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Insights into the evolutionary history of an emerging virus: *Banna virus*

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Banna virus (BAV) was initially isolated from patients with encephalitis and fever in Yunnan Province of China in 1987. Since then, BAV isolates have been obtained from pigs, cattle and kinds of blood sucking insects in China, Indonesia and Vietnam, which were mainly located in tropics and sub-tropic zones. In 2013, BAV like viruses have been reported isolated in Hungary, showing that these kinds of viruses have been extends from tropical and sub-tropic zones of Southeast Asia to North temperate regions of Europe. BAVs have been considered as an emerging pathogen. However, until now, no systematic evolutionary analysis of BAVs has been reported. In this study, we used genome sequences of segment 12 of BAVs isolated worldwide from 1987-2012 to investigate evolutionary and epidemiologic dynamics. Phylogeographic approach estimated BAVs was originated in the Indonesia region and then rapidly spread to Southeast Asia and Europe within just about 30 years. The Bayesian phylogenetic analysis of BAVs reveals the time to most recent common ancestor and initial divergence of BAVs was at about the beginning of 20th century. Population dynamics analysis indicated that the genetic diversity of BAVs declined in the late 1980s, suggesting that the virus of BAV was suffering from bottle-necked event. These results and their interpretation provide new insights into our understanding of BAV evolution and dispersal and highlight its potential for introduction into new areas.

Biography

Liu Hong has completed her PhD from State Key Laboratory for Infectious Disease Prevention and Control, Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, China. She is currently working as an Assistant Professor at School of Life Sciences, Shandong University of Technology. Her current research interest includes the detection and investigation of arboviruses and associated disease.

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