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95 Characterisationof mcr-5-harbouring plasmids and mobilegenetic elements in Salmonella usingshort-read and long-read sequencing technologies

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Background: Foodborne salmonellosis caused by non-typhoidal *Salmonella* spp. is a commonly reported gastrointestinal infection in Europe. The acquisition of antimicrobial resistance genes by *Salmonella* strains can impair antimicrobial therapy in patients and animals. The emergence and spread of mobile resistance against the last resort antibiotic colistin in Enterobacteriaceae is alarming and of major public health concern. Due to extensive use of colistin in the animal production worldwide, livestock is considered as a potential reservoir of colistin resistance genes for commensal and pathogenic bacteria. So far, eight different mobile colistin resistance genes (*mcr-1* to *mcr-8*) are described. This study is primarily focusing on *mcr-5*-harbouring *Salmonella enterica* isolates from the strain collection of the National Reference Laboratory for Salmonella in Germany. All isolates were collected between 2011 and 2018 and originated from livestock and food products.

Materials/methods: Aim of this study was to analyse 23 *mcr-5*-harbouring *Salmonella* isolates by whole genome sequencing using Illumina short-read as well as ONT MinIon or PacBio long-read technologies. Obtained data was used to build phylogenetic trees, reconstruct plasmid sequences and to analyse the association of *mcr-5* with transposable elements. Plasmid sequences were compared with NCBI Genbank entries to gain knowledge about the global distribution of *mcr-5* plasmids harboured by bacterial pathogens isolated from animals, food and patients.

Results: Altogether 5 different *mcr-5* plasmid types were observed in the analysed *Salmonella* isolates from animals and food sources in Germany. In these strains, *mcr-5* is mostly located on small multi-copy plasmids. However, due to its association with transposable elements, integration of *mcr-5* in *Salmonella* chromosomes was observed. Extended search in public databases revealed, that *mcr-5* was reported in six different bacterial species isolated from food, animals or patients in 13 different countries.

Conclusions:
Our results indicate effective *mcr-5* mobility and independent acquisition of *mcr-5*-harbouring genetic elements by individual strains. This is supported by the increasing number of publications reporting the presence of *mcr-5* in various bacterial species worldwide. Extended *mcr-5* screening is necessary to link isolates from the environment, livestock, food and patients.