

Detection of *bla*_{SPM-1} and *bla*_{SIM-2} Metallo- β -Lactamases Genes in Imipenem-Resistant *Pseudomonas aeruginosa* Clinical Isolates Recovered from Two University Hospitals in Egypt

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Supplementary Data

Table S1. Alignment of the nucleotide sequences of SIM gene detected in one *P. aeruginosa* clinical isolate and another published sequence.

Our seq1 KX 452682	TACAAGGGATTTCGGCATCGTTAAAAACAAGGCTTAGTAGTTCTTGACAATCACAAGGCA
KT013203 (China)	-----
Our seq1 KX 452682	TATCTCATCGACACTCCAGCTTCCGCAGGAGATACTGAAAAGCTAGTAAACTGGCTCGAA
KT013203 (China)	-----
Our seq1 KX 452682	AAAAATGATTTCACTGTCAATGGAAGCATTCAACACATTCCACGACGACAGTACTGCT
KT013203 (China)	-----
Our seq1 KX 452682	GGGATAGAGTGGCTTAATACAAAGTCCATCCCCACATATGCATCTAAATTGACAAATGAA
KT013203 (China)	-----
Our seq1 KX 452682	TTGCTAAATAAAAATGGCAAACTCAAGCCAAGCACTCTTTTGATAAAGAGAGCTTTTGG
KT013203 (China)	-----
Our seq1 KX 452682	TTGGTCAAAAATAAAAATTGAAATTTTTATCCAGGCCAGGACACACTCAAGATAACGAA
KT013203 (China)	-----
Our seq1 KX 452682	GTTGTCTGGATACCTAATAAAAAAATCCTATTCGGGGGCTGTTTTATAAAACCGAATGGC
KT013203 (China)	-----
Our seq1 KX 452682	CTTGGCAATCTAAGTGACGCAAATTTGGAAGCTTGCCAGACTCCGCAAAAAAATGATA
KT013203 (China)	-----
Our seq1 KX 452682	TCAAATACAGTAAGGCAAACTTGTTATCCCAAGCCACAGTGAAATCGGAGACGCATCA
KT013203 (China)	-----
Our seq1 KX 452682	CTATTGAAACTCACATGGGAACAGGCCATTA
Our seq2	-----
Our seq3	-----
KT013203 (China)	-----

Table S2. Alignment of the nucleotide sequences of SPM gene among three *P. aeruginosa* isolates and other published sequences.

Our seq1 KX 452683	AAAATCTGGGTACGCAAACGCTTATGGATTGGGTGGCTAAGACTATGAAGCCGAAGAAAG
Our seq2 KX 452683	-----
Our seq3 KX 452683	-----
AJ492820 (UK)	-----
KT454971 (Brazil)	-----
Our seq1 KX 452683	TAGTAGCCATCAATACGCACTTTCATTTGGACGGCACGGGTGGAAATGAAATTTACAAGA
Our seq2 KX 452683	-----
Our seq3 KX 452683	-----
AJ492820 (UK)	-----
KT454971 (Brazil)	-----
Our seq1 KX 452683	AGATGGGCGCGGAGACGTGGTTCGAGCGATCTGACAAAGCAGTTGCGACTTGAGGAAAACA
Our seq2 KX 452683	-----
Our seq3 KX 452683	-----
AJ492820 (UK)	-----
KT454971 (Brazil)	-----
Our seq1 KX 452683	AGAAAGACCGGATAAAAGCAGCTGAGTTCTATAAAAACGAGGATCTGAAGCGAAGGATTC
Our seq2	-----

KX 452683	
Our seq3	-----
KX 452683	
AJ492820 (UK)	-----
KT454971 (Brazil)	-----
Our seq1	TGAGTTCCCATCCTGTTCCAGCGGATAATGT
KX 452683	
Our seq2	-----
KX 452683	
Our seq3	-----
KX 452683	
AJ492820 (UK)	-----
KT454971 (Brazil)	-----

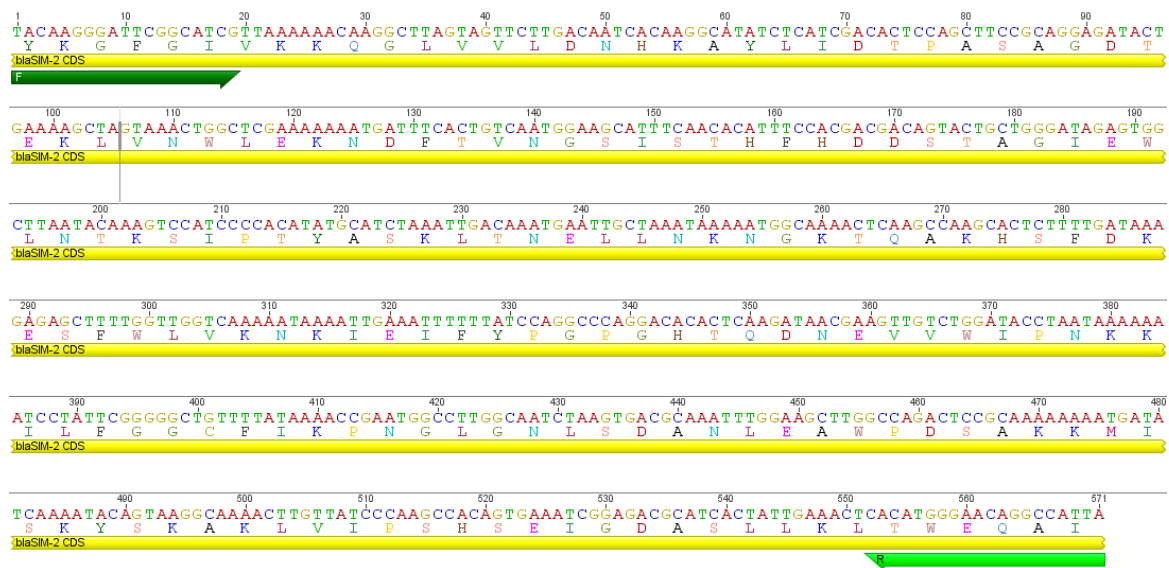


Figure S1. A representative nucleotide and protein sequence of bla_{SIM} gene from *P. aeruginosa* isolates. The dark and light green arrows refer to forward and reverse primers sequences, respectively.

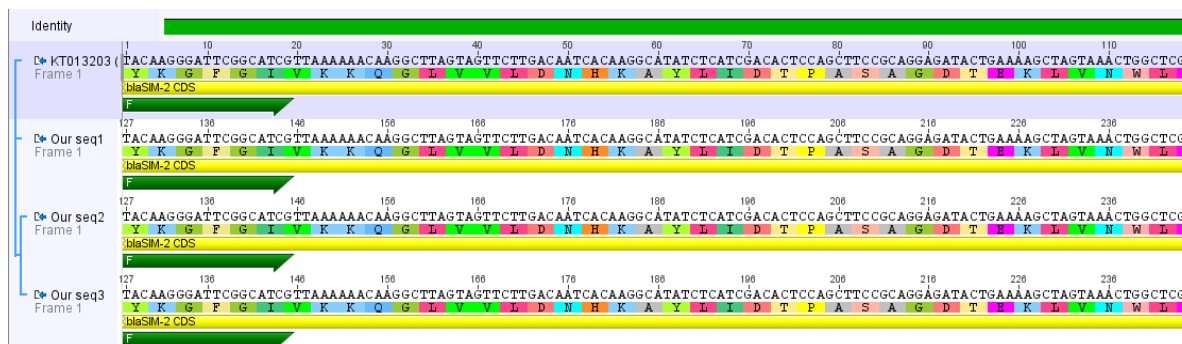


Figure S2. Alignment of the nucleotide sequences of *bla_{SPM}* gene among three *P. aeruginosa* isolates and other published sequences (software format).

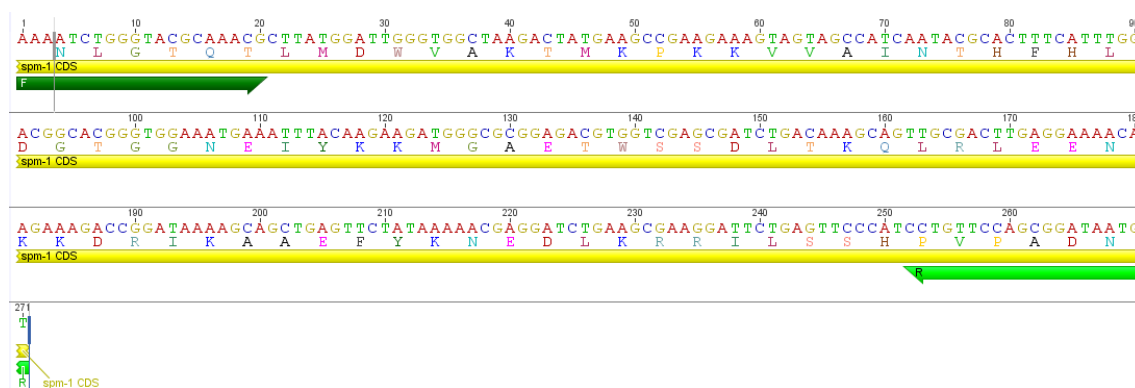


Figure S3. A representative nucleotide and protein sequence of *bla_{SPM}* gene from *P. aeruginosa* isolates. The dark and light green arrows refer to forward and reverse primers sequences, respectively.

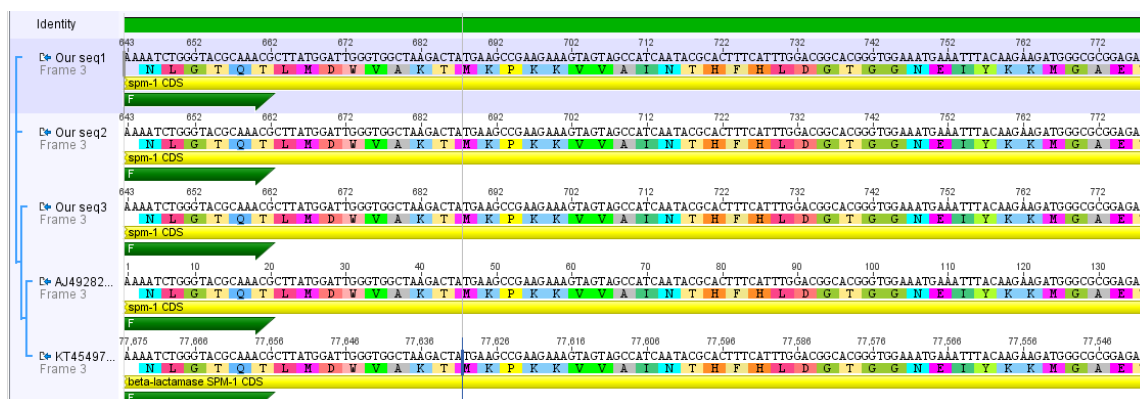


Figure S4. Alignment of the nucleotide sequences of *bla_{SPM}* gene among three *P. aeruginosa* isolates and other published sequences (software format).