BACTO-MET – a Metrological Project to Support Nosocomial Respiratory Tract Infections Monitoring

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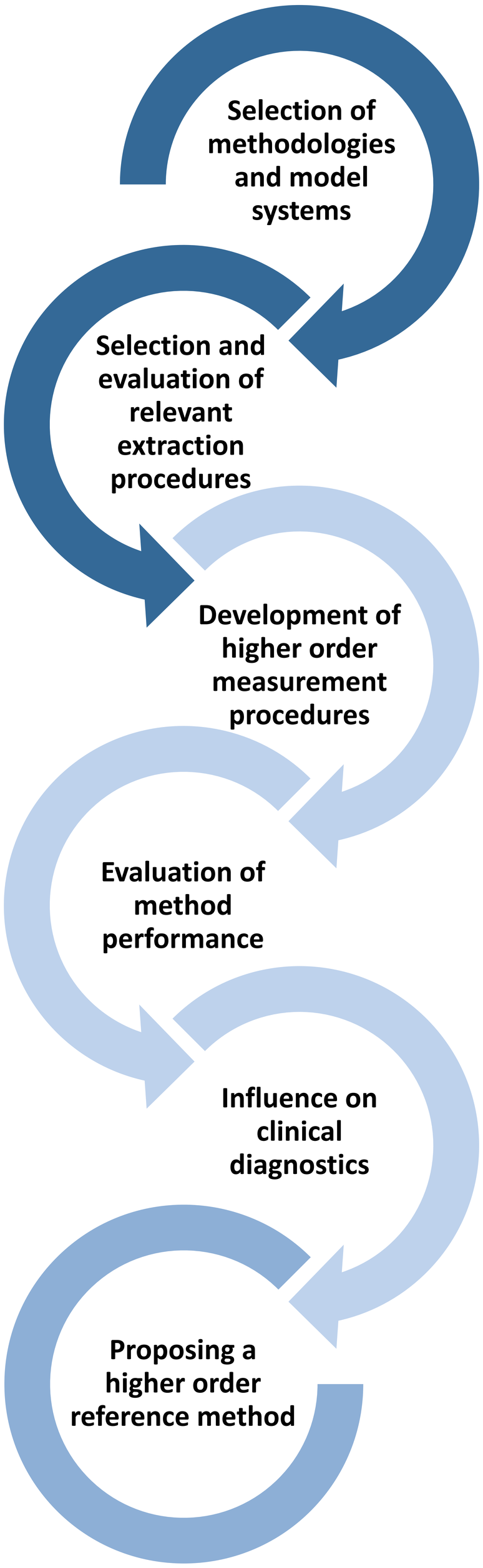
The main objectives of BACTO-MET are (1) to develop and evaluate candidate nucleic acid amplification higher order methods for accurate measurement of Gram-negative bacteria causing nosocomial respiratory tract infection, (2) to evaluate nucleic acid amplification higher order methods for measurement of susceptibility/resistance to antibiotics, (3) assign values of candidate calibrators and/or reference materials. The study will also investigate metrological support for new and innovative approaches that potentially offer the next generation of diagnostic solutions to revolutionise the fast diagnosis needed for timely management of disease.

Gram-negative bacteria cause five out of six nosocomial infections. They are responsible for 10-47% hospital-acquired pneumonia, 45–70% of ventilator-associated pneumonia, 20–30% of catheter-related bloodstream infections, and commonly cause other intensive care unit complication.

Bacterial cultures, as standard microbiological techniques, are most often used for detection and identification of bacteria. However, cultivation and phenotypic tests can take days delaying introduction of infection control measures. Infection is consequently often treated empirically with broad-spectrum antibiotics, which can lead to the emergence of antimicrobial resistance. Nucleic acid amplification methods offer shorter turnaround time and allow an early diagnosis.

Accurate diagnosis, rapid tracing of outbreak source, as well as robust approaches for assessing key epidemiological indicators, such as disease prevalence and incidence, and monitoring of drug resistance, is thus crucial. Expeditious molecular identification of Gram-negative bacteria is essential for treatment of severe infections and for infection control and prevention, surveillance and epidemiological purposes.



Following a literature survey for most relevant Gram-negative bacteria causing nosocomial respiratory tract infection and after consultation with clinic, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* and *Acinetobacter baumannii* were selected as model systems. Nucleic-acid based approaches were found to be the most relevant for detection and quantification, and nucleic-acid amplification-based methods were selected as model methods.

Quantity and quality of nucleic acids are highly dependent on extraction method, as methods selected can have a significant impact on the performance of downstream nucleic-acid amplification-based methods. Regardless of the matrix, nucleic acids should be extracted in a quantity and quality appropriate for further analysis. Three widely used manual methods have been selected to compare the extraction efficiency to an approach used in clinic.

Developed detection and quantification methods will be evaluated based on several performance criteria such as sensitivity, specificity, robustness, repeatability, and reproducibility.

Whilst emerging molecular approaches offer much promise, metrology and standardisation support is largely lacking. The lack of metrological support makes accurate detection and measurement challenging, and consequently raises the issues concerning quality, comparability and traceability. Therefore, a high degree of standardisation across laboratories throughout the world is required. Such standardisation would allow different laboratories using similar techniques to obtain the same/comparable results. After a thorough evaluation we aim to propose a higher order reference method, which will lead us one step closer in achieving standardisation.

Partners

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