

TABLE S2. Evolutionary characteristics of enterovirus 71 genogroups B and C, and their respective sub-genogroups based on the VP1 gene

Enterovirus 71 genogroup	Year first isolated (Country)	Relaxed (uncorrelated lognormal) coalescent inference	
		Exponential growth, HKY+ γ_4	Constant size, HKY+ γ_4
<i>Genogroup B</i>			
Substitution rate*		4.8 (4.5,5.0)	4.7 (4.5,4.9)
Divergence time			
B1	1972 (USA)	1967.0 (1964.8,1969.1)	1967.1 (1964.9,1969.0)
B2	1981 (USA)	1978.8 (1977.8,1979.7)	1978.9 (1978.0,1979.8)
B3	1997 (Malaysia)	1994.9 (1993.9,1995.7)	1994.7 (1993.6,1995.6)
B4	1997 (Malaysia)	1993.3 (1991.7,1994.8)	1993.3 (1991.7,1994.6)
B5	2003 (Japan)	2001.3 (2000.7,2001.9)	2001.2 (2000.7,2001.8)
<i>Genogroup C</i>			
Substitution rate		4.4 (4.1,4.6)	4.2 (4.0,4.4)
Divergence time			
C1	1986 (Australia)	1983.3 (1982.3,1984.3)	1983.2 (1982.1,1984.1)
C2	1995 (Australia)	1992.9 (1991.5,1993.9)	1992.8 (1991.6,1994.0)
C3	2000 (Korea)	1998.8 (1998.3,1999.3)	1998.8 (1998.3,1999.4)
C4	1998 (Taiwan)	1993.0 (1991.2,1994.5)	1992.8 (1990.8,1994.5)
C5	2005 (Vietnam)	2002.9 (2002.0,2003.7)	2002.7 (2001.8,2003.7)

Posterior distributions (evolutionary rates and divergence times) are estimated using a relaxed molecular clock model in the Bayesian Markov chain Monte Carlo (MCMC) framework.

* Substitution rates are expressed as 10^{-3} substitutions per site per year.