V EDICIÓN JORNADA CIENTÍFICA

Gesitra-IC

ACTUALIZACIÓN EN LA PATOLOGÍA INFECCIOSA DE PACIENTES INMUNOCOMPROMETIDOS

5 Y 6 MARZO 2026

ICOMEM

Ilustre Colegio Oficial de Médicos de Madrid

MADRID

Papel de las Paneles Sindrómicos (PPSS) en los principales modelos de infección respiratoria en inmunosuprimidos: algoritmos diagnósticos.

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Gesitra-IC
Grupo de Estudio de Infección en el Trasplante y el Huésped Inmunocomprometido
seimc

- ***Upper respiratory tract infecfion***
- ***Lower respiratory tract infection***

✓CAP *(sCAP/High-risk MDRB)*
✓HAP
✓VAT

antibiotics

MDPI

Case Report

Syndromic Testing in Infectious Diseases: From Diagnostic Stewardship to Antimicrobial Stewardship

Oana Săndulescu [1,2,*], Anca Streinu-Cercel [1,2], Maria Magdalena Moțoi [1,2], Adrian Streinu-Cercel [1,2] and Liliana Lucia Preoțescu [1,2]

- ✓ ***Syndromic (multiplexed) PCR panels***
- ✓ ***Clinical DNA/RNA metagenomics***

"A syndromic PCR panel is a single, multiplex polymerase chain reaction (PCR) test that simultaneously detects and identifies multiple microorganisms (and genotypic resistance markers) that share similar, overlapping signs and symptoms"

Syndromic vs. Multiplex PCR panels!

Syndromic/multiplexed PCR panels

Table 2 Relevant characteristics of European Community (EC)-marketed rapid multiplex molecular syndromic panels (RMMSP)

NAAT platform	*Characteristics*
BD MAX system (BD Diagnostics)	An automated real-time PCR platform utilizing TaqMan hydrolysis probes for pathogen detection
	The BD MAX instrument integrates extraction reagents and a real-time microfluidic cartridge, automating all sample handling and PCR processes
	Results are generated within a 3-h turnaround time
ePLex (GenMark Diagnostics)	A fully automated system that employs eSensor technology, utilizing electrochemical detection of ferrocene-labeled PCR amplicons via capture probes immobilized on gold-plated electrodes
	Results are available within 30 to 90 min, depending on the specific system (ePLex, ePlex NP, or eSensor XT-8)
Biofire Filmarray system (BioFire Diagnostics)	Fully automated platform performing nucleic acid extraction, real-time PCR detection and high-resolution melting for target identification
	Turnaround time less than 2 h
Unyvero System (Curetis USA)	Fully automated platform that includes a sample lysis device and a PCR panel analyzer
	The turnaround time is 4–5 h
VERIGENE system (Luminex Corporation)	Fully automated for nucleic acid extraction, purification, target amplification and hybridization of the target amplicons to a glass detection array in the test cartridge
	NanoGrid technology is used to identify target molecules. Turnaround time of around 3 h
xTAG technology (Luminex Corporation)	Multiplexed PCR coupled to bead-hybrization with a bead-specific fluorescent reporters that require offline nucleic acid extraction
	Turnaround time of 5 h

NAAT Nucleic acid amplification tests; *PCR* Polymerase chain reaction

Candel FJ, Salavert M, Cantón R, Del Pozo JL, Galán-Sánchez F, **Navarro D**, Rodríguez A, Rodríguez JC, Rodríguez-Aguirregabiria M, Suberviola B, Zaragoza R. Crit Care. 2024 Dec 30;28(1):440.

Multiplexed Respiratory viruses +/- "atypical bacterial panels

Parameter	FilmArray	Verigene	x-TAG RVP	x-TAG RVP Fast	NxTAG-RPP	eSensor RVP	ePlex
Analysis platform	FilmArray system or FilmArray Torch	Verigene system	Luminex 100/200	Luminex 100/200	Luminex Magpix	eSensor	ePlex system
No. of targets	20	16	12	8	20	14	17
Ability to detect pathogen							
Viruses							
Adenovirus	✓	✓	✓	✓	✓	✓ (differentiates subgroup B/E from C)	✓
Coronavirus							✓
Coronavirus HKU1	✓				✓		
Coronavirus NL63	✓				✓		
Coronavirus 229E	✓				✓		
Coronavirus OC43	✓				✓		
Human bocavirus					✓		
Human metapneumovirus	✓	✓	✓	✓	✓	✓	✓
Influenza A virus	✓	✓	✓	✓	✓	✓	✓
Subtype H1	✓	✓	✓	✓	✓	✓	✓
Subtype H3	✓	✓	✓	✓	✓	✓	✓
Subtype 2009 H1N1	✓					✓	✓
Influenza B virus	✓	✓	✓	✓	✓	✓	✓
Parainfluenza virus 1	✓	✓	✓		✓	✓	✓
Parainfluenza virus 2	✓	✓	✓		✓	✓	✓
Parainfluenza virus 3	✓	✓	✓		✓	✓	✓
Parainfluenza virus 4	✓	✓			✓		✓
Respiratory syncytial virus	✓			✓			
Respiratory syncytial virus A		✓	✓		✓	✓	✓
Respiratory syncytial virus B		✓	✓		✓	✓	✓
Rhinovirus/enterovirus	✓	✓	✓	✓	✓	✓	✓
Bacteria							
Chlamydophila pneumoniae	✓				✓		✓
Mycoplasma pneumoniae	✓				✓		✓
Bordetella pertussis	✓	✓					
Bordetella parapertussis-Bordetella bronchiseptica		✓					
Bordetella holmesii		✓					
Time to result (h)	~1	~2–3	~8	~6	~4	~6	~1.5

The BioFire® Respiratory 2.1 (RP2.1) Panel

1 Test. 22 Targets. ~45 Minutes.

The BioFire RP2.1 Panel Targets

VIRUSES

- Adenovirus
- Coronavirus 229E
- Coronavirus HKU1
- Coronavirus NL63
- Coronavirus OC43
- Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)
- Human Metapneumovirus
- Human Rhinovirus/Enterovirus
- Influenza A
- Influenza A/H1
- Influenza A/H3
- Influenza A/H1-2009
- Influenza B
- Parainfluenza Virus 1
- Parainfluenza Virus 2
- Parainfluenza Virus 3
- Parainfluenza Virus 4
- Respiratory Syncytial Virus

BACTERIA

- *Bordetella parapertussis*
- *Bordetella pertussis*
- *Chlamydia pneumoniae*
- *Mycoplasma pneumoniae*

	RP2.1*plus* (+ SARS-CoV-2)	SPOTFIRE R Panel
Instrument compatibility	FilmArray 2.0, TORCH	SPOTFIRE System
Assay time	~ 45 min	~ 15 min
Detection targets	23	15
Adenovirus	✓	✓
Seasonal coronavirus	Subtypes available: 229E, HKU1, NL63 & OC43	Subtypes not available
SARS-CoV-2	✓	✓
MERS-CoV	✓	X
Metapneumovirus	✓	✓
Rhinovirus/enterovirus	✓	✓
Influenza A virus	Subtypes available: H1-2009 & H3	Subtypes available: H1-2009 & H3
Influenza B virus	✓	✓
Parainfluenza virus	Subtypes available: Type 1-4	Subtypes not available
RSV	✓	✓
B. parapertussis	✓	✓
B. pertussis	✓	✓
C. pneumoniae	✓	✓
M. pneumoniae	✓	✓

Sputa/BAL/BAS/Endotracheal aspirates

BIOFIRE® FILMARRAY®
PNEUMONIA *PLUS* (PN*plus*) PANEL

1 Test. 34 Targets. ~1 Hour.

BACTERIA (Semi-Quantitative)

Acinetobacter calcoaceticus-baumannii complex
Enterobacter cloacae complex
Escherichia coli
Haemophilus influenzae
Klebsiella aerogenes
Klebsiella oxytoca
Klebsiella pneumoniae group
Moraxella catarrhalis
Proteus spp.
Pseudomonas aeruginosa
Serratia marcescens
Staphylococcus aureus
Streptococcus agalactiae
Streptococcus pneumoniae
Streptococcus pyogenes

ATYPICAL BACTERIA (Qualitative)

Chlamydia pneumoniae
Legionella pneumophila
Mycoplasma pneumoniae

VIRUSES

Adenovirus
Coronavirus
Human metapneumovirus
Human rhinovirus/enterovirus
Influenza A virus
Influenza B virus
Middle East respiratory syndrome coronavirus (MERS-CoV)
Parainfluenza virus
Respiratory syncytial virus

ANTIMICROBIAL RESISTANCE GENES

Carbapenemases
IMP
KPC
NDM
OXA-48-like
VIM

ESBL
CTX-M

Methicillin Resistance
mecA/C and MREJ (MRSA)

Lacks of *Stenothrophomonas maltophilia* and SARS-CoV-2 targets!

Hospitalized Pneumonia (HPN) Cartridge

Gram-positive bacteria

Staphylococcus aureus
Streptococcus pneumoniae

Enterobacterales

Citrobacter freundii
Escherichia coli
Enterobacter cloacae complex
Klebsiella aerogenes (E. aerogenes)
Proteus spp.
Klebsiella pneumoniae
Klebsiella oxytoca
Klebsiella variicola
Serratia marcescens
Morganella morganii

Non-fermenting bacteria

Moraxella catarrhalis
Pseudomonas aeruginosa
Acinetobacter baumannii complex
Stenotrophomonas maltophilia
Legionella pneumophila

Others/Fungi

Pneumocystis jirovecii
Haemophilus influenzae
Mycoplasma pneumoniae
Chlamydia (Chlamydophila) pneumoniae

Resistance	Gene
Macrolide/ Lincosamide	*ermB*
Oxacillin	*mecA* *mecC*
Penicillin	*tem* *shv*
3rd generation Cephalosporins	*ctx-M*
Carbapenem	*imp* *kpc* *ndm* *oxa-23* *oxa-24/40* *oxa-48* *oxa-58* *vim*
Sulfonamide	*sul1*
Fluoroquinolone	*gyrA83* *gyrA87*

Sample Types

Sputum, bronchoalveolar lavage, respiratory aspirates (tracheal and bronchial secretions)

21 Pathogens, 17 Antibiotic Resistance Markers

✓**Variable performance across platforms**

✓**Variable performance across on-panel targets**

➧ ***In general, analytical sensitivity is lower for most targets compared to mono or oligoplexed real-time PCR assays***

Anaesth Crit Care Pain Med (2023) 101300

Contents lists available at ScienceDirect

Anaesthesia Critical Care & Pain Medicine

journal homepage: www.elsevier.com

Review article

Performance evaluation of a PCR panel (FilmArray® Pneumonia Plus) for detection of respiratory bacterial pathogens in respiratory specimens: A systematic review and meta-analysis

Anne-Clotilde Moy [a], Antoine Kimmoun [b,c], Thomas Merkling [d], Béatrice Berçot [e,f], François Caméléna [e,f], Thibaut Poncin [e,f], Benjamin Deniau [a,g], Alexandre Mebazaa [a,g], Emmanuel Dudoignon [a,g,*,1], François Dépret [a,g,1], PCR Multiplex Study group (PMS group)[2], Nabil Gastli [h], Vincent Cattoir [i,j], Naouale Maataoui [k,l], Laurence Armand-Lefèvre [k,l], Barend Mitton [m,n], Jonathan Hoover [o], John R. Greenland [o,p], Brunella Posteraro [q,r], Maurizio Sanguinetti [q,s], Evdoxia Kyriazopoulou [t], Evangelos J. Giamarellos-Bourboulis [t], Giulia Menchinelli [q,s], Brune Joannard [u]

- ✓ ***Increased detection yield compared to standard culture***
- ✓ ***High negative predictive value for all targets***

Moy AC, Kimmoun A, Merkling T, Berçot B, Caméléna F, Poncin T, Deniau B, Mebazaa A, Dudoignon E, Dépret F; PCR Multiplex Study group (PMS group). Anaesth Crit Care Pain Med. 2023 Dec;42(6):101300

Candel *et al. Critical Care* (2024) 28:440
https://doi.org/10.1186/s13054-024-05224-3

Critical Care

REVIEW Open Access

The role of rapid multiplex molecular syndromic panels in the clinical management of infections in critically ill patients: an experts-opinion document

Francisco Javier Candel[1*], Miguel Salavert[2], Rafael Cantón[3,4], José Luis del Pozo[5,6], Fátima Galán-Sánchez[7,8], David Navarro[9,10,11], Alejandro Rodríguez[12], Juan Carlos Rodríguez[13,14], Montserrat Rodríguez-Aguirregabiria[15], Borja Suberviola[16] and Rafael Zaragoza[17]

"Interpretation of quantitative binned values"

- ✓ **High bacterial burdens (10(6) or ≥10 (7) generally indicate causality regardless of the number of co-detected microorganisms and lower respiratory tract sample type**

- ✓ **Lower genomic copies/ml (10 (4) or 10 (5) may also indicate causality, particularly for certain microorganisms as *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and MRSA, especially in patients receiving appropriate antimicrobial therapy.**

ELSEVIER

Contents lists available at ScienceDirect

Journal of Infection

journal homepage: www.elsevier.com/locate/jinf

Infectious Disease Practice

Performance of the BIOFIRE® Filmarray Pneumonia Plus Panel for quantifiable bacterial targets compared to semiquantitative culture methods: A systematic review and meta-analysis

Estela Giménez [a, b], María Ángeles Clari [a], Eliseo Albert [a], Nieves Carbonell [c], David Navarro [a, b, d, *]

MicrobiologyOpen

WILEY

MicrobiologyOpen Open Access

ORIGINAL ARTICLE OPEN ACCESS

Semi-Quantitative Detection of Respiratory Pathogens: A Systematic Review and Meta-Analysis of Results From the BIOFIRE FILMARRAY Pneumonia Panel and Culture

Benjamin Hommel[1] | Ophélie Hurtado[1] | Brooklyn Noble[2] | Jay Jones[2] | Florence Allantaz[1] | Tristan T. Timbrook[3] | Gennaro De Pascale[4,5] | Brunella Posteraro[5] | Maurizio Sanguinetti[6]

Hr-CAP/HAP and VAP

Start empirical broad- spectrum treatment (EBST)with coverage for MDR bacteria according to local protocol.

Request syndromic panel

Front-line antimicrobial therapy?

- MRSA no detected → withdraw coverage for MRSA
- *P. aeruginosa* no detected* → withdraw coverage for *P. aeruginosa*
- MRSA detected → Maintain or initiate coverage for MRSA
- *bla*ESBL- producing *Enterobacterales* detected → Withdraw EBST and administer Ertapenem
- *bla*OXA-48 like-producing *Enterobacterales* detected → De-escalate EBST to ceftazidime-avibactam
- *bla*KPC-producing *Enterobacterales* detected → Administer ceftazidime-avibactam or meropenem-vaborbactam or cefiderocol
- *P. aeruginosa* (no MBL producing) detected → De-escalate EBST to ceftolozane-tazobactam
- *P. aeruginosa* MBL producing detected → Administer cefiderocol or ceftazidime-avibactam plus aztreonam
- *A.baumanii* detected → Administer cefiderocol or tigecycline alone or in combination

* Consider maintaining EBST if MDR microorganisms no included in the syndromic panel is likely to be involved

de Albuquerque Pessoa dos Santos *et al. Critical Care* (2025) 29:379
https://doi.org/10.1186/s13054-025-05623-0

Critical Care

RESEARCH Open Access

Impact of syndromic molecular diagnostics on antimicrobial adequacy and time to therapy in critically ill patients with pneumonia: a systematic review and meta-analysis of randomized trials

Yuri de Albuquerque Pessoa dos Santos[1*], Bruno Martins Tomazini[1,3], Maurício Henrique Claro dos Santos[1], Eduardo Lyra de Queiroz[1], Laerte Pastore Júnior[1], Eduardo Leite Vieira Costa[1,4] and Fernando José da Silva Ramos[1,2]

Giacobbe *et al. Critical Care* (2025) 29:403
https://doi.org/10.1186/s13054-025-05632-z

Critical Care

RESEARCH Open Access

Use of a molecular syndromic panel for the etiological diagnosis of ventilator-associated bacterial pneumonia: impact on clinical outcomes and antibiotic use from a multicenter, prospective study

Daniele Roberto Giacobbe[1,2*], Greta Cattardico[1,2], Claudia Bartalucci[1], Vincenzo Di Pilato[3,36], Marco Muccio[2], Alessandro Limongelli[1,2], Alessio Signori[4], Alessandra Bandera[5,6], Bruno Cacopardo[7], Edoardo Campanella[7], Alessandro Caroli[8,9], Annamaria Cattelan[10], Marta Colaneri[11], Andrea Cortegiani[12,13], Laura Curci[14], Gennaro De Pascale[8,9], Giuseppe Vittorio De Socio[14], Filippo Del Puente[15], Antonino Di Fede[12], Chiara Fanelli[16], Nicholas Geremia[17,18], Maddalena Giannella[19,20], Giacomo Grasselli[5,21], Chiara Maci[22], Ivana Maida[16], Davide Mangioni[6], Andrea Marino[7], Maria Mazzitelli[10], Maria Chiara Meloni[16], Marco Merli[23], Elena Momesso[24], Chiara Oltolini[23], Carlo Pallotto[14], Sandro Panese[17,18], Matteo Passerini[25,26], Emanuele Pontali[15], Daniele Riccucci[19], Matteo Rinaldi[19,20], Marco Ripa[22,27], Vincenzo Scaglione[10], Francesco Saverio Serino[28], Vincenzo Spagnuolo[22,27], Giulia Spurio[12], Stefania Tigano[15], Carlo Torti[29,30], Giovanna Travi[23], Laura Magnasco[2], Federica Portunato[2], Federica Briano[2], Malgorzata Mikulska[1,2], Lorenzo Ball[3,31], Chiara Robba[3,31], Nicolò Patroniti[3,31], Denise Battaglini[3,31], Mauro Giacomini[32], Gian Maria Rossolini[33,34], Maurizio Sanguinetti[8,35], Paola Morici[36], Anna Marchese[3,36], Antonio Vena[1,2] and Matteo Bassetti[1,2] on behalf of RAPID-SITA PHENOTYPES investigators

- ✓ *Reduced time to appropriate AT*
- ✓ *Higher rate of appropriate initial AT*
- ✓ *No impact on mortality*

Detection of genotypic resistance markers....

Genotype-Phenotype discordanc

Genotype-/Phenotype+

- ✓ *Lack of allele coverage (in silico prediction)*
- ✓ *Sequence variations (Implementation of CRISPR-Cas assays?)*
- ✓ *Do not inform about the level of expression: Transcriptomic RNA-based assays (PCR/NGS)??*
- ✓ *Resistance not associated with on-target genotypic markers*

Detection of genotypic resistance markers....

Genotype-Phenotype discordances

Genotype+/Phenotype-

- ✓ **Heteroresistance**
- ✓ ***In vivo* induction or expression not captured by *in vitro* AST assays**
- ✓ **In vivo biofilm formation**
- ✓ **Culture bottlenecks and minority variants**

Contier *et al. Critical Care* (2025) 29:310
https://doi.org/10.1186/s13054-025-05528-y

Critical Care

RESEARCH Open Access

Diagnostic performance of Pneumonia multiplex PCR in critically ill immunocompromised patients

Transplant Infectious Disease

WILEY

BRIEF COMMUNICATION OPEN ACCESS

Application of Syndromic Panels for respiratory Tract Infections in Lung Transplantation: A Critical Review on Current Evidence and Future Perspectives

Andrea Lombardi[1,2] | Giulia Renisi[1] | Arianna Liparoti[1] | Chiara Bobbio[2] | Alessandra Bandera[1,2]

- **Off-panel targets to be considered in immunosuppressed individuals**

✓ *Mycobacterium tuberculosis*/Atypical Mycobacterial species/ *Nocardia* spp.
✓ Uncommon bacterial species (MDR or not)
✓ Herpesviruses: HSV/VVZ/CMV/HHV-6
✓ Fungal species (*Aspergillus* spp./*Pneumocystis carinii*/Mucorales)
✓ Protozoa: *Toxoplasma gondii*
✓ Helminths *(Strongyloides stercoralis)*

The most commonly involved agents are shared by immunocompetent and immunosuppressed patients (S. pneumoniae/CARV and MDRB)

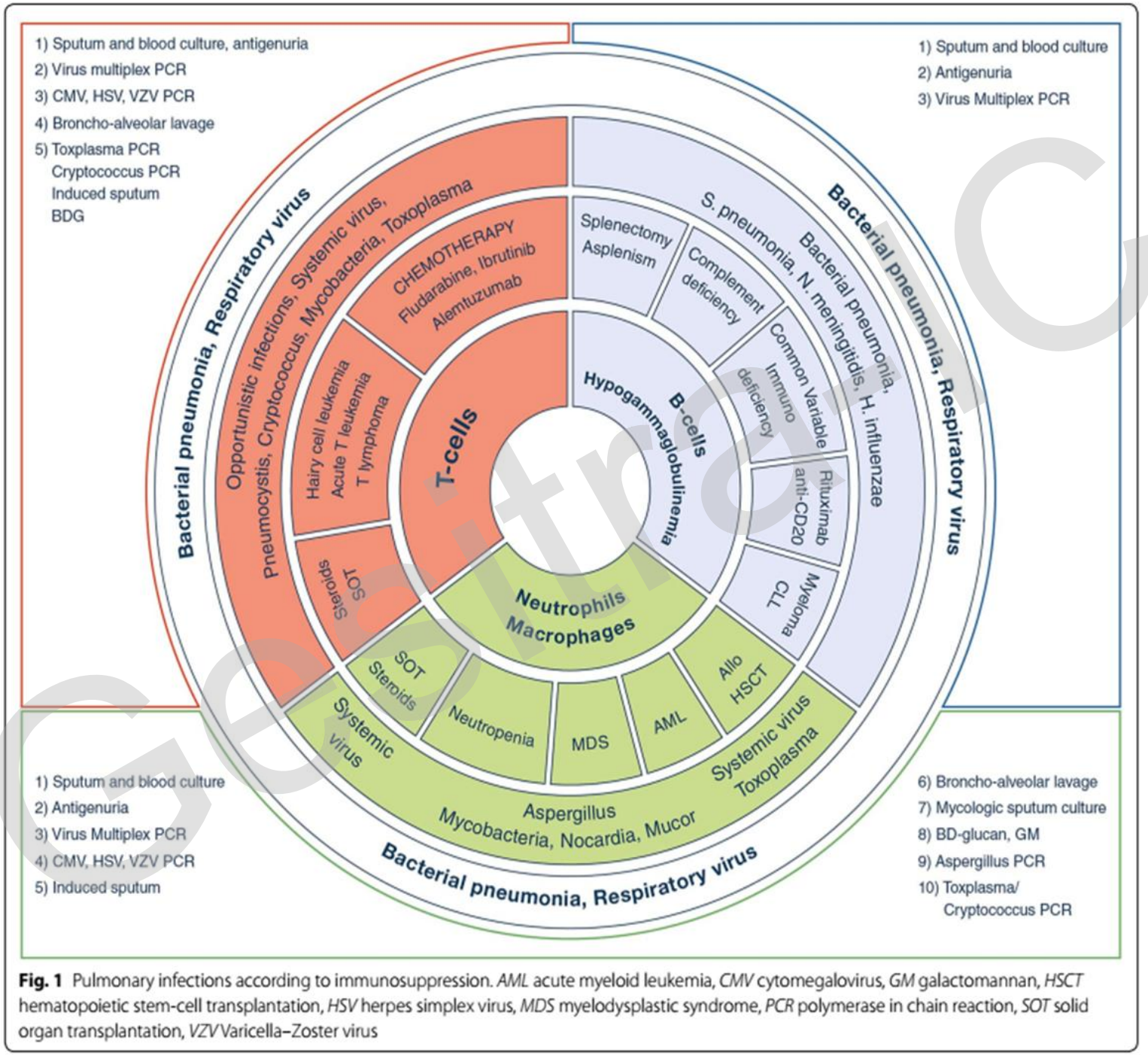


Fig. 1 Pulmonary infections according to immunosuppression. *AML* acute myeloid leukemia, *CMV* cytomegalovirus, *GM* galactomannan, *HSCT* hematopoietic stem-cell transplantation, *HSV* herpes simplex virus, *MDS* myelodysplastic syndrome, *PCR* polymerase in chain reaction, *SOT* solid organ transplantation, *VZV* Varicella–Zoster virus

Front-line use of Syndromic/multiplexed panels in immunosuppressed patients: critical factors to be considered…

- ✓ Clinical entity (Upper respiratory tract/CAP/HAP/VAT)
- ✓ Immunosuppressive condition
- ✓ Timing of appearance (TPX/CAR-T)
- ✓ Clinical and imaging data
- ✓ Multidrug-resistance bacteria (MDRB) local epidemiology
- ✓ Ongoing antimicrobial therapy
- ✓ Specimen type(s) available for testing
- ✓ Laboratory resources
- ✓ Prevalence of off-panel targets
- ✓ Cost-effectiveness

✓Upper respiratory tract infection

- Multiplexed PCR panels for CARV: Recommended

✓CAP (low risk MDRB)

- Use of syndromic panels optional
- Use of multiplexed PCR panels for CARV: Recommended

✓ CAP (high risk MDRB)sCAP/HAP/VAT

- Use of syndromic panels: Recommended

Specimen: BAL recommended/proximal airway specimens acceptable

Testing for off-panel targets upon clinical and imaging suspicion!

Community-acquired respiratory virus infections in patients with haematological malignancies or undergoing haematopoietic cell transplantation: updated recommendations from the 10th European Conference on Infections in Leukaemia

Marie von Lilienfeld-Toal, Fareed Khawaja, Francesca Compagno, Christine Robin, José-Luis Piñana, Simone Cesaro, Hermann Einsele, Per Ljungman, David Navarro, Michael Boeckh, Roy F Chemaly, Hans H Hirsch**

Diagnostic testing recommendations†	
HCT candidates or recipients presenting with URTID or LRTID should be tested for CARVs by multiplex NAT to guide infection control measures, treatment, and decisions regarding deferral of chemotherapy or HCT	AII
For all patients with RTID due to be admitted to hospital or already admitted, comprehensive diagnostic NAT (CARV multiplex NAT) is recommended, covering influenzavirus A and B, SARS-CoV-2, RSV, HPIV, HMPV, HRhV, HCoV, and HAdV	BIII
In health-care centres not providing CARV multiplex NAT, first-line diagnostic testing should be done for influenzavirus A and B, SARS-CoV-2, and RSV, and if negative, followed by second-line diagnostic testing for HMPV and HPIV 1–4 or other specific CARVs (eg, HRhV and HAdV) as epidemiologically indicated	AIIt
Specimens should be taken from the site of clinical involvement, preferably nasal, nasopharyngeal, or naso-oropharyngeal swabs for URTID, or by bronchoalveolar lavage fluids for LRTID (or tracheal aspirate if bronchoalveolar lavage is not feasible)	AII
Patients with LRTID caused by CARV should be considered for bronchoalveolar lavage and broader diagnostic testing	AII
Lung biopsy (transbronchial, thoracoscopic, or open surgery techniques) remains an extreme diagnostic measure that could be considered to evaluate clinical failure and other concomitant pulmonary conditions	CIII

Clinical Microbiology and Infection 31 (2025) 1245–1247

Contents lists available at ScienceDirect

Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com

Commentary

Revisiting diagnostics: practical application of next-generation sequencing technologies for infectious diseases

Lucía Henríquez [1, 2, *], Ander Uribarri [1, 2], Maria Eugenia Portillo [1, 2, 3]

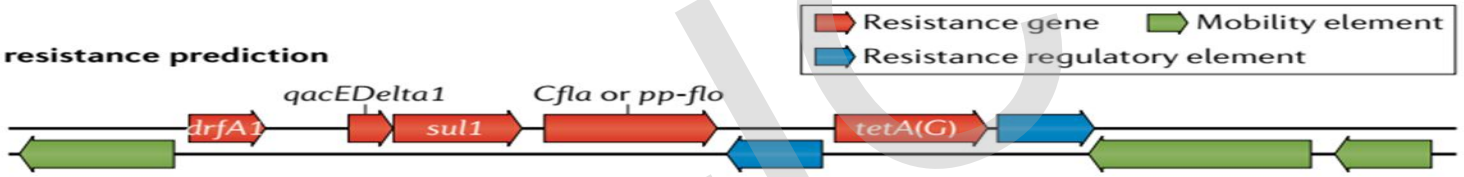
Table 1
Summary of NGS techniques: advantages, applications and sequencing platforms.

Technique	Advantages	Applications
PCR	- Rapid results - Cost-effective - High specificity for known targets	- Early diagnosis of infections - Detection of specific pathogens - Most frequent antimicrobial resistance gene detection
Targeted NGS	- Focuses on specific genetic regions - Less complex data analysis	- Bacterial (16S rRNA) and fungal (ITS/18S/28S) identification - Diagnosis of polymicrobial infections - Detection of fastidious or slow-growing pathogens - Identification of pathogens in culture-negative samples - Microbiome studies
mNGS (Shotgun)	- Detects all genetic material present - Identifies multiple microorganisms types (bacteria, virus, fungi, etc) simultaneously - Detects novel or unexpected microorganisms	- Diagnosis of polymicrobial infections - Detection of fastidious or slow-growing pathogens - Identification of pathogens in culture-negative samples - Microbiome studies
WGS	- Provides strain-level resolution - Detailed genomic information - High accuracy for mutation detection	- Epidemiological studies - Antimicrobial resistance profiling - Virulence factor detection - Outbreak investigations
Sequencing technology	**Advantages**	**Applications**
SBS	- Very low error rate (0.1–0.2%) - High accuracy for mutation detection (SNPS …)	- In-depth genomic analysis - Antimicrobial resistance studies - Epidemiological surveillance
NS	- Real-time data collection - Rapid diagnosis (within hours)- Ability to read long DNA/RNA fragments	- Point-of-care testing - Rapid clinical diagnostics - Field-based sequencing

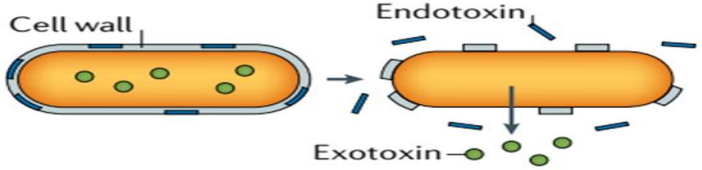
A Infectious disease diagnostics

Aa Microorganism identification

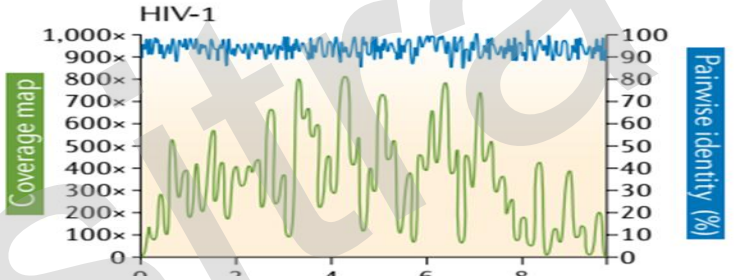
Ab Antibiotic resistance prediction

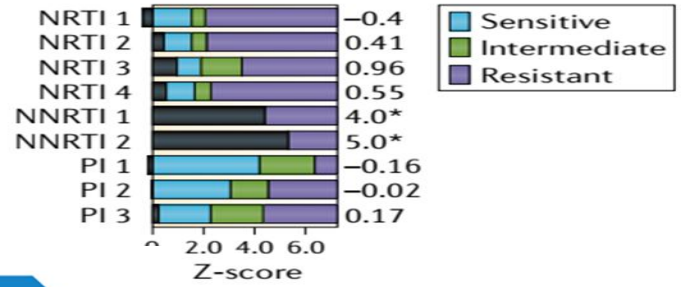


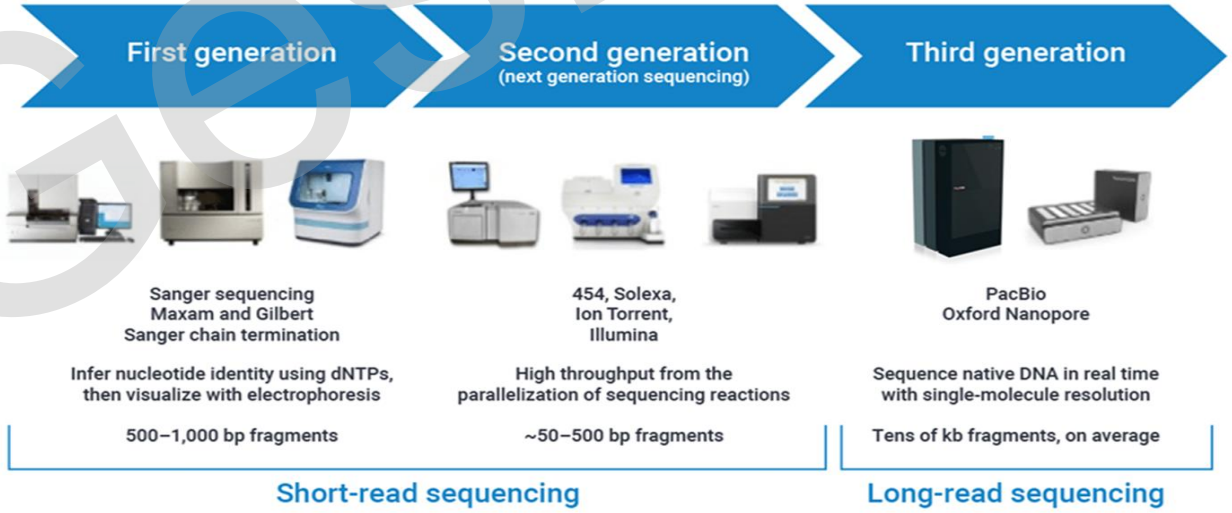
Ac Detection of virulence determinants



Ad Antiviral resistance prediction



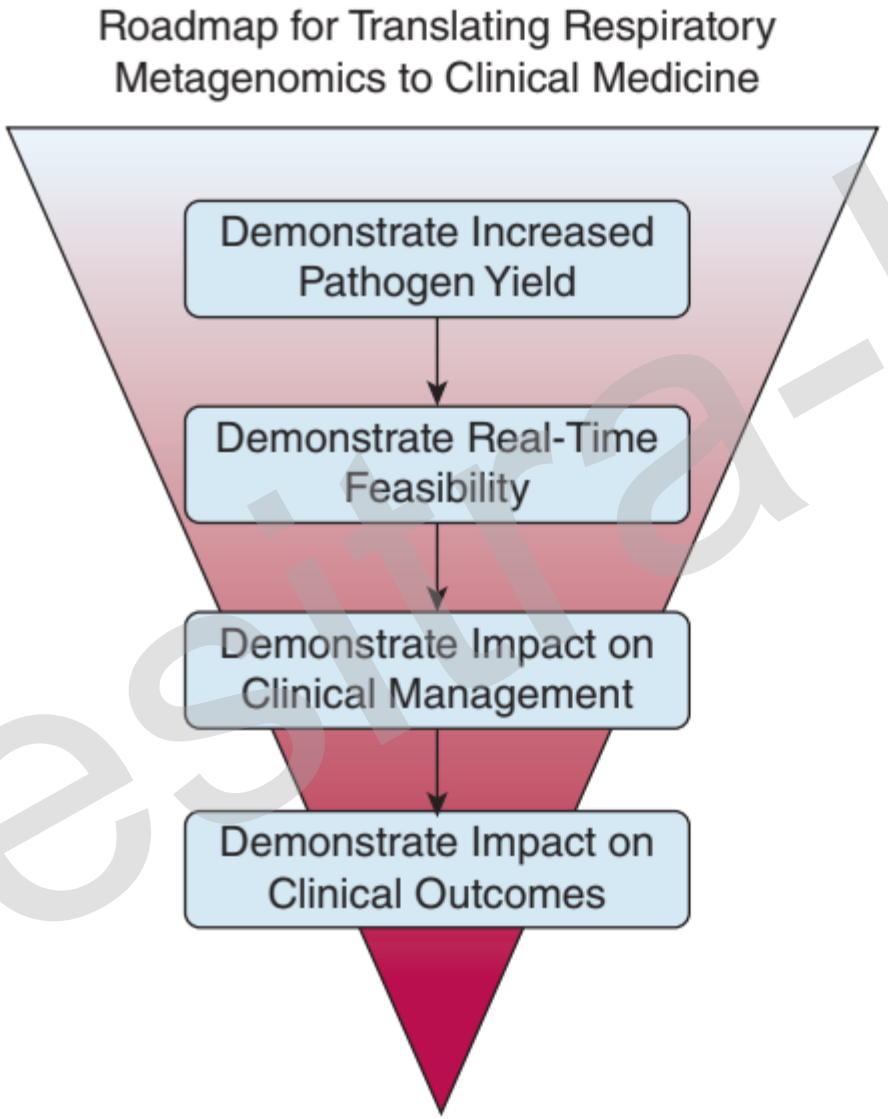




Metagenomic Sequencing for Personalized Treatment in Pneumonia

Does Better Detection Lead to Better Outcomes?

Benjamin G. Wu, MD, MSCI
New York, NY
Matt S. Zinter, MD
San Francisco, CA



Kling K, Qi C, Wunderink RG, Pickens C. Diagnostics (Basel). 2024 Jun 29;14(13):1388.

Diagnostics **2024**, *14*, 1388.

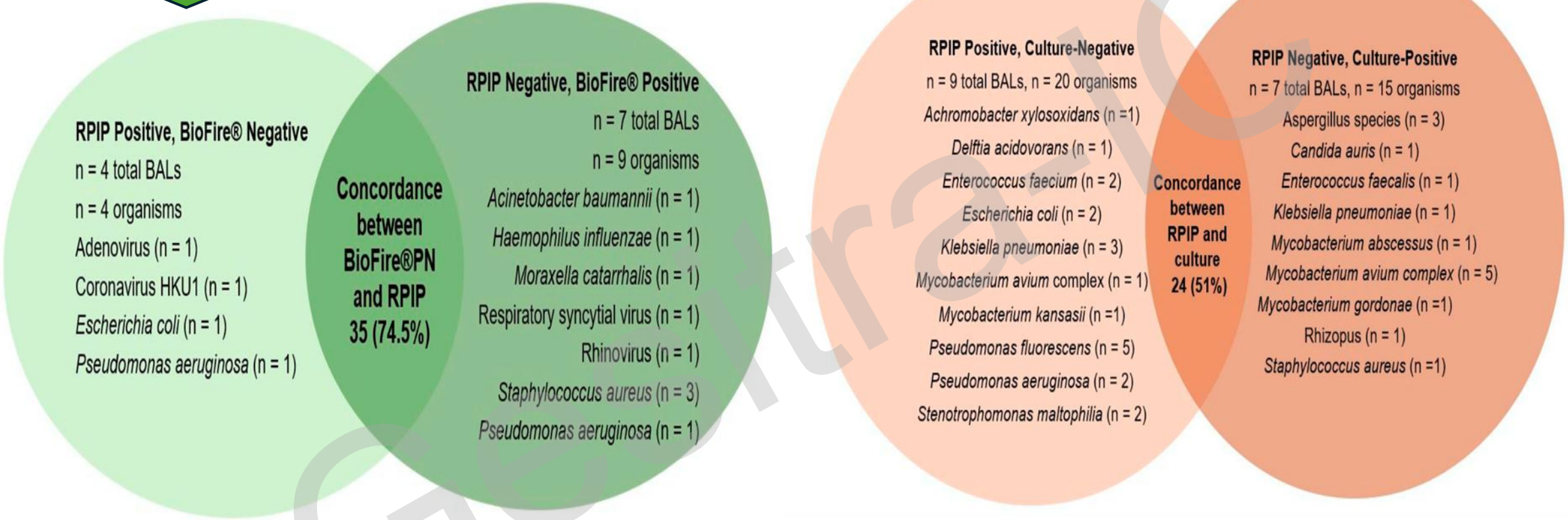
diagnostics

MDPI

Article

The Impact of Next-Generation Sequencing Added to Multiplex PCR on Antibiotic Stewardship in Critically Ill Patients with Suspected Pneumonia

Kendall Kling [1], Chao Qi [2], Richard G. Wunderink [3] and Chiagozie Pickens [3,*]



Kling K, Qi C, Wunderink RG, Pickens C. Diagnostics (Basel). 2024 Jun 29;14(13):1388.

[Chest Infections Original Research]

CHEST

Effect of Metagenomic Next-Generation Sequencing on Clinical Outcomes of Patients With Severe Community-Acquired Pneumonia in the ICU

A Multicenter, Randomized Controlled Trial