

**Table S1.** Intra- and inter- host genetic diversity for the stop-codon lineage and the std-1 lineage. For the intra-host genetic diversity, the average number of pairwise segregation sites ( $\pi$ ) and the ratios of the numbers of non-synonymous over synonymous mutations ( $d_N/d_S$ ) in each individual are examined for the stop-codon and the wt-1 lineage. For the inter-host genetic diversity, the nucleotide distances between the consensus sequences of each lineage in each individual and the reference sequence of the corresponding lineage are calculated. The reference sequence of a lineage is defined as the consensus sequence shared by the greatest number of individuals in that lineage.

	ID	Stop codon lineage					wt-1 lineage			
		No. clones	$\pi$	$d_N/d_S^a$ 5' to Stop	$d_N/d_S^a$ Stop to 3'	Nucleotide distance to the Ref. Seq.	No. clones	$\pi$	$d_N/d_S^a$	Nucleotide distance to the Ref. Seq.
Individuals with tDIP	<i>Mos194</i>	10	20.8	0.631	1.379	1	10	19.3	0.658	0
	<i>Mos206</i>	6	0.6	--	--	0	1	--	--	--
	<i>Mos305</i>	10	11.9	0.827	0.642	0	10	8.9	0.831	0
	40530	1	--	--	--	--	18	8.9	0.691	1
	47185	9	10.4	1.713	1.005	1	11	11.8	0.447	0
	47662	1	--	--	--	--	19	10.4	0.651	2
	48572	11	7.4	0.595	1.018	0	9	4.5	0.996	0
	49440	11	5.9	0.949	0.515	0	9	14.9	0.351	0
	50457	10	11.9	0.547	1.863	0	10	16.3	0.456	0
	NC416	7	20.8	1.931	1.251	5	4	20.8	0.864	0-4 <sup>b</sup>
Individuals without tDIP	<i>Mos059</i>	0	--	--	--	--	20	14.8	0.845	4
	37045	0	--	--	--	--	20	16.3	0.685	9
	38518	0	--	--	--	--	19	14.9	0.592	6
	40906	0	--	--	--	--	20	11.9	0.593	8
	43549	0	--	--	--	--	20	5.9	0.985	7

<sup>a</sup>  $d_N/d_S$  is calculated on the Datamonkey webserver (2) using the SLAC method (3).

<sup>b</sup> The consensus for 4 nucleotides of the sequences in this lineage cannot be determined.

**Table S2. Topology test results<sup>a</sup> for 3 phylogenetic trees shown Fig.S1.**

<b>Tree ID</b>	<b>Log Likelihood</b>	<b>p-values of S.H. test</b>	<b>E.L.W.</b>
<b>N</b>	-2955.47	1.0000	0.7936
<b>A</b>	-2960.01	0.1270	0.1489
<b>B</b>	-2962.77	0.0950	0.0574

<sup>a</sup> All tests used 5% significance level. 1000 resamples were performed in Shimodaira-Hasegawa (S.H.) test (4), and the Expected Likelihood Weight (E.L.W.) test (5) using the RELL method (6).

**Table S3. Maximum-likelihood estimates (MLE) of parameter values and their corresponding increase in overall DENV-1 cases during 2001 and 2002.** Seasonal forcing parameter  $\sigma=0.6$ .

Parameter	Value (C.I. <sup>a</sup> )	$R_{\text{eff,co}}$	$t_{\text{emg}}$	Neg. Log-Likelihood	Fold increase in DENV-1 cases during 2001-2002 (range of variation <sup>b</sup> )
$W_H$	1.25 (1.13-1.75)	1.25 (1.13-1.75)	Nov, 1998	4.97	2.3 (1.4-3.3)
$W_V$	1.25 (1.14-1.80)	1.25 (1.14-1.80)	Dec, 1998	5.28	2.3 (1.5-3.4)
$\gamma_{H,D}$	0.129 day <sup>-1</sup> (0.10-0.15)	1.29 (1.15-1.61)	Dec, 1998	5.67	3.1 (1.7-4.0)
$\sigma_{V,D}$	0.189 day <sup>-1</sup> (0.14-0.79)	1.24 (1.13-1.57)	Feb, 1999	4.88	2.4 (1.5-3.2)

<sup>a</sup> 95% confidence intervals that are calculated using parameter profiling.

<sup>b</sup> The ranges of variation are calculated using the estimated parameter values at the boundaries of the 95% confidence intervals.

**Table S4. Maximum-likelihood estimates of parameter values and their corresponding increase in overall DENV-1 cases during 2001 and 2002.** Seasonal forcing parameter  $\alpha=0.8$ .

Parameter	Value (C.I. <sup>a</sup> )	$R_{\text{eff,co}}$	$t_{\text{emg}}$	Neg. Log-Likelihood	Fold increase in DENV-1 cases during 2001-2002 (range of variation <sup>b</sup> )
$W_H$	1.23 (1.12-1.66)	1.23 (1.12-1.66)	Dec, 1998	5.22	2.5 (1.4-3.4)
$W_V$	1.23 (1.13-1.60)	1.23 (1.13-1.60)	Dec, 1998	5.39	2.5 (1.5-3.3)
$\gamma_{H,D}$	0.132 day <sup>-1</sup> (0.11-0.15)	1.27 (1.12-1.48)	Dec, 1998	6.26	3.3 (1.5-4.1)
$\sigma_{V,D}$	0.164 day <sup>-1</sup> (0.13-0.75)	1.19 (1.12-1.57)	Dec, 1998	4.89	2.3 (1.4-3.3)

<sup>a</sup> 95% confidence intervals that are calculated using parameter profiling.

<sup>b</sup> The ranges of variation are calculated using the estimated parameter values at the boundaries of the 95% confidence intervals.

**Table S5. Results of maximum likelihood estimations are robust across different phases of background DENV-1 dynamics.** The values of maximum likelihood estimations are shown. The corresponding simulations are shown in Fig. S3.

Parameter	Simulation time for year 2001 ( $t_{2001}$ )	Maximum Likelihood estimate	$R_{\text{eff,co}}$	Neg. Log-Likelihood	Fold increase in DENV-1 cases during 2001-2002
$W_H$	44	1.23	1.23	4.99	2.3
	46	1.32	1.32	4.92	3.4
	48	1.29	1.29	8.74	3.4
	54	1.29	1.29	6.70	3.7
	64	1.31	1.31	7.11	4.3
	74	1.32	1.32	7.06	4.6
$W_V$	44	1.23	1.23	5.26	2.4
	46	1.32	1.32	5.31	3.6
	48	1.29	1.29	9.32	3.6
	54	1.28	1.28	6.76	3.7
	64	1.31	1.31	7.18	4.3
	74	1.32	1.32	7.05	4.5
$\gamma_{H,D}$	44	0.131 day <sup>-1</sup>	1.28	5.81	3.2
	46	0.126	1.33	5.79	3.2
	48	0.128	1.30	9.32	3.2
	54	0.125 day <sup>-1</sup>	1.33	8.09	5.1
	64	0.123 day <sup>-1</sup>	1.35	8.63	6.0
	74	0.122 day <sup>-1</sup>	1.36	8.55	6.4
$\sigma_{V,D}$	44	0.186 day <sup>-1</sup>	1.24	4.88	2.5
	46	0.223	1.30	4.75	3.5
	48	0.198	1.26	8.39	3.5
	54	0.195 day <sup>-1</sup>	1.25	6.46	3.5
	64	0.203 day <sup>-1</sup>	1.27	6.81	4.1
	74	0.206 day <sup>-1</sup>	1.27	6.65	4.2

**Table S6. Description and initial values of the state variables of the ODE model.**

State variables	Description	Initial value*
<b>S</b>	Number of susceptible humans	$0.3 \cdot N_H$
<b>E</b>	Number of exposed humans who are infected with DENV-1	0
<b>I</b>	Number of infectious humans who are infected with DENV-1	1
<b>R</b>	Number of recovered humans	$0.7 \cdot N_H$
<b>T</b>	Number of humans infected with tDP only	0
<b>G</b>	Number of exposed humans who are infected with both DENV-1 and tDP	0
<b>D</b>	Number of infectious humans who are infected with both DENV-1 and tDP	0
<b>S<sub>V</sub></b>	Number of susceptible mosquitoes	$N_V$
<b>E<sub>V</sub></b>	Number of exposed mosquitoes infected with DENV-1	0
<b>I<sub>V</sub></b>	Number of infectious mosquitoes infected with DENV-1	0
<b>T<sub>V</sub></b>	Number of mosquitoes infected with tDP only	0
<b>G<sub>V</sub></b>	Number of exposed mosquitoes infected with both DENV-1 and tDP	0
<b>D<sub>V</sub></b>	Number of Infectious mosquitoes infected with both DENV-1 and tDP	0

\*  $N_H$  and  $N_V$  are the total numbers of humans and mosquitoes, respectively (see Table S6).

**Table S7. Parameter values of the full ODE model.**

Parameter	Description	Value	Ref
$N_H$	Human population in Myanmar	50,000,000	<sup>a</sup>
$N_V$	Mosquito population in Myanmar	$N_H * 2$	[2]
$\beta$	Transmission rate	70 year <sup>-1</sup>	[2]
$\mu_H$	Human host birth rate = death rate	1/60 year <sup>-1</sup>	[2]
$\mu_V$	Mosquito birth rate = death rate	365/14 year <sup>-1</sup>	[2]
$1/\sigma_H$	Average latent period of human infected with DENV-1 only	5/365 year	[2]
$1/\sigma_{H,D}$	Average latent period of dually infected human	Varies in model	
$1/\sigma_V$	Average incubation period of mosquitoes infected with DENV-1 only	10/365 year	[2]
$1/\sigma_{V,D}$	Average incubation period of dually infected mosquitoes	Varies in model	
$1/\gamma_H$	Average infectious period of human infected with DENV-1 only	6/365 year	[2]
$1/\gamma_{H,D}$	Average infectious period of dually infected human	Varies in model	
<b>a</b>	Seasonality coefficient for mosquito birth rate	0.7 (unless specified)	<sup>b</sup>
<b>b</b>	Phase of seasonality. The value of b is chosen such that the number of dengue cases peaks in July as shown in [3].	0.3	<sup>b</sup>
<b>P</b>	Relative efficiency of tDP-only transmission from dually infected individuals compared to the rate of DENV-1 transmission from singly infected individuals	Varies in model Baseline value: 0.01	
<b>Q</b>	Relative efficiency of DENV-1-only transmission from dually infected individuals compared to the rate of DENV-1 transmission from singly infected individuals	Varies in model Baseline value: 0.01	
<b>W</b>	Relative efficiency of dual transmission from dually infected individuals compared to the rate of DENV-1 transmission from singly infected individuals. When the dually infected humans and mosquitoes are considered separately, $W_H$ and $W_V$ denote the relative rates of dual transmission from dually infected humans and mosquitoes, respectively.	Varies in model Baseline value: 1.00	

<sup>a</sup> Source: Myanmar 2000, United Nations.

<sup>b</sup> The seasonality parameters are chosen such that the seasonal pattern in the model simulation is consistent with the monthly case reports in [3].