Corrigendum


Yue Li 1, Rie Uenishi 1, Saiki Hase 1, Huanan Liao, Xiao-Jie Li, Takayo Tsuchiura, Kok Keng Tee, Oliver G. Pybus, Yutaka Takebe *

The authors regret that the single shadowed triangle in the lower right side of Fig. 1 (immediately left of the box labeled BPAN) should have appeared as a red diamond. The correct figure appears below.
Fig. 1. Evolutionary characteristics of HIV-1 subtype B'. Maximum clade credibility (MCC) tree of 1.6-kb gag-pol sequences obtained by Bayesian MCMC analysis is shown (see text for details). HIV-1 subtype C sequences (86ETH2220, 95IN21068 and 92BR025d) were used as outgroups. The tips of the tree correspond to the year of sampling, and the branch lengths reflect the mean of the posterior probability density. The 95% highest probability density (HPD) for each subtype B/B' cluster is indicated as a horizontal bar at the corresponding node. Inset, distribution of the posterior probability for the tMRCA for the respective subtype B/B' lineage. The symbols for the geographic origins of the respective subtype B/B' strains are listed in the left-hand panel. The tMRCA means and 95% HPDs for the key nodes were as follows: pandemic subtype B ancestor = 1966 (1958-1973); subtype B' ancestor = 1985 (1981-1988); BFPD ancestor = 1991 (1989-1994). The asterisk indicates two subtype B' isolates from western Yunnan (Dehong district). The dagger indicates one of the earliest subtype B isolate (RF) from a Haitian immigrant living in the United States. (Gilbert et al., 2007).