ASSESSMENT

Changing carbapenemase distribution in *Klebsiella pneumoniae* and *Escherichia coli* in the EU/EEA – preliminary results from the main collection of the CRE25 survey

June 2026

Preliminary data from the main collection of the survey of carbapenem-resistant Enterobacterales 2025 (CRE25 survey) indicates a considerable change in the carbapenemase gene distribution in carbapenem-resistant or carbapenem-susceptible, increased exposure (carbapenem-R/I) *Klebsiella pneumoniae* species complex (SC). It showed a decrease of the proportion of bla_{KPC} and an increase in the proportion of bla_{NDM} carbapenemase genes in comparison to the survey of carbapenem- and/or colistin-resistant Enterobacterales (CCRE survey) from 2019. The increase in the proportion of isolates with bla_{NDM} is driven by the spread of previously circulating *K. pneumoniae* high-risk lineages (e.g. sequence type (ST) 147) carrying bla_{NDM}, the emergence of new bla_{NDM}-positive high-risk lineages (e.g. ST383, ST395, ST6260) and the acquisition of bla_{NDM} by lineages (e.g. ST258/512) previously associated with other carbapenemase genes. Alongside ongoing dissemination of bla_{NDM-1}, a pronounced increase of bla_{NDM-5} has been observed. The rising proportion of isolates carrying bla_{NDM} variants is of high concern as many newer antimicrobials developed for treating carbapenem-resistant Enterobacterales (CRE) infections, such as ceftazidime-avibactam, meropenem-vaborbactam and imipenem-relebactam, are not active against NDM-producing CRE.

For the carbapenem-R/I *Escherichia coli* dataset, comparison of the results between surveys is more difficult due to the low number of carbapenem-R/I *E. coli* isolates in the previous CCRE survey. In contrast to *K. pneumoniae* SC, there is mainly an increase in the proportion of the bla_{OXA-48}-like carbapenemase genes primarily caused by increased detection of $bla_{OXA-244}$ in *E. coli* isolates of extraintestinal pathogenic high-risk lineages (e.g. ST38, ST131, ST13730, ST69, ST10) which are known to spread in the community as well as in healthcare settings. The increase in the proportion of *E. coli* isolates carrying $bla_{OXA-244}$ is of concern due to the potential for undetected transmission of these isolates in community settings.

Enhanced efforts are required to control and reduce harm related to the spread of carbapenemase-producing Enterobacterales (CPE) in the European Union/European Economic Area. These efforts should include:

- improving national coordination and support to hospitals for implementing control measures;
- developing national CPE management plans;
- implementing enhanced infection prevention and control measures and antimicrobial stewardship programmes;
- strengthening laboratory capacity for rapid detection and characterisation of CPE, including genomic surveillance;
- strengthening innovation and access to antimicrobials indicated against CPE infections.

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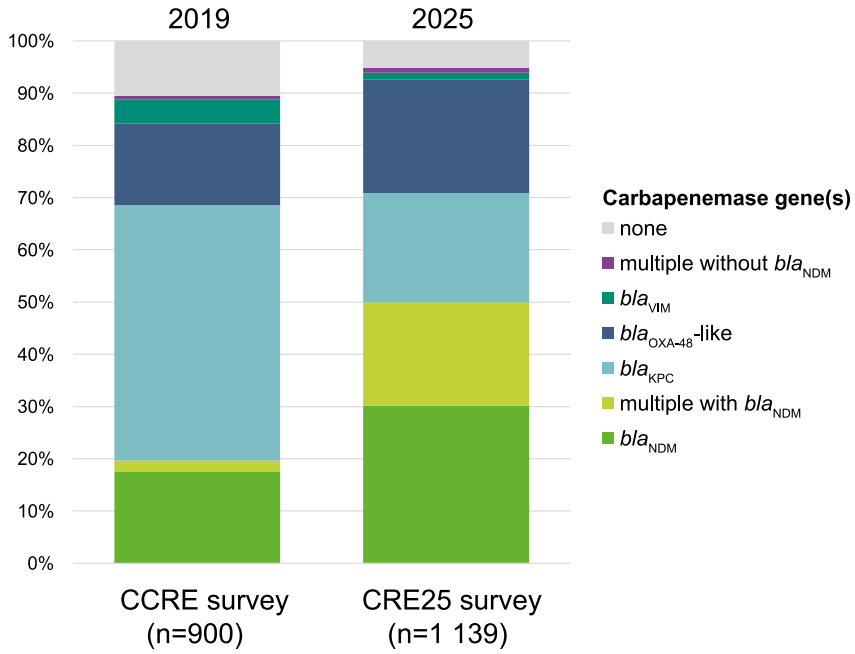
Epidemiological situation

Distribution of carbapenemase genes in *Klebsiella pneumoniae* species complex

In the preliminary dataset from the survey of carbapenem-resistant Enterobacterales 2025 (CRE25 survey), which included data from 21 countries as of 22 April 2026 (Table 1), 569 (50%) of 1 139 carbapenem-resistant or carbapenem-susceptible, increased exposure (carbapenem-R/I) *Klebsiella pneumoniae* species complex (SC) isolates carried *bla*$_{NDM}$ (alone or in combination with other carbapenemase genes) compared to only 177 (20%) of 900 isolates in the survey of carbapenem- and/or colistin-resistant Enterobacterales (CCRE survey) in 2019. In contrast, carbapenem-R/I isolates carrying *bla*$_{KPC}$ have decreased from 448 (50%) in the CCRE survey to 281 (25%) in the CRE25 survey[1] (Figure 1 and Table 2).

Figure 1. Distribution of carbapenemase genes in carbapenem-R/I *Klebsiella pneumoniae* species complex isolates in 21 countries that submitted data for the CCRE and the CRE25 survey



Among 569 CRE25 survey carbapenem-R/I *K. pneumoniae* SC isolates carrying *bla*$_{NDM}$ variants, *bla*$_{NDM-1}$, alone or in combination with other carbapenemase genes, was the variant detected most frequently in 285 isolates (50%), followed by *bla*$_{NDM-5}$ in 260 isolates (46%)[2]. These proportions changed compared to the CCRE survey, where *bla*$_{NDM-1}$ was detected in 160 (90%) of 177 isolates carrying *bla*$_{NDM}$ and *bla*$_{NDM-5}$ in only nine (5%) isolates.

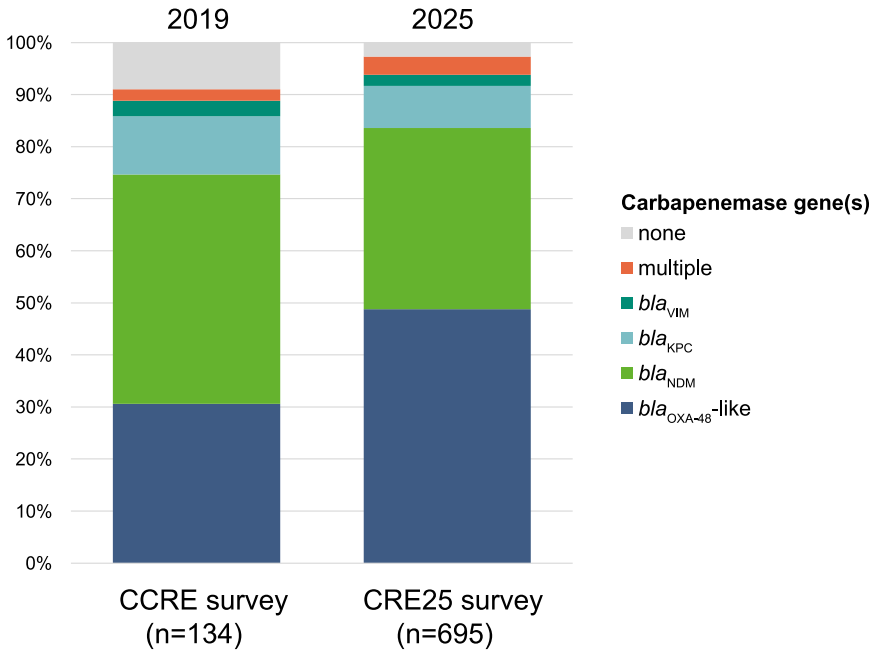
The increase of carbapenem-R/I *K. pneumoniae* SC isolates carrying *bla*$_{NDM-5}$ was associated with the increasing spread of the known high-risk sequence type (ST) 147 and emerging ST383, ST395, and ST6260 *K. pneumoniae* lineages. In addition, several isolates (25, 4%) of the high-risk lineage ST258/512, previously mainly associated with *bla*$_{KPC}$, are now carrying *bla*$_{NDM}$ variants in the CRE25 survey. The rising proportion of isolates carrying *bla*$_{NDM}$ variants is of high concern as many newer beta-lactam/beta-lactam inhibitor antimicrobials developed for treatment of CRE, e.g. ceftazidime-avibactam, meropenem-vaborbactam and imipenem-relebactam, are not active against NDM-producing Enterobacterales. This leaves very limited treatment options such as aztreonam-avibactam and cefiderocol. However, NDM-producing Enterobacterales, with resistance to these agents, have also been described [1-3].

[1] Two and 33 carbapenem-R/I *K. pneumoniae* SC isolates carried *bla*$_{NDM}$ and *bla*$_{KPC}$ and/or a third carbapenemase gene in the CCRE and CRE25 surveys, respectively, and are counted twice in this description.
[2] One *K. pneumoniae* SC isolate carried *bla*$_{NDM-1}$ and *bla*$_{NDM-5}$ together in the CRE25 survey and is counted twice in this description.

Distribution of carbapenemase genes in *Escherichia coli*

The carbapenemase distribution also shifted for carbapenem-R/I *E. coli*, with *bla*$_{OXA-48}$-like variants (alone or in combination with other carbapenemase genes), increasing from 43 (32%) out of 134 in the CCRE survey to 359 (52%) out of 695 isolates in the CRE25 survey[3] (Figure 2 and Table 2). Correspondingly, the proportions of NDM and KPC carbapenemases detected alone decreased from 44% to 35% and from 11% to 8%, respectively (Figure 2 and Table 3).

Figure 2. Distribution of carbapenemase genes in carbapenem-R/I *Escherichia coli* isolates in 21 countries that submitted data for both surveys in 2019 and 2025



Among 359 CRE25 survey carbapenem-R/I *E. coli* isolates carrying a *bla*$_{OXA-48}$-like gene, *bla*$_{OXA-244}$ alone or in combination with other carbapenemase genes was the most frequent variant, detected in 245 isolates (68%). This was followed by *bla*$_{OXA-48}$ in 78 isolates (22%) and *bla*$_{OXA-181}$ in 22 isolates (6%). This distribution contrasted with the CCRE survey, where *bla*$_{OXA-48}$ dominated in 28 (65%) of 43 isolates, while *bla*$_{OXA-244}$ and *bla*$_{OXA-181}$ were less frequent in nine (21%) and six isolates, respectively.

The spread of *E. coli* carrying *bla*$_{OXA-244}$ was polyclonal with detections across major multidrug-resistant and extraintestinal pathogenic *E. coli* (ExPEC) lineages, including ST38, ST131 and its single locus variant ST13730, ST69, and ST10. ExPEC have been detected in several non-human reservoirs including companion animals, food animals, food products, sewage and other environmental reservoirs [4]. They can be transmitted in healthcare settings as well as in the community via faecal-oral, household, sexual or food-borne routes [5] and are therefore difficult to control. Compared to OXA-48, OXA-244 has weak hydrolytic activity associated with slightly decreased carbapenem susceptibility and is therefore challenging to detect for clinical laboratories [6]. This increases the risk for undetected transmission of these strains in community settings. Despite only causing decreased susceptibility on its own, OXA-244 can contribute to high-level resistance when combined with other resistance mechanisms. Although there is a lack of data on treatment outcomes for infections with OXA-244-producing *E. coli*, OXA-48-like carbapenemases have been linked to compromised clinical efficacy of carbapenem treatment [7,8]. The European Committee on Antimicrobial Susceptibility Testing (EUCAST) recommends avoiding carbapenems for treatment of CPE even if testing susceptible, due to a potentially impaired clinical response to treatment [9].

Enhanced efforts are required to control and reduce harm related to the spread of CPE in the European Union/European Economic Area. These efforts should include improved national coordination and support to hospitals to implement control measures; develop national CPE management plans; implement enhanced infection prevention and control measures and antimicrobial stewardship programs; strengthen laboratory capacity for rapid detection and characterisation of CPE, including genomic surveillance, and strengthen innovation and access to antimicrobials indicated against CPE infections as further detailed in the ECDC rapid risk assessment on carbapenem-resistant Enterobacterales, third update [10].

[3] Two and 20 *E. coli* isolates carried *bla*$_{OXA-48}$-like and another carbapenemase gene in the CCRE and CRE25 surveys, respectively, and are counted twice in this description.

Data sources

This epidemiological update is based on the preliminary analysis of data from the CRE25 survey submitted by 21 countries (see Table 1), with 1 139 carbapenem-R/I *K. pneumoniae* SC and 695 carbapenem-R/I *E. coli* isolates (CRE25 survey main collection) sampled between 1 October 2025 and 31 December 2025.More information on the methodology of the CRE25 survey can be found in the protocol and the analysis plan [11,12]. The CRE25 survey dataset was compared with the dataset from the CCRE survey 2019 [13-15]. While there have been several protocol changes between the two surveys, the inclusion criteria for carbapenem-R/I *K. pneumoniae* and *E. coli* isolates based on EUCAST clinical breakpoints have remained stable between the CCRE survey and the CRE25 survey main collection.

Table 1. Number of carbapenem-R/I isolates in the CCRE and CRE25 survey for 21 countries that reported data as of 22 April 2026

Country	CCRE survey Carbapenem-R/I *K. pneumoniae* species complex	CRE25 survey Carbapenem-R/I *K. pneumoniae* species complex	CCRE survey Carbapenem-R/I *E. coli*	CRE25 survey Carbapenem-R/I *E. coli*
	n isolates	n isolates	n isolates	n isolates
Austria	19	45	5	23
Belgium	51	19	10	8
Bulgaria	84	60	7	2
Czechia	27	66	10	24
Denmark	3	13	6	19
Estonia	2	7	2	1
Finland	11	3	10	14
France	40	137	7	127
Germany	33	207	14	228
Greece	128	122	2	10
Hungary	40	59	1	8
Ireland	8	28	1	29
Italy	278	118	17	48
Latvia	3	18	1	16
Luxembourg	3	3	3	4
The Netherlands	23	52	10	37
Norway	7	26	5	25
Romania	66	75	0	14
Slovakia	30	40	0	15
Slovenia	24	18	7	13
Sweden	20	23	16	30
Total	**900**	**1 139**	**134**	**695**

Table 2. Distribution of carbapenemase genes in carbapenem-R/I *Klebsiella pneumoniae* species complex isolates in 21 countries that submitted data for the CCRE and the CRE25 survey

Carbapenemase gene(s)	CCRE survey, n	CCRE survey, %	CRE25 survey, n	CRE25 survey, %
bla_{NDM}	158	18	343	30
multiple with bla_{NDM}	19	2	226	20
bla_{NDM} and bla_{OXA-48}-like	16	2	190	17
bla_{NDM} and bla_{KPC}	2	<1	32	3
bla_{NDM} and bla_{VIM}	1	<1	2	<1
multiple bla_{NDM} variants	0	0	1	<1
bla_{NDM}, bla_{KPC} and bla_{OXA-48}-like	0	0	1	<1
bla_{KPC}	440	49	238	21
bla_{OXA-48}-like	141	16	248	22
bla_{VIM}	41	4	15	1
multiple without bla_{NDM}	6	1	10	1
bla_{KPC} and bla_{VIM}	5	<1	7	<1
bla_{KPC} and bla_{OXA-48}-like	1	<1	3	<1
none	95	10	59	5
Total	**900**	**100**	**1 139**	**100**

Table 3. Distribution of carbapenemase genes in carbapenem-R/I *Escherichia coli* isolates in 21 countries that submitted data for the CCRE and the CRE25 survey

Carbapenemase gene(s)	CCRE survey, n	CCRE survey, %	CRE25 survey, n	CRE25 survey, %
bla$_{OXA-48}$-like	41	31	339	49
bla$_{NDM}$	59	44	242	35
bla$_{KPC}$	15	11	56	8
bla$_{VIM}$	4	3	15	2
multiple	3	2	24	3
bla$_{NDM}$ and *bla*$_{OXA-48}$-like	2	1	19	3
bla$_{NDM}$ and *bla*$_{VIM}$	1	1	2	<1
multiple *bla*$_{NDM}$ variants	0	0	1	<1
bla$_{NDM}$ and *bla*$_{KPC}$	0	0	1	<1
bla$_{OXA-48}$-like and *bla*$_{GES}$	0	0	1	<1
none	12	9	19	3
Total	**134**	**100**	**695**	**100**

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