ELSEVIER

Preventive Veterinary Medicine 1728 (2002) 1–14

PREVENTIVE VETERINARY MEDICINE

www.elsevier.com/locate/prevetmed

Modelling bovine trypanosomosis spatial distribution by GIS in an agro-pastoral zone of Burkina Faso

Jean-François Michel[a,*], Stéphane Dray[b], Stéphane de La Rocque[a], Marc Desquesnes[a], Philippe Solano[c], Gérard De Wispelaere[d], Dominique Cuisancee[e]

[a]*CIRDES/CIRAD-EMVT, Bobo Dioulasso, Burkina Faso, France*
[b]*Université Claude Bernard Lyon I, Villeurbanne, France*
[c]*IRD/IPR, Bouake, Côte d'Ivoire, France*
[d]*CIRAD-EMVT, Maison de la télédetection, Montpellier, France*
[e]*CIRAD-EMVT, Campus International de Baillarguet, Montpellier, France*

Abstract

Modelling of the spatial distribution of bovine trypanosomosis prevalence in Sideradougou district Burkina Faso was performed by using a combination of spatial and statistical analysis. Based on a comprehensive and geographically representative census of herds and farms in the area, more than 2000 cattle were randomly chosen and their blood sampled during field survey. Data on livestock farming practices were recorded for each farm. All data were mapped within a GIS to generate new information on spatial constraints in the area.

Surveys results were analysed and serological prevalence data were modelled using logistic regression. The model allowed identification and quantification of risk factors. In a second step the statistical model was used predictively on the entire farm population in the area. This method was successful in predicting the serological prevalence for each individual herd in the sample, from their livestock management patterns and spatial location. Predicted prevalences were represented within the GIS, taking daily movements of animals into account. Spatial distribution of prevalence would illustrate specific locations at risk from an epidemiological viewpoint. It gives evidence that the hydrological network and land occupation patterns in the savanna-type countryside are playing an important part when structuring a so-called ''trypanosomosis space''.

Keywords: GIS; Spatial modelling; Logistic regression; Trypanosomosis; Epidemiology

* Corresponding author.
E-mail address: jefmichel@wanadoo.fr (J.-F. Michel).

0167-5877/02/$ – see front matter © 2002 Published by Elsevier Science B.V.
PII: S0167-5877(02)00120-4

1. Introduction

Animal trypanosomoses are one of the main pathological constraints on the development of animal production in sub-Saharan Africa (Hursey and Slingenbergh, 1995), and cause annual losses estimated at US$ 1 billion (De Haan and Bekure, 1991). Tsetse flies are the main vectors. The risk of transmission is primarily linked to the intensity of the encounters between vectors and hosts, and depends on the spatial and temporal interfaces between the protagonists in the pathogen system (host–vector–parasite) (Laveissière et al., 1986; De La Rocque et al., 1999). High-risk areas have been identified on this basis in an agro-pastoral zone of southern Burkina Faso, taking environmental and socio-economic factors into account. The available data were georeferenced, included into a geographic information system (GIS), and high-risk areas were identified by spatial modelling (De La Rocque et al., 2001), as it was performed at the other scales (Hendrickx et al., 2001).

The serological prevalence of the disease (prevalence of antibodies directed against trypanosomal antigens) was studied on a sample of cattle farms in the study area, to validate the list of epidemiological risk areas identified. However, the data obtained were both partial and spatially disjointed. The method described here was subsequently developed for estimating and modelling disease spatial distribution, with a view to making the data compatible with the layers of geographic data available for the study zone as a whole.

2. Material and methods

2.1. Study zone

The study was conducted in part (1200 km^2) of the Sidéradougou agro-pastoral zone south of Bobo-Dioulasso (Burkina Faso), 11°N and 4°W (Fig. 1). The zone has 1000–1100 mm of rainfall per year, with a dry season from November to April and a rainy season from May to October. It is typical of the Sudanian tropical climate zone, with bushy savannas and forest stands along its watercourses. These types of riverside vegetation are the preferred biotopes of the tsetse flies found in the zone, *Glossina tachinoides* and *Glossina palpalis gambiensis* (Challier, 1973; Gruvel, 1975).

2.2. Population, sampling and diagnosis

The cattle in the zone were counted exhaustively, based on the dwellings by which they are penned during the night (Michel et al., 1999). For each dwelling, the number of head, their watering points at the end of the dry season, and information on transhumance were recorded. The geographic positions of each dwelling and the watering point or points (two at most) were determined by global positioning system (GPS) (Garmin™).

Over 800 dwellings, with 16,576 head, were visited. The herds were split into three categories: (i) small units with one or two pairs of draught oxen; (ii) mixed units, generally with fewer than 20 head, including draught oxen and a few breeders; (iii) large herds of several dozen head, with transhumance often practised during the dry season. In this zone, where livestock are a major component of farming systems practised, there are many small

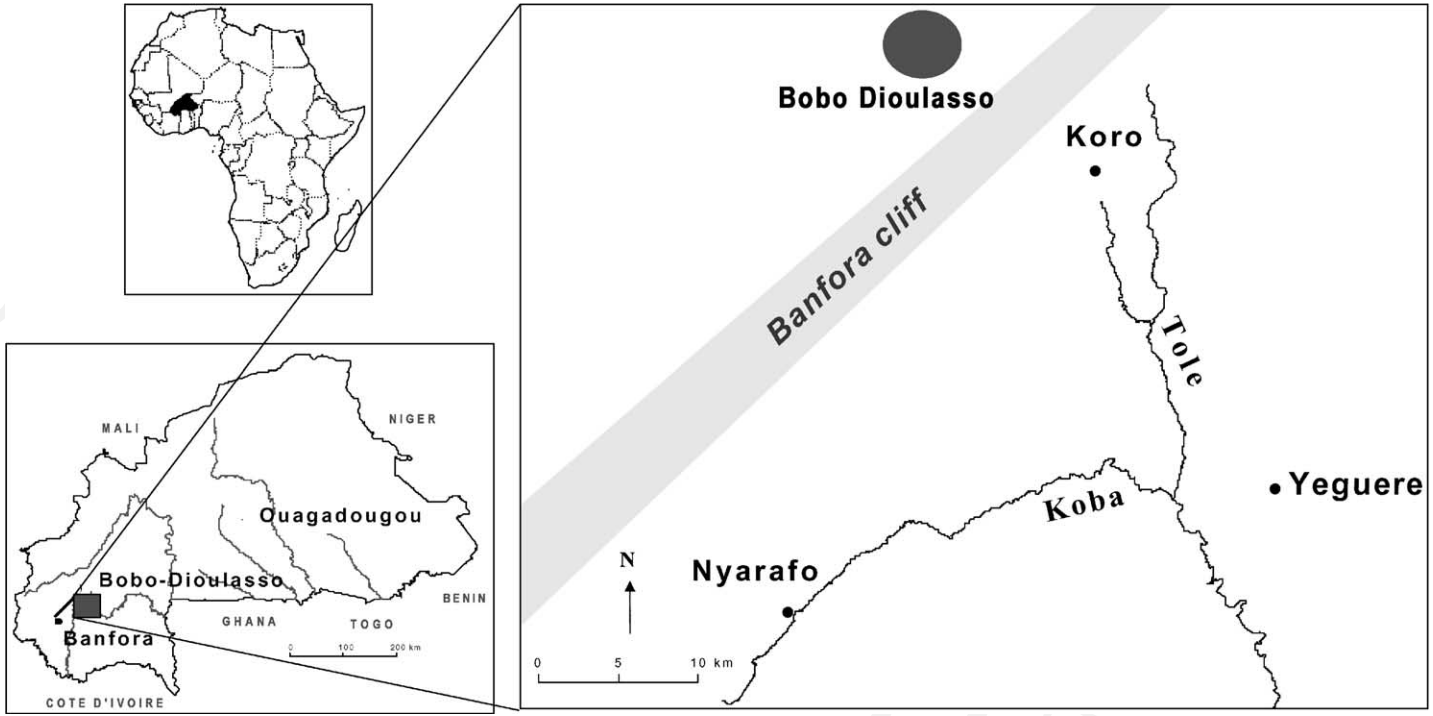

Fig. 1. Location of the study zone. The Sidéradougou agro-pastoral zone is located in the south of Bobo-Dioulasso (Burkina Faso), at 11°N and 4°W (after De La Rocque et al., 2001).

Table 1
Herd size and head number in the local population

	Herd size			
	Under five head	5–20 head	Over 20 head	Total
Number of herds	476 (59%)	188 (24%)	137 (17%)	801
Number of animals	1372 (9%)	1861 (11%)	13343 (80%)	16576

and medium-sized herds, which account for over 80% of farms but only 20% of the animals. On the other hand, 80% of the cattle in the zone are owned by 17% of the farmers (Table 1).

The herds are found in three main zones (Fig. 2): (i) an agricultural zone in which animal production is closely integrated into the farming system, with medium-sized herds, in the east (zone 1); (ii) a mixed agricultural and pastoral zone in the west, with small and large herds (zone 2); (iii) an almost exclusively pastoral zone in the south, with large herds (zone 3). This distribution corresponds to the pattern for crops (De La Rocque et al., 2001). In the whole study area, there are very few trading and non-trading exchanges of cattle.

A two-stage sampling was performed. The first sampling unit was on herd, i.e. an animal management unit subject to common animal production practices. It was easily identifiable in the field and corresponds to an epidemiological entity. The herds were drawn at random. The second sampling unit was animals which were chosen as follows: (i) exhaustive sampling in small herds (fewer than five head); (ii) 10 head at most in medium-sized herds (between five and 20 head); (iii) 20 head at most in large herds (over 20 head). Within the herds, the head were drawn at random, without replacement. For logistical reasons it was decided to sample 2000 head spread over 15% of the herds in the zone. A questionnaire on animal production practices was filled in for each herd.

Blood samples were taken from the jugular vein. The plasma was analysed in the laboratory using three indirect ELISA systems (*T. vivax*, *T. brucei* and *T. congolense*), revealing antibodies against *Trypanosoma* spp. (Desquesnes et al., 2000).

2.3. Available data and statistical model

Several types of data were used to analyse and model trypanosomosis seroprevalence in the herds:

- Serological data corresponding to the variable to be explained.
- Animal husbandry data obtained from the field survey: herd size, transhumance practices and the type of watering point used at the end of the dry season.
- Spatial data generated by the GIS from the geographic position of the different units: distance between dwelling and watering point, and proximity of dwellings to the hydrological network.

The descriptive variables were classified according to knowledge of practices (Lhoste et al., 1993), and their epidemiological significance (Table 2). The type of watering point was divided into springs and rivers (which are propitious to tsetse flies), and wells and

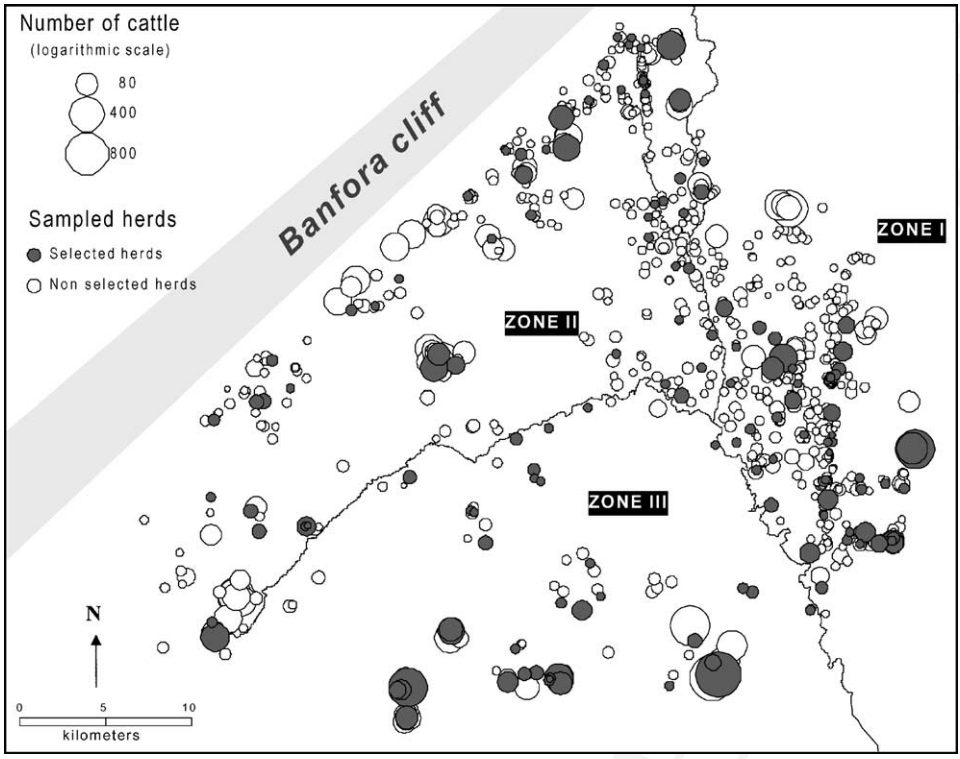

Fig. 2. Herds, sampled herds and agricultural distribution in the study zone. The size of the points varies according to the $\log_e$ of herd size. The herds are found in three main zones which are delineated by the hydrographic network: (i) an agricultural zone in which animal production is closely integrated into the farming system, with medium-sized herds, in the east; (ii) a mixed agricultural and pastoral zone in the west, with small and large herds; (iii) an almost exclusively pastoral zone in the south, with large herds. This distribution corresponds to the pattern for crops.

boreholes (which are generally found in zones not favourable to the flies). The zone classed as *neighbouring* on the hydrographic network was set at 2 km, based on known data on the tsetse fly's ability to spread (Cuisance et al., 1985).

The serological prevalence for each herd was modelled using logistic regression, since the response variable is a proportion and the error function is assumed to follow the binomial law (McCullagh and Nelder, 1989). The link function used was the logit function, defined as $\text{logit}(p) = \log_e(p/(1-p))$. An over-dispersion phenomenon often appears in using generalized linear model with a logit link when the response variable is a proportion. Over-dispersion means that the variance of the response variable exceeds the binomial variance and this problem is very common in large-scale epidemiological studies (McCullagh and Nelder, 1989). Taking into account the over-dispersion problem, we used a quasi-likelihood approach (McCullagh and Nelder, 1989) in the place of likelihood function. This led to wider confidence interval of parameters than the classical approach. For the same reasons, to test the contribution of the different descriptive variables in the model, we conducted a

Table 2
Descriptive variables used for modelling[a]

Code	Variable	Levels
typew	Type of watering point used in dry season	*Art: artificial* Nat: natural
distw	Distance between farm and watering point used in dry season	*1: <1000 m* 2: 1000–4000 m 3: >4000 m
hrdsz	Herd size	*1: small (<5)* 2: medium (5–20) 3: large (>20)
Hy2km	Farm less than 2 km from hydrographic network	*No* Yes
allyr	Animals kept by dwelling all year round	*No* Yes

[a] Reference levels for the model are shown in italic.

deviance analysis with F-test in the place of χ^2-test (Collet, 1991). The coefficients obtained in the model were interpreted by calculating the odds ratios and their confidence interval (Bouyer et al., 1995). This enabled us to quantify the risk factors associated with the levels of each of the explanatory variables in relation to a reference level.

As the model was not spatialized, it was necessary to look for autocorrelation among residuals. If the presence of autocorrelation was detected, it could imply the omission of regressor variables, the presence of non-linear relationships or that the regression model should have an autoregressive structure (Cliff and Ord, 1973). To test the autocorrelation, we firstly established neighbourhood relationships between herds using a Delaunay triangulation as proposed by Schmoyer (1994). In the second step, Geary (Geary, 1954) and Moran's (Moran, 1948) statistics (see also Cliff and Ord, 1973) were computed for residuals. By permuting the values of the residual map, we computed new values of autocorrelation statistics and the observed value is tested by comparing to the set of values obtained for the permutations. As the number of possible permutation was very large, we used a Monte-Carlo (Manly, 1991) version of the test. The same procedure has been carried out for observed and predicted prevalence values. This kind of procedure has been recently used in Kleinschmidt et al. (2000) with the non-parametric D-statistic (Walter, 1992) to measure autocorrelation of predictions from a logistic regression. When these indices were applied to observed and predicted prevalence values and the residuals of the model, they enabled us to test the capacity of a model to take account of the spatial nature of data.

The statistical model was then inverted to estimate the serological prevalence for all the herds in the zone, using the explanatory variables shared with the survey, which were the same than those used to generate the model.

All calculations were made using the R software (Ihaka and Gentleman, 1996).

2.4. Spatial model

Specific problems linked to the geographical nature of mapped objects such as herds and the "in herd" variability of measured variables have to be considered when mapping

seroprevalence: (i) herds are points that may be superimposed if they are close to one another, hence masking information; (ii) the meaning of prevalence within a herd varies with the number of head in the herd, a prevalence of 50% in a two head herd has not the same significance as a prevalence of 50% in a 100 head herd; (iii) mapping only the points corresponding to the pens used at night provides only a partial representation of reality as animals move and occupy a continuous space; (iv) spatial information on prevalence has to be compatible with the other information available in the GIS if they are to be compared. To overcome these problems, a spatial model of land occupation by cattle and of disease distribution was developed. All spatial object manipulations used the Mapinfo™ software.

The representation of land occupation by cattle in a zone as a whole is based on modelling the daily movements of the animals in each herd. In savanna zones, water availability is the main constraint at the end of the dry season, and governs movements (Boutrais, 1994). Herd movements were therefore modelled by representing the direct route between the night pen and the watering point or points, and drawing a buffer zone around the route, corresponding to the area occupied by the cattle during the day (Michel et al., 1999). This zone of daily use by the herd varies in size. The wider the herd and the nearer it is to its watering point, the larger the zone of frequentation (Fig. 3). This model was validated by monitoring the movements of a sample of herds.

The predicted prevalence for all the herds was applied to their zones of daily use. To synthesize this information, which was not yet very easy to resolve due to the superimposition of polygons, it proved necessary to aggregate it so as to shift to a smaller scale. This was done by projecting all the zones of use and the corresponding prevalences onto a regular geographic grid of 1 km^2 (Raynal et al., 1996). The cumulated distribution of antibody-prevalence in the study zone was then represented by assigning to each square the mean value of the prevalences for the herd polygons impinging on it, so as to produce a map of average prevalence (Fig. 4). The calculated mean value of prevalence was weighted by the size of herds in order to take into account for problems (ii) cited above. Smoothing by two-dimensional weighted local regression (Cleveland and Devlin, 1988) on the centroids of the squares in the grid made the maps more realistic.

3. Results

3.1. Sampling and observed seroprevalence

In total, 216 herds and 1784 head were sampled. Herd and cattle distribution in the sample showed that small herds were slightly under-represented, in favour of medium-sized herds (Table 3). On the other hand, small herds were over-represented near the hydrographic network (Fig. 2). The differences in relation to the sample initially planned can be attributed to field constraints such as herds in an out-of-the-way place or cattle breeder absent or not in agreement with taking a blood sample.

The average serological prevalence observed among the cattle was 73.4%. The map of herd prevalence, shown as points according to the corresponding dwelling, showed case distribution but was difficult to interpret (Fig. 5).

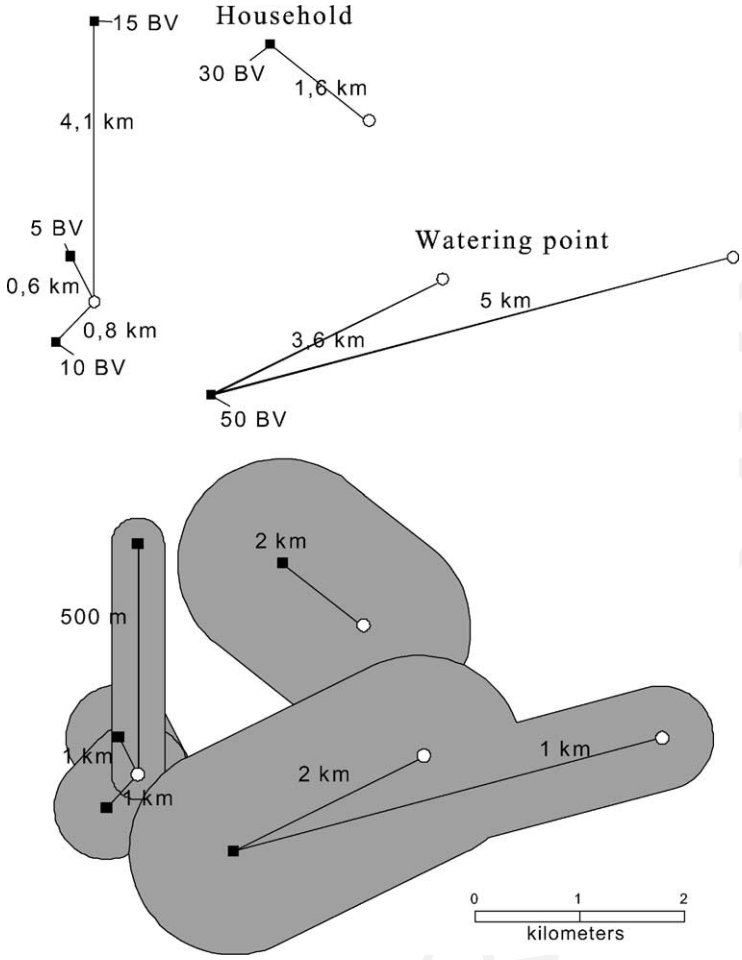

Fig. 3. Modelling of daily herd movements. Modelling herd movements consists in representing the direct route between the night pen and the watering point or points, and drawing a buffer zone around the route, corresponding to the area occupied by the cattle during the day. This zone of daily use by the herd varies in size. The larger the herd and the nearer it is to its watering point, the larger the zone of frequentation is (BV: cattle) (after De La Rocque et al., 2001).

Table 3
Herd size and head number in the sample

	Herd size			
	Under five head	5–20 head	Over 20 head	Total
Number of herds	110 (51%)	70 (32%)	36 (17%)	216
Number of animals	327 (18%)	736 (41%)	721 (41%)	1784

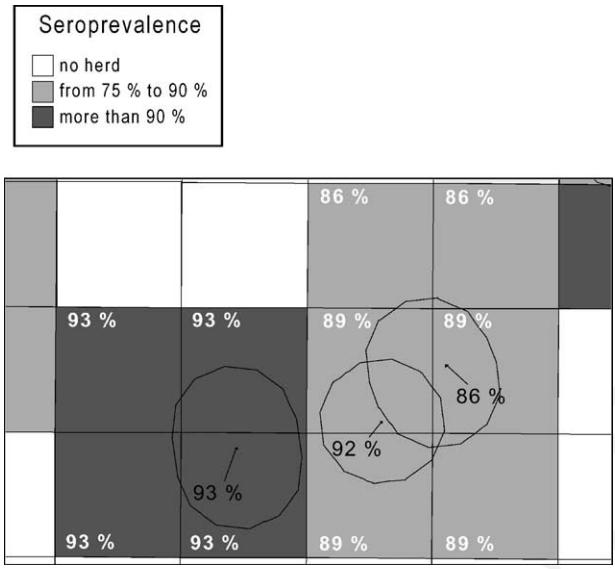

Fig. 4. Data aggregation and spatial distribution of mean prevalence. This was done by projecting all the zones of use and the corresponding prevalences onto a regular geographic grid of 1 km^2. The cumulated distribution of antibody-prevalence in the study zone was then represented by assigning to each square the mean value of the prevalences for the herd polygons impinging on it, so as to produce a map of average prevalence.

3.2. Statistical modelling: identification of risk factors

The deviance analysis showed that only the distance between cattle pen and watering point was not significant and this variable was excluded from the model. All the other variables were significant (Table 4). The dispersion parameter for the model was 2.48. The relation between the numbers of observed and predicted positives (Spearman's rank correlation $\rho = 0.45$, $P < 0.0001$) showed that the statistical model has a good fit. The spatial autocorrelation tests revealed a positive correlation between observed and predicted prevalences, whereas the residuals of the model were not correlated (Table 5). The variables used in the model thus take account of the spatial factor. The odds ratios calculated with the coefficients estimated by the model showed that proximity to the

Table 4
Deviance analysis of the model

	Degree of freedom	Deviance	Residual degree of freedom	Residual deviance	$P(>F)$
NULL	–	–	215	666.51	–
typew	1	17.66	214	648.86	<0.0082
hrdsz	2	37.37	212	611.49	<0.0006
allyr	1	59.07	211	552.41	<0.0001
hy2km	1	54.17	210	498.24	<0.0001

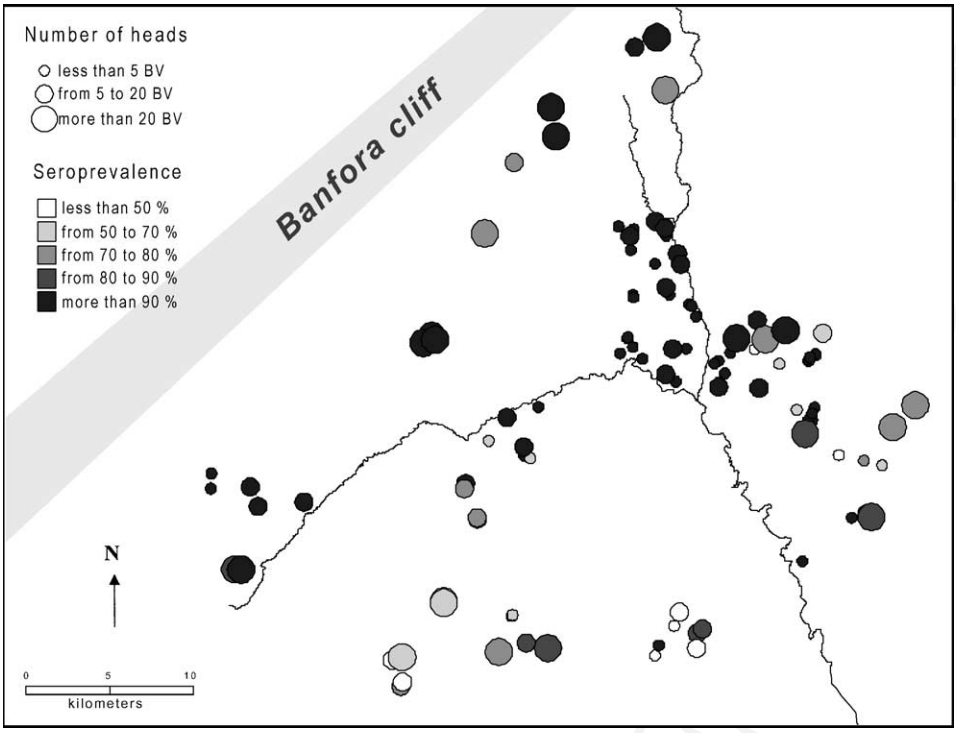

Fig. 5. Distribution of serological prevalence among the herds sampled. The map of seroprevalence for the herds sampled, shown as points according to the corresponding dwelling, indicated case distribution. BV: cattle.

hydrographic network, frequentation of natural watering points, large herd size and the fact of keeping animals near dwellings all year round were all risk factors (Table 6).

3.3. Modelling of spatial distribution of prevalence

The map of predicted serological prevalences, obtained by spatial modelling on a whole study zone scale, showed that mean serological prevalence is distributed along the hydrographic network, with focal points of high values, and that it spreads radially into the neighbouring savannas (Fig. 6).

Table 5
Spatial autocorrelation tests for the observed and the predicted prevalences and the residues of the model, using Moran's (I) and Geary's (c) indexes

Variable	I	P-values	c	P-values
Observed prevalence	0.196	<0.001	0.799	<0.001
Predicted prevalence	0.542	<0.001	0.465	<0.001
Residuals of model	0.020	0.248	0.972	0.288

Table 6
Odds ratios (OR) calculated from the coefficients of the serological model

Variable	Lower confidence interval (OR)	OR	Upper confidence interval (OR)
Intercept	0.53	1.08	2.19
typewnat	0.88	1.34	2.04
hrdsz2	0.38	0.67	1.16
hrdsz3	1.03	1.99	3.84
allyryes	1.69	2.70	4.31
hy2kmyes	1.94	3.43	6.07

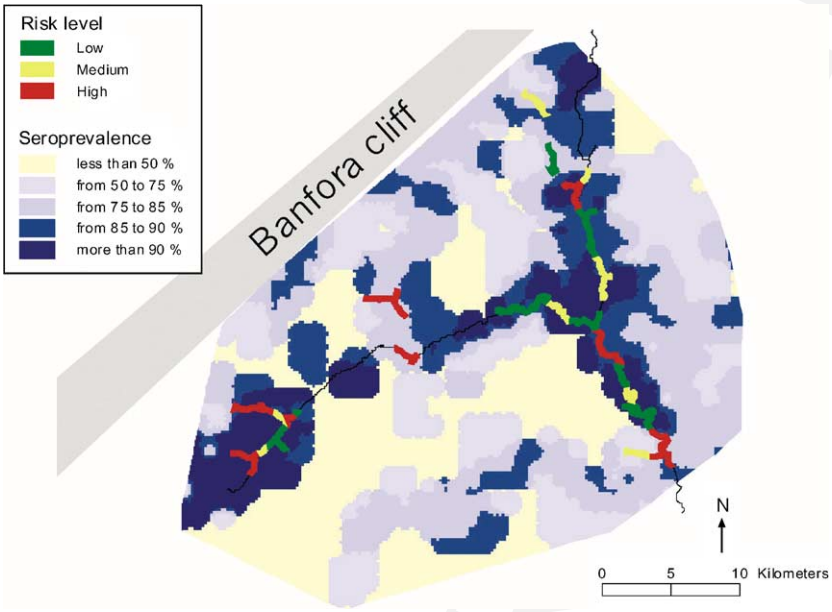

Fig. 6. Distribution of mean serological prevalence in the zone and high-transmission-risk zones. The high-transmission risk zones are delineated by a white outline. This map shows that mean serological prevalence is structured linearly along the hydrographic network, with focal points of high values, and that it spreads radially into the neighbouring savannas.

4. Discussion

4.1. Observed prevalence and statistical model

The serological results obtained from the sample confirm the enzootic situation that had already been observed for trypanosomosis in the Sidéradougou zone, with high infection levels among vectors (De La Rocque, 1997). On an animal production zone scale, parasite pressure can be evaluated more accurately by the number of antibody carriers than by direct detection of parasites (Desquesnes et al., 2000). With serological data, the statistical model

proved to be of high quality, and confirmed the risk factors conventionally identified in terms of animal trypanosomosis, such as spatial and temporal proximity to vector-propitious biotopes and intensity of contact with tsetse flies, particularly through watering practices (De La Rocque et al., 1999). The risk associated with large herds can be put down to the fact that such herds use natural watering points with sufficient capacity, which are generally located in preferred biotopes of tsetse flies.

4.2. Spatial modelling of trypanosome prevalence

Daily movements of cattle were modelled at the end of the dry season, since at such times, animal movements centre on specific sites: dwellings and watering points. Moreover, the end of the dry season is a key period for bovine trypanosomosis epidemiology: it is the period with the highest risk of parasite transmission (Rowlands et al., 1993). Lastly, modelling was conducted with a specific aim: to study the relations between cattle trypanosomosis vectors and hosts on a whole-zone scale. The model predicts the presence of cattle around the crucial points of contact between cattle and tsetse flies. It would have been possible to introduce spatial constraints into the model, to take account of the relief or of zones occupied by crops. However, these constraints are very limited at the end of the dry season, and projection onto a geographic grid would reduce its accuracy.

The attribution of prevalences to zones of use by cattle and their aggregation within a geographic grid provides continuous information in spatial terms. The map of mean prevalences, which takes account of all the predicted prevalences, is well suited to serological data.

Superimposing the map of predicted prevalences and the epidemiological risks zones identified elsewhere (De La Rocque et al., 2001) shows that prevalence distribution corresponds roughly to the zones with a high risk of disease transmission (Fig. 6). The zones in the northeast, at the foot of the Banfora Cliff and in the extreme north, which had high prevalence rates among cattle, were not subjected to the high-transmission-risk site identification procedure. The existence of high serological prevalences well away from the hydrographic network can be explained by: (i) tsetse fly dispersion during the rainy season: the flies infect cattle, which may still have antibodies when the next dry season arrives (Desquesnes, 1997); (ii) the assignment of prevalences to cattle use zones that stretch well into the savannas. It is thus crucial to take account of animal movements and land occupation if we are to obtain a realistic picture of bovine trypanosomosis prevalence distribution in the zone.

Projecting the land occupied by each herd onto the geographic grid enabled us to improve the resolution of disease representation in the zone. The choice of the size of the elementary squares in the grid is crucial, as it governs the change in scale. We chose a size of 1 km, since it corresponds (i) to a reasonable scale for taking account of variations in daily herd movements and (ii) to the scale of the study and integration in the GIS of the other topics covered in the study of disease transmission.

5. Conclusion

By taking account of animal movements and modelling the prevalence of the disease, the method described enabled us to convert specific, partial spatial information on a herd scale

into continuous information on a whole-zone scale. Spatial modelling is a robust method, and produces a realistic picture of disease epidemiology. It showed that the natural environment and animal production practices account for structure in trypanosome distribution. The data layer obtained was integrated into a GIS with a view to validating the zones with a high risk of animal trypanosomosis transmission. This opens the way for the identification of spatial indicators of a trypanosomal risk, such as the presence of crops, the spatial structure of habitats, and soil characteristics.

The approach described was based on detailed field data whose acquisition is time-consuming, such as exhaustive, georeferenced counts of herds and their watering points. One essential improvement would be to identify simple, easy to obtain indicators of the presence of cattle and their movements.

The spatialization of data, their integration into a GIS, the coupling of conventional statistical models and spatial models, and the methods available for changing scale offer new methodological and thematic prospects for studying the epidemiology of directly and indirectly transmitted diseases on different scales (Hay et al., 2000; Hendrickx et al., 2001), but also for understanding the interactions between animal production and the surrounding environment.

Acknowledgements

This work was funded by CIRAD-EMVT (Action Thématique Programmée ''Santé-Environnement'') and CNRS (Programme Interdisciplinaire ''Environnement, Vie et Société''). We are indebted to the directors of CIRDES, S.M. Toure and A. Gouro for allowing us to do the work.

References

Boutrais, J., 1994. Eleveurs, bétail et environnement. In: Blanc-Pamard, C., Boutrais, J. (Eds.), Dynamique des Systèmes Agraires: a la croisée des parcours: pasteurs, éleveurs, cultivateurs. ORSTOM, Paris, pp. 303–319.

Bouyer, J., Hémon, D., Cordier, S., Derriennic, F., Stücker, I., Stengel, B., Clavel, J., 1995. Epidémiologie, Principes et Méthodes Quantitatives. INSERM, Paris, 498 pp.

Challier, A., 1973. Ecologie de *Glossina palpalis gambiensis* Vanderplanck 1949 en Savane d'Afrique Occidentale. ORSTOM, Montpellier, 274 pp.

Cleveland, W.S., Devlin, S.J., 1988. Locally weighted regression: an approach to regression analysis by local fitting. J. Am. Stat. Assoc. 83, 596–610.

Cliff, A.D., Ord, J.K., 1973. Spatial Autocorrelation. Monographs in Spatial and Environmental Systems Analysis. Pion Limited, London, 178 pp.

Collet, D., 1991. Modelling Binary Data. Chapman & Hall, London, 384 pp.

Cuisance, D., Fevrier, J., Déjardin, J., Filledier, J., 1985. Dispersion linéaire de *Glossina palpalis gambiensis* et *G. tachinoides* dans une galerie forestière en zone soudano-guinéenne (Burkina Faso). Rev. Elev. Med. Vet. Pays Trop. 47, 69–75.

De Haan, C., Bekure, S., 1991. Animal Health Services in Sub-Saharan Africa: Initial Experiences with New Approaches. World Bank, Washington, 88 pp.

De La Rocque, S., 1997. Facteurs discriminants majeurs de la présence des glossines dans une zone agro-pastorale du Burkina Faso. Intérêt dans la prévision du risque trypanosomien. Ph.D. Thesis. Université de Montpellier, Montpellier, 162 pp.

297 De La Rocque, S., Bengaly, Z., Michel, J.F., Solano, P., Sidibé, I., Cuisance, D., 1999. Importance des interfaces
298 spatiales et temporelles entre les bovins et les glossines dans la transmission de la trypanosomose animale en
299 Afrique de l'Ouest. Rev. Elev. Med. Vet. Pays Trop. 52, 215–222.
300 De La Rocque, S., Michel, J.F., Cuisance, D., De Wispeleare, G., Solano, P., Augusseau, X., Guillobez, S.,
301 Arnaud, M., 2001. Le risque trypanosomien, une approche globale pour une décision locale. CIRAD,
302 Montpellier, France, 150 pp.
303 De La Rocque, S., Michel, J.F., De Wispeleare, G., Cuisance, D., 2001. De nouveaux outils pour l'étude des
304 trypanosomoses en zone soudanienne: modélisation de paysages épidémiologiquement dangereux par
305 télédétection et systèmes d'information géographique. Parasite 8, 171–195.
306 Desquesnes, M., 1997. Les trypanosomoses du bétail en Amérique Latine, étude spéciale dans le Plateau des
307 Guyanes. Ph.D. Thesis. Université de Lille, Lille, 409 pp.
308 Desquesnes, M., Michel, J.F., De La Rocque, S., Solano, P., Millogo, L., Sidibé, I., Cuisance, D., 2000. Enquête
309 parasitologique et sérologique (ELISA-indirectes) sur les trypanosomoses des bovins dans la zone de
310 Sidéradougou, Burkina Faso. Rev. Elev. Med. Vet. Pays Trop. 52, 223–232.
311 Geary, R.C., 1954. The contiguity ratio and statistical mapping. Incorp. Stat. 5, 115–145.
312 Gruvel, J., 1975. Données générales sur l'écologie de *Glossina tachinoides* Westwood, 1850, dans la réserve de
313 Kalamaloué, vallée du Bas-Chari. Rev. Elev. Med. Vet. Pays Trop. 28, 27–40.
314 Hay, S.I., Randolph, S.E., Rogers, D.J. (Eds.), 2000. Remote Sensing and Geographical Information Systems in
315 Epidemiology. Academic Press, London, 351 pp.
316 Hendrickx, G., De La Rocque, S., Reid, R., Wint, W., 2001. Spatial trypanosomosis management: From data-
317 layers to decision making. Parasitol. Today 17, 35–41.
318 Hursey, B.S., Slingenbergh, J., 1995. The tsetse fly and its effects on agriculture in sub-Saharan Africa. World
319 Anim. Rev. 84, 67–73.
320 Ihaka, R., Gentleman, R., 1996. R: a language for data analysis and graphics. J. Comput. Graph. Stat. 5, 299–
321 314.
322 Kleinschmidt, I., Bagayoko, M., Clarke, G.P.Y., Craig, M., Le Sueur, D., 2000. A spatial statistical approach to
323 malaria mapping. Int. J. Epidemiol. 29, 355–361.
324 Laveissière, C., Couret, D., Hervouët, J.P., 1986. Localisation et fréquence du contact homme/glossines en
325 secteur forestier de Côte d'Ivoire. 1. Recherche des points épidémiologiquement dangereux dans
326 l'environnement végétal. Cahiers de l'ORSTOM, Série Entomologie médicale et Parasitologie 14, 21–35.
327 Lhoste, P., Dollé, V., Rousseau, J., Soltner, D., 1993. Manuel de zootechnie des régions chaudes. Les systèmes
328 d'élevage. Coll. Manuels et précis d'élevage, CIRAD, Coopération Française, Paris, 288 pp.
329 Manly, B.F.J., 1991. Randomization and Monte Carlo Methods in Biology. Chapman & Hall, London, 281 pp.
330 McCullagh, P., Nelder, J.A., 1989. Generalized Linear Models, 2nd ed. Chapman & Hall, London, 512 pp.
331 Michel, J.F., Michel, V., De La Rocque, S., Touré, I., Richard, D., 1999. Modélisation de l'occupation de
332 l'espace par les bovins. Applications à l'épidémiologie des trypanosomoses animales. Rev. Elev. Med. Vet.
333 Pays Trop. 52, 25–33.
334 Moran, P.A.P., 1948. The interpretation of statistical maps. J. Roy. Stat. Soc. B Met. 10, 243–251.
335 Raynal, L., Dumolard, P., D'Aubigny, G., Weber, C., Rigaux, P., Scholl, M., Larcena, D., 1996. Gérer et générer
336 des données spatiales hiérarchisées. Rev. Int. Géo. 6, 365–382.
337 Rowlands, G.J., Mulatu, W., Authié, E., D'Ieteren, G.D.M., Leak, S.G.A., Nagda, S.M., Peregrine, A.S., 1993.
338 Epidemiology of bovine trypanosomiasis in the Ghibe valley, Southwest Ethiopia. 2. Factors associated with
339 variations in trypanosome prevalence, incidence of new infections and prevalence of recurrent infections.
340 Acta Trop. 53, 135–150.
341 Schmoyer, R.L., 1994. Permutation tests for correlation in regression errors. J. Am Stat. Assoc. 89, 1507–1516.
342 Walter, S.D., 1992. The analysis of regional patterns in health data, Part 1. Am. J. Epidemiol. 136, 730–741.