The area-wide epidemiology of bovine trypanosomosis and its impact on mixed farming in subhumid West Africa; a case study in Togo

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Abstract

This paper reports on an area wide study of all major variables determining the expression of trypanosomosis in cattle in the subhumid eco-zone of West Africa, taking Togo as an example. To enable systematic area-wide sampling, the country was divided in 311 grid-squares of 0.125×0.125 sides. Cross-sectional surveys were then conducted to generate maps or digital layers on cattle density, herd structure, ownership and breed. These data layers, except for the breed data, were subjected to a cluster analysis in order to define spatial patterns in animal husbandry systems. This analysis revealed two main systems: one is oriented towards integration with crop-agriculture and a second towards investment in cattle. These two systems could be further characterised by incorporating breed data. Zebu cattle and their crossbreeds are more favoured in the second system. The breed distribution map shows the actual situation but also serves to predict the outcome of progressive crossbreeding. An area wide trypanosomosis survey allowed the production of prevalence maps for *Trypanosoma congolense*, *T. vivax* and the associated packed cell volume (PCV) values. A simple curvi–linear relationship was established between vector density and disease prevalence. The regression between disease prevalence and PCV for taurine and zebu plus crossbreeds separately, revealed that taurine cattle maintain a comparatively high PCV level particularly in high prevalence scenarios. The relationship between the average herd PCV and cattle density suggests that herd PCV value may provide a mirror for the number of animals *not* kept because of the prevailing risk. The regression between agricultural intensity and cattle density subsequently in areas with decreasing herd PCV values reveals that the level of integration of cattle in crop production decreases with a

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decreasing PCV. Thus, despite the presence of taurine animals in Togo, the omnipresence of tsetse in particular *Glossina tachinoides*, remains a major obstacle to cattle raising and indirectly mixed farming development and intensification. It is argued that only with the present type of wide scale, spatial studies it becomes possible to clarify all the major variables influencing the expression of trypanosomosis. Spatial epidemiological studies at a macro level may form the basis for area wide trypanosomosis control in West Africa. ©1999 Elsevier Science B.V. All rights reserved.

1. Introduction

Most studies concerning the epidemiology of African animal trypanosomosis rarely consider the spatial dimension of disease prevalence but instead concentrate on the temporal aspects with longitudinal studies carried out in relatively few animals found in a limited number of places. Recent examples include studies on the vector–host relationship in The Gambia (Claxton et al., 1992; Wacher et al., 1993; Rawlings et al., 1994), studies on the relationship between tsetse challenge and disease prevalence conducted in the framework of the trypanotolerant network of the International Livestock Centre for Africa (ILCA) (e.g. Leak et al., 1990) and studies aiming at measuring the epidemiological situation in a given area before during and after tsetse control (e.g. Bauer et al., 1992, 1995).

Whilst those studies have produced valuable information, it may be argued that without a proper spatial analysis it is difficult to fully comprehend the disease dynamics or to make any sensible statement on the area-wide impact of the disease.

This paper reports on an area-wide sampling approach with data collected on the tsetse vectors, cattle, trypanosomosis prevalence, packed cell volume (PCV) and husbandry features. The coverage comprised the whole of Togo. The rationale was to explore the feasibility of assessing the impact of trypanosomosis on cattle and agriculture at a country level. It is the first attempt towards clarifying all major variables influencing the expression of trypanosomosis over such a large area.

This paper expands on the earlier publication of preliminary results (Hendrickx et al., 1995, 1996). The vector distribution and abundance surveys and their relation to ground measured and remotely sensed eco-climatical variables and agriculture are discussed in detail elsewhere (Hendrickx et al., 1999).

2. Materials and methods

2.1. The study area

Togo is a narrow West African country, 550 km long and maximum 150 km wide, east from Ghana and west from Benin with a total surface of 56,000 km^2. The country can be divided in four major seasonal clusters (Hendrickx et al., 1999) ranging from a dry monomodal climate in the north to a wet bimodal system in the south (Fig. 1). As such the country arguably is an ideal transect representative for most coastal West African countries.
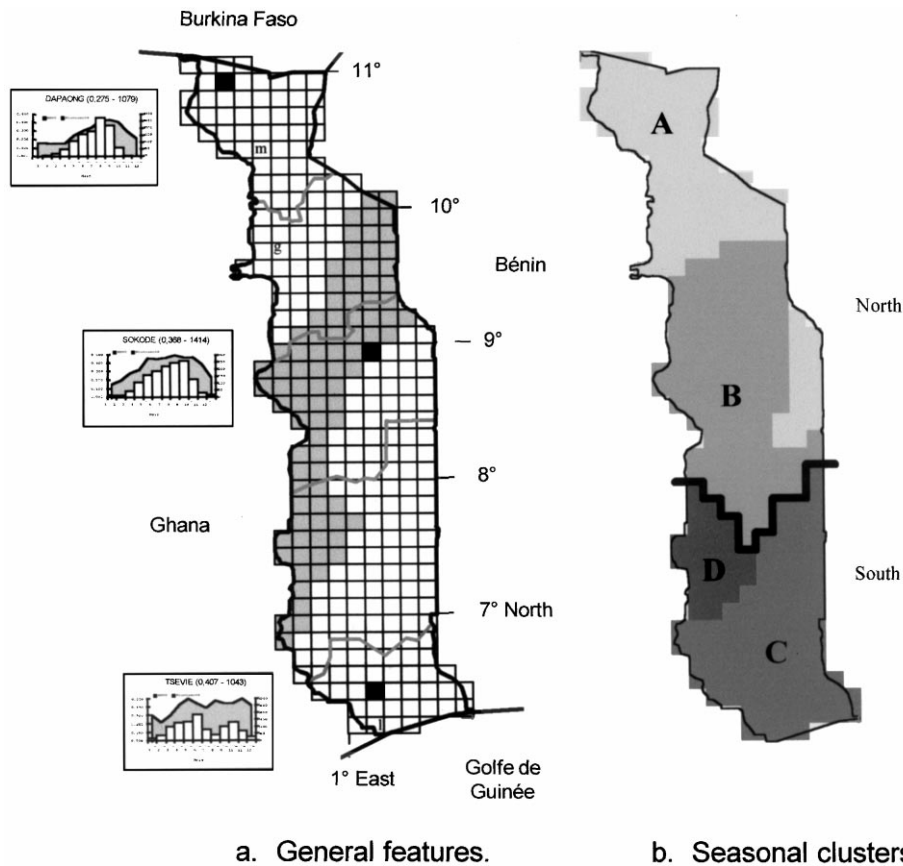
a. General features.   b. Seasonal clusters.

Fig. 1. Togo, geographical and climatic features. The small graphs show rainfall (histogram) and the greenness of vegetation (areas) depicted as satellite measured normalized difference vegetation indices (NDVI), for three sites from north to south: Dapaong, Sokodé and Tsévié, respectively, referred to by a black square in (a). Seasonal clusters were obtained after hierarchical clustering of a series of remotely sensed and ground measured eco-climatical variables (Hendrickx et al., 1999). Major differences between northern clusters (A and B) and southern clusters (C and D) are a significantly higher ratio of humid over dry months in clusters C and D, and a distinctly monomodal seasonal cycle in clusters A and B (i.e. a single long dry season).

To allow systematic area-wide surveys the country was divided in 311 grid-squares or sample units of $0.125 \times 0.125°$ sides. The different variables were sampled in every grid-square.

2.2. Factors affecting the epidemiology of African bovine trypanosomosis

To identify and highlight relationships between the main factors affecting the epidemiology of bovine trypanosomosis at a macro scale, a flowchart is given in Fig. 2. In this figure the central axis shows the links between fly habitat, vector, parasite–host–disease. The (Contact Vector–Host) box encompasses several factors acting on the transmission rate; the parasite reservoir in the hosts, fly infection rates, fly preferences in feeding, etc.
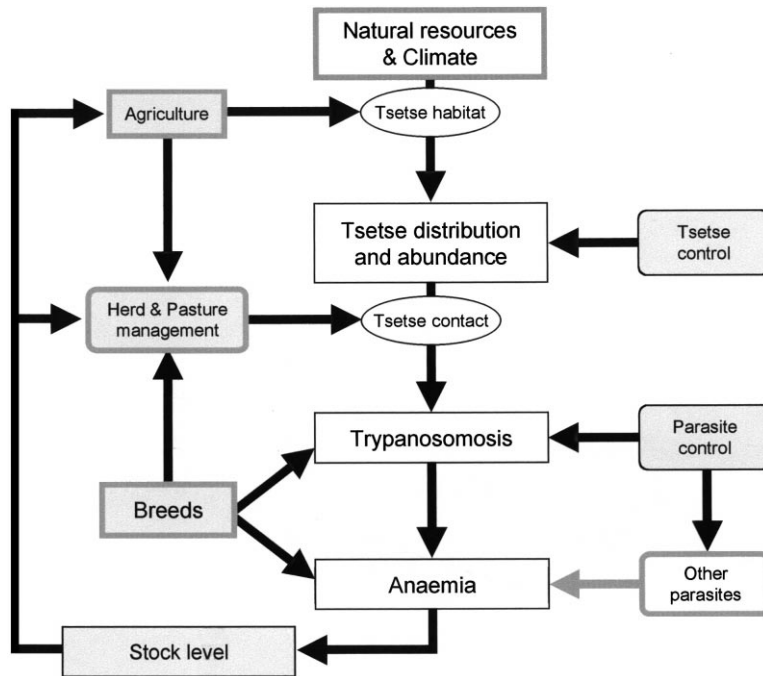
Fig. 2. Factors affecting the epidemiology of African bovine trypanosomosis. Variables included in this study are in square boxes, those influenced by man are in grey shaded boxes. See text for more details.

While the latter variables are often included in longitudinal studies at a micro scale, it is not realistic to include these in the present type macro scale, cross-sectional study. A series of external factors affect the epidemiology of bovine trypanosomosis. Some (grey frame) are influenced by eco-climatic variables such as temperature, rainfall and vegetation. Most are influenced by human activity (grey background). Square boxes depict variables included in this study. The relationship between vector and agriculture is studied elsewhere (Hendrickx et al., 1999). Factors such as herd and pasture management which influence the local vector–host interface are difficult to measure at a macro scale. However, it is possible to consider the human influence on epidemiological variables at a macro scale and to look for spatial animal husbandry patterns.

2.3. Animal husbandry systems and cattle breeds

A country wide exhaustive cattle census comprising data on herd composition and ownership was conducted during 1993. The survey was guided by the results of a previous census (PROPAT, 1990) and the local knowledge of veterinary field staff. All the sedentary herds identified were visited. During these visits a questionnaire was completed with inputs from the herdsmen. Animal numbers, sex, age and breeds were recorded. The main purpose of this survey was to produce a series of maps or digital layers depicting cattle distribution and density, herd structure and size, ownership patterns and most importantly, the breed type.

2.3.1. Cattle breeds

During the survey, breed characteristics were assessed through recording the shape of the head, the presence or absence of a hump and the size of the dewlap. On the basis of these features, the animals were grouped in three classes: taurine, zebu and their crossbred. Results are displayed either as raw data (total herd and females) or after 3×3 grid-square spatial pooling to include the movement of 'fertile' males towards surrounding grid cells. In the latter case only steers and bulls were considered. Castrated males (animal traction) were not included. The validation of the phenotype maps is elsewhere discussed (Hendrickx et al., 1996) and confirmed the strong link between the observed phenotype and measured genotype in a representative sample.

2.3.2. Animal husbandry systems

Herd owners were classified as either rural or urban. After having obtained the first results, it was decided to subdivide the owner categories. Rural owners were categorised as either crop agriculturists or mainly livestock keepers and urbanite owners were classified as civil servants, merchants, and others. The combined data set was subjected to a hierarchical cluster analysis, with the aim to demarcate and identify distinct animal husbandry systems using commercially available software (UNISTAT^{TM}). Variables were selected based on previous experience suggesting a strong relationship between ownership patterns, herd size and husbandry systems, also included were : cattle density, herd size, number of owners per herd, percentage of rural owners and the percentage of rural owners being agriculturists. To allow independent comparison of husbandry systems and cattle breed distribution patterns the latter were not included here. Prior to analysis all variables were individually regrouped into three classes: low, medium and high. Respective class limits were set as the mean value minus or plus half a standard deviation.

2.4. Trypanosomosis surveys

Most blood samples were taken during two main survey periods. A first field survey was conducted during 1991–1992 and complementary surveys were completed during 1993–1994, thus encompassing the whole country. All field surveys were conducted by five different mobile teams operating simultaneously. Each team was assigned one out of five administrative regions (Fig. 1). Only sedentary cattle herds were sampled. Herd selection was much influenced by road access. Sedentary cattle herds could be identified in 217 of the 311 grid-squares. Herds could be reached in 200 of those grids (92%). Non sampled squares concern areas where cattle densities are very low, mainly in the southern part of the country. It was aimed to sample minimum 50 head of cattle per grid square, with animals coming from three different herds, sampling at least 10% of the herds.

During this cross-sectional study a total of 26,481 head of cattle were eventually sampled in 946 different herds; on average 37% of the animals were sampled per herd. Samples were taken from the auricular vein using an heparinised capillary tube, and further processed as described by Murray et al. (1977). After measurement of the PCV, the capillary tube was cut with a diamond pencil and the buffy coat expressed on a slide. A minimum of 50 fields were examined using a standard light microscope with a X40 objective. The required dark ground

effect was simulated by adjusting the condenser light passage (ILCA, 1983). Trypanosomes were identified mainly on the basis of their movement pattern (FAO, 1986). Given that the diagnostic method herewith described does not reliably identify *T. brucei*, this species was not included in this study.

Since surveys had been carried out during different times of the year and in different places, seasonal adjustments were calculated on the basis of monthly indices, depicted from seasonal curves. Those curves were obtained by pooling the monthly prevalence data measured during the cross-sectional study, both for the northern (seasonal clusters A and B) and southern (seasonal clusters C and D) part of the country. Monthly adjustment indices were computed separately for the prevalence of *T. congolense* and *T. vivax* as well as for the average herd PCV values. Measured values were then adjusted for seasonality by multiplying them with the index of the respective sampling month per variable. To reveal overall trypanosomosis risk patterns a spatial smoothing was carried out through averaging each grid value with that of the eight, or less, adjacent grids. Missing grid-values were also replaced this way.

2.5. Tsetse surveys

The sampling and processing of fly data used in this paper is described in detail elsewhere (Hendrickx et al., 1999). Tsetse were sampled during a parallel cross-sectional study in 305 grid-squares using an average of 12 standard biconical traps (Challier and Laveissière, 1973) per trapping site. On average 2.1 sites were sampled per grid during 24 or 48 h. After $\log_{10} (x+1)$ transformation of the measured apparent fly densities per fly species data processing included seasonal adjustment and spatial smoothing as described above for trypanosomosis prevalence and herd PCV values.

The six tsetse species found in Togo were mapped including (1) two riverine tsetse species *Glossina (Nemorhina) tachinoides* Westwood (1850) and *G. (Nemorhina) palpalis palpalis* Robineau-Desvoidy (1830), (2) two savannah tsetse species *G. (Glossina) morsitans submorsitans* Newstead (1910) and *G. (Glossina) longipalpis* Wiedemann (1830) and (3) two forest tsetse species *Glossina (Austenina) medicorum* Austen (1911) and *Glossina (Austenina) fusca fusca* Walker (1849). Results included abundance maps of both riverine species and distribution maps of the other species.

3. Results

3.1. Animal husbandry systems and cattle breeds

The different variables measured during the cattle census are shown in Fig. 3. The results of the cluster analysis are given in Table 1 with map displays in Fig. 4. The mapped distribution of cattle breeds for fertile females, males and the total herd is given in Fig. 5 including a graph showing the strong regression between phenotype and genotype ($R^2 = 0.884$).

The cluster analysis reveals that the country may be divided into two major parts. A first animal husbandry system (A), mainly in the northern part of the country, is more
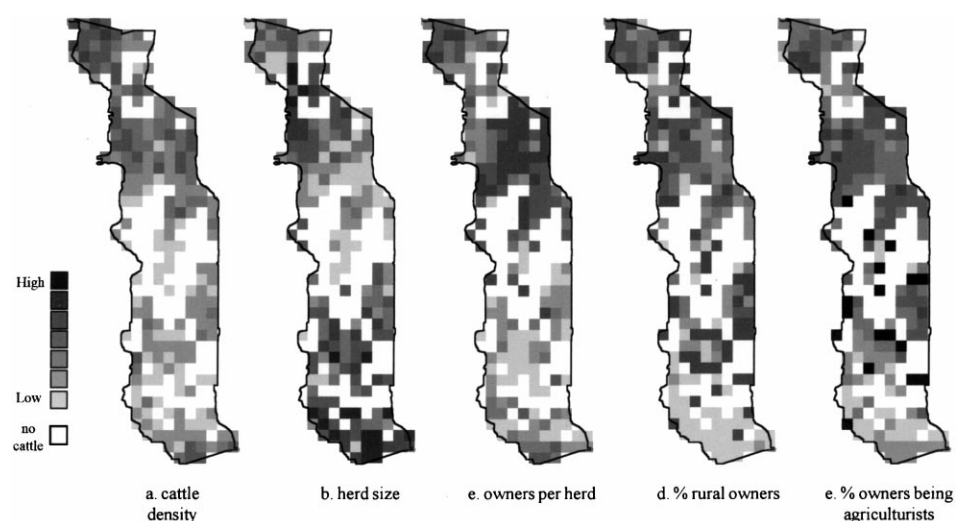
Fig. 3. Variables included in the cluster analysis to define animal husbandry patterns. Respective class limits are: (a) cattle density: 1, 5, 10, 25, >25; (b) herd size: 30, 40, 50, 75, >75; (c) number of owners per herd: 1, 2, 3, 5, >5; (d) % of rural owners: 70, 90, 95, 99, >99; (e) % of owners being agriculturists: 0, 50, 75, 90, 99, 100.

Table 1
Animal husbandry systems[a]

Cluster	n	cattle density	cattle per herd	owners per herd	% rural owners	% agric.	% taurine females	% taurine males
A	145	6.1 (0.64)	43.6 (1.66)	3.7 (0.22)	92.5 (0.74)	77.8 (1.27)	89.6 (1.53)	78.2 (1.99)
B	67	4.3 (0.68)	82.9 (1.66)	1.7 (0.12)	48.3 (4.42)	16.3 (2.21)	55.9 (4.60)	45.7 (3.38)
p (A : B)	–	<0.05	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
A1	92	7.8 (0.93)	38.6 (1.59)	4.7 (0.25)	91.8 (0.87)	77.4 (1.4)	91.7 (1.65)	86.4 (1.96)
A2	47	2.2 (0.32)	47.6 (3.15)	1.5 (0.11)	94.2 (1.45)	79.2 (2.67)	85.3 (3.37)	62.4 (3.78)
A3	2	5.1 (3.84)	91.7 (12.04)	8.8 (3.88)	82.5 (11.41)	53.7 (1.61)	86.2 (13.84)	55.0 (7.42)
A4	4	12.9 (1.46)	86.1 (3.60)	2.0 (0.30)	95.6 (2.44)	82.2 (5.83)	92.4 (3.72)	85.6 (4.44)
p (A1 : A2)	–	<0.001	<0.02	<0.001	NS	NS	NS	<0.001
B1	30	1.1 (0.18)	74.9 (10.67)	1.6 (0.14)	21.1 (4.32)	12.4 (3031)	51.6 (7.53)	43.0 (5.67)
B2	14	1.7 (0.54)	70.3 (10.68)	1.0 (0.08)	92.9 (3.79)	14.7 (4.66)	75.2 (7.20)	49.5 (6.62)
B3	20	10.8 (1.4)	108.7(13.33)	2.0 (0.18)	50.4 (5.11)	24.6 (3.87)	49.5 (8.39)	44.6 (5.81)
B4	3	4.6 (1.39)	50.2 (8.4)	3.6 (1.39)	97.9 (2.08)	8.3 (8.33)	57.1 (14.32)	61.7 (8.64)
p (B1 : B2)	–	NS	NS	<0.001	<0.001	NS	<0.02	NS
p (B1 : B3)	–	<0.001	NS	NS	<0.001	<0.02	NS	NS
p (B2 : B3)	–	<0.001	<0.05	<0.001	<0.001	NS	<0.05	NS

[a] The average values of selected variables (Fig. 3) with standard error between brackets for each animal husbandry cluster and sub cluster. A display of the mapped results is given in Fig. 4. All data were re-arranged into three classes (low, medium, high) with limits given by the mean $\pm \frac{1}{2}$ SD: cattle density: 1.9, 9.1, >9.1; herd size: 36.1, 76, >76; owners per herd: 1.8, 4.3, >4.3; % rural owners: 63.7, 93.5, >93.5; % owners being agriculturists: 41.9, 74.8, >74.8. The right part of the table shows the average values of two variables nor included in the cluster analysis: (1) percentage of females with a taurine phenotype and (2) the 3×3 pooled percentages of fertile male taurine animals.
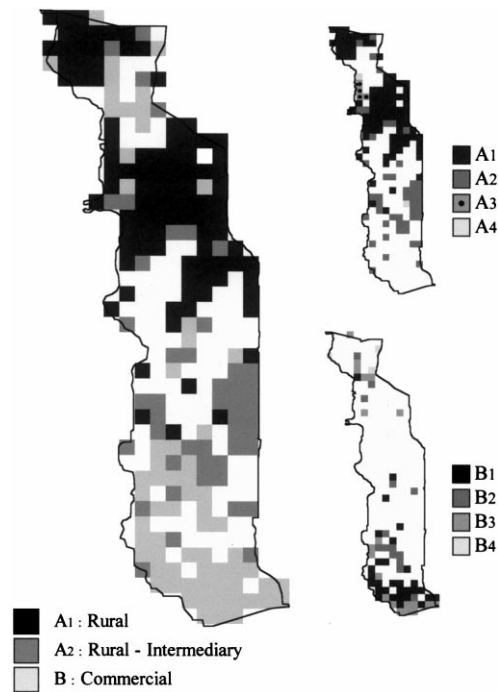
Fig. 4. Map depicting the computed animal husbandry clusters (see also Table 1). Cluster A_1: traditional rural systems with great potential to improve integration of cattle and agriculture. Cluster A_2: intermediary system. Cluster B: (peri) urban linked system with commercial potential. Additional maps separately show sub clusters $A_{1,2,3,4}$ and sub clusters $B_{1,2,3,4}$.

traditionally oriented. Characteristics here are higher cattle densities, smaller herds and more owners per herd of which almost all originate from rural areas and a high proportion of them is engaged in crop-agriculture. Most of those herds are village herds. This system shows a clear propensity towards integration of cattle and agriculture.

A second system (B), mainly in the south and in the area around Mango (m, Fig. 1(a), is more (peri) urban linked. Herds are larger in size and cattle owners per herd are fewer in number. Owners comprise civil servants and merchants investing in cattle. This system has a commercial orientation.

The difference between A and B also extends to the proportion of taurine cattle out of total cattle, although this variable was not included in the clustered set. There is a higher proportion of taurine cattle in the traditional rural system whilst crossbred are more numerous in the (peri) urban system.

Further analysis of cluster A reveals two major (A_{1-2}) sub clusters generated by the analysis. Sub cluster A_1 is distinctly more traditional as was described above whilst A_2 would appear a transitory system; most owners come from rural areas but cattle densities are lower, herds are larger and there are fewer owners per herd. Crossbreeding, employing zebu males, is also more widespread. Geographically (Fig. 4) this sub cluster also marks the limit between both systems A and B.
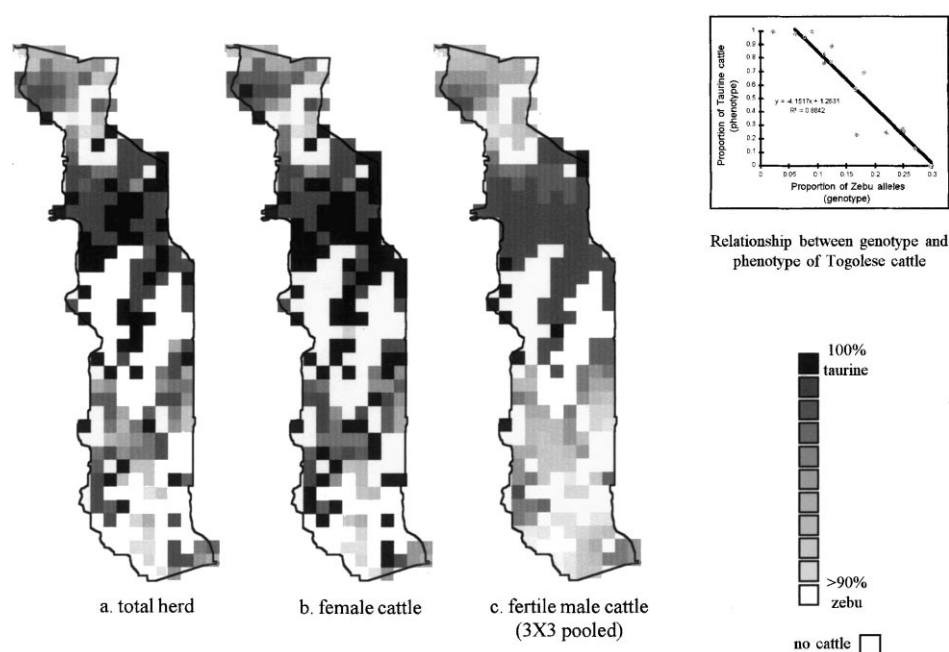
Relationship between genotype and
phenotype of Togolese cattle

a. total herd　　　b. female cattle　　　c. fertile male cattle
(3X3 pooled)

Fig. 5. Zebu introgression.The proportion of cattle with a taurine phenotype per grid-square is shown as opposed to zebu and zebu X taurine crossbreeds. Map (c) includes a 3X3 grid-square spatial smoothing to reflect a measured mobility of 14 km for bulls. Classes are 100%, 90–100, 80–90, 70–80, 60–70, 50–60, 40–50, 30–40, 20–30, 10–20, 0–10. The inlaid graph shows the linear regression between the proportion of zebu alleles (selected microsatellite markers) and the observed phenotype (morphology) expressed as the proportion of cattle with taurine characteristics ($R = 0.940$, $n = 17$, $p < 10^{-6}$). Reproduced from Hendrickx et al. (1996).

The two minor sub clusters (A_{3-4}) are less typical. In both cases herds are almost twice as large than in A_{1-2}. Sub cluster A_3 is located around Guerin Kouka (g, Fig. 1(a)), south-west of the Keran game reserve along the Ghana border. It is traditionally a cattle raising area and cattle are well integrated in the rural system. The two remaining grid-squares (A_4) are a more hybrid system, 23% of the rural owners are herdsmen and the proportion of urban linked owners is higher (17.5%) explaining the higher level of cross breeding. The first is located north of cluster A_3 and the second in the southern half of the country at the periphery of cluster A_2.

Cluster B can further be divided into three major sub clusters. Sub-cluster B_1 groups the bulk of grid-squares in the south, 79% of owners have urban links, of which 36% are civil servants and 33% are merchants. Herds are mostly kept for banking purposes.

Sub-cluster B_2 groups a series of scattered grid-squares were herds are mainly owned by a single rural owner, 54% of them are themselves herdsmen. Sub-cluster B_3 groups peri urban grid-squares mainly around Lomé (l, Fig. 1(a)) in the south and Mango (m, Fig. 1(a)) in the north. Herds are large and half of the owners originate from rural and half from urban areas. Half the rural owners (44%) are herdsmen. A minor sub cluster (B4) groups three grid-squares scattered in the extreme north of Togo, 91% of the rural owners are herdsmen; crossbreeding is common practice here.
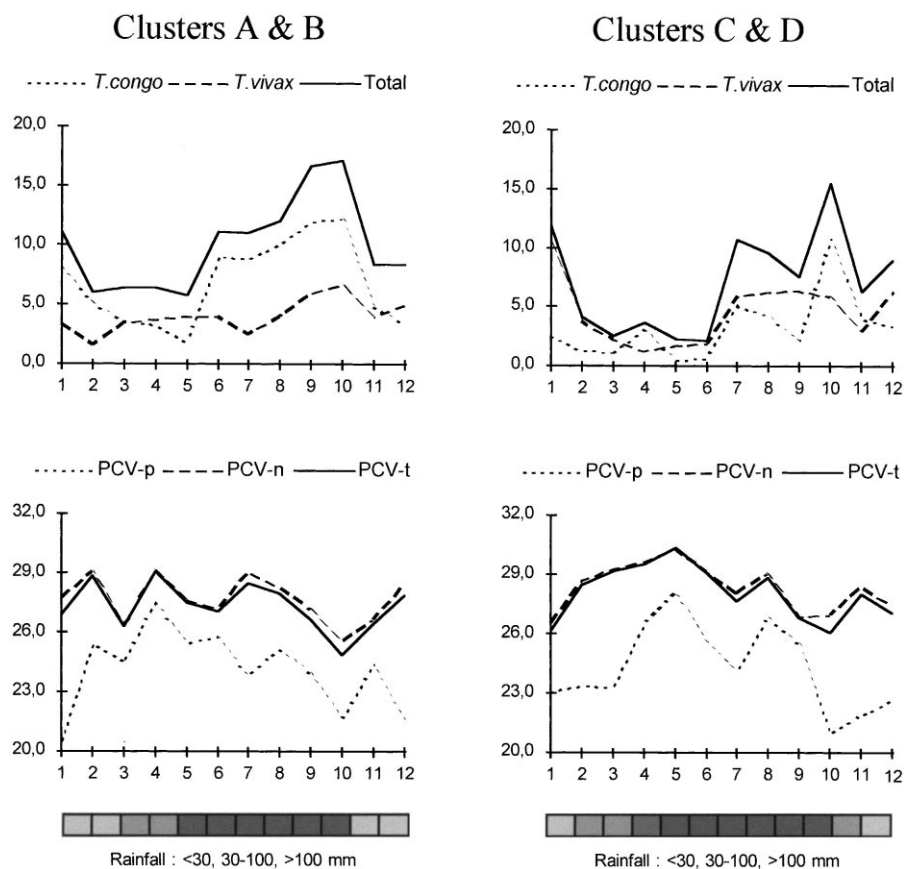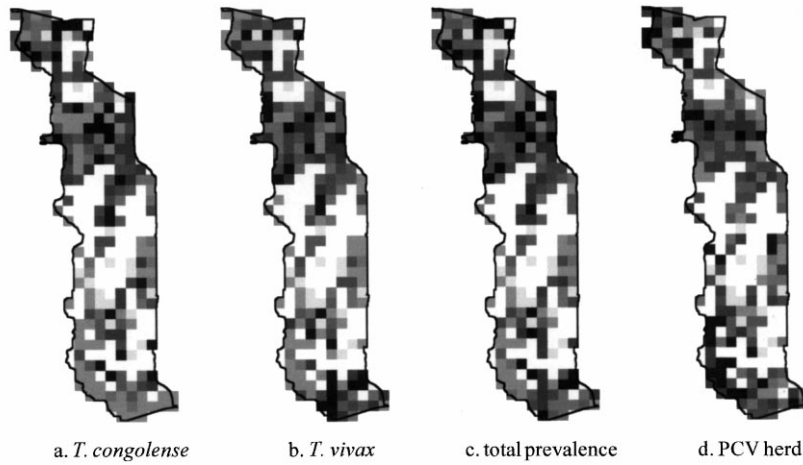
Clusters A & B

Clusters C & D

Fig. 6. The seasonal fluctuation of trypanosomosis per eco-zone. *T. congo* = *T. congolense*, Total = combined prevalence of *T. congolense* and *T. vivax*, PCV-p = PCV of positive cattle, PCV-n = PCV of negative cattle, PCV-t = PCV of all cattle = PCV herd. Bars reflect average rainfall intensity: light grey: dry months (<30 mm rain) and dark grey: humid months (>100 mm rain).

3.2. Trypanosomosis

Seasonal trypanosomosis prevalence curves are given in Fig. 6. The monthly prevalence increases during the rainy season in both the northern and southern parts of the country. The highest prevalence is recorded just after the rainy season and the lowest at the end of the dry season. The monthly prevalence of *T. congolense* and *T. vivax* range, respectively, from 1.8 to 12.3 and 1.6 to 6.7 in the north and from 0.5 to 10.8 and 1.2 to 10.4 in the south. The seasonal fluctuation of *T. vivax* is more pronounced in the south. When mixed infections are included *T. congolense* is found mainly in the north (61% of recorded cases) and *T. vivax* (57%) in the south. The PCV curves follow the trypanosomosis prevalence patterns. The highest average herd PCV value is observed when the prevalence is lowest, in April (29.1) in the north and in May (30.3) in the south. The inverse happens during times of the year when the prevalence is high. The difference between the average herd PCV values and the

A. raw data adjusted for seasonal effects

a. *T. congolense*   b. *T. vivax*   c. total prevalence   d. PCV herd

B. 3X3 pooled data adjusted for seasonal effects

a. *T. congolense*   b. *T. vivax*   c. total prevalence   d. PCV herd
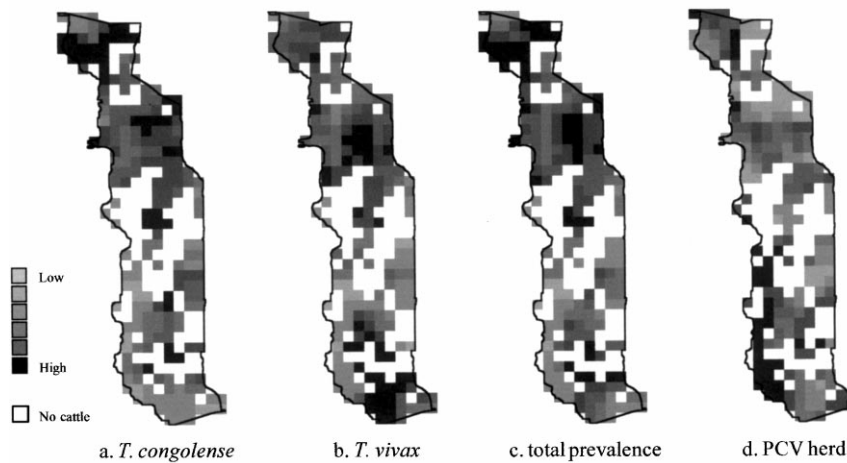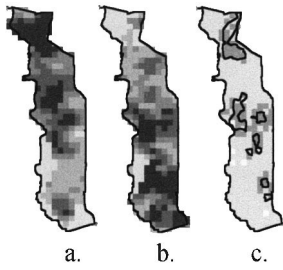
Fig. 7. Spatial distribution of trypanosomosis. (A) Raw data adjusted for seasonality; (B) see A after spatial smoothing. Class limits were set to include approximately the same number of grids per class. Class upper limits for (A) are : *T. congolense*: 0, 2.7, 4.4, 8, 12.8, >12.8; *T. vivax*: 0, 2, 3.2, 4.8, 8.1, >8.1; Total prevalence: 0, 4.7, 7.1, 11, 17.6, >17.6; PCV herd: 25.5, 26.8, 27.7, 28.4, 29.8, >29.8 and for (B) : *T. congolense*: 0, 2.7, 4.6, 6.2, 8.1, >8.1; *T. vivax*: 0, 2.2, 3.4, 4.5, 6.4, >6.4; Total prevalence: 0, 5.2, 7.8, 9.8, 12.5, >12.5; PCV herd: 26.4, 27.2, 27.6, 28, 28.8, >28.8. Except for zero class approximately the same number of grid-squares are included per class.

mean PCV of positive cattle is most pronounced and amounts to $3.2 \pm 0.5\%$ in the north and 3.8 ± 0.5 points in the south. Both curves show a similar seasonal pattern.

The map displays of trypanosomosis prevalence are given in Fig. 7 both for raw and 3×3 pooled data adjusted for seasonality. The spatial smoothing allows to highlight disease risk

Table 2
Correlation between riverine fly abundance and trypanosomosis[a]

a.   b.   c.

	Area	*T.c*	*T.v*	*T.c. + v.*	PCV
	Togo	0.559_{-6}	0.195_{-3}	0.557_{-6}	-0.338_{-6}
G. tachinoides (a)	North	0.458_{-6}	0.292_{-4}	0.474_{-6}	-0.193_{-2}
	South	0.469_{-5}	0.447_{-5}	0.612_{-6}	-0.186_{NS}
	Togo	-0.153_{-2}	0.089_{NS}	-0.121_{NS}	0.052_{NS}
G. p. palpalis (b)	North	0.028_{NS}	-0.002_{NS}	-0.083_{NS}	-0.102_{NS}
	South	0.068_{NS}	0.086_{NS}	0.151_{NS}	-0.204_{-2}

[a] Pearson correlation coefficients between riverine tsetse abundance figures and trypanosomosis data separately for the whole country the northern and the southern part: *T. congolense* = prevalence of *T. congolense*, *T. v.* = prevalence of *T. vivax*, *T. c. + v.* = combined prevalence figures, PCV: packed cell volume of all cattle sampled. Indices given reflect the significance, 10^{-10}, per observed correlation. NS: NS relationship. Maps show riverine fly abundance (a. and b.) and combined savannah fly (c., *G. m. submorsitans + G. longipalpis*) distribution data (Hendrickx et al., 1999).

areas. The results illustrate that trypanosomosis prevalence is highest in the northern part of the country. As stated above, this may be attributed to *T. congolense* whilst *T. vivax* is predominant in the south. *T. congolense* is almost absent from the coastal zone (terre de barre). In the south-west part of the country the disease is absent around the Danyi and Akposso plateau area and it is here where PCV values are highest (dark grid-squares, in the South-Western part of Togo on Fig. 7 B.d.).

Table 2 shows correlation figures between riverine tsetse abundance and trypanosomosis. Included are abundance maps of both riverine tsetse and the distribution of savannah flies. The results show a highly significant correlation for *G. tachinoides* but not for *G. p. palpalis*. The best fit is obtained for *T. congolense*. In the southern part of the country *T. vivax* is also found strongly related to *G. tachinoides*. These combined results suggest that *G. tachinoides* is a more important vector than *G. p. palpalis*.

Fig. 8 shows the existing trend to keep trypanotolerant cattle in areas of higher *G. tachinoides* abundance whilst crossbred and zebu cattle are more common in areas with lower fly abundance. This different fly ecological setting complicates a direct breed comparison.

The regression between *G. tachinoides* abundance and trypanosomosis prevalence (Fig. 9) shows that both breeds may equally well attract trypanosomosis.

In Fig. 10 the relationship between disease prevalence and PCV is compared for different levels of crossbreeding. To avoid attenuating eventual interbreed differences through correction for seasonality, raw data are used here. Results indicate that taurine animals de-
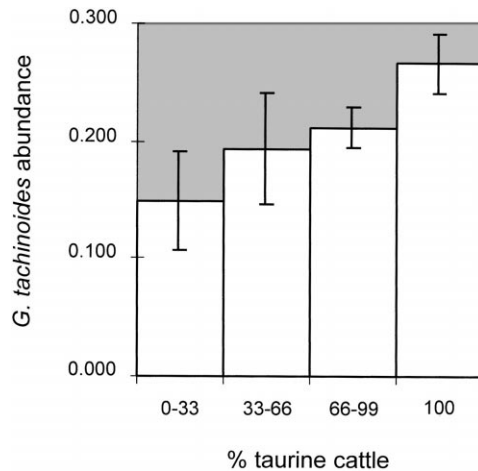
Fig. 8. Cattle breeds and vector abundance. Cattle breeds are divided in four classes: 0–33% of cattle with taurine phenotype per grid-square, 33–66%, 66–99% included, all cattle of taurine phenotype. Flags give standard error on mean. Tsetse abundance: *G. tachinoides*.
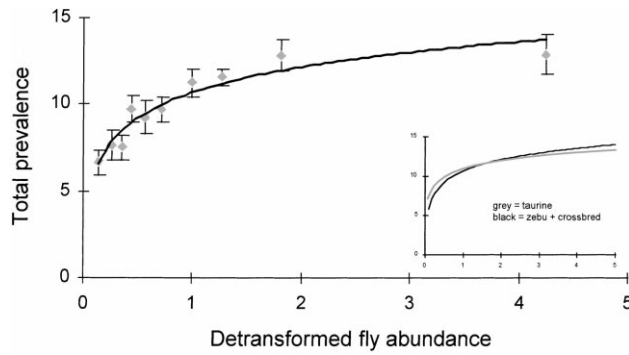

Fig. 9. Vector abundance and disease prevalence. Fly abundance is divided in 10 subsequent classes of approximately the same size. The inlaid figure shows separate regression lines for 100% taurine grid-squares and for zebu + crossbreed grids. The computed equations for the total sample were (1) for all cattle: $y = 1.8697 \ln(x) + 10.668$ ($R = 0.488$, $n = 171$, $p < 10^{-6}$); (2) for taurine cattle: $y = 1.4621 \ln(x) + 10.978$ ($R = 0.377$, $n = 45$, $p < 0.01$); for zebu + crossbreed: $y = 2.0738 \ln(x) + 10.654$ ($R = 0.533$, $n = 126$, $p < 10^{-6}$).

velop comparatively less anaemia and this feature of availing of a superior ability to control anaemia becomes progressively more pronounced with a higher disease prevalence.

The relationship between cattle density and PCV is shown in Fig. 11. To avoid interference from other factors affecting cattle density in the southern half of the country and believed to be mainly linked to a different climate and agricultural practices only the northern part of the country (seasonal clusters A and B) where cattle raising is most predominant is considered here. It is seen that disease, expressed as a degree of anaemia, negatively influences cattle density. Few cattle are kept in areas where PCV values are low and the risk of attracting trypanosomosis correspondingly higher.
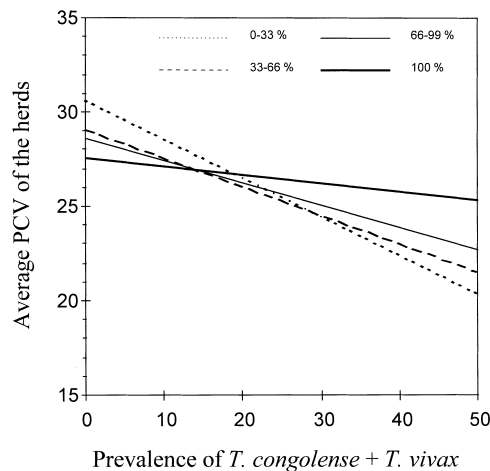
Fig. 10. Influence of the breed factor on the relationship Prevalence–PCV. Breed classes are set as: 0–33% of cattle with taurine phenotype per grid-square, 33–66%, 66–99% included, all cattle of taurine phenotype. Linear regressions: (0–33%) $y = -0.206x + 30.669$, $R^2 = 0.2591$, $n = 28$, $p < 0.006$; (33–66%) $y = -0.1509x + 29.1$, $R^2 = 0.460$, $n = 27$, $p < 10^{-6}$; (66–99%) $y = -0.1188x + 28.646$, $R^2 = 0.1158$, $n = 96$, $p < 0.0007$; (100%) $y = -0.0441x + 27.56$, $R^2 = 0.0216$, $n = 45$, not significant. Data used are raw, unadjusted for seasonal fluctuation.
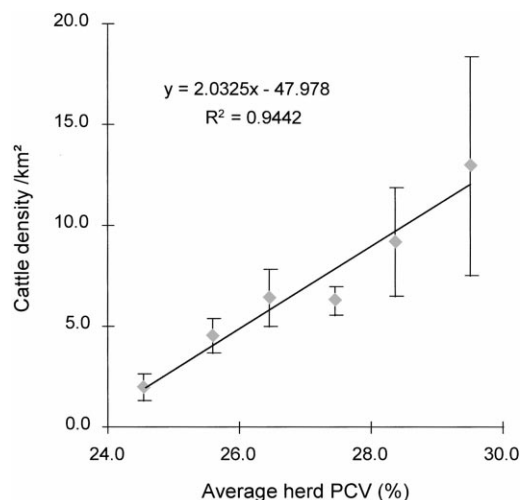

Fig. 11. Effect of PCV on cattle density. PCV classes are: <25 ($n = 9$), 25–26 ($n = 14$), 26–27 ($n = 29$), 27–28 ($n = 63$), 28–29 ($n = 23$), >29 ($n = 7$). Significance: $R = 0.972$, $n = 6$, $p = 0.0012$. The area covered includes climatic clusters A and B (Fig. 1).

Fig. 12, also for the northern part of the country, shows that trypanosomosis influences the association between crop-agriculture and cattle. In low prevalence areas cattle numbers increase proportionally with the proportion of land brought into the cultivation cycle, herewith termed the agricultural intensity. However, the level of integration of cattle in crop production decreases with a decreasing PCV.
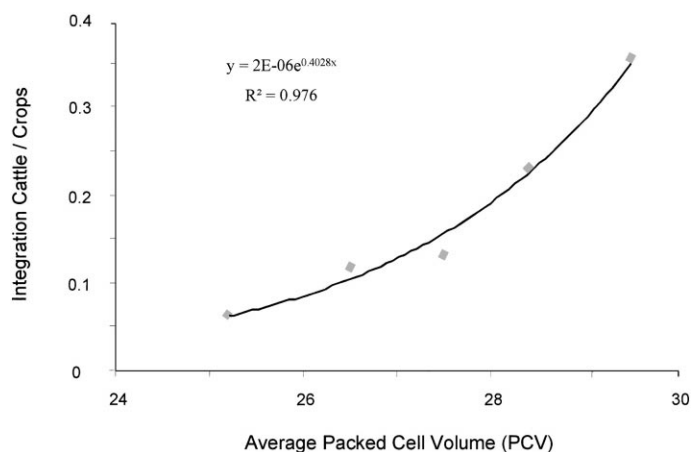
Fig. 12. PCV and the integration cattle-crops. PCV classes are: <26 ($n = 23$), 26–27 ($n = 29$), 27–28 ($n = 63$), 28–29 ($n = 23$), >29 ($n = 7$). The association between agriculture and cattle is defined as the slope from the linear regression of agriculture against cattle density per PCV class. The area covered includes climatic clusters A and B (Fig. 1). Agriculture is expressed as the % of land cultivated as digitised from maps derived from arial photographs (PNUD, 1984). Regressions are (from low to high PCV classes): (1) $y = 0.0602x + 1.4335$ ($R^2 = 0.135$, $p < 0.01$), (2) $y = 0.1188x + 1.387$ ($R^2 = 0.097$, $p < 0.01$), (3) $y = 0.1324x + 0.2756$ ($R^2 = 0.215$; $p < 0.001$), (4) $y = 0.2323x–2.3546$ ($R^2 = 0.1512$, $p < 0.01$), (5) $y = 0.3566x + 3.5711$ ($R^2 = 0.3687$, NS).

4. Discussion

The cluster analysis proved useful in the demarcation of spatial patterns in animal husbandry systems in Togo. The two dominant husbandry systems fit systems as described for cattle by PROPAT (1990): (1) a traditional extensive system, prevailing in the northern half of the country where cattle are a patrimony for future generations owned by a group or family and (2) a semi-modern system where ownership is often individual and savings are invested in cattle. Importantly, both systems can be further characterised when incorporating the phenotype data. The identification of such a set of easily measured variables opens important prospects for low cost field surveys to clarify animal husbandry systems and related taurine cattle distributions across West Africa.

Analysis of the breed distribution (Fig. 5) reveals that crossbreeding is mainly restricted to the extreme north and over a larger area in the south of the country, leaving taurine cattle mainly in the central part. Crossbreeding is achieved mainly through the purchase of zebu or crossbred bulls (see also Table 1). When taking into consideration the area-wide mobility of these bulls (3×3 pooling), it follows that all females may enter in contact with a non-taurine bull. Thus, the map displaying all cattle categories is a reflection of the situation at present, whilst the map showing fertile male cattle only, in fact provides for a prediction of the level of crossbreeding in the short to medium term. The present distribution patterns broadly fit the published maps of cattle breeds in West Africa (FAO, 1987), however, the map of genitor influences shown in this paper indicates the trend of cross breeding will go further in future.

The combined information on the animal husbandry patterns and on the seasonality of trypanosomosis facilitates the definition of trypanocidal drug regimens. Also the PCV map assist here because it shows where the animals suffer most. Taurine cattle are kept in areas of higher tsetse challenge, mainly in the traditional husbandry system where cattle owners tend to neglect a proper veterinary follow up. Crossbred and zebu cattle on the other hand are usually better looked after and veterinary inputs here turn more beneficial in economic terms. A similar trend was observed by ILCA (1990) where it was shown in Ivory Coast, The Gambia, The Republic of Central Africa and Nigeria that farmers themselves fine tune the degree of crossbreeding according to the disease risk and to socio-economic considerations such as the size and commercial value of the animals.

The regression between genotype and phenotype (Fig. 5) confirms that the observed phenotype distributions reflect a genetic reality. The link between taurine genotype and trypanotolerance, the prime characteristic of taurine breeds (Stewart, 1951), is more complex to show. It has been established that the level of anaemia is a reliable measure of the health status of an animal infected with trypanosomes (Murray and Dexter, 1988), although the degree of anaemia developed depends furthermore on the nutritional (Agyemang et al., 1990) and physiological status of the animal (Agyemang et al., 1992) as well as concurrent infections (Kaufmann et al., 1992). Studies elsewhere demonstrated that trypanotolerance may be defined as the ability to control parasitemia and anaemia, following an infection by pathogenic trypanosomes. The level of anaemia control best reflects the level of trypanotolerance, defined as the ability to produce in a tsetse infested environment (Trail et al., 1991). The results presented in this study are consistent with this finding and show that taurine cattle maintain a comparatively high PCV level particularly in high prevalence scenarios. This ability to control PCV decreases stepwise with increasing levels of crossbreeding. Furthermore, observed differences are likely to be underestimated since: (1) taurine cattle tend to control the parasitemia which might be missed by the diagnostic method used (Murray et al., 1977); (2) taurine cattle are usually kept in a more traditional environment were most owners neglect a proper veterinary follow up and nutritional aspects more than owners of zebu or crossbreeds do.

The savannah flies, *G. morsitans submorsitans* and *G. longipalpis* are known to be very efficient disease transmitters (Buxton, 1955). Both these species mainly occur in protected areas where no cattle are present (Table 2, Map c.). At the perimeter of these protected areas animals become readily infected and this risk prevents people from keeping cattle there (Dao, unpublished data). In areas of cattle presence *G. tachinoides* appears to be the major vector of trypanosomosis (Table 2). Despite the complexities in the vector–host interface not taken into consideration here, the present study reveals a simple, strong relationship between vector abundance and disease prevalence, without taking fly infection rates or fly host preferences in the risk equation. These results clearly suggest that the developed approach of spatially pooled maps indeed reflect, at a macro level, a measure of vector challenge and/or disease risk. The process of pooling turns out to be of great assistance and makes it possible to fill in blanks, remove extreme or anomalous values and enhances the process of identifying spatial trends. It is believed that the prevalence maps produced after spatial smoothing (Fig. 7(B)) reveal patterns, superior and more truthful than may be obtained from the raw data.

The correlation between fly abundance and PCV in Table 2 is less strong than for total prevalence. This may indicate the influence of other determinants of the PCV level (cf. flow chart Fig. 2). A recent cross-sectional study (Bouka, 1998) suggested that infection with *Babesia sp.* may adversely affect PCV values. However, from Fig. 6 it can readily be depicted that trypanosomosis is chiefly responsible for major PCV drops.

When fly abundance data are detransformed, i.e. non-logarithmic scale, the observed relationship with disease prevalence is curvi-linear and the curve is almost identical for both taurine and crossbred cattle (Fig. 9). Leak et al. (1990) showed a difference between curves obtained with trypanotolerant and trypanosusceptible cattle, each kept at four different sites of the African Trypanotolerant Livestock Network. Predicted relationships between tsetse challenge and trypanosomosis prevalence yielded a markedly lower prevalence for tolerant cattle at similar challenge levels. The difference with data shown here could be explained by the fact that Togo data are point prevalence figures of different cattle kept in a variety of husbandry systems whilst the ILCA network data are derived from a longitudinal study of frequently surveyed cattle. This de facto contributes to improve veterinary involvement and general herd management allowing full benefit to the expression of trypanotolerance. As for Togo (Fig. 8), tolerant cattle were kept in production systems with a higher level of challenge.

The traditional response to trypanosomosis in West Africa has been trypanotolerance (Hoste et al., 1988; Hoste, 1992). Trypanotolerance allowed cattle raising without veterinary advice in tsetse infested areas but as seen above it is at a cost. This is further stressed by the negative influence of disease, expressed as the average PCV value, on cattle densities (Fig. 11) and the disruptive effect of disease on the integration of cattle and agriculture (Fig. 12). Those results in fact suggest that herd PCV value may provide a mirror for the number of animals not kept because of the prevailing risk. Those data can be contrasted with data from outside the tsetse belt (Mali, Niger, Nigeria, Sudan and Chad) where a very strong positive relationship was found between sedentary cattle densities and agriculture intensity levels (Wint and Bourn, 1994).

The results described in this paper clearly suggest that taurine cattle do make a contribution towards reducing the trypanosomosis problem in Togo but this still does not enable farmers to keep animals as and where they wish. The presence of tsetse fly in Togo remains a major obstacle to cattle raising and constrains particularly mixed farming development and intensification.

The described approach of trypanosomosis mapping combined with maps of cattle breed phenotype and an analysis of animal husbandry systems allowed us to draw a clear picture and understand better the epidemiology of the disease in Togo at a macro level. This opens important perspectives to study and understand the problem of trypanosomosis in other parts of West Africa. Obtained results will be of invaluable help to define and implement control strategies within the framework of a geographical information system, the subject of our ongoing research.

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