idbydna

Precise Insights for Better Health

explify®

ECCMID 2022 Poster Presentations and Integrated Symposium

Poster Presentations – Genitourinary Pathogen Detection

Abstract #02724 | Poster P1189

Analytical Performance of a Precision Metagenomics Approach for Pathogen Detection in Urinary Tract Infections

Authors:
M. Mangifesta, K. Broadbent, G. Silva, R. Stinnett, A. Hanson, A. Kadam, J. Rossen, J. Lemon, R. Schlaberg

IDbyDNA, Salt Lake City, UT, USA

Analytical sensitivity, an important performance characteristic of any test, is estimated by determining the limit of detection (LoD). This study reports LoD for key uropathogens of the Urinary Pathogen ID/AMR Panel (UPIP)* workflow. Contrived samples were prepared and serially diluted in triplicate, then sequenced using the NextSeq550 sequencer (Illumina) to a depth of 1 million reads/sample. UPIP identified all expected pathogens, and the LoD ranged between 1 and 100 copies/mL (*E. coli* = 100, *Staphylococcus aureus* = 100, *Chlamydia trachomatis* = 10, *Aspergillus flavus* = 100, *Candida albicans* = 100, *HSV-2* = 10, *Trichomonas vaginalis* = 1).

Conclusion: UPIP demonstrated high analytical sensitivity for the direct detection of uropathogens.

Abstract #02327 | Poster P0333

Uropathogen Detection by Precision Metagenomics in Culture-Positive, Culture-Negative, and Volunteer Urine

Authors:
R. Stinnett, S. Stauffer, M. Mangifesta, A. Hanson, K. Broadbent, J. Lemon, J. Rossen, R. Schlaberg

IDbyDNA, Salt Lake City, UT, USA

Quantitative and sensitive molecular detection of uropathogens can be achieved directly from urine through next-generation sequencing (NGS) using the Urinary Pathogen ID/AMR Panel (UPIP)*. Remnant urine samples from patients with suspected UTI (culture-negative and culture-positive) and urine from consenting asymptomatic volunteers were analyzed with the UPIP metagenomic sequencing workflow; resulting data were analyzed using the Explify* platform (IDbyDNA). Microbial load (copies/mL) was significantly higher in culture-positive samples than in culture-negative or asymptomatic volunteer samples. Gram-negative bacterial organisms were most frequently detected in clinical samples.

Conclusion: A preliminary quantitative threshold provides high positive agreement with culture and evidence of infections missed by culture.

Abstract #03064 | Poster P1188

Precision Metagenomics for Broad Detection of Genitourinary Pathogens and Associated Antimicrobial Resistance Markers

Authors:
C. Gonzalez, M. Mangifesta, R. Stinnett, K. Broadbent, A. Hanson, K. Arora-Williams, J. Rossen, E. Kim, J. Lemon, R. Schlaberg

IDbyDNA, Salt Lake City, UT, USA

Next-generation sequencing with targeted enrichment using the Urinary Pathogen ID/AMR Panel (UPIP)* can detect, quantify and characterize hundreds of pathogens and thousands of antimicrobial resistance markers. Specimens were spiked with internal control, DNA was extracted, sequencing libraries were prepared and target-enriched in triplex with the Urinary Pathogen ID/AMR Panel (UPIP)*, sequenced using the NextSeq sequencer (Illumina), at 1 million reads/sample) and analyzed with the Explify* platform (IDbyDNA). UPIP detected at least one of the top 8 most established bacterial causes of UTI in 84% of samples and ≥ AMR marker in 95% of samples. AMR markers detected included those associated with resistance to beta-lactam antibiotics, trimethoprim/sulfamethoxazole, aminoglycosides and fluoroquinolones.

Conclusion: UPIP profiled AMR markers associated with resistance to UTI antibiotics.

* For Research Use Only. Not for use in diagnostic procedures.

Poster Presentations – Respiratory Pathogen Detection

Abstract #01663 | Poster P1192

Evaluation of the Respiratory Pathogen ID/AMR Panel Workflow Compared to Standard-of-Care for the Diagnosis of Lower Respiratory Tract Infections

Authors:
D. Gaston[1], H. Miller[1], J. Fissel[2], K. Carroll[1], P. Simner[1]

1 Johns Hopkins Hospital, Baltimore, MD, USA,
2 Children's Hospital Los Angeles, Los Angeles, CA, USA

Investigators assessed the accuracy of the Respiratory Pathogen ID/AMR Panel (RPIP)* vs. standard of care (SoC) testing from unselected bronchoalveolar lavage (BAL) specimens in the context of an analytical validation study. Results were interpreted using standardized criteria informed by characterization of the respiratory flora. Following application of these criteria, RPIP identified 73 potential pathogens from 55 BAL specimens (66% overall agreement with SoC). The target-enriched RPIP NGS workflow detected 27 bacterial, 1 mycobacterial, 42 viral and 3 fungal potential pathogens, including some that were not identified by provider-ordered testing but were confirmed by orthogonal methods, e.g. *Ureaplasma parvum*.

Conclusion: RPIP should be considered as an adjunct to SoC and can provide relevant additional detections of pathogens and AMR markers directly from BAL specimens.

Abstract #03792 | Poster P1183

Pathogen Surveillance by mNGS for Intubated Patients: A Reflex to Culture Model (RPIP)

Authors:
P. Kavaliauskas[1,2], N. Couto[3,4], B. Kuklinska[5], L. Vasovic[6], S. Vaca[5], I. Estabrooke[7], R. Stinnett[7], J. Rossen[7,8,9], R. Schlaberg[7], A. Craney[10,11]

1 Weill Cornell Medicine of Cornell University, New York, NY, USA
2 University of Maryland School of Medicine, Baltimore, MD, USA
3 University of Bath, Bath, UK
4 University of Groningen, Groningen, The Netherlands
5 New York Presbyterian Hospital Weill Cornell Campus, New York, NY, USA
6 Weill Cornell Medicine, New York, NY, USA
7 IDbyDNA, Salt Lake City, UT, USA
8 Isala Hospital, Zwolle, The Netherlands
9 University of Utah, Salt Lake City, UT, USA
10 Orlando Health Regional Medical Center, Orlando, FL, USA
11 Previously Weill Cornell Medicine, New York, NY, USA

Investigators demonstrated a proof of concept for early and accurate detection of respiratory pathogens with the Respiratory Pathogen ID/AMR Panel (RPIP)* in a retrospective analysis of tracheal aspirates from intubated patients during the first COVID-19 wave. A NextSeq2000 sequencer (Illumina) was used for sequencing at a depth of 5 million reads/sample. Bacterial or fungal pathogens were detected in 66 of 104 samples (63%) by culture, in 77 (74%) by RPIP and in 81 (78%) by both methods. In 5 of 34 patients (15%) with longitudinally collected samples available, pathogens were detected by RPIP in an average of 5.4 days prior to standard of care.

Conclusion: Culture plus RPIP provided improved and earlier detection of relevant respiratory pathogens, including cases where disease management would have changed. These findings demonstrate the potential for new reflex testing paradigms that integrate metagenomic Next-Generation Sequencing (mNGS) in the clinical microbiology laboratory.

Illumina Integrated Symposium (iS49)

Presentation—Moving Next-Generation Sequencing to Clinical Microbiology Laboratories: The Future is Now!

Monday, April 25, 2022
16:15-18:15
Hall P, iS49

John W.A. Rossen[1,2,3]

Next-generation sequencing (NGS) for dummies: How to implement metagenomics for respiratory infections.

- NGS methodology for laboratories without experience
- Practical advice for beginners: Sample extraction, library prep (workflow with and without automation), analytics and bioinformatics, technical time, time to results and estimated costs for NGS
- Demonstration using respiratory infection applications to outline clinical benefits of NGS vs. others routine techniques (culture, ID, AST, PCR, etc.)

1 LMMI Isala, Zwolle, The Netherlands
2 University Medical Center Groningen, Groningen, The Netherlands
3 University of Utah School of Medicine, Salt Lake City, UT, USA

* For Research Use Only. Not for use in diagnostic procedures.

675 Arapeen Drive, Suite 100, Salt Lake City, UT 84108

22.ID.20.01

idbydna.com