

PCR multiplex en réanimation : intérêts et implications thérapeutiques..

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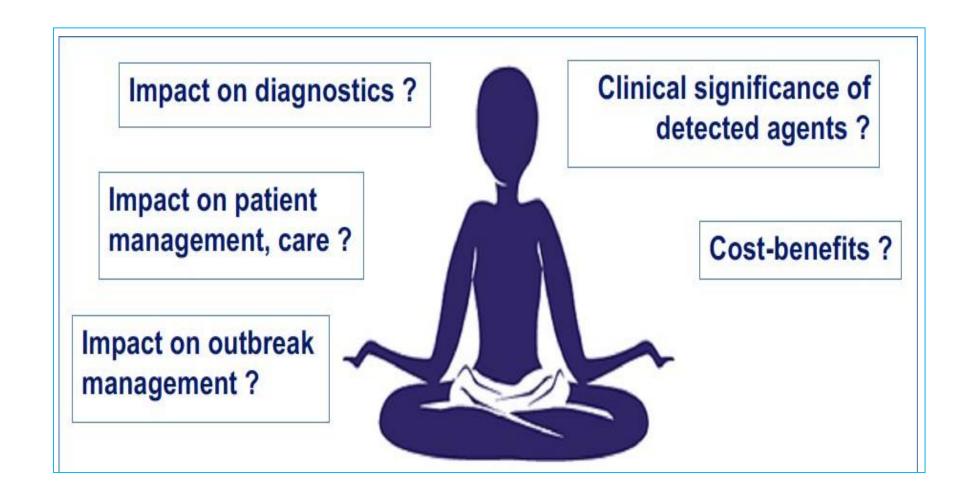
Pas de conflits d'intérêt

- La PCR multiplex est une technique de biologie moléculaire très répandue
- Principe : l'amplification de plusieurs cibles dans une seule expérience de PCR .

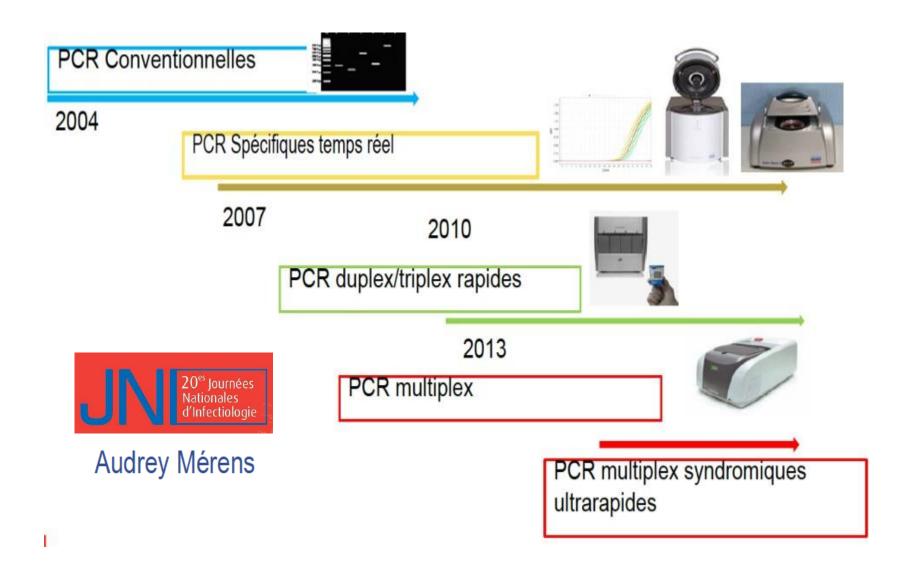
Les avantages:

- Simplicité d'un prélèvement unique
- Identification simultanée des agents pathogènes et gènes de résistance
- Possibilité de détecter des bactéries (même si sous antibiothérapie)
- Sensibilité et spécificité accrues

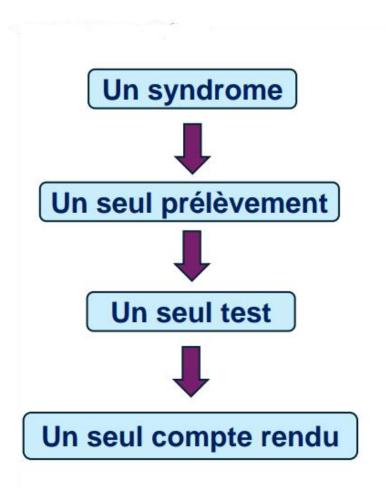
Problématiques



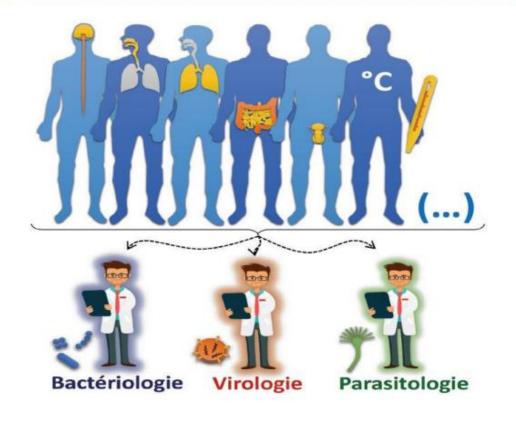
Évolution des techniques de PCR



APPROCHE SYNDROMIQUE



Plusieurs panels pour l'exploration de la quasi-totalité des infections +++



Système intégré de PCR multiplex: quels avantages?

Panels syndromiques unitaires



- Rapide
 Pour peu d'échantillons
- + Facilité d'utilisation

 Manipulation simple
- Grands nombres d'agents pathogènes détectés simultanément
- Détection de co-infections

Techniques conventionnelles (PCR classique, cultures..)

- + Efficacité
 Moins rapide mais traite un grand
 nombre d'échantillons
- Quantification possible et plus fiable
- Sensibilité souvent meilleure
- Meilleure adaptabilité
 En cas d'émergence d'un nouvel agent

Approche syndromique multiplexe en réanimation

Multiplex PCR syndromic testing in intensive care units



B. Visseaux · L. Armand-Lefèvre

Reçu le 26 février 2019 ; accepté le 26 mai 2019 © SRLF et Lavoisier SAS 2019

- Les nouveaux tests de diagnostic rapide par PCR multiplexe à visée syndromique, capables de détecter plusieurs dizaines de pathogènes en quelques heures, a entraîné un changement de paradigme en microbiologie et en pratique clinique.
- peuvent apporter une aide dans le diagnostic des infections chez les patients de réanimation.
- elles présentent cependant certains défis, comme l'évaluation de leurs performances réelles, leur coût très élevé, le choix des stratégies d'utilisation et l'interprétation clinico biologique des résultats.

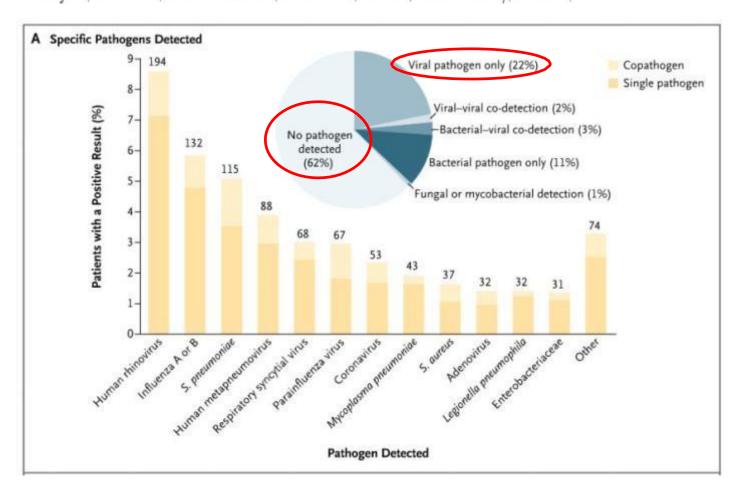
- Respiratoires +++
- Neuro méningés
- Bactériémies

Diagnostic microbiologique des infections respiratoires = véritable challenge

Community-Acquired Pneumonia Requiring Hospitalization among U.S. Adults

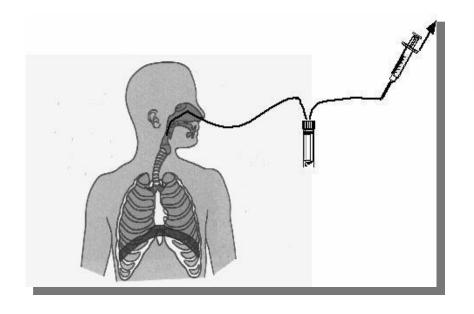


S. Jain, W.H. Self, R.G. Wunderink, S. Fakhran, R. Balk, A.M. Bramley, C. Reed,



Techniques de prélèvement

- ✓ Mise en œuvre facile et rapide
- ✓ Extraction des acides nucléiques + facile
- ✓ Ecouvillon spécifique ++++ → Nylon floqué
- ✓ milieu de transport virologique
- ✓ Emballage



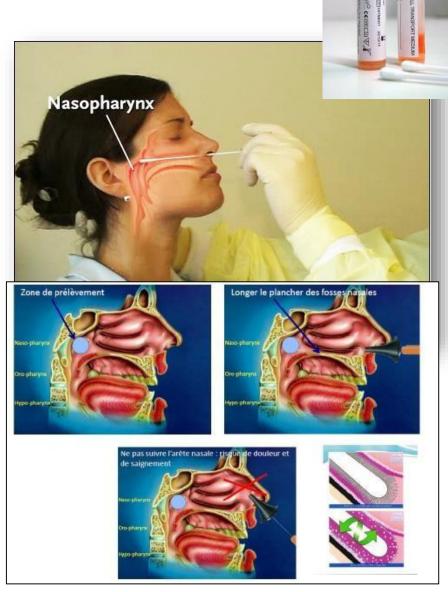


Table 1. Landscape of Food and Drug Administration—Cleared Diagnostic Tests for Acute Respiratory Tract Infection

Targets ^a	Approved Specimen Types	Time ^b	Cost ^c
CLIA-waived assays			
Influenza A/B only	NS direct, NPS direct, NP, NPS	15–30 minutes	\$\$-\$\$\$
RSV only	NPS direct, NS, NPS	15 minutes	\$\$\$
Flu A/B plus RSV	NS, NPS	20-30 minutes	\$\$-\$\$\$
Multiple viruses plus atypical bacteria	NPS	60 minutes	\$\$\$\$
Moderate- to high-complexity assays			
Influenza A/B only	NS, NPS	0.5-2 hours	\$\$
PIV only	NPS	3.5 hours	\$\$
Flu A/B plus RSV	NS, NPS, NPA, NW	0.5-3.5 hours	\$\$-\$\$\$\$
RSV plus hMPV	NS, NPS	0.75 hours	\$S
AdV, hMPV plus RV	NPS	3.5 hours	\$\$
Multiple viruses plus atypical bacteria	NPS	0.75-5 hours	\$\$\$\$
Multiple bacteria with resistance	ETA	4–5 hours	\$\$\$\$\$
Multiple viruses and bacteria with resistance	S, ETA, BAL	60 hours	\$\$\$\$\$

En TUNISIE



BACTÉRIES

(Résultats semi-quantitatifs) Acinetobacter calcoaceticusbaumannii complexe Enterobacter cloacae complexe Escherichia coli Haemophilus influenzae Klebsiella aerogenes Klebsiella oxytoca Groupe Klebsiella pneumoniae Moraxella catarrhalis Proteus spp. Pseudomonas aeruginosa Serratia marcescens Staphylococcus aureus Streptococcus agalactiae Streptococcus pneumoniae

(Résultats qualitatifs) Chlamydia pneumoniae Legionella pneumophila Mycoplasma pneumoniae

VIRUS

Adénovirus Coronavirus Métapneumovirus humain Entérovirus/rhinovirus humains Virus de la grippe A Virus de la grippe B Coronavirus du syndrome respiratoire du Moyen-Orient (MERS CoV) Virus parainfluenza Virus respiratoire syncytial

BACTÉRIES ATYPIQUES GÈNES DE RÉSISTANCE **AUX ANTIBIOTIQUES**

Résistance à la méticilline mecA/C et MREJ

Carbapénémases

IMP **KPC** NDM OXA-48-like

BLSE

VIM

CTX-M

34 cibles en 1 heure environ

Type d'échantillon :

Streptococcus pyogenes

Expectoration (AET compris) et LBA (mini-LBA compris)

05/2014

10/2015

06/2017

Q4/2018

BioFire® FilmArray® Panels

FDA-clearance: 05/2011

06/2013

RESEARCH ARTICLE

Open Access

(CrossMark

Multiplex PCR point of care testing versus routine, laboratory-based testing in the treatment of adults with respiratory tract infections: a quasi-randomised study assessing impact on length of stay and antimicrobial use



- Méthodologie: Cohorte randomisée, ouverte n= 606 (contrôle 211, interventionnel 334). Technique PCR multiplex rapide VS techniques standards
- **Inclusion:** Adultes (consultants/hospitalisés) présentant syndrome grippal, IRA, +/- infection respiratoire basse.
- Objectif principal: Comparaison de la durée moyenne de séjour
- Objectifs secondaires: Impact sur l'utilisation des antibiotiques, les réadmissions, la mortalité, le délai admission résultat

Pas de différence sur la durée moyenne de séjour Réduction du délai pour la mise en place des antiviraux Meilleur traitement pour *Mycoplasma pneumoniae*

Bacterial and Viral Infection in Patients Hospitalized for Acute Exacerbation of Chronic Obstructive Pulmonary Disease: Implication for Antimicrobial Management and Clinical Outcome

Salma Messous^{a,b}, Aida Elargoubi^b, Sylvie Pillet^c, Alain Rajoharison^d, Jonathan Hoffmann^d, Imen Trabelsi^a, Mohamed Habib Grissa^{a,e}, Riadh Boukef^{a,f}, Kaouther Beltaief^{a,e}, Maha Mastouri^b, Gláucia Paranhos-Baccalà^c Semir Nouira^{a,e}, and Bruno Pozzetto^c

Table 2. Demographics together with clinical and biological characteristics at hospital admission of the 84 patients exhibiting an exacerbation of COPD included into the study.

Patients' characteristics	All patients
Age in years, mean (SD)	67.8 (10)
Male sex, no. (%)	78 (92.9)
Smoking history in packets/year, mean (SD)	52.3 (64)
Number of previous exacerbations in	2.5 (1.7)
the last 12 months, mean (SD)	
BMI in kg/m², mean (SD)	25.7 (4.9)
GOLD severity classification	
Stage 4, no. (%)	30 (35.7)
Stage 3, no. (%)	47 (56)
Stage 2, no. (%)	7 (8.3)
PaO ₂ in kPa, mean (SD) ^a	14 (1.4)
PaCO ₂ , in kPa, mean (SD) ^a	5.9 (1.9)
pH, mean (SD)	7.3 (0.06)
WBC in cells/mm ³ *10 ³ , mean (SD)	12.4 (6)
CRP in mg/l, mean (SD)	58 (56)

^aThese values were recorded while the patients were under oxygen supplementation.

Table 3. List of pathogens recovered from the sputum samples of the patients of the study.

Conventional bacteriological cultures (n = 74)³ - Acinetobacter baumannii - Escherichia coli - Klebsiella pneumoniae - Haemophilus influenzae - Haemophilus parainfluenzae - Haemophilus parainfluenzae - Pseudomonas aeruginosa - Staphylococcus aureus - Streptococcus pneumoniae Molecular testing (n = 84) Bacteria - Chlamydia pneumoniae Viruses - Influenza virus A/HINI - Influenza virus A/H3N2 - Influenza virus B - Rhinovirus - Respiratory syncytial virus B - Parainfluenza virus type 1 - Parainfluenza virus type 1 - Parainfluenza virus type 3 - Human coronavirus VL63 - Human coronavirus NL63 - Human coronavirus HKU-1¹b - Human bocavirus - Adenovirus	Pathogen	Number				
- Escherichia coli - Klebsiella pneumoniae - Haemophilus influenzae - Haemophilus parainfluenzae - Haemophilus parainfluenzae - Pseudomonas aeruginosa - Staphylococcus aureus - Streptococcus pneumoniae Molecular testing (n = 84) Bacteria - Chlamydia pneumoniae 1 Viruses - Influenza virus A/H1N1 - Influenza virus A/H3N2 - Influenza virus B - Respiratory syncytial virus B - Respiratory syncytial virus B - Parainfluenza virus type 1 - Parainfluenza virus type 1 - Parainfluenza virus type 3 - Human coronavirus VL63 - Human coronavirus NL63 - Human coronavirus HKU-1 ^b - Human bocavirus	Conventional bacteriological cultures (n = 74) ^a					
- Klebsiella pneumoniae - Haemophilus influenzae - Haemophilus parainfluenzae - Pseudomonas aeruginosa - Staphylococcus aureus - Streptococcus pneumoniae Molecular testing (n = 84) Bacteria - Chlamydia pneumoniae Viruses - Influenza virus A/H1N1 - Influenza virus A/H3N2 - Influenza virus B - Rhinovirus - Respiratory syncytial virus B - Parainfluenza virus type 1 - Parainfluenza virus type 3 - Human coronavirus VL63 - Human coronavirus NL63 - Human coronavirus HKU-1 ^b - Human bocavirus - Respiratory syncytius HKU-1 ^b - Human coronavirus HKU-1 ^b - Human bocavirus		2				
 Haemophilus influenzae Haemophilus parainfluenzae Pseudomonas aeruginosa Staphylococcus aureus Streptococcus pneumoniae Molecular testing (n = 84) Bacteria Chlamydia pneumoniae Viruses Influenza virus A/HTNT Influenza virus A/H3N2 Influenza virus B Respiratory syncytial virus B Parainfluenza virus type 1 Parainfluenza virus type 3 Human coronavirus OC43 Human coronavirus NL63 Human coronavirus HKU-1b Human bocavirus Human bocavirus 	– Escherichia coli	1				
 Haemophilus parainfluenzae Pseudomonas aeruginosa Straphylococcus aureus Streptococcus pneumoniae Molecular testing (n = 84) Bacteria Chlamydia pneumoniae Viruses Influenza virus A/HINI Influenza virus A/H3N2 Influenza virus B Respiratory syncytial virus B Parainfluenza virus type 1 Parainfluenza virus type 3 Human coronavirus 229E Human coronavirus NL63 Human coronavirus HKU-1b Human bocavirus Human bocavirus 	– Klebsiella pneumoniae	2				
- Pseudomonas aeruginosa - Staphylococcus aureus - Streptococcus pneumoniae Molecular testing (n = 84) Bacteria - Chlamydia pneumoniae Viruses 63 - Influenza virus A/HTN1 - Influenza virus A/H3N2 - Influenza virus B - Rhinovirus - Respiratory syncytial virus B - Parainfluenza virus type 1 - Parainfluenza virus type 3 - Human coronavirus VC43 - Human coronavirus NL63 - Human coronavirus HKU-1b - Human bocavirus - Human bocavirus - Human bocavirus - Human bocavirus - Human coronavirus HKU-1b - Human bocavirus	– Haemophilus influenzae	3				
- Staphylococcus aureus - Streptococcus pneumoniae Molecular testing (n = 84) Bacteria - Chlamydia pneumoniae Viruses - Influenza virus A/HINI - Influenza virus A/H3N2 - Influenza virus B - Rhinovirus - Respiratory syncytial virus B - Parainfluenza virus type 1 - Parainfluenza virus type 3 - Human coronavirus VC43 - Human coronavirus NL63 - Human coronavirus HKU-1 ^b - Human bocavirus - Staphylococcus pneumoniae 1 2 Molecular testing (n = 84) 1 1 - Chlamydia pneumoniae 1 - Chlamydia pneumoniae 1 - Chlamydia pneumoniae 1 - Influenza virus A/H3N2 - Influenza virus B - Parainfluenza virus B - Parainfluenza virus type 1 - Parainfluenza virus type 3 - Human coronavirus OC43 - Human coronavirus NL63 - Human bocavirus	– Haemophilus parainfluenzae	1				
- Streptococcus pneumoniae Molecular testing (n = 84) Bacteria 1 - Chlamydia pneumoniae 1 Viruses 63 - Influenza virus A/HTNT / - Influenza virus A/H3N2 5 - Influenza virus B 1 - Rhinovirus 33 - Respiratory syncytial virus B 1 - Parainfluenza virus type 1 2 - Parainfluenza virus type 3 1 - Human coronavirus 229E 2 - Human coronavirus OC43 2 - Human coronavirus NL63 2 - Human coronavirus HKU-1 ^b 2 - Human bocavirus	– Pseudomonas aeruginosa	3				
Molecular testing (n = 84) Bacteria 1 - Chlamydia pneumoniae 1 Viruses 63 - Influenza virus A/HTNT 7 - Influenza virus A/H3N2 5 - Influenza virus B 1 - Rhinovirus 33 - Respiratory syncytial virus B 1 - Parainfluenza virus type 1 2 - Parainfluenza virus type 3 1 - Human coronavirus 229E 2 - Human coronavirus NL63 2 - Human coronavirus HKU-1b 2 - Human bocavirus 4						
Bacteria 1 - Chlamydia pneumoniae 1 Viruses 63 - Influenza virus A/HTNT / - Influenza virus A/H3N2 5 - Influenza virus B 1 - Rhinovirus 33 - Respiratory syncytial virus B 1 - Parainfluenza virus type 1 2 - Parainfluenza virus type 3 1 - Human coronavirus 229E 2 - Human coronavirus NL63 2 - Human coronavirus HKU-1 2 - Human bocavirus 4	– Streptococcus pneumoniae	2				
- Chlamydia pneumoniae Viruses - Influenza virus A/HTNT - Influenza virus A/H3N2 - Influenza virus B - Rhinovirus - Respiratory syncytial virus B - Parainfluenza virus type 1 - Parainfluenza virus type 3 - Human coronavirus 229E - Human coronavirus NL63 - Human coronavirus HKU-1 ^b - Human bocavirus 4	Molecular testing ($n = 84$)					
Viruses — Influenza virus A/HTNT — Influenza virus A/H3N2 — Influenza virus B — Rhinovirus — Respiratory syncytial virus B — Parainfluenza virus type 1 — Parainfluenza virus type 3 — Human coronavirus 229E — Human coronavirus NL63 — Human coronavirus HKU-1 ^b — Human bocavirus 4	Bacteria	1				
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 Influenza virus A/H3N2 Influenza virus B Rhinovirus Respiratory syncytial virus B Parainfluenza virus type 1 Parainfluenza virus type 3 Human coronavirus 229E Human coronavirus OC43 Human coronavirus NL63 Human coronavirus HKU-1b Human bocavirus 						
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 Human coronavirus OC43 Human coronavirus NL63 Human coronavirus HKU-1^b Human bocavirus 	• • • • • • • • • • • • • • • • • • • •	1				
 Human coronavirus NL63 Human coronavirus HKU-1^b Human bocavirus 	– Human coronavirus 229E					
 Human coronavirus HKU-1^b Human bocavirus 	– Human coronavirus OC43					
– Human bocavirus 4						
	– Human coronavirus HKU-1 ^b	2				
- Adenovirus 1	– Human bocavirus					
	– Adenovirus	1				

Co Infections respiratoires Pendant l'ère COVID

co-infections avec des virus respiratoires

Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study

Nanshan Chen*, Min Zhou*, Xuan Dong*, Jieming Qu*, Fengyun Gong, Yang Han, Yang Qiu, Jingli Wang, Ying Liu, Yuan Wei, Jia'an Xia, Ting Yu, Xinxin Zhang, Li Zhang

www.thelancet.com Published online lanuary 20, 2020

RESEARCH LETTER

Rates of Co-infection Between SARS-CoV-2 and Other Respiratory Pathogens

JAMA Published online April 15, 2020

23/116 COVID+ 292/1100 COVID-

Table 2. Proportions of Specimens Positive for Non-SARS-CoV-2 Respiratory Pathogens and Mean Patient Ages for Each Subgroup, by SARS-CoV-2 Result^{a,b}

	SARS-CoV-2 status						
	Negative (n = 1101)		Positive (n = 116)				
Pathogen	Proportion positive for other respiratory pathogen, No. (%) ^b	Mean age of positive patients, y	Proportion positive for other respiratory pathogen, No. (%) ^b	Mean age of positive patients, y			
Influenza							
A	29/1101 (2.6)	45.9	1/116 (0.9)	74.0			
В	8/1101 (0.7)	21.6	0/116 (0)				
RSV	32/1101 (2.9)	26.0	6/116 (5.2)	52.3			
Parainfluenza							
1	1/1101 (0.1)	71.0	1/116 (0.9)	43.0			
2	0/1101 (0)		0/116 (0)				
3	2/1101 (0.2)	40.0	1/116 (0.9)	45.0			
4	5/1101 (0.5)	26.6	1/116 (0.9)	36.0			
Metapneumovirus	47/1101 (4.3)	41.1	2/116 (1.7)	67.0			
Rhinovirus/enterovirus	133/1101 (12.1)	32.6	8/116 (6.9)	42.1			
Adenovirus	10/1101 (0.9)	14.1	0/116 (0)				
Other Coronaviridae	39/1101 (3.5)	42.2	5/116 (4.3)	40.8			
Chlamydia pneumoniae	0/1060 (0)		0/116 (0)				
Mycoplasma pneumoniae	6/1101 (0.5)	14.8	0/116 (0)				

	Patients (n=99)
(Continued from previous column)	
Infection-related biomarkers	
Procalcitonin (ng/mL; normal range 0·0–5·0)	0.5 (1.1)
Increased	6 (6%)
Interleukin-6 (pg/mL; normal range 0·0–7·0)	7-9 (6-1-10-6)
Increased	51 (52%)
Erythrocyte sedimentation rate (mm/h; normal range 0·0–15·0)	49-9 (23-4)
Increased	84 (85%)
Serum ferritin (ng/mL; normal range 21-0–274-7)	808-7 (490-7)
Increased	62 (63%)
C-reactive protein (mg/L; normal range 0·0–5·0)*	51.4 (41.8)
Increased	63/73 (86%)
Co-infection	
Other viruses	0
Bacteria	1 (1%)
Fungus	4 (4%)

Data are n (%), n/N (%), mean (SD), and median (IQR). Increased means over the upper limit of the normal range and decreased means below the lower limit of the normal range. 2019-nCoV=2019 novel coronavirus. *Data available for 73 patients.

Table 3: Laboratory results of patients with 2019-nCoV pneumonia

RESEARCH

Open Access

Bacterial and viral co-infections in patients with severe SARS-CoV-2 pneumonia admitted to a French ICU

Damien Contou^{1*}, Aurore Claudinon², Olivier Pajot¹, Maïté Micaëlo², Pascale Longuet Flandre³, Marie Dubert⁴, Radj Cally¹, Elsa Logre¹, Megan Fraissé¹, Hervé Mentec¹ and Gaëtan Plantefève¹

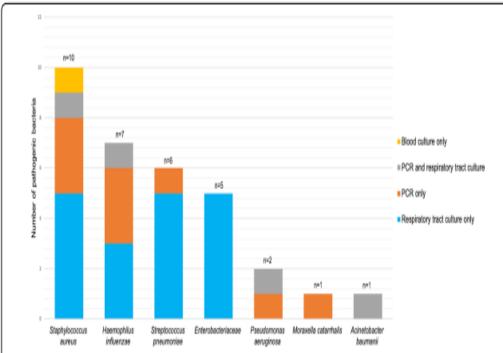


Fig. 1 Number of each species of bacteria isolated from respiratory tract cultures (blue), multiplex PCR (red), both (grey) or blood culture (yellow) among 26 critically ill patients with severe SARS-CoV-2 pneumonia

We report on a 28% rate of bacterial coinfection at ICU admission of patients with severe SARSCoV-2 pneumonia

our results encourage the systematic administration of an empiric antibiotic monotherapy with a 3rd generation cephalosporin, with a prompt de-escalation as soon as possible.

Further larger studies are needed to assess the real prevalence and the predictors of co-infection together with its prognostic impact on critically ill patients with severe SARS-CoV-2 pneumonia.

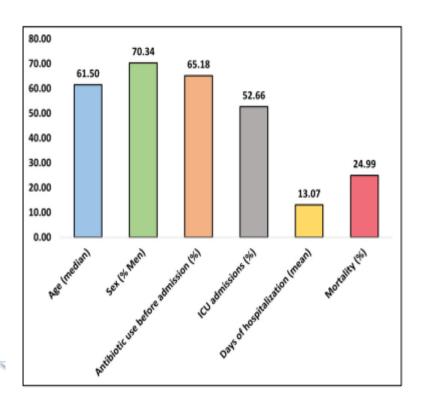




Systematic Review

The Assessment of Multiplex PCR in Identifying Bacterial Infections in Patients Hospitalized with SARS-CoV-2 Infection: A Systematic Review

Iulia Bogdan ^{1,2,3,†}, Tejaswi Gadela ⁴, Felix Bratosin ^{2,3}, Catalin Dumitru ^{5,*}, Alin Popescu ⁵, Florin George Horhat ⁶, Rodica Anamaria Negrean ^{7,†}, Razvan Mihai Horhat ⁸, Ion Cristian Mot ⁹, Adrian Vasile Bota ³, Carmen Nicoleta Stoica ¹⁰, Bogdan Feciche ^{11,*}, Andrei Nicolae Csep ¹², Roxana Manuela Fericean ¹, Gratiana Nicoleta Chicin ^{13,14,*} and Iosif Marincu ³



- Bacterial infections that are identified in COVID-19 patients can lead to more negative outcomes, particularly with a severe infection who are hospitalized with COVID-19.
- effective methods of timely diagnosis and treatment need to be implemented in order to decrease the mortality rate and prevent the misdiagnosis of infections.
- This will allow for a reduction in the number of infections that are incorrectly diagnosed.

Infections respiratoires Après l'ère COVID



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



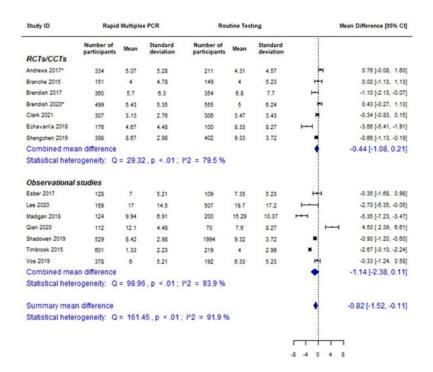
Rapid multiplex PCR for respiratory viruses reduces time to result and improves clinical care: Results of a systematic review and meta-analysis



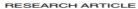
Study ID	Rapid Multiplex PCR		Routine Testing		sting		Mean Difference (95% C	
RCTs/CCTs	Number of participants	Mean	Standard deviation	Number of participants	Mean	Standard deviation		
Andrews 2017*	334	19.6	17.57	211	40.83	24.04	-	-21.23 (-24.98, -17.4)
Brendish 2017	350	2.3	1.4	354	37.1	21.5	144	-34.80 [-37.04, -32.56
Brendish 2020*	499	1,73	0.22	555	21.73	8.84		-20.00 [-20.74, -19.26
Clark 2021	307	1.23	0.22	308	22.43	9.46		-21.20 [-22.2820.14
Echavamia 2018	176	2	0.65	100	31.56	21.08		-29.56 (-33.69, -25.4)
Gelfer 2015	22	1.8	0.3	24	26.7	18	-	-24.90 (-31.30, -18.50
Gilbert 2016	59	2.1	0.7	68	28.5	15	1	-24.40 [-27.97, -20.83
Shengohen 2019	390	1.57	0.22	402	33.33	20:09	1+1	-31.76 (-33.72, -29.80
Combined m	ean differen	nce					•	-25.98 [-30.01, -21.96
Statistical het	erogeneity	Q=	264.03	p < .01; P	2 = 9	97.3 %		
Observation	al studies							
Madigan 2018	124	4.4	0.61	200	21.6	17.02	1-4	-17.20 [-19.56, -14.84
Petrit 2015	872	3.1	0.61	230	45.4	20.07	144	-43.30 [-45.89, -40.71
Poelman 2020	492	3.23	0.61	280	38	17.02	1-4	-32.77 [-34.84, -30.70
Rappo 2016a	54	1.83	0.48	158	7.5	9.88		-5.67 [-7.22, -4.12
Rappo 2016b	85	1.67	0.53	40	20.2	23.3		-18.53 (-25.75, -11.31
Roy 2018b	130	0.72	0.61	25	12	17.02		-11.28 (-17.95, -4.61
Weiss 2019	1043	3	1,17	451	27.9	20.07	(m)	-24.90 (-26.73, -23.07
Combined m	ean differen	nce					-	-22.04 (-32.76, -11.32
Statistical het	erogeneity:	Q=	822.00,	p < .01; P	2 = 9	99.3 %		
Summary me	an differen	ce					•	-24.22 [-28.70, -19.74
Statistical he	terogeneity	: Q=	1094.17	, p < .01;	1/2 =	98.7 %		

Délai de résultat du test

Apport de l'approche syndromique Delai diagnostic Durée du séjour



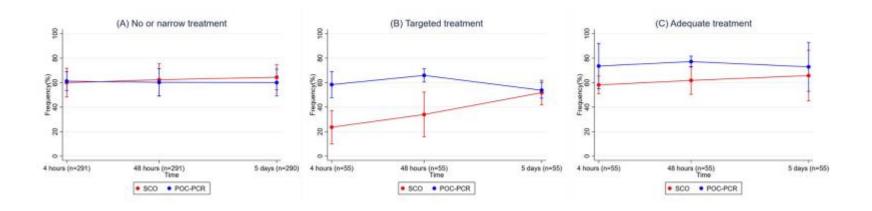
Durée du séjour



Evaluation of point-of-care multiplex polymerase chain reaction in guiding antibiotic treatment of patients acutely admitted with suspected community-acquired pneumonia in Denmark: A multicentre randomised controlled trial

Mariana Bichuette Cartuliares (1,2 *, Flemming Schønning Rosenvinge (3,4, Christian Backer Mogensen (5,2), Thor Aage Skovsted (5, Steen Lomborg Andersen (6,6), Claus Østergaard⁷, Andreas Kristian Pedersen (8,4), Helene Skjøt-arkil (5,1),





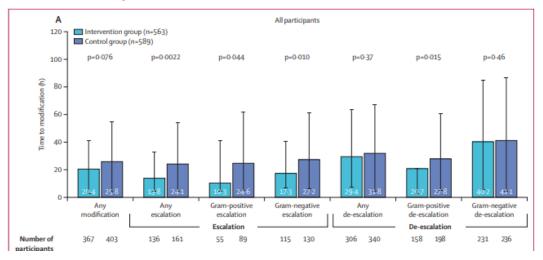
In this randomised study, adding sputum-POC-PCR to our diagnostic setup did not affect prescriptions of no or narrow-spectrum antibiotics during the first 2 days of admission, but less patients in the POC-PCR-group were treated with no or narrow-spectrum antibiotics after 5 days. Interestingly, patients in the POC-PCR-group were more likely to receive early targeted and adequate treatment. Number of readmissions, ICU admissions, and mortality were unchanged but we found a nonsignificant one-day reduction in LOS.

Rapid multiplex PCR panel for pneumonia in hospitalised patients with suspected pneumonia in the USA: a single-centre, open-label, pragmatic, randomised controlled trial

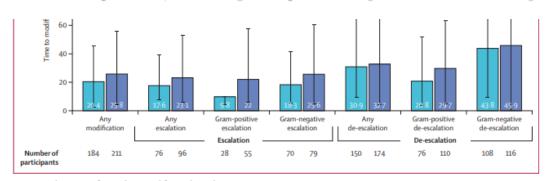


Abinash Virk, Angel P Strasburg, Kami D Kies, Alexander D Donadio, Jay Mandrekar, William S Harmsen, Ryan W Stevens, Lynn L Estes, Aaron J Tande, Douglas W Challener, Douglas R Osmon, Madiha Fida, Paschalis Vergidis, Gina A Suh, John W Wilson, Nipunie S Rajapakse, Bijan J Borah, Ruchita Dholakia, Katelyn A Reed, Lisa M Hines, Audrey N Schuetz, Robin Patel





Interpretation Clinical use of the BioFire FilmArray pneumonia panel might lead to faster antibiotic escalations, including for Gram-negative or Gram-positive bacteria, and faster antibiotic de-escalations directed at Gram-positive bacteria. Additional research is needed regarding antimicrobial de-escalation, especially when antibiotics with broad Gram-negative spectrum are being used, by use of rapid diagnostics in patients with lower respiratory tract infection.



Recommandations de l'IDSA

Clinical Infectious Diseases

VIEWPOINTS ARTICLE



Molecular Testing for Acute Respiratory Tract Infections: Clinical and Diagnostic Recommendations From the IDSA's Diagnostics Committee

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Clinical Infectious Diseases®

2020;XX(XX):1-8

PCRm virologiques en compléments des tests bactério de routine

L'approche syndromique moléculaire dans les infection respiratoire dépend de :

Sévérité intermédiaire

- Test négatif: arrêter le ttt empirique
- **Test positif**: ttt ciblé, réduire la toxicité des ttt évitables, réduit le recours aux tests inutiles

Sévérité élevée

ces tests peuvent se révéler dangereux en cas d'absence de ttt empirique contre un agent mortel

Sévérité faible

Tests non adaptée aux pays à faible ressources

D'autres études coût/bénéfice sont nécessaires

PERSPECTIVES

Table 2. Committee Recommendations for Future Respiratory Diagnostic Studies

Development of New and Innovative Diagnostics	Cost-effectiveness Studies of Available Tests	Definition of Optimal Testing Algorithms and AS Interventions
Novel biomarker discovery and host-response signa- tures that help separate viral, bacterial, fungal, and coinfections from colonization or no infection.	' '	Studies combining host-response signatures or bio- markers with pathogen detection and active AS.
Continued refinement and analytical evaluation of unbiased next-generation sequencing platforms for use in clinical settings. Targeted tests for fungi, nontuberculous mycobacteria, and Nocardia.	Specific assessments of the impact of non–influ- enza virus detections, mixed infections, and bacterial pneumonia panels with antibiotic- resistance markers.	Prospective studies of AS interventions in conjunction with NAAT results and testing algorithms in the outpatient clinic, intensive care unit, and immunocompromised host settings.

Abbreviations: AS, antimicrobial stewardship; NAAT, nucleic acid amplification test.

Conclusion

PCR multiplex et approche syndromique moléculaire

- une innovation technologique indiscutable : une révolution diagnostique et thérapeutique en réanimation.
- une démarche clinique indispensable et un dialogue étroit entre cliniciens et microbiologistes pour maximiser leur impact.
- -problème: coût et la disponibilité.
- -une opportunité d'innover et de redéfinir l'avenir de la réanimation, avec audace et pragmatisme