



ESBL in Stockholm: How WGS surveillance revealed a *K. quasipneumoniae* CTX-M-15 cluster

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Background

- Since 2018 Karolinska UH perform WGS on ESBL producing *K. pneumoniae* and *E.coli*:
 - All isolates from the ICUs
 - Blood/cerebrospinal fluid cultures from all departments
- *K pneumoniae* ST2312 with CTX-M-15, first appeared in week 19 in 2022
 - Six more cases 2022
 - 14 cases 2023
 - 10 cases 2024
- No description of this sequence type in the literature
- Could it be a silent outbreak?

PTZ	IMI	MER	ERT	AMI	TSU	CTX	CFZ	FOX	G10	CIP	Resistensgener			
											ESBL	betalakt	Kinolon	Trimeto
20	26	28	26	18	6	6	13	23	18		CTX-M-15	OKP-A-4	qnrS1	dfrA14
20	26	29	28	19	6	6	6	22	19	18	CTX-M-15	OKP-A-4	qnrS1	dfrA14
21	27	29	27	21	6	6	14	23	19	18	CTX-M-15	OKP-A-4	qnrS1	dfrA14

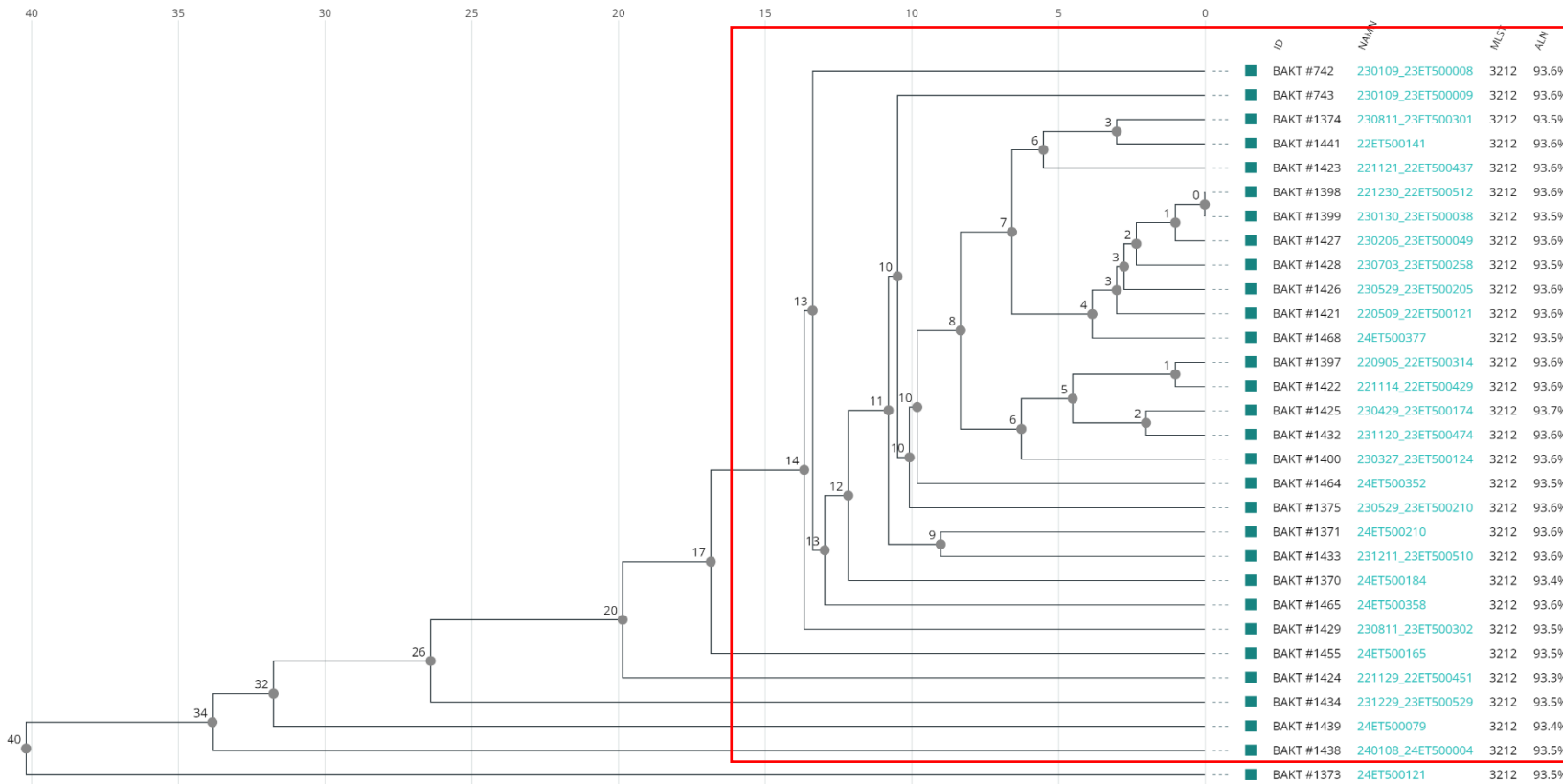
The investigation

- All sequences were uploaded to 1928 Diagnostics software
- All initial 31 isolates belonging to ST 3212 turned out to be *K. quasipneumoniae subsp. quasipneumoniae* and not *K. pneumoniae*
- Environmental species, not really considered a human pathogen
- Cluster analysis with cgMLST for *K. pneumoniae* not suitable as *K. quasipneumoniae* only carries about 45% of the core genes *K. pneumoniae* carries.
- Cluster analysis with SNP: 30 out of 31 isolates closely related.

K quasipneumoniae

- First described in 2014, most likely separated from *K. pneumoniae* six million years ago.
- Maldi-TOF can not distinguish *K quasipneumoniae* from *K. pneumoniae*
- Belongs to phylogroups KpII-A and KpII-B
 - KpII-A *K. quasipneumoniae* subsp. *quasipneumoniae*
 - KpII-B *K. quasipneumoniae* subsp. *similimpneumoniae*
- Genotypically,
 - KpII-A carries chromosomal beta-lactamase (not ESBL) OKP-A
 - KpII-B carry OKP-B.
 - *K. pneumoniae* does not carry these genes.
 - WGS needed

SNP cluster analysis

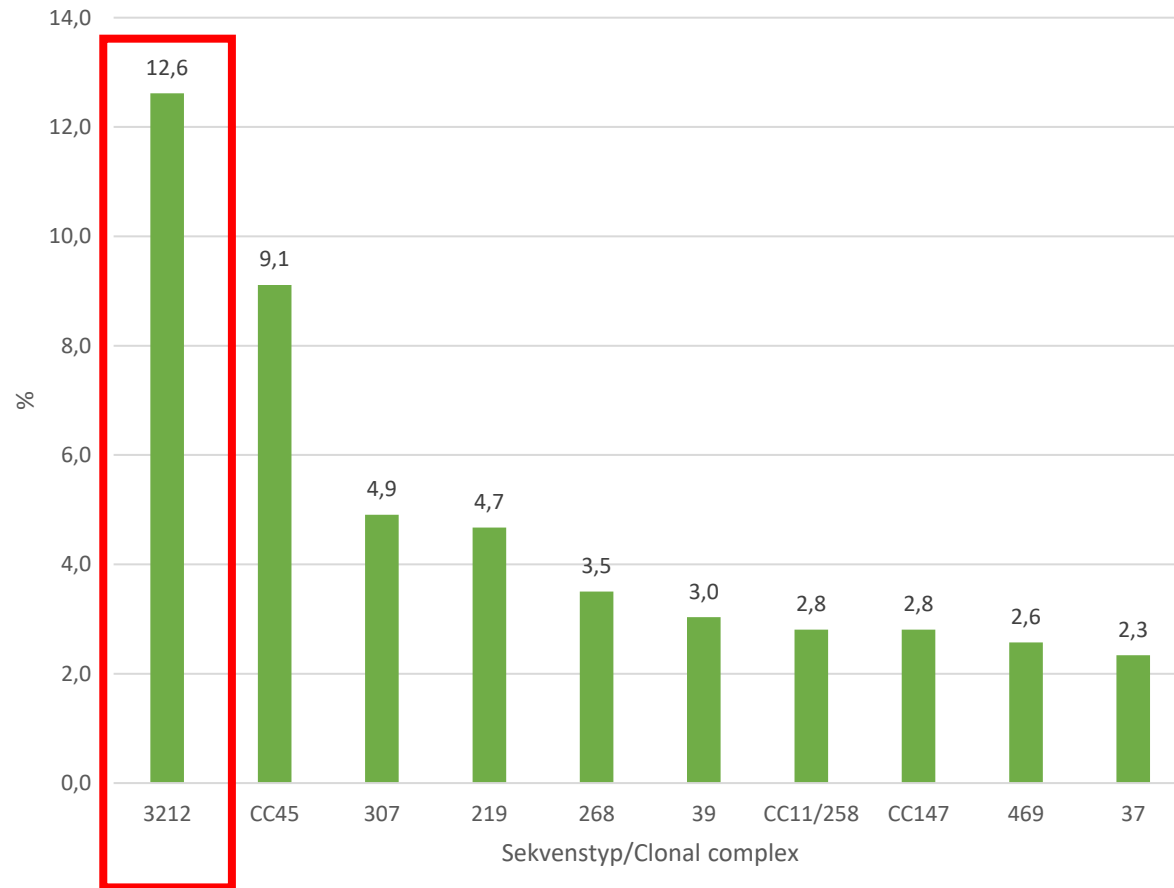


30 of 31 are considered to be genetically closely related <30 SNPs

25 of 31 isolates fall into a cluster which does not differ by more than 14 SNPs.

Since then the cluster has expanded to include 150 patients

ESBL_{A/M} *K. pneumoniae* 2025 in Stockholm



Starting in the fall of 2024 and forward, all *K. pneumoniae* have been sequenced.

A total of 428 isolates sequenced until January 2026

ST3212 is now the most common *K pneumoniae* with ESBL in the Stockholm region

Conclusion

- ESBL *K. quasipneumoniae* cluster with unusual subgroup of the *K pneumoniae* complex. Carries CTX-M 15 (and OKP-A)
- Environmental bacterium, lacks virulence factors
- WGS needed
- Very unusual ST, not found in other center in the Nordics
- Approximately 150 clinical cases since 2021. (Mostly blood + urine cultures)
- Investigation with Infection control units in Stockholm in collaboration with Clin Microbiology MRB section
 - Common source of infection in healthcare has not been confirmed. Probably community spread.

Help needed!

What is the source?

Have you found ST 3212?

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