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**Title:** The mutation characteristics of the bla<sub>CTX-M/SHV/TEM</sub>-producing *Klebsiella pneumoniae* clinical isolates in multicenter in China

Shuchang 11447 An anshuchang@sohu.com MD<sup>1</sup>, Jichao 11448 Chen chen\_htzxy@sina.com MD<sup>2</sup>, Zhanwei 11478 Wang wangzhanwei@sina.com<sup>3</sup>, Xiaorong 11488 Wang rong-100@163.com MD<sup>1</sup>, Xixin 11489 Yan yanxixin@hotmail.com MD<sup>4</sup>, Jihong 11498 Li 952224925@qq.com<sup>5</sup>, Yusheng 11501 Chen chenyushengfj@yaho.com.cn MD<sup>6</sup>, Jingping 11511 Yang yangjingping@sina.com MD<sup>7</sup>, Xiaoling 11524 Xu xxlahh08@163.com MD<sup>8</sup>, Jiabin 11535 Li lijabin948@vip.sohu.com MD<sup>9</sup>, Qi 11548 Wang wqdmu@yahoo.com.cn MD<sup>10</sup>, Hui 11555 Wang whuibj@gmail.com MD<sup>3</sup> and Zhancheng 11566 Gao zcgao@bjmu.edu.cn MD<sup>1</sup>. <sup>1</sup> Department of Respiratory and Critical Care Medicine, Peking University People's Hospital, Beijing, China ; <sup>2</sup> Department of Respiratory Medicine, The Central Hospital of China Aerospace Corporation, Beijing, China ; <sup>3</sup> Department of Clinical Laboratory, Peking University People's Hospital, Beijing, China ; <sup>4</sup> Department of Respiratory Medicine, The Second Hospital of Hebei Medical University, Shijiazhuang, China ; <sup>5</sup> Department of Clinical Laboratory, The Second Hospital of Hebei Medical University, Shijiazhuang, China ; <sup>6</sup> Department of Respiratory Medicine, Fujian Province Hospital, Fuzhou, China ; <sup>7</sup> Department of Respiratory Medicine, The Third Affiliated Hospital of the Inner Mongolia Medical College, Baotou, China ; <sup>8</sup> Department of Respiratory Medicine, Anhui Province Hospital, Hefei, China ; <sup>9</sup> Department of Infectious Diseases, The First Affiliated Hospital of Anhui Medical University, Hefei, China and <sup>10</sup> Department of Respiratory Medicine, The Second Affiliated Hospital of Dalian Medical University, Dalian, China .

**Body:** Objectives Due to the prevalence of CTX-M- and SHV-type extended-spectrum  $\beta$ -lactamase (ESBL)-producing Enterobacteriaceae in China, the base mutation characteristics of bla<sub>CTX-M/SHV/TEM</sub>-producing *Klebsiella pneumoniae* were investigated. Methods From February 2010 to July 2011, 158 *K. pneumoniae* isolates from lower respiratory tract infection patients with positive double-disk synergy tests were collected from Beijing (69), Fujian (27), Anhui (22), Hebei (15), Liaoning (14), and Inner Mongolia (11). Ninety percent isolates were collected from common wards more than 48h after hospitalization. The bla<sub>CTX-M/SHV/TEM</sub> genes were examined by PCR and sequencing. The nucleotide sequences were analysed via BLAST program. Results In total, 138 bla<sub>CTX-M</sub> were detected, including 78 bla<sub>CTX-M-14</sub>, 19 bla<sub>CTX-M-15</sub>, 17 bla<sub>CTX-M-27</sub>, 12 bla<sub>CTX-M-3</sub>, 4 bla<sub>CTX-M-55</sub>, 2 bla<sub>CTX-M-65</sub>, 2 bla<sub>CTX-M-24</sub>, 2 bla<sub>CTX-M-24a</sub>, 1 bla<sub>CTX-M-38</sub>, and 1 bla<sub>CTX-M-98</sub>. 120 bla<sub>SHV</sub> were detected, including 45 bla<sub>SHV-11</sub>, 23 bla<sub>SHV-1</sub>, 15 bla<sub>SHV-12</sub>, 7 bla<sub>SHV-5</sub>, 5 bla<sub>SHV-108</sub>, 4 bla<sub>SHV-28</sub>, 3 bla<sub>SHV-36</sub>, 3 bla<sub>SHV2a</sub>, 2 bla<sub>SHV-2</sub>, 2 bla<sub>SHV-27</sub>, 2 bla<sub>SHV-142</sub>, 1 bla<sub>SHV-1a</sub>, 1 bla<sub>SHV-26</sub>, 1 bla<sub>SHV-32</sub>, 1 bla<sub>SHV-33</sub>, 1 bla<sub>SHV-38</sub>, 1 bla<sub>SHV-60</sub>, 1 bla<sub>SHV-103</sub>, 1 bla<sub>LEN</sub>, and 1 bla<sub>LEN-22</sub>. Also, 91 bla<sub>TEM-1</sub> and 1 bla<sub>TEM-135</sub> were detected. 8 bla<sub>SHV</sub> and 1 bla<sub>TEM-135</sub> with the silent base mutations were detected, and none of the bla<sub>CTX-M</sub>.

**Conclusions** The CTX-M-14, CTX-M-15, and CTX-M-27 were predominant ESBL genes in *K. pneumoniae* in China. The diversity of bla<sub>SHV</sub> and bla<sub>CTX-M</sub>, most silent mutations in bla<sub>SHV</sub>, and only missense mutations in bla<sub>CTX-M</sub> may be of significance contributing to epidemiological and clinical challenges.