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NGS for understanding global epidemics:

How massive whole genome sequencing can inform public health

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ESGEM

ESCMID STUDY GROUP
FOR EPIDEMIOLOGICAL
MARKERS

European Society of Clinical Microbiology and Infectious Diseases

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Improving the Diagnosis of Bloodstream Infections – Advancing Technology and Quality for Better Care

NGS for understanding global epidemics

Disclaimer:

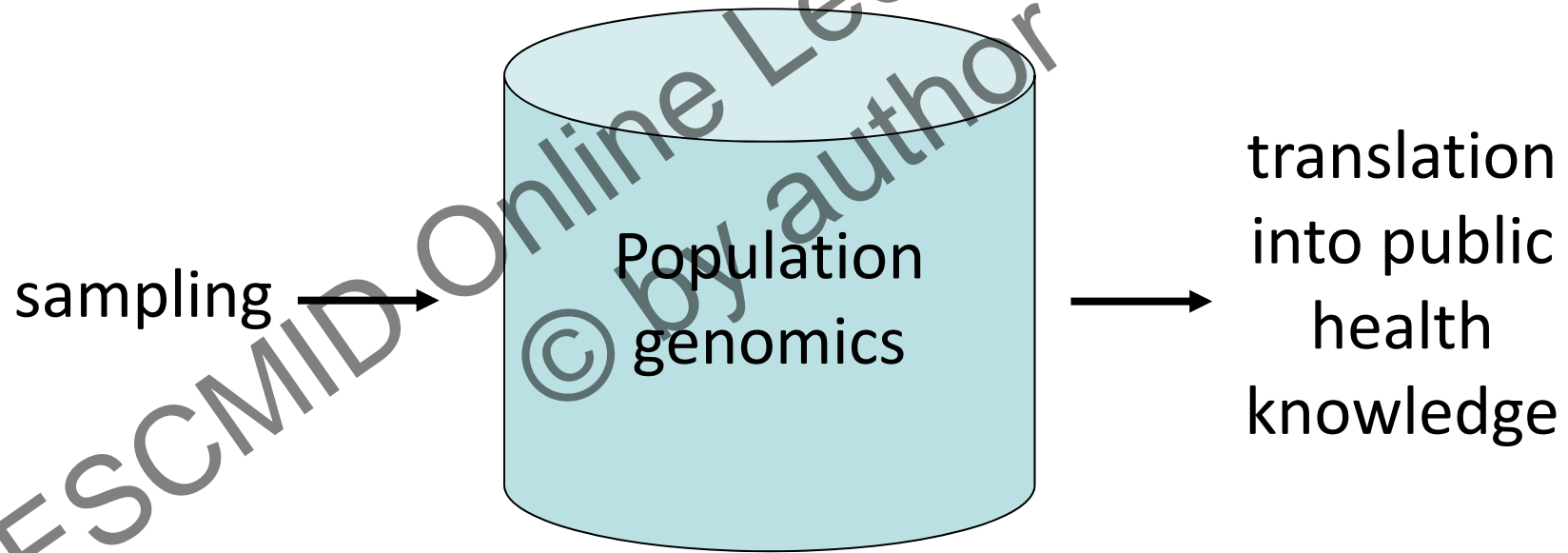
I shall not be talking about

- viral infections
- mycobacterial infections
- irrational voting behaviour

I shall mainly talk about

- cosmopolitan opportunistic bacterial pathogens

Network approaches at both ends of the pipeline



Front end network approaches

- Structured surveys
- Consistent sampling frame
- Scalable (in intensity and extensiveness)
- Syndrome or pathogen oriented
- Web-based data collection
- Multicentre, multinational, continental
- Hierarchical distributed networks

Caveats with European structured surveys

- Geo-demographic representativeness of sentinel sites
- Extra workload and extra costs
- Consistency
- Capacity
- Quality control
- Ownership
- Vision
- Teambuilding

European structured surveys

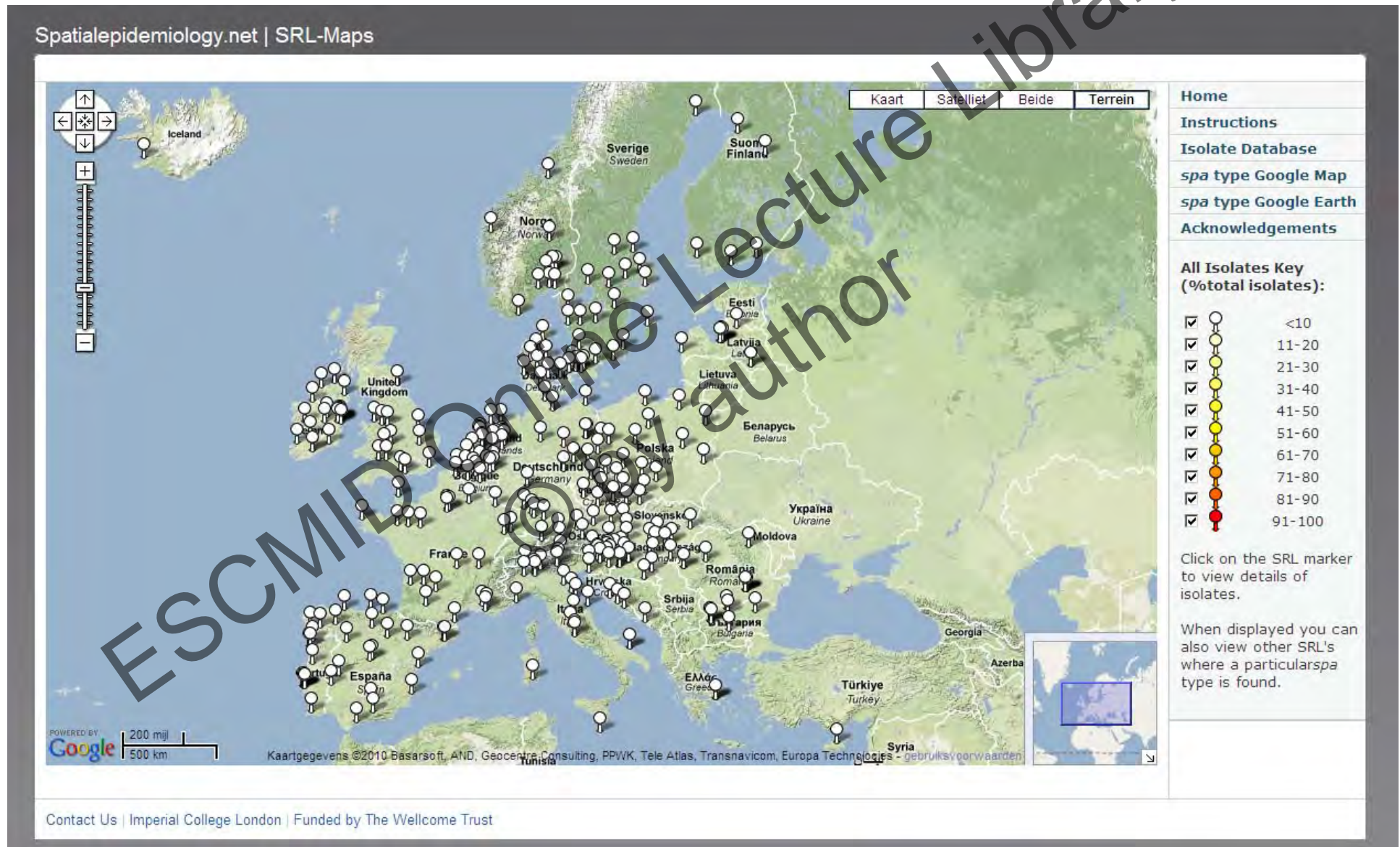
- Staphylococcal Reference Laboratory Working Group
 - Structured survey 1 (2006)
 - Structured survey 2 (2011, supported through ECDC tender)
- European Survey on Carbapenemase-producing Enterobacteriaceae (EuSCAPE, 2013 – 2014, supported through ECDC tender)

SRL-structured survey 1: Results


- 26 countries (NRLs)
- all passing a annual proficiency tests
- 450 hospitals
- 2890 invasive isolates
- 658 spa types
- providing geographical explicit tools

www.spatialepidemiology.net/srl-maps

Geographic coverage



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

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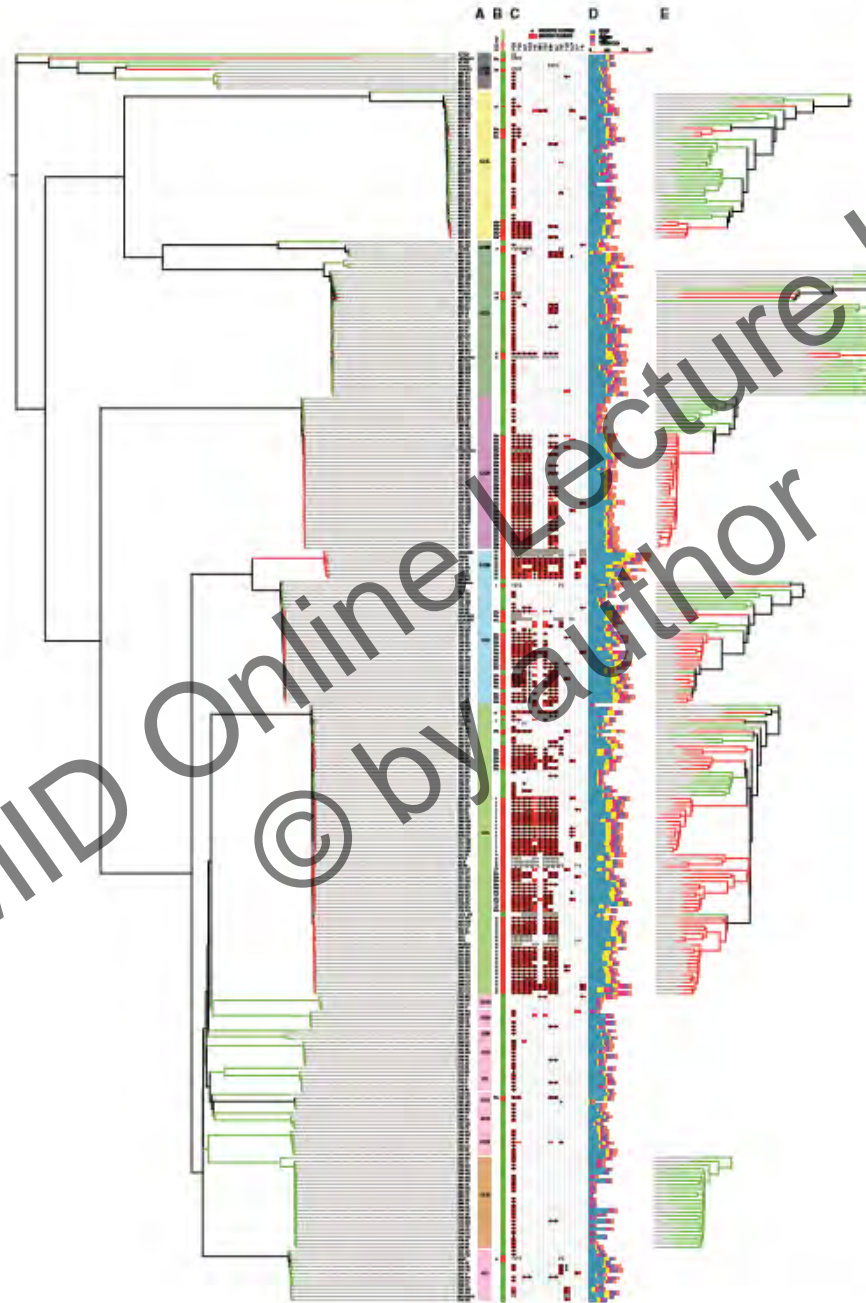
Citation Aanensen DM, Feil EJ, Holden MTC, Dordel J, Yeats CA, Fedosejev A, Goater R, Castillo-Ramírez S, Corander J, Colijn C, Chlebowicz MA, Schouls L, Heck M, Pluister G, Ruimy R, Kahlmeter G, Åhman J, Matuschek E, Friedrich AW, Parkhill J, Bentley SD, Spratt BG, Grundmann H, ESCMID Study Group on Molecular Epidemiological Markers (ESGEM), European Staphylococcal Reference Laboratory Working Group. 2016. Whole-genome sequencing for routine pathogen surveillance in public health: a population snapshot of invasive *Staphylococcus aureus* in Europe. mBio 7(3):e00444-16. doi:10.1128/mBio.00444-16.

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Identifying High Risk Clones by phylogenetic analysis

- Abundance
- Genetic relatedness
- Geographic structure

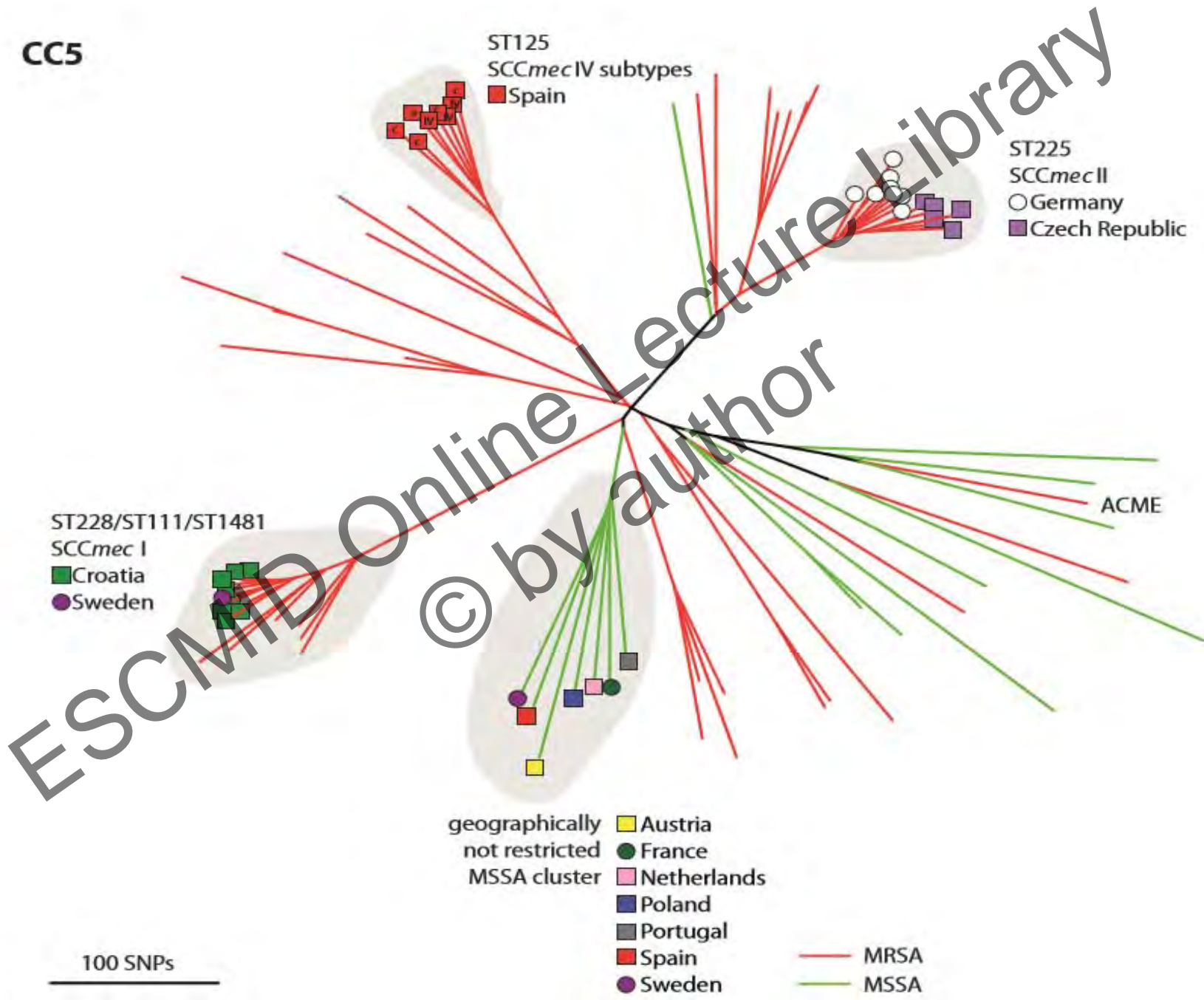
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Microreact: tool for geo-visualisation and analysis of WGS data

The screenshot displays the Microreact web interface. At the top, there is a header with the logo 'SRL-WGS', a search bar, and a count '334 of 334'. Below the header, there are map controls including 'Map', 'Satellite', and 'Labels: On'. The main area is split into two panels: a map on the left and a phylogenetic tree on the right. The map shows Europe with various colored markers (red, purple, blue, green, yellow, orange) representing different WGS data points. The phylogenetic tree on the right shows the relationships between these data points. Below the map and tree, there are configuration options for 'Shapes and Colours' and 'Labels'. The 'Shapes and Colours' section has buttons for 'None', 'country', and 'mrsa', with 'country' selected. The 'Labels' section has buttons for 'id', 'ers number', 'mlst', 'spa', 'sccmec', 'country', 'city', 'source', 'hoscom', and 'mrsa', with 'id' selected. The text 'Developed at Imperial College London' is visible in the bottom right corner of the interface.

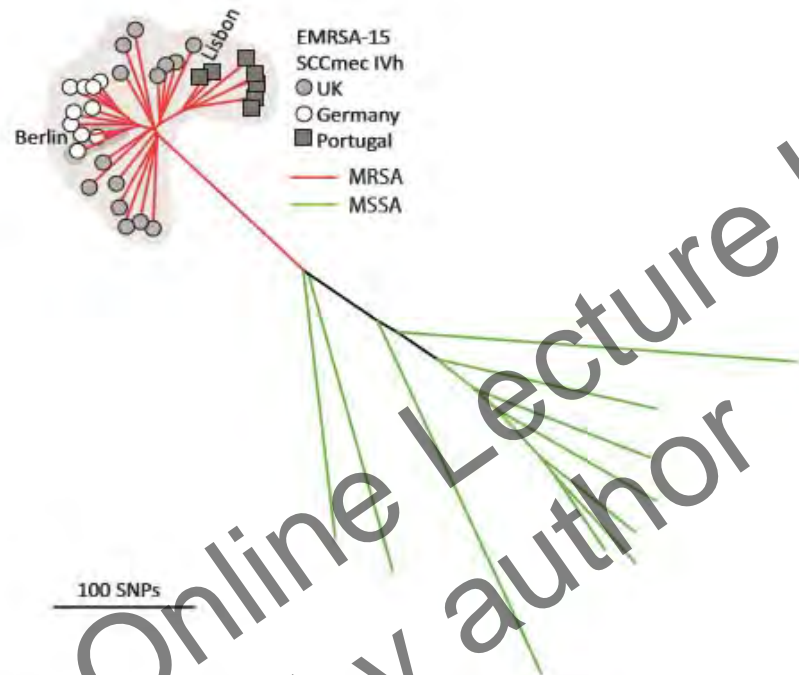
<http://www.microreact.org/project/EkUvg9uY?tt=rc>

CC5

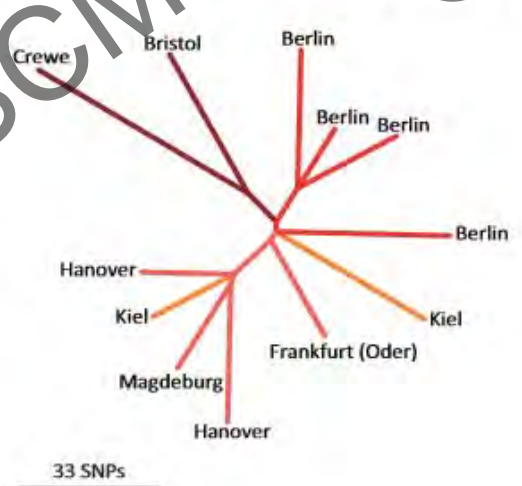


CC22

A



B Possible transmission of EMRSA-15 from the UK to Germany via Berlin (colour gradient indicates the direction inferred from phylogenetic signal)



size of circles indicates the number of isolates from that town

Results from EuSCAPE

Occurrence of carbapenemase-producing *Klebsiella pneumoniae* and *Escherichia coli* in the European survey of carbapenemase-producing Enterobacteriaceae (EuSCAPE): a prospective, multinational study



Hajo Grundmann*, Corinna Glaener*, Barbara Albiger, David M Aanensen, Chris T Tomlinson, Arjana Tambić Andrasević, Rafael Cantón, Yehuda Carmeli, Alexander W Friedrich, Christian G Giske, Youn-Gluczynski, Marek Gniadkowski, David M Livermore, Patrice Nordmann, Laurent Poirel, Gian M Rossolini, Harald Seifert, Alkiviadis Vatsopoulos, Timothy Walsh, Neil Woodford, Dominique L Monnet, and the European Survey of Carbapenemase-Producing Enterobacteriaceae (EuSCAPE) Working Group†

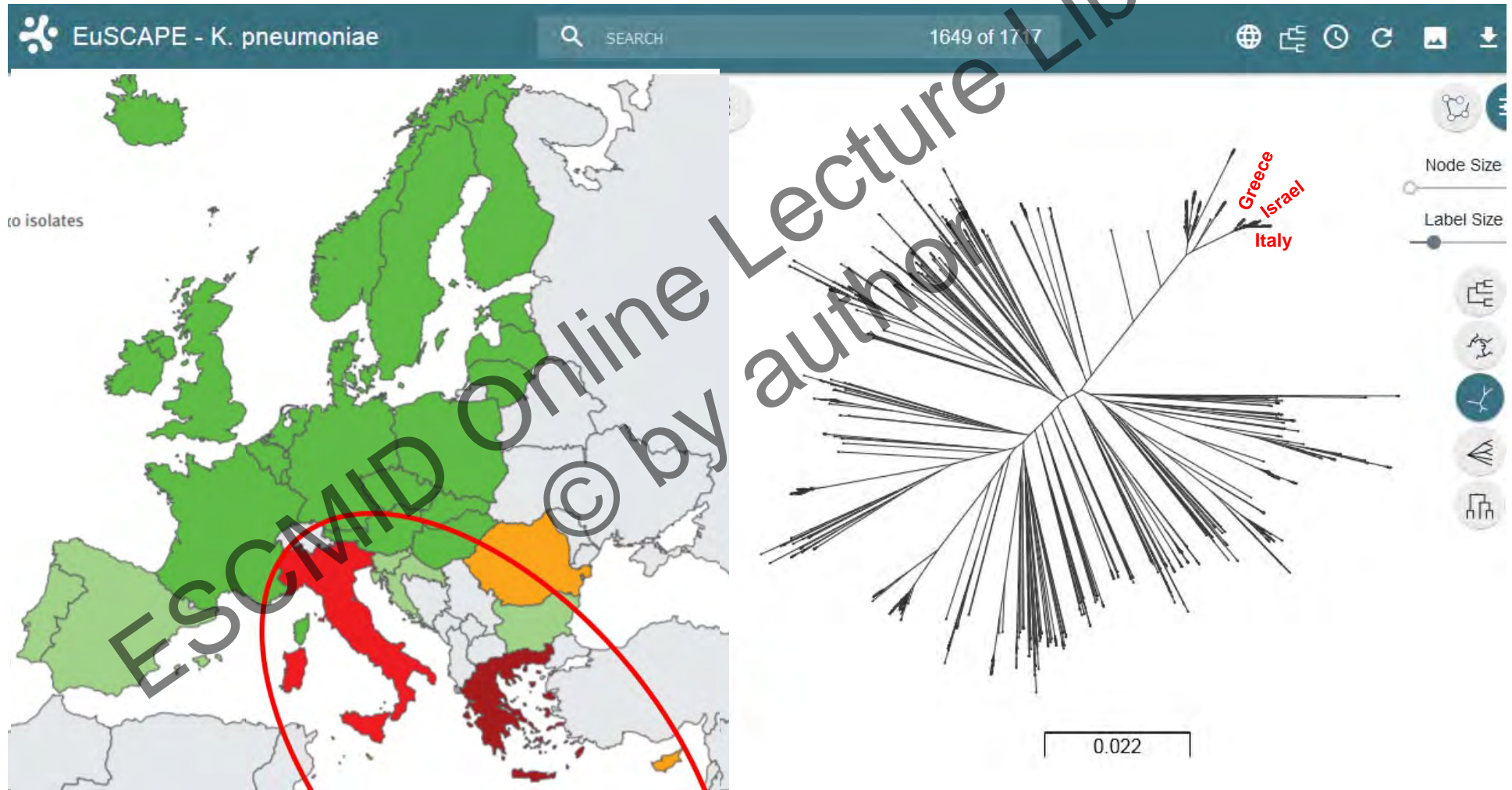
Population structure of *K. pneumoniae* from a global collection (n=328)



Population structure of *K. pneumoniae* in Europe: Clinical isolates from the EuSCAPE collection (n=1717)



Population structure of *K. pneumoniae* in Europe: Clonal expansion of KPC2-producing *K. pneumoniae* 2013



Conclusions

Network approaches are helpful at all levels of investigation

- during sampling
- for final analysis

Population genomics helps generating and testing of epidemiological hypothesis

Different health care utilisation patterns strongly influence the transmission dynamic at national and international levels

Interdisciplinary approaches will lead to better informed public health decisions and interventions

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The EuSCAPE working group

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