

**US states with SMART sites**

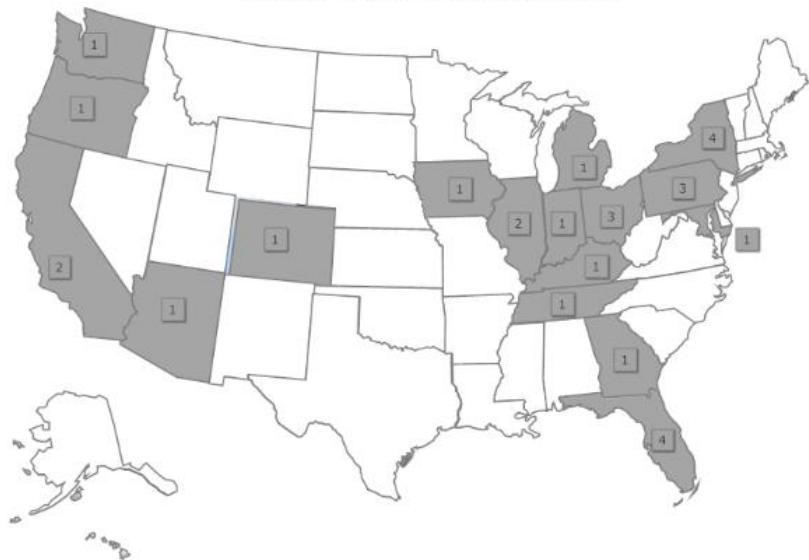


Figure S1. States with hospitals that participated in SMART between 2009 and 2013. Number of sites in each state are shown in the label.

Supplementary data.

Genomic DNA was extracted from overnight colonies grown on blood agar (Remel, Lenexa, KS) using the QIAamp DNA Mini Kit and the QIAcube instrument (Qiagen, Valencia, CA) according to the manufacturer's instructions. Genes encoding  $\beta$ -lactamases (*bla*) were detected using five separate multiplex PCR reactions: (1) *bla<sub>TEM</sub>*, *bla<sub>SHV</sub>*, *bla<sub>VEB</sub>*, *bla<sub>PER</sub>*, *bla<sub>GES</sub>*, and *bla<sub>SPM</sub>*; (2) *bla<sub>IMP</sub>*, *bla<sub>VIM</sub>*, *bla<sub>OXA-48</sub>*, *bla<sub>NDM</sub>*, and *bla<sub>KPC</sub>*; (3) *bla<sub>ACC</sub>*, *bla<sub>ACT</sub>*, *bla<sub>MIR</sub>*, *bla<sub>CMY</sub>*, *bla<sub>MOX</sub>*, *bla<sub>DHA</sub>*, and *bla<sub>FOX</sub>*; (4) *bla<sub>CTX-M-1</sub>*, *bla<sub>CTX-M-2</sub>*, and *bla<sub>CTX-M-9</sub>*; (5) *bla<sub>CTX-M-8</sub>* and *bla<sub>CTX-M-25</sub>*. Multiplex PCR reactions to detect all genes but *bla<sub>CTX-M-8</sub>* and *bla<sub>CTX-M-25</sub>* were performed using the Multiplex PCR kit (Qiagen), whereas the CTX-M-8/25 reaction was performed using the Fast Cycling PCR kit (Qiagen). All reactions were performed per the manufacturer's instructions using primers listed in Table S1. All genes were amplified for sequencing using the Fast Cycling PCR kit (Qiagen) per the manufacturer's instructions using primers listed in Table S1. Sanger sequencing of PCR amplicon was performed at ACGT, Inc. (Wheeling, IL). Sequence data was analyzed using SeqScape v.2.7 (Applied Biosystems) and compared to sequences available from the National Center for Biotechnology Information ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)) and the Lahey Clinic ([www.lahey.org](http://www.lahey.org)).

*bla<sub>SHV</sub>* and *bla<sub>TEM</sub>* encoding SHV-type and TEM-type enzymes containing amino acid substitutions common to ESBLs (SHV G238S, G238A, E240K; TEM E104K, R164S, R164C, R164H, G238S) were identified by limited sequencing or by using the Check-MDR CT101 microarray (Check-Points B.V., Wageningen, the Netherlands). Full sequence was obtained only for *bla<sub>SHV</sub>* or *bla<sub>TEM</sub>* containing substitutions common to ESBLs. All other *bla* genes were sequenced in their entirety.

**Table S1. Primers used for multiplex PCR, gene amplification, and sequencing**

Primer	Sequence (5' - 3')	Reference
<b>For <i>bla</i> gene detection by multiplex PCR</b>		
ACC-MF	AACAGCCTCAGCAGCCGGTTA	Perez-Perez and Hanson, 2002 (1)
ACC-MR	TTCGCCGCAATCATCCCTAGC	Perez-Perez and Hanson, 2002 (1)
CIT-MF (CMY-II)	TGGCCAGAACTGACAGGGAAA	Perez-Perez and Hanson, 2002 (1)
CIT-MR (CMY-II)	TTTCTCCTGAACGTGGCTGGC	Perez-Perez and Hanson, 2002 (1)
CTX-M1-F2	AAAAATCACTGCGCCAGTTC	Woodford <i>et al</i> , 2006 (2)
CTX-M1-R2	AGCTTATTCACTGCCACGTT	Woodford <i>et al</i> , 2006 (2)
CTX-M2-F2	CGACGCTACCCCTGCTATT	Woodford <i>et al</i> , 2006 (2)

<b>Primer</b>	<b>Sequence (5'- 3')</b>	<b>Reference</b>
CTX-M2-R2	CCAGCGTCAGATTTTCAGG	Woodford <i>et al</i> , 2006 (2)
CTX-M8-A	TCGCGTTAACGGATGATGC	Woodford <i>et al</i> , 2006 (2)
CTX-M25-A	GCACGATGACATTGGGG	Woodford <i>et al</i> , 2006 (2)
CTX-M8/25-B	AACCCACGATGTGGGTAGC	Woodford <i>et al</i> , 2006 (2)
CTX-M9-F2	CAAAGAGAGTGCAACGGATG	Woodford <i>et al</i> , 2006 (2)
CTX-M9-R2	ATTGGAAAGCGTTCATCAC	Woodford <i>et al</i> , 2006 (2)
DHA-MF	AACTTCACAGGTGTGCTGGGT	Perez-Perez and Hanson, 2002 (1)
DHA-MR	CCGTACGCATACTGGCTTGC	Perez-Perez and Hanson, 2002 (1)
EBC-MF (ACT/ MIR)	TCGGTAAGCCGATGTTGCGG	Perez-Perez and Hanson, 2002 (1)
EBC-MR (ACT/ MIR)	CTTCCACTGCGGCTGCCAGTT	Perez-Perez and Hanson, 2002 (1)
FOX-MF	AACATGGGGTATCAGGGAGATG	Perez-Perez and Hanson, 2002 (1)
FOX-MR	CAAAGCGCGTAACCGGATTGG	Perez-Perez and Hanson, 2002 (1)
GES-F	AGTCGGCTAGACCGGAAAG	Dallenne <i>et al</i> , 2010 (3)
GES-R	TTTGTCCGTGCTCAGGAT	Dallenne <i>et al</i> , 2010 (3)
IMP2-F	GGAATAGAGTGGCTTAAYTCTC	Poirel <i>et al</i> , 2011 (4)
IMP2-R2	GGTTAAYAAAACAACCACC	Poirel <i>et al</i> , 2011 (4)
KPCy-F	TGTCACTGTATGCCGTC	Yigit <i>et al</i> , 2001 (5)
KPCy-R	CTCAGTGCTCTACAGAAAACC	Yigit <i>et al</i> , 2001 (5)
MOX-MF	GCTGCTCAAGGAGCACAGGAT	Perez-Perez and Hanson, 2002 (1)
MOX-MR	CACATTGACATAGGTGTGGTGC	Perez-Perez and Hanson, 2002 (1)
NDM-F	CCGTATGAGTGATTGCGGCG	Lascols <i>et al</i> , 2011 (6)
NDM-R	GCCCAATATTATGCACCCGG	Lascols <i>et al</i> , 2011 (6)
OXA-48-F	GCTTGATGCCCTCGATT	Dallenne <i>et al</i> , 2010 (3)
OXA-48-R	GATTGCTCCGTGGCCGAAA	Dallenne <i>et al</i> , 2010 (3)
PER-F	GCTCCGATAATGAAAGCGT	Dallenne <i>et al</i> , 2010 (3)
PER-R	TTCGGCTTGACTCGGCTGA	Dallenne <i>et al</i> , 2010 (3)
SHV-5	CCTTAAAGTAGTGCTCTGC	This study
SHV-6	TTCGCTGACCGGCGAGTAGT	This study
SPM-F	AAAATCTGGGTACGCAAACG	Ellington <i>et al</i> , 2007 (7)
SPM-R	ACATTATCCGCTGGAACAGG	Ellington <i>et al</i> , 2007 (7)
TEM-3	CATTCCGTGTCGCCCTTATT	Dallenne <i>et al</i> , 2010 (3)
TEM-4	CGTTCATCCATAGTTGCCTGAC	Dallenne <i>et al</i> , 2010 (3)
VEB-F	CATTCCCGATGCAAAGCGT	Dallenne <i>et al</i> , 2010 (3)
VEB-R	CGAAGTTCTTGGACTCTG	Dallenne <i>et al</i> , 2010 (3)
VIM-F	GATGGTGTGGTCGCATA	Ellington <i>et al</i> , 2007 (7)
VIM-R	CGAATGCGCAGCACCAAG	Ellington <i>et al</i> , 2007 (7)
<b>For bla gene amplification and sequencing</b>		
CMY2-seqF	ATGATGAAAAAATCGTTATGCTGCGC	This study
CMY2-seqR	TTATTGCGAGCTTTCAAGAATGCGC	This study
CMY2int-seqF	GCAATGACCAGACGCGTC	This study
CMY2int-seqR	GACCGTCTGGTCATTGC	This study
CTX-M1c-F	GAATTCATGTTGTTATTTC	Mena <i>et al</i> , 2006 (8)
CTX-M1c-R	TTACAAACCGTTGGTGACG	Mena <i>et al</i> , 2006 (8)
CTX-M1-R2	AGCTTATTCATGCCACGTT	Woodford <i>et al</i> , 2006 (2)
CTX-M-1int Fseq	GACAGCTGGAGACGAAACGTTC	This study

<b>Primer</b>	<b>Sequence (5'- 3')</b>	<b>Reference</b>
KPCy-F	TGTCACTGTATGCCGTC	Yigit <i>et al</i> , 2001 (5)
KPCy-R	CTCAGTGCTCTACAGAAAACC	Yigit <i>et al</i> , 2001 (5)
KPCint-Fseq	CGCCAATTGTTGCTGAAGGAG	This study
KPCint-Rseq	ACGTGGTATGCCGATAGAGC	This study
SHV-seqF2	ATGCGTTATTCGCCTGTGT	This study
SHV-seqR	TTAGCGTTGCCAGTGCTCG	This study
SHVint-seqF	GATCGGCGACAACGTCAC	This study
SHVint-seqR	GTGACGTTGTCGCCGATC	This study
TEM-3	CATTCCGTGTCGCCCTATT	Dallenne <i>et al</i> , 2010 (3)
TEM2-extended	TTACCAATGCTTAATCAGTGAGG	This study
TEMint-seqF	GTGCTGCCATAACCATGAGTG	This study
TEMint-seqR	CACTCATGGTTATGGCAGCAC	This study

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