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Short communication

Emergence of *Echinococcus multilocularis* among Red Foxes in northern Germany, 1991–2005

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Abstract

The parasite *Echinococcus multilocularis* is currently of great concern in Europe because of its spreading behavior, which has public health implications. This study investigates the spatiotemporal distribution of *Echinococcus multilocularis* in Red Foxes. The infection status of 8459 foxes was sampled from 43 regions in the north German province of Lower Saxony over three investigation periods 1991–1994, 1994–1997 and 2003–2005. Linear empirical Bayesian smoothing within the binomial model was used to produce smoothed choropleth maps. Geostatistical kriging was applied to generate prevalence risk maps. Further geostatistical modeling of the prevalence difference between study periods facilitated spatiotemporal trend investigations. The spatial scan statistic was used for cluster detection analysis. The average prevalence risk for Lower Saxony increased from about 12 to 20% during 1991–2005. Specifically the increases from first to second and to third study periods were estimated by 3.3% (CI 95%: 0.6%–5.9%) and 8.5% (CI 95%: 5.2%–11.8%), respectively. Infections in foxes were clustering and a location stable disease cluster was detected in the south of the province. This study is the first showing evidence for steady emergence of *Echinococcus multilocularis* in Red Foxes. First cases of human Alveolar Echinococcosis were recorded recently.

Keywords: *Echinococcus multilocularis*; Fox; Geographic distribution; Germany; Spatial epidemiology

1. Introduction

Human Alveolar Echinococcosis (AE) is a serious zoonosis caused by the larval stage of the small fox tapeworm *Echinococcus multilocularis* (*E. multilocularis*) and is currently of great concern in Europe and Asia. Human infections are rare in Europe because the tapeworm develops in a mainly silvatic life cycle. But recent reports show that the parasite is spreading in Europe (Sréter et al., 2003) among its predominant definitive host population: the Red Foxes (*Vulpes vulpes*). Furthermore the zoonosis is commonly viewed an emerging disease, and temporal prevalence increases have been variously reported (König et al., 2005). However, studies were done in restricted areas over short periods, or data from studies with different sampling strategies were compared. A data analysis confirming steadily increasing infection frequencies has not yet been presented for a larger region. A review (Duscher et al., 2006) pooling investigations of Austrian foxes conducted during 1993–1997 and 1999–2004 concluded that there is no evidence in a drop of prevalence, but could not demonstrate an increase.

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Lower Saxony is a province in northern Germany, larger and more populated than for example Switzerland—one of the traditional high endemic areas in Europe. Recent studies (Berke, 2001; Berke and von Keyserlingk, 2001) showed that the prevalence of *E. multilocularis* among foxes in Lower Saxony actually increased from 1991–1994 to 1994–1997, and that the prevalence reached up to 50% and even 60% in certain areas. These numbers are reasonably comparable to those from a study in a Swiss highly endemic area that found the annual prevalence to range from 47 to 56% in the fox population (Gottstein et al., 1996).

An increasing prevalence from one to another study period does not prove a trend. Therefore, additional data sampled from foxes in 43 regions of Lower Saxony during 2003–2005 were investigated in this study.

2. Materials and methods

2.1. Description of sample data

A total of 8.459 foxes were sampled from 43 regions in the German province of Lower Saxony over three investigation periods 1991–1994, 1994–1997 and 2003–2005. The respective sample sizes for the three periods are 2748, 2617 and 3094. The infection status was diagnosed using the intestinal scraping technique (SCT) as described elsewhere (Eckert et al., 2001). The median of the raw regional prevalence of *E. multilocularis* in foxes increased from 5.8% over 11.4% to 16.9%. But these numbers do not account for regional sample size disparities and spatial correlation.

2.2. Spatial epidemiological data analysis

Linear empirical Bayesian smoothing under the binomial model (Martuzzi and Elliott, 1996) is used to produce smoothed regional prevalence risk estimates suitable for choropleth mapping. The smoothed risks are then modeled within the geostatistical framework of ordinary kriging (Berke, 2004) separately for each of the three study periods. The spatial dependence structure among the smoothed regional risks is fitted by an exponential model using maximum likelihood estimation. Ordinary kriging is then applied to generate isopleth maps of the latent prevalence risk distribution for each study period showing the temporal variation over the three study periods.

Further ordinary kriging models are fitted to the difference in prevalence risk between second and first, third and second as well as third and first study periods to investigate the significance in temporal variation. The intercept parameters of the spatial constant trend models represent the increase in the provincial average risks from one to another period.

The spatial scan statistic (Kulldorff, 1997) is used for cluster detection analysis within a binomial model. The analysis was performed for each study period separately.

3. Results

The average prevalence risk for Lower Saxony as estimated within the geostatistical model increased from the first to second, second to third and first to third study period by 3.3% (CI 95%: 0.6–5.9%), 5.1% (CI

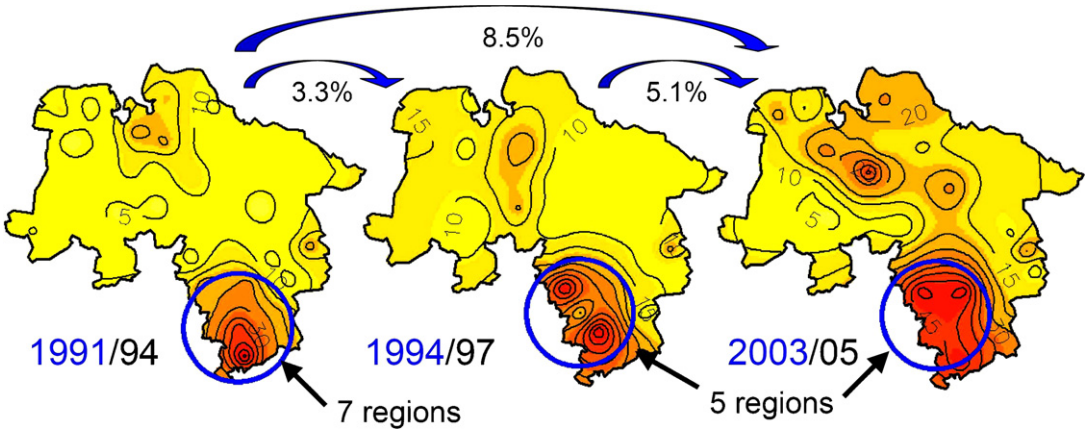

Fig. 1. Isopleth maps of the latent prevalence risk in Red Fox populations for infection with *E. multilocularis* in Lower Saxony, northern Germany. The latent risk maps resulted from interpolation via ordinary kriging from linear empirical Bayes smoothed regional prevalence risk estimates for the three study periods 1991–1994, 1994–1997 and 2003–2005. The percentages under the arrows indicate the increase in risk from one to another study period. Circles indicate the location of disease clusters as identified using the spatial scan statistic ($P \leq 0.01$).