

# National Surveillance of Legionnaires' Disease, China, 2014–2016

## Appendix

**Appendix Table 1.** MICs results for 7 *Legionella pneumophila* strains, China, 2014–2016\*

Strain ID	Antimicrobial drug, susceptible MIC, mg/dL							
	CIP, $\leq 2.0$	LVX, $\leq 1.0$	MXE, $\leq 1.0$	ERY, $\leq 0.5$	AZM, $\leq 1.0$	CLR, $\leq 0.5$	RIF, $\leq 0.032$	CXM, $\leq 1.0$
CNLP001	0.125	0.094	0.38	0.094	0.094	0.125	0.016	3
CNLP002	0.125	0.094	0.25	0.094	0.032	0.25	0.012	4
CNLP003	0.5	0.094	0.38	0.094	0.047	0.125	0.032	1.5
CNLP004	0.125	0.064	0.38	0.064	0.047	0.25	0.032	8
CNLP005	0.25	0.094	0.38	0.064	0.032	0.125	0.023	2
CNLP006	0.25	0.125	1	0.064	0.094	0.25	0.002	2
CNLP007	0.25	0.125	0.38	0.125	0.094	0.125	0.023	3

\* The MIC values with bold font are greater than the cutoff values of the specific antimicrobial agent. The MICs with normal fonts are  $\leq$  the cutoff values of the specific antimicrobial agent. AZM, azithromycin; CIP, ciprofloxacin; CLR, clarithromycin; CXM, cefuroxime; ERY, erythromycin; LVX, levofloxacin; MCE, moxifloxacin; RIF, rifampin.

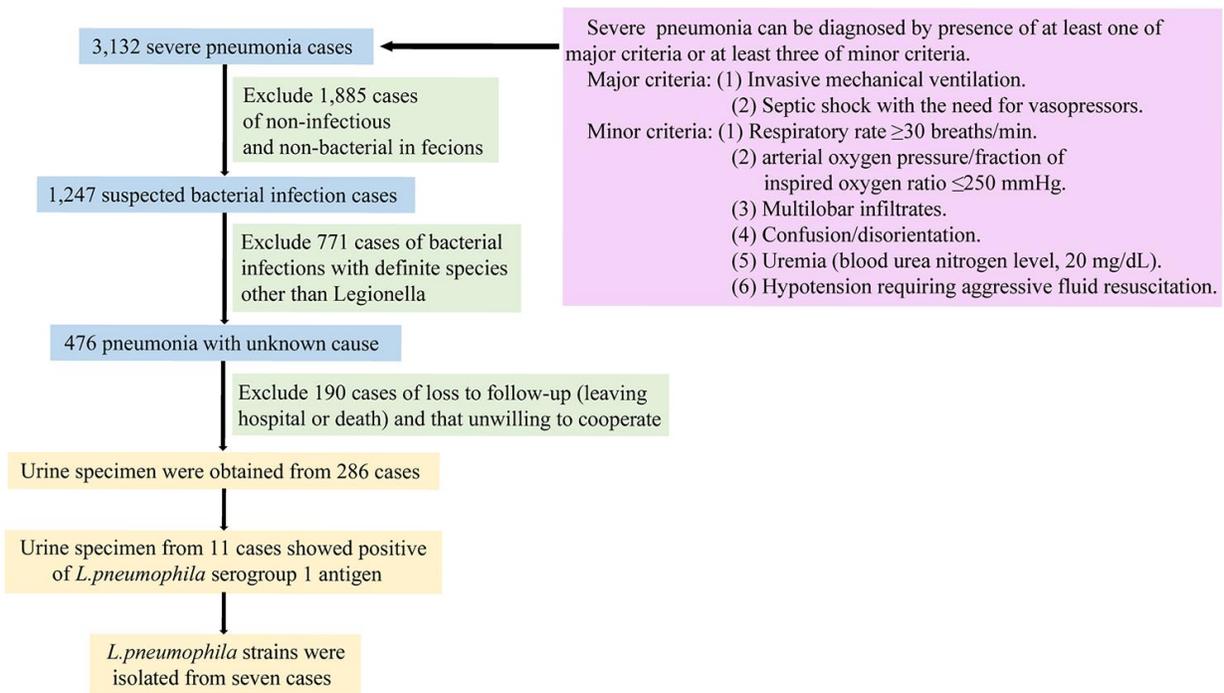
**Appendix Table 2.** Number, sources, regional distribution, and year distribution of strains of STs determined in this study in the *Legionella pneumophila* SBT database

ST	No. strains in SBT database			Regional distribution	Year distribution
	Total	Clinical	Environmental		
ST-42*	324	269	52	30 countries	1982–2017
ST-59	134	73	61	17 countries	1982–2016
ST-742	3	2	1	2 countries	2009, 2013
ST-2344	1	1	0	1 country	2014
ST-2366	1	1	0	1 country	2016
ST-2368	1	1	0	1 country	2016
ST-2369	1	1	0	1 country	2015

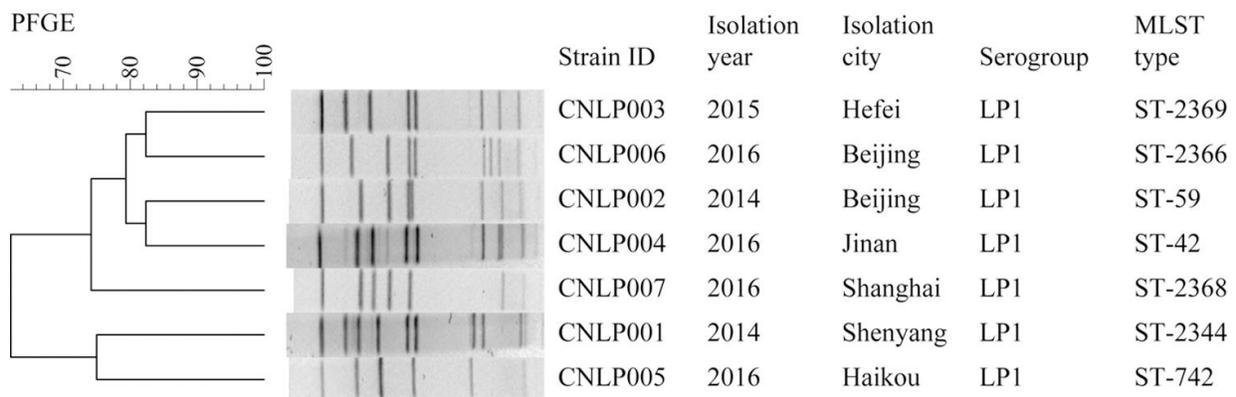
\*In the database, the sources of three ST-42 strains were unknown. SBT, sequence-based typing; ST, sequence type.



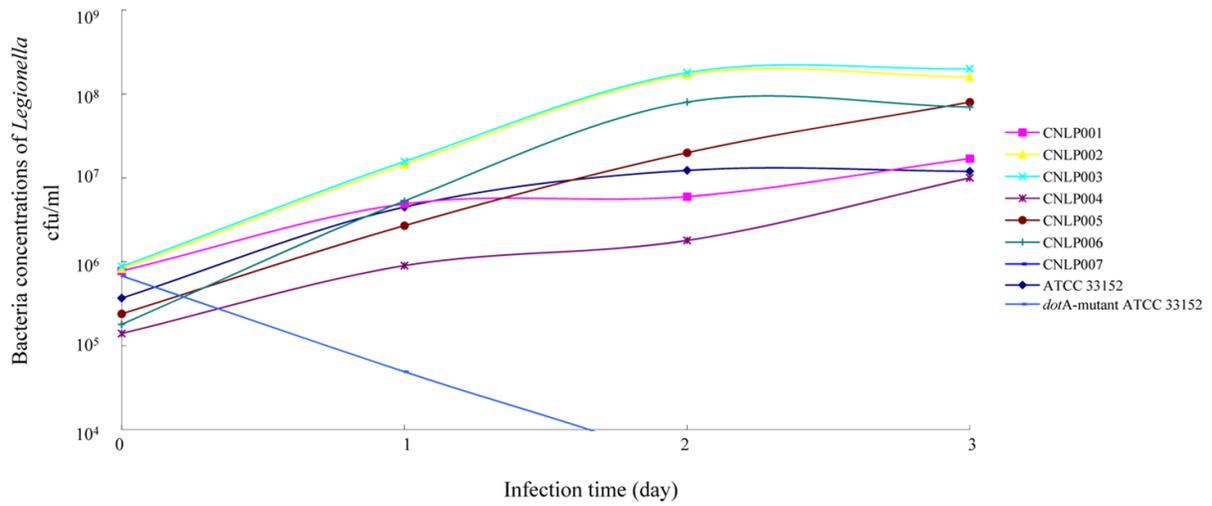
**Appendix Figure 1.** Geographic distribution of 18 hospitals (1 hospital was chosen in each city) in the national survey of *Legionella pneumophila* infections, China, 2014–2016.



**Appendix Figure 2.** Screening procedure for Legionnaires' disease in the national surveillance in 18 hospitalsChina, 2014–2016.



**Appendix Figure 3.** Clustering of the 7 clinical *Legionella pneumophila* strains based on pulsed-field gel electrophoresis patterns. The strain ID, isolation year, isolation city, serogroup, and multilocus sequence typing type of each isolate are listed to the right of the patterns.



**Appendix Figure 4.** Intracellular growth ability of 7 clinical *Legionella pneumophila* strains China, 2014–2016. The formation of colonies (colony-forming units/mL) was determined in triplicate at the times indicated, and the representative data of at least 4 independent experiments are shown. The *L. pneumophila* philadelphia-1 strain ATCC33152 and its *dotA* mutant were used as positive and negative controls, respectively.