Supporting information

Supplementary File 1. Custom code used to perform epidemiological simulations. The file contains the R script and complete instructions for installing and running the script.

Supplementary Table 1. ZIKV strains included in this study. The name of the ZIKV strains used in the study with their country of origin, original strain name, source of isolation, year of collection and the passage history prior to use in this study are indicated. TS: *Toxorhynchites splendens* mosquitoes; C6/36: *Aedes albopictus* cells; Vero: green monkey kidney cells; SM: suckling mouse brains.

Name in this	Country	Strain ID	Source	Year	Passage
study	, ,				history
F_Polynesia_2013	French	PE13/251013-18	Human serum	2013	C6/36-4
	Polynesia	1110/201010-10			00/00-4
Puerto_Rico_2015	Puerto		Human serum	2015	Vero-2: C6/36-3
	Rico	FINADC39			vero-2, co/so-s
Philippines_2012	Philippines	CPC-0740	Human serum	2012	TS-1; C6/36-2;
					Vero-1; C6/36-1
Thailand_2014	Thailand	SV0127-14	Human serum	2014	TS-1; C6/36-2;
					Vero-1; C6/36-1
Cambodia_2010	Cambodia	FSS13025	Human serum	2010	Vero 2; SM-1;
					C6/36-1
Senegal_2011	Senegal	Kedougou2011	Pool of Aedes spp.	2011	C6/36-2
			and <i>Mansonia</i> spp.		00/30-2
Senegal_2015	Senegal	Kedougou2015	Pool of Aedes spp.	2015	C6/36-2
			and <i>Mansonia</i> spp.		00/00-2

Supplementary Table 2. Parameter estimates of mosquito-to-human transmission events. The transmission kinetics of each ZIKV strain were modeled with a two-parameter log-logistic function to estimate their extrinsic incubation period (EIP) distribution. In the epidemiological simulations, the probability of mosquito-to-human transmission for each contact between a human and an infected mosquito was determined by the transmission probability inferred for each ZIKV strain from the EIP log-logistic distributions of location = log(e), and scale = 1/b.

	Log-logistic parameter			
	estimates			
ZIKV strain	е	b		
F_Polynesia_2013	16.60	-10.83		
Puerto_Rico_2015	20.74	-8.17		
Thailand_2014	18.76	-24.86		
Philippines_2012	19.01	-5.72		
Cambodia_2010	17.66	-4.99		
Senegal_2015	12.05	-3.24		

Application	Oligo	Sequence (5'-3')
ZIKV RNA	Forward	GTATGGAATGGAGATAAGGCCCA
quantification	Primer	
in mosquito	Reverse	ACCAGCACTGCCATTGATGTGC
experiments	primer	
ZIKV RNA	Forward	CCGCTGCCCAACACAAG
quantification	primer	
in mouse	Reverse	CCACTAACGTTCTTTTGCAGACAT
experiments	primer	
(Asian	Probe	6FAM/AGCCTACCT/ZEN/TGACAAGCAATCAGACACTCAA/
strains)		3'IABkFQ
ZIKV RNA	Forward	GTCGCTGTCCAACACAAG
quantification	primer	
in mouse	Reverse	CACCAGTGTTCTCTTGCAGACAT
experiments	primer	
(African	Probe	6FAM/AGCCTACCT/ZEN/TGACAAGCAATCAGACACTCAA/
strains)		3'IABkFQ
ZIKV RNA	gBlock	GAGGCATCAATATCAGACATGGCTTCTGACAGCCGCTGC
standards in		CCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGAC
mouse		ACTCAATATGTCTGCAAAAGAACGTTAGTGGACAGAGGCT
experiments		GGGGAAATGGATGTGGACT
(Asian		
strains)		
ZIKV RNA	gBlock	GAGGCATCAATATCGGACATGGCTTCGGACAGTCGCTGT
standards in		CCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGAC
mouse		ACTCAATATGTCTGCAAGAGAACACTGGTGGATAGAGGTT
experiments		GGGGAAATGGGTGTGGACT
(African		
strains)		

Supplementary Table 3. Oligonucleotides used in this study.



Supplementary Fig. 1. **Mouse-to-mosquito ZIKV transmission probability over time.** The lines represent the proportion of *Ae. aegypti* mosquitoes from Gabon (left) or Guadeloupe (right) that tested ZIKV-positive 14 days after taking a blood meal on the same triplet of *Ifnar1*^{-/-} mice inoculated with 10⁵ FFU of the Cambodia_2010 ZIKV strain on day 0. A median of 11 females per time point and per mouse (range 2-17) were tested for the Gabon population. A median of 13 females per time point and per mouse (range 0-19) were tested for the Guadeloupe population. The gold dashed lines represent the transmission probabilities for the 3 individual mice during their viremic period and the black line represent their mean. Horizontal ticks indicate the 95% confidence intervals of the probabilities. Source data are provided as a Source Data file.



Number of secondary human infections ≥ 100 < 100 None

Supplementary Fig. 2. Simulated effect of empirical variation in ZIKV transmissibility on the risk and magnitude of human outbreaks with reduced mosquito susceptibility. The figure shows the simulations results of Fig. 3 when the highly ZIKV susceptible mosquito population from Guadeloupe is replaced with a less susceptible mosquito population from Gabon (Fig. S1) to parameterize human-to-mosquito transmission events.



Supplementary Fig. 3. Variation in viremia kinetics between ZIKV strains after inoculation of a high virus dose. Time course of ZIKV viremia in AG129 mice inoculated on day 0 with 10^3 PFU of ZIKV. Viremia is expressed in log_{10} -transformed viral genome copies per ml of plasma (mean ± standard error). Each virus strain is represented by *n*=5 mice on each day, with the exception of day 6 for the Senegal_2011 and Senegal_2015 strains that are represented by *n*=10 mice. Source data are provided as a Source Data file.



Supplementary Fig. 4. Intraplacental injections of ZIKV induce subcutaneous edema. Photos show representative E14.5 embryos after intraplacental injection of mock inoculum (left; *n*=10 embryos) or Senegal_2015 ZIKV strain (right; *n*=9 embryos) at E10.5.

DAPI ACC3 ZIKV



Supplementary Fig. 5. African and Asian ZIKV strains show comparable organs tropism. Immunocompetent mouse embryos were infected at E10.5 by intraplacental injection of 500-1,000 PFU of ZIKV and examined at E14.5 by microdissection. Immunolabeling of embryonic eye, anterior and posterior spinal cord and atrium sections representative of each ZIKV strain tested (*n*=3 embryos per virus strain). Blue, green and red colors indicate DAPI, anti-cleaved caspase 3 (ACC3) and ZIKV stainings, respectively. The scale bars represent 200 μm.