Persistence of *Klebsiella pneumoniae* ST258 as the predominant clone of carbapenemase-producing Enterobacteriaceae in post-acute-care hospitals in Israel, 2008–13

Amos Adler, Omar Hussein, Debby Ben-David, Samira Masarwa, Shiri Navon-Venezia, Mitchell J. Schwaber and Yehuda Carmeli
National Center of Infection Control, Tel-Aviv, Israel

INTRODUCTION

In addition to carbapenemase-producing Enterobacteriaceae (CPE) spread in acute-care hospitals, an important component of the epidemiology of the Israeli outbreak has been the dissemination into post-acute-care hospitals (PACHs). There is ongoing bidirectional patient movement between these institutions and acute-care hospitals, and as such they have become a reservoir of CPE carriage.

As part of the Israeli national intervention to contain the spread of CPE in healthcare facilities, an initiative has been implemented in PACHs, with the goals of improving infection control practices overall and, specifically, reducing the prevalence of CPE. As a result of this program, the prevalence of CPE in PACHs decreased from 16.8% in 2008 to 12.5% in 2011.

In this study, our aim was to examine the molecular characteristics of carbapenemase-producing Enterobacteriaceae (CPE) in post-acute-care hospitals (PACHs) in Israel and to analyze the temporal changes between 2008 and 2013.

METHOD

Study design and settings

National retrospective study of CPE isolated in PACHs in Israel. Two cross-sectional prevalence surveys performed by the National Center for Infection Control (NCIC), from November 2008 to January 2009 (12 centrs) and from June 2013 to January 2014 (14 centrs).

Detection and identification of CPE

Surveillance cultures were collected by streaking rectal swabs onto selective media. Isolates were identified to species level and tested for *bla*KPC, *bla*NDM and *bla*OXA-48 by PCR and by the Carba-NP test.

Genotyping of KPC-KP isolates

Molecular typing was done by PCR for the pilv-l gene, designed for the ST258 KPC-producing *Klebsiella pneumoniae* (KPC-KP) clone. Isolates negative by pilv-l PCR were analyzed by BOX-PCR. Representative isolates of each BOX-PCR type were subjected to MLST for definitive genotyping.

RESULTS

Molecular epidemiology of CPEs in Israeli PACHs in the two surveys

- The prevalence of CPE carriage in the first survey was 184/1,147 (16 %) all isolates KPC-KP. The prevalence of CPE carriage in the second survey was substantially lower, 127/1,287 (9.9%); of these isolates 113 (89%) were KPC-KP, 9 (7%) were other KPC-producing species, and 5 (4%) were NDM- and OXA-48-producing CPE (n=1 and 4, respectively) (table 1).

- The proportion of the KPC-KP population represented by the ST-258 clone increased from 120/184 (65%) in 2008 to 91/113 (80%) in 2013.

- The second most prevalent KPC-KP clone was ST-340, co-existed with ST258 , its prevalence decreased significantly, from 41/184 (22.3%) in 2008 to 9/113 (7.9%) in 2013 (p=0.001).

- All pilv-l-negative KPC-KP isolates were from clones other than ST-258, except for 8 isolates that were positive on prp-PCR testing.

Sources of CPE acquisition, 2013 survey

- In 68% (83/122) of the KPC-CPE carriers identified in the 2013 survey, the source of acquisition was determined to be the PACH itself.

- All 4 OXA-48 CPE's were acquired either directly or indirectly from patients arriving from the Palestinian Authority or Syria.

- The single NDM-producing K. pneumoniae isolate was presumably acquired at PACH C, were NDM-producing CPE have been previously reported.

Table 1: Clonal structure of KPC-KP and other CPE isolates in Israeli PACHs, 2008–13

PACH	Year of Survey				
	2008		2013		
	KPC-producing *K. pneumoniae*		KPC-producing *K. pneumoniae*		Other CPE[b] (n)
	ST[a]-258, no.	Other STs, no	ST-258, no.	Other STs, no	
A	9	ST-340, 18	12	0	0
B	7	ST-236, 1	1	ST-147, 1	0
C	16	ST-45, 9	7	0	NDM-*K. pneumoniae* (1)
D	28	ST-1119, 1	2	ST-485, 1 ST-340, 1	0
E	7	0	9	ST-1077, 4 ST-784, 1	KPC-*K. oxytoca* (1) KPC-*Citrobacter freundii* (2)
F	8	ST-340, 2	2	ST-340, 4	0
G	6		4	0	KPC-*E. coli* (1)
H	0	ST-340, 13 ST-534, 1	14	ST-1520, 1 ST-340, 5 Unknown[c], 2	OXA-48-*K. pneumoniae* (3)
I	11	ST-16, 10	15	ST-37, 1	KPC-*E. coli* (1)
J	11	ST-340, 8	2	0	0
K	6	ST-37, 1	0		
L	11	0	9	0	KPC-*Enterobacter cloacae* (1)
M	NI[d]		9	ST-983, 1	KPC-*K. oxytoca* (1) OXA-48-*K. oxytoca* (1)
N	NI[d]		5	0	KPC-*Enterobacter* spp. (1) KPC-*K. oxytoca* (1)
Total	120	64	91	22	14

CONCLUTIONS

In this study we outline the first systematic national survey of the clonal structure of CPE, and a unique overview of the changes that have occurred in the PACH system between 2008 and 2013.

The study provides further evidence for the predominance of ST258 KPC-KP among CPE, and illustrates the similarity in clonal structure of KPC-KP in acute-care centrs and PACHs in Israel.