Occurrence of multidrug-resistant high-risk clonal Escherichia coli lineages in the Baltic Sea with simultaneous low antimicrobial selection pressures

Inhalt

Antimicrobial resistant (AMR) E. coli (EC) increasingly occurs in human medical, veterinary, and environmental settings. The World Health Organization categorized extended-spectrum β-lactamase (ESBL)-producing Enterobacterales among the top-priority pathogens for prospective antibiotic (AB) development. It has been shown that not only AB residues but also heavy metals/metalloids (HM) facilitate the spread of AMR bacteria across different locations, which poses a serious health risk for humans and animals in the One Health context. Here, we investigated correlations on the occurrence of ESBL-EC and AB/HM residues in the Baltic Sea in Western Pomerania. We examined 30 ESBL-EC from water samples collected over a period of one year. By combining whole-genome sequencing (WGS) with functional tests and UPLC-MS residue analysis, we characterized the isolates in detail and quantified selection pressures in water samples. Phenotypic data revealed resistances to some important ABs beyond ESBL resistance, such as ciprofloxacin and gentamicin while WGS suggested the presence of the high-risk clonal EC lineages of sequence types (ST)131, ST117, and ST58. We also detected genotypic AB and HM resistance genes, such as to aminoglycosides, arsenic, and mercury. While residue analysis is still ongoing, first results indicate overall low residue levels. Our findings highlight the importance of the Baltic Sea area as a hotspot for AMR bacteria even in the absence of high selection pressures.

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