

HCV基因型的差异性流行与进化

赵璐, 冯悦, 夏雪山

昆明理工大学生命科学与技术学院, 昆明 650500

ZHAO Lu, FENG Yue, XIA Xue-Shan

Faculty of Life Science and Technology, Kunming University of Science and Technology, Kunming 650500, China

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摘要 丙型肝炎病毒(Hepatitis C virus, HCV)是导致慢性肝炎的主要病原体之一, 全球感染人数大约为1.7亿。HCV基因组具有高度变异特性, 利用现代遗传分类方法, 可将HCV分为6个基因型和80多个基因亚型。不同HCV基因型、亚型的分布与流行具有明显地域特性: 1型、2型呈全球流行态势, 3型主要流行于亚洲、北美及欧洲部分地区, 4型主要流行于中非、中东和欧洲地区, 5型主要发现于非洲和欧洲部分国家, 6型则主要在东南亚和北美地区流行。我国流行的HCV有1、2、3和6四种基因型, 北方仍以1b和2a型为主要流行基因型, 近年来3型和6型在华南、西南地区快速传播。据推断, 云南将可能成为我国HCV流行与传播的重要源头, 引起目前HCV基因型/亚型分布的较大变化, 并呈现多样化的传播方式。通过溯祖理论和进化分子钟等分析方法, 了解HCV不同基因型差异性流行与进化, 对研究HCV的分子流行病学特征, 对应性制定丙型肝炎的预防控制策略具有重要意义。

关键词: HCV 流行 分子钟 进化 基因型

Abstract: Hepatitis C virus (HCV) is a prevalent and globally distributed human pathogen that currently infects an estimated 170 million people. Chronic HCV infection significantly increases the risk of chronic hepatitis. The virus exhibits a very high degree of genetic diversity that is classified six genotypes and sub-classified more than 80 subtypes by phylogenetic analysis. The various genotypes and subtypes of HCV have been associated with different epidemiological and geographical spread patterns. Genotypes 1 and 2 are globally distributed; genotype 3 is predominant in Asia, North America and parts of Europe; similar regional patterns of endemic diversity have been found for genotype 4 in Europe, Middle East and Central Africa, for genotype 5 in parts of Africa and Europe, and for genotype 6 in Southeast Asia and North America. Up to date, four HCV genotypes, including genotype 1, 2, 3 and 6, were identified in China. Genotypes 1b and 2a were mainly found in Northern China. The fast spreading of genotypes 3 and 6 in Southern and South-Western China was reported by recent studies. It's deduced that Yunnan may become an important source of HCV epidemic and spread, which will cause great changes in the distribution of HCV genotypes and subtypes, and a variety of transmission. With the development of evolution theory and related analysis methods, such as coalescent theory and evolutionary molecular, it is possible to understand the characters of virus evolution and migration. For HCV, the further understanding on the prevalence and evolution characters of various genotypes is very important for the deep investigation of HCV epidemic and the development of prevention strategy.

Keywords: HCV, prevalence, molecular clock, evolution, genotype

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通讯作者 夏雪山 Email: oliverxia2000@yahoo.com.cn

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[1] Centers for Disease Control and Prevention(CDC). Recommendations for prevention and control of hepatitis C virus (HCV) infection and HCV related chronic disease. *MMWR Recomm Rep*, 1998, 47(RR19): 1-39.

[2] Lauer GM, Walker BD. Hepatitis C virus infection. *N Engl J Med*, 2001, 345(1): 41-52. 

[3] Williams R. Global challenges in liver disease. *Hepatology*, 2006, 44(3): 521-526. 

[4] Chen YD, Liu MY, Yu WL, Li JQ, Peng M, Dai Q, Liu X, Zhou ZQ. Hepatitis C virus infections and genotypes in China. *Hepatobiliary Pancreat Dis Int*, 2002, 1(2): 194-201.











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- [5] Xia X, Luo J, Bai JL, Yu RB. Epidemiology of hepatitis C virus infection among injection drug users in China: systematic review and meta-analysis. *Public Health*, 2008, 122(10): 990-1003. [crossref](#)
- [6] Tsukiyama-Kohara K, Iizuka N, Kohara M, Nomoto A. Internal ribosome entry site within hepatitis C virus RNA. *J Virol*, 1992, 66(3): 1476-1483.
- [7] Neumann AU, Lam NP, Dahari H, Gretch DR, Wiley TE, Layden TJ, Perelson AS. Hepatitis C viral dynamics in vivo and the antiviral efficacy of interferon- α therapy. *Science*, 1998, 282(5386): 103-107.
- [8] Kang SM, Choi SH, Park CY, Kim MH, Kim TK, Park JM, Koh MS, Kang HJ, Hwang SB. Monoclonal antibody recognizing N-terminal epitope of hepatitis C virus nonstructural 5B inhibits viral RNA replication. *J Viral Hepat*, 2008, 15(4): 305-313. [crossref](#)
- [9] 张中林, 山松, 陈曦, 苏宁, 吴祥甫, 钱凯先, 沈桂芳. 丙肝病毒融合抗原基因NS3-C定点整合入衣藻叶绿体基因组的研究. *遗传*, 1999, 21(6): 1-173. [浏览](#)
- [10] Simmonds P, Holmes EC, Cha TA, Chan SW, McOmish F, Irvine B, Beall E, Yap PL, Kolberg J, Urdea MS. Classification of hepatitis C virus into six major genotypes and a series of subtypes by phylogenetic analysis of the NS-5 region. *J Gen Virol*, 1993, 74(Pt11): 2391-2399. [crossref](#)
- [11] Murphy DG, Willems B, Deschênes M, Hilzenrat N, Mousseau R, Sabbah S. Use of sequence analysis of the NS5B region for routine genotyping of hepatitis C virus with reference to C/E1 and 5' untranslated region sequences. *J Clin Microbiol*, 2007, 45(4): 1102-1112. [crossref](#)
- [12] Simmonds P. Genetic diversity and evolution of hepatitis C virus 15-years on. *J Gen Virol*, 2004, 85(Pt11): 3173-3188. [crossref](#)
- [13] Major ME, Feinstone SM. The molecular virology of hepatitis C. *Hepatology*, 1997, 25(6): 1527-1538. [crossref](#)
- [14] Pybus OG, Markov PV, Wu A, Tatem AJ. Investigating the endemic transmission of the hepatitis C virus. *Int J Parasitol*, 2007, 37(8-9): 839-849. [crossref](#)
- [15] Kuiken C, Yusim K, Boykin L, Richardson R. The Los Alamos hepatitis C sequence database. *Bioinformatics*, 2001, 17(3): 379-384.
- [16] Kryczka W, Brojer E, Zarebska-Michaluk D, Medyńska J, Urbaniak A. Factors influencing natural history of chronic hepatitis C. *Med Sci Monit*, 2001, (Suppl. 1): 212-216.
- [17] Nakano I, Fukuda Y, Katano Y, Toyoda H, Hayashi K, Hayakawa T, Kumada T, Nakano S. Interferon responsiveness in patients infected with hepatitis C virus 1b differs depending on viral subtype. *Gut*, 2001, 49(2): 263-267.
- [18] Nakano T, Lu L, Liu P, Pybus OG. Viral gene sequences reveal the variable history of hepatitis C virus infection among countries. *J Infect Dis*, 2004, 190(6): 1098-1108. [crossref](#)
- [19] Drummond AJ, Rambaut A. BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evol Biol*, 2007, 7: 214. [crossref](#)
- [20] 敖雁, 朱明星, 徐辰武. 贝叶斯统计在QTL作图中的应用研究进展. *遗传*, 2007, 29(6): 668-674. [浏览](#)
- [21] Magiorkinis G, Magiorkinis E, Paraskevis D, Ho SY, Shapiro B, Pybus OG, Allain JP, Hatzakis A. The global spread of hepatitis C virus 1a and 1b: A phylodynamic and phylogeographic analysis. *PLoS Med*, 2009, 6(12): e1000198.
- [22] Courtwright D. *Dark paradise: a history of opiate addiction in America*. Cambridge: Harvard University Press, 2001. [crossref](#)
- [23] Stimson GV. The global diffusion of injecting drug use: implications for human immunodeficiency virus infection. *Bull Narc*, 1993, 45(1): 3-17.
- [24] Markov PV, Pepin J, Frost E, Deslandes S, Labbé AC, Pybus OG. Phylogeography and molecular epidemiology of hepatitis C virus genotype 2 in Africa. *J Gen Virol*, 2009, 90(Pt9): 2086-2096.
- [25] Khan A, Tanaka Y, Azam Z, Abbas Z, Kurbanov F, Saleem U, Hamid S, Jafri W, Mizokami M. Epidemic spread of hepatitis C virus genotype 3a and relation to high incidence of hepatocellular carcinoma in Pakistan. *J Med Virol*, 2009, 81(7): 1189-1197. [crossref](#)
- [26] Verma V, Chakravarti A, Kar P. Genotypic characterization of hepatitis C virus and its significance in patients with chronic liver disease from Northern India. *Diagn Microbiol Infect Dis*, 2008, 61(4): 408-414. [crossref](#)
- [27] EMRO. Health System Organization-Health System Profile Pakistan. Regional Health Systems Observatory-World Health Organization, 2007: 28-42.
- [28] Pybus OG, Cochrane A, Holmes EC, Simmonds P. The hepatitis C virus epidemic among injecting drug users. *Infect Genet Evol*, 2005, 5(2): 131-139. [crossref](#)
- [29] Esteban JI, Sauleda S, Quer J. The changing epidemiology of hepatitis C virus infection in Europe. *J Hepatol*, 2008, 48(1): 148-162. [crossref](#)
- [30] Njouom R, Frost E, Deslandes S, Mamadou-Yaya F, Labbé AC, Pouillot R, Mbélesso P, Mbadingai S, Rousset D, Pépin J. Predominance of hepatitis C virus genotype 4 infection and rapid transmission between 1935 and 1965 in the Central African Republic. *J Gen Virol*, 2009, 90 (Pt 10): 2452-2456. [crossref](#)
- [31] Abdel-Hamid M, El-Daly M, Molnegren V, El-Kafrawy S, Abdel-Latif S, Esmat G, Strickland GT, Loffredo C, Albert J, Widell A. Genetic diversity in hepatitis C virus in Egypt and possible association with hepatocellular carcinoma. *J Gen Virol*, 2007, 88(Pt 5): 1526-1531. [crossref](#)
- [32] Pybus OG, Drummond AJ, Nakano T, Robertson BH, Rambaut A. The epidemiology and iatrogenic transmission of hepatitis C virus in Egypt: A Bayesian coalescent approach. *Mol Biol Evol*, 2003, 20(3): 381-387. [crossref](#)
- [33] Tanaka Y, Agha S, Saady N, Kurbanov F, Orito E, Kato T, Abo-Zeid M, Khalaf M, Miyakawa Y, Mizokami M. Exponential spread of hepatitis C virus genotype 4a in Egypt. *J Mol Evol*, 2004, 58(2): 191-195. [crossref](#)

- [34] Verbeeck J, Maes P, Lemey P, Pybus OG, Wollants E, Song E, Nevens F, Fevery J, Delpoort W, Van der Merwe S, Van Ranst M. Investigating the origin and spread of hepatitis C virus genotype 5a. *J Virol*, 2006, 80(9): 4220-4226.
- [35] Henquell C, Guglielmini J, Verbeeck J, Mahul A, Thibault V, Lebray P, Laperche S, Trimoulet P, Foucher J, Le Guillou-Guillemette H, Fouchard-Hubert I, Legrand- Abravanel F, Métivier S, Gaudy C, D'Alteroche L, Rosenberg AR, Podevin P, Plantier JC, Riachi G, Saoudin H, Coppere H, André E, Gournay J, Feray C, Vallet S, Nousbaum JB, Baazia Y, Roulot D, Alain S, Loustaud- Ratti V, Schvoerer E, Habersetzer F, Pérez-Serra RJ, Gourari S, Mirand A, Odent-Malaure H, Garraud O, Izopet J, Bommelaer G, Peigue-Lafeuille H, van Ranst M, Abergel A, Bailly JL. Evolutionary history of hepatitis C virus genotype 5a in France, a multicenter ANRS study. *Infection, Genetics and Evolution*, 2011, 11(2): 496-503. 
- [36] World Health Organization. Hepatitis C-global prevalence. *Wkly Epidemiol Rec*, 1997, 14(46): 341-344.
- [37] Hauri AM, Armstrong GL, Hutin YJ. The global burden of disease attributable to contaminated injections given in health care settings. *Int J STD AIDS*, 2004, 15(1): 7-16. 
- [38] Stumpf MPH, Pybus OG. Genetic diversity and models of viral evolution for the hepatitis C virus. *FEMS Microbiol Lett*, 2002, 214(2): 143-152. 
- [39] Xia XS, Lu L, Tee KK, Zhao WH, Wu JG, Yu J, Li XJ, Lin YX, Mukhtar MM, Hagedorn CH, Takebe Y. The unique HCV genotype distribution and the discovery of a novel subtype 6u among IDUs co-infected with HIV-1 in Yunnan, China. *J Med Virol*, 2008, 80(7): 1142-1152. 
- [40] Nakano T, Lu L, He YS, Fu YS, Robertson BH, Pybus OG. Population genetic history of hepatitis C virus 1b infection in China. *J Gen Virol*, 2006, 87(1): 73-82. 
- [41] Fu Y, Wang Y, Xia W, Pybus OG, Qin W, Lu L, Nelson K. New trends of HCV infection in China revealed by genetic analysis of viral sequences determined from first-time volunteer blood donors. *J Viral Hepat*, 2011, 18(1): 42-52. 
- [42] 桂亚萍, 郑惠, 沃垮, 孔令和. 九江地区丙型肝炎病毒基因分型. *实验与检验医学*, 2010, 28(5): 514-515.
- [43] 刘剑荣, 黄永建, 夏洪娇, 张勇. 丙型肝炎基因型分布特点及流行分析. *国际检验医学杂志*, 2010, 31(12): 1847-1848.
- [44] Zhang CY, Wu NN, Liu J, Ge QJ, Huang Y, Ren Q, Feng QC, He GL. HCV subtype characterization among injection drug users: implication for a crucial role of Zhenjiang in HCV transmission in China. *PLoS One*, 2011, 6(2): e16817.
- [45] Fu YS, Qin WB, Cao H, Xu R, Tan Y, Lu T, Wang HR, Tong WX, Rong X, Li G, Yuan MQ, Li CH, Abe K, Lu L, Chen GH. HCV 6a prevalence in guangdong province had the origin from Vietnam and recent dissemination to other regions of china: phylogeographic analyses. *PLoS One*, 2012, 7(1): e28006.
- [46] 洪国祜, 谭朝霞, 郭艳, 毛青. 中国西南地区丙型肝炎病毒6a亚型病毒株的传播速率. *中华肝脏病杂志*, 2011, 19(7): 502-505.
- [47] Hesketh T, Wei XZ. Health in China From Mao to market reform. *BMJ*, 1997, 314(7093): 1543-1545.
- [48] Zhang C, Yang R, Xia X, Qin S, Dai J, Zhang Z, Peng Z, Wei T, Liu H, Pu D, Luo J, Takebe Y, Ben K. High prevalence of HIV-1 and hepatitis C virus coinfection among injection drug users in the southeastern region of Yunnan, China. *J Acquir Immune Defic Syndr*, 2002, 29(2): 191-196.
- [49] Wang YZ, Xia XS, Li CH, Maneekarn N, Xia WJ, Zhao WH, Feng Y, Kung HF, Fu YS, Lu L. A new HCV genotype 6 subtype designated 6v was confirmed with three complete genome sequences. *J Clin Virol*, 2009, 44(3): 195-199. 
- [50] Xia XS, Zhao WH, Tee KK, Feng Y, Takebe Y, Li QH, Pybus OG, Lu L. Complete genome sequencing and phylogenetic analysis of HCV isolates from China reveals a new subtype, designated 6u. *J Med Virol*, 2008, 80(10): 1740-1746. 
- [51] Lu L, Nakano T, He YS, Fu YS, Hagedorn CH, Robertson BH. Hepatitis C virus genotype distribution in China: predominance of closely related subtype 1b isolates and existence of new genotype 6 variants. *J Med Virol*, 2005, 75(4): 538-549. 
- [52] Zhou YQ, Wang XH, Mao Q, Fan Y, Zhu Y, Zhang XQ, Lan L, Jiang L, Tan WT. Changes in modes of hepatitis C infection acquisition and genotypes in southwest China. *J Clin Virol*, 2009, 46(3): 230-233. 
- [53] Liu PP, Xiang KL, Tang H, Zhang W, Wang XQ, Tong X, Takebe Y, Yang RG. Molecular epidemiology of human immunodeficiency virus type 1 and hepatitis C virus in former blood donors in central China. *AIDS Res Hum Retroviruses*, 2008, 24(1): 1-6.
- [54] World Health Organization. <http://www.who.int/en/>. 2011.
- [55] Tee KK, Pybus OG, Li XJ, Han X, Shang H, Kamarulzaman A, Takebe Y. Temporal and spatial dynamics of human immunodeficiency virus type 1 circulating recombinant forms 08_BC and 07_BC in Asia. *J Virol*, 2008, 82(18): 9206-9215.
- [1] 杨泽民 陈蔚文. 幽门螺杆菌 *vacA* 和 *cagA* 基因全长分子系统发育分析[J]. *遗传*, 2012,34(7): 863-871
- [2] 张昕, 姜华, 王艳丽, 张震, 毛雪琴, 柴荣耀, 邱海萍, 杜新法, 王教瑜, 孙国昌. 真菌类过氧化物酶体增殖因子 *PEX17* 基因家族生物信息学研究[J]. *遗传*, 2012,34(5): 635-646
- [3] 叶远浓, 郭锋彪. 微生物必需基因的理论研究现状[J]. *遗传*, 2012,34(4): 420-430
- [4] 祝雯, 詹家绥. 植物病原物的群体遗传学[J]. *遗传*, 2012,34(2): 157-166
- [5] 李娟 张克勤. 微生物的遗传多样性[J]. *遗传*, 2012,34(11): 1399-1408
- [6] 陈林, 杨亮, 段康民. 从进化谈细菌细胞间的群体感应信号传递[J]. *遗传*, 2012,34(1): 33-40
- [7] 郭新军. 人类 (Homo sapiens) 肌肉增强因子2 (MEF2) 生物信息学特性比较及其进化分析[J]. *遗传*, 2011,33(9): 975-981

- [8] 钱光辉, 王义权. Wnt信号通路与后口动物体轴的进化发育[J]. 遗传, 2011,33(7): 684-694
- [9] 张丽, 王芄, 魏莎莉, 刘纯杰. 幽门螺杆菌毒力基因分型和宿主遗传多态性与胃病关系研究进展[J]. 遗传, 2011,33(6): 558-566
- [10] 陈军, 罗伟雄, 李明, 罗琼. 水稻减数分裂过程中染色体重组交换行为[J]. 遗传, 2011,33(6): 648-653
- [11] 董长征. 流感病毒基因组进化研究进展[J]. 遗传, 2011,33(3): 189-197
- [12] 李铁民, 杜波. CRISPR-Cas系统与细菌和噬菌体的共进化[J]. 遗传, 2011,33(3): 213-218
- [13] 危金普, 潘学峰, 李红权, 段斐. 简单重复DNA序列在哺乳动物mtDNA D-loop区的分布及进化特征[J]. 遗传, 2011,33(1): 67-74
- [14] 屠鞠传礼, 吕贯廷, 曾长青. 人类基因组中巢式基因对的系统分析[J]. 遗传, 2010,32(9): 914-920
- [15] 王天宇, 董园园, 李海燕, 李校堃. MicroRNAs的分子进化与调控机制[J]. 遗传, 2010,32(9): 874-880