



Escherichia coli

OXA-244

nowe zagrożenie

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Karbapenemaza OXA-244

- Karbapenemaza klasy D, CHDL (ang. carbapenem-hydrolysing class D β -lactamases)
- Wariant OXA-48; pojedyncza mutacja Arg214Gln
- Pierwsza izolacja: Malaga, Hiszpania, 2012, *Klebsiella pneumoniae* izolat oporny na ertapenem, wrażliwy na imipenem i meropenem
- W 2013 pierwsza *Escherichia coli* wytwarzająca OXA-244 (Niemcy)
- Izolowana w wielu krajach świata, głównie u *E. coli* ST38
- Izolaty dodatkowo ESBL+ (CTX-M-27 lub CTX-M-14)
- Niska aktywność hydrolityczna wobec karbapenemów
- Trudna w detekcji fenotypowej

Characterisation of OXA-244, a chromosomally-encoded OXA-48-like β -lactamase from *Escherichia coli*

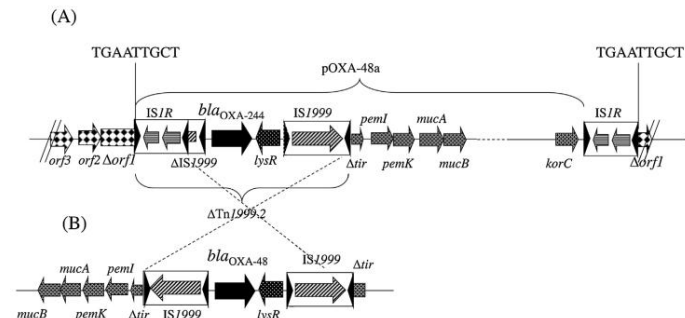


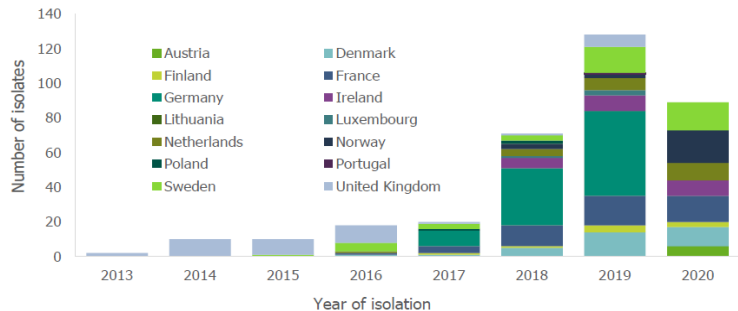
Fig. 1. Schematic map of (A) the transposon structure and surrounding sequences in *Escherichia coli* VAL and (B) the transposon Tn1999 in reference plasmid pOXA-48a. Open reading frames (ORFs) are shown as arrows or as horizontal boxes with an arrow indicating the orientation of the coding sequence. Target site duplications (TGAATTGCT) are represented by black bars. *orf1*, *orf2* and *orf3* were similar to ORFs identified on *E. coli* chromosomes.

Increase in OXA-244-producing *Escherichia coli* in the European Union/European Economic Area and the UK since 2013

18 February 2020

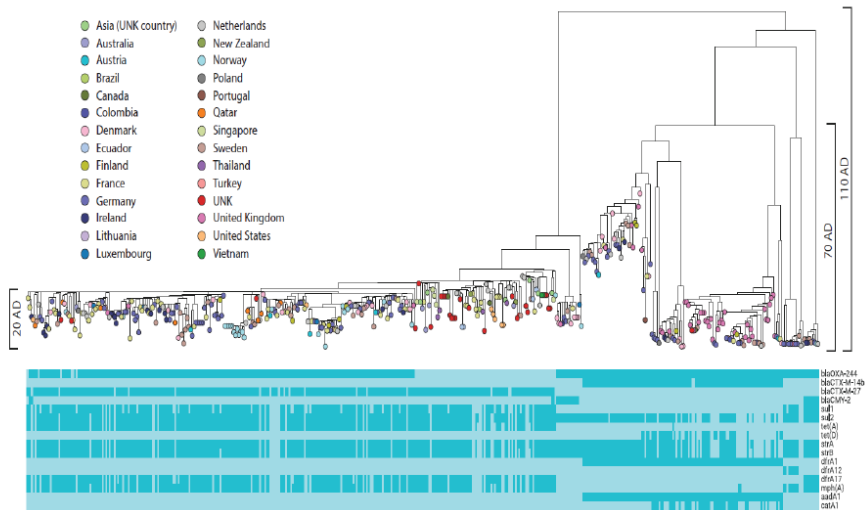


Figure 2. Number of OXA-244-producing *E. coli* ST38 isolates per year, EU/EEA and the UK, 2013–2020 (n=348)*



* The figure only includes cases for which WGS data and year of isolation are available (n=348).

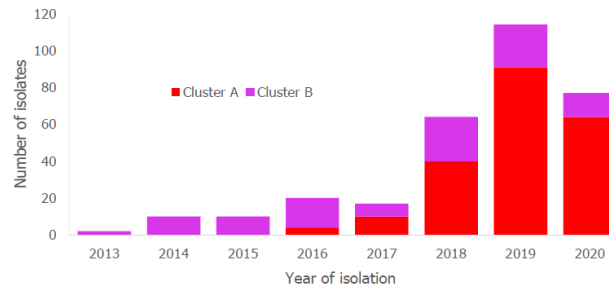
Figure 1. Neighbour joining tree of *E. coli* ST38 non-outlier sequences collected from EU/EEA countries and the UK and from the open-access databases (n=458)



Increase in OXA-244-producing *Escherichia coli* in the European Union/European Economic Area and the UK since 2013 – first update

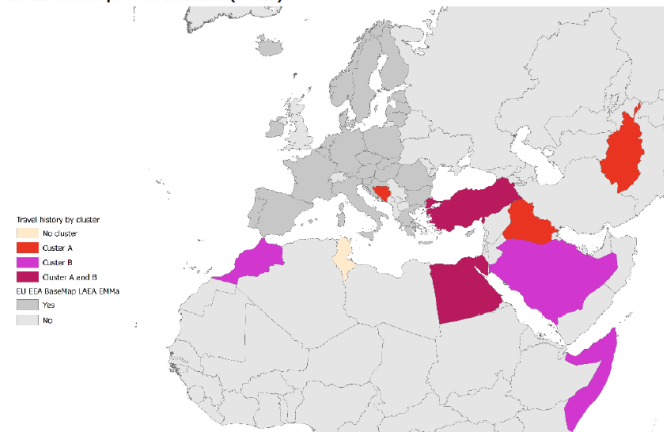
20 July 2021

Figure 3. Number of OXA-244-producing *E. coli* ST38 isolates in clusters A and B per year, EU/EEA and the UK, 2013–2020 (n=314 isolates)*



* Only cases with available year of isolation are shown.

Figure 4. Countries of travel outside of the EU/EEA for cases of OXA-244-producing *E. coli* ST38, in the 12 months prior to detection (n=28)



RAPID COMMUNICATION

Rapid spread of OXA-244-producing *Escherichia coli* ST38 in Germany: insights from an integrated molecular surveillance approach; 2017 to January 2020

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Article submitted on 13 May 2020 / accepted on 25 Jun 2020 / published on 25 Jun 2020

FIGURE 2

Phylogenetic tree of core genome multilocus sequence typed OXA-244-producing *Escherichia coli* isolates, Germany, January 2017–August 2019 (n = 148)

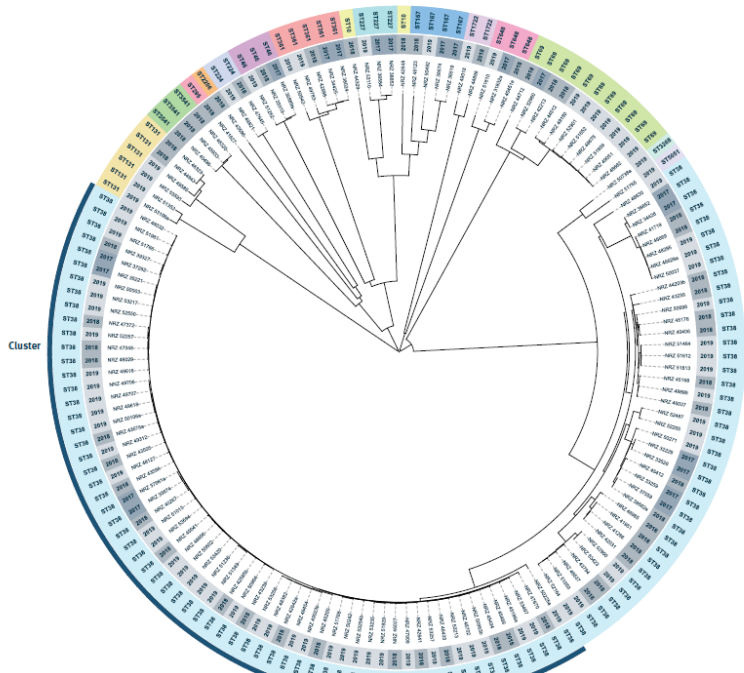


FIGURE 1

Number of detected OXA-244-producing *Escherichia coli* isolates by month, Germany, January 2017–January 2020 (n = 243)

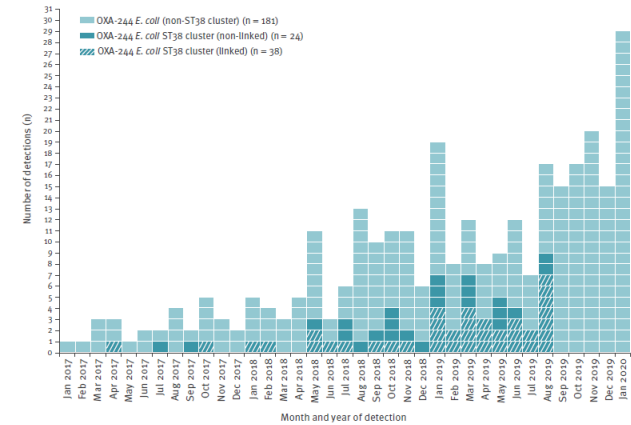
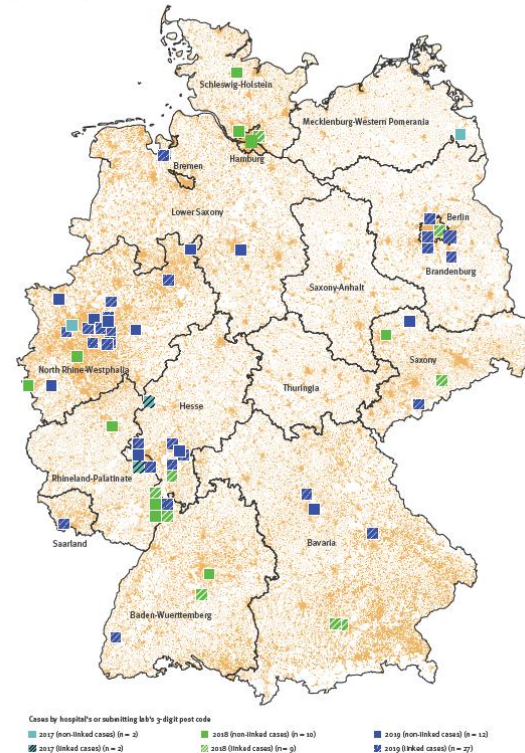


FIGURE 3

Distribution of cases with OXA-244-producing *Escherichia coli* ST38 isolates by year and notification status, Germany, January 2017–January 2020 (n = 62)



Emergence and Polyclonal Dissemination of OXA-244-Producing *Escherichia coli*, France

Cecile Emeraud, Delphine Girlich, Rémy A. Bonnin, Agnès B. Jousset, Thierry Naas, Laurent Dortet

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 27, No. 4, April 2021

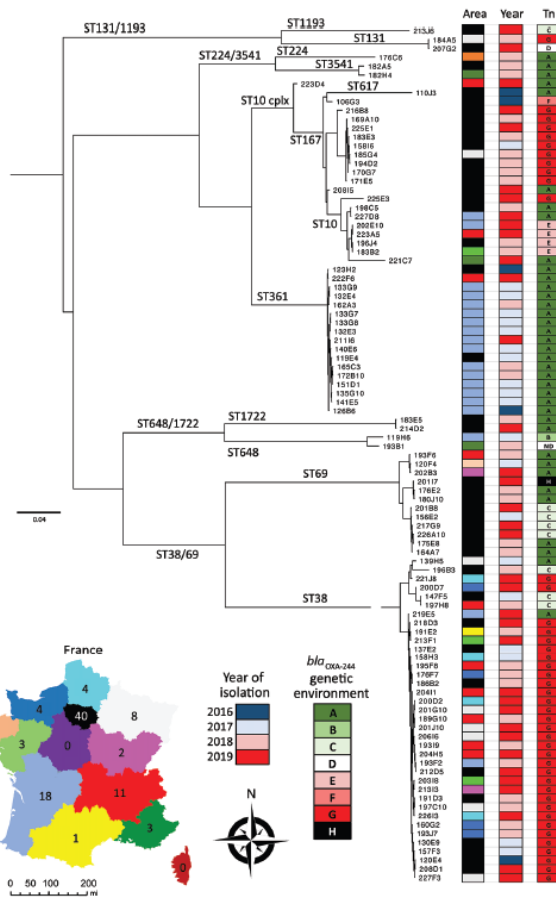
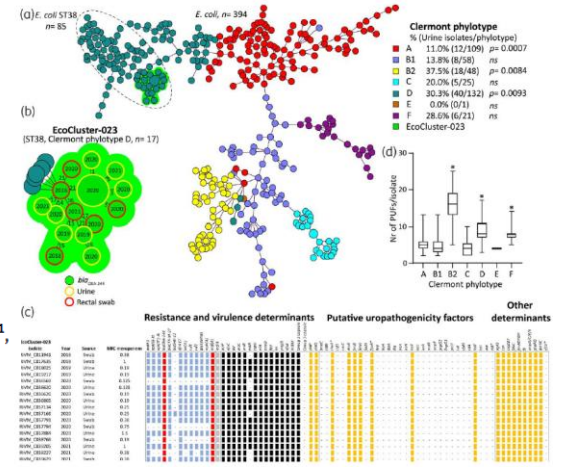


Figure 1. Phylogenetic relationship and geographic distribution of the 97 OXA-244-producing *Escherichia coli* isolates recovered in France, 2016–2019. Inset map shows regions of France; colors correspond to areas from which OXA-244-producing *E. coli* isolates were collected. The phylogenetic tree was constructed using CSIPhylogeny version 1.4 (<https://cge.obs.dtu.dk/services/CSIPhylogeny>). Scale bar indicates nucleotide substitutions per site. ND, not detected; OXA, oxacillin; ST, sequence type.

J Antimicrob Chemother 2022; **77**: 3205–3208
<https://doi.org/10.1093/jac/dkac307>
 Advance Access publication 29 September 2022

A genetic cluster of OXA-244 carbapenemase-producing *Escherichia coli* ST38 with putative uropathogenicity factors in the Netherlands

Daan W. Notermans¹, Annelot F. Schoffelen¹, Fabian Landman¹, Cornelia C. H. Wielders¹, Sandra Witteveen¹, Varisha A. Ganesh¹, Marga van Santen-Verheul¹, Sabine C. de Greeff¹, Ed J. Kuijper¹, and Antoni P. A. Hendrickx^{1*} the Dutch CPE Surveillance Study Group†



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Journal homepage: www.elsevier.com/locate/ijantmicag



Short Communication

Cross-border emergence of clonal lineages of ST38 *Escherichia coli* producing the OXA-48-like carbapenemase OXA-244 in Germany and Switzerland

Linda Falgenhauer^{a,b}, Patrice Nordmann^{c,d,e}, Can Imirzalioglu^a, Yancheng Yao^a, Jane Falgenhauer^a, Anja M. Hauri^f, Petra Heinmüller^f, Trinad Chakraborty^{g,h}

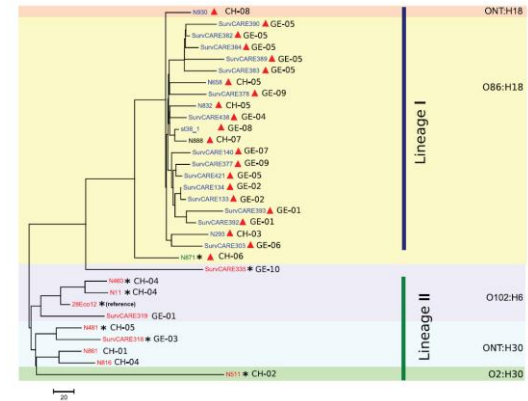


Figure 1. Circos-genome-based analysis of OXA-244-producing ST38 isolates. The colour of the isolate names indicates the carriage of additional ESBL/AmpC enzymes; CTX-M-14b, red; CTX-M-27, blue; CMY-2, green; no additional ESBL/AmpC gene, black. A star indicates the presence of a complete Tn3008 harbouring OXA-244. Red triangles indicate absence of Type I fimbriae genes. In a reference, SHV012 was used (marked as reference).

Intraregional hospital outbreak of OXA-244-producing *Escherichia coli* ST38 in Norway, 2020

Paul Christoffer Lindemann¹, Torunn Pedersen², Dortehea Hagen Oma³, Jessin Janice², Fredrik Grøvan⁴, Ghantous Milad Chedid⁵, Liv Jorunn Hafne⁵, Ellen H. Josefsen², Oliver Kacelnik⁶, Arnfinn Sundsfjord^{2,7}, Ørjan Samuelsen^{2,8}

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Article submitted on 29 Sept 2022 / accepted on 09 May 2023 / published on 06 July 2023

FIGURE 2

Comparisons of the *bla*_{OXA-244} containing chromosomal region in the outbreak clone with selected isolates of ST349, ST131 and ST38 representing three variants

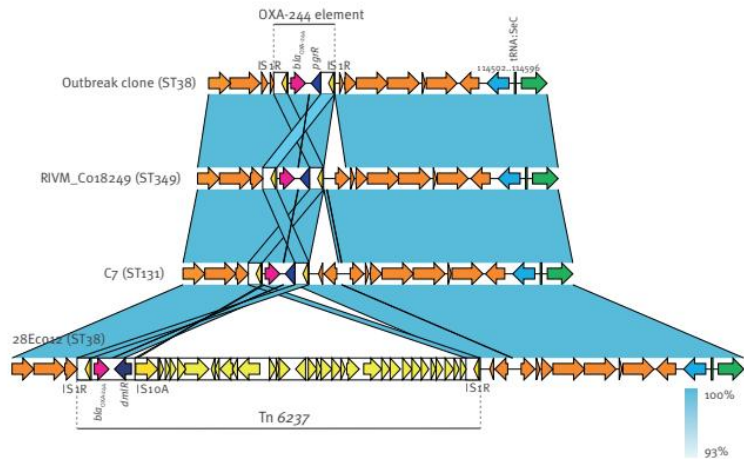
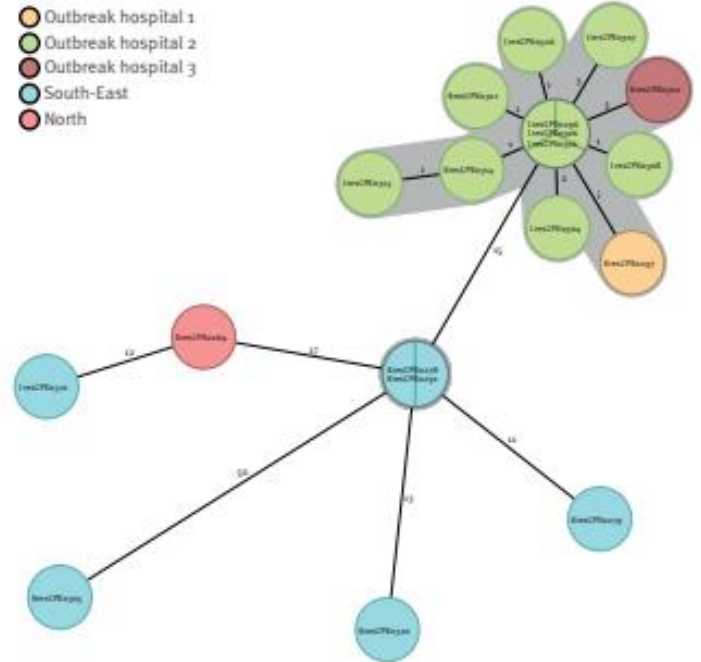


FIGURE 1

Minimum spanning tree based on the core genome allele profile of OXA-244-producing *Escherichia coli* ST38 outbreak isolates (n = 12) from Western Norway and isolates from other regions in Norway in 2020 (n = 7)



OXA: oxacillinase; MLST: multilocus sequence typing; ST: sequence type.

Each isolate is represented by a circle coloured according to the hospital involved in the outbreak or region. The number of core genome MLST allele differences between isolates is indicated with a number along the connecting lines between circles. Circles containing > 1 isolate indicate no core genome MLST allele differences. Grey shading show clusters of isolates with a core genome MLST allele difference below the cluster threshold (≤ 10 allele differences).

E. coli ST38 OXA-244 w Polsce

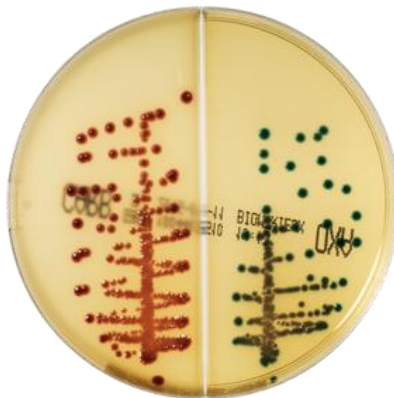
- Pierwsze izolaty:

- grudzień 2017 Kraków ($bla_{\text{CTX-M-27}}$)
- marzec 2018 Warszawa ($bla_{\text{CTX-M-14}}$)
- listopad 2018 Ostrów Wielkopolski ($bla_{\text{CTX-M-14}}$)



E. coli ST38 OXA-244 woj. lubuskie

- wiosna 2023 r. – szpital w woj. lubuskim „HF1”
- badania przesiewowe dla *Enterobacterales* wytwarzających podstawowe typy karbapenemaz (CPE)
- izolaty *E. coli*
 - chromID™ CARBA SMART, bioMerieux
 - MacConkey + ertapenem 10 µg
 - test z krążkiem z temocyliną 30 µg
 - NG-Test® CARBA 5, NG Biotech



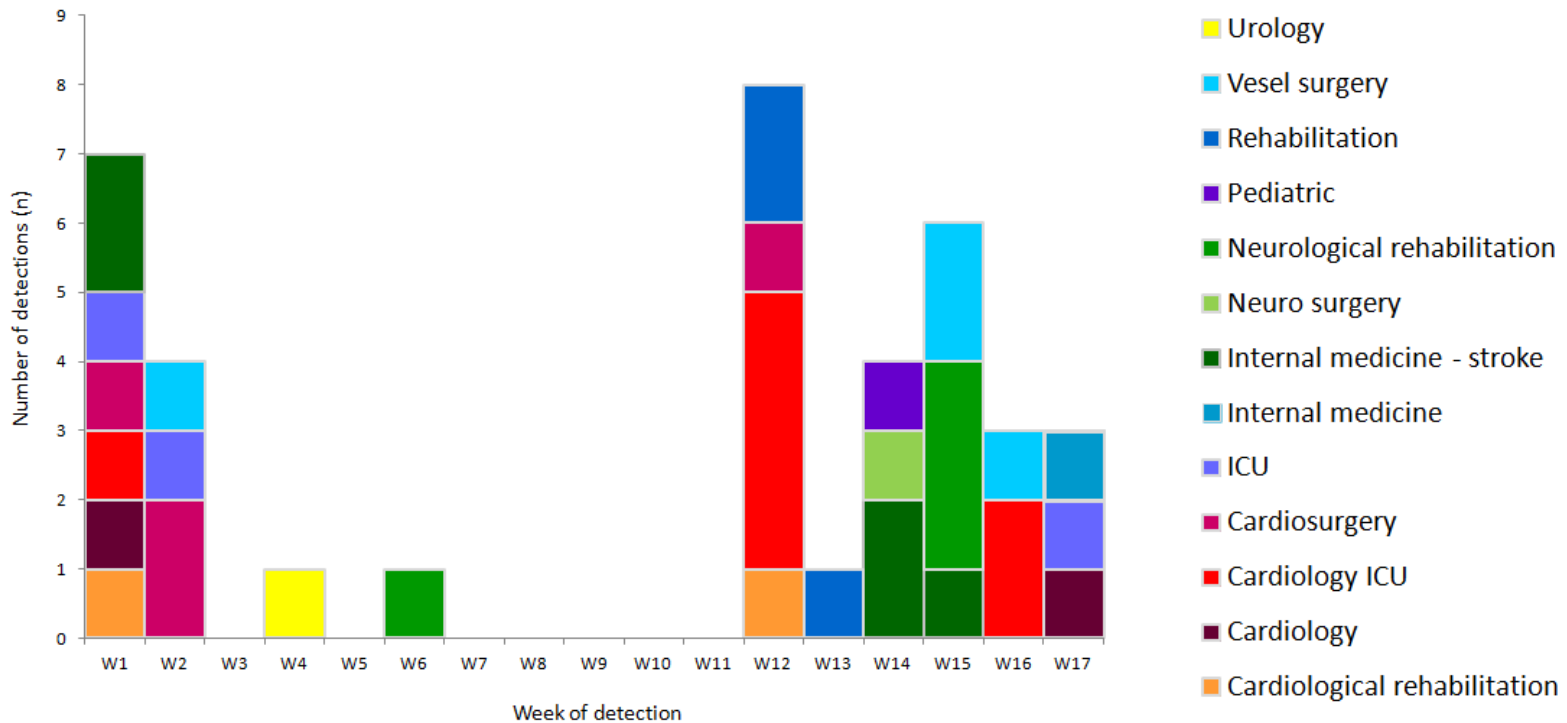
chromID™ CARBA SMART, bioMerieux



NG-Test® CARBA 5, NG Biotech

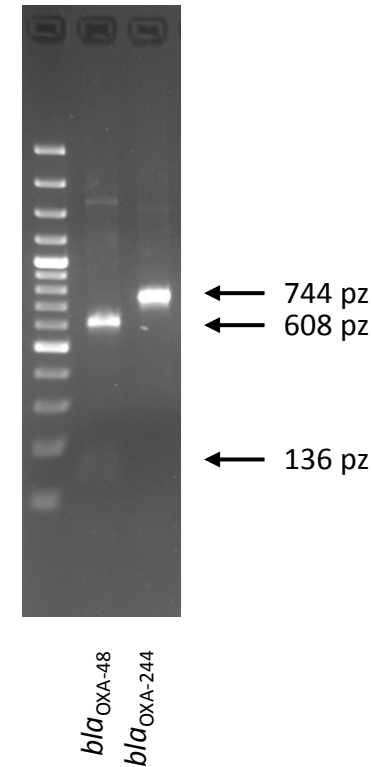
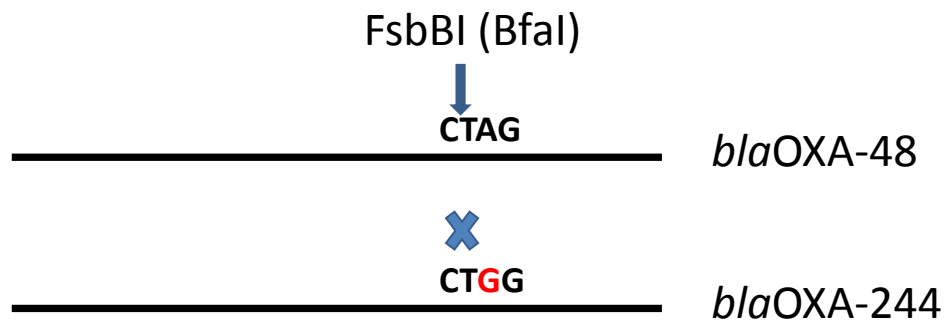
E. coli ST38 OXA-244 woj. lubuskie

- 38 izolatów szpitalnych *E. coli*, luty-czerwiec 2023
- przekazane do ZMM NIL



E. coli ST38 OXA-244 woj. lubuskie

PCR genów typu *bla*_{OXA-48} i PCR-RFLP

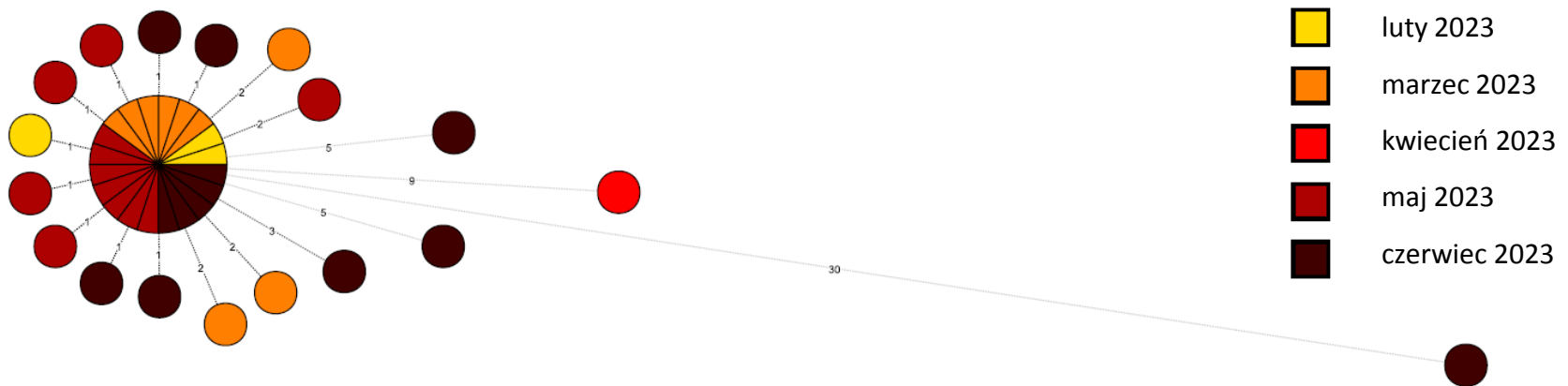


Krajowy Ośrodek Referencyjny ds. Lekowrażliwości Drobnoustrojów (KORLD) prowadzi badania PCR-RFLP wszystkich izolatów *E. coli* OXA-48 (+) w celu identyfikacji producentów OXA-244

E. coli ST38 OXA-244 woj. lubuskie

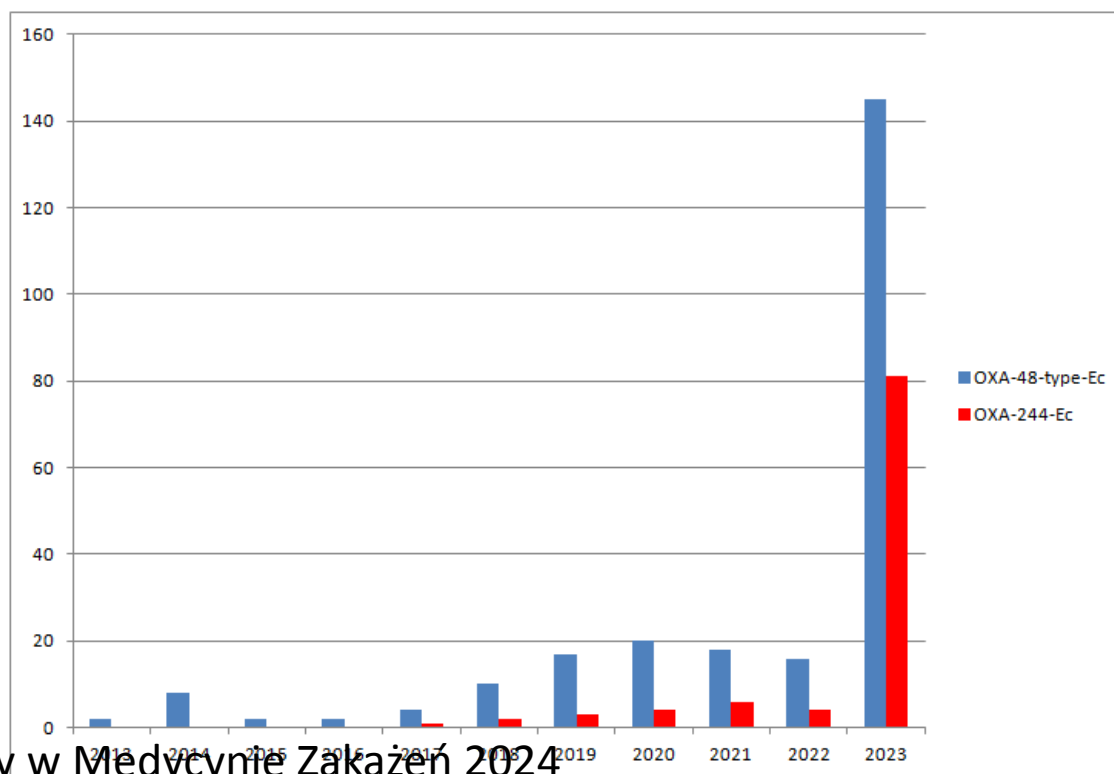
WGS, sekwencjonowanie genomowe

- MLST: ST38
- SNP, polimorfizm pojedynczego nukleotydu
 - 68 polimorficznych pozycji (~4.7 Mbp)
 - 0 - 30 polimorficznych pozycji pomiędzy pierwszym i dowolnym izolatem
 - średnia wartość 1.8 polimorficznych pozycji; mediana - 0



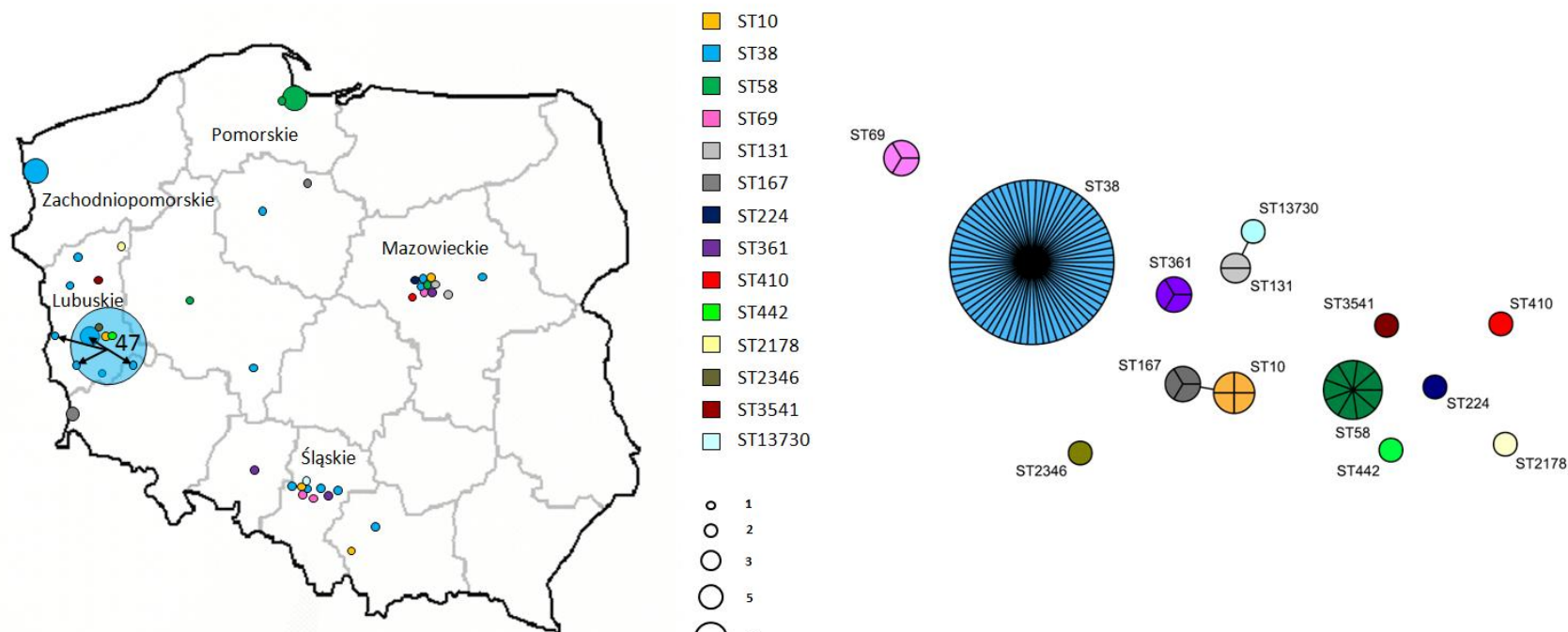
E. coli OXA-244 w Polsce

- 244 izolaty *E. coli* OXA-48-like 2013-2023
- FsbBI PCR-RFLP – 101 prawdopodobnych izolatów OXA-244 2017-2023 – WGS
- 101 *E. coli* OXA-244 - ~41% OXA-48-like (2017-2023)
- ~80% *E. coli* OXA-244 z 2023!



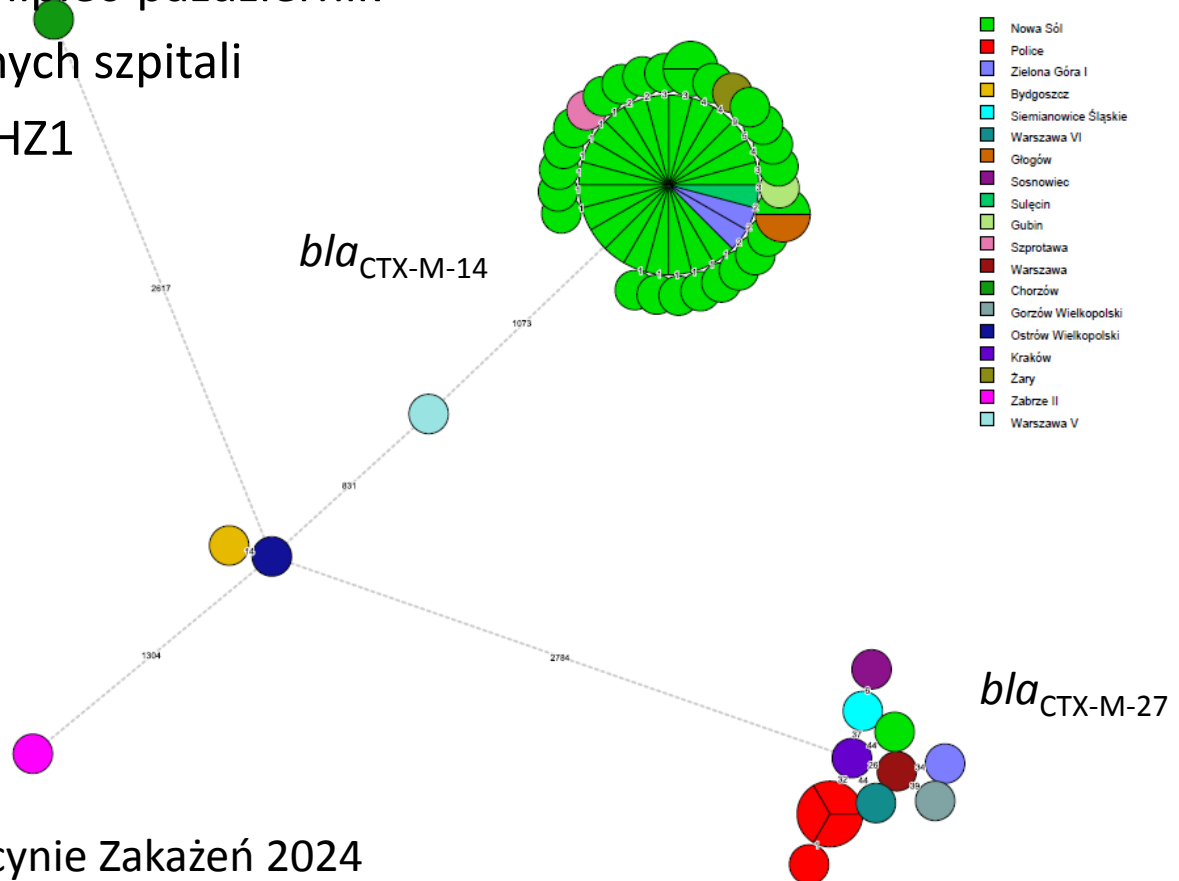
E. coli OXA-244 w Polsce

- 38 szpitali w 29 miastach 10/16 województw
- mężczyźni (62 %), kobiety (38%)
- średnia wieku 63,5 lat; od 5 dni do 97 lat
- 88% z nosicielstwa
- 14 ST: **ST38 (n=70)**, ST58 (n=9), ST10 (n=4), ST69, ST167 i ST361 (po 3), oraz ST131 (n=2)

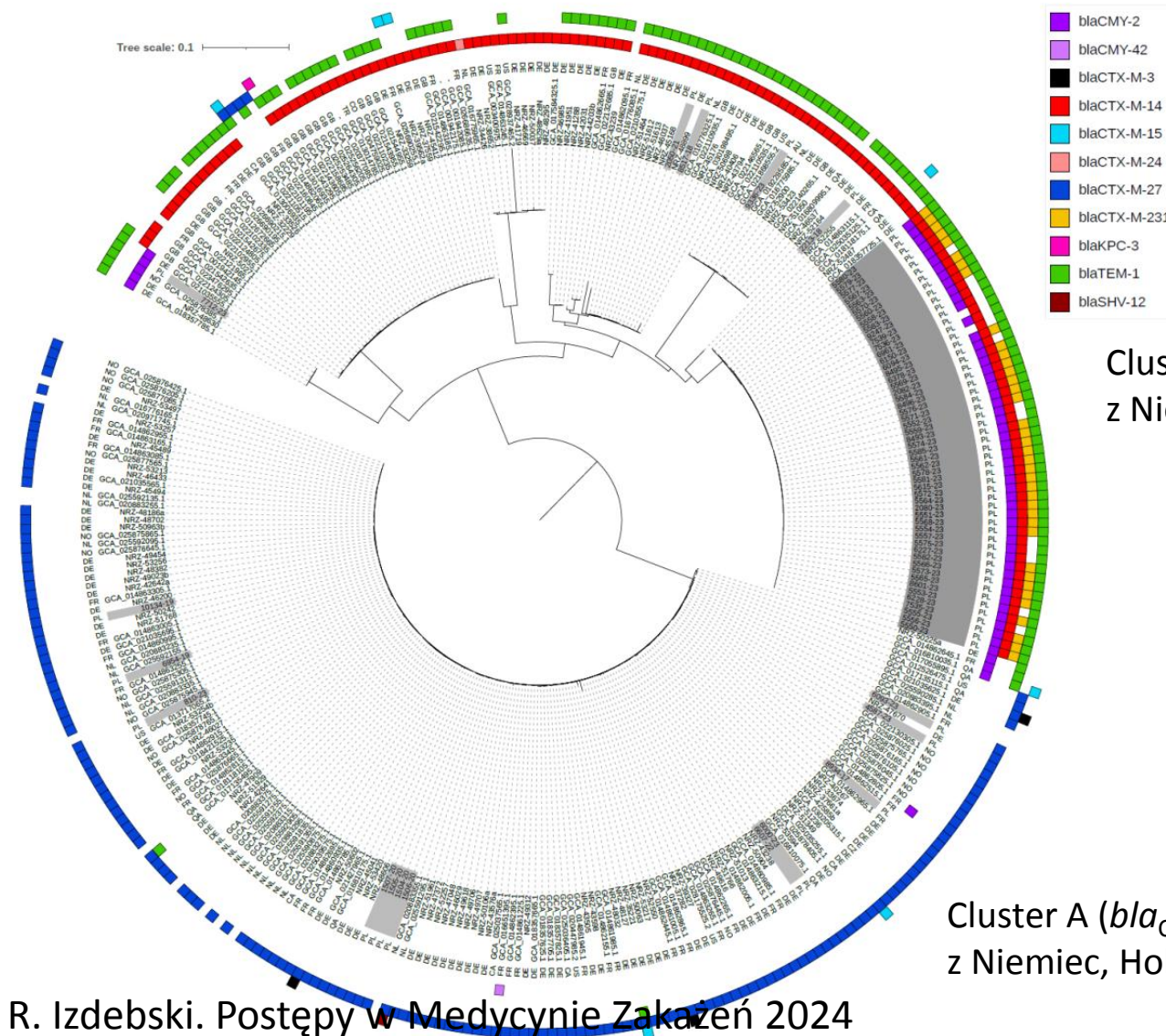


E. coli ST38 OXA-244 w Polsce

- 70 izolatów ST38
- 53 (~70% ST38) blisko spokrewnione (0-9 SNP)
- 46 w HF1 – 8 nowych lipiec-październik
- 4 przeniesienia do innych szpitali
- 4 izolaty (0-1 SNP) w HZ1



E. coli ST38 OXA-244 w Polsce



- blaCMY-2
- blaCMY-42
- blaCTX-M-3
- blaCTX-M-14
- blaCTX-M-15
- blaCTX-M-24
- blaCTX-M-27
- blaCTX-M-231
- blaKPC-3
- blaTEM-1
- blaSHV-12

Analiza filogenetyczna *E. coli* ST38 OXA-244

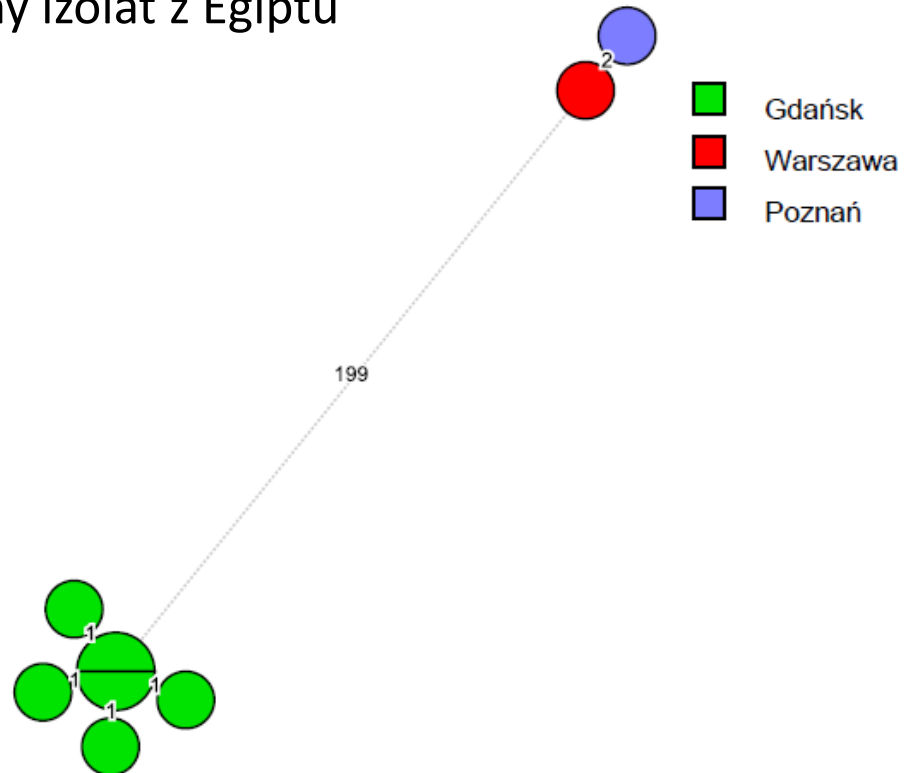
164 z 217 882 genomów z GenBank
 100 z Niemiec
 38 z Polski

Cluster B (*bla*_{CTX-M-14}) wraz z izolatami z Niemiec, Holandii i W. Brytanii

Cluster A (*bla*_{CTX-M-27}) wraz z izolatami z Niemiec, Holandii, Norwegii i Francji

E. coli ST58 OXA-244 w Polsce

- 9 izolatów z 4 szpitali z 3 miast
- 7 izolatów z HG1 i HG2 – 0-2 SNP
- Pojedynczy niespokrewniony izolat z Egiptu



Podsumowanie - *E. coli* ST38 OXA-244

- duże rozprzestrzenienie terytorialne (gł. Niemcy) *E. coli* ST38 OXA-244 głównie w środowisku pozaszpitalnym (trudności w monitorowaniu i kontroli)
- trudności w diagnostyce mikrobiologicznej
- *E. coli* OXA-244 obecna w Polsce od 2017r.; nagły wzrost izolacji w 2023r.
- Dominujący klon ST38 gł. w woj. Lubuskim
- *E. coli* ST38 OXA-244 ma potencjał epidemiczny zdolny do wywoływania ognisk szpitalnych (liczniejszych/częstszych)
- *E. coli* ST38 OXA-244 doskonałym materiałem do dalszej ewolucji oporności
- **monitoring!**

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<https://doi.org/10.1007/s10096-024-04954-0>

BRIEF REPORT



Several epidemic and multiple sporadic genotypes of OXA-244-producing *Escherichia coli* in Poland; predominance of the ST38 clone

Marta Biedrzycka¹ · Radosław Izdebski¹ · Marek Gniadkowski¹ · Dorota Zabicka²

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Podziękowania

- mikrobiolodzy kliniczni i specjaliści kontroli zakażeń z całego kraju
- Zakład Mikrobiologii Molekularnej NIL
- Krajowy Ośrodek Referencyjny ds. Lekowrażliwości Drobnoustrojów NIL



NARODOWE CENTRUM NAUKI

Dziękuję za uwagę