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Usefulness of a PCR Assay for the Identification of the *Klebsiella pneumoniae* ST258 Epidemic Clone in Latin American Clinical Isolates

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Abstract:
BACKGROUND: The worldwide dissemination of ST258 of *Klebsiellapneumoniae* (KP)-KPC producers encouraged investigators to develop a rapid typing method based on the identification of ST258 unique gene *pilv-I*, and phage related protein (*prp)* which is neither specific nor ubiquitous of ST258 *(*Adle*r et. al. DMID 2014, 78:12-15)*. Prompt identification of ST is invaluable for some Latin American (LA) countries where this clone has become endemic.**OBJECTIVES:** to evaluate a PCR developed for ST258 in KP-KPC clinical isolates from LA.**METHODS:** KPC, pilv-I and prp genes were detected by PCR and sequenced following standard procedures. Specific primers were used to detect the 3´end of PilV-like gene which is highly specific of ST258 (product size 320 bp) and *prp* gene (product size 544 bp). ST258 and non-ST258 were defined by Xba-I-PFGE and MLST. A total of 107 KP clinical isolates from 9 LA countries recovered from 2006 to 2015 where tested, of which 44 were ST258 and 63 non-ST258. **RESULTS:** The *pilv-I* gene was present only in ST258 isolates regardless of the presence of KPC (positive predictive value 100%). All *pilvI* negative isolates were non-ST258 (negative predictive value 100%). *prp* results were variable. Remarkably, four ST258 isolates were positive for *pilv-I*, negative for KPC and carried CTX-M (n=3) or NDM (n=1). **CONCLUSIONS:**The evaluation of a specific PCR for ST258 unique gene that could replace time and resource consuming methods (MLST and PFGE) was successful for the LA isolates tested. In our setting,*pilv-I* detection is enough to discriminate ST258 from other STs.

K. pneumoniae	KPC	n	*pilvI+/prp+*	*pilvI+/prp-*	*pilvI-/prp+*	*pilvI-/prp-*
ST258 n=44	+	40	16	24	0	0
	-	4	3	1	0	0
non-ST258 n=63	+	40	0	0	6	34
	-	23	0	0	1	22

Acknowledgments/ References:
Reference: Adle*r et. al. DMID 2014, 78:12-15*