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Antimicrobial regimen guided by multiplex-PCR and culture in critically ill patients with healthcare associated pneumonia: a survey-based study

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Position du problème et objectif(s) de l'étude:
Microbiological diagnosis for healthcare-associated pneumonia (HCAP) in ICU is challenged by low sensitivity of conventional methods, including culture. Multiplex PCRs (M-PCR) target the most common pathogens and resistance genes with an excellent sensitivity but may lead to antimicrobials overuse. Our aim was to describe in ICU patients with HCAP the modifications in antimicrobial regimen (ATB) guided by culture plus M-PCR vs. culture alone and to identify factors influencing modifications.

Matériel et méthodes:
We conducted a self-administered online survey-based study. Invitation was sent to French intensivists via the French Society of Anesthesiology and Intensive Care (SFAR). Survey consisted of 2 fictive clinical cases randomly selected among 8 cases. Cases were a unique combination of three characteristics including severity (septic shock: yes /no), sample type (invasive: yes /no) and risk factors for multidrug resistant bacteria (yes /no). In each case, M-PCR allowed for the identifications of more pathogens than culture. Cases were reviewed for plausibility by a multidisciplinary committee. For each case, we collected AMR in 4 situations: empirical (E-ATB), M-PCR-based (PCR-ATB), guided by culture (C-ATB), guided by culture plus M-PCR (full-ATB). ATB spectra were compared using the Weiss et al. classification.

Résultats & Discussion:
Between November 27th, 2022, and February 20th, 2023, 171 participants opened the survey. Most of participants were working in university hospitals (82%), familiar with M-PCR use (70%) and had less than 10 years of practice (75%). C-ATB and full-ATB were available for 287 cases answered by 171 participants. C-ATB and full-ATB were different in 130 cases (45% (95%CI: 0.39-0.51]), of which 63% were escalations (full-ATB spectrum wider than C-ATB spectrum), and 29% de-escalations. Modifications were also analyzed according to case characteristics' (table 1). Before availability of culture results, M-PCR led to a modification of empirical antibiotic in 69% cases (95% CI: 0.63-0.75). This modification was a de-escalation in 61% cases (E-ATB spectrum wider than PCR-ATB spectrum) whereas an escalation was observed in 21% cases. When clinicians prescribed wide spectrum E-ATB (carbapenem, piperacillin/tazobactam or 4th generation cephalosporin), M-PCR allowed de-escalation in 73% cases.

Conclusion:
This study suggests that M-PCR may largely participate in ATB decision when conventional methods are less informative. In 45% of cases, M-PCR led to a modification of ATB compared with culture alone, mainly widening ATB spectrum. Interestingly, we observed that while M-PCR impact on culture-adapted antibiotic is mostly escalations (63% cases with ATB modification), its impact on empirical antibiotic is mostly de-escalation (61% cases with ATB modification). The latter is even more evident in situations where clinicians prescribed wide spectrum empirical antibiotic.

Table 1. Modification according to patient characteristics. (N=287)

	No modification (N=157)	Modification (N=130)	p
Septic shock, yes (N=145)	84 (58%)	61 (42%)	0.26
Sample type, invasive (N=136)	48 (35%)	88 (65%)	<0.001
MDR risk factor, yes (N=145)	89 (61%)	56 (39%)	0.022

MDR: Multidrug resistant bacteria.

Data are expressed as numbers (percentages) and analyzed with Pearson chi2 test.

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