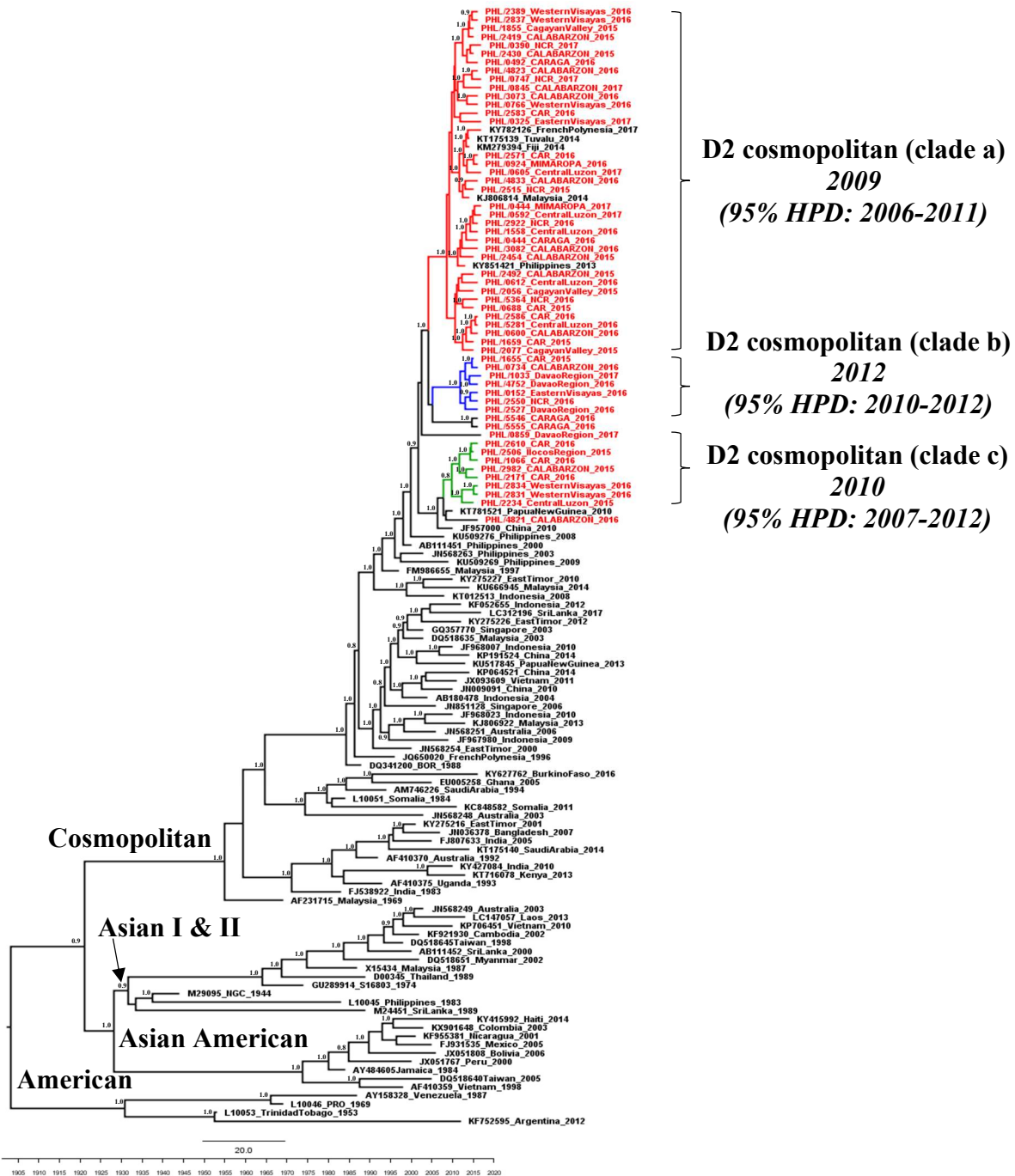
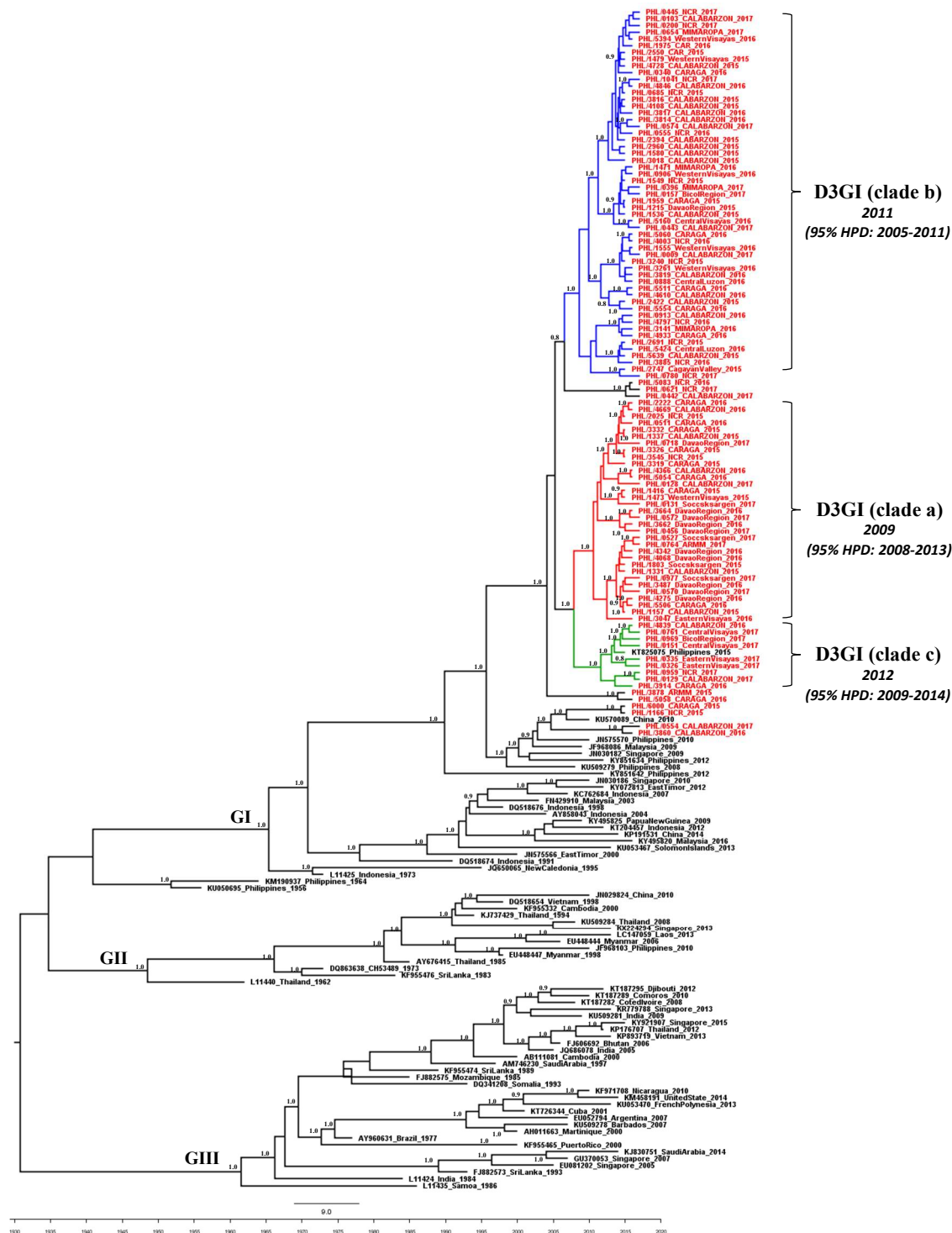


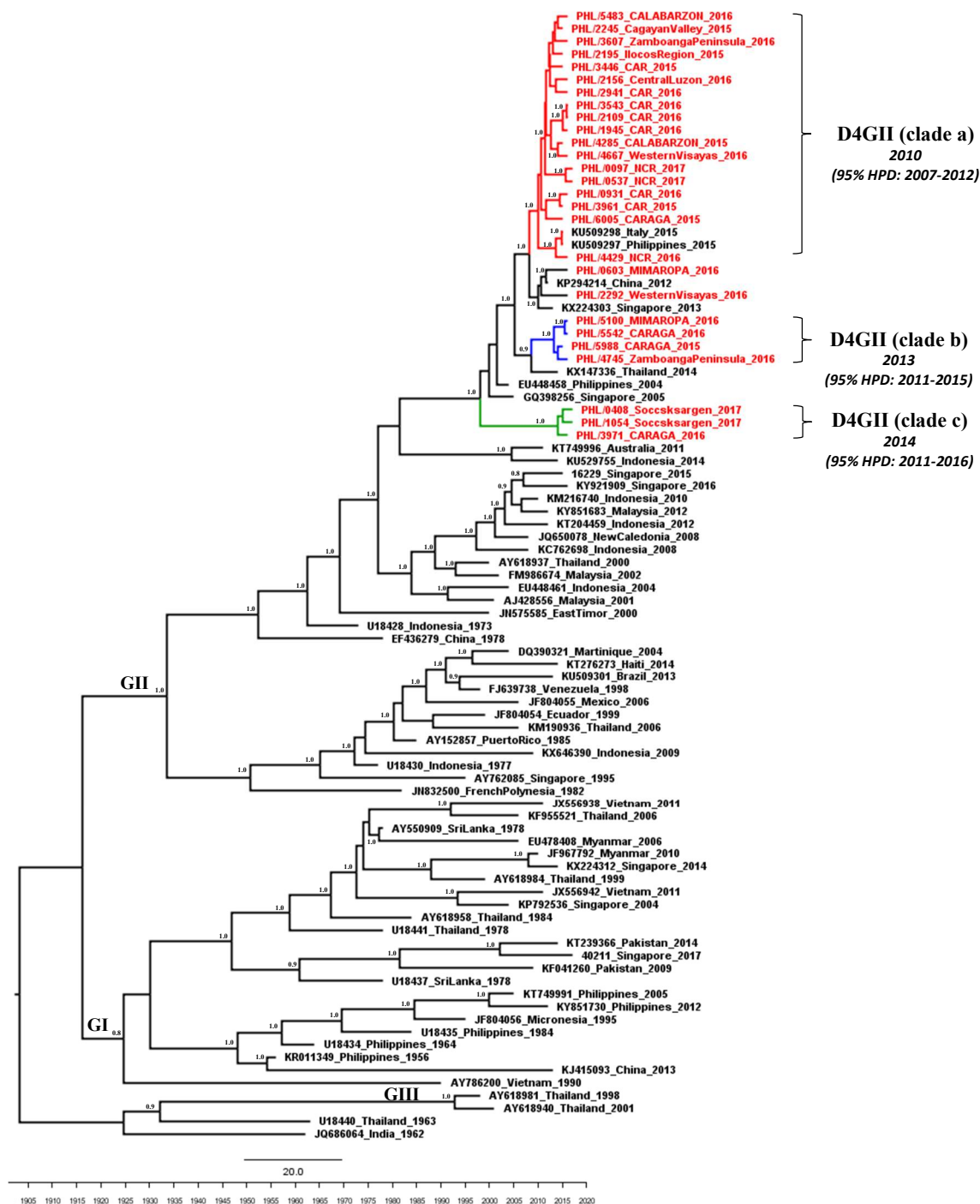
**Figure S1. Phylogenetic and tMRCA analysis of DENV-1.** Maximum clade credibility (MCC) tree of DENV-1 constructed using the Bayesian Markov Chain Monte Carlo (MCMC) method implemented in the BEAST package v1.7.4 (ref). The analysis included 89 *E* gene sequences selected to cover all possible viral genetic diversity observed during the study period (highlighted in red) and 126 sequences obtained from GenBank database. The x-axis represents the time unit (year) and the posterior probability values > 0.8 are indicated on respective branches. The tMRCA values are shown in italics for major clade only. D1=DENV-1; GI=genotype I; GII=genotype II; GIII=genotype III.



**Figure S2. Phylogenetic and tMRCA analysis of DENV-2.** Maximum clade credibility (MCC) tree of DENV-2 constructed using the Bayesian Markov Chain Monte Carlo (MCMC) method implemented in the BEAST package v1.7.4 (ref). The analysis included 55 *E* gene sequences selected to cover all possible viral genetic diversity observed during the study period (highlighted in red) and 77 sequences obtained from GenBank database. The x-axis represents the time unit (year) and the posterior probability values > 0.8 are indicated on respective branches. The tMRCA values are shown in italics for major clade only. D2=DENV-2.



**Figure S3. Phylogenetic and tMRCA analysis of DENV-3.** Maximum clade credibility (MCC) tree of DENV-3 constructed using the Bayesian Markov Chain Monte Carlo (MCMC) method implemented in the BEAST package v1.7.4 (ref). The analysis included 106 *E* gene sequences selected to cover all possible viral genetic diversity observed during the study period (highlighted in red) and 69 sequences obtained from GenBank database. The x-axis represents the time unit (year) and the posterior probability values > 0.8 are indicated on respective branches. The tMRCA values are shown in italics for major clade only. D3=DENV-3; GI=Genotype I; GII=Genotype II; GIII=Genotype III.



**Figure S4. Phylogenetic and tMRCA analysis of DENV-4.** Maximum clade credibility (MCC) tree of DENV-4 constructed using the Bayesian Markov Chain Monte Carlo (MCMC) method implemented in the BEAST package v1.7.4 (ref). The analysis included 27 *E* gene sequences selected to cover all possible viral genetic diversity observed during the study period (highlighted in red) and 62 sequences obtained from GenBank database. The x-axis represents the time unit (year) and the posterior probability values > 0.8 are indicated on respective branches. The tMRCA values are shown in italics for major clade only. D4=DENV-4; GI=Genotype I; GII=Genotype II; GIII=Genotype III.