays and transmission electron microscopy.

Results:
Lower respiratory tract samples accounted for 68% of isolates, followed by pleural effusion (14%). Species identification showed B. cenocepacia as the predominant species (83.8%). RAPD typing resolved eight molecular clusters, with a dominant cluster comprising 58% of isolates. Several wards contained isolates with highly similar RAPD patterns, suggesting localized transmission or a shared environmental source. Resistance profiling demonstrated high resistance to LVX (86%), whereas SXT retained activity with only 5% non-susceptibility. PCR detection revealed gyrA mutations (67.7%), AmpC β-lactamase genes (4.8%), and sul-family genes (1.5%), partially correlating with phenotypic susceptibility. Environmental screening recovered several BCC-infecting phages displaying Siphoviridae-like morphology and plaque-forming activity against selected isolates.

Conclusions:
Integrated molecular typing and resistance profiling revealed dominant strain clusters and heterogeneous antimicrobial resistance among clinical BCC isolates. These findings highlight the value of strain-level surveillance for understanding transmission dynamics and guiding infection-control strategies.

P18 Risk factors for cryptosporidiosis in Denmark: preliminary results from an 18-month nationwide case-control study

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Background:
Following the implementation of syndromic testing in Denmark, Cryptosporidium is increasingly recognized as a cause of gastrointestinal infection. High genetic diversity with predominantly zoonotic subtypes has been observed, but transmission pathways remain poorly understood.

Methods:
We present interim results from a nationwide, prospective case-control study conducted from May 2025 to November 2026. Cases are identified through national surveillance, and 10 unmatched controls per case are invited from the general population. Participants complete a questionnaire about exposures during the 14 days prior to symptom onset (cases) or questionnaire completion (controls). Adjusted odds ratios (aORs) with 95% confidence intervals and population attributable fractions (PAFs) are estimated.

Results:
By April 2026, 6,745 individuals had been invited, of whom 1,670 participated (386 cases, 1,284 controls). Increasing age was associated with lower odds of cryptosporidiosis. Travel abroad was associated with higher odds (aOR = 3.2 [2.1–4.9]). Important domestic exposures included contact with cattle (aOR = 9.3 [5.0–18.0]) and taking immunosuppressive medication (aOR = 3.4 [2.0–5.8]). Swimming pool exposure, an important source of infection in other high-income countries, was not significantly associated with higher odds (aOR = 1.43 [0.93–2.16].
The PAF for cattle-contact was 24%. Species- and subtype-stratified analyses showed that cattle-contact was associated with the common C. parvum subtypes IIaA15G2R1 and IIaA16G3R1. Other, less common species and subtypes showed different risk profiles; for example, C. parvum IIdA19G1 was associated with consumption of ready-to-eat salad (aOR 7.2, 95% CI 1.3–140.0).

Conclusion:
Cattle-contact appears to be an important driver of cryptosporidiosis in Denmark. Species- and subtype-specific risk factors will be subject to further analyses, but current findings indicate that cattle-contact alone does not explain the majority infections nor the diversity of infecting subtypes. Instead, multiple transmission routes are likely, highlighting the need for differentiated prevention strategies informed by continued molecular and epidemiological surveillance.

P42 Utility of metagenomic sequencing of microbial cell-free DNA as a diagnostic tool in vascular graft and endograft infections: a cross-sectional analysis

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Introduction
Vascular graft or endograft infection (VGEI) is a severe complication following vascular reconstruction, associated with high mortality and morbidity. Patients unfit for graft replacement often receive long-term or lifelong suppressive antibiotic therapy. Accurate microbiological diagnosis is crucial for targeted treatment; however, sampling from the infected area may risk bleeding or graft contamination. Blood cultures have poor sensitivity in VGEI, possibly due to prior antibiotics and transient bacteraemia in biofilm-associated infections.

Methods
We evaluated the diagnostic utility of metagenomic sequencing of microbial cell-free DNA (mcfDNA) in plasma from patients with diagnosed or suspected VGEI. Participants were included from the prospective ACHIEVE cohort of VGEI patients in the Central Denmark Region. Plasma samples and blood cultures were obtained concurrently from the same venipuncture. After blinding, plasma samples underwent metagenomic sequencing analysis. Sequencing results were adjudicated by an expert panel of infectious disease physicians and microbiologists, integrating clinical history, microbiology, imaging, and biochemistry. Paired sample-level positivity of mcfDNA sequencing and concurrent blood cultures was compared using exact McNemar's test.

Results
A total of 25 patients contributing 32 samples were included. Metagenomic sequencing detected one or more microorganisms in 23/32 sampling events (72%) with a median of two microorganisms per positive sample (IQR: 1–3.5), compared with 2/32 (6%) paired blood culture sets ($p < 0.001$). Across all samples, 77 distinct microorganisms were identified. Based on expert adjudication, two were confirmed by concurrent blood cultures, 18 were judged probable pathogens, 43 possible, nine unlikely, and five indeterminate. One patient had a positive blood culture for Staphylococcus epidermidis (1/4 bottles), which was not detected by metagenomic sequencing.

Conclusion
Plasma mcfDNA metagenomic sequencing showed higher microbiological yield than concurrent blood cultures in VGEI and may serve as a promising non-invasive diagnostic adjunct. Further studies are needed to define specificity, clinical utility, and impact on antimicrobial management.

P43 Multiplex PCR Diagnostics of Enteric Pathogens in a Nationwide Study: Experience from Centralized Diagnostics in the Faroe Islands in a 3-Year Period

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Background:
Multiplex polymerase chain reaction (PCR) has become an important tool in the diagnosis of gastrointestinal infections, enabling simultaneous detection of multiple pathogens, and improving diagnostic yield, compared to conventional methods. However, data on overall PCR testing activity and positivity rates are not consistently reported in routine clinical practice.
Methods:
We conducted a retrospective observational nationwide study of stool samples analyzed by multiplex PCR over a three-year period (2023-2025) in the Faroe Islands.Stool samples were analyzed using the QIAstat-Dx Gastrointestinal Panel 2 on the QIAstat-Dx Analyser (QIAGEN). Pathogen-specific time intervals were applied to define unique episodes and avoid duplicate results. Selected clinically relevant pathogens were analyzed, including rotavirus, norovirus, Escherichia coli pathotypes, Clostridioides difficile, Campylobacter spp., and Salmonella spp. The panel enables detection of Shiga toxin genes and differentiation between Stx1 and Stx2 (including subtype Stx2f). Incidence rates per 100,000 inhabitants were calculated using annual population estimates. Overall testing activity rates were assessed using both positive and negative PCR results.
Results:
A total of 407, 475 and 430 PCR-positive samples were identified in 2023, 2024 and 2025, respectively. The total number of PCR tests performed was 1,158 in 2023, 1,317 in 2024 and 1,281 in 2025. Corresponding positivity rates were 35.1%, 36.1% and 33.6%. The incidence of PCR-positive samples exceeded 700 per 100,000 inhabitants annually. The most frequently detected pathogens included Clostridioides difficile, E.coli EPEC, norovirus and Campylobacter spp. The distribution of pathogens remained relatively stable across the study period with moderate variation between years.
Conclusion:
Multiplex PCR enables comprehensive detection of gastrointestinal pathogens in a centralized diagnostic setting. Stable positivity rates over time suggest consistent diagnostic yield. Reporting both testing activity and incidence provides a more complete understanding of diagnostic data and may improve interpretation. Further studies are needed to assess the clinical relevance of detected pathogens.

P44 Evaluation of cefoxitin disk diffusion to determine methicillin susceptibility in Staphylococcus epidermidis

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Objectives:
Staphylococcus epidermidis, may cause serious, often foreign body-related infections. S. epidermidis expressing mecA becomes methicillin resistant through the expression of an altered penicillin binding protein. The European Committee on Antimicrobial Susceptibility Testing (EUCAST) recommends using the cefoxitin disk diffusion method to screen for methicillin resistance in staphylococci. Recently EUCAST increased the screening breakpoint for S. epidermidis to S≥27 mm and introduced an area of technical uncertainty (ATU) at 27 mm. The aim of this study was to evaluate the cefoxitin disk diffusion method using EUCAST breakpoints to detect mecA positive Staphylococcus epidermidis isolates.

Methods:
Since 2017, methicillin susceptibility in S. epidermidis from critical samples (mainly blood cultures and tissue samples from prosthetic joint infections) has been confirmed with mecA-PCR in our Department of Clinical Microbiology. Based on prospectively collected routine-data, a retrospective analysis was performed on all S. epidermidis isolates from 01.01.2017 to 31.05.2025 using R (version 4.5.2) and applying current EUCAST breakpoints.

Results:
Cefoxitin disk diffusion was performed on 17.458 S. epidermidis isolates. Confirmatory mecA-PCR was performed on 485 isolates. When analysing the first isolate per pheno-/genotype per patient, we included a total of 416 isolates in the analysis. Applying a cefoxitin zone diameter cut-off ≥27 mm, 358 S. epidermidis isolates were included, of which 27 were mecA-positive, corresponding to 7,5% (95% CI: 5,2–10,8%). Taking account for the ATU and using the cut-off ≥28 mm, 316 isolates were included, of which 22 were mecA-positive, corresponding to 7,0% (95% CI: 4,6–10,3%).

Conclusions:
The cefoxitin disk diffusion potentially misses mecA-mediated methicillin-resistance in critical isolates of S. epidermidis, even when accounting for the ATU. Based on this, we will continue our current practice. As data are only gathered from a single laboratory, generalizability is limited. Further investigations, including examination of discordant isolates on media from different manufacturers, is planned.

P45 Validation of a Novel Commercial Multiplex PCR Platform for the Diagnosis of Acute Gastroenteritis in a Hospital Laboratory Setting

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Background:
Rapid and accurate detection of gastrointestinal pathogens is essential for clinical management, infection control, and surveillance. Syndromic multiplex PCR panels enable simultaneous detection of a broad range of viral, bacterial, and parasitic pathogens directly from a single specimen, reduc-ing time to diagnosis compared with conventional methods and minimizing the need for sequential testing. These assays offer standardized workflows, high analytical sensitivity, and improved pathogen coverage, which is particularly valuable in high-throughput clinical settings. The Department of Clinical Microbiology at Hvidovre Hospital serves a catchment population of approx. 1,000,000 and processes more than one million patient samples annually, including more than 28,000 fecal samples in 2024 and 2025.

Objective:
To validate and assess assay performance of the EasyScreen™ Pan-Enteric Pathogen Detection Kit (Genetic Signatures, NSW, Australia) on clinical specimens collected in fecalSwab collection devices.

Methods:
Analytical validation will use the ZeptoMetrix GI2 panel with 24 targets and a collection of Quality Control Molecular Diagnostics (QCMD) panels from 2024, comprising 58 tests covering enteric viruses, bacteria, parasites, Clostridioides difficile, norovirus, and Escherichia coli. Clinical performance will be assessed using left-over routine clinical fecal samples stored at -80C previously analyzed with an in-house realtime PCR multiplex assay (Flow Classic, Roche, Switzerland), including 15 targets with 20 samples per target (viruses, bacteria, and parasites). Concordance, sensitivity, and specificity will be assessed against reference methods, QCMD consensus results and clinical testing.

Results:
Data collection and analysis are ongoing. Validation is scheduled for completion by May 2026, with results available for presentation at NSCMID 2026.

Conclusion:
This study will provide a comprehensive evaluation of the EasyScreen™ Pan-Enteric Pathogen Detection Kit in a high-throughput clinical setting and inform its suitability for routine diagnostics of gastrointestinal infections for patient samples collected in fecalSwab collection devices.

P46 Categorization of cefiderocol susceptibility by EUCAST disk breakpoints has low predictability of clinical outcome for MBL-producing Enterobacterales

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Cefiderocol susceptibility testing by disk diffusion is recommended by EUCAST. Based on routine clinical data collected in an observational study, we evaluated how well the current EUCAST interpretive criteria for zone diameter predicted the clinical outcomes of patients treated with cefiderocol for metallo-beta-lactamase-producing Enterobacterales (MBL-CRE) infections.
CIRCE was an observational, multicentre study performed in Spain (January 2023-April 2025) investigating the clinical outcomes of adult hospitalised patients with reported MBL-CRE infections, who received cefiderocol for ≥72 hours. Cefiderocol susceptibility was determined by disk diffusion in each centre according to EUCAST recommendations.
Clinical response and clinical cure rates at Day 14 and inhibition zones were analysed. Interpretive criteria for disk zone diameters were based on EUCAST breakpoint table v16 (Susceptible ≥23 mm, Area of Technical Uncertainty [ATU] 21-23 mm and R <23 mm).
For 133 patients in this analysis, similar clinical cure rates at Day 14 were found for isolates irrespective of their interpretive category: Susceptible (N=71): 67.6% or Resistant (N=62): 69.4%.
The distribution of patients achieving or not achieving clinical cure or clinical response by zone inhibition diameter is shown in Figure 1. The number of patients without clinical response was low, and most patients who had clinical response had MBL-CRE isolates with zone inhibition diameter between 20 and 24 mm, overlapping S, ATU and R categories.
These data showed that patients receiving cefiderocol for MBL-CRE infections achieved similar rates of clinical response irrespective of whether isolates were categorized as susceptible, resistant or falling within the ATU when using routine reported data. These results suggest a weak predictive power of current EUCAST interpretive criteria for cefiderocol disk zone diameters and a risk of over-reporting resistance. Where disk diffusion testing is used, labs should consider retesting isolates with zone diameters <23mm by a broth microdilution method.

Infection prevention and Infection control posters

Poster walk overview

Poster number	Abstract title	Poster walk number	Poster walk day
P36	Cost-Effectiveness of Cell-Based Versus Egg-Based Trivalent Influenza Vaccines in Denmark, Finland, Norway and Sweden	7	Saturday
P37	Cost-effectiveness of pneumococcal conjugate vaccine strategies in children and adults in Sweden	7	Saturday
P38	Risk of infection in pregnant women with and without cerebral palsy, and association with adverse birth outcomes	7	Saturday
P39	Molecular Investigation of ESBL-negative Enterobacterales Clinical Isolates in a Tertiary Hospital in Denmark	7	Saturday
P40	The role of infection prevention and control (IPC) contact persons in a Norwegian hospital	7	Saturday
P41	The effect of the probiotic - ASTARTE™ - on the reduction of recurrent Urinary Tract Infection in women aged 18-40 years: a randomized, double-blind, placebo-controlled study	7	Saturday

P36 Cost-Effectiveness of Cell-Based Versus Egg-Based Trivalent Influenza Vaccines in Denmark, Finland, Norway and Sweden

Prof. Lars Holger Ehlers[1], Dr. Thea Kirkegaard Kjær[1], Prof. Lars Jørgen Østergaard[2], Prof. Terho Heikkinen[3], Dr. Klaus Madsen[4], Dr. Joaquin Federico Mould-Quevedo[5]
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Background: Influenza imposes a substantial clinical and economic burden on healthcare systems across the Nordic countries, including both pediatric and working-age adult populations. In seasons affected by egg-adaptation–related antigenic drift, cell-based influenza vaccines may offer improved effectiveness over egg-based vaccines. This study evaluated the cost-effectiveness of cell-based trivalent influenza vaccines (TIVc) compared with standard-dose egg-based trivalent influenza vaccines (SD-TIVe) in pediatric and adult populations, from a healthcare payer perspective in Denmark, Finland, Norway and Sweden.

Methods: A one-year dynamic infectious disease model based on a susceptible–exposed–infected–recovered (SEIR) framework was developed and calibrated to represent an average influenza season in the Nordics. Country-specific vaccination coverage inputs were informed by national immunization programs. Pairwise incremental cost-effectiveness ratios (ICERs) were estimated for three age groups: 6 months–17 years, 18–64 years, and 6 months–64 years. Analyses incorporated indirect protection of older adults through herd-immunity effects. The relative vaccine effectiveness of TIVc compared with SD-TIVe was set at 13%, based on multiple observational test-negative design studies spanning five influenza seasons. Health outcomes included influenza cases, hospitalizations, and quality-adjusted life years (QALYs). Event-related costs were estimated using official, publicly available national data sources. Uncertainty was explored through deterministic and probabilistic sensitivity analyses.

Results: Replacing SD-TIVe with TIVc was projected to generate cost savings of €10.7 million in Denmark, €12.7 million in Finland, €5.3 million in Norway, and €17.5 million in Sweden, alongside QALY gains of 468, 231, 408, and 705, respectively. TIVc was dominant over SD-TIVe across all countries and age groups evaluated. Sensitivity analyses confirmed the robustness of these findings, with the largest net benefits observed when TIVc was offered to high-risk individuals aged 6 months to 64 years.

Conclusions: TIVc was associated with improved health outcomes and healthcare cost savings compared with SD-TIVe across Nordic countries, supporting its consideration within national influenza vaccination programs.

P37 Cost-effectiveness of pneumococcal conjugate vaccine strategies in children and adults in Sweden

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Background
PCV15 (2+1) was introduced in Sweden's pediatric national immunization program in September 2023. Since January 2026, the Swedish Public Health Agency has recommended conjugate vaccines covering ≥20 serotypes for risk groups individuals ≥2 and all adults ≥65, most who currently receive PCV20. Although PCV20 (3+1) has been available for children since March 2024, the pediatric program has not been updated. Using the same vaccine for all age groups could simplify vaccination and enhance health and economic outcomes.

Objective
Estimate the cost-effectiveness of switching from PCV15 (2+1) to PCV20 (3+1) in children and maintaining PCV20 in adults ("PCV20/PCV20") compared to maintaining PCV15 (2+1) in children and switching from PCV20 to PCV21 in adults ("PCV15/PCV21").

Methods
A decision-analytic model assessed health and economic outcomes for the Swedish population over 5 years from a healthcare perspective. Outcomes included IPD, pneumonia (inpatient and outpatient), otitis media, deaths, life-years, QALYs, and direct medical and vaccination costs (at list prices). Costs and outcomes were discounted annually at 3%. Pediatric and adult effects were assumed comparable to PCV13 for vaccine serotypes. Serotype replacement was conservatively modeled as a 1% annual increase in non-covered serotypes.

Results
Over 5 years, PCV20/PCV20 could prevent 248 more IPD cases, 6,512 more pneumonia cases, and 2,720 more OM cases compared with PCV15/PCV21, resulting in 58 additional life-years and 291 additional QALYs. The number of deaths averted were comparable among both strategies. Total costs were 158.6 million SEK lower with PCV20/PCV20 despite higher vaccination costs. PCV20/PCV20 was the dominant strategy (more effective and cost-saving) (Table 1).

Conclusions
PCV20 for both children and adults could result in greater health and economic benefits than using PCV15 in children and PCV21 in adults. Efficiencies related to one pneumococcal vaccine across ages (training, storage, etc.) were not captured and may provide further benefit.

P38 Risk of infection in pregnant women with and without cerebral palsy, and association with adverse birth outcomes

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Preliminary abstract

Background: Pregnant women with cerebral palsy (CP) have an increased risk of adverse birth outcomes (ABO). We aimed to investigate whether women with CP have a higher risk of infections during pregnancy than women without CP and if this contributes to the overall higher risk of ABO.
Methods: In this nationwide register-based cohort study, we used the Civil Personal Register number to link between Danish health registries. Pregnancies in women with CP were matched 1:10 on age and year of childbirth to pregnancies in women without CP. We assessed risk of infection as crude odds ratios (cOR) using logistic regression within a generalized estimating equation framework and evaluated the contribution of infection to the risk of ABO with four-way decomposition analysis, allowing infection to act as both mediator and interaction term.
Results: We identified 503 pregnancies in women with CP during 1997-2021. The cOR for a diagnose of infection was 1.62 (95% Confidence interval (CI): 1.01-2.59) for pregnant women with CP compared to pregnant women without CP. Pregnant women with CP had higher cOR for small-for-gestational-age (SGA): 1.48 (95% CI: 1.15-1.91), preterm birth: 2.04 (95% CI: 1.51-2.77), very preterm birth: 2.34 (95% CI: 1.24-4.41), and low birth weight (LBW): 2.06 (95% CI: 1.45-2.91) than pregnant women without CP. Figure 1 illustrates a significant interaction between CP and infection explaining 14 % (95% CI: 6-23%) of the total effect of CP on preterm birth.
Discussion: Pregnant women with CP had a higher cOR for infection, preterm birth, very preterm birth, LBW and SGA than pregnant women without CP. Combined exposure to CP and infection was associated with a significantly higher risk of preterm birth, exceeding the risk from either factor alone. Adjusted ORs accounting for potential confounders, such as CP severity, are needed before definitive conclusions can be drawn.

P39 Molecular Investigation of ESBL-negative Enterobacterales Clinical Isolates in a Tertiary Hospital in Denmark

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Background: Plasmid-based AmpC beta-lactamase (p-ampC)-producing Enterobacterales are a public health concern. This study investigated Enterobacterales isolates from blood cultures with a negative phenotypic extended-spectrum beta-lactamase (ESBL) test and estimated the prevalence of AmpC-producing clinical isolates among them.

Methods: A consecutive cohort of Enterobacterales clinical blood isolates were identified in a 5-year period from May 1st, 2021, to Jan 7th, 2026, in a single-center University Hospital in Southern Denmark. Isolates (incl. E. coli, E. hermannii, Klebsiella spp., Proteus mirabilis, Salmonella spp., Citrobacter spp. (excl. C. freundii complex), and Pantoea spp.) suspected of ESBL-production were screened, and all ESBL-negative isolates were subject to further genotypic analyses. Bacterial DNA was extracted, followed by a long-read nanopore-based Whole Genome Sequencing (WGS).

Results: A total of 1706 positive blood cultures with Enterobacterales were identified. ESBL was suspected in 131 (8%) non-duplicate Enterobacterales isolates. Of the screened isolates, 38 (29%) were ESBL-negative. One isolate was excluded due to cephalosporine susceptibility, and 37 isolates were further analyzed (Table 1). The most frequent strains were E. coli ST-73 (n=4) and ST-131 (n=3). Five (14%) AmpC-genes (blaDHA-1, blaCMY-2) were found among 37 ESBL-negative Enterobacterales isolates. Of these, three carried p-AmpC-genes (E. coli and K. pneumoniae complex). Beta-lactamase genes other than AmpC were found in 23 isolates, of which eight were plasmid-based. Eleven E. coli carried no beta-lactamase genes other than blaEC, and one E. coli isolate carried no beta-lactamase genes.

Conclusion: This study provided insight into the prevalence of p-AmpC-producing Enterobacterales in our hospital. Similarly to other multidrug-resistant pathogens, AmpC-producing Enterobacterales, as well as cephalosporin-resistant non-ESBL/non-AmpC isolates, can pose challenges to antimicrobial stewardship and infection control programs in clinical settings. In this study, some ESBL-negative isolates did not have beta-lactamase genes commonly associated with cephalosporin resistance, calling for further investigations to better understand prevalence and potential for transmission.

P40 The role of infection prevention and control (IPC) contact persons in a Norwegian hospital

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Background / Introduction
The role of IPC contact persons in Norwegian hospitals has evolved since the mid 1990s, following the introduction of infection control legislation and structured programmes. It is typically performed by a clinical nurse alongside regular duties. A similar model ("IPC link nurse") is well established in the UK, but less developed in other Nordic countries. We examined the role and responsibilities of IPC contact persons at Akershus University Hospital (Ahus), the largest acute care hospital in Norway (catchment population 600,000; 12,000 employees).
Methods
A 14 item questionnaire based on the Ahus procedure "Tasks for IPC contact persons" was distributed via Microsoft Forms to 117 IPC contact persons on January 20, 2026. The procedure defines the role as multidisciplinary, serving all professional groups within the unit, and should include a local written agreement specifying tasks and time allocation.
Results
The response rate was 39% (46/117). Most IPC contact persons were nurses (65%), while only 2% were physicians. Duration in the role was <1 year for 26%, 1-3 years for 37%, and >4 years for 37%. The majority (61%) were asked by their line leader to assume the role, whereas 27% volunteered. Only 14% reported serving all professional groups within their unit. 83% spent ≤4 hours/month on the role, and 82% lacked a local written agreement on tasks and time allocation. The most challenging IPC practices to maintain were "bare below the elbows," waste management, appropriate use of personal protective equipment, and hand hygiene. Common questions concerned isolation precautions and resistant microorganisms. Free text responses highlighted limited managerial support and a sense of working alone.
Conclusion
Improved organisational anchoring and role clarity are needed to ensure structure, time allocation, and support. Planned measures include a template for written agreements, implementation support, and annual triadic meetings with the IPC contact, manager and IPC nurse.

P41 The effect of the probiotic - ASTARTE™ - on the reduction of recurrent Urinary Tract Infection in women aged 18-40 years: a randomized, double-blind, placebo-controlled study

Khaled Saoud Ali Ghathian, Karen Angeliki Krogfelt, Niels Frimodt-Møller, Katrine Hartung Hansen, Anne Holm, Sofie Ingdam Halkjær, Andreas Munk Petersen

Background:
Urinary tract infection (UTI) is among the most common bacterial infections and a major driver of antibiotic consumption. Probiotics have shown potential in reducing infection related risk factors in both the gut and vaginal microbiome. This randomized trial investigates the effect of the orally administered probiotic combination ASTARTE™ on vaginal and gut microbial com-position and the incidence of recurrent UTIs (rUTIs) in women.
Methods:
A randomized, double-blind, placebo-controlled study in women aged 18–40 years with a history of rUTI. Participants were randomized 1:1 to receive a daily probiotic capsule (5×10^9 CFU) containing L. crispatus, L. rhamnosus, L. jensenii, and L. gasseri, or placebo, for six months. Clinical assessments included symptom questionnaires, urine culture, and shotgun-based micro-biome profiling of vaginal and rectal swabs at baseline, 2, 4, and 6 months. Follow-up visits were scheduled at 8, 10, and 12 months. The primary outcome was the incidence of sympto-matic, bacteriologically confirmed UTIs during the 6-month intervention. Secondary outcomes included changes in vaginal and gut microbiome composition.
Results:
A total of 290 participants have completed the 6-month intervention, while 46 discontinued early. Among completers, 232 (80%) experienced ≤1 UTI, whereas 58 (20%) met the definition of recurrent UTI (≥2 UTIs). These data are preliminary and blinded, and therefore no comparison between the probiotic and placebo groups is yet possible. Recruitment has progressed steadily since August 2022, and projections based on the latest 3- and 6-month recruitment rates indicate that the target of 667 participants is expected to be reached within the planned timeframe.
Conclusion:
Early results show an 80/20% distribution between non-rUTI and rUTI among participants who completed the 6-month intervention. Recruitment remains on track, and final outcomes includ-ing treatment effects and microbiome analyses will be reported when full enrollment and data collection are completed.

Microbiome posters

Poster walk overview

Poster number	Abstract title	Poster walk number	Poster walk day
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P10 The overlooked role of the seminovaginal microbiome in assisted reproductive outcomes

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Infertility affects up to 17% of couples worldwide and remains unexplained in a substantial proportion of cases. While the vaginal microbiome has been widely linked to reproductive outcomes, including success of assisted reproductive technologies (ART), the contribution of the male genital microbiome is less well defined.
Emerging evidence suggests that microbial exchange between partners may influence vaginal microbiome composition, local immune responses, and ultimately fertility outcomes, highlighting the need for a couple-based perspective.
In this study, semen and vaginal swabs are collected from couples initiating fertility treatment in a clinical setting. Bacterial isolates are identified using MALDI-TOF. In addition, 16S rRNA gene sequencing (Illumina) is used to characterize the broader microbial communities and potential sharing of taxa between partners. To resolve strain-level relatedness and confirm microbial transmission, whole-genome sequencing is performed on isolates shared within couples.
This study introduces the concept of the seminovaginal microbiome as a clinically relevant unit of analysis. By integrating culture-based and high-throughput sequencing approaches, it aims to elucidate microbial interactions within couples. Improved understanding of partner-associated microbial dynamics may identify novel biomarkers of treatment success and support development of targeted, couple-based interventions to improve reproductive outcomes.

P11 Effects of oral Probiotics on Vaginal Microbiome Dynamics during Pregnancy in Women with Obesity

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Background

The vaginal microbiome plays an important role in reproductive and pregnancy health. In normal pregnancy, the vaginal microbiome is typically characterized by relatively low microbial diversity and predominance of Lactobacillus spp. Evidence from longitudinal studies shows that the vaginal microbiome in pregnant women is more stable and compositionally distinct than in non-pregnant women. Lactobacillus spp. are thought to contribute to vaginal homeostasis through mechanisms including maintenance of a low vaginal pH and production of antimicrobial compounds.
In contrast, bacterial vaginosis (BV) is characterized by depletion of lactobacilli and increased abundance of anaerobic bacteria. BV and abnormal vaginal flora during pregnancy have been associated with adverse pregnancy outcomes, including preterm birth. Studies in non-pregnant women suggest that obesity may be associated with altered vaginal microbiota composition and a higher occurrence of BV or BV-associated microbial profiles. However, dynamics of the vaginal microbiome across pregnancy in women with obesity remain poorly characterized, as does the extent to which probiotic supplementation may influence vaginal microbiome

Aim

To investigate longitudinal changes in the vaginal microbiome during pregnancy in women with obesity and to evaluate whether oral supplementation with the multi-strain probiotic CDS22® affects vaginal microbiome compared with placebo.

Methods

This study is based on data from a randomized, double-blinded, placebo-controlled trial including 41 pregnant women with obesity (pre-pregnancy BMI ≥30 and <35 kg/m²). Participants were randomized to receive either CDS22® multi-strain probiotics (450 billion CFU/day) or placebo from gestational weeks 14–20 until delivery. Vaginal swabs were collected at three time points: baseline (gestational weeks 14–20), gestational weeks 27–30, and gestational weeks 36–37. Vaginal microbiome composition was characterized using 16S rRNA gene sequencing. Analyses will assess microbial richness, alpha- and beta-diversity, taxonomic composition, and relative abundance of predominant taxa across pregnancy and between intervention groups.

Results
Preliminary results are expected in August 2026.

P12 Previous antibiotic exposure and risk of STEC infection with/without HUS in children

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Background:
Hemolytic uremic syndrome (HUS) is a serious microangiopathic disease that can develop following infection with Shiga toxin-producing Escherichia coli (STEC). The pathophysiology of HUS is poorly understood, and the role of gut microbiota remains unclear. Antibiotics influence the gut microbiota and may play a role in disease progression.

Objective:
To investigate associations between recent antibiotic exposure, susceptibility to clinical infection following STEC exposure and risk of HUS in a large day care-centre outbreak.

Methods
Information on antibiotic use up to six months prior to STEC infection was obtained from the Directorate of Health. Medical information was obtained from the electronic medical records at Landspítali University Hospital. Logistic regression was used for statistical analysis.

Results:
The study included 133 children exposed to STEC in a day-care-centre in Reykjavík in 2024. 48 had confirmed infection and 12 developed HUS. Thirteen of the 48(27%) children with STEC had antibiotic prescriptions, as had three of the 12(25%) with HUS. Ten of the 44(22.7%) children with symptomatic STEC infection had antibiotics prescriptions, compared to three of four asymptomatic children. The risk of HUS was similar in children with and without antibiotic exposure (OR:0.96; 95%CI: 0.79-1.15; p=0.65) and risk of STEC infection was not affected by antibiotic use (OR:1.03; 95%CI: 0.94-1.12; p=0.56). Infected children who had antibiotic prescriptions were however 26% more likely to be asymptomatic compared to children without antibiotic exposure (OR=0.74; 95%CI: 0.57-0.97; p=0.030). When adjusting for age and sex, the risk ratio remained similar (OR: 0.76 ;95%CI: 0.56-1.04; p=0.084).

Conclusion:
Recent antiobiotic use does not appear to increase the risk of STEC infection or progression to HUS. Children with recent antibiotic use were however less likely to develop symptomatic infection. Further studies are needed to clarify the relationship between antibiotic use, the gut microbiota and symptomatic STEC infection.