

Welcome: and introduction.



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ESGEM mission statement

Molecular information that living cells receive and pass on through the process of inheritance can be used to identify ancestral relationships between cells. Hence inherited molecular markers such as DNA sequences are a proxy for genetic and epidemiologic relatedness.

ESGEM appraises methods that utilise these markers to draw epidemiological conclusions about the expansion and spread of pathogens within and between individuals and among populations.

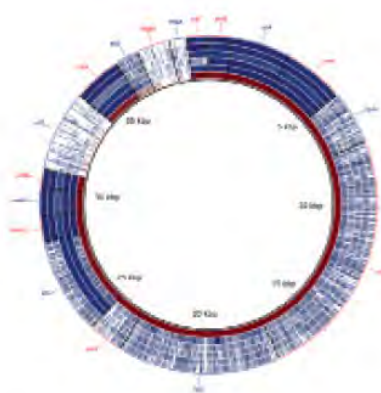
ESGEM thereby explores the usefulness and user friendliness of various techniques and promotes collaborative research to develop standardised methodologies for specific pathogens.

ESGEM also provides a forum for the exchange of ideas and the development of consensus strategies.

ESGEM works with individuals and companies active in this research area to foster the development of further technological advances in microbial typing.

ESGEM cordially invites colleagues actively interested in these areas to join this study group and contribute to the 'critical mass' in this exciting international field.

Training and Capacity Building



Target Audience

20–30 technicians, (molecular) biologists, medical microbiologists, bioinformaticians, veterinarians and public health workers involved in animal, human or food related research (one-health principle) are identified as main target of this workshop.

Faculty Members

João André Carriço, Lisbon, Portugal
Ruud Deurenberg, Groningen, Netherlands
Alexander Friedrich, Groningen, Netherlands
Corinna Glasner, Hinxton, United Kingdom
Hajo Grundmann, Groningen, Netherlands
Dag Harmsen, Münster, Germany
Jacob Moran-Gilad, Jerusalem, Israel
John Rossen, Groningen, Netherlands
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Tutors

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Scientific picture: A taxome comparison of *K. pneumoniae* isolates, © Dr Kai Zhou




ESCMID Postgraduate
Technical Workshop

**Capacity-building
Workshop: Rapid NGS for
Characterization and
Typing of Resistant
Gram-Negative Bacilli**

**Groningen, Netherlands
7 – 9 October 2015**



Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive *Staphylococcus aureus* in Europe

David M. Aanensen,^{a,b} Edward J. Feil,^c Matthew T. G. Holden,^{d,e} Janina Dordel,^{e,f} Corin A. Yeats,^{a,b} Artemij Fedosejev,^{a,b} Richard Goater,^b Santiago Castillo-Ramírez,^g Jukka Corander,^h Caroline Colijn,ⁱ Monika A. Chlebowicz,^j Leo Schouls,^k Max Heck,^k Gerlinde Pluister,^k Raymond Ruimy,^l Gunnar Kahlmeter,^m Jenny Åhman,^m Erika Matuschek,^m Alexander W. Friedrich,^j  Julian Parkhill,^e Stephen D. Bentley,^e Brian G. Spratt,ⁿ Hajo Grundmann,^o ESCMID Study Group on Molecular Epidemiological Markers (ESGEM), European Staphylococcal Reference Laboratory Working Group†

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† We deeply regret the untimely loss of our dear friend and colleague Helmut Mittermayer, to whom we dedicate this paper.

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<http://www.microreact.org/project/EkUvg9uY?tt=rc>

Guidelines for the validation and application of typing methods for use in bacterial epidemiology

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Performance indicators

- Stability
- Typability
- Discriminatory ability
- Epidemiological concordance
- Reproducibility
- **Portability**

Convenience indicators

- Flexibility
- Rapidity
- Accessibility
- Ease of use
- **Ease of interpretation**
- Cost
- Automatisations
- Interrogability

Additional indicators

Biological significance

- Information contents
- Phylogenetic signature
- Ecological or geographic signal
- Epigenetic information
- Metagenomic proximity

Clinical and public health significance

- Phenotypic predictive value
 - Virulence
 - Susceptibility
 - Tenacity