Since the mid 1980s, the ESCMID study group ESGEM has organized a tri-annual meeting called International Meeting on Microbial Epidemiological Markers (IMMEM). The 12th edition took place in Dubrovnik, Croatia, from 18th to 21st September 2019. Altogether, 275 participants from 35 countries covering all continents convened to discuss and exchange ideas on various aspects of microbial strain typing and characterization. Overall 158 abstracts were submitted and 25 were selected for an oral presentation. ESCMID granted free attendance to the conference for 10 scientists from all around the world. Major aims of IMMEM conferences are to (i) resolve outbreaks, transmission chains and population structures by the most reliable methods and techniques; (ii) determine the propensity for spread of distinct strain types and mobile genetic elements (MGE) including plasmids; (iii) describe ecological bottlenecks leading to expansions of clones and MGE at population level; and (iv) perform detailed strain characterization and comparisons in order to infer reliable markers for accurate diagnostics and robust nomenclature. This year’s meeting was held under the banner “Moving towards genome-based pathogen surveillance – lessons learnt and challenges ahead”. The programme consisted of nine scientific sessions, an opening ceremony, two morning workshops, a pro/con session and two days of poster discussions. All sessions were initiated by keynote talks and followed by short oral presentations selected from submitted abstracts. The application of next generation and whole genome sequencing to answer various research, public and veterinary (public) health questions was central to most of the topics at IMMEM-XII.

Scientific programme at day 1

The introductory session focussed on the advantages and limitations of alternatives for microbial strain typing, including metagenomics’ approaches and proteomic-based methods such as MALDI TOF MS and FTIR applications. The session was organized in collaboration with ESGMD, included keynote talks by Adrian Egli and Luisa Peixe, and was followed by two oral presentations on practical applications of FTIR typing and metagenomic sequencing for AMR genes. Session II discussed classical and novel tools for bacterial genome-wide association studies (GWAS) and was introduced by two keynote talks by Jukka Corander and Laurent Jacob. GWAS applications for studying population-based analysis were further demonstrated in two selected short talks on Staphylococcus saprophyticus and Klebsiella pneumoniae. Session II was co-organized by ESGS. The opening ceremony started with some introductory words by the chair of ESGEM, Guido Werner, and the immediate past-ESCMID president Mario Poljak. Three scientific presentations followed introducing first the work of the European Committee of Infection Control EUCIC by Alexander W. Friedrich with the title “EUCIC – from science to implementation”. The second keynote talk was given by Ben Krause-Kyora about “Ancient microbiology and genomics - new insights into the past of mankind”, wrapping up what is novel in our understanding of emergence and spread of historical plagues and diseases and movement of people. The final keynote talk was given by Nick J. Loman about applications for field diagnostics and culture-independent approaches using long-read sequencing technologies and metagenomics’ applications.
The morning workshops

There was a huge audience attention to the early bird workshops at days 2 and 3. Workshop I given by Richard Goering, João A. Carriço and Eduardo Taboada discussed issues of harmonization and standardization of genome-based typing. Aspects of backward compatibility of data, like the extraction of older typing markers out of genome data (such as MLST) were discussed as well as the harmonization of technical protocols up to standardization of core genome based approaches (cgMLST vs. SNP-based mapping). Nomenclature issues were introduced along with the biological difficulty of how to define a clone. Workshop II co-organized by ESGMD and given by Nick Loman, Sally Partridge and John W. Rossen introduced technical, infrastructural and bioinformatics aspects of AMR prediction out of genome data and included an interactive user questionnaire which was very well received by all the participants of this workshop. The request to give these kinds of scientific exchange more space at forthcoming IMMEM conferences has been acknowledged and will receive full consideration.

Scientific programme at day 2

An entire session was dedicated to the analysis of mobile genetic elements including plasmids and integrative and conjugative elements (ICE). Two keynote talks given by Eduardo Rocha on population-based analyses of MGE and Anna Sheppard on technical aspects of plasmid reconstructions based on NGS using short- and long-read sequencing data were followed by four selected abstracts on tracking transmission of plasmids between isolates of multispecies hospital outbreaks and MGE associated with niche adaptation. In collaboration with the new ESCMID study group, ESGPHM, and the ECDC a session called “Multi level genomic surveillance” was held introducing the nation-wide transfer from band-based to genome-based typing in the US by Eric Stevens and the ECDC strategic framework for genome-based surveillance by Marc Struelens in two keynote talks. Sophia David presented results of the ESGEM supported and ECDC co-funded EuSCAPE project describing the geo-temporal spread of carbapenemase-producing K. pneumoniae isolates in Europe (published in 2019 [1]). Two selected abstracts analysing the spread of Salmonella enterica ser. Heidelberg and on WGS-based influenza surveillance completed this session. The day 2-afternoon session discussed aspects of classification of types and clones in the first keynote given by Eduardo Taboada. Population-based analysis of K. pneumoniae and how to link genomics with pathogenicity was introduced by Kathryn Holt. Four selected short oral talks presented various aspects of long-term carriage of ESBL-producing E.coli, a high prevalence of functional vancomycin gene clusters in non-enterococcal gut colonizers and genome-based analysis of Chlamydia trachomatis and Serratia marcescens isolates from international strain collections.

Scientific programme at day 3

Practical applications of the implementation of WGS-based analysis into infection control and prevention activities were addressed in session 6 which was co-organized by EFWISG. First keynote talk was given by Beatriz Guerra describing activities of EFSA to implement genome-based pathogen surveillance for increasing food safety and for faster identification of foodborne related outbreaks and corresponding sources at EU level. In the second keynote talk, Amy Mathers described practical applications of WGS-based surveillance for hospital pathogens, exemplified by an extended and long-lasting multispecies outbreak in an US American hospital. How to analyse outbreaks caused by MGE carrying carbapenemase
genes and spread across isolates of different *Enterobacterales* species was one of the key topics of this IMMEM, and a matter of debate for many affected hospitals worldwide. It is not clear yet if measures for infection prevention and control have to be adapted for these kinds of outbreaks. The session was completed by four short oral presentations on virulence prediction from WGS data, intra-laboratory comparison of long read sequencing data, WGS-based retrospective analysis of highly prevalent VRE strains and WGS-based *Listeria monocytogenes* surveillance. A pro/con session on clinical metagenomics for diagnostics and typing was co-organized by ESGMD and explicitly well-received by the audience. In two keynotes the two experts Etienne Ruppé and Jacob Moran-Gilad were asked to present contrary positions on this subject followed by a lively discussion including all participants. This format was clearly popular, and will be considered for forthcoming IMMEM conferences.

**Scientific programme at day 4**

The last day of the conference started with an interdisciplinary session on One Health and AMR co-organized by ESGVM. First talk was given by Yang Wang about selection and spread of gene-based resistances to last resort antibiotics for human health in animal farming in China. Second keynote by Samuel Sheppard introduced aspects of niche adaptation, source attribution and resistance progression in *Campylobacter* spp. The following four short oral talks presented plasmid-mediated colistin resistance in *Salmonella enterica* isolates from food, emergence of tigecycline resistance genes in Gram-negative bacteria from animals and humans, an approach how to use publicly available datasets of ten thousand available *E.coli* genome for doing population-based analysis and transmission of livestock-associated MRSA through the food chain. The last session was dedicated to novel tools for genome data analysis introduced by two keynote talks by Alison Mather and Torsten Seeman and followed by four short oral presentations on ontologies, platforms for integrating genomic and epidemiological data, pangenome analysis tools and multidimensional sequence typing.

**Poster sessions on days 2 and 3**

Altogether 115 posters were presented and discussed at two days of the conference, and grouped into different poster categories. Most submissions fell into the topic (i) WGS-based typing: method harmonization, applications and surveillance, which was further divided into subjects (a) food- and waterborne diseases, (b) nosocomial infections, (c) sexually-transmitted diseases, (d) outpatient/ambulatory care, and (e) general. Additional poster categories were (ii) GWAS, proteomics and metagenomics; (iii) MGE, plasmids, virulence and resistance gene prediction; (iv) Veterinary and One health, resistances to last resort antibiotics; and (v) Long read sequencing applications and novel bioinformatics tools. Poster discussions were scheduled for two 90 – 120 min afternoon sessions on days 2 and 3, leaving sufficient time especially for most of the younger attendants to present their own work. Poster areas were always crowded and posters were intensely discussed throughout all sessions as usual for IMMEM conferences. The ESGEM Executive committee awarded five posters with a Poster Prize: (i) Natalie Effelsberg et al., LA-MRSA in German pigsty workers- Recolonization or persistence?; (ii) Casper Jamin et al., International occurrence of an OXA-48 encoding plasmid in four European countries; (iii) Yingbo Shen et al., Integrated aquaculture contributes to the transfer of mcr-1 between animals and humans via the aquaculture supply chain; (iv) Lisandra Aguilar Butlet et al., In-host genetic diversity and persistence of ESBL-producing
Enterobacteriales over time; and (v) Susanne Schjørring et al., High comparability despite use of different laboratory and analysis approaches for L. monocytogenes cluster identification by WGS.

Organizing committee

This IMMEM-XII conference was co-organized by several ESCMID study groups as a collaborative effort of ESGEM and ESGMD, EFWISG, ESGPHM, ESGS, and ESGVM. Representatives of European agencies such as EFSA and ECDC actively participated in establishing the scientific programme and performing abstract evaluation. Esteemed colleagues from Europe, America, Asia and Australia supported IMMEM visibility and scientific excellence as additional members of the scientific committee. Special thanks to all former and present members of the ESGEM Executive Committee Hajo Grundmann, Frederic Laurent, Ana Budimir, Natacha Couto, Ed Feil, João A. Carriço, Guido Werner and the ESGEM conference coordinator Sandra Reuter, to Carla Seiler from the ESCMID staff for an excellent organizational support and Mario Poljak for ESCMID and local support.

Resume

IMMEM started as an ESCMID-initiated, European conference in 1987, but from the very beginning already with international support and contribution. IMMEM-XII again managed to attract an international audience and clearly demonstrated that the key issues of IMMEM and the aims and objectives of ESGEM work are more current and in demand than ever. Use of a few key technologies for WGS worldwide does not always simplify aspects of methods harmonization, nomenclature and (integrated) data interpretation. Looking deeper into transmission of strains and their MGE, into population structures and phylogenies quite often raises more questions than answers. Consequently, the slogan of IMMEM-XII summed up perfectly that the implementation of WGS-based typing has told us many new and interesting aspects ("lessons learnt"), but a lot of work is still ahead of us ("challenges ahead").
Speakers at the opening ceremony. From left to right: Alexander W. Friedrich, Ben Krause-Kyora, Mario Poljak, Nick J. Loman, Guido Werner.

Awarded Poster presenters. From left to right: Guido Werner (conference chair); Yingbo Shen, Natalie Effelsberg, Lisandra Aguilar Butlet, Susanne Schjørring, Casper Jamin.
Crowded lecture hall during the opening ceremony.

Poster discussions
Photos Dubrovnik