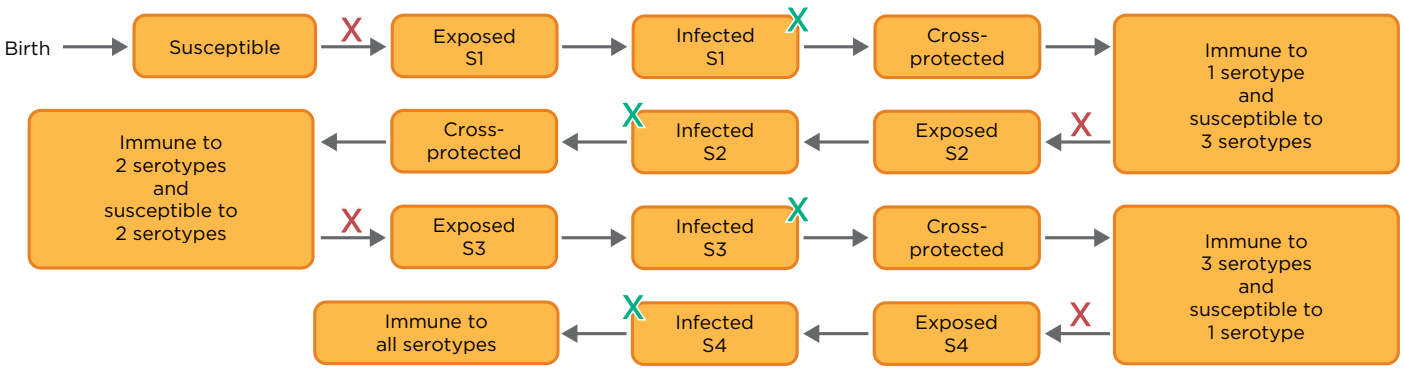
Supplementary Materials

SUPPLEMENTARY FIGURE: DYNAMIC TRANSMISSION DETERMINISTIC COMPARTMENTAL MODEL STRUCTURE



X Exposure via an effective bite of an infectious vector

X Possibility of virus transmission to a susceptible mosquito, given a bite

S1 to S4 denote the serotypes DENV-1 to DENV-4 in the order of infecting of hosts. The model considers all possible combinations of serotypes acquisition and tracks serotypes not acquired yet, but not the order of infecting by serotypes already acquired. The transition from the state "susceptible" to the state "exposed" (for each serotype) occurs upon an effective bite of a vector carrying the serotype in question. In the state "infected" the hosts are able to transmit the serotype they are infected with to a susceptible vector upon an effective bite. Co-infection is assumed impossible. During the period of cross-protection the hosts are assumed to be fully protected from a heterologous infection.

Supplementary Figure has been reproduced with permission from the poster "Disease Impact of a New Dengue Vaccine (TAK-003) in Thailand" presented at the International Society for Infectious Diseases 2022 congress.

S1, serotype of first infection; S2, serotype of second infection; S3, serotype of third infection; S4, serotype of fourth infection.

SUPPLEMENTARY TABLE: MODEL INPUT PARAMETERS

Model Input		Value	Source
Population/epidemiology			
Population, n		66,486,458	Reference 1
Expansion factor	Symptomatic cases	8.37	Reference 2
	Hospitalized cases	2.94	
Duration of cross-protection, mo		6	References 3-6
Probability of symptomatic dengue (given an infection), %	Primary/secondary/post secondary	30/60/10	Reference 7
Probability of hospitalized dengue (given a symptomatic infection), %	Primary/secondary/post secondary	15.9/30.0/7.5	Reference 8
Probability of severe dengue (given a symptomatic infection), %	Primary/secondary/post secondary	6.3/11.8/2.9	Reference 9
Probability of dengue death (given hospitalization for severe dengue), %		0.26	Reference 8
Infection parameters			
Adult female vectors per host (annual average)		2	References 10-12
Vector life expectancy, days		14	References 13,14
Duration of latent period in vectors, days		10	References 13-16
Vector biting rate, bites per day		0.7	Reference 17
Amplitude of the seasonal sine function		0.34	Fitted[a]
Horizontal shift of the seasonal sine function		–0.59	Fitted[a]
Probability of virus transmission from an infectious host to a susceptible vector, given a bite, %		30	Reference 13
Probability of virus transmission from an infectious vector to a susceptible host, given a bite (age-specific), %		4.6–27.9	Fitted[b]
Duration of latent period in hosts, days		5	References 13, 18, 19
Duration of viremia in hosts, days		4.5	References 4, 18, 20-22
Vaccination strategy inputs			
Age of routine vaccination, y		11	Based on the observed HPV vaccination program (Ref 23)
Coverage of routine vaccination, %		87	Based on HPV vaccination cohort and coverage in Thailand (Ref 23)
Efficacy parameters			
Non-hospitalized symptomatic dengue		Constructed efficacy curves by serostatus based on DEN-301 data	Efficacy is computed by a power function (decay function) with the decline of the curve informed by DEN-301 data
Hospitalized dengue		84.4% (no waning)	Cumulative efficacy informed by DEN-301 data; efficacy against hospitalized dengue was not observed to wane over time in DEN-301
Asymptomatic dengue		50% of the efficacy against non-hospitalized symptomatic dengue[c]	Assumption; DEN-301 data
Model assumptions			
Transmissibility of symptomatic infection (relative to asymptomatic)		2	References 4, 24
Natural boosting		Each breakthrough infection boosts the level of vaccine protection	The assumption fits within the dengue framework (Ref 25)

HPV, human papilloma virus.

[a]Calibrated to fit the average rate of symptomatic dengue (corrected for underreporting) observed in each calendar month from 2011 to 2020.

[b]The probability of virus transmission from an infectious vector to susceptible host was calibrated by fitting the model output to the average age-specific incidence rate of symptomatic dengue (corrected for underreporting) observed in 2011-2020. Age-specific coefficients applied to this probability were estimated separately based on a simple static simulation and then used in the fitting process.

[c]Precedence in Coudeville and Garnett 2016.[18]

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