Temporal and geographic analysis of human trichinellosis incidence in Chile with risk assessment

Carlos Landaeta-Aqueveque (clandaeta@udec.cl)
Universidad de Concepcion Facultad de Ciencias Veterinarias https://orcid.org/0000-0002-7398-6099
Salvador Ayala
Instituto de Salud Publica de Chile
Denis Poblete-Toledo
Universidad de Concepción Facultad de Ciencias Veterinarias
Mauricio Canals
Universidad de Chile Facultad de Medicina

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Abstract

Trichinellosis is a foodborne disease caused by several *Trichinella* species around the world. In Chile, the domestic cycle was fairly well-studied in previous decades, but has been neglected in recent years. The aims of this study were to analyze, geographically, the incidence of trichinellosis in Chile to assess the relative risk, as well as to analyze the temporal fluctuation in the incidence rates in the last decades. Using temporal data spanning 1964–2019, as well as geographical data from 2010–2019, the time series of cases was analyzed with ARIMA models to explore trends and periodicity. The Dickey–Fuller test was used to study trends, and the Portmanteau test was used to study white noise in the model residuals. The Besag–York–Mollie (BYM) model was used to create Bayesian maps of the level of risk relative to that expected by the overall population. The association of the relative risk with the number of farmed swine was assessed with Spearman's correlation. The number of annual cases varied between 5 and 220 (mean: 65.13); the annual rate of reported cases varied between 0.03 and 1.9 cases per 10^5 inhabitants (mean: 0.53). The cases of trichinellosis in Chile showed a downward trend that has become more evident since the 1980s. No periodicities were detected via the autocorrelation function. Communes (the smallest geographical administrative subdivision) with high incidence rates and high relative risk were mostly observed in the Araucanía region. The relative risk of the commune was significantly associated with the number of farmed pigs and boar (*Sus scrofa* Linnaeus, 1758). The results allowed us to state that trichinellosis is not an (re)emerging disease in Chile, but local conditions must be further studied to identify the factors favoring the presence of outbreaks in some communes, particularly in Araucanía.

Background

Trichinellosis is a foodborne disease with a worldwide distribution, and is caused by the *Trichinella* species [1]. Several *Trichinella* species have been described and are transmitted by meat/muscle consumption, circulating among carnivore and omnivore vertebrates, including humans [1]. Human trichinellosis is mainly associated with the household slaughter of pigs (*Sus scrofa domestica* Linnaeus, 1758) or the consumption of game animals without veterinary inspection, especially when the meat has been poorly cooked [2, 3, 4]. After consumption, the infection can vary from asymptomatic to lethal, and may present with systemic symptoms associated with the circulation of larvae and infection of the muscles or other tissues [3, 5, 6].

Currently, there are 13 genotypes of *Trichinella* around the world, 10 of which are recognized as different species [1, 7]. In South America, *Trichinella* has been detected in Brazil, Ecuador (via antibody detection), Bolivia, Argentina, and Chile (via larvae isolation), and most studies have focused on the domestic cycle; Argentina and Chile were found to have the largest number of human cases [8, 9, 10]. Four *Trichinella* species have been reported in this continent, mainly in Argentina: *T. spiralis* Owen, 1835; *T. patagoniensis* Krivokapich et al. 2012; *T. britovi* Pozio et al. 1992; and *T. pseudospiralis* Garkavi, 1972 [8]. Conversely, *T. spiralis* is the sole species to be reported in Chile, and while studies on wild animals have increased recently [11, 12, 13, 14], the domestic cycle was fairly well-studied in previous decades [9], but has been neglected in recent years. Thus, the aim of this study was to analyze geographically the incidence of trichinellosis in Chile. In particular, the goal was to assess the relative risk, as well as to analyze the temporal fluctuations of the incidence of this disease over the past few decades, assessing the presence or absence of cyclic tendencies.

Human trichinellosis is a disease that requires mandatory and immediate reporting to public health authorities. Those reports pass through several institutions, from local to national levels of the Ministry of Health. In addition, some regulatory laws support the transparency of this information, making it possible to request non-sensitive information regarding this disease.

To analyze the time series of trichinellosis, the information of yearly cases from 1964–2019 was obtained from the yearly reports of mandatory notifiable diseases. For spatial analyses, cases spanning 2010–2019 were obtained from the Regional Secretaries of the Ministry of Health for each commune (the smallest geographical administrative sub-division), as per the requirements for this transparent system. When information was not completed through the transparent system, reports from the Instituto de Salud Pública de Chile were used to provide more comprehensive information, but it only featured details from the administrative regions (see Table S1 in Supporting Information for case details per commune and year).

The yearly time series of cases spanning 1964–2019 was analyzed with autoregressive integrated moving average (ARIMA) models, which examined overall trends and periodicity. The autocorrelation and partial autocorrelation functions were used to select the model. The Dickey–Fuller test was used to study trends, and the Portmanteau test was used to study white noise from the residuals in the model. The 2010–2019 series was used to study the absolute and relative risk by locality. The Besag–York–Mollie (BYM) model was used to make Bayesian maps of relative risks to those expected by population size [15], using WinBUGS and ArcGIS software. The BYM model assumes that the number of cases (O_{it}) in area i and period t follows a Poisson distribution with the mean:

$$m_{it} = e_{it} \cdot r_{it},$$

where r_{it} is the relative risk and e_{it} is the expected number of cases, with e_{it} depending on non-spatial random variation (U_{it}) and the spatially structured variability (S_{it}: neighborhood structure; [15, 16, 17]. The relative risk is given as:

$$r_{it} = ae_{it} + U_{it} + S_{it},$$

with a representing the global rate. The expected number of cases was estimated as:

$$e_{it} = P_{it} I_t,$$

where P_{it} is the total population of the locality and I_t is the average reported number of cases per 10^5. The population sizes for each locality and over time were obtained from the National Institute of Statistics of

Chile (INE)[18], and the annually reported cases per 10^5 inhabitants were obtained from the Database of Notifiable Diseases.

Finally, the association between the mean relative risk with the number of farmed pigs and boars (*S. scrofa*) was assessed with Spearman's correlation. The number of farmed pigs and boars was obtained from 2007 agricultural census data [19], given that no recent data have been published (see Table S2 in Supporting Information for the detailed number of pigs and boars per commune).

From 1964–2019, the number of annual cases varied from 5–220, with a mean of 65.13 and a standard deviation (SD) of 41.06 cases. The annual rate of reported cases varied between 0.03 and 1.9 cases/10^5 inhabitants, with an average and SD of 0.53±0.41 cases/10^5 inhabitants. The annual rate series of reported cases of trichinellosis in Chile shows a downward trend that has become more evident since the 1980s. ($R=-0.59$, $F_{1,54}=29.5$; $P<0.001$; Figure 1a). This trend was removed by first-order differentiation, resulting in a detrended time series (Dickey–Fuller test=-11.9; $P<0.001$). No periodicities were detected via the autocorrelation function. An ARIMA model was fitted, obtaining an ARIMA (0,1,1) model (see Table S3 in Supporting Information for the model details). An autocorrelation analysis of errors showed adequate adjustment with a Portmanteau Q test=22.83 ($P=0.59$). The model then corresponded to a first-order moving average model, indicating a weak dependence on random fluctuations from the previous year.

Communes with at least one case, an incidence rate >0 cases/10^5 inhabitants, and a high relative risk (>1 case/10^5 inhabitants) were mostly observed in the Araucanía region, followed by the Los Ríos and Los Lagos regions (Figures 1b, 1c). The relative risk of the commune was significantly associated with the number of farmed pigs and boar (Spearman's rho=0.45; $P<0.001$).

The decrease in the incidence over time coincides with what has been found in Europe, where the frequency of trichinellosis outbreaks caused by pig consumption had decreased [20]. It was also aligned with the current low global burden [21], supporting the idea that this is not currently an emerging disease in Chile. During the period spanning 2010–2013, most cases around the world were caused by the consumption of game meat [20]. However, in Chile, most cases are consistently due to domestic pig meat consumption, which corresponds to the association between the level of risk and the number of farmed pigs in a commune; the one exception is that there was a single case of wild boar consumption [22]. These findings are expected because the hunting of native carnivore mammals is prohibited by law [23], as only the hunting of introduced species is permitted. Introduced feral carnivore mammals, such as American minks or feral dogs are not usually hunted, other than for sanitary or ecological control. Thus, wild boar is the sole feral species hunted for consumption in Chile that can act as a direct source of human infection.

The temporal decrease in the incidence rate is in agreement with the reduction in the number of pig farms over the last decade, but not with the reduction of pig production [24], which means that production has been concentrated in larger industrialized farms, which face a low risk of *Trichinella* infection [2]. No studies have examined the change in practices among household breeders over time; hence, there is no evidence to support that the decrease in the incidence is due to a change in household-breeding practices. Only a few studies have assessed the knowledge and practices related to *Trichinella* infection in Chile; it was noted that the general population possesses higher knowledge levels and better practices when compared with those for other zoonotic diseases [25, 26]. However, those studies have been performed in communes of the Ñuble region, which have a low relative risk. Since recommendations include focusing on building awareness, among other measures, to prevent trichinellosis outbreaks [27, 28], more studies are needed in other communes with higher risks and incidence rates, particularly those belonging to the Araucanía and Los Ríos regions.

There were no ≤3-year cycles observed; thus, no evidence was found to support the presence of regular temporal fluctuations. Rather, a small correlation between long-term decreases in relation to time was found. Few of the reports analyzed in this study included the number of outbreaks and individual cases, as well as the number of cases per commune in a year. In those reports, most cases were due to a few outbreaks (i.e., a sole source of infection), and few cases were individual cases. This suggests that the variations between years could have been due to a few outbreaks that occurred in years with higher incidences, favoring the randomness in temporal variations.

The geographic visualization of the risks does not suggest a latitudinal variation – i.e., the risks did not increase in the south; rather, the highest risks were seen in communes of the Araucanía region, which is explained by the number of pigs bred there. The Araucanía region has the third-largest number of domestic pigs, after the Metropolitan and O'Higgins regions [19]; however, pigs from these latter two regions belong mostly to industrial farms [24]. Therefore, Araucanía is the region with the largest number of household-bred pigs, and it is also the region with the highest proportion of communes with a high relative risk (>1), which supports the fact that the number of swine animals is a significant factor for the risk of human trichinellosis. Araucanía is also a region with the largest concentration of Mapuche Indigenous peoples in Chile [18] and is characterized by the most severe economic poverty rate [29], a factor that has been associated with the reemergence of trichinellosis elsewhere [30].

Feral or wild animals reported to be infected by *Trichinella* in Chile correspond to two cougars (*Puma concolor* Linnaeus, 1771) and five wild boars [11, 12, 14], most of which were found in the two regions with the highest proportion of communes featuring high relative risks: Araucanía and Los Ríos. Thus, the evidence suggests that there is a small association between human cases and the presence of the parasite in feral animals. However, it is also true that the most sampling efforts to examine those animals have been made in these two regions; hence, more rigorous and unbiased studies are needed to further assess this association.

Thus, our results support the notion that trichinellosis is not a (re)emerging disease in Chile, but local conditions must be further studied to identify the factors that favor the presence of outbreaks in some communes, particularly in the Araucanía region.

Abbreviations

ARIMA
Autoregressive integrated moving average
BYM
Besag–York–Mollie test
INE
National Institute of Statistics of Chile
SD
Standard deviation
R
Correlation coefficient

Declarations

Ethics approval and consent

The Comité de Ética of the Facultad de Ciencias Veterinarias of the Universidad de Concepción approved this study (Certify CBE-30-2020).

Consent for publication

Not applicable

Availability of data and materials

All data generated or analysed during this study are included in this published article and its supplementary information files.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

CLA and MC designed the study, DPT and MC obtained the data, SA and MC made the data analyses, CLA wrote the first draft, all authors read and approve the final manuscript.

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Not applicable

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Figures

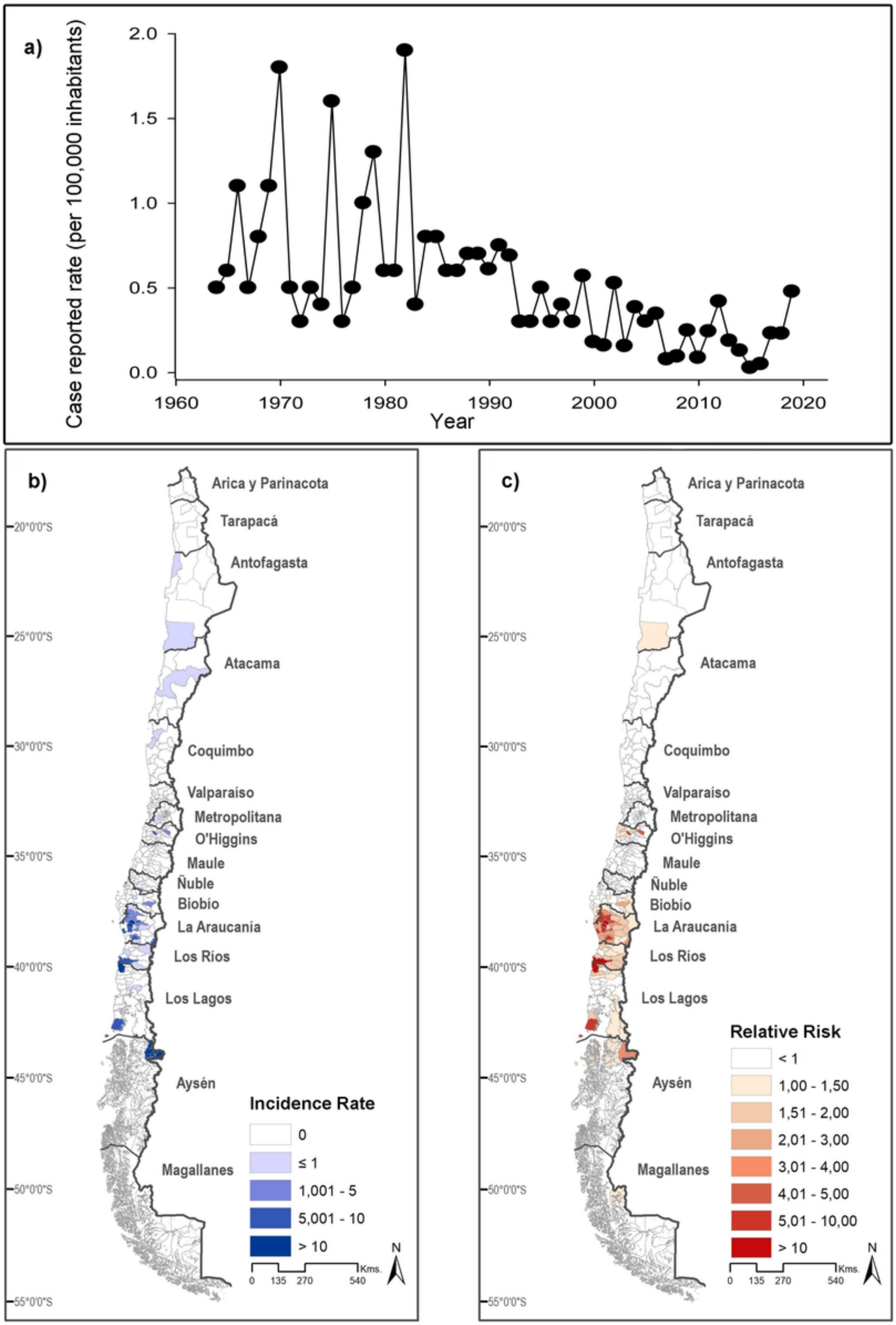

Figure 1

Temporal and geographic variation of human trichinellosis in Chile (a) Evolution of the incidence rate of trichinellosis from 1964–2019 in Chile. (b) Maps of Chile featuring the incidence rate distribution of trichinellosis in Chile (cases per 100,000 inhabitants) from 2010–2019. (c) Maps of Chile featuring the relative risk distribution of trichinellosis in Chile from 2010–2019. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

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