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Identification and impact of macrolide hemi-resistance in the foodborne pathogen *Campylobacter* spp.

Inhalt

Thermotolerant *Campylobacter* spp. are the leading cause of foodborne infections in the European Union, with macrolides being the antibiotics of choice. The point mutation A2075G in the 23S rRNA gene is the most common resistance determinant conferring high-level erythromycin resistance.

We observed that prediction of phenotypic resistance from short-read sequence assemblies failed for some isolates carrying one or two of the three copies of the 23S rRNA gene with the resistant point mutation A2075G. This hemi-resistant genotype conferred only intermediate resistance to macrolides. However, it facilitated the acquisition of a complete set of mutated 23S rRNA gene copies upon erythromycin selection, in turn conferring high-level resistance. Transition states from one to three 23S rRNA A2075G gene copies were resolved at single 23S rRNA gene loci by Oxford Nanopore sequencing.

Without antibiotic selection and upon nutrient depletion and cold stress in the water environment, the hemi-resistant genotype was stable, even upon entry into and exit from the viable but non-culturable state. It may represent a memory of macrolide resistance in *Campylobacter* from antibiotic selection in the animal (and human) host, relevant in the One Health context and currently eluding and/or perturbing detection in routine diagnostics.

Keywords

Campylobacter, AMR, Macrolides

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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