Carbapenemase-producing Enterobacteriaceae and Pseudomonas spp. are increasingly reported in many countries all over the world. Due to the resistance of those bacteria to almost all antibiotics (e.g. beta-lactams, aminoglycosides, fluoroquinolones), treatment options are seriously limited. In the Czech Republic, the incidence of carbapenemase-producing Enterobacteriaceae seems to be low, restricted to only three cases detected between 2009 and 2010. Here, we describe molecular typing of 15 carbapenemase-producing Klebsiella pneumoniae isolates identified in the Czech Republic during 2011. Five VIM-1-producing isolates belonging to sequence type (ST) 11 and one VIM-4-producing isolate of ST1029 have been detected. bla$_{VIM-1}$ and bla$_{VIM-4}$ as a part of class 1 integrons were chromosomally located or carried by a plasmid belonging to A/C replicon type (bla$_{VIM-1}$). KPC-3-producing isolates of ST512, recovered from six patients, caused an outbreak. Three more isolates producing KPC-2 enzyme belonged to ST258. Both bla$_{KPC}$ genes were part of the Tn$_{4401}$a transposon carried on plasmids of the pKpQIL type. The isolates were resistant to all antibiotics tested except colistin and/or gentamicin. Four of these 15 strains were recovered from patients repatriated to the Czech Republic from Greece and Italy. This is the first report of outbreaks caused by carbapenemase-producing Enterobacteriaceae in the Czech Republic.

Introduction

Spread of carbapenemase-producing Enterobacteriaceae and Pseudomonas spp. has been observed in many countries across the world [1-3]. Carbapenemase producers are usually resistant to almost all of the effective antibiotics (such as beta-lactams, aminoglycosides, fluoroquinolones). Therapy of infections caused by such bacteria is limited to few choices (such as colistin and/or a combination therapy) with unpredictable effect [4]. Therefore, prevention of their spread in healthcare settings and in the community is a big challenge for medicine today.

In the Czech Republic, occurrence of carbapenemase-producing bacteria seemed to be rare with only sporadic cases of carbapenemase-producing Klebsiella pneumoniae (VIM-1, KPC-2), Serratia marcescens (VIM-1) and metallo-beta-lactamase-producing Pseudomonas aeruginosa (VIM-2, IMP-7) [1,5-7]. In 2011, however, the incidence of such bacteria increased, especially in K. pneumoniae and P. aeruginosa. The aim of this study was to analyse carbapenemase-producing K. pneumoniae isolates recovered from Czech hospitals in 2011.

Methods

Bacterial isolates, identification and susceptibility testing

In 2011, a total of 102 Enterobacteriaceae isolates, non-susceptible to carbapenems according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines [8], were sent to the Czech national reference laboratory (NRL) for Antibiotics from local microbiology laboratories, for verification of carbapenemase production. All isolates were tested for carbapenemase production by MALDI-TOF mass spectrometry (MS) meropenem hydrolysis assay [9,10]. Phenotypic identification of carbapenemases was performed by an inhibitor-based method [11]. Species identification was performed using a MALDI Biotyper Version 3.0 (Bruker Daltonik GmbH., Bremen, Germany). Minimum inhibitory concentrations (MICs) to 12 antibiotics (piperacillin, piperacillin/tazobactam, cefotaxime, ceftazidime, cefepime, meropenem, ciprofloxacin, gentamicin, amikacin, colistine, chloramphenicol, trimethoprime/sulfamethoxazole) were determined according to the EUCAST recommendations [12].
Typing
All isolates were typed by pulsed-field gel electrophoresis (PFGE) [13] using the restriction enzyme XbaI; the results were interpreted according to Tenover et al. [14]. All isolates were also subjected to multilocus sequence typing (MLST) as described previously [15]. The database available at www.pasteur.fr/recherche/genopole/PF8/mlst/Kpneumoniae.html was used for assigning sequence types (STs).

Beta-lactamase identification, bla gene environment mapping
Detection of bla genes, encoding important carbapenemase types, was performed by PCR using specific primers for bla\textsubscript{OXA-48}, bla\textsubscript{IMP}, bla\textsubscript{NDM}, bla\textsubscript{VIM} and bla\textsubscript{KPC} [2,16-18]. The gene environment of bla\textsubscript{KPC} was determined by PCR mapping as proposed by Naas et al. [17]. Mapping of the VIM-encoding integrons was performed by PCR [16]. For detection of bla\textsubscript{CMY}-type genes, a PCR assay was employed [19]. PCR products were sequenced on both strands.

Conjugation and transformation
To check transferability of the resistance genes on a conjugative plasmid, conjugal transfer was carried out by broth mating, using rifampin-resistant Escherichia coli A15 as previously described [20]. Transconjugants were selected with 50 mg/L ampicillin and 60 mg/L rifampin. Transformation experiments were performed with plasmid extracts, purified using a Qiagen Plasmid Maxi Kit (Qiagen GmbH, Hilden, Germany), and E. coli DH\textsubscript{5alpha} chemically competent cells as a recipient. Transformants were selected with 50 mg/L ampicillin.

Plasmid analysis
Plasmid content was visualised after S1 linearisation followed by PFGE separation [21]. Localisation of bla\textsubscript{VIM}, bla\textsubscript{KPC} and bla\textsubscript{CMY} genes was analysed by hybridisation. The bla-specific probes were prepared from PCR amplicons using a BrightStar Psoralen-Biotin kit (Applied Biosystems, Prague, Czech Republic). DNA after S1 linearisation and PFGE separation was transferred on BrightStar-Plus Positively Charged Nylon Membrane (Applied Biosystems, Prague, Czech Republic) according to manufacturer recommendations, and hybridised for 24 h at 42 °C. Detection of membranes was performed by BrightStar BioDetect Kit (Applied Biosystems, Prague, Czech Republic). PCR-based replicon typing (PBRT) of plasmids was performed as proposed by Carattoli et al. [22], using total DNA from transconjugants/transformants or from clinical isolates that were non-successful in conjugation and transformation experiments. IncF plasmids were further characterised by replica sequence typing (RST) [23]. Plasmids carrying bla\textsubscript{KPC} were identified by PCR mapping as proposed by Baraniak et al. [24].

Results
MALDI-TOF MS meropenem hydrolysis assay confirmed carbapenemase activity in 15 of the 102 isolates analysed. Ethylene-diamine tetra-acetic acid (EDTA)-meropenem combined disk test confirmed metallo-beta-lactamase production in six of the isolates. The respective aminophenylboronic acid–meropenem test was positive for KPC production in the remaining nine isolates. All of the suspected isolates based on the phenotypic tests were positive in MALDI-TOF MS meropenem hydrolysis assay.

VIM-producing isolates
Five of the six VIM-1-producing K. pneumoniae were isolated from one hospital (A5) in Prague (Table 1). In all five isolates, MICs of meropenem were in the susceptible category according to the EUCAST criteria, ranging from 1 to 2 mg/L. The five isolates were resistant to all antibiotics tested, except colistin. The variable region of their class 1 integron containing bla\textsubscript{VIM-1} gene is described in Table 1. Neither transconjugants nor transformants were obtained from any of the five isolates detected in hospital A5. A bla\textsubscript{VIM-1} specific probe hybridised strongly with a band corresponding to the chromosomal material, which confirmed the chromosomal location of the bla\textsubscript{VIM-1}-containing integron. All isolates belonged to ST11, which is a common clone of K. pneumoniae that possesses extended spectrum (ESBL)- and AmpC-beta-lactamases [25,26].

<table>
<thead>
<tr>
<th>Strain number</th>
<th>Isolation date</th>
<th>Hospital</th>
<th>ST</th>
<th>Conjugation</th>
<th>Replicon type</th>
<th>Gene cassettes</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>V554</td>
<td>1 Sep</td>
<td>A5</td>
<td>11</td>
<td>-</td>
<td>-</td>
<td>aac(6')-Ib, bla\textsubscript{VIM-1}</td>
<td></td>
</tr>
<tr>
<td>V555</td>
<td>24 Aug</td>
<td>A5</td>
<td>11</td>
<td>-</td>
<td>-</td>
<td>aac(6')-Ib, bla\textsubscript{VIM-1}</td>
<td></td>
</tr>
<tr>
<td>V564</td>
<td>26 May</td>
<td>A5</td>
<td>11</td>
<td>-</td>
<td>-</td>
<td>aac(6')-Ib, bla\textsubscript{VIM-1}</td>
<td></td>
</tr>
<tr>
<td>V602</td>
<td>10 Oct</td>
<td>A5</td>
<td>11</td>
<td>-</td>
<td>-</td>
<td>aac(6')-Ib, bla\textsubscript{VIM-1}</td>
<td></td>
</tr>
<tr>
<td>V633</td>
<td>21 Oct</td>
<td>A5</td>
<td>11</td>
<td>-</td>
<td>-</td>
<td>aac(6')-Ib, bla\textsubscript{VIM-1}</td>
<td></td>
</tr>
<tr>
<td>V624</td>
<td>17 Oct</td>
<td>NJ</td>
<td>1029</td>
<td>+</td>
<td>A/C</td>
<td>bla\textsubscript{VIM-4}</td>
<td>Import from Greece</td>
</tr>
</tbody>
</table>

ST: sequence type.
The sixth VIM-4-producing strain was detected in October 2011 in a patient admitted to the hospital in the Czech Republic after the medically assisted repatriation from a hospital in Northern Greece. Carbapenem-resistant *K. pneumoniae* (isolate no. V624; Table 1) was isolated from blood immediately after the admission to the hospital. The isolate belonged to ST1029, a novel sequence type, which is a single locus variant (SLV) of ST383 and was first reported in Greece in 2009 [19]. The strain produced VIM-4 and CMY-4 beta-lactamases as described in ST383 by Papagiannitsis et al. [19]. However, no production of KPC enzyme was identified in our strain, contrary to the Greek strain. The class 1 integron consisting of a sole *bla*<sub>VIM-4</sub> gene cassette was harboured by a conjugative plasmid of A/C replicon type. A similar plasmid harbouring *bla*<sub>VIM-1</sub> was described by Samuelsen et al. in a patient repatriated from Greece in 2005 [27]. Immediately after the isolation of the carbapenem-resistant *K. pneumoniae* isolate, recommended isolation precautions were set up in the hospital and no transfer of the strain to another patient was found.

### Table 2
Characterisation of KPC-producing *Klebsiella pneumoniae* isolates recovered from Czech hospitals in 2011 (n=9)

<table>
<thead>
<tr>
<th>Strain number</th>
<th>Isolation date</th>
<th>Hospital</th>
<th>ST</th>
<th>KPC type</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>V514</td>
<td>13 Jul</td>
<td>A41</td>
<td>ST512</td>
<td>KPC-3</td>
<td>Import from Italy, index case</td>
</tr>
<tr>
<td>V556</td>
<td>18 Aug</td>
<td>A41</td>
<td>ST512</td>
<td>KPC-3</td>
<td></td>
</tr>
<tr>
<td>V557</td>
<td>18 Aug</td>
<td>A41</td>
<td>ST512</td>
<td>KPC-3</td>
<td></td>
</tr>
<tr>
<td>V573</td>
<td>8 Aug</td>
<td>A41</td>
<td>ST512</td>
<td>KPC-3</td>
<td></td>
</tr>
<tr>
<td>V646</td>
<td>14 Nov</td>
<td>A41</td>
<td>ST512</td>
<td>KPC-3</td>
<td></td>
</tr>
<tr>
<td>V719</td>
<td>28 Dec</td>
<td>A41</td>
<td>ST512</td>
<td>KPC-3</td>
<td></td>
</tr>
<tr>
<td>V597</td>
<td>4 Oct</td>
<td>A6</td>
<td>ST258</td>
<td>KPC-2</td>
<td>Import from Greece, index case</td>
</tr>
<tr>
<td>V640</td>
<td>7 Nov</td>
<td>A6</td>
<td>ST258</td>
<td>KPC-2</td>
<td></td>
</tr>
<tr>
<td>V601</td>
<td>21 Oct</td>
<td>A51</td>
<td>ST258</td>
<td>KPC-2</td>
<td>Import from Greece</td>
</tr>
</tbody>
</table>

ST: sequence type.

### KPC-producing isolates
In the Czech Republic, the first KPC-producing *K. pneumoniae* isolate was obtained from a patient repatriated from a hospital in Italy to hospital A41 in Prague in July 2011. A carbapenem-resistant isolate producing KPC-3 was cultivated from a urine sample (isolate no. V514; Table 2). From August till December, five more KPC-3-producing *K. pneumoniae* strains were identified in different patients. Their molecular and epidemiological characteristics are summarised in Table 2. Three of these patients were hospitalised on the same ward as, but without direct contact to, the index case, while the remaining two patients were hospitalised in the same time period but in different hospital wards (Figure 1).

Another KPC-producing isolate was recovered from a patient repatriated from a hospital on Greece to hospital A6 in Prague (isolate no. V597; Table 2). The strain was recovered from a blood sample. A second patient (isolate no. V640; Table 2) hospitalised in the same room as the previous one, was colonised with a strain of the same PFGE pattern and ST.
The last case was detected in hospital A51 in Prague. This strain (isolate no. V601; Table 2) was obtained from the respiratory tract of a patient repatriated from a hospital on Crete (Greece). No spread to other patients was detected. No difference was detected in the PFGE patterns of ST258 and ST512 isolates. According to the EUCAST criteria, the detected KPC-producing isolates were susceptible only to gentamicin (Table 3). MICs of colistin, which is sometimes the drug of the last choice in carbapenemase-producing Enterobacteriaceae infections, were in the resistant category (8–16 mg/L). Plasmid profiling with S1 linearisation of all clinical isolates showed a common profile with plasmids approximately 40, 110 and 200 kb in size [24]. All KPC-producing isolates harboured blaKPC-positive plasmids of similar size (approximately 110 kb). Those blaKPC-encoded plasmids were negative for all replicon sequences included in the PBRT panel. However, by the RST method, the KPC-encoding plasmids were positive for the FII replicon. Using PCR-based mapping, the plasmids were identified as the pKpQIL type [24]. Both blaKPC2 and blaKPC3 were part of the transposon Tn4401, isoform a. No transconjugants were obtained from KPC producers. KPC-encoding plasmids were only transferred by transformation of plasmid DNA obtained from isolate V597. MICs of the transformant are shown in Table 3.

All of the patients repatriated to the Czech Republic had been hospitalised in intensive care units in the countries they were repatriated from. In two hospitals in the Czech Republic (A6 and A51), isolation precautions were set up immediately after the identification of carbapenem-resistant *K. pneumoniae* isolate.

Discussion

Carbapenemase-producing enterobacteria seem to be uncommon in the Czech Republic with only three reported cases in the period of 2009 and 2010 and six cases in 2012 [1,5,7]. In 2011, two outbreaks and a few cases of VIM- and KPC-producing *K. pneumoniae* were reported. The *K. pneumoniae* species was the only member of the *Enterobacteriaceae* family found to produce carbapenemases in that year in the Czech Republic. We believe that the situation is not underestimated because, since the mandatory official guideline was issued by the Ministry of Health in 2012, all carbapenem-resistant enterobacteria have been sent to the NRL for Antibiotics for confirmation of carbapenemase production and epidemiological typing.

The situation of VIM-1-producing *K. pneumoniae* in the hospital A5 seems to have been endemic. Even if no epidemiological connection among the isolates could be found (such as hospitalisation on the same ward, use of the same medical procedure or the same medical personnel), most of them were recovered the same time period between May and October 2011 (Table 1, Figure 2). Therefore, the occurrence of these isolates could be considered as an outbreak, but we were not able to identify an index case nor reservoir of the strains. Therefore, our hypothesis was based on molecular typing of the isolates only.

The increasing incidence of KPC-producing *K. pneumoniae* observed in the Czech Republic in 2011 was initially caused by the repatriation of infected patients from Italy (KPC-3, ST512) and Greece (KPC-2, ST258), followed by an outbreak with an ST512 strain in Hospital A41. All isolates showed identical PFGE

### Table 3

<table>
<thead>
<tr>
<th>Strain number</th>
<th>Species</th>
<th>Beta-lactamase</th>
<th>MICs [mg/L]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>PIP</td>
<td>TZP</td>
</tr>
<tr>
<td>V554</td>
<td><em>K. pneumoniae</em></td>
<td></td>
<td></td>
</tr>
<tr>
<td>V624</td>
<td><em>K. pneumoniae</em></td>
<td>&gt;64</td>
<td>&gt;64</td>
</tr>
<tr>
<td>CONJ V624</td>
<td><em>Escherichia coli</em></td>
<td>&gt;64</td>
<td>&gt;64</td>
</tr>
<tr>
<td>V614</td>
<td><em>K. pneumoniae</em></td>
<td>&gt;64</td>
<td>&gt;64</td>
</tr>
<tr>
<td>V597</td>
<td><em>K. pneumoniae</em></td>
<td>&gt;64</td>
<td>&gt;64</td>
</tr>
<tr>
<td>TRAN V597</td>
<td><em>E. coli</em></td>
<td>&gt;64</td>
<td>&gt;64</td>
</tr>
<tr>
<td>V601</td>
<td><em>K. pneumoniae</em></td>
<td>&gt;64</td>
<td>&gt;64</td>
</tr>
</tbody>
</table>

AMK: amikacin; CAZ: ceftazidime; CHL: chloramphenicol; CIP: ciprofloxacin; CST: colistin; CTX: cefotaxime; FEP: cefepime; GEN: gentamicin; MEM: meropenem; MIC: minimum inhibitory concentration; PIP: piperacillin; SXT: trimethoprim/sulfamethoxazole; TZP: piperacillin with tazobactam.

a CONJ V624: transconjugant of the strain no V624.
b TRAN V597: transformant of V597.

As the MICs of isolates of the same clone were similar, we show in the Table only representative isolates of each clone and their transformant/transconjugant.
patterns and belonged to ST512, supporting the theory of an outbreak.

This ST is a single locus variant of a widely spread KPC-2-producing ST258 clone. ST512 was first reported from Israel among the isolates producing KPC-3 carbapenemase [28]. All KPC-producing isolates detected in this study were resistant to colistin. Resistance to this drug in KPC-producing *K. pneumoniae* isolates is being described more and more frequently [29,30]. Treatment options for infections caused by carbapenemase-producing *Enterobacteriaceae* are seriously limited until new classes of antibiotics are found; therefore it is necessary to understand the epidemiological principles of the spread of such bacteria and to set up efficient infection control measurements.

It can be assumed that the repatriated patients acquired the carbapenemase-producing *Enterobacteriaceae* in the foreign countries, since their transport was organised through specialised medical assistance and they were admitted to a Czech hospital without delay. Molecular typing data also confirm this theory. In all of the described patients, screening (such as rectal swab, sputum, urine, wound swab etc.) for identification of carbapenemase-producing *Enterobacteriaceae* was performed in the intensive care units abroad in a way corresponding to what is recommended in the national guidelines issued by the NRL for Antibiotics [31].

Until mid-2012, there was no official document in the Czech Republic on isolation precautions for patients colonised or infected by carbapenemase-producing *Enterobacteriaceae*. However, recommendations regarding diagnostic procedures, screening, and specific hygienic measurements were available from the NRL for Antibiotics [31]. Recently, an official guideline for the management of imported cases of carbapenemase-producing *Enterobacteriaceae* including infection control procedures has been approved and published through a bulletin of the Ministry of Health of the Czech Republic [32]. In this document, screening procedures on medical wards with confirmed occurrence of carbapenemase-producing *Enterobacteriaceae* are described in detail. The recommended screening is based on rectal swabs collected from patients hospitalised on the same ward or in possible contact with an infected or colonised patient. Other tissues sampled for standard screening in intensive care units (such as sputum, urine, different swabs) should also be tested for carbapenemase-producing *Enterobacteriaceae*. For patients with suspected or proven carbapenemase-producing *Enterobacteriaceae*, strict isolation procedures have to be set up.

In 2012 and 2013, there has not been a further increase in the occurrence of carbapenemase-producing *Enterobacteriaceae* in the Czech Republic, and only one outbreak (five patients) and four sporadic cases have been noted until mid-2013 (data not shown). An almost similar number of carbapenem-non-susceptible isolates has been sent for confirmation of carbapenemase production from routine laboratories in 2012 as in 2011. Only two imported cases of VIM-1-producing *K. pneumoniae* and NDM-4-producing *Enterobacter cloacae* have been detected [33]. This situation signals that the proposed preventive recommendations have been able to stabilise or even decrease the incidence of carbapenemase-producing *Enterobacteriaceae* in our country.

Czech participants of European Antimicrobial Resistance Surveillance Network in 2011

Vaclava Adamkova, First Faculty of Medicine and University Hospital, Charles University, Prague; Natasa Bartonikova, Bata’s Hospital, Zlin; Markyta Bartova, Thomayer’s Hospital, Prague; Eva Bendova, Third Faculty of Medicine and University Hospital in Kralovske Vinohrady, Charles University, Prague; Tamara Bergerova, Faculty of Medicine and University Hospital in Plzen, Charles University, Plzen; Zdena Bohunova, Hospital in Liberec, Liberec; Eva Capova, Hospital in Tabor, Tabor; Eva Chmelarova, Institute for Public Health in Ostrava, Ostrava; Marie Dovalova, Novy Jicin; Marian Glasnak, Rudolf’s and Stefanie’s Hospital in Benesov, Benesov; Marketa Hanslianova, University Hospital in Brno, Brno; Vera Haskova, Institute of Public Health in Kolín, Horovice; Blanka Heinigeova, Hospital in Jindrichuv Hradec, Jindrichuv Hradec; Magdalena Hornikova, Hospital
in Ceske Budejovice, Ceske Budejovice; Blanka Horova, Hospital in Bulovka, Prague; Jana Janeckova, Hospital in Litomyšl, Litomyšl; Petr Jezek, Hospital in Pribram, Pribram; Vlastimil Jindrak, Hospital Na Homolce, Prague; Milan Kolár, Faculty of Medicine and University Hospital, Palacky University, Olomouc; Lenka Kolarova, SYNLAB, Prague; Věra Kūrková, Hospital in Písek, Písek; Petr Linhart, Hospital in Havlíčkův Brod, Havlíčkův Brod; Helena Nedvědová, Hospital in Klatovy, Klatovy; Jana Niemczykova, Institute of Public Health in Ostrava, Havrivo; Otakar Nyc, Second Faculty of Medicine and University Hospital in Motol, Charles University, Prague; Vladimir Petkov, Institute for Clinical and Experimental Medicine, Prague; Zora Pokorna, BIOPLUS, Brno; Jan Pomykal, Hospital in Kolín, Kolín; Blanka Puchalkova, Hospital in Karlovy Vary, Karlovy Vary; Milošslava Rumlerova, Institute of Public Health in Kolín, Kolino; Lenka Ryskova, Faculty of Medicine and University Hospital in Hradec Kralove, Hradec Kralove; Josef Scharfen, Hospital in Trutnov, Trutnov; Anna Sekacova, Hospital in Vsetin, Vsetin; Helena Skacaniova, Hospital in Jihlava, Jihlava; Eva Simeckova, Hospital in Strakonice, Strakonice; Martina Sokolova, Hospital in Opava, Opava; Eva Stastna, Hospital in Praha, Praha; Alena Steinerova, Military Hospital Praha; Marta Stolbova, Masaryk’s Hospital, Usti nad Labem; Renata Tekjalova, Faculty of Medicine and University Hospital of St. Anna, Masaryk’s University, Brno; Ladislav Trojan, Hospital in Trebic, Trebic; Hana Typovska, P+R LAB, Sternberk; Eva Uhlirova, NsP, Uherske Hradiste; Eva Vesela, Hospital in Nachod, Nachod; Eva Zalabska, Hospital in Pardubice, Pardubice; Dana Zamazalova, Hospital in Nove Mesto Na Morave, Nove Mesto Na Morave; Robert Zaruba, Hospital in Most, Most;

Acknowledgements

This work was supported by the research project grants NT10326/2010 from the Ministry of Health of the Czech Republic and by the Charles University Research Fund (project number P36). C.C. Papagiannitsis was supported by the project: „Support of establishment, development, and mobility of quality research teams at the Charles University”, project number P36). C.C. Papagiannitsis was supported by the project: „Support of establishment, development, and mobility of quality research teams at the Charles University“, registration number CZ.1.07/2.3.00/30.0022, financed by The Education for Competitiveness Operational Programme (ECOP) funded by the ESF and the government budget of the Czech Republic. We thank platform Genotyping of Pathogens and Public Health (Institut Pasteur, Paris, France) for coding MLST alleles and profiles available at www.pasteur.fr/mlst.

Conflict of interest

None declared.

Authors’ contributions

J.Hrabak and C.C.Papagiannitsis performed molecular typing, and prepared the manuscript. V.Studentová was responsible for performing some typing methods. V.Jakubu, M.Fridrichova, H.Zemlickova collected the isolates and the data about the patients from local laboratories and performed phenotypic tests for the detection of resistance mechanisms and determined MICs.

References

PMid:21444429


15. Dianecourt L, Passet V, Verhoel I, Grimaud PA, Brisse S. Multilocus sequence typing of Klebsiella pneumoniae

www.eurosurveillance.org