

SUPPLEMENTARY MATERIAL

A Zika virus from America is more efficiently transmitted than an Asian virus by *Aedes aegypti* mosquitoes from Asia

Short title: Difference in ZIKV transmissibility between American and Asian strains

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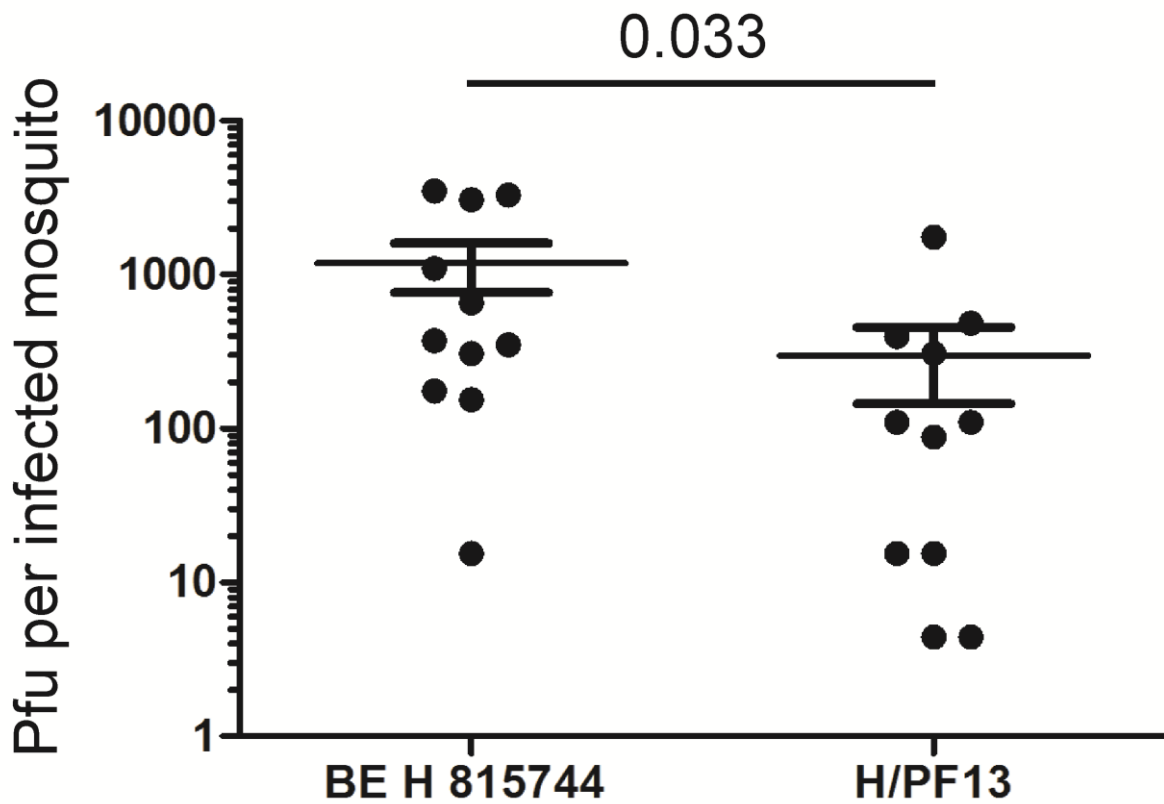


Figure S1. Virus titer in whole mosquitoes 3 days post-infection with ZIKV from the American (BE H 815744) or Asian (H/PF13) lineage.

Mosquitoes were orally infected with the two viruses and collected for titration 3 days p.i. Each point represents a mosquito. T-test statistical difference is shown.

Table S1. Summary of consensus level changes between the virus inoculum and the published KU365780 sequence

Position	Reference (KU365780)	Virus inoculum	Amino Acid coding	Codon changed in the virus stock ?
836	C	T	H	no
863	U	C	F	no
923	G	A	T	no
1034	C	T	T	no
1433	U	C	I	no
1475	A	G	K	no
1904	U	C	T	no
3137	U	C	H	no
3534	A	G	M --> V	yes
3566	C	T	D	no
5267	C	T	R	no
5270	C	T	T	no
5315	G	A	E	no
5438	A	G	R	no
6320	C	T	N	no
6671	C	T	F	no
6803	U	C	F	no
6959	U	C	H	no
6983	G	A	G	no
7493	G	A	G	no
8213	G	A	K	no
8327	U	C	Y	no
8408	U	A	P	no
8439	G	A	D --> N	yes
8867	C	T	F	no
8978	U	C	D	no
9242	U	C	R	no
9344	A	G	E	no
9560	A	G	L	no
10447	-	C	N/A	N/A
836	C	T	H	no
863	U	C	F	no
923	G	A	T	no
1034	C	T	T	no
1433	U	C	I	no
1475	A	G	K	no
1904	U	C	T	no
3137	U	C	H	no

3534	A	G	M --> V	yes
3566	C	T	D	no
5267	C	T	R	no
5270	C	T	T	no
5315	G	A	E	no
5438	A	G	R	no
6320	C	T	N	no
6671	C	T	F	no
6803	U	C	F	no
6959	U	C	H	no
6983	G	A	G	no
7493	G	A	G	no
8213	G	A	K	no
8327	U	C	Y	no
8408	U	A	P	no
8439	G	A	D --> N	yes
8867	C	T	F	no
8978	U	C	D	no
9242	U	C	R	no
9344	A	G	E	no
9560	A	G	L	no
10447	-	C	N/A	N/A

Table S2. Analysis of low frequency variants in the viral inoculum

Position	Consensus	Variant	Depth of Coverage	Allele frequency
326	G	A	14572	0.0122
436	T	C	20630	0.0051
1028	T	G	23218	0.0067
1278	T	C	21663	0.0064
2400	T	C	18196	0.0058
3147	A	G	22397	0.0054
3535	T	C	22939	0.0581
4106	A	G	19790	0.0055
7416	A	G	16086	0.0052
7499	T	C	11179	0.0062
9227	A	G	22884	0.0071
9434	A	G	20014	0.0065
9548	T	C	20185	0.0051
9917	C	A	16861	0.0199
10220	T	C	17801	0.0050
10666	T	A	11990	0.0067
10717	A	G	7013	0.0093
10772	A	G	2834	0.0159

Table S3. Code and origin of the strain used for genome comparison

Continent	Country	Date of collection	GenBank ID	
Americas	Brazil	2015	KU365780 ¹	
			KX280026	
			KU527068	
			KU321639	
			KU497555	
			KX197205	
			KU365778	
			KX520666	
			KR872956	
			KU365780	
			KU365777	
			KU365779	
			KU707826	
	KU729217			
	KU729218			
	2016		KY014320	
			KY014307	
			KY014317	
			KY014301	
			KY014297	
			KX197192	
			KX811222	
			KY014296	
KU820897				
KX087102				
KX548902				
2016		KX247646		
Ecuador	2016	KX879603		
		KX879604		
French Guiana	2015	KU758877		
		KU312312		
Suriname	2015	KU312312		
		2016	KU937936	
Venezuela	2016	KX893855		
		KX702400		
Asia	Cambodia	2010	KU955593	
			KX369547 ¹	
	French Polynesia	2013	KX369547 ¹	
	Philippines	2012	KU681082	
	Thailand	2013	KX694532	
			2014	KU681081
			2016	KY272987
	Singapore	2016	KX827309	
KX813683				

¹ Virus used in the oral infection study.