Antibiotic resistance mechanism continues to spread

A recently discovered genetic mechanism allowing bacteria to develop and transfer resistance to colistin, one of the last-resort antibiotics, has been present in many countries across the world for more than a decade, according to late-breaking data presented at ECCMID.

9 April 2016, Amsterdam: Researchers presented findings on the prevalence of the mcr-1 gene, a transferable genetic mechanism of antimicrobial-resistance to colistin - the last resort antibiotic in a number of circumstances. At a session dedicated to late-breaking abstracts on colistin resistance, researchers presented evidence on the prevalence of the gene in bacteria (including Enterobacteriaceae such as Escherichia coli, Salmonella or Klebsiella). Scientists also presented evaluations of treatment and management options, as well as new diagnostic methods and assays to help identify mcr-1. The late-breaking data was released at ECCMID 2016 – the annual meeting of the European Society of Clinical Microbiology and Infectious Disease (ESCMID).

The mcr-1 gene is particularly significant as it can be carried by plasmids, small DNA molecules, which can be transferred between single-celled organisms, such as bacteria, through so-called horizontal gene transfer. These genes can then be transferred sideways to other strains or species, not just vertically down to the offspring by replication. Horizontal gene transfer is the primary reason for antibiotic resistance.

The mechanism, first discovered in an E. coli strain from a pig in China in November 2015, has over the past months been identified in bacterial samples across the world. The increased prevalence of plasmid-mediated resistance is causing major concern among infectious disease specialists, because it threatens to reduce options to treat infections and is creating new resistant bacterial strains.

Abstract No.: 7426 No trend towards increasing mcr-1 prevalence between 2004 and 2014 in food-producing animals in Europe

The study evaluated the prevalence and evolution of the mcr-1 gene from 2004 - 2014 in E. coli and Salmonella samples isolated from food-producing animals. The results showed that the gene has been present in animals for more than a decade and has already spread across Europe. However, the researchers did not observe a trend towards an increase in the mcr-1 prevalence during the 10-year period studied.

Abstract No.: 7069 Human as a source of colistin resistance: presence of mcr-1 gene in gut microbiome

In an abstract on the current prevalence of the mcr-1 gene in the human gut microbiome – one of the major reservoirs of resistance in the ecosystem – the researches evaluated samples from 344 Chinese and 145 European individuals. Six of the Chinese individuals
harboured the mcr-1 gene and close homologues of the plasmid in their gut microbiota, whereas no related genetic elements were found in the European cohort.

**Abstract No.: 7430 The occurrence of the colistin resistance gene mcr-1 in Salmonella enterica and E. coli isolates from humans, livestock and retail meat in the Netherlands**

A study from the Netherlands found that the antibiotic resistant gene mcr-1 was not identified in human Salmonella, but was retrospectively detected at low levels in Salmonella from poultry sources (1.0%), as well as in E. coli from faeces of Dutch livestock (0.3%) and retail meat (1.7%). The authors concluded retrospective screening with selective isolation procedures is needed to assess the current spread of the gene in bacterial populations from animal sources.

**Abstract No.: 7101 Extended-spectrum beta-lactamase and carbapenemase encoding Enterobacteriaceae isolates harbouring the novel mcr-1 colistin resistance gene**

Researchers undertook whole genome sequencing from 600 Enterobacteriaceae isolates from different sources (humans, livestock, companion animals, environment) in Germany. They found that the resistance gene mcr-1 has been present since at least 2010.

**Abstract No.: 7590 Prevalence of colistin resistance gene (mcr-1)-containing Enterobacteriaceae in feces of patients admitted to a tertiary-care hospital in the Netherlands**

A Dutch study evaluated 624 faecal samples from patients admitted to a tertiary hospital. The researchers observed the mcr-1 gene at a low prevalence of about 0.3% within the Dutch population. Remarkably, the presence of the mcr-1 gene did not result in a colistin-resistant phenotype, and was found in ESBL-negative E. coli isolates that contained a plasmid-mediated enzyme.

**Abstract No.: 7281 Genetic diversity of colistin-resistant mcr-1-carrying E. coli isolates from global travellers**

A global study evaluated the distribution (prevalence and presence) of the mcr-1 gene in Enterobacteriaceae and the diversity of its isolates – the latter gives an indication of the rapidity of the gene’s spread. The researchers found ESBL isolates carrying the mcr-1 gene in travellers returning from three different continents. The findings suggest that a horizontal transfer is likely across many clones. The variety of plasmid backbones carrying the mcr-1 gene indicates efficient transposition mechanisms. These observations indicate a promiscuous spread of the mcr-1 gene, which likely facilitated the observed dissemination across the globe, the authors concluded.

**Abstract No.: 7437 Colistin-resistance can be detected by semi-automated systems**

A study examines the quality of colistin-resistance detection methods. The authors showed that automated systems underestimated colistin resistance in 19% of a sample of carbapenem-resistant Klebsiella pneumoniae (KPC) strains. The research has concluded, this underestimation may lead to major errors in clinical interpretation and cause therapeutic failure.
Abstract No.: 7471 Detection of the plasmid-mediated colistin-resistance gene *mcr-1* in clinical isolates and stool specimens using a newly developed real-time PCR assay

The researchers validated a newly developed real-time PCR assay for the detection of *mcr-1*. The new assay specifically detects the *mcr-1* gene and was validated to accurately confirm the presence of this new gene in colistin-resistant clinical isolates. The assay may facilitate rapid *mcr-1* identification in stool specimens and can therefore be important to further improve clinical management and infection control.

Abstract No.: 7386 Molecular characterization of colistin-resistant *Klebsiella pneumoniae* causing bacteremia in a large teaching hospital in South India

A study from India evaluated the molecular characteristics of colistin resistance in *Klebsiella pneumoniae*. The researchers found that mutations in the *mgrB* gene, and not the mobile *mcr-1* gene, were responsible for resistance at the hospital. Due to the emergence of resistance to reserve drugs, there is a need for combination therapies for carbapenem-resistant *K. pneumoniae*, and colistin must be judiciously used.

Abstract No.: 7485 The *mcr-1* gene: is it useful for detecting colistin resistance in carbapenem-resistant *Klebsiella pneumoniae* (CR-KP) from clinical isolates?

A Malaysian study evaluated *mcr-1* detection in Enterobacteriaceae. The researchers support the evidence that the detection of the *mcr-1* gene in colistin-resistant Enterobacteriaceae may be useful for rapid detection in clinical isolates. Rapid detection is needed for better patient management and to promptly implement effective infection control measures. They also suggest that the detection methods should include other molecular mechanisms that may contribute to the resistance of colistin in CR-KP.

Prof. Winfried Kern, Programme Director of ECCMID comments: “The *mcr-1* gene has recently taken centre stage in the on-going fight against antibiotic resistance as we are concerned that resistance this colistin resistance mechanism may be transferred between different bacterial species. The antibiotic colistin is in some cases already the only treatment option clinicians have left. Today’s research gives some indication of its prevalence, its spread and its genetic diversity, adding further data on its role and transference. Understanding the spread of *mcr-1* and the underlying resistance mechanism will allow us to develop more effective diagnostics, treatments and stewardship programmes to better manage infections caused by multi-resistant pathogens.”

-ENDS-

Notes to editors:
Two special tracks were opened for late-breaking abstracts on topics that not only are of high scientific importance, but are also relevant on a global scale: colistin resistance and migrant health. A total of 340 late-breaker abstracts have been submitted, 25 related to refugee health, 44 on colistin resistance, and 271 on other topics. The ECCMID Programme Committee selected the most interesting and scientifically significant late-breaking abstracts to be presented in three dedicated oral sessions and additional poster presentations.
Media information

For a full programme of educational workshops, poster presentations and oral sessions at ECCMID 2016, please visit: http://eccmidlive.org/

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About ECCMID 2016: The annual meeting of the European Society of Clinical Microbiology and Infectious Diseases will this year take place from April 9 - 12 in Amsterdam. As the world’s largest congress focused on infectious diseases and clinical microbiology, researchers will present more than 3,000 abstracts with the latest findings and recommendations, which are set to help improve diagnosis, prevention and the clinical care given to patients. The congress offers more than 150 presentations, including keynote lectures, symposia, oral sessions, educational workshops and meet-the-experts session, as well as more than 2,000 poster presentations. In total, more than 10,000 scientists and clinicians are expected.