Published in final edited form as:

Transfusion. 2014 August ; 54(8): 1911–1915. doi:10.1111/trf.12790.

Chikungunya virus – new risk to transfusion safety in the Americas

Lyle R. Petersen, MD, MPH and

Division of Vector-Borne Diseases, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, 3156 Rampart Road, Fort Collins, CO 80525

Jay S. Epstein, MD

Office of Blood Research and Review, Center for Biologics Evaluation and Research, Food and Drug Administration, WO71-4230, 10903 New Hampshire Avenue, Silver Spring, Maryland 20993-0002

On December 5, 2013, the French National Reference Centre for Arboviruses confirmed autochthonous chikungunya virus (CHIKV) transmission on the Caribbean island of St. Martin.[1,2] This mosquito-borne virus, so-named in the Makonde language for its ability to cause crippling arthralgia, has caused large outbreaks in multiple locations in Africa, Asia, and the Western Pacific in the last decade.[3,4] Prior to its arrival in St. Martin, few doubted that CHIKV would eventually emerge and take hold in the Western Hemisphere given the widespread presence of competent mosquito vectors and opportunities for the virus to be introduced through travel and commerce.[5–9] The virus' subsequent swift spread from St. Martin throughout the Caribbean[4] and onto South America have created considerable concern regarding its eventual extent and intensity of transmission in the Western Hemisphere, and hence its impact on transfusion safety.

Although transfusion-associated CHIKV transmission has not been reported, most likely due to the difficulty in identifying and proving CHIKV transfusion-associated transmission in the context of large-scale community mosquito-borne outbreaks, the AABB Transfusion Transmitted Diseases Committee deemed CHIKV a priority area of concern[10,11] given its high-level viremia[12–15] and high incidence during outbreaks.[6,16–18] As with other arboviruses, four factors will determine the impact of CHIKV on transfusion medicine in the Americas: (1) prevalence of viremia among blood donors, (2) clinical impact on infected transfusion recipients, (3) availability of measures to reduce transfusion transmission when required, and (4) the cost and disruption incurred by those measures.[19]

The prevalence of viremia among blood donors relates to the incidence of infection in the population-at-large, and in this regard, the outlook for CHIKV in tropical America is grim. CHIKV, like dengue, is transmitted efficiently in urban settings in a human-mosquito-human transmission cycle by *Aedes aegypti* mosquitoes, whose distribution extends from the southern United States to northern Argentina (Figure). The Pan American Health Organization recorded more than 2.3 million dengue cases in 2013; the actual number of dengue infections likely vastly exceeded this number given disease underreporting and that most dengue virus infections remain asymptomatic.[20–22] One study estimated the true

number of apparent and inapparent dengue infections in the Americas in 2010 was 13.3 and 40.5 million, respectively.[23] Thus, CHIKV can be expected to spread throughout much of tropical America and cause explosive outbreaks involving tens or hundreds of thousands of persons as it has done in other dengue endemic areas of the Old World.

The potential for large CHIKV outbreaks on the fringes of the *Aedes aegypti* distribution, such as the southern United States, is much less certain.[24] Dengue outbreaks in Florida and Texas in recent years have been relatively focal and self-limited, likely due to sociological conditions that limit contact with the indoor-biting *Aedes aegypti* mosquito, such as the frequent use of air conditioning.[25–27] While this suggests that CHIKV may follow a similar pattern, the transmission potential for CHIKV relative to dengue virus in these settings is unknown. In addition, *Aedes albopictus,* the outdoor-biting Asian tiger mosquito, is endemic in much of the southern and eastern United States (Figure).[28] Since this mosquito is also a competent vector for CHIKV,[29] it could also help drive outbreaks, particularly in temperate areas where *Aedes aegypti* does not exist, as was demonstrated by an outbreak in northern Italy involving more than 300 persons. The Italian outbreak was caused by a southern/central/east African genotype CHIKV containing an envelope protein mutation (E1 A226V) that increases viral fitness in *Aedes albopictus* mosquitoes (references).[30,31] Although the Asian genotype CHIKV now circulating in the Americas does not possess this mutation,[2,32] A recent study indicated that *Aedes albopictus* mosquitoes collected throughout the Americas are generally competent to transmit the Asian genotype CHIKV strain.[33]

In this issue of *Transfusion*, Appassakij and colleagues report on a study in which they adapted a modeling approach originally created to estimate West Nile virus transfusion transmission risk in the United States[34,35] to estimate the prevalence of viremic blood donors during a CHIKV outbreak in Thailand involving an estimated 71,000 ill persons (5.3%) in a population of 1,344,000.[36] Assuming a 1.5-day viremia before symptoms and either a total 9.5-day or 18.5-day viremia for asymptomatic persons, the model yielded a mean weekly prevalence of viremic donations of 38.2 and 52.3, respectively, per 100,000 donations, with a maximum weekly prevalence of 237.0 and 267.1, respectively, per 100,000. The authors validated their model findings by comparing CHIKV nucleic acid amplification test (NAT) results (0.10% positive) of donations collected for a 5-week period during the waning period of the outbreak with their model results for the corresponding time frame (estimated prevalence 0.20–0.33%). Of note, the authors predicted that 11 CHIKV-contaminated donations would have been received during the epidemic. Even if all of these donations were transfused, the resultant infections in recipients would have represented a tiny fraction of the estimated 71,000 cases in the population.

Two similar previously published models have estimated the risk of CHIKV prevalence in donors during outbreaks. During a large outbreak on Reunion Island involving approximately 244,000 persons, or 35% of the island's population, the model indicated a substantial prevalence (132 per 100,000 donations; maximum 1500 per 100,000 donations) of chikungunya viremic donors.[16,37] This model assumed a 1.5-day viremia before symptoms and a total 7.5-day viremia for those asymptomatic. As with the Thai study, the Reunion Island model results (estimated prevalence 0.7%) compared favorably with the proportion of NAT-positive donations (0.4%) during a 4-month period during the outbreak,

thus confirming the validity of the model results. Another study using the same modeling approach during the much smaller CHIKV outbreak in northern Italy involving 337 suspected cases (0.03%) in a population of 1,040,000, the maximum weekly prevalence of viremic donations was estimated at 1.05 per 100,000 donations.[38,39] This model assumed a 2-day viremia before symptoms and a total 8-day viremia for those symptomatic.

All of these models estimated the proportion of donations that were viremic as measured by the duration of NAT positivity; however, this duration may not correlate with the actual duration of risk of transfusion transmission. Extensive experience with West Nile virus indicates that the measured duration of NAT positivity depends on the sensitivity of the assay, whether samples are pooled for testing, and the number of replicates tested.[40] Furthermore, CHIKV specific IgM antibodies develop around six days after illness onset, a period shorter than the duration of NAT positivity.[12,15] If CHIKV is similar to West Nile virus in which NAT-positive donations containing West Nile virus specific IgM antibodies rarely transmit infection to recipients,[41,42] the duration of CHIKV transmission risk may be shorter than the duration of NAT positivity. In addition, not all recipients may be susceptible to infection, particularly if high population background immunity develops. While current background CHIKV immunity in populations in the Western Hemisphere is extremely low or nonexistent, this will evolve as the current epidemic continues.

Despite these limitations, the model results from both Reunion Island and Thailand indicate a significant short-term risk of transfusion-associated CHIKV transmission during the large outbreaks that will likely occur in tropical America, while the Italian model suggests a small, but quantifiable risk that may exceed accepted safety standards during smaller, focal outbreaks that may occur in temperate areas of the United States. This risk is likely to have clinical significance as upwards of 80% of those infected with CHIKV become symptomatic, often with considerable morbidity and occasional mortality among the elderly and those with preexisting conditions.[17,43–45] To mitigate this risk during the Thai outbreak, blood centers enhanced pre-donation screening questions about CHIKV-related symptoms and implemented an enhanced post-donation notification system.[36] In addition, components from donors at high risk were quarantined for 7 days after donation, at which time donors were called to ascertain symptoms. It was not stated how the authors defined “high risk”. Of the 299 donations initially deemed high-risk, 11 developed symptoms suggestive of CHIKV infection.

In the Reunion Island CHIKV outbreak, routine blood collections were suspended except for platelets, which were then photochemically inactivated.[46] Two (0.4%) of 500 platelet donations were found to be NAT-positive; thus, documenting the possible benefit of this approach.[37] During the northern Italian CHIKV outbreak, all collections were suspended in affected areas until the expected prevalence of viremic donors fell below one in 380,000 and visitors to affected areas were initially deferred from donation for 21 days.[39] Blood products were imported from areas of continuing blood collections and efforts were made to reduce blood product usage. The economic costs associated with the Italian efforts exceeded 1.3 million Euros. No data exist regarding the efficacy of deferring potential donors returning from areas experiencing outbreaks; however, one mathematical model suggested that

deferring the approximately 4500 Dutch tourists visiting Thai CHIKV outbreak areas would result in an expected reduction of 0.068 infected donors annually.[47]

Possible mitigation strategies to reduce CHIKV transfusion risk in the Western Hemisphere are indicated in the table. Curtailing donations during outbreaks, NAT screening, and photochemical inactivation of platelets are likely to be highly effective, but expensive. Screening potential donors, enhanced post-donation notification of symptoms by donors, or deferring potential donors who have traveled to outbreak areas will be less expensive, but could lack specificity and thus eliminate many low-risk donors. Three mitigation strategies are now implemented on two Caribbean islands experiencing CHIKV outbreaks (Martinique and Guadeloupe): photochemical inactivation of platelets, CHIKV NAT screening of red cells, and importation of plasma from France. In anticipation of the possible need for interventions in the United States and its territories, the U.S. Food and Drug Administration (FDA) is facilitating further development of CHIKV NAT assays for donor screening, in part, by providing candidate manufacturers reference panels to assure test kit sensitivity. Additionally, FDA plans a survey in cooperation with AABB to estimate donor losses if a policy of temporary deferral were implemented for travelers to outbreak regions.

The inherent uncertainties regarding the timing and extent of transmission of CHIKV or other emergent arboviruses will continue to complicate decisions regarding implementation of mitigation strategies to reduce their transfusion transmission risk. Fortunately, as now demonstrated for the West Nile and chikungunya viruses, the transfusion risk model has proven a robust indicator of arboviral transfusion transmission risk from which to guide mitigation strategies once an outbreak begins. CHIKV is the latest, but certainly not the last, emerging pathogen to threaten blood safety. Until effective, practical and cost-effective pathogen inactivation techniques applicable to all components of blood collections in a wide range of settings are developed, we must rely on a menu of costly and imperfect options to ensure blood safety.

References

1. Cassadou S, Boucau S, Petit-Sinturel M, Huc P, Leparc-Goffart I, Ledrans M. Emergence of chikungunya fever on the French side of Saint Martin island, October to December 2013. Euro Surveill 2014;19.
2. Leparc-Goffart I, Nougairede A, Cassadou S, Prat C, de Lamballerie X. Chikungunya in the Americas. Lancet 2014;383: 514. [PubMed: 24506907]
3. Burt FJ, Rolph MS, Rulli NE, Mahalingam S, Heise MT. Chikungunya: a re-emerging virus. Lancet 2012;379: 662–71. [PubMed: 22100854]
4. Van Bortel W, Dorleans F, Rosine J, Blateau A, Rousseau D, Matheus S, Leparc-Goffart I, Flusin O, Prat CM, Cesaire R, Najioullah F, Ardillon V, Balleydier E, Carvalho L, Lemaitre A, Noel H, Servas V, Six C, Zurbaran M, Leon L, Guinard A, van den KJerhof J, Henry M, Fanoy E, Braks M, Reimerink J, Swaan C, Georges R, Brooks L, Freedman J, Sudre B, Zeller H. Chikungunya outbreak in the Caribbean region, December 2013 to March 2014, and the significance for Europe. Euro Surveill 2014;19: pii=20759. [PubMed: 24721539]
5. Chaves Tdo S, Pellini AC, Mascheretti M, Jahnel MT, Ribeiro AF, Rodrigues SG, Vasconcelos PF, Boulos M. Travelers as sentinels for chikungunya fever, Brazil. Emerg Infect Dis 2012;18: 529–30. [PubMed: 22377013]
6. Powers AM, Logue CH. Changing patterns of chikungunya virus: re-emergence of a zoonotic arbovirus. J Gen Virol 2007;88: 2363–77. [PubMed: 17698645]

7. Gibney KB, Fischer M, Prince HE, Kramer LD, St George K, Kosoy OL, Laven JJ, Staples JE. Chikungunya fever in the United States: a fifteen year review of cases. Clin Infect Dis 2011;52: e121–6. [PubMed: 21242326]

8. Savini H, Gautret P, Gaudart J, Field V, Castelli F, Lopez-Velez R, Lim PL, Shaw M, von Sonnenburg F, Loutan L, Simon F, GeoSentinel Surveillance N. Travel-associated diseases, Indian Ocean Islands, 1997–2010. Emerg Infect Dis 2013;19: 1297–301. [PubMed: 23876977]

9. Organization' PAH. Preparedness and Response for Chikungunya Virus Washington, D.C.: PAHO, 2011.

10. Stramer SL, Hollinger FB, Katz LM, Kleinman S, Metzel PS, Gregory KR, Dodd RY. Emerging infectious disease agents and their potential threat to transfusion safety. Transfusion 2009;49 Suppl 2: 1S–29S. [PubMed: 19686562]

11. Atreya C, Nakhasi H, Mied P, Epstein J, Hughes J, Gwinn M, Kleinman S, Dodd R, Stramer S, Walderhaug M, Ganz P, Goodrich R, Tibbetts C, Asher D. FDA workshop on emerging infectious diseases: evaluating emerging infectious diseases (EIDs) for transfusion safety. Transfusion 2011;51: 1855–71. [PubMed: 21392016]

12. Lanciotti RS, Kosoy OL, Laven JJ, Panella AJ, Velez JO, Lambert AJ, Campbell GL. Chikungunya virus in US travelers returning from India, 2006. Emerg Infect Dis 2007;13: 764–7. [PubMed: 17553261]

13. Staikowsky F, Talarmin F, Grivard P, Souab A, Schuffenecker I, Le Roux K, Lecuit M, Michault A. Prospective study of Chikungunya virus acute infection in the Island of La Reunion during the 2005–2006 outbreak. PLoS One 2009;4: e7603. [PubMed: 19893613]

14. Thiberville SD, Boisson V, Gaudart J, Simon F, Flahault A, de Lamballerie X. Chikungunya fever: a clinical and virological investigation of outpatients on Reunion Island, South-West Indian Ocean. PLoS Negl Trop Dis 2013;7: e2004. [PubMed: 23350006]

15. Panning M, Grywna K, van Esbroeck M, Emmerich P, Drosten C. Chikungunya fever in travelers returning to Europe from the Indian Ocean region, 2006. Emerg Infect Dis 2008;14: 416–22. [PubMed: 18325256]

16. Renault P, Solet JL, Sissoko D, Balleydier E, Larrieu S, Filleul L, Lassalle C, Thiria J, Rachou E, de Valk H, Ilef D, Ledrans M, Quatresous I, Quenel P, Pierre V. A major epidemic of chikungunya virus infection on Reunion Island, France, 2005–2006. Am J Trop Med Hyg 2007;77: 727–31. [PubMed: 17978079]

17. Sergon K, Njuguna C, Kalani R, Ofula V, Onyango C, Konongoi LS, Bedno S, Burke H, Dumilla AM, Konde J, Njenga MK, Sang R, Breiman RF. Seroprevalence of Chikungunya virus (CHIKV) infection on Lamu Island, Kenya, October 2004. Am J Trop Med Hyg 2008;78: 333–7. [PubMed: 18256441]

18. Krishnamoorthy K, Harichandrakumar KT, Krishna Kumari A, Das LK. Burden of chikungunya in India: estimates of disability adjusted life years (DALY) lost in 2006 epidemic. J Vector Borne Dis 2009;46: 26–35. [PubMed: 19326705]

19. Petersen LR, Busch MP. Transfusion-transmitted arboviruses. Vox Sang 2010;98: 495–503. [PubMed: 19951309]

20. Porter KR, Beckett CG, Kosasih H, Tan RI, Alisjahbana B, Rudiman PI, Widjaja S, Listiyaningsih E, Ma'Roef CN, McArdle JL, Parwati I, Sudjana P, Jusuf H, Yuwono D, Wuryadi S. Epidemiology of dengue and dengue hemorrhagic fever in a cohort of adults living in Bandung, West Java, Indonesia. Am J Trop Med Hyg 2005;72: 60–6. [PubMed: 15728868]

21. Rigau-Perez JG. Surveillance for an emerging disease: dengue hemorrhagic fever in Puerto Rico, 1988–1997. P R Health Sci J 1999;18: 337–45. [PubMed: 10730300]

22. Rodriguez-Figueroa L, Rigau-Perez JG, Suarez EL, Reiter P. Risk factors for dengue infection during an outbreak in Yanes, Puerto Rico in 1991. Am J Trop Med Hyg 1995;52: 496–502. [PubMed: 7611553]

23. Bhatt S, Gething PW, Brady OJ, Messina JP, Farlow AW, Moyes CL, Drake JM, Brownstein JS, Hoen AG, Sankoh O, Myers MF, George DB, Jaenisch T, Wint GR, Simmons CP, Scott TW, Farrar JJ, Hay SI. The global distribution and burden of dengue. Nature 2013;496: 504–7. [PubMed: 23563266]

24. Eisen L, Moore CG. Aedes (Stegomyia) aegypti in the continental United States: a vector at the cool margin of its geographic range. J Med Entomol 2013;50: 467–78. [PubMed: 23802440]
25. Brunkard JM, Robles Lopez JL, Ramirez J, Cifuentes E, Rothenberg SJ, Hunsperger EA, Moore CG, Brussolo RM, Villarreal NA, Haddad BM. Dengue fever seroprevalence and risk factors, Texas-Mexico border, 2004. Emerg Infect Dis 2007;13: 1477–83. [PubMed: 18257990]
26. Ramos MM, Mohammed H, Zielinski-Gutierrez E, Hayden MH, Lopez JL, Fournier M, Trujillo AR, Burton R, Brunkard JM, Anaya-Lopez L, Banicki AA, Morales PK, Smith B, Munoz JL, Waterman SH, Dengue Serosurvey Working G. Epidemic dengue and dengue hemorrhagic fever at the Texas-Mexico border: results of a household-based seroepidemiologic survey, December 2005. Am J Trop Med Hyg 2008;78: 364–9. [PubMed: 18337327]
27. Radke EG, Gregory CJ, Kintziger KW, Sauber-Schatz EK, Hunsperger EA, Gallagher GR, Barber JM, Biggerstaff BJ, Stanek DR, Tomashek KM, Blackmore CG. Dengue outbreak in Key West, Florida, USA, 2009. Emerg Infect Dis 2012;18: 135–7. [PubMed: 22257471]
28. Benedict MQ, Levine RS, Hawley WA, Lounibos LP. Spread of the tiger: global risk of invasion by the mosquito Aedes albopictus. Vector Borne Zoonotic Dis 2007;7: 76–85. [PubMed: 17417960]
29. Reiskind MH, Pesko K, Westbrook CJ, Mores CN. Susceptibility of Florida mosquitoes to infection with chikungunya virus. Am J Trop Med Hyg 2008;78: 422–5. [PubMed: 18337338]
30. Lambrechts L Quantitative genetics of Aedes aegypti vector competence for dengue viruses: towards a new paradigm? Trends Parasitol 2011;27: 111–4. [PubMed: 21215699]
31. Tsetsarkin KA, Vanlandingham DL, McGee CE, Higgs S. A single mutation in chikungunya virus affects vector specificity and epidemic potential. PLoS Pathog 2007;3: e201. [PubMed: 18069894]
32. Lanciotti RS, Valadere AM. Transcontinental movement of Asian genotype chikungunya virus Emerg Infect Dis 2014.
33. Vega-Rua A, Zouache K, Girod R, Failloux AB, Lourenco-de-Oliveira R. High level of vector competence of Aedes aegypti and Aedes albopictus from ten American countries as a crucial factor in the spread of chikungunya virus. J Virol 2014;88: 6294–306. [PubMed: 24672026]
34. Biggerstaff BJ, Petersen LR. Estimated risk of West Nile virus transmission through blood transfusion during an epidemic in Queens, New York City. Transfusion 2002;42: 1019–26. [PubMed: 12385413]
35. Biggerstaff BJ, Petersen LR. Estimated risk of transmission of the West Nile virus through blood transfusion in the US, 2002. Transfusion 2003;43: 1007–17. [PubMed: 12869104]
36. Appassakij H, Promwong C, Rujirojindakul P, Wutthanarungsan R, Silpapojakul K. The risk of blood transfusion-associated Chikungunya fever during the 2009 epidemic in Songkhla Province, Thailand. Transfusion 2014.
37. Brouard C, Bernillon P, Quatresous I, Pillonel J, Assal A, De Valk H, Desenclos JC, workgroup "Quantitative Estimation of the Risk of Blood Donation Contamination by Infectious A. Estimated risk of Chikungunya viremic blood donation during an epidemic on Reunion Island in the Indian Ocean, 2005 to 2007. Transfusion 2008;48: 1333–41. [PubMed: 18298600]
38. Rezza G, Nicoletti L, Angelini R, Romi R, Finarelli AC, Panning M, Cordioli P, Fortuna C, Boros S, Magurano F, Silvi G, Angelini P, Dottori M, Ciufolini MG, Majori GC, Cassone A, group Cs. Infection with chikungunya virus in Italy: an outbreak in a temperate region. Lancet 2007;370: 1840–6. [PubMed: 18061059]
39. Liumbruno GM, Calteri D, Petropulacos K, Mattivi A, Po C, Macini P, Tomasini I, Zucchelli P, Silvestri AR, Sambri V, Pupella S, Catalano L, Piccinini V, Calizzani G, Grazzini G. The Chikungunya epidemic in Italy and its repercussion on the blood system. Blood Transfus 2008;6: 199–210. [PubMed: 19112735]
40. Busch MP, Kleinman SH, Tobler LH, Kamel HT, Norris PJ, Walsh I, Matud JL, Prince HE, Lanciotti RS, Wright DJ, Linnen JM, Caglioti S. Virus and antibody dynamics in acute West Nile virus infection. J Infect Dis 2008;198: 984–93. [PubMed: 18729783]
41. Centers for Disease Control and Prevention. West Nile virus transmission through blood transfusion--South Dakota, 2006. MMWR Morb Mortal Wkly Rep 2007;56: 76–9. [PubMed: 17268405]

42. Centers for Disease C, Prevention. Fatal West Nile virus infection after probable transfusion-associated transmission--Colorado, 2012. MMWR Morb Mortal Wkly Rep 2013;62: 622–4. [PubMed: 23925171]

43. Sissoko D, Moendandze A, Malvy D, Giry C, Ezzedine K, Solet JL, Pierre V. Seroprevalence and risk factors of chikungunya virus infection in Mayotte, Indian Ocean, 2005–2006: a population-based survey. PLoS One 2008;3: e3066. [PubMed: 18725980]

44. Queyriaux B, Simon F, Grandadam M, Michel R, Tolou H, Boutin JP. Clinical burden of chikungunya virus infection. Lancet Infect Dis 2008;8: 2–3. [PubMed: 18156079]

45. Economopoulou A, Dominguez M, Helynck B, Sissoko D, Wichmann O, Quenel P, Germonneau P, Quatresous I. Atypical Chikungunya virus infections: clinical manifestations, mortality and risk factors for severe disease during the 2005–2006 outbreak on Reunion. Epidemiol Infect 2009;137: 534–41. [PubMed: 18694529]

46. Rasongles P, Angelini-Tibert MF, Simon P, Currie C, Isola H, Kientz D, Slaedts M, Jacquet M, Sundin D, Lin L, Corash L, Cazenave JP. Transfusion of platelet components prepared with photochemical pathogen inactivation treatment during a Chikungunya virus epidemic in Ile de La Reunion. Transfusion 2009;49: 1083–91. [PubMed: 19309473]

47. Lieshout-Krikke RW, Zaaijer HL, Prinsze FJ. The yield of temporary exclusion of blood donors, exposed to emerging infections abroad. Vox Sang 2013;104: 12–8. [PubMed: 22775433]

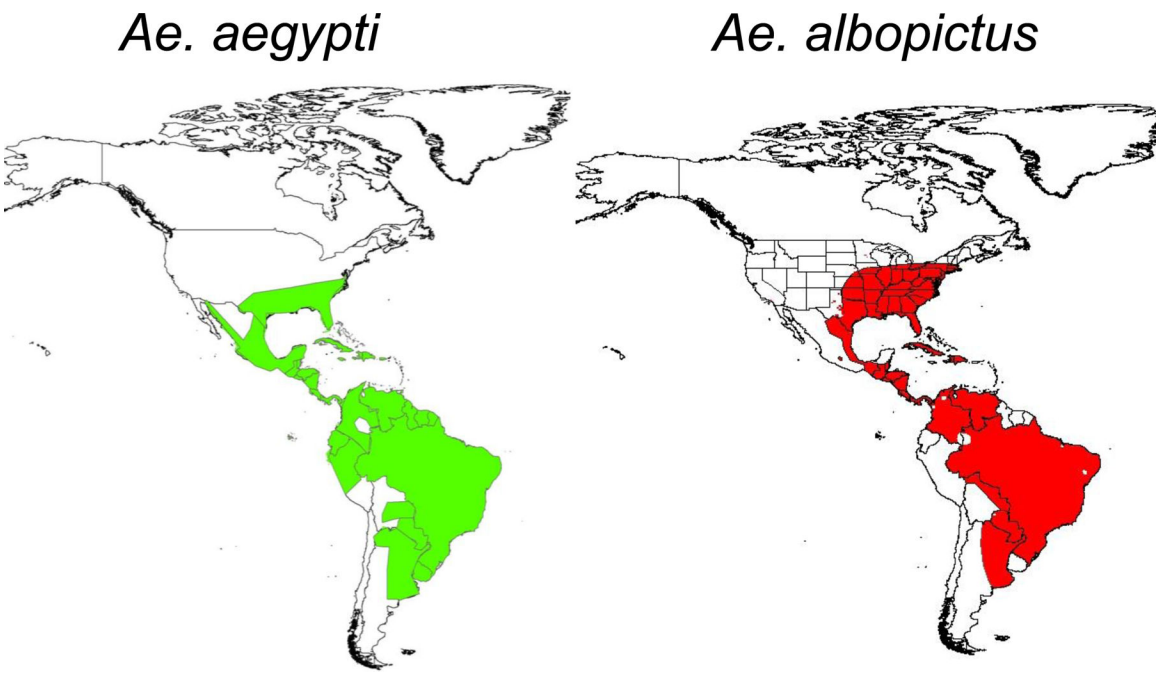

Figure.
Distribution of *Aedes aegypti* and *Aedes albopictus* in the Western Hemisphere.

Table:

Possible mitigation strategies to reduce the risk of CHIKV transfusion transmission in the Americas

Mitigation strategy	Setting	Comment
Enhanced donor pre-donation symptom screening	Areas with outbreaks or at risk for outbreaks	Will not identify viremic persons who are asymptomatic. Will have low predictive value in areas with low infection incidence, resulting in unnecessary loss of donors.
Enhanced post-donation illness notification by blood donors	Areas with outbreaks or travelers from areas experiencing outbreaks	No impact on components already transfused from donors who remain asymptomatic. Could be combined with short-term quarantine of components. Will have low predictive value in areas with low infection incidence, resulting in unnecessary component loss.
Defer donors returning from areas with outbreaks	Areas without outbreaks	Difficult to define outbreak areas as well as the associated risk of a traveler acquiring CHIKV in those areas. Potential for extensive donor loss with little improvement in safety. Optimal deferral period uncertain.
Curtail routine collections during outbreaks	Areas with focal, limited outbreaks	Likely to be disruptive and expensive. Only feasible upon availability of imported blood supplies. Trigger-on and trigger-off strategies could be based on predicted prevalence of viremic donations.
Photochemical inactivation of platelets	Areas with focal, limited outbreaks	Expensive and depends on availability of inactivation equipment. Currently exists only as investigational technology in the U.S.
CHIKV-specific nucleic acid amplification testing	Large outbreaks or focal use in small outbreak areas	Expensive. No licensed blood donor screening test is available in the U.S. Efficacy expected to be very high.