### Review

Introduction to the symposium on cestode zoonoses in Asia and the Pacific at the 21st Pacific Science Congress

# *Echinococcus Multilocularis*: Why are *multidisciplinary* and *multiscale* approaches essential in infectious disease ecology?

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**Abstract:** Understanding the transmission ecology of parasites involves the challenge of studying the complexity of life-cycles at multiple levels of biological organisation and at various space-time scales. We think that a single field of science alone cannot fully address this issue and that a way to understand such complexity is to connect various fields of science, to consider the whole transmission system, and to identify which are the variables reasonably accessible to measurement and the relevant scales at which they may provide information about transmission processes and indicate a higher risk of transmission/emergence. Based on ongoing studies carried out in Europe and in China, the aim of the present paper is to discuss this approach and to show how results obtained from mass-screening of human populations may be combined to those obtained from small mammal and landscape ecology studies and modelling to promote an understanding of *Echinococcus multilocularis* transmission and to determine how differences in the time-space scales at which human infection and small mammal population dynamic processes occur may complicate the analysis.

Key words: complexity, landscape ecology, epidemiology, small mammal community, fox, cestode zoonosis

#### INTRODUCTION

An understanding of the emergence or re-emergence of zoonotic pathogens requires knowledge of the ecological conditions enhancing their population dynamics and/or vicinity to humans. When transmission concerns parasite life cycles involving various host species and different development stages, this knowledge addresses the challenge of understanding the complexity of a life-cycle at multiple levels of organisation. For instance, on a cellular level, a parasite must accept its host and be accepted, while on a population level, host and parasite density and behaviours must make meeting likely, that is, the survival of free living stages may be affected by environmental factors, etc. Although dozens of host species may be involved in transmission and several fields of science are obviously required at each level of organisation with a systems approach, relatively few articles addressing complexity issues in parasitology are based on multidisciplinary studies. For instance, a query of the Scopus database on parasite/parasitology identifies 497 articles also indexed on complexity from 1973 to 2006 while only 66 were indexed on multidisciplinary studies over the same period. In both cases 50% of them were published from 2000 onwards, indicating that complexity and multidisciplinary have been issues of increasing interest only recently.

The emergence of a wildlife pathogen depends largely on 2 factors: the effect of environmental change on prevalence in wild populations and the frequency of human and domestic animal contact with wildlife reservoirs [1]. However, the infection rates of numerous wildlife populations can be extremely low, a general pattern before emergence. The relevant parameters of wildlife populations may never been monitored with reasonable precision such as population density, age structure and dispersion. for deterministic modelling and prediction. Furthermore, in many cases sub-

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populations of interest do not exist in isolation but interact, via (un-quantified) dispersion, with other conspecific subpopulations across a larger region. In this case, the inadequacy of traditional (e.g. non-spatial) approaches to determining population and transmission dynamics becomes apparent. Although new quantitative approaches are currently enabling better use of scarce data [2], it is probably ridiculous to think that the way to understand complexity is to dig deeper and narrower at one spatial and temporal scale in a single field of science alone. Thus, the challenge is to find ways to connect various fields of science and to consider the transmission system as a whole. Moreover, this implies identifying the variables reasonably observable in such systems and detecting the relevant spatial and temporal scales at which they may indicate a higher risk of parasite trans-

mission. Observational studies are essential at this stage, and processes underlying the observed patterns could then be reasonably hypothesized and investigated experimentally on this basis. Then it is necessary to quantitatively link descriptive results at various temporal and spatial scales from several disciplines. The way to do this remains an open question.

The aim of the present paper is to show how results obtained from massscreening of human populations may be combined to those obtained from small mammal community studies to understand the transmission of Echinococcus multilocularis and how differences in the time-space scales at which human infection and small mammal population dynamic processes occur may complicate the analysis. Primary data have

been obtained from ongoing multidisciplinary research carried out in Europe and China (see eg [3-5]).

## ECHINOCOCCUS MULTILOCULARIS ECOLOGY, SCALE DEPENDENCE AND SYSTEMS APPROACH

The cestode *E. multilocularis* exploits predator-prey relationships between canid definitive hosts and small mammal intermediate hosts. Human infection arises from accidental ingestion of *E. multilocularis* eggs. The red fox (*Vulpes vulpes*) is regarded as the principal definitive host responsible for sustaining transmission in a wildlife cycle throughout much of paleartic Euro-Asia. The southern limit of this endemic area is imposed by the susceptibility of *E. multilocularis* eggs to desiccation in hot or dry conditions

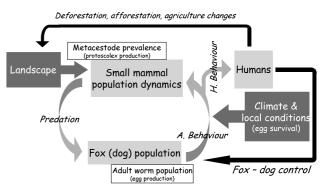


Fig. 1: Life cycle of Echinoccocus multilocularis and ecological factors regulating transmission. H. behaviour, human behaviour; A. behaviour, animal behaviour (after [4]).

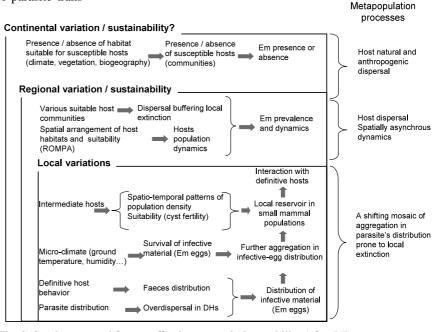


Fig. 2: Spatio-temporal factors affecting transmission stability (after [5])

[6]. Fig. 1 shows the life cycle in a rather classical form. It also summarizes the main environmental and behavioural parameters that have been shown to interact with transmission (see [4] for details). It draws attention to the fact that interactions cannot be studied from the perspective of a single discipline alone and that human and animal epidemiology, immunology, small mammal intermediate host and definitive host ecology, ethology and anthropology should be included to fully address relevant issues of transmission. Furthermore, such a system takes place in space and time. Fig. 2 shows how accounting for time-space processes adds much more complexity (see [5] for details). Here three critical spatial extents are described as the range at which the parasite populations stabilise. As suggested by the hierarchy theory [7], at each spatial extent corresponds a time span at

which processes occur. For instance, at the extremely local range, egg survival is determined by humidity and temperature that can kill eggs within hours and change drastically within a day and according to seasons. The distribution of faeces with infective eggs depends on various definitive host behaviours, and the large over-dispersion of parasites in hosts is conducive to the local aggregation of parasites prone to local extinction. At a larger range, intermediate and definitive host population dynamics are determined by regional factors such as spatial arrangements of favourable habitats and population dispersal (see below). Population dynamics are generally affected by seasonal and interannual variations of host densities, and the periods of higher densities are expected to be more conducive to transmission. At the continental scale, the bio-geographical distribution of species and thus community composition takes roots in the phylogenic history of the area. At that scale, the presence in a community of susceptible species prone to sustain higher population density in favourable conditions (if conditions are met at the regional scale) makes population outbreaks and intensive transmission likely. The time (tens of thousands of years or more for small mammals) needed to establish sustainable communities over a continental range is, of course, much longer than the time (a few years) needed to establish stable population dynamic patterns at the regional scale, itself much longer than the time (some hours) taken to vary viable egg distribution and host meeting via the prey /predator relationship and individual dispersal. This link between spatial range and temporal extent of processes is often pictured on a log-log scale as shown in Fig. 3.

Log area (km<sup>2</sup>)

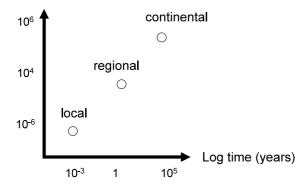


Fig. 3: Interdependence between study spatial and temporal extents. Processes occurring over large areas are slower than those over small areas.

Typical transmission parameters such as host infection rates (including those in humans, foxes, dogs and small mammals) are the global result of processes considered at various degrees as black box and often not explicitly referring to the various resolutions, spatial and temporal extents

where they occur and interact. In humans, for instance, the larva primary target organ is the liver where it proliferates slowly. Thus the disease has a long (5-20 years) asymptomatic stage and metacestode growth speed varies largely between individuals [8]. Human epidemiology studies are generally grounded on hospital records or the result of active screening of populations on a regional level. E. multilocularis prevalence is relatively low in humans (about 1‰ in the endemic areas of Western Europe and >1% in some foci of Western China). This means that using E. multilocularis prevalence in human to map parasite transmission intensity just cumulates unknown events including human exposure for the last 5-20 years before the screening and that the poor statistical power due to low prevalence rates generally prevents obtaining significant gradients at any extent lower than regional. Ironically, parasites can still be detected in an area where they are already extinct in wildlife and domestic animals, a fact demonstrated in Southern Gansu, China [4, 9]. Moreover, they have also not been detected in humans in areas where they have been shown to actually circulate such as European cities [10, 11]. However, it has been shown that in some cases, E. multilocularis prevalence in humans was correlated to landscape composition at regional scale. Although this pattern may not be as general as believed initially [6] this has been the case in the Jura mountains, Eastern France [12], in a study area of southern Gansu, China [9, 13, 4, 14, 15], and in the south of the Ningxia Autonomous Region of China (Pleydell et al. unpublished).

## LANDSCAPE APPROACH, TRANSMISSION ECOLOGY AND MODELLING

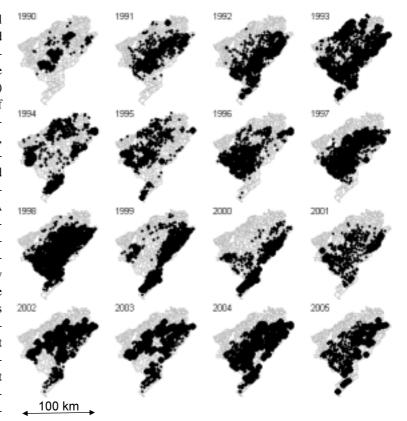
Assessing transmission intensity via studies carried out on the fox population (directly from necropsy or from faeces collection) is theoretically feasible in Western Europe where the species is abundant and not protected but logistically heavy at such a point that no long-term monitoring has ever been undertaken. Studies carried out at the regional level exceeding 1-2 years are exceptional (but see [16]) and results are generally pooled over time. Attempts are made to model spatial distributions on this basis, and the results have shown that infection in foxes may also be responsive to landscape composition [17-19]. However, such studies cannot help to explain either temporal patterns of infection (seasonal, multi-annual) or the detailed distribution of infective material such as faeces at fine grain.

The low prevalence in small mammals (<1‰ on the regional level in highly endemic areas, >10% locally in some over-dispersed foci) prevents any estimation of transmission intensity on a large extent at relevant resolutions.

The plasticity of small mammal dynamics is well known for some species as voles and pikas and vole populations have been shown to be extremely responsive to landscape composition. The ratio of optimal to marginal patch area (ROMPA) hypothesis is an attempt to describe the effects of both primary production and landscape composition on small mammal population dynamics [20, 21]. ROMPA refers to the ratio of optimal to marginal patch areas and is most frequently expressed as the proportion of a landscape composed of optimal habitat for the target species. The ROMPA could influence the probability that small mammal population densities undergo multiannual cycles, as a combined effect of dispersal and predation. If optimal habitats were scarce (low ROMPA), then the landscape matrix would serve as a large dispersal sink, and population densities would be very stable and small. At very high ratios, rodent densities would also be stable but relatively large (vole dispersal occurs within optimal habitats and sink area and predation is not enough to reduce population density). At intermediate ROMPA, multiannual rodent population cycles would be more likely. The hypothesis sug- Fig. 4: Population outbreaks of Arvicola terrestris in the Doubs department,

gests that the availability of optimal habitat in the landscape influences the growth rate of small mammal populations, but for grassland rodents high ROMPA in general implies little suitable habitat for generalist predators, and thus different cyclic patterns may emerge depending on available habitat. Percentage cover is perhaps the sim-

plest and most popular metric by which small mammal population dynamic patterns have been compared to the environment [22-24] although in grassland areas the dampening effect of hedgerow networks and mosaic landscapes has been proven [25-27]. Moreover long term monitoring of focal populations has shown that complex space-time patterns such as travelling waves can emerge with higher ROMPA (Fig. 4) [23]. This means that local short-term surveys of small mammal communities can be dramatically misleading with regard to the question of which species sustains large population densities at a larger extent and longer time-span (Fig. 5). This issue is essential when considering the areas where the long term population dynamics of community species have not yet been assessed. This is generally the case in China where dozens of different communities coexist in discrete sub-areas of various sizes, here called regions [4-6, 28]. The ROMPA hypothesis may however provide a way to link the range over which small mammal community surveys are carried out (local and very short



France. Black circles are proportional to population densities (maximum 500-100 individual/ha in grassland). Four population cycles are recognized (1990-1994, 1995-1999, 2000-2003, 2004-2005 cycle not achieved). Population surges start from epicentres located on a NE-SW strip and spread like a wave toward other areas of the department (data Fédération Régionale de Protection des cultures et Service Régional de protection des végétaux).

term) and the range over which human screenings are achieved (result of cumulated events on a region for 5-20 years). When long-term monitoring cannot be supported, it can also help delineating areas where larger population densities of focal species are likely.

The foremost question is how to objectively define the optimal habitat of each species of a community and to characterise community distributions according to habitat features. By necessity the habitat classifications defined in the field are based on physiological characteristics of vegetation. These classifications typically contain more classes than required to identify observable differences in the community structure of small mammals since different vegetation cover types often provide functionally similar levels of protection from predation and sources of nutrition, etc. At the regression stage of the landscape analysis this results in more regression parameters being estimated than necessary and thus sub-optimal conditions in terms of parsimony. Our current view is that this classification redundancy reduction

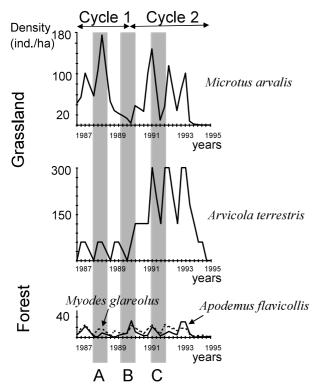


Fig. 5: small mammal population dynamics at le Souillot, Doubs department, from 1987 to 1995 (after [30]). Short term surveys (grey boxes A, B and C) would have shown different community structures and abundances. Studies in A and B would have failed to detect the importance of *A. terrestris*, and *A. terrestris* and *M. arvalis* respectively, although those two species represent, on average, the main prey biomass for foxes over the study period.

problem translates into a model selection problem. Under this paradigm information theory-based criterion can help identify the thresholds within a vegetation classification which fail to identify thresholds in small mammal community data. The starting point under this paradigm is the expression of a suitable likelihood function, and, since a single trap result is one of a set of mutually exclusive categorical variables, the multinomial distribution is a natural choice. Moreover, a multinomial regression model can include habitat type and other sampling-related factors such as trap type or trapping night. The Akaike Index Criterion (AIC) of this baseline model can be compared to that of the same model fitted under the constraint that regression coefficients for two different habitat types are equivalent. An exhaustive pairwise search can then identify the habitat pair for which there is the least evidence for differences in the trapping frequency distributions and indicate if a class merger can increase parsimony. The sequence of model comparison, selection and class merging can then be iterated until every super-class in the classification is associated 297

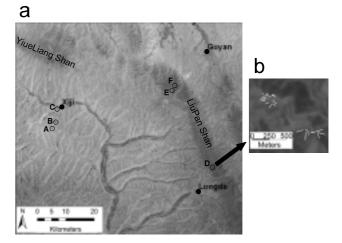


Fig. 6: differences in study extents in Southern Ningxia. Box a, study area used for mass screening of human populations; circles A, B, C, D, E, F: small mammal sampling locations. Box b: trapline locations in circle D. Each trapline consist in 25 traps set for 3 nights and controlled every morning. Although on the whole area sampling represents 5821 trap nights and all kinds of habitat there, traplines were clustered on 0.0003% of the total area under study for unavoidable logistic reasons.

with a unique trapping frequency distribution i.e. a unique small mammal assemblage (Raoul et al., unpublished). An open research question relating to this technique remains, that is, the incorporation of the dynamics inherent in temporal series.

At present we also face the challenge of how best to upscale from local trapping studies to mapping habitat suitability and epidemiological importance for intermediate host species across China (Fig. 6). Luckily an increasingly wide range of remote sensing data products are becoming available, as shown in a recent review [29]. These products enable space-time series to be mapped easily across the globe and can provide a baseline dataset upon which small mammal species or community data can be modelled and extrapolated. We are currently exploring the use of soft classification techniques combined with Bayesian prediction in the interest of assessing uncertainty in the known distributional extents of key intermediate host species. Such analyses are undoubtedly invaluable for targeting of those habitats or eco-zones associated with the greatest uncertainty when manpower and resources are limited.

Although necessary here, attempts to derive global parameters on a regional level from studies undertaken on smaller areas should nevertheless be considered cautiously. For instance, grassland ratio derived from CORINE Land Cover (a European spatial dataset related to environmental, agriculture and spatial planning http://terrestrial.eionet. europa.eu/CLC 2000) extrapolated to southern Germany and south-west Czech Republic failed to describe the fox prevalence (Echinorisk Network, unpublished). This probably represents a resolution mismatch between the geographical data at hand and the phenomenon giving rise to transmission: namely, that a network of small microtine patches undetectable in the CORINE dataset appears to sustain transmission in southern Germany and the Czech Republic (Romig, Martinek, personal communication). These and other uncertainties and the nested hierarchy of transmission systems (see Fig. 2) prohibit fully deterministic modelling. To address this problem and to explore the local particularities under favourable environmental conditions, transmission models need to be coupled with more flexible approaches capable of detecting unknown spatial patterns and non-linearities. The diversity of small mammal host communities and landscape worldwide offer a number of systems that sustain transmission of E. multilocularis at various time-space scales. It is expected that further advances will come from methods combining quantification of host communities from field surveys, landscape via remote sensing and parasite transmission via population screenings conducted on definitive hosts (e.g. dogs in villages in China or foxes in Europe) and humans, in a spatially explicit context. The combination of multi-level field approaches with modern regression techniques coupled with traditional transmission models may provide a unique opportunity to investigate how the diversity of small mammal communities and anthropogenic landscapes can regulate parasite transmission [6].

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