



A global systematic review of Chagas disease prevalence among migrants



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ABSTRACT

Human migration has been identified as a potential factor for increased Chagas disease risk and has transformed the disease from a Latin American problem to a global one. We conducted a systematic review of the scientific literature between 2004–2014 in order to: summarize recent seroprevalence estimates of Chagas disease among Latin American migrants, in both endemic and non-endemic settings; compare seroprevalence estimates in migrants to countrywide prevalence estimates; and identify risk factors for Chagas disease among migrants. A total of 320 studies were screened and 23 studies were included. We found evidence that the prevalence of Chagas disease is higher than expected in some migrant groups and that reliance on blood donor screening prevalence estimates underestimates the burden of disease. Overall there is a dearth of high quality epidemiologic studies on the prevalence of Chagas disease in migrants, especially among intra-regional migrants within Latin America. Given that this zoonotic disease cannot likely be eradicated, improved surveillance and reporting is vital to continuing control efforts. More accurate health surveillance of both Latin American migrants and the Chagas disease burden will help countries appropriately scale up their response to this chronic disease. Overall, improved estimates of Chagas disease among migrants would likely serve to highlight the real need for better screening, diagnostics, and treatment of individuals living with the disease.

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1. Introduction

One of the current challenges in combating Chagas disease (American trypanosomiasis) is that human migration is changing the distribution of disease in both endemic and non-endemic countries (Gascon et al., 2010; Pinazo and Gascon, 2015). This shift is so great that Chagas disease is now co-classified as both a re-emerging infection and a neglected tropical disease (Hotez et al., 2008; Mackey and Liang, 2012; Mackey et al., 2014; World Health Organization, 2013). Human migration represents both a risk for the re-emergence of new infections in countries with the vector and for the expansion of the geographical distribution of chronic Chagas cases to non-endemic countries.

Caused by the protozoan parasite *Trypanosoma cruzi* (*T. cruzi*), Chagas disease results in the largest burden of disease in disability-

adjusted-life-years of any parasitic disease in the Americas (Lee et al., 2013; World Health Organization, 2012). Depending on the region, 20–30% of patients chronically infected with Chagas disease go on to develop cardiac and/or gastrointestinal damage and an estimated 10,000 people will die from Chagas each year (World Health Organization, 2010). The morbidity and mortality associated with Chagas disease results in a staggering annual global economic burden of US\$7.2 billion (Lee et al., 2013).

The main mode of transmission of *T. cruzi* to humans is vector borne, which occurs only in the Americas. Traditionally considered a disease of poverty, risk of Chagas disease has been associated with housing in rural areas, of poor construction quality (e.g., palm roof, cracks in the walls), and with domestic pets and livestock in or near the house (Enger et al., 2004; Molina-Garza et al., 2014; Ramsey et al., 2005; World Health Organization, 2002). Coordinated efforts by endemic countries in the 1990's were instrumental in shrinking the domestic vector infestation and thus the population at risk for Chagas disease (Coura and Dias, 2016; Dias and Schofield, 1999; Dias et al., 2002).

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Despite the success of spraying campaigns, the disease persists through its alternate transmission mechanisms, primarily congenital and blood transfusion, and to a lesser extent oral ingestion (Alarcon de Noya et al., 2010; Carlier et al., 2015; Coura, 2015; Rassi Jr. et al., 2010). Multiple transmission mechanisms, coupled with the chronic, often asymptomatic nature of the disease and lack of effective and accessible treatment for patients means the burden of disease continues to remain high (Pan American Health Organization, 2014).

Within Latin America, migration into urban areas and an increase in urban poverty has transformed this once rural disease to an urban disease as well (Briceno-Leon and Galvan, 2007). There are an estimated 127 million people living below the poverty line in urban and peri-urban communities in Latin America (Ault, 2007) and sub-standard housing conditions within these urban settings have facilitated the domiciliation of triatomines (Gürtler, 2009; Levy et al., 2006; Medrano-Mercado et al., 2008). A 2013 review of qualitative research on socio-cultural aspects of Chagas disease found that changes in land use may both drive human migration and provide new homes for the vector (Ventura-Garcia et al., 2013). For example, in Peru it was found that human settlement patterns created shantytowns with favorable conditions for triatomines and seasonal agricultural workers may have carried the vector to communities through their work (Bayer et al., 2009). Agricultural workers may be at greater personal risk through exposure to the vector during outdoor labor (Ventura-Garcia et al., 2013; World Health Organization, 2010).

Migration has also changed the distribution of Chagas disease from a health problem only in Latin America, to a global one. As of 2013 there were an estimated 36.7 million people who had migrated out of Latin America and the Caribbean and were residing elsewhere in the world, predominantly in North America (United Nations Department of Economic and Social Affairs, 2013b).

Generally, migrants are at greater risk of infectious diseases because of the existing poverty driving them to migrate and the social and economic inequalities they often face once relocating (Cabieses et al., 2013; Carballo and Nerukar, 2001). A 2013 review of qualitative research uncovered migration as a socio-structural risk factor for Chagas disease (Ventura-Garcia et al., 2013). After migrating, structural barriers to diagnosis and treatment include cost, language, lack of insurance, fear of deportation (in the case of undocumented migrants), and stigma against migrants (Bayer et al., 2009; Jackson et al., 2012; Minneman et al., 2012; Ventura-Garcia et al., 2013).

Current prevalence estimates of Chagas disease in non-endemic countries are largely extrapolations of countrywide prevalence from endemic birth countries multiplied by the proportion of immigrants from that country (Basile et al., 2011; Bern and Montgomery, 2009; Gascon et al., 2010; Schmunis, 2007). While country prevalence estimates provide a good starting point for estimating the burden among migrant populations, there are some substantial drawbacks. First, regional variations in migration rates and Chagas disease burden may be masked by the use of a single prevalence estimate for an endemic country. Secondly, these estimates do not take into account characteristics specific to migrants, who tend to be demographically different from the average person in any given country of origin (Weeks, 2015). Migrants often come from rural areas, have a different age profile (i.e., are younger), and are of a different socioeconomic status than the general population (Bern and Montgomery, 2009).

Determining accurate prevalence estimates of Chagas disease among migrants may enable health systems to more precisely gauge the true burden of disease and target populations most at risk. Further, given the heterogeneity of Chagas disease distribution within countries, there remain questions as to whether migrants are at heightened personal risk for this disease.

Therefore the purpose of this review was to: summarize current seroprevalence estimates of Chagas disease among Latin American migrants, in both endemic and non-endemic settings and compare seroprevalence estimates in migrants to countrywide prevalence estimates. We also report on risk factors for Chagas disease among migrants.

2. Methods

We conducted a systematic review of the literature from January 2004 to July 2014 using the PubMed and Scopus databases. We also searched relevant grey literature from international and governmental organizations, including the Pan American Health Organization (PAHO), World Health Organization (WHO), and the U.S. Centers for Disease Control and Prevention. Search terms included combinations of the following keywords: (1) Chagas; American trypanosomiasis; or *T. cruzi*; (2) migra*; mobil*; immigra*; or non-endemic; (3) epidemi*; prevalence; or seroprevalence. Searches were not restricted by language. Reference lists of selected articles were examined for additional citations.

Articles were included in the present analysis if they met the following criteria: (i) original data on the prevalence of Chagas disease among human migrants in endemic or non-endemic countries. “Migrants” were defined as individuals living in a country different than that of their birth or who moved from an area of endemicity to one without vector transmission. Articles were excluded if they: (i) had obvious selection bias (i.e., only included participants with known Chagas disease, or sampled tropical disease hospital or cardiac patients) (ii) did not have full text available (iii) did not include migration status of participants.

First, all duplicates and papers published prior to 2004 were removed. Next, titles and abstracts were screened for relevancy and papers that were off-topic, not original research (e.g., review articles, guidelines, case studies), and those that were not epidemiological studies on humans (e.g., drug development, vector studies). The full text for each of the remaining articles was screened again for inclusion/exclusion criteria.

The following data were abstracted for the included studies, if available: first author, year of publication, country of study, study design, study setting, population of interest, mean/median age of participants, number of migrants tested, prevalence, dates of data collection, and screening tests used.

2.1. Comparison data

We took a two pronged approach to exploring whether migrants have a higher prevalence of Chagas disease than the general population. First, we compared whether current countrywide prevalence estimates for non-endemic countries were similar to studies of migrants living within non-endemic countries.

According to the UN, the top 10 destination countries for Latin American migrants are: the United States, Spain, Italy, Canada, Japan, Portugal, France, the United Kingdom, China, and Australia. (United Nations Department of Economic and Social Affairs, 2013a) Major destinations from the highest Chagas disease prevalence sending countries (Bolivia, Argentina, El Salvador, Honduras, and Paraguay) are the United States, Argentina, and Spain. (United Nations Department of Economic and Social Affairs, 2013a)

We used three sources for non-endemic countrywide prevalence estimates. Gascon et al. (2010), Bern and Montgomery (2009), and Basile et al. (2011) were based on PAHO prevalence estimates for endemic countries and documented and undocumented immigrant populations by country of origin (Basile et al., 2011; Bern and Montgomery, 2009; Gascon et al., 2010). These three sources estimated countrywide prevalence for the top 10 Latin Ameri-

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