

Accepted Manuscript

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Authors: Dechun Lin, Liqiang Li, Tian Xie, Qingqing Yin, Nitin Saxena, Rangke Wu, Wanyu Li, Geyang Dai, Jinmin Ma, Xiaohong Zhou, Xiao-Guang Chen



PII: S0168-1702(17)30597-X
DOI: <https://doi.org/10.1016/j.virusres.2018.01.014>
Reference: VIRUS 97332

To appear in: *Virus Research*

Received date: 4-8-2017
Revised date: 26-1-2018
Accepted date: 29-1-2018

Please cite this article as: Lin, Dechun, Li, Liqiang, Xie, Tian, Yin, Qingqing, Saxena, Nitin, Wu, Rangke, Li, Wanyu, Dai, Geyang, Ma, Jinmin, Zhou, Xiaohong, Chen, Xiao-Guang, Codon usage variation of Zika virus: the potential roles of NS2B and NS4A in its global pandemic. *Virus Research* <https://doi.org/10.1016/j.virusres.2018.01.014>

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Codon usage variation of Zika virus: the potential roles of NS2B and NS4A in its global pandemic

Dechun Lin^{1,2,3#}, Liqiang Li^{2,3#*}, Tian Xie⁴, Qingqing Yin⁴, Nitin Saxena^{2,3}, Rangke Wu⁵, Wanyu Li⁴, Geyang Dai⁴, Jinmin Ma^{2,3,5*}, Xiaohong Zhou^{4*} and Xiao-Guang Chen^{4**†}

¹BGI Education Center, University of Chinese Academy of Sciences, Shenzhen 518083, Guangdong, China

²BGI-Shenzhen, Shenzhen 518083, Guangdong, China

³China National Genebank, BGI-Shenzhen, Shenzhen 518083, Guangdong, China

⁴Department of Pathogen Biology, Key Laboratory of Prevention and Control for Emerging Infectious Diseases of Guangdong Higher Institutes, Guangdong Provincial Key Laboratory of Tropical Disease Research, School of Public Health, Southern Medical University, Guangzhou 510515, Guangdong, China

⁵The School of Foreign Studies, Southern Medical University, Guangzhou 510515, Guangdong, China

⁶Department of Biology, University of Copenhagen, Copenhagen, Denmark

#Co-first authors

*Correspondence: xgchen2001@hotmail.com (Xiao-Guang Chen)

daizhouxh@163.com (Xiaohong Zhou)

liliqiang@genomics.cn (Liqiang Li)

majinmin@genomics.cn (Jinmin Ma)

†Lead Contact: xgchen2001@hotmail.com (Xiao-Guang Chen)

Highlights

- Codon usage pattern of ZIKVs were characterized to be gene specific and their variation might be constraint by respective gene function.
- Common over-represented codons are selected and their variation between the Africa lineage and Asian lineage were analyzed.

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