Molecular detection evaluation of pneumonia-associated fastidious pathogens and comparison to conventional microbiological results

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Introduction: Microbiological diagnosis for pneumonia causing pathogens refractory to cultivation is frequently slow for clinical decision taking. Fastidious pathogen identification using new molecular techniques might accelerate appropriate antibiotic treatment start in patients. Objectives: We investigated a prototype multiplexed pneumonia test covering the three pneumonia-causing fastidious pathogens Legionella pneumophila, Chlamydia pneumoniae, Moraxella catarrhalis and 22 resistance genes.

Methods: Results were obtained in 302 hospitalized patients with suspected pneumonia by examining BAL, tracheal secretion and sputum material. Molecular test results were compared to conventional culture, biochemical test, serology and antimicrobial susceptibility testing (AST) results as validated methods. Discrepant results were evaluated in context of patient treatment and outcome in order to assess impact and relevance of molecular results.

Results: Among 302 patients, potentially relevant fastidious pathogens were detected in only 4 patients by molecular analysis: L. pneumophila (n = 3), C. pneumoniae (n = 1), M. catarrhalis (n = 1). Of these, only the signal for M. catarrhalis was above the threshold proposed by the manufacturer. The device detected possibly associated resistance markers: ermB (L. pneumophila, C. pneumoniae), ermC (L. pneumophila) and mefA (M. catarrhalis). These resistance markers were not associated to the pathogens identified by the molecular technique. In contrast, the conventional culture technique identified Enterococcus faecium (n = 1), Enterobacter aerogenes (n = 2) and Acinetobacter baumannii (n = 1) with relevant resistances: gentamicin high-level (E. faecium), piperacillin/tazobactam and ceftazidim (E. aerogenes), and ampicillin/sulbactam and ciprofloxacin (A. baumannii).

Conclusion: Of the cases in which fastidious bacterial DNA could be detected, only one case (M. catarrhalis) was relevant according to system threshold, but clinical relevance remained unclear. Erythromycin-resistance was indicated by the system without corresponding pathogen identification. It appears that detected resistance genes were associated with respiratory flora, thereby possibly misleading the clinician. On the other hand, nosocomial pathogens detected by conventional techniques were not sufficiently covered by the system. Taken together it seems that system specificity for fastidious pneumonia pathogens might be sufficient but results for resistance genes did not correspond to results of pathogen identification.