

Detecting the Prevalence of Chagas Disease among People Living with HIV/AIDS in Los Angeles County, California

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Abstract

Background: Chagas disease (CD) is a well-known tropical parasitic disease with a historical footprint in Latin America. Special populations, including people living with HIV/AIDS (PLWHA), may be at a higher risk of CD and its progression to adverse outcomes. The objective of this study is to measure the prevalence of CD among Latin American foreign-born PLWHA residing in Los Angeles (LA) County (LAC), CA.

Methods: Retrospective data analysis of Latin American foreign-born PLWHA aged 18 years and older seeking primary care services at AIDS Healthcare Foundation (AHF) Healthcare Centers between 05/01/2017 and 03/31/2018. Descriptive analyses were performed using frequency distributions and nonparametric Chi-square tests to examine the prevalence of CD.

Results: Two clients out of a sub-population of 179 were identified as CD-positive ($p < 0.01$): one male and one female, both originating from Honduras. The prevalence documented at AHF Healthcare Centers (1.11%) is slightly lower than the 1.24% prevalence reported previously in LAC (1.24%).

Conclusion: While this is a relatively small sample size, the statistically significant results suggest developing CD testing and treatment guidelines among Latin American foreign-born PLWHA—a prominent subpopulation in LAC.

Keywords: Chagas disease; Travel; Infectious disease; Tropical disease; People living with HIV/AIDS

Introduction

Chagas disease (CD) is a well-known and complex zoonosis caused by the protozoan parasite *Trypanosoma cruzi* with a historical footprint in 21 Latin American countries [1]. While the infection is often asymptomatic, it has the potential to cause significant chronic disease—particularly affecting the gastrointestinal and cardiovascular systems [2,3]. While the burden of disease is well documented in nations of classically high prevalence, its detection in the global north has not been well characterized until recently [4] having said that, a systematic system of detection is certainly lacking—especially among special populations [3]. According to the Centers for Disease Control and Prevention (CDC), there are 300,000 cases estimated in the US alone [2]. What was not clear until recently was a description of the burden of disease among American migrants from nations without well-established prevalence ratios. However, Meymandi et al. published a recent analysis of foreign-born Latin Americans currently living in Los Angeles (LA) county (LAC), CA, and reported a 1.24% general prevalence [5].

In addition to a general dearth of surveillance in the global north, what is not well known is which populations may be at higher risk for CD. People living with HIV/AIDS (PLWHA) represent a high-risk population for disease transmission as well as a number of adverse outcomes. Consequently, it has been theorized that a pre-existing HIV

infection may lead to a greater risk of CD infection as well as a likely progression to more adverse events [6]. To that point, Almeda et al performed a literature review of co-morbidity cases of HIV/AIDS and CD between 1980 and 2010, and documented a wide range of prevalence ratios from more than 75% in Brazil ($n=222$), followed by Argentina (19.2%) ($n=56$), the US (1.7%) ($n=5$), Chile (1.7%) ($n=5$), and Spain (1.0%) ($n=3$) [7]. In addition to higher suspected rates of CD transmission, published on higher rates of parasitemia among PLWHA [8]. Moreover, PLWHA with lower CD4 T-cell counts are at higher risk of CD reactivation, which results in an increased risk of fatality [6,9,10].

While this heightened risk of CD among PLWHA has been documented, what is not clear is prevalence of CD/HIV co-infectivity in the US. Consequently, this study aims to explore the prevalence of CD among Latin American foreign-born PLWHA residing in LAC who sought clinic services at the AIDS Healthcare Foundation (AHF), the largest nonprofit provider of primary care services for PLWHA in the US [11].

Materials and Methods

Study design and population

We conducted a retrospective analysis of 179 patients HIV⁺ patients who sought primary care services at AHF Healthcare Centers between May 1, 2017 and April 30, 2018. AHF serves over 50,000 patients in the US with over 7000 (mostly HIV⁺) in the US. They provide HIV

specialist services in addition to general primary care. Clients were included in the analysis if they were 1. Between the ages of 18 years and 15 years; 2. Born in any country in Latin America, 3. Diagnosed with HIV; 4. Sought primary care service at AHF in LAC; and 5. Received a test for CD during the study period. Clients were excluded if they did not receive a test for CD and were over age 50.

Independent variables

Data collection using AHF’s electronic medical record system (Centricity Practice Solution, GE Healthcare) explored the following predictor variables: age, gender, country of origin, and year of immigration.

Dependent variables

The outcome variable of interest was CD status, which was determined by qualitative assay using the FDA-approved Abbott Prism Chagas assay (Abbott Laboratories, Lake Bluff, IL). Any preliminary positive result was sent to the LAC department of public health laboratory, which was further sent to the CDC to perform a confirmatory testing. Confirmatory testing was provided by combined ELISA/western blot sequencing.

Data analysis

A descriptive analysis was performed using frequency distributions and non-parametric Chi-square tests to examine the prevalence of CD by age, gender and country of origin. Frequency distributions were used to describe the participants’ demographics and CD status. Categorical predictor variables were compared between CD-positive and CD-negative groups using Fisher’s exact test. Statistical analyses were conducted using SPSS Statistics 23 (IBM Corporation, Armonk, NY).

Results

Out of the 179 clients in the study, 150 (83.8%) self-identified as male, 13 self-identified as female, and 16 self-identified as transgender (either male-to-female or female-to-male). More than half (n=103; 57.5%) of the study population migrated from Mexico, followed by 26 (14.5%) from El Salvador, 18 (10.1%) from Guatemala, 15 (8.4%) from Colombia, and seven (3.9%) from Honduras. The majority of the study population (n=118; 65.9%) identified Spanish as their primary language. The mean age based on the clients’ dates of birth was 47 years old (SD: 11 years). 68 participants (38.0%) reported the year of their migration, and the mean age at migration was 25 years (SD: 9 years). Table 1 shows the demographic characteristics of the study population.

Variable	n(SD)	%
Mean Age in Years	47 (11)	
Mean Age in Years at First Migration*	25 (9)	
Gender		
Female	13	7.3
Male	150	83.8
Transgender	16	8.9

Country of Origin		
Mexico	103	57.5
El Salvador	26	14.5
Guatemala	18	10.1
Colombia	15	8.4
Honduras	7	3.9
Other	10	5.6
Primary Language		
Spanish	118	65.9
English	61	34.1
SD: Standard Deviation.		
*Sixty-eight participants reported the year of their migration.		

Table 1: Demographic characteristics of the study population (N=179).

While we had 5 preliminary positive results (based on the Abbot prism assay), the CDC test (describe here again) only confirmed 2 of these cases, with an overall prevalence of 1.11%. There were clinical findings, found in both patients (found on EKG). This was slightly lower than Meymandi et al. [5] findings described above (1.24%) [3] Of the 2 cases, there was one cis male and female. Both of the CD-positive cases migrated from Honduras, with a specific prevalence of 28.6% (p=0.257). Our findings found no statistically significant association between age, gender, and CD status. However, we did find a statistically significant association between country of origin and CD status. Table 2 illustrates this data further.

Variable	CD+ Cases (%)	CD- Cases (%)	CD Prevalence (95% CI)	p-value
Total	2 (1.1)	177 (98.9)	1.1% (-0.004, 0.026)	<0.001
Age Group in Years				1*
24-34	0 (0.0)	26 (14.7)	-	-
35-44	1 (50.0)	47 (26.6)	2.1% (-0.020, 0.062)	<0.001
45-54	1 (50.0)	68 (38.4)	1.4% (-0.014, 0.042)	<0.001
55+	0 (0.0)	36 (20.3)	-	-
Gender				0.148*
Female	1 (50.0)	12 (6.8)	7.7% (-0.068, 0.222)	0.002
Male	1 (50.0)	149 (84.2)	0.7% (-0.006, 0.020)	<0.001
Transgender	0 (0.0)	16 (9.0)	-	
Country of Origin				0.001*
Mexico	0 (0.0)	103 (58.2)	-	-
El Salvador	0 (0.0)	26 (14.7)	-	-
Guatemala	0 (0.0)	18 (10.2)	-	-
Colombia	0 (0.0)	15 (8.5)	-	-

Honduras	2 (100.0)	5 (2.8)	28.6% (-0.049, 0.621)	0.257
Other	0 (0.0)	10 (5.6)	-	-

CD: Chagas Disease; CI: Confidence Interval.
*Fisher's Exact Test.

Table 2: Prevalence of Chagas disease by age, gender, and country of origin.

Discussion

CD was first discovered in LAC in 1984. While CD prevalence in LAC has been documented, this study is one of only a few that investigated CD comorbidity among PLWHA, and the first to describe it among US migrants. These findings provide a better understanding of the current prevalence of CD among PLWHA residing in a bordering area to Latin America.

While the CD prevalence was lower than expected, and CD does not appear to be higher among PLWHA, a prevalence of >1% provides further evidence to advocate for better surveillance systems to detect this deleterious disease. What was also of interest was that both reported cases were from Honduras, with no other cases reported in Latin America. This was not consistent with the data reported by Meymandi et al. [5]. While we do not demonstrate a need for a heightened surveillance system for PLWHA, we believe we have provided evidence for more systematic surveillance systems in migrants living in the US.

Limitations

There are several limitations that should be considered when interpreting our findings. First, this retrospective study utilized secondary data that were not initially intended to study prevalence of CD. As a result, there were a limited number of predictor variables to include in the analysis as well as possible confounders that could not

be measured or controlled. Second, clients who sought primary care service at AHF Healthcare Centers may experience recall bias when answering providers' questions. Third, the sample size of our population was too small to measure risk of CD co-infection among PLWHA.

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