



Original article

Peri-urbanisation, counter-urbanisation, and an extension of residential exposure to ticks: A clue to the trends in Lyme borreliosis incidence in the Czech Republic?

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ARTICLE INFO

Article history:

Received 18 April 2014

Received in revised form 23 June 2014

Accepted 13 July 2014

Available online 10 August 2014

Keywords:

Lyme borreliosis

Disease emergence

Suburbanisation

Counter-urbanisation

Amenity migrants

ABSTRACT

The incidence of tick-borne human diseases (TBD) in the Czech Republic (CZ) is on the increase, driven by infections increasingly acquired in residential locations, earlier in spring and later in autumn, and among children and the elderly. To interpret these trends, data on Lyme borreliosis (LB) incidence between 1997 and 2010 were analysed in the context of population migration flows registered in the CZ during the same period. Analysis showed that a migration stream of families with children, and of the elderly, flowed from more urbanized and densely populated localities to those more rural and less populated, where the chance of acquiring LB in the home vicinity was greater than in the urban settings. By contrast, a stream of people in the life phase between early adulthood and family formation flowed reversely, corresponding to a prominent absence of this age category from the patient spectrum. The data further showed that the more the residential exposure became prevalent, the more people were in year-round (rather than in summertime only) contact with ticks, which accounts for an extension of the cases' seasonal distribution as well as for an overall increase in case numbers. Finally, the fact that majority of the urban-to-rural migrants could be categorised as wealthier people could explain the previously noticed lack of low-status people among TBD patients in the CZ.

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Introduction

The recent increase in the incidence of tick-borne human diseases (TBD), primarily Lyme borreliosis (LB) and tick-borne encephalitis (TBE), in many parts of Europe, has aroused considerable public health concern (WHO, 2004). An explanation of reasons behind this trend is required to improve preventative measures and control plans (Heinz et al., 2013). There is, however, no general consensus as yet over causes of this development, and various factors, largely divergent, have been cited. It is assumed that a broad complex of miscellaneous interacting factors of abiotic, biotic and anthropic nature could in fact be collectively responsible (Randolph, 2010; Jaenson et al., 2012a).

An overall increase in morbidity is accompanied by some conspicuous changes in distributional patterns of the disease cases, independently reported by various authors:

- (1) **Distribution in space.** Systematic shifts at the distributional fringes, both latitudinal and altitudinal, of the vector ticks can be convincingly explained by global warming (e.g. Lindgren et al., 2000; Materna et al., 2008; Jore et al., 2011; Tokarevich et al., 2011; Jaenson et al., 2012b). But, changes observed in long-established endemic regions, where the vast majority of new cases have been recorded, show little consistency with climatic conditions (Randolph, 2004). In particular, there is conflict between omnipresence and great uniformity of the climate change on the one hand, and noticeable heterogeneity or even the converse in disease trends on the other; these are registered even in geographically very close areas (Süss et al., 2004; Sumilo et al., 2007; Zeman et al., 2010). Moreover, a detailed analysis of places of contraction in the Czech Republic (CZ) showed that the population's exposure to TBDs is becoming increasingly confined to the nearest surroundings of residences, morbidity is closely correlated with this trend, and, as a consequence, the observed rise in disease numbers is solely made up of cases acquired at or near patients' homes while the number of cases acquired further away is simultaneously decreasing (Zeman and Benes, 2013).

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- (2) **Seasonal distribution.** There is a noticeable extension of the season of disease occurrence beyond the so far typical warm period: More cases are now recorded both earlier in spring and later in autumn than had been observed a decade or two ago (Pazdiora et al., 2008, 2012; Svihrova et al., 2011; Kriz et al., 2012; Trajer et al., 2013).
- (3) **Age distribution.** The elderly, mainly 50–65-year-old people, increasingly dominate the patient age spectrum. They prevail among new cases in regions of disease emergence (Walder et al., 2008; Lundkvist et al., 2011), as well as showing an increase among patients reported from pre-existing endemic regions (Süss et al., 2010). In the CZ, for example, this contrasts with the situation 20–30 years ago when the highest TBE rate befell adolescents (Pazdiora et al., 2008; Zeman et al., 2010; Kriz et al., 2012). In addition to the elderly, the second most affected cohort has become children of about 10 years of age; this minor peak has been reported, among others, in (East) Germany, Slovakia, the CZ and Slovenia, but not in Austria (Fülöp and Poggensee, 2008; Svihrova et al., 2011; Heinz et al., 2013; Wilking and Stark, 2014).
- (4) **Distribution of patients' economic status.** The coincidence of the political turnover in Eastern Europe in the early 1990s with a prominent outbreak of TBD incidence warrants the deduction that the socio-economical transformation, following the fall of socialism in those countries, must have promoted the incidence rise (Randolph, 2008). Although some authors argue it was due to a decline in the economy and subsequent pauperisation of people—pushing them to a greater contact with wild and uncultivated, tick-infested habitats—in the CZ, increased incidence turned out to be more associated with a higher economic status: The number of unemployed TBE patients is less than the average for the whole country, most new TBE cases have been registered in a region with the lowest unemployment rate (Kriz et al., 2004), and medium- to well-paid professions tend to be over-represented among TBE patients (Zeman et al., 2010).

In this paper we show that these apparently disconnected patterns can be explained by a single process of population outflow from cities and towns which occurs in industrialized countries. This process includes a re-distribution of town inhabitants out of town cores to the surrounding suburbs and hinterland, i.e. 'peri-urbanisation' (syn. 'suburbanisation' or 'rurbanisation'), as well as migration to more distant rural areas, i.e. 'counter-urbanisation' (Frey, 1988). The two migration streams differ somewhat from each other in motivation and their geographic, sociologic and/or demographic characteristics which have different epidemiological implications, and may vary geographically within and between countries (Piorr et al., 2011). Herein, we analyse data on LB incidence in the CZ during the last two decades.

Material and methods

Epidemiological data

The data used in this analysis were extracted from a register of compulsorily notifiable diseases in the National Institute of Public Health in Prague. Altogether 44,360 cases of LB reported between 1997 and 2010 were selected for which both the patient's residential address and self-reported place of infection were available; positional data have been translated into geographical coordinates (geo-coded) as described previously (Zeman and Benes, 2013). An additional 30,612 geo-coded cases of animal bite (ICD code: W54/55), reported during the same period, were included in the

study as a control data-set; these controls are also 'noncontagious', associated with outdoor activities and of a comparable prevalence to LB.

Population data

Official data on migration and demographic changes between 1997 and 2010 were obtained from the Czech Statistical Office; geographic resolution of this data ranged from the administrative district level (NUTS4; international/internal migration, demography) to the municipality/parish level (NUTS5; number of residents).

Study design

The hypothesis to be evaluated in this study is that the population migrates from residential localities of lower LB risk to localities of higher risk (which can itself—without the contribution of any other factor—account for an increase in disease incidence), and that the character of the migrants predetermines the incidence patterns. There are several obstacles, however, to testing it unequivocally: the migration of interest occurs on a fine geographical scale (often within the same town/municipality), but scarcity of the disease cases and over-dispersion of case counts on too minute a surveying scale (i.e. extra-Poisson variation) prevent detailed spatial analysis. On a grosser scale, a spatial continuum of migration trends is lacking, and abrupt contrasts between immediately neighbouring localities thwarts the application of statistical smoothing approaches. Moreover, since the disease incidence depends equally on the number of people exposed as well as on the background rate of zoonotic risk, even a massive in-migration to a locality may coincide with no disease cases if the risk is insignificant, and vice versa. Hence, these circumstances demand a substantial aggregation of the data based on a criterion following as closely as possible the pattern of internal migration flows but independent of the geographical proximity and morbidity rate factors.

Analytical approaches

Previous analysis of the data (Zeman and Benes, 2013) showed that there was a ca. two-fold increase in LB incidence during the study period which was made up solely of infections acquired at or nearby the patients' residence. Therefore, to distinguish cases that primarily contribute to the disease rise, the infections were classified as 'local' or 'remote', depending on whether the indicated distance between residence and place of infection exceeded a 5-km limit (adjusted with respect to the spatial resolution of the data so that acquisitions within this radius showed an increasing trend while those outside the radius were decreasing during the study period).

Whether a settlement gains or loses population through the current process of population re-distribution has been documented to be predictable from the settlement's (population) size: It is typical that inhabitants of larger settlements tend to migrate to smaller, less densely populated ones (Mitchell, 2004). Thus, employing size as a proxy for migration trends, municipalities were classified among disjunctive size categories (sets) according to the mean number of residents registered in the period of study. Each set of municipalities was then characterized by an average 'risk' level estimated as the number of local cases divided by the number of residents registered in each year of the study period:

$$\text{risk} = \frac{\sum_{yr=1997}^{2010} \text{No.local cases}_{yr}}{\sum_{yr=1997}^{2010} \text{No.inhab.}_{yr}}$$

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