

ECHINOCOCCUS MULTILOCULARIS: THE ROLE OF SATELLITE REMOTE SENSING, GIS AND SPATIAL MODELLING

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Abstract. Satellite remote sensing is now widely used in epidemiology to derive information on disease host and vector distributions through relationships with land cover, climatology or other environmental variables. This spatial information is normally managed within a Geographical Information Systems (GIS) which provides a means of storing, manipulating, and visualizing the data. Increasingly spatial models of disease transmission patterns are now developed within a GIS environment and the outputs used to map transmission risk. This paper reviews the way in which these technologies are being used in an integrated way to study the ecology of the transmission of the fox parasite *Echinococcus multilocularis* which causes the highly pathogenic disease human alveolar echinococcosis (AE). The paper also outlines the first results of an investigation that examined the relationships between landscape ecology metrics and human AE prevalence in an *E. multilocularis* endemic area in central China.

INTRODUCTION

The transmission of *Echinococcus multilocularis* in wildlife is an indirect parasite life cycle that depends on the spatial interaction of an infected canid definitive host with a small mammal intermediate host, often a microtine rodent species. The adult tapeworm attaches itself to the intestine of the definitive host, typically a fox or other canid species, and sheds proglottids containing *E. multilocularis* eggs. The availability of eggs in the environment is, therefore, determined by the home range of the infected fox, which is typically 2-5 km in rural areas. Scats are not randomly distributed within the fox home range, however, but are preferentially distributed along tracks or field boundaries. Furthermore, the tapeworm is over-dispersed in the fox population with 75% of the biomass in 12% of the foxes observed in one study (Raoul *et al.*, 2001). As a consequence of these processes, the spatial distribution of *E. multilocularis* eggs in the environment is likely to be highly clustered.

In favorable conditions, *E. multilocularis* eggs may remain viable for several months, but experimental research has shown that hot and dry climatic conditions reduce egg viability (Veit *et al.*, 1995). At a regional scale this may explain the spatial distribution of *E. multilocularis* in wildlife, but at a local or patch scale it is likely to lead to further spatial aggregation of

infective eggs. Sustainable *E. multilocularis* transmission requires ingestion of viable eggs by an intermediate microtine rodent host, which implies that susceptible species, which generally have a home range of only a few tens of meters, are located within the fox home range. The parasite transmission cycle is completed when foxes predate on infected rodents, and clearly this activity must take place within the fox home range (Morgan *et al.*, 2004).

It is clear that there is a range of factors which affect the pattern and intensity of *E. multilocularis* transmission in wildlife, and that these factors operate at a range of spatial scales. Transmission to humans adds further complexity, however, as it requires either the direct ingestion of eggs from infected animals (*eg*, domestic dog) or indirectly through contaminated food or water. Patterns of human infection at regional scale are correlated with landscapes that can sustain *E. multilocularis* transmission in wildlife, and at local scale with the proximity of human populations to particular landscape configurations that can sustain high population densities of microtine rodents (Danson *et al.*, 2003). This paper reviews the recent contributions that remote sensing, geographical information systems (GIS) and spatial modelling have made to understanding the effects of landscape on *E. multilocularis* transmission and provides an example of how landscape structure may be analysed and related to human AE risk.

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ROLE OF SATELLITE REMOTE SENSING, GIS AND SPATIAL MODELLING

The key role of satellite remote sensing in the

context of disease epidemiology is in landscape mapping. Satellite remote sensing can provide images of most of the Earth's surface with spatial resolutions between about 60 cm and 1m (Danson *et al.*, 2003). These images may be processed to provide information on topography, land surface temperature, land cover, and a wide range of other variables. Satellite remote sensing has been used in epidemiological studies for more than three decades with applications to locate parasite, vector and host habitats, monitor temporal changes in the landscape and predict spatial and temporal changes in host populations (Kitron, 1998). These data are often managed within a GIS which provides a means for managing, manipulating, interrogating, and visualizing multiple data sets that are geographically referenced to a known grid mapping system.

Once the landscape data are imported into a GIS they may be combined with data on other epidemiologically important variables, such as vector or host distribution, climatic data or the location of human populations. For example, remotely sensed data have been used to map the habitat of larval mosquito populations that are associated fresh or brackish water (Wood *et al.*, 1992). This information has been imported into a GIS and simple spatial measures of distance between village and mosquito habitat used to estimate risk of malaria transmission (Rejmankova *et al.*, 1995; Beck *et al.*, 1997; Thomas and Lindsay, 1999). A review of GIS and remote sensing in the study of human helminth infections indicated that environmental factors, such as temperature, humidity, and altitude, which affect the distribution of helminth infections, may be determined from remotely sensed data and used within a GIS environment to better understand transmission (Brooker and Michael, 2000). The authors set up a GIS to collate prevalence survey data on schistosome and hookworms but found that a key problem was the comparability of data derived from numerous disparate studies, using different data collection methodologies and working towards different end goals. However, the GIS highlighted areas where data is currently sparse and it was suggested that GIS would in future allow efficient storage, presentation and analysis of data on helminths as it becomes available.

Spatial analysis tests for spatial patterns in epidemiological data and may be used to develop predictive models of disease distribution. Such analyses are critical when it is hypothesized that there is a correlation between the spatial distribution of vector-borne disease, the geographical range of the vector hosts, and the preferred habitat of the vector

hosts. Spatial analysis within GIS facilitates quantitative analysis of features in heterogeneous landscapes such as patch size, patch shape, edge distance and corridor features. It has been suggested that such features may be more revealing than traditional ecological concepts of equilibrium when modelling epidemiological risk, highlighting a further role for GIS in disease modelling (Kitron, 1998).

APPLICATION OF REMOTE SENSING AND GIS TO *E. MULTILOCULARIS* TRANSMISSION

To date there have been two main approaches to examining the spatial aspects of *E. multilocularis* transmission. The first has examined patterns of infection in foxes and related these patterns to landscape and other variables, and the second has been to examine patterns of infection in humans and relate these to spatial and aspatial risk factors. Infection rates in the intermediate hosts are often very low (<1 in 1,000) and it is impractical to map spatial variation in these animals. In the case of fox infection rates, the approach has been either to map culled foxes, or to collect fox feces and apply copro-antigen enzyme linked immuno assay (ELISA) tests. Staubach *et al.* (2001) examined the landscape in 2.5 km radius buffer zones around the positions of 3,521 culled foxes and found that infected foxes were more likely to be found in areas with higher pasture cover and lower forest cover. They also used data derived from satellite imagery to identify areas of moist soil as an additional explanatory variable. Raoul *et al.* (2001) found that the use of Em ELISA differentiated between high and low edemicity zones in eastern France and Stieger *et al.* (2002) found that the prevalence of ELISA positive fox feces was highest in the periphery of the urban area of Zurich.

In the case of human AE, Danson *et al.* (2003) used regional scale land cover data derived from the NOAA AVHRR to correlate the spatial distribution of human AE in China with the spatial distribution of the grassland land cover hypothesized to be suitable for *E. multilocularis* intermediate hosts. At a local scale, research in an *E. multilocularis* endemic area in southern Gansu Province, China, found a significant correlation between landscape composition derived from land use maps, and human AE prevalence in 31 agricultural villages (Craig *et al.*, 2000; Giraudoux *et al.*, 2002). This work was extended by Danson *et al.* (2004) who examined the landscape around the villages using archived data from the Landsat Multispectral Scanning (MSS) system with a 79m spatial resolution. Standard image processing techniques were used, with

data collected on the ground, to produce a map with five land cover classes: forest, tree/shrub, grass/shrub, grassland, and agricultural fields corresponding to those used in an earlier ecological survey (Giraudoux *et al*, 1998). The proportions of each land cover type were determined for circular 'buffer-zones' of different sizes (500-3,500m radius in 250m increments) around each village and the linear correlation between land cover proportions and village AE prevalence computed. The results showed a maximum linear correlation coefficient of 0.51 between human AE prevalence and the proportion of grassland in a 1,750m buffer around the villages determined from a satellite image recorded in 1975. Although the bivariate correlation only explained about 25% of the spatial variation in village AE prevalence, a multiple regression model, based on the proportions of shrubland and grassland habitat in the area around villages, explained 75% of the variation in village AE prevalence and illustrated the strong link between landscape and AE transmission risk (Danson *et al*, 2004).

LANDSCAPE STRUCTURE AND HUMAN AE

A key influence of landscape on *E. multilocularis* transmission is its control on the spatial distribution and population dynamics of the intermediate hosts. In the south Gansu study area, villages surrounded by shrubland and grassland were found to have higher human AE prevalence rates and it was hypothesized that such areas could sustain cyclically high population densities of susceptible intermediate hosts (Craig *et al*, 2000; Giraudoux *et al*, 2002; Danson *et al*, 2003). It was also hypothesized that such grassland and shrubland areas within about 2,000 m of village centers would be easily accessible to domestic dogs that could be infected through consuming infected rodents. The relationship between landscape and rodent population dynamics has been studied extensively and related to the ratio of optimal to marginal patch area (ROMPA) hypothesis that indicates that cyclically high population densities are likely in areas with a large ratio of optimal habitat to marginal habitat (Pleydell *et al*, 2004). However, the spatial organization of habitat patches will also influence population distributions and dynamics, and landscape ecology provides a theoretical framework within which to study such patterns. It is now straightforward to derive a range of 'landscape metrics' within a GIS to describe the spatial organization of habitats within a given area.

To test the relationships between landscape metrics and human AE in south Gansu, a range of metrics were

computed using the land cover map derived from the 1975 Landsat MSS data. A 2,000m buffer zones centered on each of the 31 villages was interrogated using the FRAGSTATS program (McGarigal *et al*, 2002) and set of landscape metrics extracted. The metrics may either represent attributes of the whole landscape, for example, the average landscape patch size, or may represent attributes of individual land cover classes, for example the average patch size of forest. Included within the metrics was the land cover proportion measurement used in the previous study (Danson *et al*, 2004). In this initial analysis, linear correlations between the metrics and village AE prevalence were computed.

The results showed that the strongest correlation between AE prevalence and the landscape metrics was with the *grassland mean patch size* in the 2,000m buffer area around villages (Table 1). The positive correlation indicated that as the mean grassland patch size increased, village AE prevalence increased providing an indication that the large patches of grassland close to villages represent a risk factor for *E. multilocularis* transmission. This is consistent with the hypothesis that the grassland patches provide a suitable habitat for the intermediate host and furthermore suggests a link to the ROMPA hypothesis.

In our previous study in Gansu, the strongest correlation was with the percentage of grassland around villages, which, in the current work, was ranked fourth out of the set of landscape metrics computed (Table 1). However, landscape metrics are known to exhibit co-correlation, and in this data set, there were statistically significant linear correlations between the four landscape metrics with the highest correlation with human AE (Fig 1). Grassland mean patch size was strongly positively correlated with grassland mean shape index and less strongly correlated with grassland and forest percent cover. It is clear, therefore, that these landscape metrics do not provide independent correlates with human AE, but rather they confirm that particular sets of landscape characteristics are likely to support high density populations of the intermediate hosts.

DISCUSSION AND CONCLUSIONS

This paper has outlined the factors affecting the transmission of *E. multilocularis* in wildlife and to human populations and highlighted the role of satellite remote sensing, GIS and spatial modelling in understanding the ecology of transmission. Significant advances in parasite detection over the past 10 years are now being coupled with spatial data on landscape characteristics, host distributions and dynamics, and

Table 1
 Linear correlation coefficient between landscape metrics and human AE prevalence. All correlations were significant ($p < 0.05$, $n = 31$).

Landscape metrics within 2,000m radius buffer	Metric description	Correlation coefficient
Mean patch size (MPS) – Grassland	Mean size (m ²) of grassland patches	0.537
Mean shape index (MSI) – Grassland	Grassland shape complexity 1=regular circles or square, greater than 1 for irregular patch shapes	0.513
Percentage cover (PC) – Forest	Percentage of buffer occupied by forest	0.510
Percentage cover (PC) – Grassland	Percentage of buffer occupied by grassland	0.503
Edge density (ED) – Agriculture	Amount of agriculture edge relative to total agriculture area	-0.494
Total edge (TE) – Agriculture	Sum of a perimeter of all agriculture patches	-0.494
Edge density (ED) – Forest	Amount of forest edge relative to total forest area	0.473
Total edge (TE) – Forest	Sum of a perimeter of all forest patches	0.473
Mean shape index (MSI)– Landscape	All landscape patch shape complexity	0.466
Percentage cover (PC) – Agriculture	Percentage of buffer occupied by agriculture	-0.461

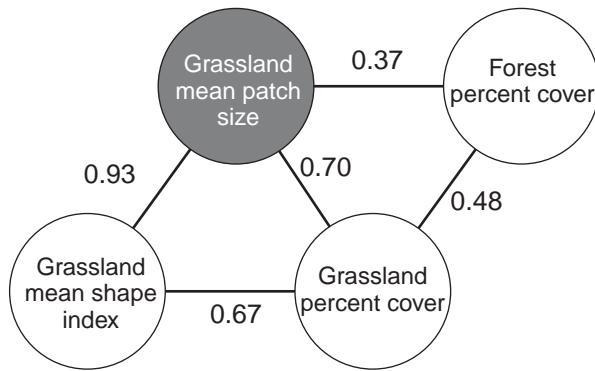


Fig 1- Linear correlation between landscape metrics. All correlation coefficients are significant ($p < 0.05$, $n = 31$). There was no significant correlation between forest percent cover and grassland mean shape index.

patterns of human infection. Spatial modelling techniques are being applied to study both fox infection patterns and the incidence of human AE providing new insights into the spatial risk factors for parasite transmission (Danson *et al*, 2003; Pleydell *et al*, 2004). Ecologists have previously explored the relationships between landscape composition and the population dynamics of susceptible intermediate hosts (Delattre

et al, 1996) and more recently satellite remote sensing and GIS have been used to test relationships with landscape metrics (Graham *et al*, 2004). There is, however, a considerable challenge ahead to relate such landscape characteristics to quantitative data on rodent populations, and also to link such data to systems-based models describing *E. multilocularis* transmission. Recent work by Hansen *et al* (2004) has provided a useful modelling framework for such studies and remote sensing, GIS and spatial modelling are likely to play a key role in providing quantitative data to parameterise, calibrate, and test such models

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