

# Transmission origin of HIV-1 CRF01\_AE and B subtype among injecting drug user in Taiwan



Yu-Ching Lan\*, Yi-Chen Yang, Szu-An Chen, Ji-Rong Sin, Ju-Pei Chang and Yu-Jiun Luo

Department of Health Risk Management, China Medical University, Taichung, Taiwan (R.O.C)



## Introduction

The major of HIV-1 subtype are CRF07\_BC, B and CRF01\_AE in Taiwan. This study supported the evidence of origin and transmission pathway of HIV-1 CRF01\_AE genotype in Taiwan.

## Materials and methods

The study collected HIV-1 seropositive blood samples (N=310) from hospital in Taiwan in 2007. We use phylogenetic analysis to detect HIV-1 virus strains of the subtypes in *env* gene. The coalescent theory and molecular clock analysis were used to estimate the evolution rate and time for "The Most Recent Common Ancestors (TMRCA).

## Results

There is clustering phenomenon after phylogenetic analysis revealed that a total of 9 CRF01\_AE sequences, and the bootstrap values is greater than 75%. The variation of our cases and the sequences before Taiwan 2007 (n=20) is 0.098.

Our cases are 89% from male and the average age is 35.7. Five of all sequences are IDUs (56%). The evolution rate of CRF01\_AE is  $8.2 \times 10^{-3}$  ( $4.9 \times 10^{-3}$ - $11.6 \times 10^{-3}$ ) and subtype B is  $6.2 \times 10^{-3}$  ( $4.2 \times 10^{-3}$ - $8.2 \times 10^{-3}$ ). The TMRCA of CRF01\_AE in Taiwan were dated to 1984.6 (1978.2-1989) and subtype B in central Taiwan (cluster 1) were dated to 1991.9 (1985.8-1997.4), and the skyline plot showed the CRF01\_AE origin from 1985 and subtype B origin from 1980 in Taiwan.

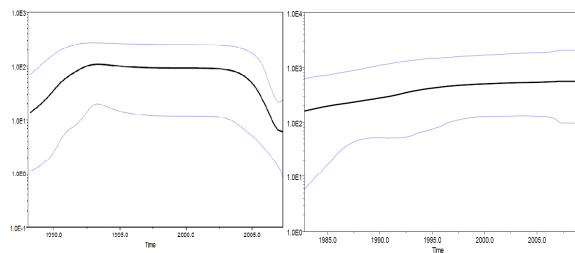


Fig.1 - Skyline plot of CRF01\_AE (GTR model).

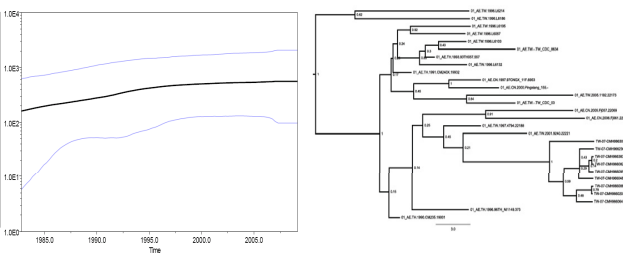


Fig.2 - Skyline plot of Subtype B (GTR model).

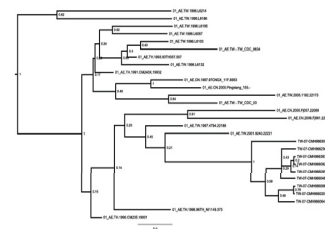


Fig. 3 - Maximum-likelihood phylogenetic analysis of CRF01\_AE (GTR model).

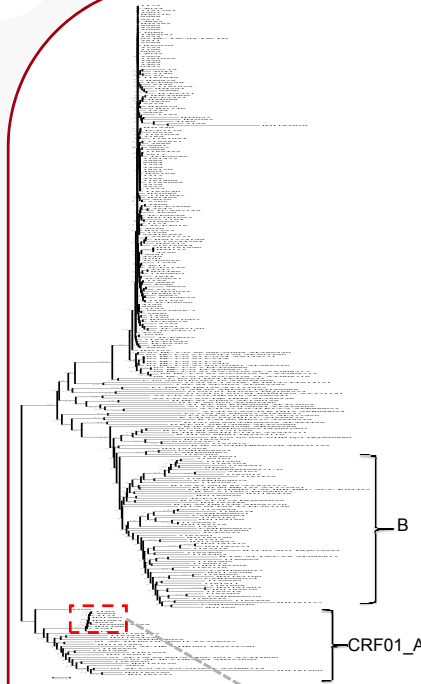


Fig. 4 - Phylogenetic analysis. CRF01\_AE cluster (HIV-1 *env* NJ tree bootstrap 1000) (bootstrap:100%)

Table 1 - Evolutionary characteristics of CRF01\_AE and Subtype B.

HIV-1 subtype and location	Genetic region	Value (HPD) <sup>a</sup> of the evolutionary parameter according to the indicated model	
		Constant size	
		Rate of evolution <sup>b</sup>	TMRCA <sup>c</sup>
CRF01_AE		8.2 (4.9-11.6)	
Taiwan	<i>env</i>		1984.6 (1978.2-1989.9)
Subtype B		6.2 (4.2-8.2)	
Middle of (Cluster-1)	<i>env</i>		1991.9 (1985.8-1997.4)
Middle of (Cluster-2)	<i>env</i>		1988.8 (1981.9-1995.0)
Taiwan (past 2007)	<i>env</i>		1976.7 (1968.2-1984.2)
Thailand and	<i>env</i>		1975.8 (1968.1-1982.5)

## Conclusions

Our estimate of CRF01\_AE of Taiwan is 1984.6 (1978.2-1989.9) and the evolution rate is  $8.2 \times 10^{-3}$  and subtype B in central Taiwan is 1991.9 (1985.8-1997.4) and the evolution rate is  $6.2 \times 10^{-3}$  ( $4.2 \times 10^{-3}$ - $8.2 \times 10^{-3}$ ).

This study first presents the origin estimation of CRF01\_AE in Taiwan and subtype B in central Taiwan.

## References

- UNAIDS. 2008 Report on the global AIDS epidemic. < <http://www.unaids.org/en/KnowledgeCentre/HIVData/GlobalReport/2008/> > Accessed 2010 Sep 23.
- Centers for disease control, R.O.C. (Taiwan). Statistics of HIV/AIDS. < <http://www.cdc.gov.tw/public/Attachment/0161612171.xls> > Accessed 2010 Sep 23.
- Chen, Y.M. and Kuo, S.H. 2007. HIV-1 in Taiwan. *Lancet* 369:623-625.
- Chen, Y.J., Huang, Y.H., Chuang, S.Y., et al. 2010. Molecular epidemiology of HIV-1 subtype B, CRF01\_AE, and CRF07\_BC infection among injection drug users in Taiwan. *J Acquir Immune Defic Syndr* 53:425-39.

## Acknowledgments

This work was partially supported by grant NSC96-2314-B-039-003-MY2 and NSC96-2314-B-039-003-MY3 from the National Science Council, and CMU96-117 and CMU96-190 from China Medical University.

\*Correspondence to: Assistant Prof. Yu-Ching Lan PhD. Department of Health Risk Management, China Medical University, No. 91, Hsueh-Shih Road, Taichung, Taiwan 404 (R.O.C.) (E-mail: yclan@mail.cmu.edu.tw; Phone : +886-4-2205-3366 ext 6507).