

Satellite imagery, tsetse and trypanosomiasis in Africa

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ABSTRACT

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This paper describes the application of remote sensing to studies on the African trypanosomiasis causing sleeping sickness in man and 'nagana' in domestic animals. After giving some biological background to the problem, an important relationship between the risk of infection of domestic animals, tsetse fly numbers and fly infection rates is presented. An understanding of the latter leads to a prediction of risk in cattle. The problems of analysing and interpreting the distribution and abundance patterns of flies are explored, and a mortality climogram approach is described in which the important meteorological variables appear to be temperature and saturation deficit. This approach, which can be applied to data collected at only very few sites, leads to extensive predictions of the distributional limits of the tsetse *Glossina morsitans* Westwood. These predictions are supported by the known distribution of this species throughout Africa.

A similarity noted between published whole-Africa normalised difference vegetation indices (NDVI) and tsetse distribution leads to an exploration of the usefulness of NDVI for such vector studies. The likely information content of the images is identified through principal component analysis, and correlations are shown between NDVI values and annual temperature, saturation deficit and rainfall figures for more than 300 sites throughout the sub-Saharan region of the continent. NDVI values are highly correlated with both saturation deficit and rainfall figures.

Significant correlations are shown between vector mortality rates and mean monthly NDVI values, and between the physical size of the vectors (known to reflect the mortality rates affecting the parental population) and NDVI along an approximately 700 km transect across a whole range of eco-climate conditions in West Africa. Reasons are suggested for the localisation of human sleeping sickness to just one of several regions sampled by the transect.

Finally, seasonal changes in case numbers of human sleeping sickness in both Uganda and Kenya are correlated with mean monthly NDVI from the areas concerned. The first of these correlations is negative, the second positive. Explanations for this difference are given in terms of the different vector species and epidemiological situations in these long-standing foci in East Africa.

It is concluded that the rather limited amount of information available in NDVI has already proved enormously useful, and a plea is made for a more complete exploration of National Oceanic and Atmospheric Administration (NOAA) data, especially at the highest available resolution, whilst not neglecting the vitally important ground-based studies that made possible the results presented in this paper.

INTRODUCTION

Tropical diseases may be studied at many different levels. On the one hand, historical geographers deal with vast sweeps of space and time, and each disease is given a thumbnail sketch fitting into the overall tapestry (Kjekshus, 1977). On the other hand molecular biologists examine areas a fraction of an electron microscope field wide and deal with events occupying only minutes or seconds of time. Researchers often spend the whole of their careers looking at one level of the problem (the threads, the warp, the icons, the panels), without grasping the whole epidemiological picture. Yet, epidemiology should be determining the questions researchers ask in their day-to-day activities, and should not be used as a post hoc, often weak justification for the answers they have found to a quite different set of questions.

Much of this article deals not with satellite imagery, but with the ground-based studies that provided an understanding of one very important set of tropical diseases, the African trypanosomiases, *Trypanosoma* spp., *Nannomonas* spp. and *Duttonella* spp., transmitted by blood-sucking tsetse flies, *Glossina* spp. These studies were an extended prelude to the fugue of the last few years when remotely sensed images have been readily available, not so much to give answers to new sets of questions, but rather to provide a means of arriving at the same answers to the original set of questions more quickly. Epidemiological studies still depend on a researcher being curious about a relationship, and curiosity is not yet a notable feature of image-processing microchips. Satellite imagery will really come of age when it helps us to formulate and answer questions that we could not even dream of from our ground-based studies.

After briefly describing the diseases in question, a theoretical framework is set and an example given of how an intensive study in one or two places may be used to make extensive predictions about vector and disease distribution and abundance. It is then shown how extensive studies may be used to explain why the diseases transmitted by these vectors occur in some areas, but not in others. Finally, it is demonstrated how the seasonal incidence of disease in two ecologically different sites can be explained only with some prior knowledge of the very different vector ecologies in the regions concerned.

THE AFRICAN TRYPANOSOMIASSES

The African trypanosomiases are zoonoses caused by species of the flagellate Protozoan genera *Trypanosoma*, *Nannomonas* and *Duttonella* (Hoare, 1972). Each genus contains several species, not all of equal epidemiological or epizootiological significance. Only two sub-species of *Trypanosoma brucei*, *T.b. gambiense* and *T.b. rhodesiense*, affect man, causing sleeping sickness of the 'typical' West and East African forms, respectively. West African human

sleeping sickness tends to be endemic and man is possibly a major (but by no means the only) reservoir. East African human sleeping sickness is a clear zoonosis, the role of domestic or wild animals varying locally. It is a much more acute disease than the West African form and tends to occur in periodic epidemics in the human population, perhaps as a result of hitherto unrecorded events within the non-human hosts. Human trypanosomiasis is not found throughout the distributional range of its vectors, but is instead a focal disease, almost certainly because the threshold for transmission is very much higher than is the case for the animal trypanosomiasis (Rogers, 1988a).

All subspecies of *T. brucei* (i.e. including *T.b. brucei*) and species of *Nannomonas* and *Duttonella* (each of which used to be included within *Trypanosoma* itself) infect a variety of wild and domestic animals, with varying effects. As a broad generality, animals with a long African evolutionary history are thought to be rather little affected by trypanosomiasis (either because they are rarely bitten by the vectors or because they have a high degree of natural immunity) and races of domestic cattle with longer periods of residence in Africa are more tolerant of the disease than more recently arrived stock (Ford, 1971). The relatively recently arrived (i.e. about 5000 years BP) and widespread zebu race is both frequently fed upon by the vectors and susceptible to debilitating trypanosomiasis, *Nannomonas congolense* and *Duttonella vivax* being much more important in this respect than *Trypanosoma* spp. (for which, nevertheless, cattle are a very good reservoir). Trypanosomiasis in cattle is sometimes referred to by its East African name, 'nagana'. The proportion of cattle infections that are *D. vivax* tends to be higher in West Africa than in East Africa, possibly associated with the major West African vectors being relatively less infectible with *N. congolense*. The susceptibility of zebu (the major livestock of Africa) to trypanosomiasis excludes them from most of the tsetse-affected regions of the continent, an area of about 10 million km² (roughly equal to that of the continental USA) and makes this group of diseases a major constraint on agricultural development. An alternative view periodically appears, that tsetse have prevented larger-scale repetition of the over-grazing and soil degradation seen in some cattle-rearing areas (Ormerod, 1976, 1986). Such observations highlight the need for careful planning of land use following tsetse eradication, but cannot really be used to permanently fix African agricultural production at its present inadequate level (Harrison, 1987; Rogers and Randolph, 1988).

TSETSE FLIES

Tsetse are all placed in a single family, the Glossinidae, currently restricted to Africa (although occurring in the 40-million-year-old Florissant deposits of the Oligocene era in North America). There are three species groups: the ancestral fusca group, whose present-day members still inhabit forests and are

in general of little epidemiological or epizootiological significance; the palpalis group, forest and riverine species of major importance in human sleeping sickness transmission; and the morsitans group, mostly savannah species of great importance in the transmission of animal trypanosomiasis. Tsetse have a highly specialised life cycle during which each mature female produces one fully grown larva approximately every 10 days. These are deposited in shady places and emerge after three or more weeks. The relatively long adult lifespan, coupled with the short incubation period of the trypanosomes within the flies (of between about 10 and 30 days), makes tsetse particularly good potential vectors. This potential is rarely realised in infections with *Trypanosoma* and *Nannomonas*, however, because all but newly emerged flies appear to be remarkably insusceptible to infection with these species. Nevertheless, once infected, flies are likely to be able to transmit these trypanosomes for the remainder of their lives.

IMPORTANT PATTERNS IN THE EPIDEMIOLOGY AND EPIZOOTIOLOGY OF THE AFRICAN TRYPANOSOMIASIS

The relationship between the risk of susceptible zebu contracting trypanosomiasis and the 'challenge' presented by the local tsetse population is shown in Fig. 1 (redrawn from Rogers (1985)). Each measure of vectorial challenge tends to differ from all others; even within the field of trypanosomiasis, there are several working definitions. The horizontal axis in Fig. 1 is the simple product of tsetse apparent density (a crude measure of abundance which, in

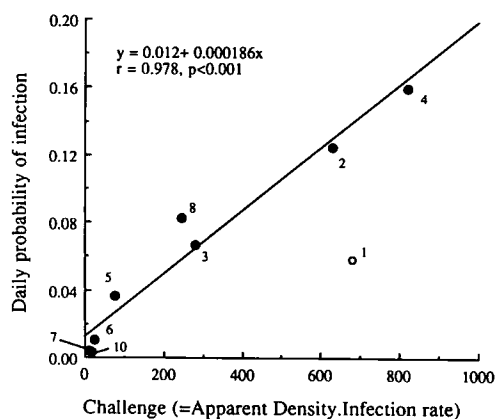


Fig. 1. Relationship between the daily probability of trypanosome infection (all species) of zebu cattle and the challenge presented by the local tsetse population (redrawn from Rogers (1985)). Numbered sites were: 1, Shinyanga (Tanzania); 2 and 3, Lugala, Uganda; 4, Ankole (Uganda); 5 and 6, Kenya; 7, Tanzania; 8, Uganda; 10, Simba (Kenya). The rather anomalous Site 1 was omitted from the regression calculations for reasons given in the original paper.

several studies both ancient and recent, correlates remarkably well with absolute population size) and infection rate.

Whilst it appears likely that similar relationships will occur within the foci of human trypanosomiasis (thus, for example, a reduction of fly numbers in known human foci is associated with a proportionate reduction in human sleeping sickness), comparisons cannot be made across large geographical areas in much of which no human trypanosomiasis occurs.

Figure 1 is an important pattern of the African trypanosomiasis which allows us to define more clearly the problems we have to solve. The figure suggests that wherever there are flies, there is some measurable risk of cattle disease (fly density is a far more variable component of the challenge axis in Fig. 1 than is infection rate) and that the more flies there are, the greater is the risk of disease transmission. It follows that if we can determine the distributional limits of the vectors, we have also defined the distributional limits of the disease; and if we can determine the abundance of the vectors we have gone some way towards predicting the prevalence of disease within these distributional limits. In drawing these conclusions it must be appreciated that many other factors come into play to determine just how much disease there is at any particular level of fly abundance and infection rate (i.e. as measured by the slope of the line in Fig. 1). Most of the information in Fig. 1 comes from East African sites and the fact that the data appear to fit a single regression quite well suggests that these other transmission factors may apply over quite wide geographical ranges. There are, unfortunately, very few appropriate data sets for West Africa to make more extensive comparisons.

THE ROLE OF CLIMATE IN DETERMINING TSETSE DISTRIBUTION

An earthworm the size of a tsetse fly, living where flies live and in the way that flies do, would lose its own body weight of water every hour. The remarkable capacity of insects to resist desiccation in extreme environments has clearly contributed to the success of the Class Insecta. Water relationships, nevertheless, remain the Achilles heel of many insects and, directly or indirectly, are thought to limit insect distributions in dry environments. In the case of tsetse, Nash (1948) showed a correspondence between the northern (i.e. dry) distributional limits of *Glossina morsitans* Westwood and the number of dry months of the year. He could find no such simple correspondence for the southern (i.e. wet) limits of this species, which he imagined to be the result of some interaction of climate and vegetation rather than climate alone. Attempts to correlate distribution (which can be temporarily redefined as a non-zero abundance) and climate are, however, misdirected, since climate cannot determine abundance directly, but only via its effect on one (or more) of four demographically important rates—of birth, death, immigration and

emigration. Climate affects these parameters and thus shifts the demographic balance one way or the other.

A more general approach to define distributional limits, therefore, starts with the following inequality

$$\sum_{n=1}^{12} f_n \geq \sum_{n=1}^{12} \text{d.i.m.}_n \quad (1)$$

where f is the fertility (plus immigration) and d.i.m. is the density-independent mortality (plus emigration) for each of the $n=12$ months of the year (from Rogers, 1979). Density-independent mortality (often resulting from the weather) must be distinguished from density-dependent mortality (always resulting from biological factors such as competitors, parasites and predators) because whilst it plays no part in the regulation of animal abundance within the distributional limits, it is often vital in determining those limits (at the edge of a distribution, densities are generally so low that density dependence is insignificant).

Laboratory studies, and rather limited field experience, suggest that the left-hand side of the inequality in eqn. (1) is determined solely by temperature (because they have rarely been quantified, immigration and emigration are omitted from the following discussion). Flies have reduced inter-larval intervals as temperature rises and there appears to be little or no effect of atmospheric moisture. Mortality, on the other hand, is often strongly correlated with both temperature and atmospheric moisture, the latter, generally more important, being expressed as saturation deficit (Rogers, 1979; Rogers and Randolph, 1986). An example of an attempt to illustrate this inequality with the results of the analysis of data for *G. morsitans submorsitans* Newstead in the Yankari Game Reserve of Nigeria is shown in Fig. 2 (redrawn from Rogers and Randolph (1986)). The horizontal plane contains information more usually referred to as a climogram, the monthly changes of temperature and saturation deficit near the sample site. The vertical axis is the mortality rate (expressed as a monthly k -value; see Rogers (1979) for more details). The resulting irregular 12-sided figure is called a mortality climogram. Slicing almost horizontally through the climogram is a more or less flat plane that represents the fertility rate at each temperature, expressed on the same scale as the mortality rate. There are clearly months when mortality exceeds fertility (and, therefore, when the population of flies in the Yankari Game Reserve falls) and others where the fertility exceeds the mortality (and the population rises).

The 12 points on the mortality climogram of Fig. 2 are 12 sample points on a continuous mortality surface that covers the whole range (and beyond) of the horizontal axes of the climogram. With some care, this mortality surface may be estimated by interpolation and extrapolation, and used to make pre-

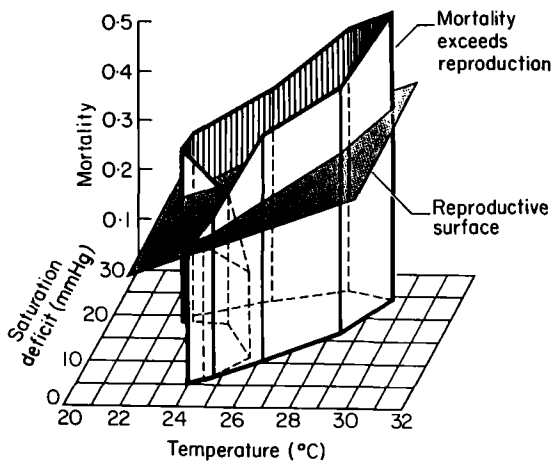


Fig. 2. Mortality climogram for *G.m. submorsitans* in the Yankari Game Reserve, Nigeria. The horizontal axes record the meteorological conditions during the 12 months of the year at Bauchi, Nigeria (near the game reserve), and the vertical axis is a measure of the fly mortality rate, expressed as a k -value (derived from Moran curve analysis of tsetse fly data; Rogers, 1979. See Varley et al. (1973) for a definition of k -values). The shaded plane cutting through the mortality climogram records the reproductive rate of tsetse at the different temperatures. Redrawn from Rogers and Randolph (1986).

dictions of the distributional limits of the flies over very wide geographical ranges. The assumption is made that if any point on the map of Africa is characterised by an annual average temperature and saturation deficit that, according to Fig. 2, results in fertility exceeding mortality, then the species can occur, whilst if the prediction is that mortality exceeds fertility the species cannot occur. These predictions are obtained by taking vertical sections through the mortality surface at any particular temperature. The resulting mortality profile shows how mortality changes with saturation deficit at that temperature. The line of intersection of the reproductive surface with this mortality profile cuts off ranges of saturation deficit where fertility exceeds mortality from other ranges where it does not. Thus, at the specified temperature, the saturation deficit range of the species is defined. By taking vertical sections at a whole range of temperatures and by reading off the saturation deficit limits for each, a bioclimatic range can be defined for the species. The bioclimatic range predicted from the *G.m. submorsitans* data are shown in Fig. 3, together with that predicted for another subspecies, *G.m. morsitans* Vanderplank, from data collected in northeastern Zambia. Areas within the rather irregular 'bubbles' are predicted to be suitable, whilst areas outside are not. Figure 3 also shows the average annual meteorological conditions for a range of sites throughout the present known distribution of *G. morsitans* (from

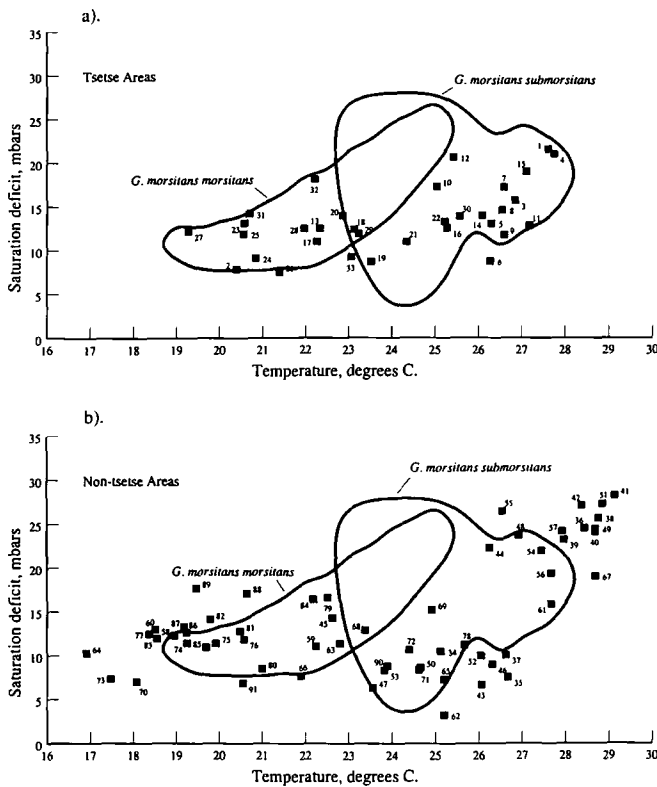


Fig. 3. The irregular 'bubbles' are the bioclimatic limits of *G.m. morsitans* and *G.m. submorsitans* predicted from the analysis of single data sets from Zambia and Nigeria, respectively. Each black square records the average annual meteorological conditions from 33 known tsetse areas (a) and from 58 non-tsetse areas (on average only 189 km away from the nearest tsetse area) (b) throughout Africa, from Senegal to South Africa. (χ^2 for the difference in the proportions of sites within or on the predicted limits in (a) and (b) is 18.1; $P < 0.001$). Redrawn from Rogers (1979) with the points numbered as in the Appendix of that paper.

Senegal through Africa to Botswana; Fig. 3(a)) and for a selection of sites relatively near to (on average 189 km away from) the local limits of this species' distribution (Fig. 3(b)). There is a dramatic and significant difference between the distribution of the data points relative to the predicted limits in Fig. 3(a) and 3(b); 94% (31/33) of the sites within the present (or very recent) known distribution of *G. morsitans* fall on or within the predicted bioclimatic limits, whilst points for the non-tsetse areas are equally divided. Figure 3 illustrates one very important result which is likely to confound presence/absence predictions made by this, and similar, techniques of analysis. Whilst we may be able to say with some degree of certainty that a species cannot occur in any particular place (because the environment is too adverse for it), it will not be possible to say that the species definitely does occur

within all those sites that are climatically suitable for it. Many sites throughout Africa appear to be climatically suitable for *G. morsitans* (and indeed some of these are known to have been infested more than 100 years ago, before the rinderpest pandemic) but do not harbour them at present. Such sites should be viewed, nevertheless, as being 'at risk' from invasion.

The exciting prospect raised by Fig. 3 is that intensive study of a vector at only a very few sites may be used to make extensive predictions of that vector's distribution. This is particularly valuable when a pest's distribution extends across country boundaries. Political and economic events in Africa have contributed to the present inadequacy of good, long-term tsetse data for many of the most important sites.

A shorthand way of viewing the dependence of tsetse mortality rates on climatic conditions is to carry out simple linear regressions/correlations, using the single most important climatic variable. Experience has shown that in some cases it is better both to calculate bi-monthly density-independent mortalities (the average of the previous and present monthly density-independent mortalities) and to lag the correlations by 1 month (i.e. the bi-monthly d.i.m. of one month is correlated with the value of the climatic variable of the previous month). The result of doing this in the case of *G.m. submorsitans* is shown in Fig. 4 (when bi-monthly d.i.m. is plotted against the saturation deficit of the same month, the correlation coefficient, (r) is 0.626 and $P < 0.05$; when the d.i.m. itself is plotted against the saturation deficit of the same month, $r = 0.729$ and $P < 0.01$; and when it is plotted against the saturation deficit of the previous month, $r = 0.835$ and $P < 0.001$).

Tsetse mortality rates are clearly important in determining distributional

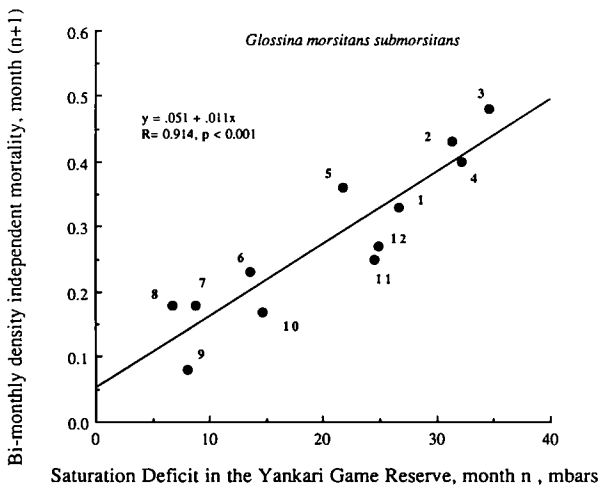


Fig. 4. Relationship between the bi-monthly density-independent mortality of *G.m. submorsitans* in the Yankari Game Reserve and the mean saturation deficit of the previous month. The number against each point refers to the month, n (1 = January, etc.).

limits. They are also important in determining the disease transmission potential of the local population. Epidemiological models for vector-transmitted diseases are particularly sensitive to changes in these rates (Rogers, 1988a,b).

THE ABUNDANCE OF TSETSE

It is much more difficult to make predictions about the abundance of flies within their distributional limits since abundance is some, rarely simple, function of the difference between the two sides of the inequality given in eqn. (1), above. An attempt has been made to predict where in Africa *G. morsitans* might be expected to be particularly abundant, and these predictions are to some extent supported by their local coincidence with known 'problem areas' in several countries, in both East and West Africa (see Rogers and Randolph (1986) for predictions and examples).

THE ROLE OF SATELLITE IMAGERY IN VECTOR STUDIES

The potential role of satellite imagery in monitoring African vegetation types was illustrated by Tucker et al. (1985). The processed images accompanying the article seemed also to contain information relevant to tsetse, since in a number of places discontinuities in the images appeared to coincide with the edge of the ranges of one or more tsetse species. The images were obtained from the advanced very high resolution radiometer (AVHRR) sensor of the National Oceanic and Atmospheric Administration (NOAA) series of meteorological satellites and were processed to provide normalised difference vegetation indices or NDVI. These indices are the ratio of the difference of the Channel 2 (near-infrared) and Channel 1 (visible red) radiances over their sum; a combination chosen because active photosynthetic tissue absorbs the visible red and reflects the infrared, and ratioed in order to diminish the variation introduced into the raw waveband information by varying atmospheric absorption and view-angle differences.

Monthly average NDVI for the whole of Africa (at about 20 km spatial resolution) were kindly donated by John Townshend for the present study, whilst those for particular countries (at about 7 km spatial resolution) were obtained from the ARTEMIS service of the Food and Agriculture Organisation (FAO), Rome. Preliminary principal component analysis tended to confirm the original conclusions of Tucker et al. (1985). About 95% of the variation in the 12 whole-Africa images was captured by the first three components. The first component (accounting for about 80% of total variation) appeared to correlate with total vegetation biomass; the second and third components (accounting for a further 10 and 4% of total variation) seemed to be associated with the seasonality of the environments, with the second

component especially picking out the humid savannah zone across the top of the sub-Saharan region, and the third component picking out the structurally similar (although specifically different) southern savannah regions. The eigenvectors of the second and third components cycled through the year, with a positive peak for the second component in July/August and for the third in December. These months correspond to the months of maximum rainfall in the northern and southern zones of the continent, respectively.

In trying to determine the utility of these images for tsetse studies, correlations were examined between NDVI and the 'standard' meteorological variables. Long-term average values of these variables were taken from the UK Meteorological Office data sets (HMSO, 1983), and the 12 monthly NDVI for Africa were averaged to give an annual value at each of the meteorological station sites. The correlations between NDVI and temperature, saturation deficit and rainfall are shown in Figs. 5–7. There is no obvious relationship with temperature (Fig. 5), a significant linear relationship with saturation deficit (Fig. 6) and a curvilinear relationship (described by a logistic curve) with rainfall (Fig. 7). This analysis, therefore, tended to confirm the results of the principal component analysis and highlights the importance of rain and/or atmospheric moisture in determining NDVI values.

Once the likely information content of the NDVI was established and found

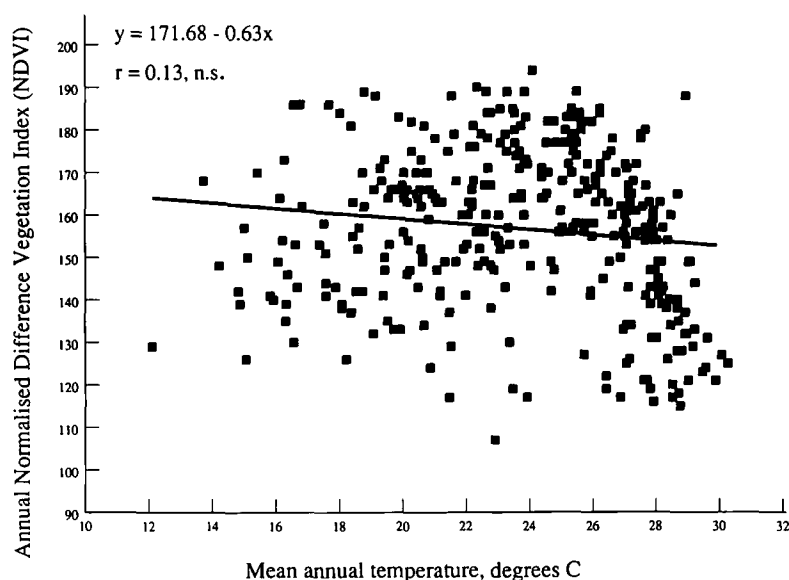


Fig. 5. Relationship between the annual NDVI and mean annual temperature at sites throughout Africa below latitude 20°N. All sites recorded in HMSO (1983) were included in this analysis, except coastal stations (for which image registration was occasionally poor and where human activity associated with ports makes the interpretation of NDVI problematic). NDVI here and later is expressed on the 8 bit scale 0–255.

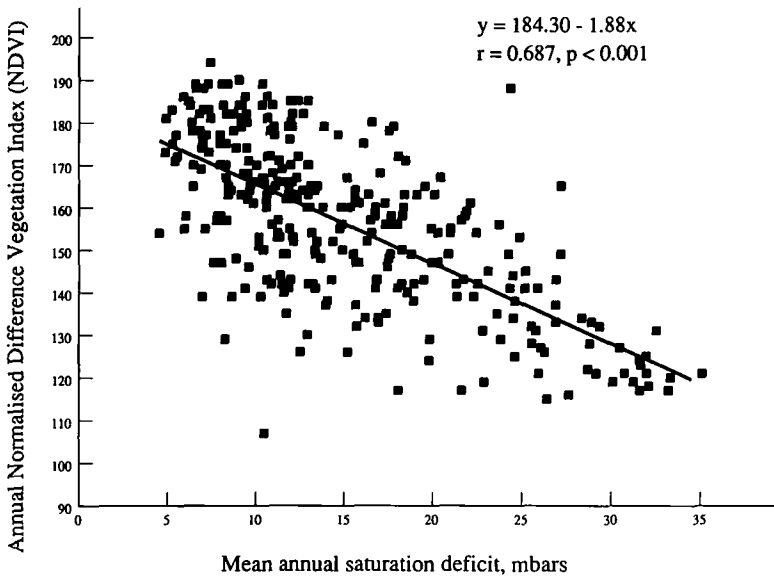


Fig. 6. The relationship between the annual NDVI and mean annual saturation deficit for the sites referred to in Fig. 5.

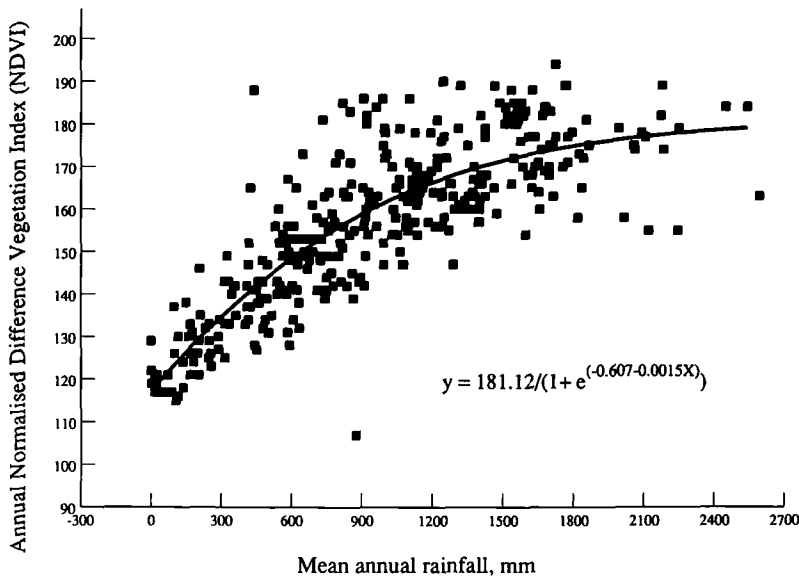


Fig. 7. The relationship between the annual NDVI and mean annual rainfall for the sites referred to in Fig. 5. The fitted line is essentially a logistic curve, with each parameter significantly different from zero.

to be relevant for tsetse studies (where moisture also plays a key role; Fig. 4), the relationships were examined between the ground-based estimates of fly mortality rates and the satellite NDVI for the sample sites. Examples from West and East Africa are shown in Fig. 8 for *G.m. submorsitans* and Fig. 9 for

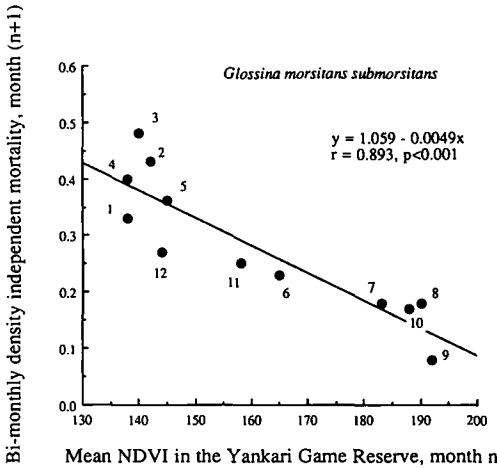


Fig. 8. The relationship between the bi-monthly density-independent mortality rate (expressed as a *k*-value) of *G.m. submorsitans* from the Yankari Game Reserve, Nigeria, and the mean monthly NDVI of the previous month, from 7 km resolution ARTEMIS images (NDVI on the same scale as in Figs. 5–7). The number against each point refers to the month, *n* (1 = January, etc.).

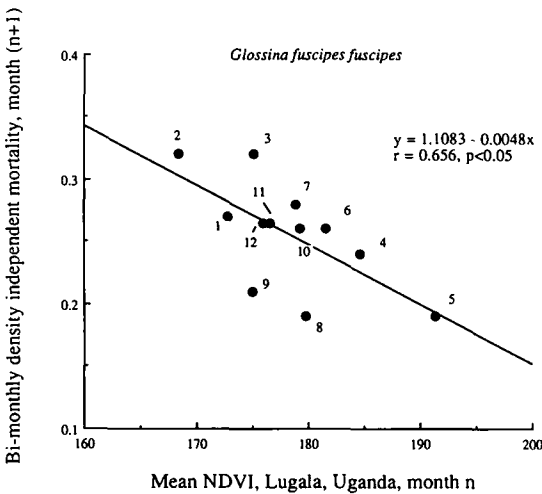


Fig. 9. The relationship between the bi-monthly density-independent mortality rate (expressed as a *k*-value) of *G. fuscipes fuscipes* near Lugala, Uganda, and the mean monthly NDVI of the previous month. The number against each point refers to the month, *n* (1 = January, etc.).

Glossina fuscipes fuscipes Newstead. Figures 4 and 8 show the power of either ground-based or remotely sensed data, respectively, in predicting tsetse mortality rates. The remarkably high level of correlation shown in Fig. 8 suggests that, with care, satellite imagery may be used in the same way as in Figs. 2 and 4 to make the same predictions about tsetse distribution and abundance. A simple classification of the annual NDVI for Africa tended to confirm this. Tsetse population models developed to test the method of fly data analyses (Rogers, 1979) predict maximum rates of population increase of around two per month (i.e. populations double from one month to the next). If all of this population production is killed by density-independent mortality, it is impossible for the species to survive. A potential rate of increase of 2.0 would be completely suppressed by a mortality rate of 0.3 on the scale shown on Fig. 8 (which is logarithmic; $\log 2 = 0.3$), which is, therefore, a threshold for the presence or absence of this species of tsetse. The value of NDVI in Fig. 8 associated with a mean mortality rate of 0.3 was read from the graph and used to classify the annual NDVI image into areas of higher NDVI (where, according to Fig. 8, the fly mortality rate is less than the threshold value) and those of lower NDVI (where mortality rates are predicted to be above the threshold value). Tsetse could survive in the first sort of area, but not the second. The classification exercise satisfactorily identified areas where flies would not occur (broad bands at the top and bottom of the continent) and also those where it could (a band in-between the other two). The present-day distribution of *G. morsitans* lay almost entirely within this second band, but did not occupy it completely. Once again, therefore, as with the analysis using mortality climograms, it is not possible to state where the vectors will occur, only where they will not.

EXTENSIVE STUDIES ON TSETSE POPULATIONS

Within the range of any tsetse, the flies may pose a serious epidemiological risk in one place, but not in another. As part of a United Nations Development Programme (UNDP)/World Health Organisation (WHO)/World Bank/Special Programme for Research and Training in Tropical Diseases, a 700 km transect was sampled in West Africa during the 1983/1984 wet and dry seasons. The transect, which ran approximately north-south through the Ivory Coast and Burkina Faso, covered many different vegetation types, in each of which could be found *Glossina palpalis* (Robineau-Desvoidy), the local vector of Gambian sleeping sickness. The human disease is, in fact, a major problem only in the central region of the transect, and the study was designed to investigate the characteristics of the fly population along the transect that might explain the localisation of disease. Eight sample sites were used in the study, more or less equally spaced and 100 km apart. The full results of this study will be published elsewhere. Of remote sensing interest

was the relationship between the mean wing vein length of the fly samples at each site and the NDVI values of those sites in the previous month (images again obtained from ARTEMIS). Fly vein length is a crude measure of fly size and is thought to reflect stress on the parental female population at the time that they are nurturing the larvae that eventually turn into the adults whose size is measured (this developmental time delay is of the order of 1 month, thus justifying the use of NDVI values of the months prior to each survey). Figure 10 shows that fly vein length is more or less constant throughout the transect during the wet season (when all NDVI are high), but is significantly positively correlated with the NDVI for each site during the dry season; the northerly sites along the transect have lower NDVI and the flies have shorter vein lengths than do the southerly sites. Although the variation in mean vein length may appear slight, work by Dransfield et al. (1989) shows that in the case of *Glossina pallidipes* Austen in Kenya, a similar change in vein length is associated with a four-fold change in the mortality rate of the fly population. It therefore appears that there are demonstrable differences in *G. palpalis* across its range in West Africa, that these differences are seasonal and that they are associated with changes in parameter values (in this case mortality rates) of crucial epidemiological significance. Once again, it appears that remote sensing may be used to monitor changes in seasonal risk factors across wide geographical ranges.

We are still uncertain as to why the disease should be a problem only in the

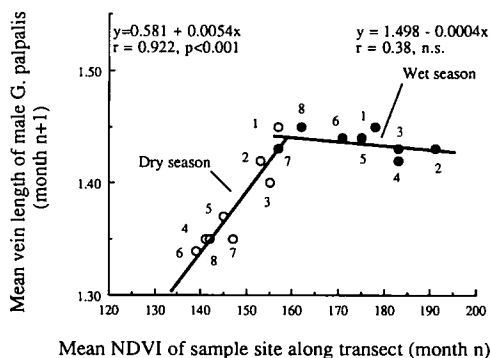


Fig. 10. Relationship between the mean length of the hatchet cell vein in populations of *G. palpalis* (arbitrary units) at eight sample sites along an approximately 700 km north-south transect in West Africa (from near Sassandra, Ivory Coast, to near Bobo Dioulasso, Burkina Faso) and the NDVI of the previous month at each sample site in the wet and dry seasons of 1983 and 1984, respectively. Nutritional stress on the parental female population is clearly reflected in the vein length of their offspring in the dry season, but is absent in the wet season. Sample sites were approximately 100 km apart as follows: 1, Pauli Brousse (near Sassandra); 2, Antonihio (near Gagnoa); 3, Degbézéré (near Bouaflé); 4, Bo'Pri (near Bouaké); 5, River N'zi (east of Niakaramandougou); 6, Komborodougou (near Korhogo); 7, Oulokoussou (near Banfora); 8, La Guingette (near Bobo Dioulasso).

middle part of the transect, although the results described above suggest a reasonable hypothesis. It is possible that man is bitten infrequently in the south because although there are many tsetse with low mortality rates, the flies are not stressed enough by climatic extremes to bite him. In the north, on the other hand, there are too few flies and their mortality rate is too high to pose a serious risk. In the middle of the transect, there may be just a sufficient number of flies experiencing intermediate mortality rates and being just sufficiently stressed to bite man more frequently than elsewhere.

WILL REMOTE SENSING ON ITS OWN BE SUFFICIENT?

Before the euphoria for remote sensing becomes uncontrolled, it is necessary to inject a note of caution. The idea that scientists will be able, in the future, to perform epidemiological studies from their image-processing facilities remote from the study site may be an attractive one, but it is misleading. We do not yet know whether the correlations we have found locally between fly mortality rates and NDVI will apply over large areas, or over a wider range of NDVI values. Theoretically, the relationships should be non-linear (for the same sorts of reason that mortality profiles are non-linear) and will certainly vary from species to species. There is much work still to be done and a final example illustrates the likely complexity of the task.

HUMAN TRYPANOSOMIASIS IN UGANDA AND KENYA—TWO CASE STUDIES

Human sleeping sickness caused by *T.b. rhodesiense* has waxed and waned around the Lake Victoria basin since the first colonial records were made, more than 100 years ago. On the northern shores of Lake Victoria, in the Busoga District of Uganda, tens of thousands of people died of the disease in the early years of this century. About 30–40 years after this major epidemic, the disease recurred in the same area, though with less severity. After a similar interval of time, the disease occurred yet again, with the number of cases increasing from the mid-1970s, peaking at 8465 cases in 1980, and declining thereafter, although not equally in all places (Mbulamberi, 1989). (I am grateful to Dr. D.B. Mbulamberi for providing the sleeping sickness case data for the present analysis.) Opinions vary as to the important vector species in the three major epidemic events, but it is quite clear that the vector presently responsible is *G.f. fuscipes* Newstead, a palpalis group fly and the only species found throughout the sleeping sickness zone. As with other palpalis group species, *G.f. fuscipes* tends to take a higher proportion of its blood meals from primates, including man, than do flies in the morsitans group.

Across Lake Victoria, in Kenya, is the Lambwe Valley, a game reserve surrounded by human settlements. This is one of the very few sites in Kenya where sleeping sickness continues to occur periodically. A small epidemic in

the Lambwe Valley (perhaps mirroring the situation in Uganda) occurred in the early 1980s and was the subject of an intensive epidemiological study (Welde, 1989) which provided sleeping sickness case data for the present analysis. The vector in the Lambwe valley is *G. pallidipes*, a morsitans group species which, like most members of this group, relies heavily on wild animals for its blood meals.

NDVI images used in the present analysis were obtained from the ARTEMIS programme of FAO in the form of monthly composites from January 1982 onwards, and so could be compared with the contemporary sleeping sickness data. Again, the detailed results of this analysis will be given elsewhere, but those of present interest are shown in Figs. 11 and 12 for Uganda and Kenya, respectively. There is a significant negative correlation between the 1984–88 mean monthly numbers of cases of human sleeping sickness in the Kigulu District of Uganda (one of the most heavily affected districts in the recent epidemic) and the NDVI values for the previous month over the same period of time (Fig. 11). In this example, case numbers increase as NDVI values fall and there is, therefore, a peak seasonal incidence in the dry season. In the Lambwe Valley, however, mean monthly case numbers are positively correlated with the NDVI values of the previous month; the monthly incidence, therefore, peaks in the wet season (Fig. 12). Figures 11 and 12 provide the first examples of correlations between case numbers in any vector-borne disease and NDVI, and contain an important message of site-to-site variation which is likely to haunt us for a very long time to come. It is possible to explain the different (negative or positive) correlations in Figs. 11 and 12 only with some knowledge of the habits and habitats of the local vector species. In Uganda, *G. fuscipes* co-exists throughout the year with man

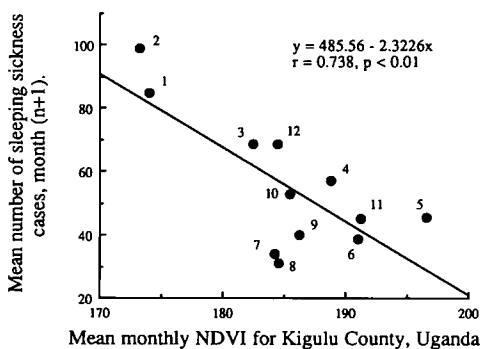


Fig. 11. Relationship between the mean monthly number of cases of human sleeping sickness recorded from Kigulu County, Uganda, between 1984 and 1988, and the mean monthly NDVI for Kigulu over the same period. The number against each point refers to the month, *n* (1 = January, etc.).

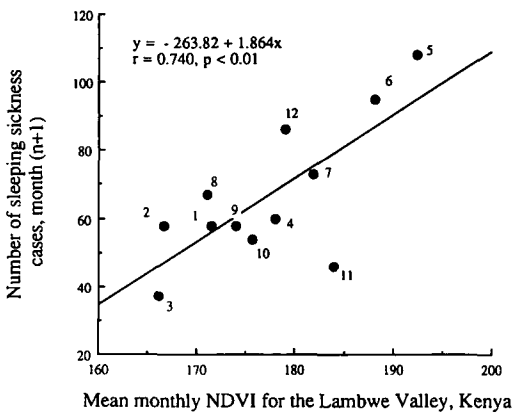


Fig. 12. Relationship between the number of cases of human sleeping sickness recorded in the Lambwe Valley, Kenya from 1963 to 1984 (data from Welde (1989)) and the mean monthly NDVI for Lambwe from 1984 to 1988. The number against each point refers to the month, n (1 = January, etc.).

and in a number of places has become totally peri-domestic. Although it may bite man throughout the year, it prefers other hosts and so only bites humans appreciably in the dry season, thus giving rise to larger numbers of sleeping sickness cases. In Kenya, however, *G. pallidipes* spends most of the year out of contact with man, in the thickets in the centre of the game reserve. With the coming of the rainy season, the humid conditions allow the flies to spread out from the central thickets, to come into contact with humans around the edges of the reserve (Welde (1989), and others before, comments that people complain of being bitten by flies only in the wet season). Sleeping sickness transmission, therefore, increases in the wet season.

CONCLUSIONS

Although the amount of information available in the images referred to in this article would appear to be rather small, it has, nevertheless, been shown to be potentially of great value in monitoring tsetse mortality rates and the seasonal incidence of sleeping sickness in the human population. It is to be hoped that other vector-borne diseases are equally amenable to such analysis.

What is required now is a research program to investigate the utility of other satellite information (either raw waveband information or alternative ratioing methods) to establish robust correlations operating over space and time. It is highly unlikely that NDVI, the first images chosen, are necessarily the best way of expressing or using the information available from satellites.

When suitable robust correlations have been found, we are obliged to investigate the causal mechanisms, if any, which link predicted and predictor variables. Predicting seasonal incidence from NDVI values may be useful,

but the prediction cannot be changed (i.e. disease cannot be reduced) unless we understand the underlying relationships. Predictions based on correlations are, in any case, in the category of what might be called status quo models: they work only as long as the future is like the past. In the present era of rapid environmental change, status quo models will become less satisfactory as whole ecosystems adjust to anthropogenic changes. In this case, we need the more certain durability of dynamic models (the 'strategic models' of Conway (1977)) that are able to predict the response of biological systems to such changes through an understanding of the underlying mechanisms at work.

Tropical countries have many pressing needs and for them remote sensing might seem an ill-affordable luxury; a recording of the ultimate disaster movie. There are also many ways in which remote sensing may help, however, in development planning and monitoring agricultural forest and fuel-wood production, in disease risk prediction and avoidance, in water resources management and many others. In recording environmental changes via satellites, we have a simple choice. Should we use remote sensing the better to watch the Titanic sinking, or as a lifeboat to help the survivors?

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