

# 6<sup>th</sup> Euro Virology Congress and Expo

March 10-12, 2016 Madrid, Spain

## Hepatitis C virus subtype distribution and evolution characteristic among drug users, men who have sex with men and the general population in Beijing

Liyang Ma<sup>1</sup>, Xiaoxi Zhang<sup>4</sup>, Yang Jiao<sup>1,2</sup>, Chen Wang<sup>2</sup>, Shuming Li<sup>2</sup>, Li Li<sup>2</sup>, Jie Liu<sup>2</sup>, Katharine J Bar<sup>3</sup>, Huamian Wei<sup>1</sup>, Yao Hu<sup>2</sup>, Ping Huang<sup>2</sup>, Zhaoli Zeng<sup>2</sup>, Shulin Jiang<sup>2</sup>, Jialiang Du<sup>4</sup>, David Metzger<sup>3</sup> and Yiming Shao<sup>1</sup>

<sup>1</sup>National Center for AIDS/STD Control and Prevention, China

<sup>2</sup>Beijing Chaoyang District Centre for Disease Control and Prevention, China

<sup>3</sup>University of Pennsylvania, USA

<sup>4</sup>National Institutes for Food and Drug Control, China

Hepatitis C Virus (HCV) is a rapidly evolving pandemic disease that has increasing importance in China. To characterize the current molecular epidemiology of HCV infection in Beijing, China, whole blood samples and behavioral data were collected from a total of 10,354 subjects, including DUs, MSM and general population, in Beijing from 2010 to 2011. Samples were tested for HCV infection using ELISA and real-time PCR. In total, 217 subjects (2.1%) tested positive for HCV by antibody or vRNA-based testing. HCV prevalence rates for DUs, MSM and general population were, 26.2%, 0.54% and 0.37%, respectively. The 156 HCV RNA positive samples were then sequenced by nested PCR over core/E1 and NS5B regions. Nine HCV genotypes, including 1a, 1b, 2a, 3a, 3b, 6a, 6n, 6u and 6v, were detected. The most prevalent subtypes were 3b (36.09%), 1b (32.54%) and 3a (16.57%). Bayesian evolutionary analysis by sampling trees of sequences of the three major subtypes revealed the origin and history of HCV in Beijing. The origin time of subtype 1b was 2004.1 (1997.7, 2007.7). Subtype 1b showed most sequences from DUs and all sequences from no-DUs were in different groups. Subtype 1b of Beijing and Shanghai may have migration trend or they may have the same evolutionary origins. The origin time of subtype 3a was 2006.5 (1983.4, 2010). They had close relationship with the sequences of Yunnan, Guangzhou, Hong Kong and Jiangsu. The origin time of subtype 3b was 2006.2 (2001.4, 2009.2). The migration trend appeared to have been from Yunnan, Guangdong and Hong Kong to Beijing among subtype 3b. Our results suggest that HCV prevalence in Beijing is complicated. The mixing of nine HCV subtypes and the evolution characteristic indicated that the migration pattern of HCV in Beijing is complex. Beijing plays a pivotal role in HCV transmission following a large amount of floating population in China.

### Biography

Liyang Ma is a Professor and Leader of Pathogen Biology Branch of Department of Immunology and Virology of National Center for AIDS/STD Control and Prevention, PI in State Key Laboratory of Infectious Disease Prevention and Control, Chinese Center for Disease Control and Prevention. She was graduated from West China University of Medicine for her PhD degree in 1998. During 2001-2005, she was trained in Sixth University of Paris and New York University and Blood Center. In 2005, she came back to China. Her research focuses on HIV pathogenesis and drug resistance. She is undertaking National Natural Science Foundation Projects, NIH-NSF SINO-US Cooperation Project as a PI, European Seventh Framework Program as co-PI. Her working group major on systematic studying on evolution and viral fitness of HIV/HCV epidemic strains in China, HIV, HIV drug resistance and drug targets combined with free antiretroviral treatment in China. She has published more than 70 papers in AIDS, JAIDS, Nano letters, Retrovirology, JAC, JMC and AAC etc. Five patents were applied so far and two patents were authorized. She got China Preventive Medicine Association of Science and Technology Award and Beijing Municipal Science and Technology Award.

[mal@chinaaids.cn](mailto:mal@chinaaids.cn)

### Notes: