

Molecular detection to improve surveillance of multi-resistant bacteria

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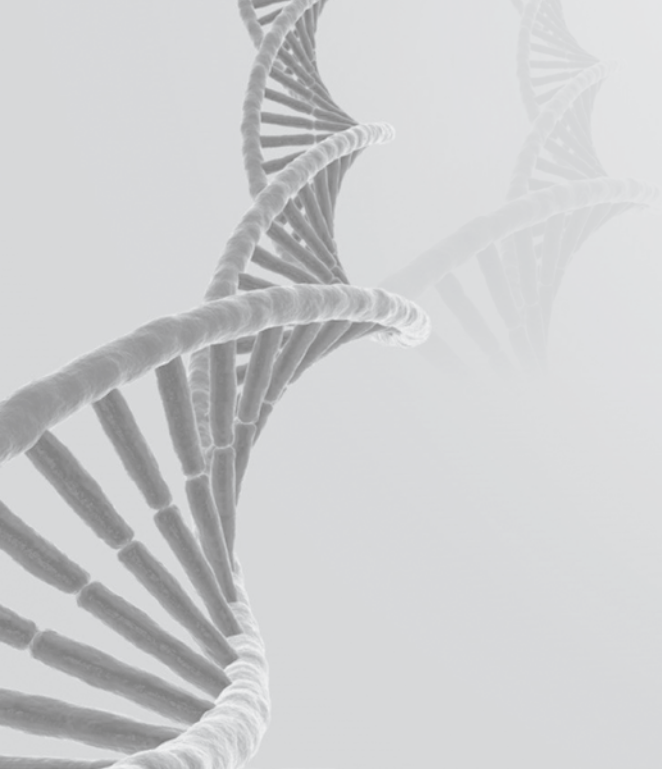
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VALORIZATION PARAGRAPH

Worldwide, an emerging increase in antimicrobial resistance is observed. This is alarming since antimicrobial resistance might not only be responsible for increased morbidity and mortality for the individual patient, but has also been responsible for major hospital outbreaks.

The aim of this research was to study different strategies and methods to improve the laboratory detection of highly resistant micro-organisms (HRMOs) and at the same time decrease the time to result. The rapid and correct detection of HRMOs is of utmost importance for the individual patient, in order to obtain the adequate treatment as rapid as possible. Moreover, the improved laboratory detection of HRMOs is important for the implementation of the correct infection prevention measures within hospitals.

The results of the research in chapter 2 showed that phenotypical detection of extended-spectrum beta-lactamases (ESBLs) can produce false positive results, compared to the molecular detection of ESBL. Since the current Dutch guideline recommends to nurse ESBL positive patients in isolation, these false positive results can consequently be responsible for installing incorrect isolation procedures. Next to the additional costs associated with isolated nursing, it is also very inconvenient and stressful for both patient and nursing personnel. Therefore, the use of molecular detection to confirm ESBL suspected isolates is important to prevent unnecessary costs and frustration associated with incorrect isolation procedures.

All studies presented in this thesis, describe a molecular method that is responsible for a reduction in time to result, when compared to conventional phenotypical methods. This reduction in time to result is important to prevent further spread of HRMOs within the hospital, since corresponding infection prevention measures can be installed earlier. Moreover, when an accidental HRMO is identified from a sample obtained from a hospitalized patient, molecular methods as described in this thesis can be used in order to rapidly generate an overview on the possible spread of the corresponding HRMO. Both the early prevention of further spread of multi-resistant bacteria and the possibility to avoid unnecessary isolation days (because of the rapid detection of HRMOs) will save hospitals a high amount of money. Consequently, this saved money can be used elsewhere in the hospital for further improvement of healthcare.

Eventually, when molecular methods as described in this thesis are widely introduced, the rapid and correct detection of HRMOs and the consequences as described above will be responsible for reducing worldwide spread of HRMOs, which is one of the focus points of the World Health Organization (WHO). This reduction in worldwide spread of HRMOs hopefully gives time for the development of new antimicrobial agents to treat the current HRMOs.

The results reported in this thesis are of considerable interest to clinical microbiologists, molecular biologists and infection prevention workers. Moreover, the results can also be helpful to policymakers. The current Dutch guideline for the laboratory detection of HRMOs, as developed by a working group of the Dutch society for medical microbiology (NVMM), describes recommendations that are mainly based on conventional phenotypical methods. With the results of the research as presented in this thesis, new insights on the genotypic detection of HRMOs are obtained. These insights can be used when the current guideline for the laboratory detection of HRMOs is revised.

In the past decade, a number of different techniques, developed by different researchers or companies, have been introduced for the laboratory detection of HRMOs. The results of the research as described in this thesis will provide a solid basis for near future molecular diagnostic assays as well as for improvement of currently available methods. In chapter 3, we describe the distribution of ESBL genes found in the east of the Netherlands. The results of this study, combined with other studies, will be important to companies that develop molecular assays for the rapid detection of ESBL genes. The scientific evidence described in this thesis and other studies will enable companies to make decisions on the relevant genes that have to be included into a new assay. The same holds true for the results of chapters 4 and 5, in which respectively the different types of MRSA and CPE are described that have been identified with our routine screening method.

During the studies performed for this thesis, a wide variety of clinical isolates have been analyzed. These clinical isolates are stored and included in the corresponding collection and database of the Laboratory for Medical Microbiology and Medical Immunology. Since the presence and type of resistance-genes in these clinical isolates is well known, this collection can be very valuable for future studies and validation of (commercial) molecular diagnostic assays. The results of such validations can both be used for publications in peer reviewed journals, as well as for CE marking of products.

To conclude, the prevalence of antibiotic resistance is increasing, resulting in a worldwide spread of these highly resistant micro-organisms. This thesis described evaluations and implementations of molecular methods for the correct and rapid detection of HRMOs. These methods can therefore contribute to the prevention of further spread of HRMOs, resulting in time needed to develop new antimicrobial agents to be used for the treatment of infections caused by the HRMOs.