An Estimate of the Burden of Chagas Disease in the United States

Caryn Bern and Susan P. Montgomery

Division of Parasitic Diseases, National Center for Zoonotic, Vector-Borne and Enteric Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia

Chagas disease causes the highest burden of any parasitic disease in the Western hemisphere. By applying published seroprevalence figures to immigrant populations, we estimate that 300,167 individuals with *Trypanosoma cruzi* infection live in the United States, with 30,000–45,000 cardiomyopathy cases and 63–315 congenital infections annually. *T. cruzi* causes a substantial disease burden in the United States.

Chagas disease, caused by the protozoan *Trypanosoma cruzi,* is responsible for a greater disease burden than any other parasitic disease in the New World [1]. Infection occurs when the triatomine vector defecates during its blood meal and fecal material containing the parasite is inoculated through the bite wound or mucous membranes [2]. Vector-borne transmission occurs only in the Americas, where an estimated 8 million people are currently infected with *T. cruzi* [3]. Historically, transmission was concentrated in rural Latin America, but successful vector-control programs have greatly decreased transmission in areas where the disease was formerly endemic, whereas migration has brought infected individuals to cities in Latin America, as well as to the United States, Europe, and Japan [4].

The United States cannot be classified as an area of nonendemicity for Chagas disease in the same sense as Europe or Asia. The southern states have enzootic *T. cruzi* transmission that involves at least 11 triatomine species and hosts such as raccoons, opossums, and domestic dogs [5, 6]. Nevertheless, the vast majority of *T. cruzi*–infected individuals are immigrants from areas of endemicity in Latin America. Only 7 autochthonous vector-borne cases of infection (4 in Texas and 1 each in California, Tennessee, and Louisiana) have been reported in the United States since 1955 [7]. The rarity of vector-borne transmission in the United States, compared with Latin America, is thought to be the result of better housing conditions and lower efficiency of North American vectors.

Estimation of the number of *T. cruzi*–infected individuals in the United States is challenging, because the underlying data are sparse. Previous calculations have relied on a patchwork of *T. cruzi* prevalence estimates, derived from blood donor screening data and surveys from Latin America applied to the immigrant population [8, 9]. The highest early estimate (~370,000 infected US residents in 1992) used a Latin America–wide prevalence rather than country-specific estimates and was therefore likely to be a substantial overestimation [10]. Published US disease burden figures range from 50,000 to 1 million, but the lowest estimate is now 15 years old [8], and the highest estimate [11] was based on an extrapolation of the highest early estimate [10], thereby compounding the likely overestimation.

In 2006, the Pan American Health Organization (PAHO) published updated country-specific estimates of the prevalence and burden of *T. cruzi* infection [3]. These figures represent the first attempt since 1990 to produce integrated estimates that are based on the best currently available national data, while recognizing that data completeness and precision vary by country. Some

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Reprints or correspondence: Dr. Caryn Bern, Div. of Parasitic Diseases, MS F-22, 4770 Buford Highway NE, National Center for Zoonotic, Vector-Borne and Enteric Diseases, Centers for Disease Control and Prevention, Atlanta, GA 30341 (CBern@cdc.gov).

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Table 1. Calculated Prevalence of *Trypanosoma cruzi* Infections in Latin American–Born Persons living in the United States in 2005

Country of origin	Immigrant population living in the United States	*T. cruzi* prevalence in country of origin, %	Estimated no. of immigrants with *T. cruzi* infection in the United States
Mexico	16,963,851	1.03	174,388
El Salvador	1,458,014	3.37	49,164
Guatemala	1,014,669	1.98	20,131
Honduras	567,002	3.05	17,311
Argentina	223,931	4.13	9246
Ecuador	345,204	1.74	6003
Colombia	554,821	0.96	5304
Brazil	501,036	1.02	5106
Bolivia	61,453	6.75	4149
Nicaragua	223,931	1.14	2553
Peru	371,980	0.69	2552
Venezuela	151,350	1.16	1754
Chile	92,761	0.99	914
Costa Rica	95,761	0.53	509
Paraguay	16,707	2.54	425
Uruguay	51,737	0.66	339
Belize	42,130	0.74	312
Panama	107,601	0.01	6
Total	22,843,939	1.31	300,167

NOTE. Data adapted from [3, 14, 15].

countries have representative serial survey data [12], whereas others continue to rely on extrapolations from blood donor screening and modelling based on measured vector distribution, density, and infection rates [13].

Applying birth country prevalence estimates to immigrant populations entails a number of inherent sources of uncertainty. First, *T. cruzi* transmission is not uniformly distributed across a national population. Rural populations that live in areas with ecology that is hospitable to vector infestation have a disease prevalence that is many times that found among urban populations, whereas urban populations originating in areas of endemicity have prevalence rates that are higher than rates among rural populations living in conditions that are hostile to the vectors (eg, at high altitudes). Equally important, immigrant populations who come from specific regions may have a higher or lower risk of *T. cruzi* infection, compared with the national population. Finally, the age structure of immigrant populations is likely to differ from that of the total population in their country of origin; an immigrant population will likely contain fewer older adults, who would have a disease prevalence higher than that for the general population, but will also likely contain fewer children, whose disease prevalence would be lower than that for the general population. Currently available data are not sufficient to refine our estimates on the basis of these differences. We summed the estimates for the authorized Latin American immigrant population made by the Pew Hispanic Center, which were based on US Census data and the American Community Survey [14], and those for unauthorized immigrant populations published by the Department of Homeland Security [15]. We then applied the seroprevalence figures for each country [3] to total immigrant populations by country of birth to arrive at an estimate of 300,167 persons with *T. cruzi* infection living in the United States in the year 2005 (table 1).

Widespread blood donation screening for *T. cruzi* began in January 2007, increasing the visibility of Chagas disease in the United States [16]. The US Food and Drug Administration–approved Ortho *T. cruzi* enzyme-linked immunosorbent assay (ELISA) test system, which is based on parasite lysate antigen, is currently used as the initial screening assay. Like many other serological tests for *T. cruzi,* the Ortho ELISA has cross-reactivity with leishmaniasis. For blood donor testing, ELISA-repeat reactive units are confirmed using the radioimmune precipitation assay [16]. Since screening began, 797 confirmed seropositive donations have been detected in 42 states, with the largest numbers found in California, Florida, and Texas [17]. The majority of persons with *T. cruzi* infection show no signs or symptoms of chronic Chagas disease and are considered to have the indeterminate form. However, data from Latin America suggests that 20%–30% of infected individuals will experience disease progression over the course of their lives to

clinically evident Chagas disease (most commonly, cardiomyopathy) [2]. The disease usually becomes clinically evident, with conduction system disease and/or ventricular arrhythmias, when patients are between 20 and 50 years of age and may subsequently progress to dilated cardiomyopathy and congestive heart failure. Because the immigrant population is younger than the US population as a whole, we used a conservative proportion of 10%–15% with clinical disease; this calculation results in a total of 30,000–45,000 individuals likely to have undiagnosed Chagas cardiomyopathy.

Finally, we estimated the number of newborns at risk of congenital *T. cruzi* infection on the basis of annual births to women born in countries in which infection is endemic [14] and the PAHO seroprevalance figures for each country. Because the rate of transmission from infected mother to child varies widely in published reports, we assumed a range of 1%–5%, yielding an estimate of 63–315 congenital *T. cruzi* infections per year in the United States. This estimate would place the prevalence of congenital Chagas disease in the range of that for phenylketonuria (254 births per year) or congenital adrenal hyperplasia (121 births per year), which are conditions that appear in the American College of Genetics recommended newborn screening panel [18].

Despite the uncertainties described above, we believe that the figures in this analysis represent the most balanced attempt to estimate the current US Chagas disease burden. We hope that these estimates provide an impetus to collect the data needed for improved assessment of the impact of this important parasitic disease in the United States.

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