

Epidemiology of Surra: Unanswered Questions

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ABSTRACT

Trypanosoma evansi occurs in a variety of ecological regions in both the Old and the New World and although it affects many different domesticated livestock species, there is a dearth of information on its distribution, prevalence and/or incidence and economic significance throughout its geographical range. Although reproductive wastage has been identified occasionally as a source of economic loss, the impact of *T. evansi* on productivity is recognized usually only when epidemic outbreaks of disease cause widespread loss. The possibility that economically significant production losses might occur also when less acute forms of disease exist has not been considered. The absence of accurate information distorts the overall picture: only outbreaks of disease with a high mortality tend to be quoted in discussions of the effects of surra. Deficiencies in our knowledge of the epidemiology of *T. evansi* contribute to this situation. These shortfalls include our knowledge and understanding of the natural history of the disease, the absence of any strategies for effective monitoring and surveillance, and the inability to design and implement cost-effective, appropriate strategies for control of the disease. Furthermore, the inadequate data on the effects of *T. evansi* infection on milk and meat production, draught power, or reproductive efficiency tend to diminish its importance as a disease, and has a negative influence on the attitude of national government and international funding organizations to implement measures to control the disease or to undertake research. Until it is possible to put in place reliable methods for identifying infected animals, estimating morbidity and assessing the economic impact of surra, this situation will continue to prevail.

INTRODUCTION

Efforts to control *Trypanosoma evansi*, the causative organism of surra, are still directed towards the treatment of individual animals that exhibit either overt signs of disease or parasitological evidence of infection. Such strategies benefit the individual animal, and are important to the smallholder farmers' livelihood. However, this policy does little to decrease the number of cases as effectively as treating all infected individuals. Also, such an approach fails to address the underlying problem of animals that have only covert evidence of infection and that comprise a far larger proportion of the population than animals with patent infections. Animals with non-patent infections thereby contribute more significantly to the overall morbidity and also act as reservoirs of infection and danger to uninfected, susceptible livestock. There has been considerable effort to develop diagnostic tests that will identify animals with cryptic infections; indeed, emphasis is often placed on the use of techniques for the rapid, "penside" diagnosis of infection. However, in order to enable effective decision-making at the individual level a thorough knowledge of the range of disease in the population is essential if the results of diagnostic tests are to be properly interpreted and appropriate action taken. Only by understanding the disease in the animal population, including the effects of sub-clinical infections on productivity, will it be possible

to assemble significant data to allow a proper assessment of the disease's economic impact and the efficacy and cost-effectiveness of control measures. Although surra is considered to be an economically important disease, there are such considerable deficiencies in knowledge of its epidemiology that the ability to determine its impact different livestock production systems is absent in most, if not all, of the countries where *T. evansi* occurs. Such is the variety of ecological systems involved and livestock species affected, it might require a number of different control options designed for specific situations. This review therefore addresses a number of questions concerning the epidemiology of *T. evansi* that are relevant to the control and management of surra. Specifically, these are (1) how effective are the currently available diagnostic techniques? (2) where and how often does disease occur? (3) what are the factors that determine the transmission and maintenance of infection? and (4) how effective is treatment?

THE ECOLOGY AND NATURAL HISTORY OF *TRYPANOSOMA EVANSI*

The relationship between *T. evansi* and its mammalian hosts is a complex, dynamic process whose outcome is influenced by several factors. The host species, and age, previous experience of infection and physiological condition determine the level of susceptibility to infection and the manifestation of disease. The degree of infection in the host population, the stage of infection (chronic or acute) and the level of parasitaemia in an individual animal are likely to influence transmission by insect vectors. Trypanosome populations can vary in terms of pathogenicity and in their sensitivity to trypanocidal drugs. Seasonal and environmental influences will affect the population density of the insect vectors and hence the opportunities for transmission. Morbidity will also be influenced by husbandry practices such as the removal of sick animals that could act as reservoirs of infection, the introduction of infected animals that might lead to outbreak of disease in the herd where they are placed, or the introduction of susceptible livestock into infected herds where they might succumb rapidly to infection.

The Host. All species of domesticated livestock can be infected with *T. evansi* although, the principle host varies geographically. In Africa beyond the northernmost limits of the tsetse fly and in parts of eastern Africa camels are the most important host (Dia et al. 1997), whilst in Central and South America the horse is principally affected (Monzon et al. 1995a; Silva et al. 1995). In Asia, a much wider range of hosts is involved including bactrian and dromedary camels, cattle, buffalo, horses and pigs (Pathak et al. 1993; Partoutomo et al. 1994; Tuntasuvan et al. 1996). Interestingly, in Africa and South America there is very little evidence to suggest that domesticated livestock other than camels and horses respectively are clinically affected or indeed, infected with *T. evansi* although there are reports of serological evidence of infection in goats and sheep from the Sudan (Boid et al. 1981) and in cattle from Brazil (Franke et al. 1994a) and both goats and cattle have been considered as potential reservoirs of infection (Clark and Dunn 1933; Dennig 1989). Farm livestock can act as a source of infection for other animals to which they come into contact; this could be due to the presence of infection with less pathogenic strains of *T. evansi* in cattle or buffalo that then act as symptomless carriers of infection (Clark and Dunn 1933). Equally, horses with fulminating infections are a dangerous source of infection for cattle or buffalo (Luckins 1996). Although these events are reported in the literature, virtually nothing is known of the circumstances which lead to the dissemination of infection, and the nature of the relationship between symptomless carriers, the vectors, transmission and disease.

It is not clear to what extent, if any, there exist true wild-animal foci of infection that operate independently of the domesticated animals/farm/ranch situation. Infections, both natural and artificial, have been shown in various wild animals including capybara (*Hydrochoerus hydrochoerus*), wild dogs, (*Canis azarae*) and deer (*Axis axis*, *Rusa timorensis*). There have been no attempts to investigate such relationships properly, and there are a number of factors that might preclude its occurrence. First, throughout its geographical range, *T. evansi* was introduced as a parasite of domesticated livestock, and any wild animals infections are acquired secondarily, hence the disease is often fatal in wild animals (Clark and Dunn 1933). Second, in some instances, the ecological conditions might preclude any close contact with wild animals - e.g. in cold or hot deserts for instance (Africa, northern China, India) or in densely populated, intensively farmed regions (Indonesia, Vietnam, Thailand, the Philippines, southern China). However, *T. evansi* shows a wide range of pathogenicity, and chronic infections in wild animals do sometimes occur, as in South America, where the capybara might be a reservoir (Arias et al. 1997; Franke et al. 1994a, b; Stevens et al. 1989). Some reports indicate that capybara are highly susceptible to *T. evansi* (Migone 1910), but more recent work Franke et al. (1994a) considered capybara were implicated as reservoirs of infection in a ranch in the Pantanal region of Brazil. The situation was complicated however, since cattle and dogs were found to harbour trypanosomes and might also be involved. Dogs probably acquired infection from being fed capybara and were considered highly suspect since they associated closely with horses. This interesting situation requires much more intensive investigation of the relationships between capybara, dogs, cattle and horses; the feeding preferences of flies and the characteristics of the strains of trypanosomes isolated from the different hosts.

The Vector. *Trypanosoma evansi* lacks the genes necessary for mitochondrial development (Borst et al. 1987) and therefore is unable to undergo growth and differentiation in the insect vector. Nevertheless this has not precluded transmission by insects. Indeed, the widespread occurrence of *T. evansi* is largely due to its being spread by the bites of haematophagous flies. Transmission by biting flies is not the sole means by which infection is perpetuated; ingestion of meat from infected carcasses by carnivores can result in infections too (Ware 1928) and in South America, vampire bats are said to be of importance both as reservoirs of infection and as vectors (Dunn 1932). However, there has never been any definitive study to confirm their role in the epidemiology of trypanosomiasis and it is not really clear how important they are. Ayala and Wells (1974) questioned the significance of vampire bats, concluding that large numbers of bats would be required to maintain and transmit infections and where there are few bats, their role is negligible. They might merely serve as indicators of the presence of infection in domesticated livestock.

The link between the disease, surra, and the presence of large biting flies was well known to livestock owners long before the causal agent and its vector were identified. Experimental evidence for the role of the tabanid fly was first reported by Rogers (1901), using an unidentified species of fly to transmit infection to the dog, horse and guinea-pig. Since that report, many hundreds of experiments have been reported in which attempts have been made to transmit *T. evansi* with *Tabanus*, *Lyperosia*, *Haematopota*, *Chrysops* and *Stomoxys* spp. Most studies have been carried out with *Tabanus* spp and it is generally accepted that this genus contains the most important vectors (Leese 1909;1912), although there are relatively few field data - apart from strong circumstantial evidence - to support this contention. *Tabanid* flies are aggressive feeders, and their vigorous attacks on the host

cause defensive reactions that disturb the flies so that they attack again and again, often choosing other hosts, in order to complete their blood meal. This form of interrupted feeding enables transmission of the trypanosomes; flies initially feeding on an infected animal initially, may complete feeding in an uninfected host. Successful transmission depends on the survival of the trypanosomes present in blood trapped in the fly's mouthparts.

More than 20 different species of *Tabanus* have been shown experimentally to transmit *T. evansi*, including:- *Tabanus albitriangularis*, *T. albimediis*, *T. bicallus*, *T. bilateralis*, *T. brunripes*, *T. ceylonicus*, *T. ditaeniatus*, *T. flavivittatus*, *T. fumifer*, *T. griseipalpis*, *T. hilaris*, *T. inmanis*, *T. latifascies*, *T. macer*, *T. malayaensis*, *T. minimus*, *T. nemocallosus*, *T. nemoralis*, *T. partitus*, *T. reducens*, *T. rubidus*, *T. rufiventris*, *T. stilatus*, *T. tropica*, *T. vagus*, *T. venecki* and *T. virgo* (Cross 1923; Cross and Patel 1921; Fraser and Symonds 1908; Kelser 1927; Lingard 1906; Mitzmain 1913; Nieschulz 1926a, 1928a, b; Nieschulz and Ponto 1927; Singh 1925; Yutuc 1940). Many transmission experiments have been conducted to define the conditions under which *T. evansi* can be transmitted. There is often considerable variation in success rates obtained in different experiments or by different workers but comparisons are difficult - variations occur fly numbers, fly species, host species and trypanosome isolates. Successful experiments have usually involved feeding large numbers of flies on hosts with high parasitaemias, but in other instances even a single fly was found to transmit infection on several occasions (Nieschulz and Ponto 1927). The few experiments conducted in which trypanosomes were absent from the peripheral blood of the donor host were unsuccessful. Survival periods of trypanosomes on the flies mouthparts varied from as short as a few minutes to as long as three days, but it is generally agreed that transmission succeeds if feeding take place within one hour of the infective feed. The probability of transmission is 0.05 within 5 minutes of an infective feed, decreasing to 0.04 by 60 minutes, 0.001 within 3 hours and 0.0003 at 24 hours (Leclercq 1952).

The role of tabanid flies other than *Tabanus* spp is not well documented, because few studies have been undertaken, but successful experimental transmission has been obtained with both *Haematopota*, *Lyperosia* and *Chrysops* (Fraser 1909; Nieschulz 1926b, 1927a, b). The position of *Stomoxys* is equivocal; a number of successful experimental transmissions have been carried out with *S. nigra* and *S. calcitrans* (Mitzmain 1912; Sergent and Donatien 1922), although the success rate is possibly less than that obtained with tabanids. *Stomoxys nigra* was considered to be the principle vector of surra in Mauritius (Moutia 1928) but in other studies in the Philippines (Mitzmain 1912) *Stomoxys* was thought to be unimportant. Since *Stomoxys*, *Haematopota* and *Lyperosia* complete their blood meals on a single animal their efficiency as vectors may be low. However, other authors consider that in certain situations, such as in stables, *Stomoxys* is important in spreading infection due to the presence of large numbers of these flies, whereas in open conditions, *tabanids* are more important (Leese 1912; Sergent and Donatien 1922).

Although the mode of mechanical transmission is well established, its dynamics are not understood. Considerable experimentation therefore is still required to attempt to define quantitatively the effect of the host species, the duration of infection in the host and the level of parasitaemia, the period between feeds and the relative efficiency of different vector species in ensuring successful transmission. In the field, studies should investigate transmission in relation to the prevalence of *T. evansi* infection in the host species, the seasonal abundance of biting flies and the relative importance of particular species of biting flies amongst those found feeding on the animal hosts.

The Parasite. It is hypothesised that *T. evansi* originated from *T. brucei* by adaptation to a non-cyclical mode of transmission and loss of the ability to undergo growth and differentiation in the fly vector (Hoare 1957). Camels that came into contact with tsetse flies at the northern most limit of their distribution acquired infections then when camels moved to non-tsetse areas, transmission was spread by other haematophagous flies. The disease was further disseminated by camel caravans traveling to north Africa, the Middle East and further east into South Asia. In a similar manner, horses were probably the means by which surra reached South America, principally by movement of the animals from West Africa in the 16th century; evidence from isoenzyme studies and characterization of nuclear and kinetoplast support this hypothesis and suggest only a limited evolutionary origin of *T. evansi* (Gibson et al. 1983; Songa et al. 1990). In spite of this, the parasite has achieved a wide geographical distribution, infects numerous host species and shows a range of pathogenicity that indicate the possibility of a range of genotypes. Stocks of *T. evansi* isolated from several different areas of Kenya were found to conform to a homogeneous pattern of zymodemes and were similar to the patterns observed in another three isolates from South America, Nigeria and Sudan (Gibson et al. 1983). Similar work on 12 isolates, isolated from buffalo, camels and horses from different parts China confirmed that isolates of *T. evansi* formed a homogeneous group irrespective of their origin (Lun et al. 1992a). This homogeneity was also seen among stocks of trypanosomes that were isolated from dogs and capybara and differed in their virulence. Although there were marked behavioural difference between the nine stocks examined, all were found to have similar zymodeme patterns and to resemble zymodemes from Africa and other parts of South America (Stevens et al. 1989). Identical zymodemes were also found in dogs, horses and capybara (Franke et al. 1994). In South East Asia, stocks of *T. evansi* from Java were shown to form a homogeneous group with similar characteristics to stocks isolated elsewhere (Boyd 1985). The level of discrimination between isolates was improved by the use molecular karyotyping; stocks that were indistinguishable by isoenzyme analysis were found to fall into several karyotype groups (Lun et al. 1992b). An isolate of *T. evansi* from the north west of China that had been isolated from a camel differed from the karyotype expressed by other stocks, suggesting that *T. evansi* might have been introduced into China on more than one occasion, once from the south (Luckins 1988) and also from the north. Characterization of stocks from China, Africa and South America and the Philippines by restriction fragment length polymorphism revealed that the Chinese stocks were identical, but differed from isolates from elsewhere (Zhang and Baltz 1994). In camels in Kenya, eight different karyotypes were identified amongst trypanosomes isolated from two herds that had been under different therapeutic regimes (Waitumbi and Young 1994). In a herd that had been protected by the long-term use of quinapyramine prosalt given prophylactically, all but one isolate conformed to a single karyotype. In contrast, in a herd where treatment had been administered to camels when they became parasitologically positive, eight different karyotypes were present (Waitumbi and Young 1994). *Trypanosoma evansi* resistant to the effects of quinapyramine were found to express two different karyotypes (Waitumbi et al. 1994). No polymorphisms in *T. evansi* stocks from camels in Kenya were revealed by random amplified polymorphic DNA (RAPD-PCR), even though karyotype differences were observed (Waitumbi and Murphy 1993). In Indonesia, over 40 karyotypes were found amongst 80 isolates collected from different parts of the country (Sukanto, personal communication), and unlike the study in Kenya a limited RAPD polymorphism was shown by these isolates; four patterns were described. A similar karyotype diversity was found

amounts isolates of *T. evansi* collected from several villages in a much smaller geographical area over an 18-month period (Rae and Luckins, unpublished observations) but the 80 stocks examined showed an identical RAPD pattern.

Clearly, molecular characterisation has considerable potential in understanding the epidemiology of *T. evansi*, particularly in determining the relationship between strains isolated from domesticated livestock and the putative reservoir hosts, the origin of strains and their spread amongst individuals in a herd, their possible association with disease outbreaks, the seasonal changes in disease and the presence of the parasite, the effects of trypanocidal treatment (or other intervention) and the presence of drug resistance. This information could provide valuable information for developing control methodology. Unfortunately, relatively few isolates have been examined comprehensively and, currently, our knowledge of the molecular characteristics of *T. evansi* in relation to the overall epidemiology of the disease is very limited.

DESCRIPTIVE AND ANALYTICAL ASPECTS OF DISEASE DISTRIBUTION

Trypanosoma evansi is the most widely distributed of the pathogenic animal trypanosomiasis, affecting domesticated livestock in Asia, Africa and Central and South America. Its spread into South East Asia has occurred only relatively recently, and the serious epidemics of surra in that were recorded towards the end of the 19th century and early years of the present century in Indonesia and the Philippines, suggest that it could have spread into these regions within the last 100 years (Luckins, 1988; Lun et al. 1993). This pathogenic form of disease is observed less frequently, but while epidemic outbreaks of disease do still occur in Indonesia, The Philippines, Vietnam, Thailand and China (Luckins, 1988, 1996; Lun et al. 1993) it is now more probable that in many countries it is a disease with a high morbidity and low mortality. However, to properly evaluate this assumption it is necessary to have data on its occurrence and distribution. Currently, there is a lack of data that is used too frequently to suggest that *T. evansi* is of little economic importance - a judgment based on ignorance of the true situation, rather than fact.

Diagnosis. Diagnostic testing is the key to determining the importance of a disease. At the herd level it gives an indication of the frequency of disease within the population; at the individual level it can be used to target animals for treatment and assess the efficacy of chemotherapy. Although there has been considerable development in diagnostic techniques applicable to surra, their evaluation, standardization, application and deployment has not been forthcoming. Consequently, diagnosis is still based on traditional parasitological methods or even clinical signs of disease. Parasitological detection methods have a poor diagnostic sensitivity, often < 50% and clinical signs are not pathognomonic for *T. evansi* (Luckins 1992; Monzon et al. 1990; Nantulya 1990). It is therefore likely that in most situations *T. evansi* is under-diagnosed and the level of infection is greater than is frequently reported. How therefore will the various technological developments in diagnosis contribute to disease control? It is important to ask what particular diagnostic test is used and what will be done if the test is positive. These two questions have probably not been addressed sufficiently. Consequently, diagnosis is more often driven by current trends in techniques and perceived wisdom - increased sensitivity, increased specificity, penicillin diagnosis - rather than whether a test is for screening or clinical diagnosis and the implications that might have in its interpretation. There is a false impression amongst many scientists working with *T. evansi* that the sensitivity and specificity of a test can be used to predict an actual test result and there seems to be a complete negation of the veterinarian's role in intuitive reasoning.

based on whether a test result (positive or negative) is from an animal at high risk (high prevalence) or low risk (low prevalence). In addition, little cognisance is taken of predictive values and the consequences of the implementation of a control programme that will alter the degree of risk within a population such that prevalence will decline necessitating introduction of alternative test strategies and decision making.

Currently, three types of assays are being used for diagnosis of *T. evansi*, enzyme linked immunosorbent assays (ELISA), card agglutination tests (CATT) and latex agglutination tests (LAT). Under experimental conditions these tests have been shown to detect trypanosome antibodies or antigens soon after infection. Antibody detection-ELISAs (Ab-ELISAs) have been used to detect infection in camels (Luckins et al. 1979), buffalo and cattle (Payne et al. 1991). However, data on sensitivity and specificity of the tests are not always available and it is not possible to determine how well the assays might predict the disease status of an animal. However, in a later study (Rae et al. 1989) in camels in the Sudan, a rigorous evaluation of Ab-ELISA and antigen detection ELISA (Ag-ELISA) showed that Ab-ELISA could be used to identify camels with patent or (more importantly) non-patent infections. Ab-ELISAs are robust and simple and usually based on non-defined antigens which could be problematic if universal standardization was required. In contrast, CATT tests are already standardized and work well in studies in buffalo, cattle, camel and horses (Songa et al. 1989). Antigen detection assays based on ELISA have shown considerable potential (Monzon et al. 1995; Nantulya et al. 1989a, b) but are currently not viewed favourably due to the low sensitivity and specificity, whereas latex agglutination tests for antigen detection are held to overcome the problems of specificity inherent in the Ag-ELISA (Olaho-Mukani et al. 1996). Although the foregoing tests have been used, extensively, adequate validation has not always been done. However, Davison (1997) carried out critical evaluation of Ab-ELISA, CATT and Ag-ELISA in buffalo in Indonesia and was able to show that the antibody assays had a higher sensitivity and specificity than Ag-ELISA. Comparison of the assays by calculation of post-test probabilities of infection, and likelihood ratios suggested that Ab-ELISA would be less likely to miss infection, and CATT would be less likely than Ab-ELISA tests to wrongly classify uninfected buffaloes as infected. Hence Ab-ELISA tests could be used for initial screening of large numbers of samples to identify animals at risk and CATT could be used for confirming diagnosis and as a rationale for treatment. A similar approach is required for other animal species, but it is important that any new test is accorded much more critical evaluation than has hitherto been allowed if serological assays are going to be a reliable factor in formulating control strategy.

Distribution and Prevalence. Estimates of the prevalence of *T. evansi* almost invariably derive from studies carried out in response to serious outbreaks of disease. Even then, diagnosis is often restricted to parasitological techniques or clinical signs. Reports of the serological prevalence of infection have usually been based on small number of samples, without attempting to institute proper sampling survey procedures (Lohr et al. 1985; Monzon et al. 1995). A possible exception are the studies done in China (Lun et al 1993) where hundreds of thousands of animals have been tested serological. Sometimes, multiple diagnostic testing has been used (Dia et al. 1997) but the results can be problematic since without proper validation interpretation can be difficult. Where rigorous validation and survey criteria have been applied, the results are more informative.

THE MANAGEMENT OF DISEASE - PLANNING AND MONITORING CONTROL

Disease. In the early years of this century devastating epidemics of trypanosomiasis

caused by *T. evansi* affected the Philippines, Mauritius, Indonesia and India (Luckins, 1988). This situation is not frequently seen nowadays, but epidemics do still occur (Luckins, 1996). The clinical and haematological characteristics of infection is similar amongst the different species of hosts animals and includes a progressive anaemia, high temperature, marked depression, dullness, loss of condition and in some cases, death. There is a tendency to ascribe the occurrence of severe and often fatal disease to the horse and camel, and milder disease in cattle, but the range of susceptibility of the livestock and the variation in pathogenicity of the trypanosome strains is so great that this is an unrealistic view. Experimental studies have shown that marked immunosuppression to vaccine antigens occurs in sheep that have only sub-clinical infections (Onah et al. 1998), hence even in situations where *T. evansi* does not apparently cause any overt signs of illness, it could be compromising vaccine efficacy or leading to severe disease with other intercurrent infections. In the field, reports of disease in camels, buffalo, cattle, horses and pigs are well documented and among the affects seen are death (Tuntasuvan et al. 1997) abortion (Lohr et al. 1986), weight loss (Luckins, unpublished observations) and reduced draught power. Where epidemics involving thousands of animals have occurred the economic consequences of these losses have not been quantified, the cost of controlling the outbreaks with trypanocidal drugs has not been determined and there have been no long term surveillance, so it is often impossible to determine the impact of the control strategy. Epidemics of disease draw attention to the existence of *T. evansi*, but the relevance of surra and its impact on productivity where sub-clinical infections occur is largely ignored and there have been few detailed studies either experimentally, or in the field, so that there are few sound data.

Treatment and Control. Various preventive measures have been used by livestock owners for many years to decrease the nuisance presented by biting flies. These include stabling animals, the use of smudge fires to discourage flies and the use of netting to protect dairy cattle. It is not known how effective these measures might be in reducing the transmission of trypanosomiasis because no studies have been undertaken. Treatment with trypanocidal drugs is the usual method of control of *T. evansi* and five compounds, namely suramin, diminazene, isometamidium, quinapyramine and cymelarsen have been used to treat camels, cattle, buffalo, horses and pigs. Suramin has been the mainstay of treatment for all host species for over 70 years even though its intravenous route of administration can be problematic in the field. Quinapyramine has been used in camels and horses whilst diminazene and isometamidium have been used for treatment of cattle and buffalo. Cymelarsen has been introduced only recently for treatment of surra in camels. Diminazene has been used successfully to treat cattle and buffalo in India and Thailand, but there are some doubts about its efficacy at the recommended dose rate of 3.5 mg/kg; some authorities suggest a higher dose (e.g. 7 mg/kg body weight). Although the drugs have been in use for many years the reports of drug resistance from the field are surprisingly few. Nevertheless, a number of studies have indicated that drug resistant strains of trypanosomes are present in Kenya and Vietnam (Maina et al. 1996; Le Ngoc My et al. 1998; Waitumbi et al. 1994). Resistance was determined on the basis of in vitro assay or mouse inoculation tests, so it is not known what the actual degree of resistance was in the host animals. Since there have been few studies on drug resistance its actual extent and importance in various hosts and different regions is unknown.

There have been no planned campaigns to control *T. evansi* infections using modern methods of fly control or chemotherapy; in most cases, control is limited to treating those animals that are considered to be infected on the basis of the unreliable clinical signs, or

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information, we do have available at present technologies that can be used for establishing control or eradication programmes. In addition, we should also address the requirements for improving, modifying and resolving other issues that are peripheral to the actual control methodology, but might enhance the design and effectiveness of control options. The most important needs are informational and there are several steps by which these can be achieved. Specifically, these are (1) application of validated, standardized diagnostic tests at local and regional levels; (2) development of appropriate monitoring and surveillance procedures to evaluate risk; (3) estimation of the national and regional occurrence of *T. evansi*; (4) quantification of the economic costs of trypanosomiasis in terms of productivity as well as socio-economic effects, in different production systems and including the consequences of sub-clinical infection; (5) development of predictive models for planning control programmes in different production system, and (6) application of chemotherapy and analysis of its cost effectiveness.

A number of research issues would be important adjunct to these strategies. These would include (1) continued development of diagnostic tests, particularly simple penside tests; (2) identification of the principle vector species responsible for transmission in different ecological situations; (3) improving understanding of the dynamics of mechanical transmission in endemic and epidemic situations; (4) investigating the potential for vector control in the management of disease; (5) determining the efficacy of different trypanocidal drugs, the extent of drug-resistance and its importance; (6) determining what factors precipitate epidemic outbreaks of disease and (7) determining if wild-animal reservoirs have any role in the epidemiology of trypanosomiasis caused by *T. evansi*.

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