Reconstructing the epidemic history of HIV-1 circulating recombinant forms CRF07_BC and CRF08_BC in East Asia: The relevance of genetic diversity and phylodynamics for vaccine strategies

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Abstract

HIV-1 CRF07_BC and CRF08_BC are closely related circulating recombinant forms (CRFs) with serious public health consequences in China. The temporal and spatial dynamics of these CRFs were determined by estimating their dates of emergence using phylogenetic and Bayesian coalescent methods. Estimates of the times of origin of CRF07_BC and CRF08_BC were obtained from these estimates both by their engine in Vietnam province. The present study highlights the relevance of incorporating evolutionary and molecular coalescent analysis methods in depth understanding of the genetic evolution of HIV epidemics, providing information for determining regional and global public health policies, including future vaccine strategies.

Keywords: HIV-1; CRF07_BC and CRF08_BC; China; Vietnam; Molecular epidemiology

1. Introduction

The high genetic diversity of HIV-1 adds considerable complexity to the development of effective vaccines [1,2]. The complex genetic structure of HIV-1 epidemics can be seen in regions such as China, where various HIV-1 strains are co-circulating within and among different risk populations. Widespread circulation of HIV-1 strains in Asia [3] indicate subtypes B and F (from Thailand variant of subtype B, also referred to as Thai-B) [4,5] and subtype C, as well as the circulating recombinant forms (CRFs) CRF01_AE [6], CRF105_BC [7], and CRF02_AG [8]. New CRFs have been reported in several regions in Asia, including CRF02_AG [9] and CRF94591.1 [10] in Thailand [10,11] and CRF31.01b in Malaya [12]. Moreover, many unique recombinant forms (URFs) have been detected in Asia, particularly in Myanmar and the western Vietnam province of Gia Lai [13].

CRF07_BC and CRF08_BC are two closely related recombinants derived from Thai subtype B and Indian subtype C genomes that have been generated in drug users among injecting drug users (IDUs) in China since their discoveries in 1997 in Xining and Guangzhou [14,15], respectively. Their origins are located back to the Vietnamese province of 12,64 of southwestern China that borders the Golden Triangle region of Southeast Asia and which was the world's largest heroin producing region, Vietnam plays an important role as an entry point for heroin smuggling into China [16] and is considered to be an epicenter of HIV/AIDS. It was first detected among injecting drug users (IDUs) in Yunnan in 1999 [12,13,16].

The early phase of the HIV-1 epidemic in Vietnam was initiated by subtype B strains of both North American and Southeast Asian (SA) origin [17,18], with subtype B subsequently becoming the dominant strain among IDUs in the region [18,19]. The subtype distribution changed in the early 1990s after a subtype C cluster of index viremia was introduced, which then became the predominant circulating strain [20]. Co-circulation of subtypes B and C in the region led to the formation of various phylogenetically distinct BF recombinants, most notably CRF07_BC and CRF08_BC.