EXPERT REVIEWS

Highlights from the 7th European Meeting on Molecular Diagnostics

Expert Rev. Mol. Diagn. 12(1), 17–19 (2012)

Anne JM Loonen[1,2], Rob Schuurman[3] and Adriaan JC van den Brule*[1,2]

[1]*Jeroen Bosch Hospital, Laboratory for Molecular Diagnostics, Department of Medical Microbiology and Pathology, 's-Hertogenbosch, The Netherlands*
[2]*Fontys University of Applied Science, Department of Medical Molecular Diagnostics, Eindhoven, The Netherlands*
[3]*University Medical Centre Utrecht, Department of Virology, Utrecht, The Netherlands*
**Author for correspondence:*
Tel.: +31 73 5538480
Fax: +31 73 5536475
a.v.d.brule@jbz.nl

The 7th European Meeting on Molecular Diagnostics

Scheveningen, The Hague, The Netherlands, 12–14 October 2011

This report presents the highlights of the 7th European Meeting on Molecular Diagnostics held in Scheveningen, The Hague, The Netherlands, 12–14 October 2011. The areas covered included molecular diagnostics applications in medical microbiology, virology, pathology, hemato-oncology, clinical genetics and forensics. Novel real-time amplification approaches, novel diagnostic applications and new technologies, such as next-generation sequencing, PCR electrospray-ionization TOF mass spectrometry and techniques based on the detection of proteins or other molecules, were discussed. Furthermore, diagnostic companies presented their future visions for molecular diagnostics in human healthcare.

Keywords: EMMD • molecular diagnostics • next-generation sequencing • PCR • personalized medicine

This year's European Meeting on Molecular Diagnostics (EMMD) was the seventh in a series of meetings devoted to molecular applications in human disease diagnostics and pathology. The 'Scheveningen Meeting' is organised every 2 years. Poster sessions and industrial exhibits are an integrated part of the meeting.

Approximately 350 participants, the majority from European countries, attended the seventh EMMD; 140 posters were presented and more than 30 diagnostic companies presented their latest innovations. As not all scientific presentations can be covered in this meeting report, only the keynotes and other highlights will be discussed.

After the opening ceremony, the symposium started with a session on molecular diagnostics in clinical microbiology. In the keynote lecture by Jacques Schrenzel (Geneva University Hospital, Switzerland), as well as in several oral and poster presentations, new developments in sample preparation were elaborated on, mainly focusing on whole blood for detection of bloodstream infections. A few examples that were discussed are the Spinomix MagPhase™ technology and the Polaris approach (Philips/Biocartis). Both focus on the use of large sample volumes to enable the detection of the low pathogen loads present in septic patients (1–10 colony-forming units/ml). Future applications of those types of patient samples should include antibiotic sensitivity testing (AST) using molecular tools and a better understanding of the clinical value of DNAemia (presence of DNA in blood). DNAemia is not a concept that is recognized in medicine yet. What does circulating DNA mean? Clinical significance needs to be proven in large multicenter studies.

Paul Savelkoul (VU University Medical Center, Amsterdam, The Netherlands) discussed a method for general amplification to investigate microbial communities called interspace region profiling. Every bacterial species has its own characteristic length of IS, which makes this technique suitable for amplification-based identification of species in a bacterial community, such as the gut or skin flora. The method is fast (3–4 h), easy, reproducible and cheap and results in reflections of the overall microbial profiles of individuals, also called microbiota. These microbiota can be used to identify abnormalities associated with certain diseases (i.e., obesity).

The state of the art of molecular diagnostics in the forensics was presented by Peter de Knijff (Leiden University Medical Centre, The Netherlands). He discussed the Dutch forensic DNA landscape, issues of counter-expertise, the use of short tandem repeat (STR) DNA

 10.1586/ERM.11.89 ISSN 1473-7159

analysis for case finding and the possibilities of next-generation sequencing (NGS) for STR detection. By massive parallel pyrosequencing instead of fragment analysis, a more detailed result (on the STR profile) can be provided. A problem encountered with this approach was that repeated sequences were automatically deleted by the NGS data analysis software. This software issue has now been addressed and resolved. This technique has not yet been implemented for routine applications, but is used in complex cases where more detailed answers are needed.

Human papilloma virus (HPV) in relation to cervical cancer was discussed by Peter Snijders (VU University Medical Center, Amsterdam, The Netherlands). He highlighted the involvement of high-risk HPVs in the pathogenesis of cervical cancer and the consequences for cervical cancer screening. Several studies have shown that testing for HPV is much more sensitive compared with normal cytology. In addition, the possibility of self-sampling (mainly in nonattendees) might increase the screening compliance and this may improve the early detection rate of cervical abnormalities in women.

The virology keynote lecture was given by Marc van Ranst (Catholic University Leuven, Belgium). In his opinion, the continuous increase in the use of molecular diagnostics for the detection of causative agents will continue during the coming years. Tests and equipment need to be smaller, faster, easier, cheaper and allow ubiquitous use. In the long term, molecular diagnostic assays will develop towards point-of-care tests. The relationships and possibilities of therapies and diagnostics will become closer and interdependent, ultimately resulting in theranostics – the key for personalized medicine.

Edwin Cuppen (Hubrecht Institute, Utrecht, The Netherlands) was the keynote lecturer in the field of pathology and clinical genetics. Developments in and applications of DNA sequencing were discussed, as well as how to interpret whole-genome information. It is a necessity to understand the role of genetic variations between healthy individuals (for prediction of disease and risk prevention) and patients (for diagnostics). It is clear that identification of variants in the genome (or exome) and their correlations to specific diseases or predispositions is a difficult task. Sequencing of a so-called 'mini cancer genome' – that is, a collection of genes that harbor markers associated with certain cancers – might be a good step in the direction of personalized cancer treatment. The extensive and growing amount of genetic data that can be generated nowadays may also lead to the identification of gene alterations that are not related to the disorder being investigated, called coincidental findings. Questions like "do patients have the 'right not to know' about these coincidental findings?" and "when should coincidental findings be reported to the patient?" were addressed by Helger Yntema (Radboud University Nijmegen Medical Center, The Netherlands). The 'right not to know' causes dilemmas for doctors and demands for new policies. In her institute, an independent multidisciplinary expert committee has been appointed to decide what information to report on a patient-by-patient basis. This committee consists of a clinical (molecular) geneticist, a social worker, a lawyer, an ethics specialist and a medical doctor. It was clear from several other talks as well that this is an issue that is very much alive in the field of molecular diagnostics.

Besides the detection of DNA and RNA, proteins and other molecules can also play a role in the molecular laboratory, as was addressed by Alex van Belkum (R&D, Biomérieux, Mary l'Etoile, France) and others. Techniques such as Luminex® and MALDI-TOF mass spectrometry (MS) have proven to be successful. Luminex is basically an ELISA-based method that is highly multiplexed. It allows scientists to investigate antibody levels over time against a pathogen or study IgG levels, for example. However, there are also applications based on detection of nucleic acids. MALDI-TOF MS allows identification of pathogens from bacterial culture (protein profile) and was quickly embraced by many laboratories. AST is still not well developed in these more advanced techniques, enabling rapid pathogen identification but not an AST profile at the same speed. MALDI-TOF MS is also not (yet) very sensitive; this will probably be solved in the near future. Several other interesting applications were also discussed, such as the electronic nose device. Out of the exhaled air of chronic obstructive pulmonary disease or tuberculosis patients, for example, molecules can be extracted and measured, resulting in breath profiles for each patient. The measured molecules are released by all kinds of microorganisms. It is believed that this new approach of breath (air) analysis offers potential for rapid, noninvasive diagnosis of respiratory conditions, for example.

Quality control and automation are very important aspects in the diagnostic laboratory. Several presentations and posters covered this issue, ranging from the use of 2D barcodes on standard components for fast data entry, middleware to connect laboratory information systems to standard laboratory workflow (as used by LabHelp, Bodégro and Roche) and the use of personal digital assistant applications to control and simplify laboratory processes.

An issue of importance that was brought to the attention of the audience was the thermal variability across the heating block of a thermocycler. This variability has been observed between different pieces of the same model and brand as well as within individual thermocyclers. Laboratories should be aware of this aspect to circumvent false-negative results.

NGS was discussed in many presentations, but Wilhelm Ansorge (Ecole Polytechnique Fédérale de Lausanne, Switzerland) provided a well-structured overview of NGS techniques and applications. Second to fourth generation sequencing was explained and the key aspects of several applications were briefly reviewed. NGS offers novel and rapid ways for genome-wide characterization and profiling of mRNAs, small RNAs, transcription factor regions, structure of chromatin and DNA methylation patterns, microbiological pathogens and metagenomics. The interplay of the latest technology and medical needs is key to personalized healthcare, which is expected to be one of the main areas of development in the near future.

Several companies (e.g., Roche, BD, Qiagen, Abbott and Focus Diagnostics) presented their future visions for molecular diagnostics. All agreed on the fact that new techniques should focus

on sample preparation, cost–effectiveness, ease of use, open access and flexibility, and should have an impact on patient outcome.

Besides the aforementioned keynotes, many oral presentations, as well as posters, were presented dealing with either novel technologies or novel diagnostic applications. Based on the continually increasing interest in attending the EMMD meetings, the international character of the meeting, as well as the extensive participation of the diagnostic industries, we are looking forward to the next EMMD, to be held in October 2013 in Schevingen, The Netherlands. In summary, the seventh EMMD was a successful event facilitating interactions between clinical molecular biologists, clinicians, laboratory staff and industries in an informal but scientifically stimulating atmosphere and sharing the ongoing innovation in the exciting field of molecular diagnostics.

Financial & competing interests disclosure

Two of the authors, R Schuurman and AJC van den Brule, are members of the organizing committee of the European Meeting on Molecular Diagnostics. The authors have no other relevant affiliations or financial involvement with any organization or entity with a financial interest in or financial conflict with the subject matter or materials discussed in the manuscript apart from those disclosed.

No writing assistance was utilized in the production of this manuscript.