The major circulating HIV-1 subtypes in Japan have been subtype B (B) followed by CRF01_AE (AE), with prevalences of 86% and 7%, respectively, in newly diagnosed HIV/AIDS cases.

These two subtypes have distinct epidemiological characteristics: B predominates in men who have sex with men (MSM), whereas AE is observed mostly in heterosexuals.

Transmission networks of these risk populations appear to be crossing over and diffusing. In our newly diagnosed populations, there have been some cases where the subtypes were not consistent between pol and env regions.

We investigated potential AE-B recombinations and analyzed transmission networks in Japan.

**Materials and Methods**

**Patients**

Newly diagnosed 1070 cases in Nagoya Medical Center from June 1997 to April 2012

**Determination of Subtype (MEGA v5.2.1.)**

Phylogenetic analysis using the neighbor-joining method (1000 bootstrap replicates)

gap MA (396 bps) pol PR-RT (1017 bps) pol IN (864 bps) env CV3 (221 bps)

**Analysis of near full-length sequences**

**Phylogenetic trees of HIV-1 isolates identified in this study**

13 cases (blue filled circles and letters) were assumed as AE (gag/B/pol/AE) recombinant HIV-1. We analyzed 7 cases of them for the near full-length sequences.

**2) Determinations of breakpoints of HIV-1 AE-B recombinants**

6 cases shared an identical recombination structure of the AE-B strains, which differs from any previously reported types. They were designated as CRF69_O18 by the Los Alamos HIV sequence database.

**Results**

Three of the ancestral recombination event originating in CRF69_O18

**3) the time of the ancestral recombination event originating in CRF69_O18**

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Baysian MCMC evolutionary parameters for HIV-1 novel CRF in Japan

**Figure 1: Phylogenetic tree of CRF69_O18**

Phylogenetic tree of CRF69_O18 with sequences detected in Asian countries registered on the Los Alamos sequence database.

**Figure 2: Determinations of breakpoints of HIV-1 AE-B recombinants**

13 cases (blue filled circles and letters) were assumed as AE (gag/B/pol/AE) recombinant HIV-1. We analyzed 7 cases of them for the near full-length sequences.

**Figure 3: Results**

Three of the ancestral recombination event originating in CRF69_O18

**Table 1: Demographic and clinical characteristics of patients infected with HIV-1 AE-B recombinant form (n=13)**

Demographic and clinical characteristics of patients infected with HIV-1 AE-B recombinant form (n=13)

**Figure 4: Conclusions**

A new recombinant strain composed of AE and B, CRF69_O18, was identified in Japan.

The mRCA analysis revealed that CRF69_O18 emerged between 1993 and 1997, soon after AE was introduced from neighboring countries in mid 1990s.

Phylogenetic analyses indicated that the AE and B fragments of CRF69_O18 are genetically close to AE and B in Japanese heterosexual and MSM populations, respectively. This suggests that the recombination seems to take place in the Japanese populations.

Previous epidemiological data describing distinct socio-epidemiological characteristics for Japanese MSM and heterosexual populations, our data indicate crossing over between the two populations.

The knowledge of epidemic strains is important for diagnosis and treatment of HIV/AIDS, it should be monitored through continuous surveillance of HIV-1 subtypes.